

Appendix H. Excluded Studies

Breast Cancer

1. Aalders KC, Kuijter A, Straver ME, et al. Characterisation of multifocal breast cancer using the 70-gene signature in clinical low-risk patients enrolled in the EORTC 10041/BIG 03-04 MINDACT trial. *European Journal of Cancer*. 2017;79:98-105. Exclude: No outcome of interest.
2. Abba MC, Lacunza E, Nunez MI, et al. Rhomboid domain containing 2 (RHBDD2): a novel cancer-related gene over-expressed in breast cancer. *Biochimica et Biophysica Acta*. 2009;1792(10):988-997. Exclude: Not intervention of interest.
3. Abd El-Rehim DM, Ball G, Pinder SE, et al. High-throughput protein expression analysis using tissue microarray technology of a large well-characterised series identifies biologically distinct classes of breast cancer confirming recent cDNA expression analyses. *International Journal of Cancer*. 2005;116(3):340-350. Exclude: Date.
4. Abdel-Fatah TM, Agarwal D, Liu DX, et al. SPAG5 as a prognostic biomarker and chemotherapy sensitivity predictor in breast cancer: a retrospective, integrated genomic, transcriptomic, and protein analysis. *Lancet Oncology*. 2016;17(7):1004-1018. Exclude: Not intervention of interest.
5. Abdel-Fatah TM, Albarakati N, Bowell L, et al. Single-strand selective monofunctional uracil-DNA glycosylase (SMUG1) deficiency is linked to aggressive breast cancer and predicts response to adjuvant therapy. *Breast Cancer Research & Treatment*. 2013;142(3):515-527. Exclude: Not intervention of interest.
6. Abdel-Fatah TM, Powe DG, Agboola J, et al. The biological, clinical and prognostic implications of p53 transcriptional pathways in breast cancers. *Journal of Pathology*. 2010;220(4):419-434. Exclude: Not intervention of interest.
7. Abdel-Fatah TM, Russell R, Albarakati N, et al. Genomic and protein expression analysis reveals flap endonuclease 1 (FEN1) as a key biomarker in breast and ovarian cancer. *Molecular Oncology*. 2014;8(7):1326-1338. Exclude: No outcome of interest.
8. Abramovitz M, Williams C, Loibl S, Leyland-Jones B. Dual Blockade of HER-2 Provides a Greater Magnitude of Benefit in Patients With Hormone-Negative Versus Hormone-Positive Breast Cancer. *Clinical Breast Cancer*. 2016;16(6):444-455. Exclude: Not intervention of interest.
9. Acharya CR, Hsu DS, Anders CK, et al. Gene expression signatures, clinicopathological features, and individualized therapy in breast cancer.[Retraction in Acharya CR, Hsu DS, Anders CK, Anguiano A, Salter KH, Walters KS, Redman RC, Tuchman SA, Moylan CA, Mukherjee S, Barry WT, Dressman HK, Ginsburg GS, Marcom KP, Garman KS, Lyman GH, Nevins JR, Potti A. *JAMA*. 2012 Feb 1;307(5):453; PMID: 22228686]. *JAMA*. 2008;299(13):1574-1587. Exclude: Publication type-letter.
10. Acs G, Esposito NN, Kiluk J, Loftus L, Laronga C. A mitotically active, cellular tumor stroma and/or inflammatory cells associated with tumor cells may contribute to intermediate or high Oncotype DX Recurrence Scores in low-grade invasive breast carcinomas. *Modern Pathology*. 2012;25(4):556-566. Exclude: No outcome of interest.
11. Acs G, Kiluk J, Loftus L, Laronga C. Comparison of Oncotype DX and Mammostrat risk estimations and correlations with histologic tumor features in low-grade, estrogen receptor-positive invasive breast carcinomas. *Modern Pathology*. 2013;26(11):1451-1460. Exclude: No outcome of interest.
12. Adamo B, Vidal M, Gomez Pardo P, et al. VENTANA (SOLTI-1501): oral metronomic vinorelbine combined with endocrine therapy in luminal/HER-2-negative early breast cancer: a window of opportunity

- trial. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
13. Ademuyiwa FO, Miller A, O'Connor T, et al. The effects of oncotype DX recurrence scores on chemotherapy utilization in a multi-institutional breast cancer cohort. *Breast Cancer Res Treat*. 2011;126(3):797-802. Exclude: In included systematic review.
14. Ademuyiwa FO, Tao Y, Luo J, Weilbaecher K, Ma CX. Differences in the mutational landscape of triple-negative breast cancer in African Americans and Caucasians. *Breast Cancer Research & Treatment*. 2017;161(3):491-499. Exclude: No outcome of interest.
15. Ademuyiwa FO, Thorat MA, Jain RK, Nakshatri H, Badve S. Expression of Forkhead-box protein A1, a marker of luminal A type breast cancer, parallels low Oncotype DX 21-gene recurrence scores. *Modern Pathology*. 2010;23(2):270-275. Exclude: No outcome of interest.
16. Adris S, Chuluyan E, Bravo A, et al. Mice vaccination with interleukin 12-transduced colon cancer cells potentiates rejection of syngeneic non-organ-related tumor cells. *Cancer Research*. 2000;60(23):6696-6703. Exclude: Date.
17. Afentakis M, Dowsett M, Sestak I, et al. Immunohistochemical BAG1 expression improves the estimation of residual risk by IHC4 in postmenopausal patients treated with anastrozole or tamoxifen: a TransATAC study. *Breast Cancer Research & Treatment*. 2013;140(2):253-262. Exclude: Not intervention of interest.
18. Afghahi A, Mathur M, Thompson CA, et al. Use of Gene Expression Profiling and Chemotherapy in Early-Stage Breast Cancer: A Study of Linked Electronic Medical Records, Cancer Registry Data, and Genomic Data Across Two Health Care Systems. *Journal of oncology practice/American Society of Clinical Oncology*. 2016;12(6):e697-709. Exclude: No outcome of interest.
19. Agarwal S, Gertler FB, Balsamo M, et al. Quantitative assessment of invasive mena isoforms (Menacalc) as an independent prognostic marker in breast cancer. *Breast Cancer Research*. 2012;14(5):R124. Exclude: Not intervention of interest.
20. Ahn S, Port ER. Lymphedema Precautions: Time to Abandon Old Practices? *Journal of Clinical Oncology*. 2016;34(7):655-658. Exclude: Not intervention of interest.
21. Ahn SG, Lee HM, Lee HW, et al. Prognostic discrimination using a 70-gene signature among patients with estrogen receptor-positive breast cancer and an intermediate 21-gene recurrence score. *International Journal of Molecular Sciences*. 2013;14(12):23685-23699. Exclude: No outcome of interest.
22. Ahn SG, Lee JH, Lee HW, et al. Comparison of standardized uptake value of 18F-FDG-PET-CT with 21-gene recurrence score in estrogen receptor-positive, HER2-negative breast cancer. *PLoS ONE [Electronic Resource]*. 2017;12(4):e0175048. Exclude: No outcome of interest.
23. Ahr A, Karn T, Solbach C, et al. Identification of high risk breast-cancer patients by gene expression profiling. *Lancet*. 2002;359(9301):131-132. Exclude: Date.
24. Akashi-Tanaka S, Shimizu C, Ando M, et al. 21-Gene expression profile assay on core needle biopsies predicts responses to neoadjuvant endocrine therapy in breast cancer patients. *Breast*. 2009;18(3):171-174. Exclude: No outcome of interest.
25. Akslen LA, Straume O, Geisler S, et al. Glomeruloid microvascular proliferation is associated with lack of response to chemotherapy in breast cancer. *British Journal of Cancer*. 2011;105(1):9-12. Exclude: Not intervention of interest.

26. Albain KS, Barlow WE, Shak S, et al. Prognostic and predictive value of the 21-gene recurrence score assay in postmenopausal women with node-positive, oestrogen-receptor-positive breast cancer on chemotherapy: a retrospective analysis of a randomised trial. *Lancet Oncology*. 2010;11(1):55-65. Exclude: No outcome of interest.
27. Albain KS, Paik S, van't Veer L. Prediction of adjuvant chemotherapy benefit in endocrine responsive, early breast cancer using multigene assays. *Breast*. 2009;18 Suppl 3:S141-145. Exclude: No outcome of interest.
28. Albanell J, Gonzalez A, Ruiz-Borrego M, et al. Prospective transGEICAM study of the impact of the 21-gene Recurrence Score assay and traditional clinicopathological factors on adjuvant clinical decision making in women with estrogen receptor-positive (ER+) node-negative breast cancer. *Ann Oncol*. 2012;23(3):625-631. Exclude: In included systematic review.
29. Albanell J, Svedman C, Gligorov J, et al. Pooled analysis of prospective European studies assessing the impact of using the 21-gene Recurrence Score assay on clinical decision making in women with oestrogen receptor-positive, human epidermal growth factor receptor 2-negative early-stage breast cancer. *Eur J Cancer*. 2016;66:104-113. Exclude: Publication type-not systematic review.
30. Aleskandarany MA, Rakha EA, Ahmed MA, et al. PIK3CA expression in invasive breast cancer: a biomarker of poor prognosis. *Breast Cancer Research & Treatment*. 2010;122(1):45-53. Exclude: Not intervention of interest.
31. Ali HR, Dawson SJ, Blows FM, Provenzano E, Pharoah PD, Caldas C. Cancer stem cell markers in breast cancer: pathological, clinical and prognostic significance. *Breast Cancer Research*. 2011;13(6):R118. Exclude: Not intervention of interest.
32. Ali HR, Rueda OM, Chin SF, et al. Genome-driven integrated classification of breast cancer validated in over 7,500 samples. *Genome Biology*. 2014;15(8):431. Exclude: No outcome of interest.
33. Ali-Khan SE, Black L, Palmour N, Hallett MT, Avar D. Socio-Ethical Issues in Personalized Medicine: A Systematic Review of English Language Health Technology Assessments of Gene Expression Profiling Tests for Breast Cancer Prognosis. *International Journal of Technology Assessment in Health Care*. 2015;31(1-2):36-50. Exclude: No outcome of interest.
34. Allison KH, Kandalaft PL, Sitlani CM, Dintzis SM, Gown AM. Routine pathologic parameters can predict Oncotype DX recurrence scores in subsets of ER positive patients: who does not always need testing? *Breast Cancer Research & Treatment*. 2012;131(2):413-424. Exclude: No outcome of interest.
35. Allott EH, Cohen SM, Geradts J, et al. Performance of Three-Biomarker Immunohistochemistry for Intrinsic Breast Cancer Subtyping in the AMBER Consortium. *Cancer Epidemiology, Biomarkers & Prevention*. 2016;25(3):470-478. Exclude: No outcome of interest.
36. Alshatwi AA, Shafi G, Hasan TN, et al. Differential expression profile and genetic variants of microRNAs sequences in breast cancer patients. *PLoS ONE [Electronic Resource]*. 2012;7(2):e30049. Exclude: Not intervention of interest.
37. Alvarado M, Carter DL, Guenther JM, et al. The impact of genomic testing on the recommendation for radiation therapy in patients with ductal carcinoma in situ: A prospective clinical utility assessment of the 12-gene DCIS score result. *J Surg Oncol*. 2015;111(8):935-940. Exclude: Not intervention of interest.
38. Alvarado MD, Prasad C, Rothney M, et al. A Prospective Comparison of the 21-Gene Recurrence Score and the PAM50-Based Prosigna in Estrogen Receptor-Positive Early-Stage Breast Cancer. *Advances in Therapy*. 2015;32(12):1237-1247. Exclude: No outcome of interest.

39. Anderson WF, Rosenberg PS, Prat A, Perou CM, Sherman ME. How many etiological subtypes of breast cancer: two, three, four, or more? *Journal of the National Cancer Institute*. 2014;106(8). Exclude: Not intervention of interest.
40. Andre F, Domont J, Delaloge S. What can breast cancer molecular sub-classification add to conventional diagnostic tools? *Annals of Oncology*. 2007;18 Suppl 9:ix33-36. Exclude: Publication type-commentary.
41. Andre F, Mazouni C, Liedtke C, et al. HER2 expression and efficacy of preoperative paclitaxel/FAC chemotherapy in breast cancer. *Breast Cancer Research & Treatment*. 2008;108(2):183-190. Exclude: Not intervention of interest.
42. Andre F, Michiels S, Dessen P, et al. Exonic expression profiling of breast cancer and benign lesions: a retrospective analysis. *Lancet Oncology*. 2009;10(4):381-390. Exclude: Not intervention of interest.
43. Andreason M, Zhang C, Onitilo AA, et al. Treatment differences between urban and rural women with hormone receptor-positive early-stage breast cancer based on 21-gene assay recurrence score result. *J Community Support Oncol*. 2015;13(5):195-201. Exclude: No outcome of interest.
44. Anjanappa M, Cardoso A, Cheng L, et al. Individualized Breast Cancer Characterization through Single-Cell Analysis of Tumor and Adjacent Normal Cells. *Cancer Research*. 2017;77(10):2759-2769. Exclude: No outcome of interest.
45. Anonymous. NSABP study confirms oncotype DX predicts chemotherapy benefit in breast cancer patients. *Oncology (Williston Park)*. 2006;20(7):789-790. Exclude: Date.
46. Anonymous. Oncotype DX DCIS score predicts recurrence. *Cancer Discovery*. 2015;5(2):OF3. Exclude: No outcome of interest.
47. Anonymous. MammaPrint Reduces Breast Cancer Overtreatment. *Cancer Discovery*. 2016;6(6):OF4. Exclude: Publication type-commentary.
48. Antoni MH, Lutgendorf SK, Blomberg B, et al. Cognitive-behavioral stress management reverses anxiety-related leukocyte transcriptional dynamics. *Biological Psychiatry*. 2012;71(4):366-372. Exclude: Not intervention of interest.
49. Araki K, Ito Y. [A Review Multigene Assays for Clinical Utility in Breast Cancer]. *Gan To Kagaku Ryoho*. 2016;43(11):1332-1340. Exclude: Not English.
50. Arango BA, Rivera CL, Gluck S. Gene expression profiling in breast cancer. *American Journal Of Translational Research*. 2013;5(2):132-138. Exclude: Publication type-not systematic review.
51. Arao T, Matsumoto K, Maegawa M, Nishio K. What can and cannot be done using a microarray analysis? Treatment stratification and clinical applications in oncology. *Biological & Pharmaceutical Bulletin*. 2011;34(12):1789-1793. Exclude: Publication type-commentary.
52. Aristizabal-Pachon AF, de Carvalho TI, Carrara HH, de Andrade JM, Takahashi CS. Detection of human mammaglobin A mRNA in peripheral blood of breast cancer patients before treatment and association with metastasis. *Journal of Egyptian National Cancer Institute*. 2015;27(4):217-222. Exclude: Not intervention of interest.
53. Arnutti P, Kotepui M, Asanprakit W, et al. Determination of whole transcription profiles and specific pathways in invasive ductal breast carcinoma. *International Journal of Clinical & Experimental Pathology*. 2013;6(6):1112-1120. Exclude: Not intervention of interest.

54. Arora A, Abdel-Fatah TM, Agarwal D, et al. Transcriptomic and Protein Expression Analysis Reveals Clinicopathological Significance of Bloom Syndrome Helicase (BLM) in Breast Cancer. *Molecular Cancer Therapeutics*. 2015;14(4):1057-1065. Exclude: Not intervention of interest.
55. Arpino G, Generali D, Sapino A, et al. Gene expression profiling in breast cancer: a clinical perspective. *Breast*. 2013;22(2):109-120. Exclude: Publication type-commentary.
56. Arranz EE, Vara JA, Gamez-Pozo A, Zamora P. Gene signatures in breast cancer: current and future uses. *Translational Oncology*. 2012;5(6):398-403. Exclude: Publication type-commentary.
57. Asad J, Jacobson AF, Estabrook A, et al. Does oncotype DX recurrence score affect the management of patients with early-stage breast cancer? *Am J Surg*. 2008;196(4):527-529. Exclude: In included systematic review.
58. Ascierto ML, Kmiecik M, Idowu MO, et al. A signature of immune function genes associated with recurrence-free survival in breast cancer patients. *Breast Cancer Research & Treatment*. 2012;131(3):871-880. Exclude: Not intervention of interest.
59. Ashraf AB, Daye D, Gavenonis S, et al. Identification of intrinsic imaging phenotypes for breast cancer tumors: preliminary associations with gene expression profiles. *Radiology*. 2014;272(2):374-384. Exclude: Not intervention of interest.
60. Asleh-Aburaya K, Sheffield BS, Kos Z, et al. Basal biomarkers nestin and INPP4b identify intrinsic subtypes accurately in breast cancers that are weakly positive for oestrogen receptor. *Histopathology*. 2017;70(2):185-194. Exclude: Not intervention of interest.
61. Aswad L, Yenamandra SP, Ow GS, Grinchuk O, Ivshina AV, Kuznetsov VA. Genome and transcriptome delineation of two major oncogenic pathways governing invasive ductal breast cancer development. *Oncotarget*. 2015;6(34):36652-36674. Exclude: Not intervention of interest.
62. Auerbach J, Kim M, Fineberg S. Can features evaluated in the routine pathologic assessment of lymph node-negative estrogen receptor-positive stage I or II invasive breast cancer be used to predict the Oncotype DX recurrence score? *Archives of Pathology & Laboratory Medicine*. 2010;134(11):1697-1701. Exclude: No outcome of interest.
63. Augustovski F, Soto N, Caporale J, Gonzalez L, Gibbons L, Ciapponi A. Meta-Analysis of Decision Impact and Net Decision Change in Adjuvant Chemotherapy Allocation in Early Stage Node-Negative, Estrogen Receptor-Positive Breast Cancer with a 21-Gene Assay. *Value Health*. 2014;17(7):A662. Exclude: Publication type-conference abstract.
64. Augustovski F, Soto N, Caporale J, Gonzalez L, Gibbons L, Ciapponi A. Response to real-life decision-making impact of Oncotype DX. *Breast Cancer Research & Treatment*. 2015;154(1):211. Exclude: Publication type-letter.
65. Aure MR, Vitelli V, Jernstrom S, et al. Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. *Breast Cancer Research*. 2017;19(1):44. Exclude: Not intervention of interest.
66. Avraham A, Cho SS, Uhlmann R, et al. Tissue specific DNA methylation in normal human breast epithelium and in breast cancer. *PLoS ONE [Electronic Resource]*. 2014;9(3):e91805. Exclude: Not intervention of interest.
67. Azim HA, Jr., Davidson NE, Ruddy KJ. Challenges in Treating Premenopausal Women with Endocrine-Sensitive Breast Cancer. *American Society of Clinical Oncology Educational Book*. 2016;35:23-32. Exclude: Publication type-commentary.

68. Azim HA, Jr., Michiels S, Bedard PL, et al. Elucidating prognosis and biology of breast cancer arising in young women using gene expression profiling. *Clinical Cancer Research*. 2012;18(5):1341-1351. Exclude: No outcome of interest.
69. Azim HA, Jr., Michiels S, Zagouri F, et al. Utility of prognostic genomic tests in breast cancer practice: The IMPAKT 2012 Working Group Consensus Statement. *Annals of Oncology*. 2013;24(3):647-654. Exclude: Publication type-not systematic review.
70. Azim HA, Jr., Nguyen B, Brohee S, Zoppoli G, Sotiriou C. Genomic aberrations in young and elderly breast cancer patients. *BMC Medicine*. 2015;13:266. Exclude: No outcome of interest.
71. Baba M, Takahashi M, Yamashiro K, et al. Strong cytoplasmic expression of NF-kappaB/p65 correlates with a good prognosis in patients with triple-negative breast cancer. *Surgery Today*. 2016;46(7):843-851. Exclude: Not intervention of interest.
72. Bacchi CE, Prisco F, Carvalho FM, Ojopi EB, Saad ED. Potential economic impact of the 21-gene expression assay on the treatment of breast cancer in Brazil. *Rev Assoc Med Bras (1992)*. 2010;56(2):186-191. Exclude: In included systematic review.
73. Badve S, Nakshatri H. Oestrogen-receptor-positive breast cancer: towards bridging histopathological and molecular classifications. *Journal of Clinical Pathology*. 2009;62(1):6-12. Exclude: No outcome of interest.
74. Badve SS, Baehner FL, Gray RP, et al. Estrogen- and progesterone-receptor status in ECOG 2197: comparison of immunohistochemistry by local and central laboratories and quantitative reverse transcription polymerase chain reaction by central laboratory.[Erratum appears in J Clin Oncol. 2008 Jul 10;26(20):3472 Note: Perez, Edith D [corrected to Perez, Edith A]]. *Journal of Clinical Oncology*. 2008;26(15):2473-2481. Exclude: Publication type-commentary.
75. Bae SY, Kim S, Lee JH, et al. Poor prognosis of single hormone receptor- positive breast cancer: similar outcome as triple-negative breast cancer. *BMC Cancer*. 2015;15:138. Exclude: Not intervention of interest.
76. Baehner FL. The analytical validation of the Oncotype DX Recurrence Score assay. *Ecancermedalscience*. 2016;10:675. Exclude: No outcome of interest.
77. Baehner FL, Achacoso N, Maddala T, et al. Human epidermal growth factor receptor 2 assessment in a case-control study: comparison of fluorescence in situ hybridization and quantitative reverse transcription polymerase chain reaction performed by central laboratories. *Journal of Clinical Oncology*. 2010;28(28):4300-4306. Exclude: Not intervention of interest.
78. Baehner FL, Gray R, Childs BH, et al. HER2 concordance between central laboratory immunohistochemistry and quantitative reverse transcription polymerase chain reaction in Intergroup Trial E2197. *Journal of Clinical Oncology*. 2008;26(15_suppl):22009. Exclude: Publication type-commentary.
79. Baitchu Y, Apffelstaedt JP. Application of Gene Profiling in Selection of Adjuvant Therapy in Breast Cancer in a Developing Country. *South African Journal of Surgery*. 2017;55(2):42-43. Exclude: No outcome of interest.
80. Baker H. 21-gene assay identifies patients who can avoid chemotherapy. *Lancet Oncology*. 2015;16(15):e531. Exclude: No outcome of interest.
81. Baker J. Genomic Health, Inc. *Pharmacogenomics*. 2007;8(4):397-399. Exclude: Publication type-commentary.

82. Bandyopadhyay D, Redkar A, Bharde S, Dani H, Sampat M, Mittra I. Prognostic association of c-erbB-2 oncogene amplification and protein overexpression in human breast cancer using archival tissues. A comparative study. *Acta Oncologica*. 1994;33(5):493-498. Exclude: Date.
83. Bandyopadhyay N, Kahveci T, Goodison S, Sun Y, Ranka S. Pathway-Based Feature Selection Algorithm for Cancer Microarray Data. *Advances in Bioinformatics Print*. 2009:532989. Exclude: Not intervention of interest.
84. Bao T, Davidson NE. Gene expression profiling of breast cancer. *Advances in Surgery*. 2008;42:249-260. Exclude: Publication type-commentary.
85. Bao Y, Ruan LJ, Mo JF. Low trichorhinophalangeal syndrome 1 gene transcript levels in basal-like breast cancer associate with mesenchymal-to-epithelial transition. *Chinese Medical Sciences Journal*. 2013;28(3):129-134. Exclude: Not intervention of interest.
86. Barajas-Castaneda LM, Cortes-Gutierrez E, Garcia-Rodriguez FM, et al. Overexpression of MMP-3 and uPA with Diminished PAI-1 Related to Metastasis in Ductal Breast Cancer Patients Attending a Public Hospital in Mexico City. *Journal of Immunological Research*. 2016;2016:8519648. Exclude: Not intervention of interest.
87. Barcenas CH, Raghavendra A, Sinha AK, et al. Outcomes in patients with early-stage breast cancer who underwent a 21-gene expression assay. *Cancer*. 2017;123(13):2422-2431. Exclude: No comparator.
88. Bargallo JE, Lara F, Shaw-Dulin R, et al. A study of the impact of the 21-gene breast cancer assay on the use of adjuvant chemotherapy in women with breast cancer in a Mexican public hospital. *J Surg Oncol*. 2015;111(2):203-207. Exclude: In included systematic review.
89. Bargallo-Rocha JE, Lara-Medina F, Perez-Sanchez V, et al. Cost-effectiveness of the 21-gene breast cancer assay in Mexico. *Adv Ther*. 2015;32(3):239-253. Exclude: In included systematic review.
90. Barinoff J, Anastasiadou L, Brandi C, et al. 21-gene recurrence score in patients with primary metastatic ER+ HER2-breast cancer. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
91. Baron P, Beitsch P, Boselli D, et al. Impact of Tumor Size on Probability of Pathologic Complete Response After Neoadjuvant Chemotherapy. *Annals of Surgical Oncology*. 2016;23(5):1522-1529. Exclude: Not intervention of interest.
92. Barrett MT, Anderson KS, Lenkiewicz E, et al. Genomic amplification of 9p24.1 targeting JAK2, PD-L1, and PD-L2 is enriched in high-risk triple negative breast cancer. *Oncotarget*. 2015;6(28):26483-26493. Exclude: Not intervention of interest.
93. Barrow TM, Barault L, Ellsworth RE, et al. Aberrant methylation of imprinted genes is associated with negative hormone receptor status in invasive breast cancer. *International Journal of Cancer*. 2015;137(3):537-547. Exclude: Not intervention of interest.
94. Bartlett JM, Bayani J, Marshall A, et al. Comparing Breast Cancer Multiparameter Tests in the OPTIMA Prelim Trial: No Test Is More Equal Than the Others. *Journal of the National Cancer Institute*. 2016;108(9). Exclude: No outcome of interest.
95. Bartlett JM, Bloom KJ, Piper T, et al. Mammostrat as an immunohistochemical multigene assay for prediction of early relapse risk in the tamoxifen versus exemestane adjuvant multicenter trial pathology study. *Journal of Clinical Oncology*. 2012;30(36):4477-4484. Exclude: No outcome of interest.

96. Bartlett JM, Starczynski J. Quantitative reverse transcriptase polymerase chain reaction and the Oncotype DX test for assessment of human epidermal growth factor receptor 2 status: time to reflect again? *Journal of Clinical Oncology*. 2011;29(32):4219-4221. Exclude: No outcome of interest.
97. Bartlett JM, Thomas J, Ross DT, et al. Mammostrat as a tool to stratify breast cancer patients at risk of recurrence during endocrine therapy. *Breast Cancer Research*. 2010;12(4):R47. Exclude: No outcome of interest.
98. Bartlett JMS, Stein RC, Bayani J, et al. Comparison of multiparameter tests in the UK OPTIMA-Prelim trial. *Cancer research*. 2015;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
99. Barton MK. Researchers find discordance between standard human epidermal growth factor receptor 2 (HER2) testing and HER2 status reported on Oncotype DX. *CA: a Cancer Journal for Clinicians*. 2012;62(2):71-72. Exclude: No outcome of interest.
100. Basavanhally A, Feldman M, Shih N, et al. Multi-field-of-view strategy for image-based outcome prediction of multi-parametric estrogen receptor-positive breast cancer histopathology: Comparison to Oncotype DX. *Journal of Pathology Informatics*. 2011;2:S1. Exclude: No outcome of interest.
101. Basho RK, de Melo Gagliato D, Ueno NT, et al. Clinical outcomes based on multigene profiling in metastatic breast cancer patients. *Oncotarget*. 2016;7(47):76362-76373. Exclude: No outcome of interest.
102. Bastien RR, Rodriguez-Lescure A, Ebbert MT, et al. PAM50 breast cancer subtyping by RT-qPCR and concordance with standard clinical molecular markers. *BMC Medical Genomics [Electronic Resource]*. 2012;5:44. Exclude: No outcome of interest.
103. Baxter E, Gondara L, Lohrisch C, et al. Using proliferative markers and Oncotype DX in therapeutic decision-making for breast cancer: the B.C. experience. *Current Oncology*. 2015;22(3):192-198. Exclude: No outcome of interest.
104. Bayraktar S, Royce M, Stork-Sloots L, de Snoo F, Gluck S. Molecular subtyping predicts pathologic tumor response in early-stage breast cancer treated with neoadjuvant docetaxel plus capecitabine with or without trastuzumab chemotherapy. *Medical Oncology*. 2014;31(10):163. Exclude: No outcome of interest.
105. Bear HD, Wan W, Robidoux A, et al. Using the 21-gene assay from core needle biopsies to choose neoadjuvant therapy for breast cancer: a multi-center trial. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
106. Beca F, Kensler K, Glass B, Schnitt SJ, Tamimi RM, Beck AH. EZH2 protein expression in normal breast epithelium and risk of breast cancer: results from the Nurses' Health Studies. *Breast Cancer Research*. 2017;19(1):21. Exclude: Not intervention of interest.
107. Bedard PL, Mook S, Piccart-Gebhart MJ, Rutgers ET, Van't Veer LJ, Cardoso F. MammaPrint 70-gene profile quantifies the likelihood of recurrence for early breast cancer. *Expert Opinion on Medical Diagnostics*. 2009;3(2):193-205. Exclude: No outcome of interest.
108. Bedard PL, Singhal SK, Ignatiadis M, et al. Low residual proliferation after short-term letrozole therapy is an early predictive marker of response in high proliferative ER-positive breast cancer. *Endocrine-Related Cancer*. 2011;18(6):721-730. Exclude: Not intervention of interest.
109. Bedognetti D, Hendrickx W, Marincola FM, Miller LD. Prognostic and predictive immune gene signatures in breast cancer. *Current Opinion in Oncology*. 2015;27(6):433-444. Exclude: Not intervention of interest.

110. Beeghly-Fadiel A, Kataoka N, Shu XO, et al. Her-2/neu amplification and breast cancer survival: results from the Shanghai breast cancer study. *Oncology Reports*. 2008;19(5):1347-1354. Exclude: Not intervention of interest.
111. Beitsch P, Whitworth P, Baron P, et al. Genomic Impact of Neoadjuvant Therapy on Breast Cancer: Incomplete Response is Associated with Altered Diagnostic Gene Signatures. *Annals of Surgical Oncology*. 2016;23(10):3317-3323. Exclude: No outcome of interest.
112. Bellocq JP, Luporsi E, Barriere J, et al. [uPA/PAI-1, Oncotype DX™, MammaPrint®]. Prognosis and predictive values for clinical utility in breast cancer management]. *Annales de Pathologie*. 2014;34(5):349-351. Exclude: No outcome of interest.
113. Bellocq JP, Luporsi E, Barriere J, et al. [uPA/PAI-1, Oncotype DX, MammaPrint®(R)]. Prognosis and predictive values for clinical utility in breast cancer management]. *Ann Pathol*. 2014;34(5):349-351. Exclude: Not English.
114. Belyavskaya VA, Prudnikova TY, Domanitskaya NV, et al. GLCE rs3865014 (Val597Ile) polymorphism is associated with breast cancer susceptibility and triple-negative breast cancer in Siberian population. *Gene*. 2017;628:224-229. Exclude: Not intervention of interest.
115. Bennett L, Quinn J, McCall P, et al. High IKKalpha expression is associated with reduced time to recurrence and cancer specific survival in oestrogen receptor (ER)-positive breast cancer. *International Journal of Cancer*. 2017;140(7):1633-1644. Exclude: Not intervention of interest.
116. Bergamaschi A, Christensen BL, Katzenellenbogen BS. Reversal of endocrine resistance in breast cancer: interrelationships among 14-3-3zeta, FOXM1, and a gene signature associated with mitosis. *Breast Cancer Research*. 2011;13(3):R70. Exclude: Not intervention of interest.
117. Bergamaschi A, Kim YH, Wang P, et al. Distinct patterns of DNA copy number alteration are associated with different clinicopathological features and gene-expression subtypes of breast cancer. *Genes, Chromosomes & Cancer*. 2006;45(11):1033-1040. Exclude: Date.
118. Bergenfelz C, Larsson AM, von Stedingk K, et al. Systemic Monocytic-MDSCs Are Generated from Monocytes and Correlate with Disease Progression in Breast Cancer Patients. *PLoS ONE [Electronic Resource]*. 2015;10(5):e0127028. Exclude: Not intervention of interest.
119. Bergqvist J, Ohd JF, Smeds J, et al. Quantitative real-time PCR analysis and microarray-based RNA expression of HER2 in relation to outcome. *Annals of Oncology*. 2007;18(5):845-850. Exclude: Not intervention of interest.
120. Bernau C, Riester M, Boulesteix AL, et al. Cross-study validation for the assessment of prediction algorithms. *Bioinformatics*. 2014;30(12):i105-112. Exclude: No outcome of interest.
121. Bernhardt SM, Dasari P, Walsh D, Townsend AR, Price TJ, Ingman WV. Hormonal Modulation of Breast Cancer Gene Expression: Implications for Intrinsic Subtyping in Premenopausal Women. *Frontiers in Oncology*. 2016;6:241. Exclude: Publication type-commentary.
122. Berns K, Horlings HM, Hennessy BT, et al. A functional genetic approach identifies the PI3K pathway as a major determinant of trastuzumab resistance in breast cancer. *Cancer Cell*. 2007;12(4):395-402. Exclude: Not intervention of interest.
123. Berry DA, Muss HB, Thor AD, et al. HER-2/neu and p53 expression versus tamoxifen resistance in estrogen receptor-positive, node-positive breast cancer. *Journal of Clinical Oncology*. 2000;18(20):3471-3479. Exclude: Date.

124. Berstein LM, Iyevleva AG, Vasilyev D, Poroshina TE, Imyanitov EN. Genetic polymorphisms potentially associated with response to metformin in postmenopausal diabetics suffering and not suffering with cancer. *Cell Cycle*. 2013;12(23):3681-3688. Exclude: Not intervention of interest.
125. Bertelli G, Holt S. Real-life decision-making impact of Oncotype DX. *Breast Cancer Research & Treatment*. 2015;154(1):209-210. Exclude: Publication type-letter.
126. Bertucci F, Finetti P, Viens P, Birnbaum D. EndoPredict predicts for the response to neoadjuvant chemotherapy in ER-positive, HER2-negative breast cancer. *Cancer Letters*. 2014;355(1):70-75. Exclude: No outcome of interest.
127. Besic N, Satej N. Insulin glargine versus other types of basal insulin-clinical and tumor characteristics in patients with breast carcinoma. *BMC Research Notes*. 2013;6:416. Exclude: Not intervention of interest.
128. Beumer I, Witteveen A, Delahaye L, et al. Equivalence of MammaPrint array types in clinical trials and diagnostics. *Breast Cancer Research & Treatment*. 2016;156(2):279-287. Exclude: No outcome of interest.
129. Beumer IJ, Persoon M, Witteveen A, et al. Prognostic Value of MammaPrint<sup> in Invasive Lobular Breast Cancer. *Biomark Insights*. 2016;11:139-146. Exclude: No outcome of interest.
130. Bhandari V, Boutros PC. Comparing continuous and discrete analyses of breast cancer survival information. *Genomics*. 2016;108(2):78-83. Exclude: Not intervention of interest.
131. Bhargava R, Dabbs DJ. Oncotype DX test on unequivocally HER2-positive cases: potential for harm. *Journal of Clinical Oncology*. 2012;30(5):570-571. Exclude: No outcome of interest.
132. Bhatavdekar JM, Patel DD, Sherbet GV, et al. Prognostic significance of plasma prolactin in breast cancer: comparison with the expression of c erb B-2 oncoprotein. *European Journal of Surgical Oncology*. 1993;19(5):409-413. Exclude: Date.
133. Bhushann Meka P, Jarjapu S, Vishwakarma SK, et al. Influence of BCL2-938 C>A promoter polymorphism and BCL2 gene expression on the progression of breast cancer. *Tumour Biology*. 2016;37(5):6905-6912. Exclude: Not intervention of interest.
134. Bianchi S, Palli D, Falchetti M, et al. ErbB-receptors expression and survival in breast carcinoma: a 15-year follow-up study. *Journal of Cellular Physiology*. 2006;206(3):702-708. Exclude: Date.
135. Bianchini G, Iwamoto T, Qi Y, et al. Prognostic and therapeutic implications of distinct kinase expression patterns in different subtypes of breast cancer. *Cancer Research*. 2010;70(21):8852-8862. Exclude: Not intervention of interest.
136. Bianchini G, Pusztai L, Karn T, et al. Proliferation and estrogen signaling can distinguish patients at risk for early versus late relapse among estrogen receptor positive breast cancers. *Breast Cancer Research*. 2013;15(5):R86. Exclude: Not intervention of interest.
137. Bianchini G, Qi Y, Alvarez RH, et al. Molecular anatomy of breast cancer stroma and its prognostic value in estrogen receptor-positive and -negative cancers.[Erratum appears in J Clin Oncol. 2010 Nov 10;28(32):4868], [Erratum appears in J Clin Oncol. 2012 Feb 20;30(6):679]. *Journal of Clinical Oncology*. 2010;28(28):4316-4323. Exclude: Not intervention of interest.
138. Bieche I, Lazar V, Nogues C, et al. Prognostic value of chorionic gonadotropin beta gene transcripts in human breast carcinoma. *Clinical Cancer Research*. 1998;4(3):671-676. Exclude: Date.
139. Bieche I, Lerebours F, Tozlu S, Espie M, Marty M, Lidereau R. Molecular profiling of inflammatory breast cancer: identification of a poor-prognosis gene expression signature. *Clinical Cancer Research*. 2004;10(20):6789-6795. Exclude: Date.

140. Bieche I, Onody P, Lerebours F, et al. ERBB2 status and benefit from adjuvant tamoxifen in ERalpha-positive postmenopausal breast carcinoma. *Cancer Letters*. 2001;174(2):173-178. Exclude: Date.
141. Bieche I, Tozlu S, Girault I, Lidereau R. Identification of a three-gene expression signature of poor-prognosis breast carcinoma. *Molecular Cancer*. 2004;3(1):37. Exclude: Date.
142. Bienkowska JR, Dalgin GS, Batliwalla F, et al. Convergent Random Forest predictor: methodology for predicting drug response from genome-scale data applied to anti-TNF response. *Genomics*. 2009;94(6):423-432. Exclude: Not intervention of interest.
143. Bighin C, Del Mastro L, Canavese G, et al. Use in current clinical practice of 70-gene signature in early breast cancer. *International Journal of Cancer*. 2010;127(11):2736-2737. Exclude: No outcome of interest.
144. Bilal E, Dutkowski J, Guinney J, et al. Improving breast cancer survival analysis through competition-based multidimensional modeling. *PLoS Computational Biology*. 2013;9(5):e1003047. Exclude: Not intervention of interest.
145. Bilecova-Rabajdova M, Urban P, Gregova K, et al. Breast carcinoma progression and tumour vascular markers related to apoptotic mechanisms. *Disease Markers*. 2014;2014:156034. Exclude: Not intervention of interest.
146. Biroschak JR, Schwartz GF, Palazzo JP, et al. Impact of Oncotype DX on treatment decisions in ER-positive, node-negative breast cancer with histologic correlation. *Breast J*. 2013;19(3):269-275. Exclude: In included systematic review.
147. Bitran JD, Samuels B, Trujillo Y, Klein L, Schroeder L, Martinec J. Her2/neu overexpression is associated with treatment failure in women with high-risk stage II and stage IIIA breast cancer (>10 involved lymph nodes) treated with high-dose chemotherapy and autologous hematopoietic progenitor cell support following standard-dose adjuvant chemotherapy. *Clinical Cancer Research*. 1996;2(9):1509-1513. Exclude: Date.
148. Blakely CM, Stoddard AJ, Belka GK, et al. Hormone-induced protection against mammary tumorigenesis is conserved in multiple rat strains and identifies a core gene expression signature induced by pregnancy.[Erratum appears in Cancer Res. 2007 Jan 15;67(2):844-6]. *Cancer Research*. 2006;66(12):6421-6431. Exclude: Date.
149. Blank PR, Filipits M, Dubsky P, et al. Cost-effectiveness analysis of prognostic gene expression signature-based stratification of early breast cancer patients. *Pharmacoeconomics*. 2015;33(2):179-190. Exclude: In included systematic review.
150. Blazadonakis ME, Zervakis ME. Comparison and unification of genomic signatures in breast cancer. *Conference Proceedings: Annual International Conference of the IEEE Engineering in Medicine & Biology Society*. 2009;2009:3869-3872. Exclude: Publication type-conference abstract.
151. Blohmer JU, Rezai M, Kummel S, et al. Using the 21-gene assay to guide adjuvant chemotherapy decision-making in early-stage breast cancer: a cost-effectiveness evaluation in the German setting. *J Med Econ*. 2013;16(1):30-40. Exclude: In included systematic review.
152. Blok EJ, van de Velde CJ, Smit VT. 70-Gene Signature in Early-Stage Breast Cancer. *New England Journal of Medicine*. 2016;375(22):2199. Exclude: Publication type-letter.
153. Bloomfield DJ, Arbon A, Cox J, et al. Patient/oncologist decisions about adjuvant chemotherapy in ER+ve, HER2ve early breast cancer following endopredict testing. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.

154. Boccia RV. Translating Research into Practice: the Prosigna (PAM50) Gene Signature Assay. *Clinical Advances in Hematology & Oncology*. 2015;13(6 Suppl 6):3-13. Exclude: No outcome of interest.
155. Bock C, Rack B, Huober J, Andergassen U, Jeschke U, Doisneau-Sixou S. Distinct expression of cytokeratin, N-cadherin and CD133 in circulating tumor cells of metastatic breast cancer patients. *Future Oncology*. 2014;10(10):1751-1765. Exclude: Not intervention of interest.
156. Bogaerts J, Cardoso F, Buyse M, et al. Gene signature evaluation as a prognostic tool: challenges in the design of the MINDACT trial. *Nature Clinical Practice Oncology*. 2006;3(10):540-551. Exclude: Date.
157. Bombard Y, Rozmovits L, Trudeau M, Leighl NB, Deal K, Marshall DA. The value of personalizing medicine: medical oncologists' views on gene expression profiling in breast cancer treatment. *Oncologist*. 2015;20(4):351-356. Exclude: No outcome of interest.
158. Bomeisl PE, Thompson CL, Harris LN, Gilmore HL. Comparison of Oncotype DX Recurrence Score by Histologic Types of Breast Carcinoma. *Archives of Pathology & Laboratory Medicine*. 2015;139(12):1546-1549. Exclude: No outcome of interest.
159. Bonastre J, Marguet S, Lueza B, Michiels S, Delaloge S, Saghatchian M. Cost effectiveness of molecular profiling for adjuvant decision making in patients with node-negative breast cancer. *J Clin Oncol*. 2014;32(31):3513-3519. Exclude: In included systematic review.
160. Bonechi M, Guarducci C, Meoni G, et al. Metabolomic analysis by nuclear magnetic resonance spectroscopy discriminates hormone receptor positive/HER2 negative breast cancer cell lines resistant to palbociclib. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
161. Bonnefoi H, Potti A, Delorenzi M, et al. Validation of gene signatures that predict the response of breast cancer to neoadjuvant chemotherapy: a substudy of the EORTC 10994/BIG 00-01 clinical trial.[Retraction in Bonnefoi H, Potti A, Delorenzi M, Mauriac L, Campone M, Tubiana-Hulin M, Petit T, Rouanet P, Jassem J, Blot E, Becette V, Farmer P, Andre S, Acharya CR, Mukherjee S, Cameron D, Bergh J, Nevins JR, Iggo RD. *Lancet Oncol*. 2011 Feb;12(2):116; PMID: 21277543]. *Lancet Oncology*. 2007;8(12):1071-1078. Exclude: No outcome of interest.
162. Bonnet F, Guedj M, Jones N, et al. An array CGH based genomic instability index (G2I) is predictive of clinical outcome in breast cancer and reveals a subset of tumors without lymph node involvement but with poor prognosis. *BMC Medical Genomics [Electronic Resource]*. 2012;5:54. Exclude: Not intervention of interest.
163. Bonnetterre J, Prat A, Galvan P, Morel P, Giard S. Value of a gene signature assay in patients with early breast cancer and intermediate risk: a single institution retrospective study. *Curr Med Res Opin*. 2016;32(5):835-839. Exclude: No outcome of interest.
164. Borg A, Tandon AK, Sigurdsson H, et al. HER-2/neu amplification predicts poor survival in node-positive breast cancer. *Cancer Research*. 1990;50(14):4332-4337. Exclude: Date.
165. Bosl A, Spitzmuller A, Jasarevic Z, Rauch S, Jager S, Offner F. MammaPrint versus EndoPredict: Poor correlation in disease recurrence risk classification of hormone receptor positive breast cancer. *PLoS ONE [Electronic Resource]*. 2017;12(8):e0183458. Exclude: No outcome of interest.
166. Bostner J, Skoog L, Fornander T, Nordenskjold B, Stal O. Estrogen receptor-alpha phosphorylation at serine 305, nuclear p21-activated kinase 1 expression, and response to tamoxifen in postmenopausal breast cancer. *Clinical Cancer Research*. 2010;16(5):1624-1633. Exclude: Not intervention of interest.

167. Bowles DW, Rabinovitch R, Borges V, et al. A young woman with a small ER-positive breast cancer, a micrometastatic axillary lymph node, and an intermediate oncotype DX recurrence score. *Oncology (Williston Park)*. 2007;21(10):1212-1217. Exclude: No outcome of interest.
168. Bradshaw SH, Pidutti D, Gravel DH, Song X, Marginean EC, Robertson SJ. Predicting OncoDx recurrence scores with immunohistochemical markers. *Applied Immunohistochemistry & Molecular Morphology*. 2013;21(6):490-496. Exclude: No outcome of interest.
169. Brandao RD, Veeck J, Van de Vijver KK, et al. A randomised controlled phase II trial of pre-operative celecoxib treatment reveals anti-tumour transcriptional response in primary breast cancer. *Breast Cancer Research*. 2013;15(2):R29. Exclude: Not intervention of interest.
170. Brase JC, Kronenwett R, Petry C, Denkert C, Schmidt M. From High-Throughput Microarray-Based Screening to Clinical Application: The Development of a Second Generation Multigene Test for Breast Cancer Prognosis. *Microarrays*. 2013;2(3):243-264. Exclude: No outcome of interest.
171. Braunstein LZ, Taghian AG, Harris JR. PRECISION (Profiling Early Breast Cancer for Radiotherapy Omission): a phase II study of breast-conserving surgery without adjuvant radiotherapy for favorable-risk breast cancer. *Cancer research Conference: 107th annual meeting of the american association for cancer research, AACR*. 2016;76(14 Supplement). Exclude: Publication type-conference abstract.
172. Brewer NT, Richman AR, DeFrank JT, Reyna VF, Carey LA. Improving communication of breast cancer recurrence risk. *Breast Cancer Research & Treatment*. 2012;133(2):553-561. Exclude: Not intervention of interest.
173. Brockton NT, Gill SJ, Laborge SL, et al. The Breast Cancer to Bone (B2B) Metastases Research Program: a multi-disciplinary investigation of bone metastases from breast cancer. *BMC Cancer*. 2015;15:512. Exclude: Not intervention of interest.
174. Brownlie D, Chatterjee S, Saad Z, Wilson G, Bashir M. Impact of Oncotype DX on the decision for adjuvant chemotherapy: Retrospective analysis of the Salford Royal Foundation Trust cohort. *European Journal of Surgical Oncology*. 2015;Conference: Association of Breast Surgery Conference and AGM, ABS. 2015 Bournemouth United Kingdom. Conference Start: 20150615 Conference End: 20150616. Conference Publication:(var.pagings) 41 (6):S74. Exclude: No outcome of interest.
175. Brufsky AM. Predictive and prognostic value of the 21-gene recurrence score in hormone receptor-positive, node-positive breast cancer. *American Journal of Clinical Oncology*. 2014;37(4):404-410. Exclude: Publication type-not systematic review.
176. Brufsky AM, Davidson NE. Multiparametric Genomic Assays for Breast Cancer: Time for the Next Generation? *Clinical Cancer Research*. 2016;22(20):4963-4965. Exclude: Publication type-commentary.
177. Budczies J, Bockmayr M, Denkert C, et al. Classical pathology and mutational load of breast cancer - integration of two worlds. *The Journal of Pathology Clinical Research*. 2015;1(4):225-238. Exclude: Not intervention of interest.
178. Budczies J, Pfitzner BM, Gyorffy B, et al. Glutamate enrichment as new diagnostic opportunity in breast cancer. *International Journal of Cancer*. 2015;136(7):1619-1628. Exclude: Not intervention of interest.
179. Bueno RC, Canevari RA, Villacis RA, et al. ATM down-regulation is associated with poor prognosis in sporadic breast carcinomas. *Annals of Oncology*. 2014;25(1):69-75. Exclude: Not intervention of interest.

180. Bueno-de-Mesquita JM, Linn SC, Keijzer R, et al. Validation of 70-gene prognosis signature in node-negative breast cancer. *Breast Cancer Research & Treatment*. 2009;117(3):483-495. Exclude: No outcome of interest.
181. Bueno-de-Mesquita JM, Sonke GS, van de Vijver MJ, Linn SC. Additional value and potential use of the 70-gene prognosis signature in node-negative breast cancer in daily clinical practice. *Annals of Oncology*. 2011;22(9):2021-2030. Exclude: No outcome of interest.
182. Bueno-de-Mesquita JM, van Harten WH, Retel VP, et al. Use of 70-gene signature to predict prognosis of patients with node-negative breast cancer: a prospective community-based feasibility study (RASTER).[Erratum appears in *Lancet Oncol*. 2008 Jan;9(1):10]. *Lancet Oncology*. 2007;8(12):1079-1087. Exclude: In included systematic review.
183. Butt S, Borgquist S, Anagnostaki L, Landberg G, Manjer J. Breastfeeding in relation to risk of different breast cancer characteristics. *BMC Research Notes*. 2014;7:216. Exclude: Not intervention of interest.
184. Buus R, Sestak I, Kronenwett R, et al. Comparison of EndoPredict and EPclin With Oncotype DX Recurrence Score for Prediction of Risk of Distant Recurrence After Endocrine Therapy. *Journal of the National Cancer Institute*. 2016;108(11). Exclude: No outcome of interest.
185. Buyse M, Loi S, van't Veer L, et al. Validation and clinical utility of a 70-gene prognostic signature for women with node-negative breast cancer. *Journal of the National Cancer Institute*. 2006;98(17):1183-1192. Exclude: Date.
186. Caan BJ, Sweeney C, Habel LA, et al. Intrinsic subtypes from the PAM50 gene expression assay in a population-based breast cancer survivor cohort: prognostication of short- and long-term outcomes. *Cancer Epidemiology, Biomarkers & Prevention*. 2014;23(5):725-734. Exclude: No outcome of interest.
187. Cadenas C, Franckenstein D, Schmidt M, et al. Role of thioredoxin reductase 1 and thioredoxin interacting protein in prognosis of breast cancer. *Breast Cancer Research*. 2010;12(3):R44. Exclude: Not intervention of interest.
188. Cadoo KA, Fornier MN, Morris PG. Biological subtypes of breast cancer: current concepts and implications for recurrence patterns. *The Quarterly Journal of Nuclear Medicine & Molecular Imaging*. 2013;57(4):312-321. Exclude: Publication type-commentary.
189. Cai H, Li X, Li J, et al. Tamoxifen therapy benefit predictive signature coupled with prognostic signature of post-operative recurrent risk for early stage ER+ breast cancer. *Oncotarget*. 2015;6(42):44593-44608. Exclude: Not intervention of interest.
190. Cai S, Geng S, Jin F, Liu J, Qu C, Chen B. POU5F1/Oct-4 expression in breast cancer tissue is significantly associated with non-sentinel lymph node metastasis. *BMC Cancer*. 2016;16:175. Exclude: Not intervention of interest.
191. Caiazza F, McCarthy NS, Young L, Hill AD, Harvey BJ, Thomas W. Cytosolic phospholipase A2-alpha expression in breast cancer is associated with EGFR expression and correlates with an adverse prognosis in luminal tumours. *British Journal of Cancer*. 2011;104(2):338-344. Exclude: Not intervention of interest.
192. Calabro A, Beissbarth T, Kuner R, et al. Effects of infiltrating lymphocytes and estrogen receptor on gene expression and prognosis in breast cancer. *Breast Cancer Research & Treatment*. 2009;116(1):69-77. Exclude: Not intervention of interest.
193. Camillo ND, Dos Santos GT, Prolla JC, et al. Impact of cell arrangement of pleural effusion in survival of patients with breast cancer. *Acta Cytologica*. 2014;58(5):446-452. Exclude: Not intervention of interest.

194. Campone M, Campion L, Roche H, et al. Prediction of metastatic relapse in node-positive breast cancer: establishment of a clinicogenomic model after FEC100 adjuvant regimen. *Breast Cancer Research & Treatment*. 2008;109(3):491-501. Exclude: Not intervention of interest.
195. Cardoso F, Piccart-Gebhart M, Van't Veer L, Rutgers E, Consortium T. The MINDACT trial: the first prospective clinical validation of a genomic tool. *Molecular Oncology*. 2007;1(3):246-251. Exclude: No outcome of interest.
196. Cardoso F, Piccart-Gebhart MJ, Rutgers EJ, et al. Standard anthracycline-based vs. Docetaxel-capecitabine in early breast cancer: results from the chemotherapy randomization (R-C) of EORTC 10041/BIG 3-04 MINDACT phase III trial. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
197. Cardoso F, Slaets L, De Snoo F, et al. Can surrogate pathological subtyping replace molecular subtyping? Outcome results from the MINDACT trial. *Cancer research Conference: 39th annual CTSC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
198. Cardoso F, Van't Veer L, Rutgers E, Loi S, Mook S, Piccart-Gebhart MJ. Clinical application of the 70-gene profile: the MINDACT trial. *Journal of Clinical Oncology*. 2008;26(5):729-735. Exclude: No outcome of interest.
199. Carey LA, Berry DA, Cirincione CT, et al. Molecular Heterogeneity and Response to Neoadjuvant Human Epidermal Growth Factor Receptor 2 Targeting in CALGB 40601, a Randomized Phase III Trial of Paclitaxel Plus Trastuzumab With or Without Lapatinib. *Journal of Clinical Oncology*. 2016;34(6):542-549. Exclude: Not intervention of interest.
200. Carlson JJ, Roth JA. The impact of the Oncotype Dx breast cancer assay in clinical practice: a systematic review and meta-analysis. *Breast Cancer Res Treat*. 2013;141(1):13-22. Exclude: Publication type-older systematic review.
201. Carlsson H, Petersson S, Enerback C. Cluster analysis of S100 gene expression and genes correlating to psoriasin (S100A7) expression at different stages of breast cancer development. *International Journal of Oncology*. 2005;27(6):1473-1481. Exclude: Date.
202. Carr DN, Vera N, Sun W, et al. Menopausal status does not predict Oncotype DX recurrence score. *Journal of Surgical Research*. 2015;198(1):27-33. Exclude: No outcome of interest.
203. Carter SL, Eklund AC, Kohane IS, Harris LN, Szallasi Z. A signature of chromosomal instability inferred from gene expression profiles predicts clinical outcome in multiple human cancers. *Nature Genetics*. 2006;38(9):1043-1048. Exclude: Date.
204. Cascione L, Gasparini P, Lovat F, et al. Integrated microRNA and mRNA signatures associated with survival in triple negative breast cancer. *PLoS ONE [Electronic Resource]*. 2013;8(2):e55910. Exclude: Not intervention of interest.
205. Casimiro S, Luis I, Fernandes A, et al. Analysis of a bone metastasis gene expression signature in patients with bone metastasis from solid tumors. *Clinical & Experimental Metastasis*. 2012;29(2):155-164. Exclude: Not intervention of interest.
206. Cecene G, Ak S, Eskiler GG, et al. Circulating miR-195 as a Therapeutic Biomarker in Turkish Breast Cancer Patients. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2016;17(9):4241-4246. Exclude: Not intervention of interest.

207. Cejalvo JM, Martinez de Duenas E, Galvan P, et al. Intrinsic Subtypes and Gene Expression Profiles in Primary and Metastatic Breast Cancer. *Cancer Research*. 2017;77(9):2213-2221. Exclude: No outcome of interest.
208. Cespedes Feliciano EM, Kwan ML, Kushi LH, et al. Body mass index, PAM50 subtype, recurrence, and survival among patients with nonmetastatic breast cancer. *Cancer*. 2017;123(13):2535-2542. Exclude: No outcome of interest.
209. Chae EY, Moon WK, Kim HH, et al. Association between Ultrasound Features and the 21-Gene Recurrence Score Assays in Patients with Oestrogen Receptor-Positive, HER2-Negative, Invasive Breast Cancer. *PLoS ONE [Electronic Resource]*. 2016;11(6):e0158461. Exclude: No outcome of interest.
210. Chalabi N, Bernard-Gallon DJ, Bignon YJ, et al. Comparative clinical and transcriptomal profiles of breast cancer between French and South Mediterranean patients show minor but significative biological differences.[Erratum appears in *Cancer Genomics Proteomics*. 2008 Nov-Dec;5(6):353], [Erratum appears in *Cancer Genomics Proteomics*. 2009 Jan-Feb;6(1):73]. *Cancer Genomics & Proteomics*. 2008;5(5):253-261. Exclude: Not intervention of interest.
211. Chan M, Liaw CS, Ji SM, et al. Identification of circulating microRNA signatures for breast cancer detection. *Clinical Cancer Research*. 2013;19(16):4477-4487. Exclude: Not intervention of interest.
212. Chan SR, Vermi W, Luo J, et al. STAT1-deficient mice spontaneously develop estrogen receptor alpha-positive luminal mammary carcinomas. *Breast Cancer Research*. 2012;14(1):R16. Exclude: Not intervention of interest.
213. Chang HY, Nuyten DS, Sneddon JB, et al. Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. *Proceedings of the National Academy of Sciences of the United States of America*. 2005;102(10):3738-3743. Exclude: Date.
214. Chang JC, Makris A, Gutierrez MC, et al. Gene expression patterns in formalin-fixed, paraffin-embedded core biopsies predict docetaxel chemosensitivity in breast cancer patients. *Breast Cancer Research & Treatment*. 2008;108(2):233-240. Exclude: No outcome of interest.
215. Chang JC, Wooten EC, Tsimelzon A, et al. Gene expression profiling for the prediction of therapeutic response to docetaxel in patients with breast cancer. *Lancet*. 2003;362(9381):362-369. Exclude: Date.
216. Chang JM, McCullough AE, Dueck AC, et al. Back to Basics: Traditional Nottingham Grade Mitotic Counts Alone are Significant in Predicting Survival in Invasive Breast Carcinoma. *Annals of Surgical Oncology*. 2015;22 Suppl 3:S509-515. Exclude: Not intervention of interest.
217. Chang MC, Souter LH, Kamel-Reid S, et al. Clinical utility of multigene profiling assays in early-stage breast cancer. *Current Oncology*. 2017;24(5):e403-e422. Exclude: No outcome of interest.
218. Chanrion M, Negre V, Fontaine H, et al. A gene expression signature that can predict the recurrence of tamoxifen-treated primary breast cancer. *Clinical Cancer Research*. 2008;14(6):1744-1752. Exclude: Not intervention of interest.
219. Chapman JW, Liu S, Leung S, Nielsen TO. Competing Risks of Mortality by PAM50 Intrinsic Subtype of British Columbia Tamoxifen-Treated Cohort of Postmenopausal Patients With Breast Cancer. *Clinical Breast Cancer*. 2017;17(4):e215-e224. Exclude: No outcome of interest.
220. Charafe-Jauffret E, Ginestier C, Bertucci F, et al. ALDH1-positive cancer stem cells predict engraftment of primary breast tumors and are governed by a common stem cell program. *Cancer Research*. 2013;73(24):7290-7300. Exclude: Not intervention of interest.

221. Chaudhary LN, Jawa Z, Szabo A, Visotcky A, Chitambar CR. Relevance of progesterone receptor immunohistochemical staining to Oncotype DX recurrence score. *Hematology/oncology & stem cell therapy*. 2016;9(2):48-54. Exclude: No outcome of interest.
222. Cheang MC, Chia SK, Voduc D, et al. Ki67 index, HER2 status, and prognosis of patients with luminal B breast cancer. *Journal of the National Cancer Institute*. 2009;101(10):736-750. Exclude: Not intervention of interest.
223. Cheang MC, Martin M, Nielsen TO, et al. Defining breast cancer intrinsic subtypes by quantitative receptor expression. *Oncologist*. 2015;20(5):474-482. Exclude: No outcome of interest.
224. Cheang MC, Voduc KD, Tu D, et al. Responsiveness of intrinsic subtypes to adjuvant anthracycline substitution in the NCIC.CTG MA.5 randomized trial. *Clinical Cancer Research*. 2012;18(8):2402-2412. Exclude: Not intervention of interest.
225. Cheang MCU, Bliss J, Dowsett M, et al. Concordance of intrinsic subtyping and risk of recurrence (ROR) scores between matched primary and metastatic tissue from Triple Negative Breast Cancer Trial (TNT). *Journal of clinical oncology*. 2015;33(15 SUPPL. 1):CONFERENCE START: 2015 May 2029 CONFERENCE END: 2015 Jun 2012. Exclude: No outcome of interest.
226. Cheang MCU, Morden J, Gao Q, et al. The impact of intrinsic subtypes and molecular features on aromatase inhibitor induced reduction of proliferation marker of Ki67 in primary ER+ breast cancer: a POETIC study (CRUK/07/015). *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
227. Cheang MCU, Perou CM, Whelan TJ, et al. Evaluation of the adjuvant radiation treatment-effect heterogeneity using genomic signature for locoregional relapse and long-term outcome. *Journal of clinical oncology*. 2014;32(15 SUPPL. 1):CONFERENCE START: 2014 May 2030 CONFERENCE END: 2014 Jun 2013. Exclude: Publication type-conference abstract.
228. Chen C, Dhanda R, Tseng WY, Forsyth M, Patt DA. Evaluating use characteristics for the oncotype dx 21-gene recurrence score and concordance with chemotherapy use in early-stage breast cancer. *Journal of oncology practice/American Society of Clinical Oncology*. 2013;9(4):182-187. Exclude: Date.
229. Chen E, Tong KB, Malin JL. Cost-effectiveness of 70-gene MammaPrint signature in node-negative breast cancer. *Am J Manag Care*. 2010;16(12):e333-342. Exclude: In included systematic review.
230. Chen JL, Espinosa I, Lin AY, Liao OY, van de Rijn M, West RB. Stromal responses among common carcinomas correlated with clinicopathologic features. *Clinical Cancer Research*. 2013;19(18):5127-5135. Exclude: Not intervention of interest.
231. Chen L, Huang TG, Meseck M, Mandeli J, Fallon J, Woo SL. Rejection of metastatic 4T1 breast cancer by attenuation of Treg cells in combination with immune stimulation. *Molecular Therapy: the Journal of the American Society of Gene Therapy*. 2007;15(12):2194-2202. Exclude: Not intervention of interest.
232. Chen N. Incorporate gene signature profiling into routine molecular testing. *Applied & Translational Genomics*. 2013;2:28-33. Exclude: Publication type-commentary.
233. Chen RS. [Study of Her-2/neu oncogene in relation to prognosis of human breast cancer]. *Chung-Hua Ping Li Hsueh Tsa Chih - Chinese Journal of Pathology*. 1993;22(5):291-293. Exclude: Date.
234. Chen X, Lin X, Zhao J, et al. A tumor-selective biotherapy with prolonged impact on established metastases based on cytokine gene-engineered MSCs. *Molecular Therapy: the Journal of the American Society of Gene Therapy*. 2008;16(4):749-756. Exclude: Not intervention of interest.

235. Chen XS, Shen KW. [Multi-gene assay profiling testing and individualized therapy in breast cancer]. *Chung-Hua Wai Ko Tsa Chih [Chinese Journal of Surgery]*. 2017;55(2):99-103. Exclude: Not intervention of interest.
236. Chen YZ, Xue JY, Chen CM, et al. PPAR signaling pathway may be an important predictor of breast cancer response to neoadjuvant chemotherapy. *Cancer Chemotherapy & Pharmacology*. 2012;70(5):637-644. Exclude: Not intervention of interest.
237. Cheng J, Lin H, Liang X. [Study on the relationship between PS2 protein expression and prognosis in invasive breast carcinoma]. *Chung-Hua Ping Li Hsueh Tsa Chih - Chinese Journal of Pathology*. 1997;26(6):331-333. Exclude: Date.
238. Cheng V, Markarian A, De Lemos M, Schaff K. Evaluation of the impact of oncotype DX test results on systemic therapy in breast cancer patients at the BC cancer agency (BCCA). *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
239. Cheung PS, Tong AC, Leung RC, Kwan WH, Yau TC. Initial experience with the Oncotype DX assay in decision-making for adjuvant therapy of early oestrogen receptor-positive breast cancer in Hong Kong. *Hong Kong Medical Journal*. 2014;20(5):401-406. Exclude: In included systematic review.
240. Chia SK, Bramwell VH, Tu D, et al. A 50-gene intrinsic subtype classifier for prognosis and prediction of benefit from adjuvant tamoxifen. *Clinical Cancer Research*. 2012;18(16):4465-4472. Exclude: No outcome of interest.
241. Chibon F. [Prediction of the metastatic potential of sarcomas on the basis of a gene expression signature related to genome complexity]. *M S-Medecine Sciences*. 2011;27(1):22-24. Exclude: Not English.
242. Chikkanna-Gowda CP, Sheahan BJ, Fleeton MN, Atkins GJ. Regression of mouse tumours and inhibition of metastases following administration of a Semliki Forest virus vector with enhanced expression of IL-12. *Gene Therapy*. 2005;12(16):1253-1263. Exclude: Date.
243. Cho WC. Conquering cancer through discovery research. *IUBMB Life*. 2010;62(9):655-659. Exclude: Publication type-commentary.
244. Chowdary D, Lathrop J, Skelton J, et al. Prognostic gene expression signatures can be measured in tissues collected in RNAlater preservative. *Journal of Molecular Diagnostics*. 2006;8(1):31-39. Exclude: Date.
245. Chowdhury N, Sapru S. Association of Protein Translation and Extracellular Matrix Gene Sets with Breast Cancer Metastasis: Findings Uncovered on Analysis of Multiple Publicly Available Datasets Using Individual Patient Data Approach. *PLoS ONE [Electronic Resource]*. 2015;10(6):e0129610. Exclude: Not intervention of interest.
246. Christgen M, Geffers R, Kreipe H, Lehmann U. IPH-926 lobular breast cancer cells are triple-negative but their microarray profile uncovers a luminal subtype. *Cancer Science*. 2013;104(12):1726-1730. Exclude: Not intervention of interest.
247. Christgen M, Harbeck N, Gluz O, Nitz U, Kreipe HH. Recognition and handling of discordant negative human epidermal growth factor receptor 2 classification by Oncotype DX in patients with breast cancer. *Journal of Clinical Oncology*. 2012;30(26):3313-3314; author reply 3314-3315. Exclude: No outcome of interest.
248. Chung C, Christianson M. Predictive and prognostic biomarkers with therapeutic targets in breast, colorectal, and non-small cell lung cancers: a systemic review of current development, evidence, and

recommendation. *J Oncol Pharm Pract.* 2014;20(1):11-28. Exclude: Publication type-older systematic review.

249. Ciocca V, Daskalakis C, Ciocca RM, Ruiz-Orrico A, Palazzo JP. The significance of GATA3 expression in breast cancer: a 10-year follow-up study. *Human Pathology.* 2009;40(4):489-495. Exclude: Not intervention of interest.

250. Cizeron-Clairac G, Lallemand F, Vacher S, Lidereau R, Bieche I, Callens C. MiR-190b, the highest up-regulated miRNA in ERalpha-positive compared to ERalpha-negative breast tumors, a new biomarker in breast cancers? *BMC Cancer.* 2015;15:499. Exclude: Not intervention of interest.

251. Clark BZ, Dabbs DJ, Cooper KL, Bhargava R. Impact of progesterone receptor semiquantitative immunohistochemical result on Oncotype DX recurrence score: a quality assurance study of 1074 cases. *Applied Immunohistochemistry & Molecular Morphology.* 2013;21(4):287-291. Exclude: No outcome of interest.

252. Clark-Langone KM, Sangli C, Krishnakumar J, Watson D. Translating tumor biology into personalized treatment planning: analytical performance characteristics of the Oncotype DX Colon Cancer Assay. *BMC Cancer.* 2010;10:691. Exclude: No outcome of interest.

253. Coates AS, Winer EP, Goldhirsch A, et al. Tailoring therapies--improving the management of early breast cancer: St Gallen International Expert Consensus on the Primary Therapy of Early Breast Cancer 2015. *Ann Oncol.* 2015;26(8):1533-1546. Exclude: Publication type-not systematic review.

254. Cobain EF, Hayes DF. Indications for prognostic gene expression profiling in early breast cancer. *Current Treatment Options in Oncology.* 2015;16(5):23. Exclude: No outcome of interest.

255. Cobleigh MA, Tabesh B, Bitterman P, et al. Tumor gene expression and prognosis in breast cancer patients with 10 or more positive lymph nodes. *Clinical Cancer Research.* 2005;11(24 Pt 1):8623-8631. Exclude: Date.

256. Cockburn JG, Hallett RM, Gillgrass AE, et al. The effects of lymph node status on predicting outcome in ER+ /HER2- tamoxifen treated breast cancer patients using gene signatures. *BMC Cancer.* 2016;16:555. Exclude: No outcome of interest.

257. Cody HS, 3rd. SLN biopsy for large and/or multicentric breast cancers: should we worry? *European Journal of Surgical Oncology.* 2011;37(5):386-387. Exclude: Not intervention of interest.

258. Cohen O, Lam G, Karp N, Choi M. Determining the Oncologic Safety of Autologous Fat Grafting as a Reconstructive Modality: An Institutional Review of Breast Cancer Recurrence Rates and Surgical Outcomes. *Plastic & Reconstructive Surgery.* 2017;140(3):382e-392e. Exclude: Not intervention of interest.

259. Coibion M, Lifrange E, Jossa V, et al. Should modified radical mastectomy be modified? A phase 1 study to evaluate infraradical mastectomy for invasive breast cancer. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states.* 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

260. Confalonieri S, Quarto M, Goisis G, et al. Alterations of ubiquitin ligases in human cancer and their association with the natural history of the tumor. *Oncogene.* 2009;28(33):2959-2968. Exclude: Not intervention of interest.

261. Conlin AK, Seidman AD. Use of the Oncotype DX 21-gene assay to guide adjuvant decision making in early-stage breast cancer. *Molecular Diagnosis & Therapy.* 2007;11(6):355-360. Exclude: Publication type-commentary.

262. Conlon N, Ross DS, Howard J, Catalano JP, Dickler MN, Tan LK. Is There a Role for Oncotype Dx Testing in Invasive Lobular Carcinoma? *Breast Journal*. 2015;21(5):514-519. Exclude: No outcome of interest.
263. Corvalan A. [Gene expression profiles for therapeutic decisions in breast cancer]. *Revista Medica de Chile*. 2007;135(2):257-263. Exclude: Not English.
264. Cosler LE, Lyman GH. Economic analysis of gene expression profile data to guide adjuvant treatment in women with early-stage breast cancer. *Cancer Invest*. 2009;27(10):953-959. Exclude: In included systematic review.
265. Cottu PH, Duhoux F, Lemonnier J, et al. NEOPAL: A randomized phase II study comparing RCB response to neoadjuvant chemotherapy or letrozole-palbociclib in PAM50 defined postmenopausal luminal breast cancer. *Cancer research*. 2015;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
266. Cowherd S, Miller LD, Melin SA, et al. A phase II clinical trial of weekly paclitaxel and carboplatin in combination with panitumumab in metastatic triple negative breast cancer. *Cancer Biology & Therapy*. 2015;16(5):678-683. Exclude: Not intervention of interest.
267. Craig DW, O'Shaughnessy JA, Kiefer JA, et al. Genome and transcriptome sequencing in prospective metastatic triple-negative breast cancer uncovers therapeutic vulnerabilities. *Molecular Cancer Therapeutics*. 2013;12(1):104-116. Exclude: Not intervention of interest.
268. Crawford NP, Qian X, Ziogas A, et al. Rrp1b, a new candidate susceptibility gene for breast cancer progression and metastasis. *PLoS Genetics*. 2007;3(11):e214. Exclude: Not intervention of interest.
269. Creighton CJ, Kent Osborne C, van de Vijver MJ, et al. Molecular profiles of progesterone receptor loss in human breast tumors. *Breast Cancer Research & Treatment*. 2009;114(2):287-299. Exclude: Not intervention of interest.
270. Creighton CJ, Sada YH, Zhang Y, et al. A gene transcription signature of obesity in breast cancer. *Breast Cancer Research & Treatment*. 2012;132(3):993-1000. Exclude: Not intervention of interest.
271. Cress RD, Chen YS, Morris CR, Chew H, Kizer KW. Underutilization of gene expression profiling for early-stage breast cancer in California. *Cancer Causes & Control*. 2016;27(6):721-727. Exclude: No outcome of interest.
272. Criscitiello C, Bagnardi V, Viale G, et al. HER2 Equivocal Status in Early Breast Cancer Is Not Associated with Higher Risk of Recurrence. *Anticancer Research*. 2016;36(7):3537-3540. Exclude: Not intervention of interest.
273. Cronin M, Sangli C, Liu ML, et al. Analytical validation of the Oncotype DX genomic diagnostic test for recurrence prognosis and therapeutic response prediction in node-negative, estrogen receptor-positive breast cancer. *Clinical Chemistry*. 2007;53(6):1084-1091. Exclude: No outcome of interest.
274. Cuadros M, Llanos A. [Validation and clinical application of MammaPrint in patients with breast cancer]. *Medicina Clinica*. 2011;136(14):627-632. Exclude: Not English.
275. Culhane AC, Quackenbush J. Confounding effects in "A six-gene signature predicting breast cancer lung metastasis". *Cancer Research*. 2009;69(18):7480-7485. Exclude: Not intervention of interest.
276. Cummings MC, Simpson PT, Reid LE, et al. Metastatic progression of breast cancer: insights from 50 years of autopsies. *Journal of Pathology*. 2014;232(1):23-31. Exclude: Not intervention of interest.
277. Curigliano G, Bagnardi V, Bertolini F, et al. Antiangiogenic therapy in recurrent breast cancer with lymphangitic spread to the chest wall: A randomized phase II trial of bevacizumab with sequential or

concurrent oral vinorelbine and capecitabine. *Breast*. 2015;24(3):263-271. Exclude: Not intervention of interest.

278. Curtit E, Mansi L, Maisonneville-Escot Y, Sautiere JL, Pivot X. Prognostic and predictive indicators in early-stage breast cancer and the role of genomic profiling: Focus on the Oncotype DX Breast Recurrence Score Assay. *European Journal of Surgical Oncology*. 2017;43(5):921-930. Exclude: Publication type-not systematic review.

279. Cusumano PG, Generali D, Ciruelos E, et al. European inter-institutional impact study of MammaPrint. *Breast*. 2014;23(4):423-428. Exclude: In included systematic review.

280. Cuzick J, Dowsett M, Pineda S, et al. Prognostic value of a combined estrogen receptor, progesterone receptor, Ki-67, and human epidermal growth factor receptor 2 immunohistochemical score and comparison with the Genomic Health recurrence score in early breast cancer. *Journal of Clinical Oncology*. 2011;29(32):4273-4278. Exclude: No outcome of interest.

281. Da Ros L, Indelli M, Santini A, et al. Multigene prognostic and predictive tests in Luminal breast cancer patients: Relation between Mammprint results and nodal status in a retrospectively monocentric analysis. *Annals of Oncology Conference: 17th National Congress of Medical Oncology Rome Italy Conference Start*. 2015;26. Exclude: Publication type-conference abstract.

282. Dabbs DJ. A Comparison of Breast Cancer Multianalyte Assays With Algorithmic Analyses (MAAA) for Their Net Predictive/Prognostic Value. *Clinical Advances in Hematology & Oncology*. 2015;13(6 Suppl 6):14-24. Exclude: No outcome of interest.

283. Dabbs DJ, Klein ME, Mohsin SK, Tubbs RR, Shuai Y, Bhargava R. High false-negative rate of HER2 quantitative reverse transcription polymerase chain reaction of the Oncotype DX test: an independent quality assurance study. *Journal of Clinical Oncology*. 2011;29(32):4279-4285. Exclude: No outcome of interest.

284. DaCosta Byfield S, Buck PO, Blauer-Peterson C, et al. ReCAP: Treatment Patterns and Cost of Care Associated With Initial Therapy Among Patients Diagnosed With Operable Early-Stage Human Epidermal Growth Factor Receptor 2-Overexpressed Breast Cancer in the United States: A Real-World Retrospective Study. *Journal of oncology practice/American Society of Clinical Oncology*. 2016;12(2):159-167. Exclude: Not intervention of interest.

285. Dahl E, Kristiansen G, Gottlob K, et al. Molecular profiling of laser-microdissected matched tumor and normal breast tissue identifies karyopherin alpha2 as a potential novel prognostic marker in breast cancer. *Clinical Cancer Research*. 2006;12(13):3950-3960. Exclude: Date.

286. Dai X, Li Y, Bai Z, Tang XQ. Molecular portraits revealing the heterogeneity of breast tumor subtypes defined using immunohistochemistry markers. *Scientific Reports*. 2015;5:14499. Exclude: No outcome of interest.

287. D'Alfonso TM, van Laar RK, Vahdat LT, et al. BreastPRS is a gene expression assay that stratifies intermediate-risk Oncotype DX patients into high- or low-risk for disease recurrence. *Breast Cancer Research & Treatment*. 2013;139(3):705-715. Exclude: No outcome of interest.

288. Dalgin GS, Delisi C. Simple discriminant functions identify small sets of genes that distinguish cancer phenotype from normal. *Genome Informatics*. 2005;16(1):245-253. Exclude: Date.

289. Dall P, Heider KH, Sinn HP, et al. Comparison of immunohistochemistry and RT-PCR for detection of CD44v-expression, a new prognostic factor in human breast cancer. *International Journal of Cancer*. 1995;60(4):471-477. Exclude: Date.

290. Dalton L. Invasive breast cancer: stratification of histological grade by gene-based assays: a still relevant example from an older data set. *Histopathology*. 2014;65(3):429-433. Exclude: No outcome of interest.
291. Damasco C, Lembo A, Somma MP, Gatti M, Di Cunto F, Provero P. A signature inferred from *Drosophila* mitotic genes predicts survival of breast cancer patients. *PLoS ONE [Electronic Resource]*. 2011;6(2):e14737. Exclude: Not intervention of interest.
292. Damelin M, Bankovich A, Park A, et al. Anti-EFNA4 Calicheamicin Conjugates Effectively Target Triple-Negative Breast and Ovarian Tumor-Initiating Cells to Result in Sustained Tumor Regressions. *Clinical Cancer Research*. 2015;21(18):4165-4173. Exclude: Not intervention of interest.
293. Danaher P, Skewis L, Mashadi-Hosseini A, et al. Development of a Prosigna (PAM50)-based classifier for the selection of advanced triple negative breast cancer (TNBC) patients for treatment with enzalutamide. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
294. Dati C, Muraca R, Tazartes O, et al. c-erbB-2 and ras expression levels in breast cancer are correlated and show a co-operative association with unfavorable clinical outcome. *International Journal of Cancer*. 1991;47(6):833-838. Exclude: Date.
295. Davidson JA, Cromwell I, Ellard SL, et al. A prospective clinical utility and pharmacoeconomic study of the impact of the 21-gene Recurrence Score(R) assay in oestrogen receptor positive node negative breast cancer. *Eur J Cancer*. 2013;49(11):2469-2475. Exclude: In included systematic review.
296. Davies SR, Watkins G, Douglas-Jones A, Mansel RE, Jiang WG. Bone morphogenetic proteins 1 to 7 in human breast cancer, expression pattern and clinical/prognostic relevance. *Journal of Experimental Therapeutics & Oncology*. 2008;7(4):327-338. Exclude: Not intervention of interest.
297. Davis BA, Aminawung JA, Abu-Khalaf MM, et al. Racial and Ethnic Disparities in Oncotype DX Test Receipt in a Statewide Population-Based Study. *J Natl Compr Canc Netw*. 2017;15(3):346-354. Exclude: No outcome of interest.
298. Davis JE, Nemesure B, Mehmood S, et al. Her2 and Ki67 Biomarkers Predict Recurrence of Ductal Carcinoma in Situ. *Applied Immunohistochemistry & Molecular Morphology*. 2016;24(1):20-25. Exclude: Not intervention of interest.
299. de Boer M, Voogd AC, Tjan-Heijnen VC. [A plea for selective use of the MammaPrint test]. *Nederlands Tijdschrift voor Geneeskunde*. 2017;161(0):D1160. Exclude: No outcome of interest.
300. de Boer RH, Baker C, Speakman D, Chao CY, Yoshizawa C, Mann GB. The impact of a genomic assay (Oncotype DX) on adjuvant treatment recommendations in early breast cancer. *Med J Aust*. 2013;199(3):205-208. Exclude: In included systematic review.
301. de Lima Lopes G, Chien R, Hornberger J. Cost-benefit of the 21-gene breast cancer recurrence score assay for patients in Singapore. *Breast J*. 2013;19(2):220-221. Exclude: Publication type-letter.
302. De P, Carlson JH, Leyland-Jones B, Dey N. Role of "oncogenic nexus" of CIP2A in breast oncogenesis: how does it work? *American Journal of Cancer Research*. 2015;5(9):2872-2891. Exclude: No outcome of interest.
303. De P, Carlson JH, Wu H, Marcus A, Leyland-Jones B, Dey N. Wnt-beta-catenin pathway signals metastasis-associated tumor cell phenotypes in triple negative breast cancers. *Oncotarget*. 2016;7(28):43124-43149. Exclude: Not intervention of interest.

304. de Rinaldis E, Gazinska P, Mera A, et al. Integrated genomic analysis of triple-negative breast cancers reveals novel microRNAs associated with clinical and molecular phenotypes and sheds light on the pathways they control. *BMC Genomics*. 2013;14:643. Exclude: Not intervention of interest.
305. de Snoo F, Bender R, Glas A, Rutgers E. Gene expression profiling: decoding breast cancer. *Surgical Oncology*. 2009;18(4):366-378. Exclude: Publication type-commentary.
306. Debled M, Tunon de Lara C, MacGrogan G. A 21-Gene Expression Assay in Breast Cancer. *New England Journal of Medicine*. 2016;374(14):1385-1386. Exclude: Publication type-letter.
307. DeFrank JT, Salz T, Reeder-Hayes K, Brewer NT. Who gets genomic testing for breast cancer recurrence risk? *Public Health Genomics*. 2013;16(5):215-222. Exclude: No outcome of interest.
308. Degenhardt T, Gluz O, Thomssen C, et al. Abstract P2-09-05: Risk Group Selection in Primary Breast Cancer According to ASCO Recommended Biomarkers Onkotype DX and uPA/PAI-1: First Experience from Prospective Multicenter WSG Plan B Trial. 2010. Exclude: No outcome of interest.
309. Del Casar JM, Martin A, Garcia C, et al. Characterization of breast cancer subtypes by quantitative assessment of biological parameters: relationship with clinicopathological characteristics, biological features and prognosis. *European Journal of Obstetrics, Gynecology, & Reproductive Biology*. 2008;141(2):147-152. Exclude: No outcome of interest.
310. Delahaye L, Drukker CA, Dreezen C, et al. A breast cancer gene signature for indolent disease. *Breast Cancer Research & Treatment*. 2017;164(2):461-466. Exclude: No outcome of interest.
311. Denkert C. [Gene expression analysis in breast cancer. A new diagnostic tool in pathology]. *Pathologe*. 2013;34(5):413-418. Exclude: Not English.
312. Denkert C, Kronenwett R, Schlake W, et al. Decentral gene expression analysis for ER+/Her2- breast cancer: results of a proficiency testing program for the EndoPredict assay. *Virchows Archiv*. 2012;460(3):251-259. Exclude: No outcome of interest.
313. Denkert C, Pfitzner BM, Heppner BI, Dietel M. [Molecular pathology for breast cancer: Importance of the gene expression profile]. *Pathologe*. 2015;36(2):145-153. Exclude: Not English.
314. Dennison JB, Molina JR, Mitra S, et al. Lactate dehydrogenase B: a metabolic marker of response to neoadjuvant chemotherapy in breast cancer. *Clinical Cancer Research*. 2013;19(13):3703-3713. Exclude: Not intervention of interest.
315. Dennison JB, Shahmoradgoli M, Liu W, et al. High Intratumoral Stromal Content Defines Reactive Breast Cancer as a Low-risk Breast Cancer Subtype. *Clinical Cancer Research*. 2016;22(20):5068-5078. Exclude: Not intervention of interest.
316. DeRose YS, Wang G, Lin YC, et al. Tumor grafts derived from women with breast cancer authentically reflect tumor pathology, growth, metastasis and disease outcomes. *Nature Medicine*. 2011;17(11):1514-1520. Exclude: Not intervention of interest.
317. Descotes F, Jezequel P, Spyrtos F, et al. Identification of potential prognostic biomarkers for node-negative breast tumours by proteomic analysis: a multicentric 2004 national PHRC study. *International Journal of Oncology*. 2012;41(1):92-104. Exclude: Not intervention of interest.
318. Desmedt C, Di Leo A, de Azambuja E, et al. Multifactorial approach to predicting resistance to anthracyclines. *Journal of Clinical Oncology*. 2011;29(12):1578-1586. Exclude: No outcome of interest.
319. Desmedt C, Haibe-Kains B, Wirapati P, et al. Biological processes associated with breast cancer clinical outcome depend on the molecular subtypes. *Clinical Cancer Research*. 2008;14(16):5158-5165. Exclude: No outcome of interest.

320. Desmedt C, Majjaj S, Kheddoumi N, et al. Characterization and clinical evaluation of CD10+ stroma cells in the breast cancer microenvironment. *Clinical Cancer Research*. 2012;18(4):1004-1014. Exclude: No outcome of interest.
321. Desmedt C, Ruiz-Garcia E, Andre F. Gene expression predictors in breast cancer: current status, limitations and perspectives. *European Journal of Cancer*. 2008;44(18):2714-2720. Exclude: No outcome of interest.
322. Deverka PA, Schully SD, Ishibe N, et al. Stakeholder assessment of the evidence for cancer genomic tests: insights from three case studies.[Erratum appears in Genet Med. 2013 Jan;15(1):91]. *Genetics in Medicine*. 2012;14(7):656-662. Exclude: No outcome of interest.
323. Dey N, Barwick BG, Moreno CS, et al. Wnt signaling in triple negative breast cancer is associated with metastasis. *BMC Cancer*. 2013;13:537. Exclude: Not intervention of interest.
324. Dey N, Sun Y, Carlson JH, et al. Anti-tumor efficacy of BEZ235 is complemented by its anti-angiogenic effects via downregulation of PI3K-mTOR-HIF1alpha signaling in HER2-defined breast cancers. *American Journal of Cancer Research*. 2016;6(4):714-746. Exclude: Not intervention of interest.
325. Dey N, Young B, Abramovitz M, et al. Differential activation of Wnt-beta-catenin pathway in triple negative breast cancer increases MMP7 in a PTEN dependent manner. *PLoS ONE [Electronic Resource]*. 2013;8(10):e77425. Exclude: Not intervention of interest.
326. Dialani V, Gaur S, Mehta TS, et al. Prediction of Low versus High Recurrence Scores in Estrogen Receptor-Positive, Lymph Node-Negative Invasive Breast Cancer on the Basis of Radiologic-Pathologic Features: Comparison with Oncotype DX Test Recurrence Scores. *Radiology*. 2016;280(2):370-378. Exclude: No outcome of interest.
327. Dias K, Dvorkin-Gheva A, Hallett RM, et al. Claudin-Low Breast Cancer; Clinical & Pathological Characteristics. *PLoS ONE [Electronic Resource]*. 2017;12(1):e0168669. Exclude: Not intervention of interest.
328. Diaz LK, Cristofanilli M, Zhou X, et al. Beta4 integrin subunit gene expression correlates with tumor size and nuclear grade in early breast cancer. *Modern Pathology*. 2005;18(9):1165-1175. Exclude: Date.
329. Dieci MV, Guarneri V, Giarratano T, et al. First prospective multicenter Italian study on the impact of the 21-Gene Recurrence Score (RS) in adjuvant clinical decisions for ER+/HER2-early breast cancer (BC) patients. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
330. Dieci MV, Guarneri V, Mion M, et al. First prospective multicenter Italian study on the impact of the 21-gene recurrence score (RS) in adjuvant clinical decisions for ER + /HER2-early breast cancer patients. *Annals of oncology Conference: 41st european society for medical oncology congress, ESMO*. 2016;27(no pagination). Exclude: Publication type-conference abstract.
331. Dieci MV, Prat A, Tagliafico E, et al. Integrated evaluation of PAM50 subtypes and immune modulation of pCR in HER2-positive breast cancer patients treated with chemotherapy and HER2-targeted agents in the CherLOB trial. *Annals of Oncology*. 2016;27(10):1867-1873. Exclude: No outcome of interest.
332. Dieras V, Campone M, Yardley DA, et al. Randomized, phase II, placebo-controlled trial of onartuzumab and/or bevacizumab in combination with weekly paclitaxel in patients with metastatic triple-negative breast cancer. *Annals of Oncology*. 2015;26(9):1904-1910. Exclude: Not intervention of interest.
333. Dinan MA, Mi X, Reed SD, Hirsch BR, Lyman GH, Curtis LH. Initial Trends in the Use of the 21-Gene Recurrence Score Assay for Patients With Breast Cancer in the Medicare Population, 2005-2009. *JAMA Oncology*. 2015;1(2):158-166. Exclude: No outcome of interest.

334. Dinan MA, Mi X, Reed SD, Lyman GH, Curtis LH. Association Between Use of the 21-Gene Recurrence Score Assay and Receipt of Chemotherapy Among Medicare Beneficiaries With Early-Stage Breast Cancer, 2005-2009. *JAMA Oncology*. 2015;1(8):1098-1109. Exclude: Date.
335. Dirix L, Van Dam P, Vermeulen P. Genomics and circulating tumor cells: promising tools for choosing and monitoring adjuvant therapy in patients with early breast cancer? *Current Opinion in Oncology*. 2005;17(6):551-558. Exclude: Date.
336. Divino CM, Chen SH, Yang W, Thung S, Brower ST, Woo SL. Anti-tumor immunity induced by interleukin-12 gene therapy in a metastatic model of breast cancer is mediated by natural killer cells. *Breast Cancer Research & Treatment*. 2000;60(2):129-134. Exclude: Date.
337. Dobbe E, Gurney K, Kiekow S, Lafferty JS, Kolesar JM. Gene-expression assays: new tools to individualize treatment of early-stage breast cancer. *American Journal of Health-System Pharmacy*. 2008;65(1):23-28. Exclude: Publication type-commentary.
338. Dogan L, Atalay C, Yilmaz KB, Ozaslan C. Prognosis in hormon receptor negative breast cancer patients according to ERBB2 status. *Neoplasma*. 2008;55(6):544-548. Exclude: Not intervention of interest.
339. Dolled-Filhart M, Ryden L, Cregger M, et al. Classification of breast cancer using genetic algorithms and tissue microarrays. *Clinical Cancer Research*. 2006;12(21):6459-6468. Exclude: Date.
340. Dowsett M. Biomarker investigations from the ATAC trial: the role of TA01. *Breast Cancer Research & Treatment*. 2004;87 Suppl 1:S11-18. Exclude: Date.
341. Dowsett M, Cuzick J, Wale C, et al. Prediction of risk of distant recurrence using the 21-gene recurrence score in node-negative and node-positive postmenopausal patients with breast cancer treated with anastrozole or tamoxifen: a TransATAC study. *Journal of Clinical Oncology*. 2010;28(11):1829-1834. Exclude: No outcome of interest.
342. Dowsett M, Dunbier AK. Emerging biomarkers and new understanding of traditional markers in personalized therapy for breast cancer. *Clinical Cancer Research*. 2008;14(24):8019-8026. Exclude: Publication type-commentary.
343. Dowsett M, Salter J, Zabaglo L, et al. Predictive algorithms for adjuvant therapy: TransATAC. *Steroids*. 2011;76(8):777-780. Exclude: No outcome of interest.
344. Dowsett M, Sestak I, Buus R, et al. Estrogen Receptor Expression in 21-Gene Recurrence Score Predicts Increased Late Recurrence for Estrogen-Positive/HER2-Negative Breast Cancer. *Clinical Cancer Research*. 2015;21(12):2763-2770. Exclude: No outcome of interest.
345. Dowsett M, Sestak I, Lopez-Knowles E, et al. Comparison of PAM50 risk of recurrence score with oncotype DX and IHC4 for predicting risk of distant recurrence after endocrine therapy. *Journal of Clinical Oncology*. 2013;31(22):2783-2790. Exclude: No outcome of interest.
346. Dressman HK, Hans C, Bild A, et al. Gene expression profiles of multiple breast cancer phenotypes and response to neoadjuvant chemotherapy. *Clinical Cancer Research*. 2006;12(3 Pt 1):819-826. Exclude: Date.
347. Drews-Elger K, Brinkman JA, Miller P, et al. Primary breast tumor-derived cellular models: characterization of tumorigenic, metastatic, and cancer-associated fibroblasts in dissociated tumor (DT) cultures. *Breast Cancer Research & Treatment*. 2014;144(3):503-517. Exclude: No outcome of interest.
348. Dreyfus C, Ballester M, Gligorov J, et al. [Impact of the 21-gene assay in decision-making during multidisciplinary breast meeting: A French experience]. *Gynecologie, Obstetrique & Fertilité*. 2015;43(12):780-785. Exclude: Not English.

349. Drukker CA, Bueno-de-Mesquita JM, Retel VP, et al. A prospective evaluation of a breast cancer prognosis signature in the observational RASTER study. *International Journal of Cancer*. 2013;133(4):929-936. Exclude: In included systematic review.
350. Drukker CA, Elias SG, Nijenhuis MV, et al. Gene expression profiling to predict the risk of locoregional recurrence in breast cancer: a pooled analysis.[Erratum appears in Breast Cancer Res Treat. 2015 Jan;149(2):567]. *Breast Cancer Research & Treatment*. 2014;148(3):599-613. Exclude: No outcome of interest.
351. Drukker CA, Nijenhuis MV, Bueno-de-Mesquita JM, et al. Optimized outcome prediction in breast cancer by combining the 70-gene signature with clinical risk prediction algorithms. *Breast Cancer Research & Treatment*. 2014;145(3):697-705. Exclude: No outcome of interest.
352. Drukker CA, Schmidt MK, Rutgers EJ, et al. Mammographic screening detects low-risk tumor biology breast cancers. *Breast Cancer Research & Treatment*. 2014;144(1):103-111. Exclude: No outcome of interest.
353. Drukker CA, Schmidt MK, van Dalen T, van der Hoeven JJ, Linn SC, Rutgers EJ. [Gene expression classifiers in the prognosis of breast cancer]. *Nederlands Tijdschrift voor Geneeskunde*. 2014;158:A7001. Exclude: No outcome of interest.
354. Drukker CA, van den Hout HC, Sonke GS, et al. Risk estimations and treatment decisions in early stage breast cancer: agreement among oncologists and the impact of the 70-gene signature. *Eur J Cancer*. 2014;50(6):1045-1054. Exclude: In included systematic review.
355. Drukker CA, van Tinteren H, Schmidt MK, et al. Long-term impact of the 70-gene signature on breast cancer outcome. *Breast Cancer Res Treat*. 2014;143(3):587-592. Exclude: No outcome of interest.
356. Drury S, Salter J, Baehner FL, Shak S, Dowsett M. Feasibility of using tissue microarray cores of paraffin-embedded breast cancer tissue for measurement of gene expression: a proof-of-concept study. *Journal of Clinical Pathology*. 2010;63(6):513-517. Exclude: No outcome of interest.
357. Du CZ, Li HP, Hou KY, Li Q, Zhao HM, Wang MP. [Expression of epidermal growth factor receptor-2 in Chinese breast cancer patients: a meta-analysis]. *Beijing da Xue Xue Bao Yi Xue Ban/Journal of Peking University Health Sciences*. 2006;38(2):184-188. Exclude: Date.
358. Du J, Yang S, An D, et al. BMP-6 inhibits microRNA-21 expression in breast cancer through repressing deltaEF1 and AP-1. *Cell Research*. 2009;19(4):487-496. Exclude: Not intervention of interest.
359. Dubsy P, Brase JC, Jakesz R, et al. The EndoPredict score provides prognostic information on late distant metastases in ER+/HER2- breast cancer patients. *British Journal of Cancer*. 2013;109(12):2959-2964. Exclude: No outcome of interest.
360. Dubsy P, Filipits M, Jakesz R, et al. EndoPredict improves the prognostic classification derived from common clinical guidelines in ER-positive, HER2-negative early breast cancer. *Annals of Oncology*. 2013;24(3):640-647. Exclude: No outcome of interest.
361. Duchnowska R, Jarzab M, Zebracka-Gala J, et al. Brain Metastasis Prediction by Transcriptomic Profiling in Triple-Negative Breast Cancer. *Clinical Breast Cancer*. 2017;17(2):e65-e75. Exclude: Not intervention of interest.
362. Duchnowska R, Jassem J, Goswami CP, et al. Predicting early brain metastases based on clinicopathological factors and gene expression analysis in advanced HER2-positive breast cancer patients. *Journal of Neuro-Oncology*. 2015;122(1):205-216. Exclude: Not intervention of interest.

363. Duffy MJ, Harbeck N, Nap M, et al. Clinical use of biomarkers in breast cancer: Updated guidelines from the European Group on Tumor Markers (EGTM). *European Journal of Cancer*. 2017;75:284-298. Exclude: Publication type-not systematic review.
364. Duffy MJ, O'Donovan N, McDermott E, Crown J. Validated biomarkers: The key to precision treatment in patients with breast cancer. *Breast*. 2016;29:192-201. Exclude: Publication type-commentary.
365. Duffy MJ, Walsh S, McDermott EW, Crown J. Biomarkers in Breast Cancer: Where Are We and Where Are We Going? *Advances in Clinical Chemistry*. 2015;71:1-23. Exclude: Publication type-commentary.
366. Dumeaux V, Ursini-Siegel J, Flatberg A, et al. Peripheral blood cells inform on the presence of breast cancer: a population-based case-control study. *International Journal of Cancer*. 2015;136(3):656-667. Exclude: Not intervention of interest.
367. Dun MD, Chalkley RJ, Faulkner S, et al. Proteotranscriptomic Profiling of 231-BR Breast Cancer Cells: Identification of Potential Biomarkers and Therapeutic Targets for Brain Metastasis. *Molecular & Cellular Proteomics*. 2015;14(9):2316-2330. Exclude: Not intervention of interest.
368. Dunbier AK, Anderson H, Ghazoui Z, et al. Association between breast cancer subtypes and response to neoadjuvant anastrozole. *Steroids*. 2011;76(8):736-740. Exclude: Not intervention of interest.
369. Dunn J, Marshall A, Campbell A, et al. Using adaptive designs for decision making within the optimal trial: Optimal personalized treatment of early breast cancer using multi-parameter tests. *Trials*. 2013;14(18). Exclude: No outcome of interest.
370. Dunn L, Demichele A. Genomic predictors of outcome and treatment response in breast cancer. *Molecular Diagnosis & Therapy*. 2009;13(2):73-90. Exclude: No outcome of interest.
371. Dvinge H, Git A, Graf S, et al. The shaping and functional consequences of the microRNA landscape in breast cancer. *Nature*. 2013;497(7449):378-382. Exclude: Not intervention of interest.
372. Dvorak L, Dolan M, Fink J, Varghese L, Henriksen J, Gulbahce HE. Correlation between HER2 determined by fluorescence in situ hybridization and reverse transcription-polymerase chain reaction of the oncotype DX test. *Applied Immunohistochemistry & Molecular Morphology*. 2013;21(3):196-199. Exclude: No outcome of interest.
373. Dzimitrowicz H, Mougalian S, Storms S, et al. Impacts of early guideline-directed 21-gene recurrence score testing on adjuvant therapy decision making. *Journal of Oncology Practice*. 2017;Jop2017022731. Exclude: No outcome of interest.
374. Ebbert MT, Bastien RR, Boucher KM, et al. Characterization of uncertainty in the classification of multivariate assays: application to PAM50 centroid-based genomic predictors for breast cancer treatment plans. *Journal of Clinical Bioinformatics*. 2011;1:37. Exclude: No outcome of interest.
375. Eden P, Ritz C, Rose C, Ferno M, Peterson C. "Good Old" clinical markers have similar power in breast cancer prognosis as microarray gene expression profilers. *European Journal of Cancer*. 2004;40(12):1837-1841. Exclude: Date.
376. Eiermann W, Rezai M, Kummel S, et al. The 21-gene recurrence score assay impacts adjuvant therapy recommendations for ER-positive, node-negative and node-positive early breast cancer resulting in a risk-adapted change in chemotherapy use. *Ann Oncol*. 2013;24(3):618-624. Exclude: In included systematic review.
377. Ein-Dor L, Kela I, Getz G, Givol D, Domany E. Outcome signature genes in breast cancer: is there a unique set? *Bioinformatics*. 2005;21(2):171-178. Exclude: Date.

378. Elias D, Vever H, Laenkholm AV, et al. Gene expression profiling identifies FYN as an important molecule in tamoxifen resistance and a predictor of early recurrence in patients treated with endocrine therapy. *Oncogene*. 2015;34(15):1919-1927. Exclude: Not intervention of interest.
379. Ellis MJ, Chen B, Chapman JA, et al. CADER prognostic gene signature for disease free survival in hormone receptor positive breast cancer: NCIC CTG MA.12 phase III placebo-controlled tamoxifen trial. *Cancer research*. 2015;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
380. Ellis MJ, Suman VJ, Hoog J, et al. Ki67 Proliferation Index as a Tool for Chemotherapy Decisions During and After Neoadjuvant Aromatase Inhibitor Treatment of Breast Cancer: Results From the American College of Surgeons Oncology Group Z1031 Trial (Alliance). *Journal of Clinical Oncology*. 2017;35(10):1061-1069. Exclude: Not intervention of interest.
381. Ellis MJ, Suman VJ, Hoog J, et al. Randomized phase II neoadjuvant comparison between letrozole, anastrozole, and exemestane for postmenopausal women with estrogen receptor-rich stage 2 to 3 breast cancer: clinical and biomarker outcomes and predictive value of the baseline PAM50-based intrinsic subtype--ACOSOG Z1031. *Journal of Clinical Oncology*. 2011;29(17):2342-2349. Exclude: No outcome of interest.
382. Ellis PG, Brufsky AM, Beriwal S, et al. Pathways Clinical Decision Support for Appropriate Use of Key Biomarkers. *Journal of oncology practice/American Society of Clinical Oncology*. 2016;12(6):e681-687. Exclude: No outcome of interest.
383. Elloumi F, Hu Z, Li Y, et al. Systematic bias in genomic classification due to contaminating non-neoplastic tissue in breast tumor samples. *BMC Medical Genomics [Electronic Resource]*. 2011;4:54. Exclude: No outcome of interest.
384. Ellsworth RE, Lovejoy L, Costantino N, Sheiver CD. Relationship between obesity and breast tumor pathology in a contemporary set of patients. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
385. Elsayegh N, Gutierrez Barrera AM, Kuerer HM, Hernandez ND, Litton JK, Arun BK. CPM rate among individuals with breast cancer who underwent multiplex gene testing for hereditary cancer: single institution experience. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
386. Emmadi R, Canestrari E, Arbieva ZH, et al. Correlative Analysis of miRNA Expression and Oncotype Dx Recurrence Score in Estrogen Receptor Positive Breast Carcinomas. *PLoS ONE [Electronic Resource]*. 2015;10(12):e0145346. Exclude: No outcome of interest.
387. Endesfelder D, McGranahan N, Birkbak NJ, et al. A breast cancer meta-analysis of two expression measures of chromosomal instability reveals a relationship with younger age at diagnosis and high risk histopathological variables. *Oncotarget*. 2011;2(7):529-537. Exclude: Not intervention of interest.
388. Endo Y, Dong Y, Kondo N, et al. Exome sequencing of human breast cancer tissues resistant to taxanes. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
389. Enewold L, Geiger AM, Zujewski J, Harlan LC. Oncotype Dx assay and breast cancer in the United States: usage and concordance with chemotherapy. *Breast Cancer Research & Treatment*. 2015;151(1):149-156. Exclude: No outcome of interest.

390. Engebraaten O, Silwal-Pandit L, Krohn M, et al. Molecular response in breast cancer treated with neoadjuvant chemotherapy with and without bevacizumab: Results from NeoAva - a randomized phase II study. *Cancer research*. 2013;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
391. Eng-Wong J, Isaacs C. Prediction of benefit from adjuvant treatment in patients with breast cancer. *Clinical Breast Cancer*. 2010;10 Suppl 1:E32-37. Exclude: No outcome of interest.
392. Eng-Wong J, Zujewski JA. Current NCI-sponsored Cooperative Group trials of endocrine therapies in breast cancer. *Cancer*. 2008;112(3 Suppl):723-729. Exclude: Not intervention of interest.
393. Epstein AJ, Wong YN, Mitra N, et al. Adjuvant chemotherapy use and health care costs after introduction of genomic testing in breast cancer. *J Clin Oncol*. 2015;33(36):4259-4267. Exclude: In included systematic review.
394. Eric-Nikolic A, Matic IZ, Dordevic M, et al. Serum DPPIV activity and CD26 expression on lymphocytes in patients with benign or malignant breast tumors. *Immunobiology*. 2011;216(8):942-946. Exclude: Not intervention of interest.
395. Eroles P, Bosch A, Perez-Fidalgo JA, Lluch A. Molecular biology in breast cancer: intrinsic subtypes and signaling pathways. *Cancer Treatment Reviews*. 2012;38(6):698-707. Exclude: No outcome of interest.
396. Esmaeili R, Majidzadeh AK, Farahmand L, Ghasemi M, Salehi M, Khoshdel AR. AKAP3 correlates with triple negative status and disease free survival in breast cancer. *BMC Cancer*. 2015;15:681. Exclude: Not intervention of interest.
397. Espinel CF, Keating S, Hibshoosh H, et al. MammaPrint Feasibility in a Large Tertiary Urban Medical Center: An Initial Experience. *Scientifica*. 2012;2012:942507. Exclude: No outcome of interest.
398. Espinosa E, Cejas P, Redondo A, et al. Phospholipid hydroperoxide glutathione peroxidase overexpression is associated with a poor overall survival in human breast cancer. *Journal of Clinical Oncology*. 2005;23(16_suppl):635. Exclude: Date.
399. Espinosa E, Gamez-Pozo A, Sanchez-Navarro I, et al. The present and future of gene profiling in breast cancer. *Cancer & Metastasis Reviews*. 2012;31(1-2):41-46. Exclude: Publication type-commentary.
400. Espinosa E, Sanchez-Navarro I, Gamez-Pozo A, et al. Comparison of prognostic gene profiles using qRT-PCR in paraffin samples: a retrospective study in patients with early breast cancer. *PLoS ONE [Electronic Resource]*. 2009;4(6):e5911. Exclude: No outcome of interest.
401. Espinosa E, Vara JA, Redondo A, et al. Breast cancer prognosis determined by gene expression profiling: a quantitative reverse transcriptase polymerase chain reaction study. *Journal of Clinical Oncology*. 2005;23(29):7278-7285. Exclude: Date.
402. Esserman LJ, Berry DA, Cheang MC, et al. Chemotherapy response and recurrence-free survival in neoadjuvant breast cancer depends on biomarker profiles: results from the I-SPY 1 TRIAL (CALGB 150007/150012; ACRIN 6657). *Breast Cancer Research & Treatment*. 2012;132(3):1049-1062. Exclude: No outcome of interest.
403. Esserman LJ, Berry DA, DeMichele A, et al. Pathologic complete response predicts recurrence-free survival more effectively by cancer subset: results from the I-SPY 1 TRIAL--CALGB 150007/150012, ACRIN 6657. *Journal of Clinical Oncology*. 2012;30(26):3242-3249. Exclude: Not intervention of interest.
404. Esserman LJ, Shieh Y, Rutgers EJ, et al. Impact of mammographic screening on the detection of good and poor prognosis breast cancers. *Breast Cancer Research & Treatment*. 2011;130(3):725-734. Exclude: Publication type-commentary.

405. Esserman LJ, Yau C, Thompson CK, et al. Identification of breast cancers with an indolent disease course: 70 gene indolent threshold validation in a Swedish randomized trial of tamoxifen vs. not, with 20 year outcomes. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
406. Esteva FJ, Sahin AA, Cristofanilli M, et al. Prognostic role of a multigene reverse transcriptase-PCR assay in patients with node-negative breast cancer not receiving adjuvant systemic therapy. *Clinical Cancer Research*. 2005;11(9):3315-3319. Exclude: Date.
407. Ethier JL, Amir E. The Role of the 21-Gene Recurrence Score in Breast Cancer Treatment. *Molecular Diagnosis & Therapy*. 2016;20(4):307-313. Exclude: Publication type-commentary.
408. Ettl J, Klein E, Hapfelmeier A, et al. Decision impact and feasibility of different ASCO-recommended biomarkers in early breast cancer: Prospective comparison of molecular marker EndoPredict and protein marker uPA/PAI-1. *PLoS One*. 2017;12(9):e0183917. Exclude: Not appropriate comparator.
409. Euhus D, Bu D, Xie XJ, et al. Tamoxifen downregulates ets oncogene family members ETV4 and ETV5 in benign breast tissue: implications for durable risk reduction. *Cancer Prevention Research*. 2011;4(11):1852-1862. Exclude: Not intervention of interest.
410. Evaluation of Genomic Applications in P, Prevention Working G. Recommendations from the EGAPP Working Group: can tumor gene expression profiling improve outcomes in patients with breast cancer? *Genetics in Medicine*. 2009;11(1):66-73. Exclude: Publication type-not systematic review.
411. Exner R, Bago-Horvath Z, Bartsch R, et al. The multigene signature MammaPrint impacts on multidisciplinary team decisions in ER+, HER2- early breast cancer. *Br J Cancer*. 2014;111(5):837-842. Exclude: In included systematic review.
412. Facheris P, Perrone F, Menard S, et al. Study of the biological and prognostic significance of the antigen CaMBr8 on breast carcinoma. *British Journal of Cancer*. 1992;65(3):466-470. Exclude: Date.
413. Faggioli F, Soldati S, Scanziani E, et al. Effects of IL-12 gene therapy on spontaneous transgenic and transplanted breast tumors. *Breast Cancer Research & Treatment*. 2008;110(2):223-226. Exclude: Not intervention of interest.
414. Falato C, Tobin NP, Lorent J, Lindstrom LS, Bergh J, Foukakis T. Intrinsic subtypes and genomic signatures of primary breast cancer and prognosis after systemic relapse. *Molecular Oncology*. 2016;10(4):517-525. Exclude: No outcome of interest.
415. Fan C, Oh DS, Wessels L, et al. Concordance among gene-expression-based predictors for breast cancer. *New England Journal of Medicine*. 2006;355(6):560-569. Exclude: Date.
416. Fan C, Prat A, Parker JS, et al. Building prognostic models for breast cancer patients using clinical variables and hundreds of gene expression signatures. *BMC Medical Genomics [Electronic Resource]*. 2011;4:3. Exclude: Not intervention of interest.
417. Faneca H, Cabrita AS, Simoes S, Pedroso de Lima MC. Evaluation of the antitumoral effect mediated by IL-12 and HSV-tk genes when delivered by a novel lipid-based system. *Biochimica et Biophysica Acta*. 2007;1768(5):1093-1102. Exclude: Not intervention of interest.
418. Farrugia DJ, Landmann A, Zhu L, et al. Magee Equation 3 predicts pathologic response to neoadjuvant systemic chemotherapy in estrogen receptor positive, HER2 negative/equivocal breast tumors. *Modern Pathology*. 2017;30(8):1078-1085. Exclude: Not intervention of interest.
419. Fazilaty H, Mehdi-pour P. Genetics of breast cancer bone metastasis: a sequential multistep pattern. *Clinical & Experimental Metastasis*. 2014;31(5):595-612. Exclude: Not intervention of interest.

420. Felts JL, Zhu J, Han B, Smith SJ, Truica CI. An Analysis of Oncotype DX Recurrence Scores and Clinicopathologic Characteristics in Invasive Lobular Breast Cancer. *Breast Journal*. 2017;23(6):677-686. Exclude: No outcome of interest.
421. Feng X, Li H, Dean M, et al. Low ATM protein expression in malignant tumor as well as cancer-associated stroma are independent prognostic factors in a retrospective study of early-stage hormone-negative breast cancer. *Breast Cancer Research*. 2015;17:65. Exclude: Not intervention of interest.
422. Feng Y, Li X, Sun B, et al. Evidence for a transcriptional signature of breast cancer. *Breast Cancer Research & Treatment*. 2010;122(1):65-75. Exclude: Not intervention of interest.
423. Feng YM, Li XQ, Sun BC, et al. [Prognostic molecular classification of breast cancers based on gene expression profiling]. *Chung-Hua Chung Liu Tsa Chih [Chinese Journal of Oncology]*. 2006;28(12):900-906. Exclude: Date.
424. Fernandez-Martinez A, Pascual T, Perrone G, et al. Limitations in predicting PAM50 intrinsic subtype and risk of relapse score with Ki67 in estrogen receptor-positive HER2-negative breast cancer. *Oncotarget*. 2017;8(13):21930-21937. Exclude: No outcome of interest.
425. Ferrucci PF, Rabascio C, Gigli F, et al. A new comprehensive gene expression panel to study tumor micrometastasis in patients with high-risk breast cancer. *International Journal of Oncology*. 2007;30(4):955-962. Exclude: Not intervention of interest.
426. Feugeas JP, Belmiloudi S, Boyer-Guittaut M, Peixoto P, Hervouet E. Relationships between breast cancer subtypes and expression of autophagy related genes. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
427. Fiets WE, Nortier JW. A multigene RT-PCR assay used to predict recurrence in early breast cancer: two presentations with contradictory results. *Breast Cancer Research*. 2004;6(5):185-187. Exclude: Date.
428. Figueroa JD, Yang H, Garcia-Closas M, et al. Integrated analysis of DNA methylation, immunohistochemistry and mRNA expression, data identifies a methylation expression index (MEI) robustly associated with survival of ER-positive breast cancer patients. *Breast Cancer Research & Treatment*. 2015;150(2):457-466. Exclude: Not intervention of interest.
429. Filipits M, Nielsen TO, Rudas M, et al. The PAM50 risk-of-recurrence score predicts risk for late distant recurrence after endocrine therapy in postmenopausal women with endocrine-responsive early breast cancer. *Clinical Cancer Research*. 2014;20(5):1298-1305. Exclude: No outcome of interest.
430. Filipits M, Rudas M, Jakesz R, et al. A new molecular predictor of distant recurrence in ER-positive, HER2-negative breast cancer adds independent information to conventional clinical risk factors. *Clinical Cancer Research*. 2011;17(18):6012-6020. Exclude: No outcome of interest.
431. Finak G, Bertos N, Pepin F, et al. Stromal gene expression predicts clinical outcome in breast cancer. *Nature Medicine*. 2008;14(5):518-527. Exclude: Not intervention of interest.
432. Finetti P, Guille A, Adelaide J, Birnbaum D, Chaffanet M, Bertucci F. ESPL1 is a candidate oncogene of luminal B breast cancers. *Breast Cancer Research & Treatment*. 2014;147(1):51-59. Exclude: Not intervention of interest.
433. Fischer L, Arnold M, Kirsch F, Leidl R. [Cost-Effectiveness of the 21 Gene Assay in Patients with Node-Positive Breast Cancer]. *Gesundheitswesen*. 2016;78(11):772-780. Exclude: Not English.
434. Fitzal F, Filipits M, Rudas M, et al. The genomic expression test EndoPredict is a prognostic tool for identifying risk of local recurrence in postmenopausal endocrine receptor-positive, her2neu-negative

breast cancer patients randomised within the prospective ABCSG 8 trial. *British Journal of Cancer*. 2015;112(8):1405-1410. Exclude: No outcome of interest.

435. Fitzal F, Filipits MF, Rudas M, et al. Tailoring local therapy in post-menopausal endocrine responsive HER2neu negative breast cancer patients based on their genetic risk profile using Endopredict. *European journal of cancer*. 2014;50(19). Exclude: No outcome of interest.

436. Flanagan MB, Dabbs DJ, Brufsky AM, Beriwal S, Bhargava R. Histopathologic variables predict Oncotype DX recurrence score. *Modern Pathology*. 2008;21(10):1255-1261. Exclude: No outcome of interest.

437. Fleischer T, Edvardsen H, Solvang HK, et al. Integrated analysis of high-resolution DNA methylation profiles, gene expression, germline genotypes and clinical end points in breast cancer patients. *International Journal of Cancer*. 2014;134(11):2615-2625. Exclude: No outcome of interest.

438. Folgueira MA, Brentani H, Katayama ML, et al. Gene expression profiling of clinical stages II and III breast cancer. *Brazilian Journal of Medical & Biological Research*. 2006;39(8):1101-1113. Exclude: Date.

439. Folgueira MA, Carraro DM, Brentani H, et al. Gene expression profile associated with response to doxorubicin-based therapy in breast cancer. *Clinical Cancer Research*. 2005;11(20):7434-7443. Exclude: Date.

440. Forero A, Yee D, Buxton MB, et al. Efficacy of Hsp90 inhibitor ganetespib plus standard neoadjuvant therapy in high-risk breast cancer: results from the I-SPY 2 trial. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

441. Foukakis T, Falato C, Bergh J. A 21-Gene Expression Assay in Breast Cancer. *New England Journal of Medicine*. 2016;374(14):1386-1387. Exclude: Publication type-letter.

442. Foukakis T, Lovrot J, Sandqvist P, et al. Gene expression profiling of sequential metastatic biopsies for biomarker discovery in breast cancer. *Molecular Oncology*. 2015;9(7):1384-1391. Exclude: No outcome of interest.

443. Fox BP, Kandpal RP. Invasiveness of breast carcinoma cells and transcript profile: Eph receptors and ephrin ligands as molecular markers of potential diagnostic and prognostic application. *Biochemical & Biophysical Research Communications*. 2004;318(4):882-892. Exclude: Date.

444. Frazier TG, Fox KR, Smith JS, et al. A retrospective study of the impact of 21-gene recurrence score assay on treatment choice in node positive micrometastatic breast cancer. *Pharmaceuticals (Basel, Switzerland)*. 2015;8(1):107-122. Exclude: No comparator.

445. Freitas MR, Simon SD. Comparison between Oncotype DX test and standard prognostic criteria in estrogen receptor positive early-stage breast cancer. *Einstein*. 2011;9(3):354-358. Exclude: No outcome of interest.

446. Freres P, Wenric S, Boukerroucha M, et al. Circulating microRNA-based screening tool for breast cancer. *Oncotarget*. 2016;7(5):5416-5428. Exclude: Not intervention of interest.

447. Fresno C, Gonzalez GA, Merino GA, et al. A novel non-parametric method for uncertainty evaluation of correlation-based molecular signatures: its application on PAM50 algorithm. *Bioinformatics*. 2017;33(5):693-700. Exclude: No outcome of interest.

448. Fried G, Moskovitz M. Treatment decisions in estrogen receptor-positive early breast cancer patients with intermediate oncotype DX recurrence score results. *Springerplus*. 2014;3:71. Exclude: In included systematic review.

449. Fritz P, Cabrera CM, Dippon J, et al. c-erbB2 and topoisomerase IIalpha protein expression independently predict poor survival in primary human breast cancer: a retrospective study. *Breast Cancer Research*. 2005;7(3):R374-384. Exclude: Date.
450. Fu WJ, Carroll RJ, Wang S. Estimating misclassification error with small samples via bootstrap cross-validation. *Bioinformatics*. 2005;21(9):1979-1986. Exclude: Date.
451. Fuentes-Mattei E, Velazquez-Torres G, Phan L, et al. Effects of obesity on transcriptomic changes and cancer hallmarks in estrogen receptor-positive breast cancer. *Journal of the National Cancer Institute*. 2014;106(7). Exclude: Not intervention of interest.
452. Gabos Z, Sinha R, Hanson J, et al. Prognostic significance of human epidermal growth factor receptor positivity for the development of brain metastasis after newly diagnosed breast cancer. *Journal of Clinical Oncology*. 2006;24(36):5658-5663. Exclude: Date.
453. Gage MM, Rosman M, Mylander WC, et al. A Validated Model for Identifying Patients Unlikely to Benefit From the 21-Gene Recurrence Score Assay. *Clinical Breast Cancer*. 2015;15(6):467-472. Exclude: No outcome of interest.
454. Galanina N, Bossuyt V, Harris LN. Molecular predictors of response to therapy for breast cancer. *Cancer Journal*. 2011;17(2):96-103. Exclude: No outcome of interest.
455. Galatenko VV, Lebedev AE, Nechaev IN, Shkurnikov MY, Tonevitskii EA, Podol'skii VE. On the construction of medical test systems using greedy algorithm and support vector machine. *Bulletin of Experimental Biology & Medicine*. 2014;156(5):706-709. Exclude: Not intervention of interest.
456. Gamez-Pozo A, Perez Carrion RM, Manso L, et al. The Long-HER study: clinical and molecular analysis of patients with HER2+ advanced breast cancer who become long-term survivors with trastuzumab-based therapy. *PLoS ONE [Electronic Resource]*. 2014;9(10):e109611. Exclude: Not intervention of interest.
457. Gamez-Pozo A, Trilla-Fuertes L, Berges-Soria J, et al. Functional proteomics outlines the complexity of breast cancer molecular subtypes. *Scientific Reports*. 2017;7(1):10100. Exclude: Not intervention of interest.
458. Gangi A, Topham A, Lee MC, Sun W, Laronga C. Genomic Assays in Ductal Carcinoma In Situ: Implications for Management Decisions. *Southern Medical Journal*. 2017;110(10):649-653. Exclude: No outcome of interest.
459. Garattini E, Bolis M, Gianni M, Paroni G, Fratelli M, Terao M. Lipid-sensors, enigmatic-orphan and orphan nuclear receptors as therapeutic targets in breast-cancer. *Oncotarget*. 2016;7(27):42661-42682. Exclude: Not intervention of interest.
460. Gasparini G, Gullick WJ, Bevilacqua P, et al. Human breast cancer: prognostic significance of the c-erbB-2 oncoprotein compared with epidermal growth factor receptor, DNA ploidy, and conventional pathologic features. *Journal of Clinical Oncology*. 1992;10(5):686-695. Exclude: Date.
461. Gavila J, Saura C, Oliveira M, et al. CORALLEEN: a phase 2 clinical trial of chemotherapy or letrozole plus ribociclib as neoadjuvant treatment for postmenopausal patients with luminal B/HER2-negative breast cancer. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
462. Gayyed MF, El-Maqsoud NM, Tawfik ER, El Gelany SA, Rahman MF. A comprehensive analysis of CDC20 overexpression in common malignant tumors from multiple organs: its correlation with tumor grade and stage. *Tumour Biology*. 2016;37(1):749-762. Exclude: Not intervention of interest.

463. Gazinska P, Grigoriadis A, Brown JP, et al. Comparison of basal-like triple-negative breast cancer defined by morphology, immunohistochemistry and transcriptional profiles. *Modern Pathology*. 2013;26(7):955-966. Exclude: No outcome of interest.
464. Gee HE, Buffa FM, Harris AL, et al. MicroRNA-Related DNA Repair/Cell-Cycle Genes Independently Associated With Relapse After Radiation Therapy for Early Breast Cancer. *International Journal of Radiation Oncology, Biology, Physics*. 2015;93(5):1104-1114. Exclude: Not intervention of interest.
465. Geffen DB, Abu-Ghanem S, Sion-Vardy N, et al. The impact of the 21-gene recurrence score assay on decision making about adjuvant chemotherapy in early-stage estrogen-receptor-positive breast cancer in an oncology practice with a unified treatment policy. *Ann Oncol*. 2011;22(11):2381-2386. Exclude: In included systematic review.
466. Geffen DB, Amir N, Sion-Vardy N, et al. Stage I breast cancer in a regional oncology practice in Israel 2002-2006: clinicopathologic features, risk estimation and planned therapy of 328 consecutive patients. *Breast*. 2009;18(5):316-321. Exclude: In included systematic review.
467. Geisler S, Lonning PE, Aas T, et al. Influence of TP53 gene alterations and c-erbB-2 expression on the response to treatment with doxorubicin in locally advanced breast cancer. *Cancer Research*. 2001;61(6):2505-2512. Exclude: Date.
468. Geradts J, Bean SM, Bentley RC, Barry WT. The oncotype DX recurrence score is correlated with a composite index including routinely reported pathobiologic features. *Cancer Investigation*. 2010;28(9):969-977. Exclude: No outcome of interest.
469. Gerson Cwilich R, Alban de la Torre LF, Villalobos Prieto A, Serrano Olvera JA. [Clinicopathological features, prognosis and influence in the adjuvant treatment of the risk recurrence groups determined by the 21 gene expression profile, Oncotype Dx, in early breast cancer]. *Gaceta Medica de Mexico*. 2012;148(2):117-124. Exclude: Not English.
470. Gertz J, Reddy TE, Varley KE, Garabedian MJ, Myers RM. Genistein and bisphenol A exposure cause estrogen receptor 1 to bind thousands of sites in a cell type-specific manner. *Genome Research*. 2012;22(11):2153-2162. Exclude: Not intervention of interest.
471. Geutjes EJ, Tian S, Roepman P, Bernardis R. Deoxycytidine kinase is overexpressed in poor outcome breast cancer and determines responsiveness to nucleoside analogs. *Breast Cancer Research & Treatment*. 2012;131(3):809-818. Exclude: Not intervention of interest.
472. Gevensleben H, Gohring UJ, Buttner R, et al. Comparison of MammaPrint and TargetPrint results with clinical parameters in German patients with early stage breast cancer. *International Journal of Molecular Medicine*. 2010;26(6):837-843. Exclude: In included systematic review.
473. Gianni L, Zambetti M, Clark K, et al. Gene expression profiles in paraffin-embedded core biopsy tissue predict response to chemotherapy in women with locally advanced breast cancer. *Journal of Clinical Oncology*. 2005;23(29):7265-7277. Exclude: Date.
474. Gilcrease MZ. Body Mass Index, PAM50 Subtype, and Outcomes in Node-Positive Breast Cancer: CALGB 9741 (Alliance) Ligibel JA, Cirrincione CT, Liu M, et al (Dana-Farber Cancer Inst, Boston, MA; Alliance Statistics and Data Ctr, Durham, NC; Mayo Clinic, Rochester, MN; Et al) *J Natl Cancer Inst* 107:djv179, 2015. *Breast Diseases*. 2016;27(2):130-131. Exclude: No outcome of interest.
475. Gilcrease MZ, Kilpatrick SK, Woodward WA, et al. Coexpression of alpha6beta4 integrin and guanine nucleotide exchange factor Net1 identifies node-positive breast cancer patients at high risk for distant

metastasis. *Cancer Epidemiology, Biomarkers & Prevention*. 2009;18(1):80-86. Exclude: Not intervention of interest.

476. Gillesby BE, Zacharewski TR. pS2 (TFF1) levels in human breast cancer tumor samples: correlation with clinical and histological prognostic markers. *Breast Cancer Research & Treatment*. 1999;56(3):253-265. Exclude: Date.

477. Giordano SH, Lin YL, Kuo YF, Hortobagyi GN, Goodwin JS. Decline in the use of anthracyclines for breast cancer. *Journal of Clinical Oncology*. 2012;30(18):2232-2239. Exclude: Not intervention of interest.

478. Giuliano AE, Connolly JL, Edge SB, et al. Breast Cancer-Major changes in the American Joint Committee on Cancer eighth edition cancer staging manual.[Erratum appears in CA Cancer J Clin. 2017 Jul 8;67(4):345; PMID: 28689371]. *CA: a Cancer Journal for Clinicians*. 2017;67(4):290-303. Exclude: No outcome of interest.

479. Glas AM, Floore A, Delahaye LJ, et al. Converting a breast cancer microarray signature into a high-throughput diagnostic test. *BMC Genomics*. 2006;7:278. Exclude: Date.

480. Gligorov J, Pivot XB, Jacot W, et al. Prospective clinical utility study of the use of the 21-gene assay in adjuvant clinical decision making in women with estrogen receptor-positive early invasive breast cancer: results from the SWITCH study. *Oncologist*. 2015;20(8):873-879. Exclude: In included systematic review.

481. Glinsky GV, Higashiyama T, Glinskii AB. Classification of human breast cancer using gene expression profiling as a component of the survival predictor algorithm. *Clinical Cancer Research*. 2004;10(7):2272-2283. Exclude: Date.

482. Gluck S, de Snoo F, Peeters J, Stork-Sloots L, Somlo G. Molecular subtyping of early-stage breast cancer identifies a group of patients who do not benefit from neoadjuvant chemotherapy. *Breast Cancer Research & Treatment*. 2013;139(3):759-767. Exclude: No outcome of interest.

483. Gluck S, Ross JS, Royce M, et al. TP53 genomics predict higher clinical and pathologic tumor response in operable early-stage breast cancer treated with docetaxel-capecitabine +/- trastuzumab. *Breast Cancer Research & Treatment*. 2012;132(3):781-791. Exclude: Not intervention of interest.

484. Gluck S, Yip AY, Ng EL. Can we replace the microscope with microarrays for diagnosis, prognosis and treatment of early breast cancer? *Expert Opinion on Therapeutic Targets*. 2012;16 Suppl 1:S17-22. Exclude: Publication type-commentary.

485. Gluz O, Hofmann D, Wurstlein R, Liedtke C, Nitz U, Harbeck N. Genomic profiling in luminal breast cancer. *Breast Care*. 2013;8(6):414-422. Exclude: No outcome of interest.

486. Gluz O, Kreipe H, Christgen M, et al. Abstract P3-10-12: Pilot Phase of the Randomized PlanB Trial: Prospective Comparison of Molecular Classification, Oncotype DX(R) and Clinical-Pathological Characteristics in Hormone-Receptor (HR) Positive Primary Breast Cancer. 2010. Exclude: No outcome of interest.

487. Gluz O, Liedtke C, Prat A, et al. Association of molecular subtype, proliferation, and immune genes with efficacy of carboplatin versus gemcitabine addition to taxane-based, anthracycline-free neoadjuvant chemotherapy in early triple-negative breast cancer (TNBC): results of the randomized WSG ADAPT-TN trial. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.

488. Gluz O, Nitz U, Kreipe HH, et al. Clinical impact of risk classification by central/local grade or luminal-like subtype vs. Oncotype DX: First prospective survival results from the WSG phase III planB trial. *European Journal of Cancer*. 2015;51(25). Exclude: No outcome of interest.

489. Gluz O, Nitz UA, Christgen M, et al. West German Study Group Phase III PlanB Trial: First prospective outcome data for the 21-gene recurrence score assay and concordance of prognostic markers by central and local pathology assessment. *Journal of Clinical Oncology*. 2016;34(20):2341-2349. Exclude: No outcome of interest.
490. Glynn RW, Miller N, Kerin MJ. 17q12-21 - the pursuit of targeted therapy in breast cancer. *Cancer Treatment Reviews*. 2010;36(3):224-229. Exclude: Not intervention of interest.
491. Gnant M, Filipits M, Greil R, et al. Predicting distant recurrence in receptor-positive breast cancer patients with limited clinicopathological risk: using the PAM50 Risk of Recurrence score in 1478 postmenopausal patients of the ABCSG-8 trial treated with adjuvant endocrine therapy alone. *Annals of Oncology*. 2014;25(2):339-345. Exclude: No outcome of interest.
492. Gnant M, Filipits M, Mlineritsch B, et al. Clinical validation of the PAM50 risk of recurrence (ROR) score for predicting residual risk of distant-recurrence (DR) after endocrine therapy in postmenopausal women with ER+ early breast cancer (EBC): An ABCSG study 54. *Cancer Research*. 2012;72(24 Supplement):Abstract no: P2-10-02. Exclude: No outcome of interest.
493. Gnant M, Sestak I, Filipits M, et al. Identifying clinically relevant prognostic subgroups of postmenopausal women with node-positive hormone receptor-positive early-stage breast cancer treated with endocrine therapy: a combined analysis of ABCSG-8 and ATAC using the PAM50 risk of recurrence score and intrinsic subtype. *Annals of Oncology*. 2015;26(8):1685-1691. Exclude: No outcome of interest.
494. Godoy P, Cadenas C, Hellwig B, et al. Interferon-inducible guanylate binding protein (GBP2) is associated with better prognosis in breast cancer and indicates an efficient T cell response. *Breast Cancer*. 2014;21(4):491-499. Exclude: Not intervention of interest.
495. Goeman JJ. L1 penalized estimation in the Cox proportional hazards model. *Biometrical Journal*. 2010;52(1):70-84. Exclude: Not intervention of interest.
496. Goetz MP, Suman VJ, Ingle JN, et al. A two-gene expression ratio of homeobox 13 and interleukin-17B receptor for prediction of recurrence and survival in women receiving adjuvant tamoxifen. *Clinical Cancer Research*. 2006;12(7 Pt 1):2080-2087. Exclude: Date.
497. Gohring UJ, Eustermann I, Becker M, Neuhaus W, Rein DT, Schondorf T. Lack of prognostic significance of nm23 expression in human primary breast cancer. *Oncology Reports*. 2002;9(6):1205-1208. Exclude: Date.
498. Gokmen-Polar Y, Badve S. Molecular profiling assays in breast cancer: are we ready for prime time? *Oncology (Williston Park)*. 2012;26(4):350-357, 361. Exclude: Publication type-commentary.
499. Gokmen-Polar Y, Badve S. Upregulation of HSF1 in estrogen receptor positive breast cancer. *Oncotarget*. 2016;7(51):84239-84245. Exclude: No outcome of interest.
500. Gokmen-Polar Y, Goswami CP, Toroni RA, et al. Gene Expression Analysis Reveals Distinct Pathways of Resistance to Bevacizumab in Xenograft Models of Human ER-Positive Breast Cancer. *Journal of Cancer*. 2014;5(8):633-645. Exclude: No outcome of interest.
501. Gokmen-Polar Y, Neelamraju Y, Goswami CP, et al. Expression levels of SF3B3 correlate with prognosis and endocrine resistance in estrogen receptor-positive breast cancer. *Modern Pathology*. 2015;28(5):677-685. Exclude: Not intervention of interest.
502. Gokmen-Polar Y, Vladislav IT, Neelamraju Y, Janga SC, Badve S. Prognostic impact of HOTAIR expression is restricted to ER-negative breast cancers. *Scientific Reports*. 2015;5:8765. Exclude: Not intervention of interest.

503. Goldstein L, Ravdin P, Gray R, et al. Prognostic utility of the 21-gene assay compared with Adjuvant! in hormone receptor (HR) positive operable breast cancer with 0-3 positive axillary nodes treated with adjuvant chemohormonal therapy (CHT): an analysis of intergroup trial E2197. 2007. Exclude: No outcome of interest.
504. Goldstein LJ, Gray R, Badve S, et al. Prognostic utility of the 21-gene assay in hormone receptor-positive operable breast cancer compared with classical clinicopathologic features.[Erratum appears in J Clin Oncol. 2009 Jul 20;27(21):3566]. *Journal of Clinical Oncology*. 2008;26(25):4063-4071. Exclude: No outcome of interest.
505. Goldvaser H, Gal O, Rizel S, et al. The association between smoking and breast cancer characteristics and outcome. *BMC Cancer*. 2017;17(1):624. Exclude: Not intervention of interest.
506. Goldvaser H, Rizel S, Hendler D, et al. The Association between Treatment for Metabolic Disorders and Breast Cancer Characteristics. *International Journal of Endocrinology Print*. 2016;2016:4658469. Exclude: No outcome of interest.
507. Goldvaser H, Rizel S, Hendler D, et al. The Association between Angiotensin Receptor Blocker Usage and Breast Cancer Characteristics. *Oncology*. 2016;91(4):217-223. Exclude: Not intervention of interest.
508. Golmohammadi R, Pejhan A. The prognostic value of the P53 protein and the Ki67 marker in breast cancer patients. *JPM - Journal of the Pakistan Medical Association*. 2012;62(9):871-875. Exclude: Not intervention of interest.
509. Goncalves A, Finetti P, Sabatier R, et al. Poly(ADP-ribose) polymerase-1 mRNA expression in human breast cancer: a meta-analysis. *Breast Cancer Research & Treatment*. 2011;127(1):273-281. Exclude: Not intervention of interest.
510. Goncalves R, Bose R. Using multigene tests to select treatment for early-stage breast cancer. *Journal of the National Comprehensive Cancer Network*. 2013;11(2):174-182; quiz 182. Exclude: Publication type-not systematic review.
511. Gong C, Tan W, Chen K, et al. Prognostic Value of a BCSC-associated MicroRNA Signature in Hormone Receptor-Positive HER2-Negative Breast Cancer. *EBioMedicine*. 2016;11:199-209. Exclude: Not intervention of interest.
512. Gonzalez MA, Tachibana KE, Chin SF, et al. Geminin predicts adverse clinical outcome in breast cancer by reflecting cell-cycle progression. *Journal of Pathology*. 2004;204(2):121-130. Exclude: Date.
513. Gonzalez-Angulo AM, Barlow WE, Gralow J, et al. SWOG S1007: A phase III, randomized clinical trial of standard adjuvant endocrine therapy with or without chemotherapy in patients with one to three positive nodes, hormone receptor (HR)-positive, and HER2-negative breast cancer with recurrence score (RS) of 25 or less. *Journal of clinical oncology*. 2011;29(15 SUPPL. 1):CONFERENCE START: 2011 Jun 2013 CONFERENCE END: 2011 Jun 2017. Exclude: Publication type-conference abstract.
514. Gonzalez-Angulo AM, Iwamoto T, Liu S, et al. Gene expression, molecular class changes, and pathway analysis after neoadjuvant systemic therapy for breast cancer. *Clinical Cancer Research*. 2012;18(4):1109-1119. Exclude: No outcome of interest.
515. Gori S, Inno A, Fiorio E, et al. The Promher Study: An Observational Italian Study on Adjuvant Therapy for HER2-Positive, pT1a-b pN0 Breast Cancer.[Erratum appears in PLoS One. 2015;10(9):e0139650; PMID: 26406908]. *PLoS ONE [Electronic Resource]*. 2015;10(9):e0136731. Exclude: Not intervention of interest.
516. Goswami T, Shah M, Isaacs C. Novel molecular prognostic markers in breast cancer. *Expert Opinion on Medical Diagnostics*. 2009;3(5):523-532. Exclude: Publication type-not systematic review.

517. Gradishar WJ, Hansen NM, Susnik B. Clinical roundtable monograph: a multidisciplinary approach to the use of oncotype DX in clinical practice. *Clinical Advances in Hematology & Oncology*. 2009;7(4):1-7. Exclude: Publication type-commentary.
518. Graeser MK, Engel C, Rhiem K, et al. Contralateral breast cancer risk in BRCA1 and BRCA2 mutation carriers. *Journal of Clinical Oncology*. 2009;27(35):5887-5892. Exclude: Not intervention of interest.
519. Grant KA, Apffelstaedt JP, Wright CA, et al. MammaPrint Pre-screen Algorithm (MPA) reduces chemotherapy in patients with early-stage breast cancer. *S Afr Med J*. 2013;103(8):522-526. Exclude: No outcome of interest.
520. Grant KA, Pienaar FM, Brundyn K, et al. Incorporating microarray assessment of HER2 status in clinical practice supports individualised therapy in early-stage breast cancer. *Breast*. 2015;24(2):137-142. Exclude: Not intervention of interest.
521. Gravier E, Pierron G, Vincent-Salomon A, et al. A prognostic DNA signature for T1T2 node-negative breast cancer patients. *Genes, Chromosomes & Cancer*. 2010;49(12):1125-1134. Exclude: Not intervention of interest.
522. Green AR, Caracappa D, Benhasouna AA, et al. Biological and clinical significance of PARP1 protein expression in breast cancer. *Breast Cancer Research & Treatment*. 2015;149(2):353-362. Exclude: Not intervention of interest.
523. Greenberg R, Barnea Y, Schneebaum S, Kashtan H, Kaplan O, Skornik Y. Detection of hepatocyte growth factor/scatter factor receptor (c-Met) and MUC1 from the axillary fluid drainage in patients after breast cancer surgery. *Israel Medical Association Journal: Imaj*. 2003;5(9):649-652. Exclude: Date.
524. Gregoire JM, Fleury L, Salazar-Cardozo C, et al. Identification of epigenetic factors regulating the mesenchyme to epithelium transition by RNA interference screening in breast cancer cells. *BMC Cancer*. 2016;16:700. Exclude: Not intervention of interest.
525. Grenader T, Plotkin Y, Geffen DB. The preoperative neutrophil/lymphocyte ratio does not correlate with the 21-gene recurrence score in estrogen receptor-positive breast cancer patients. *Oncology Research and Treatment*. 2015;38(1-2):24-27. Exclude: No outcome of interest.
526. Grenader T, Yerushalmi R, Tokar M, et al. The 21-gene recurrence score assay (Oncotype DXTM) in estrogen receptor-positive male breast cancer: experience in an Israeli cohort. *Oncology*. 2014;87(1):1-6. Exclude: No outcome of interest.
527. Groenendijk FH, Zwart W, Floore A, Akbari S, Bernards R. Estrogen receptor splice variants as a potential source of false-positive estrogen receptor status in breast cancer diagnostics. *Breast Cancer Research & Treatment*. 2013;140(3):475-484. Exclude: Not intervention of interest.
528. Group EoGAiPaPEW. Recommendations from the EGAPP Working Group: does the use of Oncotype DX tumor gene expression profiling to guide treatment decisions improve outcomes in patients with breast cancer? *Genet Med*. 2016;18(8):770-779. Exclude: Publication type-not systematic review.
529. Grunda JM, Steg AD, He Q, et al. Differential expression of breast cancer-associated genes between stage- and age-matched tumor specimens from African- and Caucasian-American Women diagnosed with breast cancer. *BMC Research Notes*. 2012;5:248. Exclude: Not intervention of interest.
530. Guarneri V, Dieci MV, Frassoldati A, et al. Prospective Biomarker Analysis of the Randomized CHER-LOB Study Evaluating the Dual Anti-HER2 Treatment With Trastuzumab and Lapatinib Plus Chemotherapy as Neoadjuvant Therapy for HER2-Positive Breast Cancer. *Oncologist*. 2015;20(9):1001-1010. Exclude: Not intervention of interest.

531. Guiu S, Michiels S, Andre F, et al. Molecular subclasses of breast cancer: how do we define them? The IMPAKT 2012 Working Group Statement. *Annals of Oncology*. 2012;23(12):2997-3006. Exclude: Publication type-not systematic review.
532. Gumireddy K, Li A, Kossenkova AV, et al. The mRNA-edited form of GABRA3 suppresses GABRA3-mediated Akt activation and breast cancer metastasis. *Nature communications*. 2016;7:10715. Exclude: Not intervention of interest.
533. Guth AA, Chun Kim J, Schwartz S, et al. The Relationship of Race, Oncotype DX, and Ki67 in a Population Highly Screened For Breast Cancer. *Breast J*. 2017;23(2):177-181. Exclude: No outcome of interest.
534. Guth AA, Fineberg S, Fei K, Franco R, Bickell N. Utilization of Oncotype DX to predict chemotherapy use in an inner-city population. *Journal of clinical oncology*. 2011;29(15 SUPPL. 1):CONFERENCE START: 2011 Jun 2013 CONFERENCE END: 2011 Jun 2017. Exclude: Publication type-conference abstract.
535. Guth AA, Fineberg S, Fei K, Franco R, Bickell NA. Utilization of Oncotype DX in an Inner City Population: Race or Place? *Int J Breast Cancer*. 2013;2013:653805. Exclude: No outcome of interest.
536. Gu-Trantien C, Loi S, Garaud S, et al. CD4+ follicular helper T cell infiltration predicts breast cancer survival. *Journal of Clinical Investigation*. 2013;123(7):2873-2892. Exclude: Not intervention of interest.
537. Gwin K, Pinto M, Tavassoli FA. Complementary value of the Ki-67 proliferation index to the oncotype DX recurrence score. *International Journal of Surgical Pathology*. 2009;17(4):303-310. Exclude: No outcome of interest.
538. Gyanchandani R, Lin Y, Lin HM, et al. Intratumor Heterogeneity Affects Gene Expression Profile Test Prognostic Risk Stratification in Early Breast Cancer. *Clinical Cancer Research*. 2016;22(21):5362-5369. Exclude: No outcome of interest.
539. Gyorffy B, Benke Z, Lanczky A, et al. RecurrenceOnline: an online analysis tool to determine breast cancer recurrence and hormone receptor status using microarray data. *Breast Cancer Research & Treatment*. 2012;132(3):1025-1034. Exclude: No outcome of interest.
540. Gyorffy B, Bottai G, Fleischer T, et al. Aberrant DNA methylation impacts gene expression and prognosis in breast cancer subtypes. *International Journal of Cancer*. 2016;138(1):87-97. Exclude: Not intervention of interest.
541. Gyorffy B, Hatzis C, Sanft T, Hofstadter E, Aktas B, Pusztai L. Multigene prognostic tests in breast cancer: past, present, future. *Breast Cancer Research*. 2015;17:11. Exclude: Publication type-commentary.
542. Gyorffy B, Karn T, Sztupinski Z, Weltz B, Muller V, Pusztai L. Dynamic classification using case-specific training cohorts outperforms static gene expression signatures in breast cancer. *International Journal of Cancer*. 2015;136(9):2091-2098. Exclude: No outcome of interest.
543. Gyorffy B, Lanczky A, Eklund AC, et al. An online survival analysis tool to rapidly assess the effect of 22,277 genes on breast cancer prognosis using microarray data of 1,809 patients. *Breast Cancer Research & Treatment*. 2010;123(3):725-731. Exclude: Not intervention of interest.
544. Gyorffy B, Schafer R. Meta-analysis of gene expression profiles related to relapse-free survival in 1,079 breast cancer patients. *Breast Cancer Research & Treatment*. 2009;118(3):433-441. Exclude: No outcome of interest.
545. Gyorffy B, Serra V, Jurchott K, et al. Prediction of doxorubicin sensitivity in breast tumors based on gene expression profiles of drug-resistant cell lines correlates with patient survival. *Oncogene*. 2005;24(51):7542-7551. Exclude: Date.

546. Haakensen VD, Nygaard V, Greger L, et al. Subtype-specific micro-RNA expression signatures in breast cancer progression. *International Journal of Cancer*. 2016;139(5):1117-1128. Exclude: Not intervention of interest.
547. Haakensen VD, Steinfeld I, Saldova R, et al. Serum N-glycan analysis in breast cancer patients--Relation to tumour biology and clinical outcome. *Molecular Oncology*. 2016;10(1):59-72. Exclude: Not intervention of interest.
548. Haas S, Gevensleben H, Rabstein S, et al. Expression of heregulin, phosphorylated HER-2, HER-3 and HER-4 in HER-2 negative breast cancers. *Oncology Reports*. 2009;21(2):299-304. Exclude: Not intervention of interest.
549. Habel LA, Quesenberry CP, Jacobs M, et al. Gene expression and breast cancer mortality in Northern California Kaiser Permanente Patients: A large population-based case control study. *Journal of Clinical Oncology*. 2005;23(16_suppl):603. Exclude: Date.
550. Habel LA, Sakoda LC, Achacoso N, et al. HOXB13:IL17BR and molecular grade index and risk of breast cancer death among patients with lymph node-negative invasive disease. *Breast Cancer Research*. 2013;15(2):R24. Exclude: Not intervention of interest.
551. Habel LA, Shak S, Jacobs MK, et al. A population-based study of tumor gene expression and risk of breast cancer death among lymph node-negative patients. *Breast Cancer Research*. 2006;8(3):R25. Exclude: Date.
552. Habermann JK, Doering J, Hautaniemi S, et al. The gene expression signature of genomic instability in breast cancer is an independent predictor of clinical outcome. *International Journal of Cancer*. 2009;124(7):1552-1564. Exclude: No outcome of interest.
553. Hachim IY, Shams A, Lebrun JJ, Ali S. A favorable role of prolactin in human breast cancer reveals novel pathway-based gene signatures indicative of tumor differentiation and favorable patient outcome. *Human Pathology*. 2016;53:142-152. Exclude: Not intervention of interest.
554. Hadi NI, Jamal Q. "OMIC" tumor markers for breast cancer: A review. *Pakistan Journal of Medical Sciences*. 2015;31(5):1256-1262. Exclude: Not intervention of interest.
555. Hafez MM, Hassan ZK, Zekri AR, et al. MicroRNAs and metastasis-related gene expression in Egyptian breast cancer patients. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2012;13(2):591-598. Exclude: Not intervention of interest.
556. Hagemann IS. Molecular Testing in Breast Cancer: A Guide to Current Practices. *Archives of Pathology & Laboratory Medicine*. 2016;140(8):815-824. Exclude: No outcome of interest.
557. Haibe-Kains B, Desmedt C, Loi S, et al. A three-gene model to robustly identify breast cancer molecular subtypes. *Journal of the National Cancer Institute*. 2012;104(4):311-325. Exclude: Not intervention of interest.
558. Haibe-Kains B, Desmedt C, Piette F, et al. Comparison of prognostic gene expression signatures for breast cancer. *BMC Genomics*. 2008;9:394. Exclude: No outcome of interest.
559. Haibe-Kains B, Desmedt C, Sotiriou C, Bontempi G. A comparative study of survival models for breast cancer prognostication based on microarray data: does a single gene beat them all? *Bioinformatics*. 2008;24(19):2200-2208. Exclude: No outcome of interest.
560. Hall P, McCabe C, Hulme C, et al. Efficient design of a phase III trial of competing tests for personalised cancer treatment in the absence of gold standard outcome data: Challenges and potential solutions. *Trials*. 2013;14(18). Exclude: No outcome of interest.

561. Hall P, Ploner A, Bjohle J, et al. Hormone-replacement therapy influences gene expression profiles and is associated with breast-cancer prognosis: a cohort study. *BMC Medicine*. 2006;4:16. Exclude: Date.
562. Hall P, Smith A, Hulme C, et al. The use of early decision modelling and value of information analysis in an adaptive trial design: results from the OPTIMA preliminary study. *Trials Conference: 3rd international clinical trials methodology conference United kingdom*. 2015;16(no pagination). Exclude: Publication type-conference abstract.
563. Hall PS, McCabe C, Stein RC, Cameron D. Economic evaluation of genomic test-directed chemotherapy for early-stage lymph node-positive breast cancer. *J Natl Cancer Inst*. 2012;104(1):56-66. Exclude: In included systematic review.
564. Hallett RM, Dvorkin-Gheva A, Bane A, Hassell JA. A gene signature for predicting outcome in patients with basal-like breast cancer. *Scientific Reports*. 2012;2:227. Exclude: Not intervention of interest.
565. Halpern N, Sonnenblick A, Uziely B, et al. Oncotype Dx recurrence score among BRCA1/2 germline mutation carriers with hormone receptors positive breast cancer. *International Journal of Cancer*. 2017;140(9):2145-2149. Exclude: No outcome of interest.
566. Han H, Cao FL, Wang BZ, Mu XR, Li GY, Wang XW. Expression of angiogenesis regulatory proteins and epithelial-mesenchymal transition factors in platelets of the breast cancer patients. *TheScientificWorldJournal*. 2014;2014:878209. Exclude: Not intervention of interest.
567. Han HS, Wilks S, Paplomata E, et al. Efficacy results of a phase 1/2 study of glucocorticoid receptor (GR) antagonist mifepristone (MIFE) in combination with eribulin in GR-positive triple-negative breast cancer (TNBC). *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
568. Han L, Ma P, Liu SM, Zhou X. Circulating long noncoding RNA GAS5 as a potential biomarker in breast cancer for assessing the surgical effects. *Tumour Biology*. 2016;37(5):6847-6854. Exclude: Not intervention of interest.
569. Han W, Jung EM, Cho J, et al. DNA copy number alterations and expression of relevant genes in triple-negative breast cancer. *Genes, Chromosomes & Cancer*. 2008;47(6):490-499. Exclude: Not intervention of interest.
570. Hanna MG, Bleiweiss IJ, Nayak A, Jaffer S. Correlation of Oncotype DX Recurrence Score with Histomorphology and Immunohistochemistry in over 500 Patients. *International Journal of Breast Cancer*. 2017;2017:1257078. Exclude: No outcome of interest.
571. Hanna W. Testing for HER2 status. *Oncology*. 2001;61 Suppl 2:22-30. Exclude: Date.
572. Hannafon BN, Trigos YD, Calloway CL, et al. Plasma exosome microRNAs are indicative of breast cancer. *Breast Cancer Research*. 2016;18(1):90. Exclude: Not intervention of interest.
573. Hannemann J, Oosterkamp HM, Bosch CA, et al. Changes in gene expression associated with response to neoadjuvant chemotherapy in breast cancer. *Journal of Clinical Oncology*. 2005;23(15):3331-3342. Exclude: Date.
574. Hannouf MB, Xie B, Brackstone M, Zaric GS. Cost-effectiveness of a 21-gene recurrence score assay versus Canadian clinical practice in women with early-stage estrogen- or progesterone-receptor-positive, axillary lymph-node negative breast cancer. *BMC Cancer*. 2012;12:447. Exclude: In included systematic review.
575. Hannouf MB, Xie B, Brackstone M, Zaric GS. Cost effectiveness of a 21-gene recurrence score assay versus Canadian clinical practice in post-menopausal women with early-stage estrogen or progesterone-

receptor-positive, axillary lymph-node positive breast cancer. *Pharmacoeconomics*. 2014;32(2):135-147. Exclude: In included systematic review.

576. Hanrahan EO, Valero V, Gonzalez-Angulo AM, Hortobagyi GN. Prognosis and management of patients with node-negative invasive breast carcinoma that is 1 cm or smaller in size (stage 1; T1a,bN0M0): a review of the literature. *Journal of Clinical Oncology*. 2006;24(13):2113-2122. Exclude: Date.

577. Hao C, Wang Z, Gu Y, Jiang WG, Cheng S. Prognostic Value of Osteopontin Splice Variant-c Expression in Breast Cancers: A Meta-Analysis. *BioMed Research International*. 2016;2016:7310694. Exclude: Not intervention of interest.

578. Harbeck N, Sotlar K, Wuerstlein R, Doisneau-Sixou S. Molecular and protein markers for clinical decision making in breast cancer: today and tomorrow. *Cancer Treat Rev*. 2014;40(3):434-444. Exclude: Publication type-not systematic review.

579. Harbeck N, Thomssen C. A new look at node-negative breast cancer. *Oncologist*. 2010;15 Suppl 5:29-38. Exclude: Publication type-commentary.

580. Harbeck N, Thomssen C. A new look at node-negative breast cancer. *Oncologist*. 2011;16 Suppl 1:51-60. Exclude: Publication type-commentary.

581. Harbeck N, Wuerstlein R. [Breast cancer. Individualized therapy concepts]. *Internist*. 2013;54(2):194-199. Exclude: Not English.

582. Harowicz MR, Robinson TJ, Dinan MA, et al. Algorithms for prediction of the Oncotype DX recurrence score using clinicopathologic data: a review and comparison using an independent dataset. *Breast Cancer Res Treat*. 2017;162(1):1-10. Exclude: No outcome of interest.

583. Harris LN, Ismaila N, McShane LM, et al. Use of biomarkers to guide decisions on adjuvant systemic therapy for women with early-stage invasive breast cancer: American Society of Clinical Oncology Clinical Practice Guideline. *Journal of Clinical Oncology*. 2016;34(10):1134-1150. Exclude: Publication type-not systematic review.

584. Hartkopf A, Wallwiener M, Kommoss S, Brucker S, Taran FA. Detection of disseminated tumor cells from the bone marrow of patients with early breast cancer is associated with high 21-gene recurrence score. *Oncology Research and Treatment Conference*. 2016;39(165). Exclude: Publication type-conference abstract.

585. Hartkopf AD, Wallwiener M, Kommoss S, Taran FA, Brucker SY. Detection of disseminated tumor cells from the bone marrow of patients with early breast cancer is associated with high 21-gene recurrence score. *Breast Cancer Research & Treatment*. 2016;156(1):91-95. Exclude: No outcome of interest.

586. Hartmann S, Gerber B, Elling D, Heintze K, Reimer T. The 70-gene signature as prognostic factor for elderly women with hormone receptor-positive, HER2-negative breast cancer. *Breast Care (Basel)*. 2012;7(1):19-24. Exclude: In included systematic review.

587. Hassett MJ, Silver SM, Hughes ME, et al. Adoption of gene expression profile testing and association with use of chemotherapy among women with breast cancer. *Journal of Clinical Oncology*. 2012;30(18):2218-2226. Exclude: In included systematic review.

588. Hatzis C, Pusztai L, Valero V, et al. A genomic predictor of response and survival following taxane-anthracycline chemotherapy for invasive breast cancer. *JAMA*. 2011;305(18):1873-1881. Exclude: No outcome of interest.

589. Hayashi S, Yamaguchi Y. Basic research for hormone-sensitivity of breast cancer. *Breast Cancer*. 2006;13(2):123-128. Exclude: Date.

590. Hayashi T, Yoshida K, Ohishi W, Kyoizumi S, Kusunoki Y, Nakachi K. Assessment of breast cancer risk among atomic-bomb survivors based on ATM polymorphisms, radiation dose, and age at exposure. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
591. Hayes DF. Clinical utility of genetic signatures in selecting adjuvant treatment: Risk stratification for early vs. late recurrences. *Breast*. 2015;24 Suppl 2:S6-s10. Exclude: Publication type-not systematic review.
592. He DX, Xia YD, Gu XT, Jin J, Ma X. A 20-gene signature in predicting the chemoresistance of breast cancer to taxane-based chemotherapy. *Molecular Biosystems*. 2014;10(12):3111-3119. Exclude: Not intervention of interest.
593. He M, Mangiameli DP, Kachala S, et al. Expression signature developed from a complex series of mouse models accurately predicts human breast cancer survival. *Clinical Cancer Research*. 2010;16(1):249-259. Exclude: No outcome of interest.
594. He YD. Genomic approach to biomarker identification and its recent applications. *Cancer Biomarkers: Section A of Disease Markers*. 2006;2(3-4):103-133. Exclude: Date.
595. Health CAFdaTi. CADTH Rapid Response Reports. In: *Oncotype DX in Women and Men with ER-Positive, HER2-Negative Early Stage Breast Cancer who are Lymph Node Negative: A Review of Clinical Effectiveness and Guidelines*. Ottawa (ON): Canadian Agency for Drugs and Technologies in Health Copyright (c) 2014 Canadian Agency for Drugs and Technologies in Health.; 2014.
596. Hedjazi L, Le Lann MV, Kempowsky T, Dalenc F, Aguilar-Martin J, Favre G. Symbolic data analysis to defy low signal-to-noise ratio in microarray data for breast cancer prognosis. *Journal of Computational Biology*. 2013;20(8):610-620. Exclude: Not intervention of interest.
597. Heimes AS, Madjar K, Edlund K, et al. Prognostic significance of interferon regulating factor 4 (IRF4) in node-negative breast cancer. *Journal of Cancer Research & Clinical Oncology*. 2017;143(7):1123-1131. Exclude: Not intervention of interest.
598. Hein S, Muller V, Kohler N, et al. Biologic role of activated leukocyte cell adhesion molecule overexpression in breast cancer cell lines and clinical tumor tissue. *Breast Cancer Research & Treatment*. 2011;129(2):347-360. Exclude: Not intervention of interest.
599. Heindl A, Sestak I, Naidoo K, Cuzick J, Dowsett M, Yuan Y. Relevance of Spatial Heterogeneity of Immune Infiltration for Predicting Risk of Recurrence After Endocrine Therapy of ER+ Breast Cancer. *Journal of the National Cancer Institute*. 2018;110(2):01. Exclude: Not intervention of interest.
600. Heng YJ, Lester SC, Tse GM, et al. The molecular basis of breast cancer pathological phenotypes. *Journal of Pathology*. 2017;241(3):375-391. Exclude: No outcome of interest.
601. Henry LR, Prindiville SA, Swain SM, Cordes R, Soballe MDP. The influence of a gene expression profile on breast cancer decisions. *Journal of Clinical Oncology*. 2008;26(15_suppl):11546. Exclude: Publication type-conference abstract.
602. Henry LR, Stojadinovic A, Swain SM, Prindiville S, Cordes R, Soballe PW. The influence of a gene expression profile on breast cancer decisions. *J Surg Oncol*. 2009;99(6):319-323. Exclude: In included systematic review.
603. Henry NL, Braun TM, Ali HY, et al. Associations between use of the 21-gene recurrence score assay and chemotherapy regimen selection in a statewide registry. *Cancer*. 2017;123(6):948-956. Exclude: No outcome of interest.

604. Henry NL, Hayes DF. Use of gene-expression profiling to recommend adjuvant chemotherapy for breast cancer. *Oncology (Williston Park)*. 2007;21(11):1301-1309; discussion 1311, 1314, 1319. Exclude: Publication type-commentary.
605. Henry NL, Somerfield MR, Abramson VG, et al. Role of Patient and Disease Factors in Adjuvant Systemic Therapy Decision Making for Early-Stage, Operable Breast Cancer: American Society of Clinical Oncology Endorsement of Cancer Care Ontario Guideline Recommendations. *Journal of Clinical Oncology*. 2016;34(19):2303-2311. Exclude: Publication type-not systematic review.
606. Hertz DL, Henry NL, Kidwell KM, et al. ESR1 and PGR polymorphisms are associated with estrogen and progesterone receptor expression in breast tumors. *Physiological Genomics*. 2016;48(9):688-698. Exclude: Not intervention of interest.
607. Heskamp S, Boerman OC, Molkenboer-Kuenen JD, et al. Upregulation of IGF-1R expression during neoadjuvant therapy predicts poor outcome in breast cancer patients. *PLoS ONE [Electronic Resource]*. 2015;10(2):e0117745. Exclude: Not intervention of interest.
608. Hicks J, Krasnitz A, Lakshmi B, et al. Novel patterns of genome rearrangement and their association with survival in breast cancer. *Genome Research*. 2006;16(12):1465-1479. Exclude: Date.
609. Higgins GS, Harris AL, Prevo R, Helleday T, McKenna WG, Buffa FM. Overexpression of POLQ confers a poor prognosis in early breast cancer patients. *Oncotarget*. 2010;1(3):175-184. Exclude: Not intervention of interest.
610. Hirsch FR, Varella-Garcia M, Franklin WA, et al. Evaluation of HER-2/neu gene amplification and protein expression in non-small cell lung carcinomas. *British Journal of Cancer*. 2002;86(9):1449-1456. Exclude: Date.
611. Hollestelle A, Pelletier C, Hooning M, et al. Prevalence of the variant allele rs61764370 T>G in the 3'UTR of KRAS among Dutch BRCA1, BRCA2 and non-BRCA1/BRCA2 breast cancer families. *Breast Cancer Research & Treatment*. 2011;128(1):79-84. Exclude: Not intervention of interest.
612. Holm J, Eriksson L, Ploner A, et al. Assessment of Breast Cancer Risk Factors Reveals Subtype Heterogeneity. *Cancer Research*. 2017;77(13):3708-3717. Exclude: No outcome of interest.
613. Holt S, Bertelli G, Humphreys I, et al. A decision impact, decision conflict and economic assessment of routine Oncotype DX testing of 146 women with node-negative or pN1mi, ER-positive breast cancer in the U.K. *Br J Cancer*. 2013;108(11):2250-2258. Exclude: In included systematic review.
614. Horak C, Pusztai L, Mudenda B, et al. Abstract PD07-02: {beta}III Tubulin Expression by Immunohistochemistry (IHC) and mRNA in a Randomized Phase 2 Neoadjuvant Breast Cancer (BC) Study of Ixabepilone (ixa) Compared to Paclitaxel (pac). 2010. Exclude: Publication type-conference abstract.
615. Horiguchi J, Iino Y, Takei H, et al. c-erbB-2 status is an independent predictor of survival after first recurrence. *International Journal of Oncology*. 1998;12(1):123-128. Exclude: Date.
616. Horiguchi J, Iino Y, Takei H, Yokoe T, Ishida T, Morishita Y. Immunohistochemical study on the expression of c-erbB-2 oncoprotein in breast cancer. *Oncology*. 1994;51(1):47-51. Exclude: Date.
617. Horimoto Y, Arakawa A, Harada-Shoji N, et al. Low FOXA1 expression predicts good response to neoadjuvant chemotherapy resulting in good outcomes for luminal HER2-negative breast cancer cases. *British Journal of Cancer*. 2015;112(2):345-351. Exclude: Not intervention of interest.
618. Horlings HM, Lai C, Nuyten DS, et al. Integration of DNA copy number alterations and prognostic gene expression signatures in breast cancer patients. *Clinical Cancer Research*. 2010;16(2):651-663. Exclude: No outcome of interest.

619. Hornberger J, Alvarado MD, Rebecca C, Gutierrez HR, Yu TM, Gradishar WJ. Clinical validity/utility, change in practice patterns, and economic implications of risk stratifiers to predict outcomes for early-stage breast cancer: a systematic review. *J Natl Cancer Inst*. 2012;104(14):1068-1079. Exclude: Publication type-older systematic review.
620. Hornberger J, Chien R, Krebs K, Hochheiser L. US insurance program's experience with a multigene assay for early-stage breast cancer. *American Journal of Managed Care*. 2011;17(5 Spec No):e194-202. Exclude: In included systematic review.
621. Hornberger J, Cosler LE, Lyman GH. Economic analysis of targeting chemotherapy using a 21-gene RT-PCR assay in lymph-node-negative, estrogen-receptor-positive, early-stage breast cancer.[Erratum appears in Am J Manag Care. 2005 Aug;11(8):476]. *American Journal of Managed Care*. 2005;11(5):313-324. Exclude: Date.
622. Hornberger J, Cosler LE, Lyman GH. Economic analysis of targeting chemotherapy using a 21-gene RT-PCR assay in lymph-node-negative, estrogen-receptor-positive, early-stage breast cancer. *Am J Manag Care*. 2005;11(5):313-324. Exclude: Date.
623. Hornberger J, Lyman GH, Chien R. Economic implications of 21-gene recurrence score assay: US multicenter experience. *J Clin Oncol*. 2010;28(22):e382; author reply e383. Exclude: Publication type-letter.
624. Hou MF, Chuang HY, Ou-Yang F, et al. Comparison of breast mammography, sonography and physical examination for screening women at high risk of breast cancer in taiwan. *Ultrasound in Medicine & Biology*. 2002;28(4):415-420. Exclude: Date.
625. Hou Y, Tozbikian G, Zynger DL, Li Z. Using the Modified Magee Equation to Identify Patients Unlikely to Benefit From the 21-Gene Recurrence Score Assay (Oncotype DX Assay). *American Journal of Clinical Pathology*. 2017;147(6):541-548. Exclude: No outcome of interest.
626. Hou Y, Zynger DL, Li X, Li Z. Comparison of Oncotype DX With Modified Magee Equation Recurrence Scores in Low-Grade Invasive Carcinoma of Breast. *American Journal of Clinical Pathology*. 2017;148(2):167-172. Exclude: No outcome of interest.
627. Hsiao TH, Chiu YC, Hsu PY, et al. Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. *Scientific Reports*. 2016;6:23035. Exclude: Not intervention of interest.
628. Hu Y, Bai L, Geiger T, et al. Genetic background may contribute to PAM50 gene expression breast cancer subtype assignments. *PLoS ONE [Electronic Resource]*. 2013;8(8):e72287. Exclude: No outcome of interest.
629. Hu ZI, Liu C, Fisher PR, Cohen JA. Intracystic Papillary Carcinoma of the Breast in a Male Patient. *Rare Tumors*. 2016;8(1):6050. Exclude: Not intervention of interest.
630. Hua J, Lowey J, Xiong Z, Dougherty ER. Noise-injected neural networks show promise for use on small-sample expression data. *BMC Bioinformatics*. 2006;7:274. Exclude: Date.
631. Huang CC, Tu SH, Huang CS, Lien HH, Lai LC, Chuang EY. Multiclass prediction with partial least square regression for gene expression data: applications in breast cancer intrinsic taxonomy. *BioMed Research International*. 2013;2013:248648. Exclude: No outcome of interest.
632. Huang CC, Tu SH, Lien HH, et al. Refinement of breast cancer risk prediction with concordant leading edge subsets from prognostic gene signatures. *Breast Cancer Research & Treatment*. 2014;147(2):353-370. Exclude: No outcome of interest.

633. Huang CC, Tu SH, Lien HH, et al. Prediction consistency and clinical presentations of breast cancer molecular subtypes for Han Chinese population. *Journal of Translational Medicine*. 2012;10 Suppl 1:S10. Exclude: No outcome of interest.
634. Huang F, Reeves K, Han X, et al. Identification of candidate molecular markers predicting sensitivity in solid tumors to dasatinib: rationale for patient selection. *Cancer Research*. 2007;67(5):2226-2238. Exclude: Not intervention of interest.
635. Huang J, Morehouse C, Streicher K, et al. Altered expression of insulin receptor isoforms in breast cancer. *PLoS ONE [Electronic Resource]*. 2011;6(10):e26177. Exclude: Not intervention of interest.
636. Hubackova M, Vaclavikova R, Ehrlichova M, et al. Association of superoxide dismutases and NAD(P)H quinone oxidoreductases with prognosis of patients with breast carcinomas. *International Journal of Cancer*. 2012;130(2):338-348. Exclude: Not intervention of interest.
637. Huth L, Rose M, Kloubert V, et al. BDNF is associated with SFRP1 expression in luminal and basal-like breast cancer cell lines and primary breast cancer tissues: a novel role in tumor suppression? *PLoS ONE [Electronic Resource]*. 2014;9(7):e102558. Exclude: Not intervention of interest.
638. Hyams DM. Understanding tumor profiling and assessing treatment. *Managed Care*. 2008;17(7 Suppl 7):4-8; discussion 17-18. Exclude: Publication type-commentary.
639. Iglehart JD, Valero MG. Commentary on "The role of the breast cancer surgeon in personalized cancer care: clinical utility of the 21-gene assay". *American Journal of Surgery*. 2012;203(6):759-760. Exclude: Publication type-commentary.
640. Ignatiadis M, Azim HA, Jr., Desmedt C, et al. The Genomic Grade Assay Compared With Ki67 to Determine Risk of Distant Breast Cancer Recurrence. *JAMA Oncology*. 2016;2(2):217-224. Exclude: Not intervention of interest.
641. Ignatiadis M, Sotiriou C. Breast cancer: Should we assess HER2 status by Oncotype DX? *Nature Reviews Clinical Oncology*. 2011;9(1):12-14. Exclude: Publication type-commentary.
642. Ithemelandu CU, Leffall LD, Jr., Dewitty RL, et al. Molecular breast cancer subtypes in premenopausal African-American women, tumor biologic factors and clinical outcome. *Annals of Surgical Oncology*. 2007;14(10):2994-3003. Exclude: Not intervention of interest.
643. Iida J, Dorchak J, Slavik J, Clancy R, Cutler ML, Shriver CD. NEDD9 promotes breast cancer metastasis by regulating mitochondrial functions. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
644. Imielinski M, Cha S, Rejtar T, Richardson EA, Karger BL, Sgroi DC. Integrated proteomic, transcriptomic, and biological network analysis of breast carcinoma reveals molecular features of tumorigenesis and clinical relapse. *Molecular & Cellular Proteomics*. 2012;11(6):M111.014910. Exclude: Not intervention of interest.
645. Imyanitov EN, Chernitsa OI, Serova OM, Nikoiforova IF, Pluzhnikova GF, Knyazev PG. Amplification of HER-2(erbB-2/neu) oncogene as the most significant prognostic factor in a group of Russian breast cancer patients. *Neoplasma*. 1993;40(1):35-39. Exclude: Date.
646. Ingoldsby H, Webber M, Wall D, Scarrott C, Newell J, Callagy G. Prediction of Oncotype DX and TAILORx risk categories using histopathological and immunohistochemical markers by classification and regression tree (CART) analysis. *Breast*. 2013;22(5):879-886. Exclude: No outcome of interest.

647. Iorio MV, Casalini P, Piovani C, Braccioli L, Tagliabue E. Breast cancer and microRNAs: therapeutic impact. *Breast*. 2011;20 Suppl 3:S63-70. Exclude: Not intervention of interest.
648. Isakoff SJ, Mayer EL, He L, et al. TBCRC009: A Multicenter Phase II Clinical Trial of Platinum Monotherapy With Biomarker Assessment in Metastatic Triple-Negative Breast Cancer. *Journal of Clinical Oncology*. 2015;33(17):1902-1909. Exclude: Not intervention of interest.
649. Ishibe N, Schully S, Freedman A, Ramsey SD. Use of Oncotype DX in Women with Node-Positive Breast Cancer. *PLoS currents*. 2011;3:RRN1249. Exclude: Publication type-not systematic review.
650. Ishioka C. [Breast cancer and molecular markers]. *Gan to Kagaku Ryoho [Japanese Journal of Cancer & Chemotherapy]*. 2008;35(8):1261-1268. Exclude: Not English.
651. Ishitobi M, Goranova TE, Komoike Y, et al. Clinical utility of the 70-gene MammaPrint profile in a Japanese population. *Jpn J Clin Oncol*. 2010;40(6):508-512. Exclude: No outcome of interest.
652. Issa AM, Chaudhari VS, Marchant GE. The value of multigene predictors of clinical outcome in breast cancer: an analysis of the evidence. *Expert Rev Mol Diagn*. 2015;15(2):277-286. Exclude: No outcome of interest.
653. Ito KI, Oba T, Aogi K, et al. The first report of multicenter validation study on curebest 95GC breast, a multigene assay to predict prognosis of node negative and ER positive breast cancer patients. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
654. Itoh M, Iwamoto T, Matsuoka J, et al. Estrogen receptor (ER) mRNA expression and molecular subtype distribution in ER-negative/progesterone receptor-positive breast cancers. *Breast Cancer Research & Treatment*. 2014;143(2):403-409. Exclude: No outcome of interest.
655. Iwamoto T, Booser D, Valero V, et al. Estrogen receptor (ER) mRNA and ER-related gene expression in breast cancers that are 1% to 10% ER-positive by immunohistochemistry. *Journal of Clinical Oncology*. 2012;30(7):729-734. Exclude: No outcome of interest.
656. Iwamoto T, Kelly C, Mizoo T, et al. Relative Prognostic and Predictive Value of Gene Signature and Histologic Grade in Estrogen Receptor-Positive, HER2-Negative Breast Cancer. *Clinical Breast Cancer*. 2016;16(2):95-100.e101. Exclude: No outcome of interest.
657. Iwamoto T, Lee JS, Bianchini G, et al. First generation prognostic gene signatures for breast cancer predict both survival and chemotherapy sensitivity and identify overlapping patient populations. *Breast Cancer Research & Treatment*. 2011;130(1):155-164. Exclude: No outcome of interest.
658. Jaafar H, Bashir MA, Taher A, Qawasmeh K, Jaloudi M. Impact of Oncotype DX testing on adjuvant treatment decisions in patients with early breast cancer: a single-center study in the United Arab Emirates. *Asia-Pacific Journal of Clinical Oncology*. 2014;10(4):354-360. Exclude: In included systematic review.
659. Jacquemier J, Penault-Llorca F, Viens P, et al. Breast cancer response to adjuvant chemotherapy in correlation with erbB2 and p53 expression. *Anticancer Research*. 1994;14(6B):2773-2778. Exclude: Date.
660. Jafarzadeh A, Minaee K, Farsinejad AR, et al. Evaluation of the circulating levels of IL-12 and IL-33 in patients with breast cancer: influences of the tumor stages and cytokine gene polymorphisms. *Iranian Journal of Basic Medical Sciences*. 2015;18(12):1189-1198. Exclude: Not intervention of interest.
661. Jahn B, Rochau U, Kurzthaler C, et al. Personalized treatment of women with early breast cancer: a risk-group specific cost-effectiveness analysis of adjuvant chemotherapy accounting for companion prognostic tests OncotypeDX and Adjuvant!Online. *BMC Cancer*. 2017;17(1):685. Exclude: Not intervention of interest.

662. Jahn B, Rochau U, Kurzthaler C, et al. Cost effectiveness of personalized treatment in women with early breast cancer: the application of OncotypeDX and Adjuvant! Online to guide adjuvant chemotherapy in Austria. *Springerplus*. 2015;4:752. Exclude: In included systematic review.
663. Jahn B, Rochau U, Kurzthaler C, et al. Lessons Learned from a Cross-Model Validation between a Discrete Event Simulation Model and a Cohort State-Transition Model for Personalized Breast Cancer Treatment. *Medical Decision Making*. 2016;36(3):375-390. Exclude: No outcome of interest.
664. Jain S, Gradishar WJ. The application of Oncotype DX in early-stage lymph-node-positive disease. *Current Oncology Reports*. 2014;16(1):360. Exclude: Publication type-not systematic review.
665. Janat-Amsbury MM, Yockman JW, Lee M, et al. Combination of local, nonviral IL12 gene therapy and systemic paclitaxel treatment in a metastatic breast cancer model. *Molecular Therapy: the Journal of the American Society of Gene Therapy*. 2004;9(6):829-836. Exclude: Date.
666. Janat-Amsbury MM, Yockman JW, Lee M, et al. Local, non-viral IL-12 gene therapy using a water soluble lipopolymer as carrier system combined with systemic paclitaxel for cancer treatment. *Journal of Controlled Release*. 2005;101(1-3):273-285. Exclude: Date.
667. Janes H, Brown MD, Crager MR, Miller DP, Barlow WE. Adjusting for covariates in evaluating markers for selecting treatment, with application to guiding chemotherapy for treating estrogen-receptor-positive, node-positive breast cancer. *Contemporary Clinical Trials*. 2017;63:30-39. Exclude: No outcome of interest.
668. Jankowitz RC, Cooper K, Erlander MG, et al. Prognostic utility of the breast cancer index and comparison to Adjuvant! Online in a clinical case series of early breast cancer. *Breast Cancer Research*. 2011;13(5):R98. Exclude: No outcome of interest.
669. Jankowitz RC, McGuire KP, Davidson NE. Optimal systemic therapy for premenopausal women with hormone receptor-positive breast cancer. *Breast*. 2013;22 Suppl 2:S165-170. Exclude: Not intervention of interest.
670. Jansen MP, Sas L, Sieuwerts AM, et al. Decreased expression of ABAT and STC2 hallmarks ER-positive inflammatory breast cancer and endocrine therapy resistance in advanced disease. *Molecular Oncology*. 2015;9(6):1218-1233. Exclude: Not intervention of interest.
671. Jarzab M, Rozanowski P, Kowalska M, et al. Optimization of the method of RNA isolation from paraffin blocks to assess gene expression in breast cancer. *Polish Journal of Pathology*. 2008;59(2):85-91. Exclude: Not intervention of interest.
672. Jegadeesh NK, Kim S, Prabhu RS, et al. The 21-gene recurrence score and locoregional recurrence in breast cancer patients. *Annals of Surgical Oncology*. 2015;22(4):1088-1094. Exclude: No outcome of interest.
673. Jenkins EO, Deal AM, Anders CK, et al. Age-specific changes in intrinsic breast cancer subtypes: a focus on older women. *Oncologist*. 2014;19(10):1076-1083. Exclude: No outcome of interest.
674. Jensen TW, Ray T, Wang J, et al. Diagnosis of Basal-Like Breast Cancer Using a FOXC1-Based Assay. *Journal of the National Cancer Institute*. 2015;107(8). Exclude: Not intervention of interest.
675. Jerevall PL, Ma XJ, Li H, et al. Prognostic utility of HOXB13:IL17BR and molecular grade index in early-stage breast cancer patients from the Stockholm trial. *British Journal of Cancer*. 2011;104(11):1762-1769. Exclude: Not intervention of interest.
676. Jerzak KJ, Pritchard KI. The 21-gene recurrence score assay in node-negative early breast cancer: Prognostic, predictive or presumptuous? *European Journal of Cancer*. 2016;68:173-175. Exclude: No outcome of interest.

677. Jeselsohn RM, Barry WT, Zhao J, et al. TransCONFIRM: The correlative analysis of breast tumors from patients with advanced hormone receptor positive disease identifies a genetic signature associated with decreased benefit from single agent fulvestrant. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
678. Jezequel P, Loussouarn D, Guerin-Charbonnel C, et al. Gene-expression molecular subtyping of triple-negative breast cancer tumours: importance of immune response. *Breast Cancer Research*. 2015;17:43. Exclude: Not intervention of interest.
679. Jiang D, Zhao N. A clinical prognostic prediction of lymph node-negative breast cancer by gene expression profiles. *Journal of Cancer Research & Clinical Oncology*. 2006;132(9):579-587. Exclude: Date.
680. Jiang G, Zhang S, Yazdanparast A, et al. Comprehensive comparison of molecular portraits between cell lines and tumors in breast cancer. *BMC Genomics*. 2016;17 Suppl 7:525. Exclude: No outcome of interest.
681. Jiang Y, Liu L, Shan W, Yang ZQ. An integrated genomic analysis of Tudor domain-containing proteins identifies PHD finger protein 20-like 1 (PHF20L1) as a candidate oncogene in breast cancer. *Molecular Oncology*. 2016;10(2):292-302. Exclude: Not intervention of interest.
682. Jiang YZ, Liu YR, Xu XE, et al. Transcriptome Analysis of Triple-Negative Breast Cancer Reveals an Integrated mRNA-lncRNA Signature with Predictive and Prognostic Value. *Cancer Research*. 2016;76(8):2105-2114. Exclude: Not intervention of interest.
683. Jiao S, Liu W, Wu M, Peng C, Tang H, Xie X. Nrdp1 expression to predict clinical outcome and efficacy of adjuvant anthracyclines-based chemotherapy in breast cancer: A retrospective study. *Cancer Biomarkers: Section A of Disease Markers*. 2015;15(2):115-123. Exclude: Not intervention of interest.
684. Joerger M, Thurlimann B. Chemotherapy regimens in early breast cancer: major controversies and future outlook. *Expert Review of Anticancer Therapy*. 2013;13(2):165-178. Exclude: Publication type-commentary.
685. Joh JE, Esposito NN, Kiluk JV, et al. The effect of Oncotype DX recurrence score on treatment recommendations for patients with estrogen receptor-positive early stage breast cancer and correlation with estimation of recurrence risk by breast cancer specialists. *Oncologist*. 2011;16(11):1520-1526. Exclude: In included systematic review.
686. Johannes M, Brase JC, Frohlich H, et al. Integration of pathway knowledge into a reweighted recursive feature elimination approach for risk stratification of cancer patients. *Bioinformatics*. 2010;26(17):2136-2144. Exclude: Not intervention of interest.
687. Johansson I, Nilsson C, Berglund P, et al. Gene expression profiling of primary male breast cancers reveals two unique subgroups and identifies N-acetyltransferase-1 (NAT1) as a novel prognostic biomarker. *Breast Cancer Research*. 2012;14(1):R31. Exclude: Not intervention of interest.
688. Johnson RC, Ricci A, Jr., Cartun RW, Ackroyd R, Tsongalis GJ. p185HER2 overexpression in human breast cancer using molecular and immunohistochemical methods. *Cancer Investigation*. 2000;18(4):336-342. Exclude: Date.
689. Johnson RH, Hu P, Fan C, Anders CK. Gene expression in "young adult type" breast cancer: a retrospective analysis. *Oncotarget*. 2015;6(15):13688-13702. Exclude: Not intervention of interest.
690. Jones LW, Kwan ML, Weltzien E, et al. Exercise and Prognosis on the Basis of Clinicopathologic and Molecular Features in Early-Stage Breast Cancer: The LACE and Pathways Studies. *Cancer Research*. 2016;76(18):5415-5422. Exclude: Not intervention of interest.

691. Jonsdottir K, Assmus J, Slewa A, et al. Prognostic value of gene signatures and proliferation in lymph-node-negative breast cancer. *PLoS ONE [Electronic Resource]*. 2014;9(3):e90642. Exclude: No outcome of interest.
692. Jonsson G, Staaf J, Vallon-Christersson J, et al. Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. *Breast Cancer Research*. 2010;12(3):R42. Exclude: Not intervention of interest.
693. Jorgensen CL, Nielsen TO, Bjerre KD, et al. PAM50 breast cancer intrinsic subtypes and effect of gemcitabine in advanced breast cancer patients. *Acta Oncologica*. 2014;53(6):776-787. Exclude: No outcome of interest.
694. Jorgensen CLT, Nielsen TO, Bjerre KD, et al. Association between PAM50 breast cancer intrinsic subtypes and effect of gemcitabine in advanced breast cancer patients. *Cancer research*. 2012;72(24 SUPPL. 3):CONFERENCE START: 2012 Dec 2014 CONFERENCE END: 2012 Dec 2018. Exclude: Publication type-conference abstract.
695. Jorns JM, Thomas DG, Healy PN, et al. Estrogen receptor expression is high but is of lower intensity in tubular carcinoma than in well-differentiated invasive ductal carcinoma. *Archives of Pathology & Laboratory Medicine*. 2014;138(11):1507-1513. Exclude: Not intervention of interest.
696. Juppunen M, Gruvberger-Saal S, Kauraniemi P, et al. Basal-like phenotype is not associated with patient survival in estrogen-receptor-negative breast cancers. *Breast Cancer Research*. 2007;9(1):R16. Exclude: Not intervention of interest.
697. Kaigorodova EV, Zavyalova MV, Bogatyuk MV, Tarabanovskaya NA, Slonimskaya EM, Perelmuter VM. Relationship between the expression of phosphorylated heat shock protein beta-1 with lymph node metastases of breast cancer. *Cancer Biomarkers: Section A of Disease Markers*. 2015;15(2):143-150. Exclude: Not intervention of interest.
698. Kaklamani V. A genetic signature can predict prognosis and response to therapy in breast cancer: Oncotype DX. *Expert Review of Molecular Diagnostics*. 2006;6(6):803-809. Exclude: Date.
699. Kaklamani VG, Gradishar WJ. Gene expression in breast cancer. *Current Treatment Options in Oncology*. 2006;7(2):123-128. Exclude: Date.
700. Kalife ET, Sung CJ, Singh K. To Oncotype or Not: Knowledge of Histologic Grade and Subtype May Help. *Archives of Pathology & Laboratory Medicine*. 2016;140(11):1184-1185. Exclude: No outcome of interest.
701. Kalinsky K, Lim EA, Andreopoulou E, et al. Increased expression of tumor proliferation genes in Hispanic women with early-stage breast cancer. *Cancer Investigation*. 2014;32(9):439-444. Exclude: No outcome of interest.
702. Kamal AH, Loprinzi CL, Reynolds C, et al. Breast medical oncologists' use of standard prognostic factors to predict a 21-gene recurrence score. *Oncologist*. 2011;16(10):1359-1366. Exclude: hypothetical or scenario-based outcome.
703. Kao KJ, Chang KM, Hsu HC, Huang AT. Correlation of microarray-based breast cancer molecular subtypes and clinical outcomes: implications for treatment optimization. *BMC Cancer*. 2011;11:143. Exclude: No outcome of interest.
704. Karami S, Lin FM, Kumar S, Ren J, Bahnassy S, Bawa-Khalfe T. Non-nuclear SUMO dynamics regulate mammary epithelial cell transformation. *Cancer research Conference: 39th annual CTRC AACR san antonio*

breast cancer symposium United states. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

705. Kardas I, Seitz G, Limon J, et al. Retrospective analysis of prognostic significance of the estrogen-inducible pS2 gene in male breast carcinoma. *Cancer*. 1993;72(5):1652-1656. Exclude: Date.

706. Karlsson E, Delle U, Danielsson A, et al. Gene expression variation to predict 10-year survival in lymph-node-negative breast cancer. *BMC Cancer*. 2008;8:254. Exclude: Not intervention of interest.

707. Karn T, Pusztai L, Holtrich U, et al. Homogeneous datasets of triple negative breast cancers enable the identification of novel prognostic and predictive signatures. *PLoS ONE [Electronic Resource]*. 2011;6(12):e28403. Exclude: No outcome of interest.

708. Karsten M, Stempel M, Radosa J, Patil S, King TA. Oncotype DX in Bilateral Synchronous Primary Invasive Breast Cancer. *Annals of Surgical Oncology*. 2016;23(2):471-476. Exclude: No outcome of interest.

709. Kato K. Algorithm for in vitro diagnostic multivariate index assay. *Breast Cancer*. 2009;16(4):248-251. Exclude: Not intervention of interest.

710. Katz G, Romano O, Foa C, et al. Economic impact of gene expression profiling in patients with early-stage breast cancer in France. *PLoS One*. 2015;10(6):e0128880. Exclude: In included systematic review.

711. Kaufman CS, Hall W, Behrndt V, et al. Use of a 3-D bioabsorbable tissue marker in 61 patients over two years. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

712. Kaufmann M, Pusztai L, Biedenkopf Expert Panel M. Use of standard markers and incorporation of molecular markers into breast cancer therapy: Consensus recommendations from an International Expert Panel. *Cancer*. 2011;117(8):1575-1582. Exclude: Publication type-not systematic review.

713. Kaya H, Ragazzini T, Aribal E, Guney I, Kotiloglu E. Her-2/neu gene amplification compared with HER-2/neu protein overexpression on ultrasound guided core-needle biopsy specimens of breast carcinoma. *Pathology Oncology Research*. 2001;7(4):279-283. Exclude: Date.

714. Keenan T, Moy B, Mroz EA, et al. Comparison of the Genomic Landscape Between Primary Breast Cancer in African American Versus White Women and the Association of Racial Differences With Tumor Recurrence. *Journal of Clinical Oncology*. 2015;33(31):3621-3627. Exclude: No outcome of interest.

715. Kelly CM, Bernard PS, Krishnamurthy S, et al. Agreement in risk prediction between the 21-gene recurrence score assay (Oncotype DX) and the PAM50 breast cancer intrinsic Classifier™ in early-stage estrogen receptor-positive breast cancer. *Oncologist*. 2012;17(4):492-498. Exclude: No outcome of interest.

716. Kelly CM, Krishnamurthy S, Bianchini G, et al. Utility of oncotype DX risk estimates in clinically intermediate risk hormone receptor-positive, HER2-normal, grade II, lymph node-negative breast cancers. *Cancer*. 2010;116(22):5161-5167. Exclude: No outcome of interest.

717. Kelly CM, Warner E, Tsoi DT, Verma S, Pritchard KI. Review of the clinical studies using the 21-gene assay. *Oncologist*. 2010;15(5):447-456. Exclude: No outcome of interest.

718. Kempowsky-Hamon T, Valle C, Lacroix-Triki M, et al. Fuzzy logic selection as a new reliable tool to identify molecular grade signatures in breast cancer--the INNODIAG study. *BMC Medical Genomics [Electronic Resource]*. 2015;8:3. Exclude: Not intervention of interest.

719. Kerr DA, 2nd, Wittliff JL. A five-gene model predicts clinical outcome in ER+/PR+, early-stage breast cancers treated with adjuvant tamoxifen. *Hormones & Cancer*. 2011;2(5):261-271. Exclude: Not intervention of interest.

720. Khaleel SS, Andrews EH, Ung M, DiRenzo J, Cheng C. E2F4 regulatory program predicts patient survival prognosis in breast cancer. *Breast Cancer Research*. 2014;16(6):486. Exclude: Not intervention of interest.
721. Khan SS, Karn T, Symmans WF, et al. Genomic predictor of residual risk of recurrence after adjuvant chemotherapy and endocrine therapy in high risk estrogen receptor-positive breast cancers. *Breast Cancer Research & Treatment*. 2015;149(3):789-797. Exclude: No outcome of interest.
722. Khawaja S, Thomas D, Udayasankar S, et al. A simulation study depicting the inconsistency of adjuvant online compared to genomic testing when determining the benefit of chemotherapy. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
723. Khoury T, Huang X, Chen X, Wang D, Liu S, Opyrchal M. Comprehensive Histologic Scoring to Maximize the Predictability of Pathology-generated Equation of Breast Cancer Oncotype DX Recurrence Score. *Applied Immunohistochemistry & Molecular Morphology*. 2016;24(10):703-711. Exclude: No outcome of interest.
724. Khoury T, Yan L, Liu S, Bshara W. Oncotype DX RT-qPCR assay for ER and PR correlation with IHC: a study of 3 different clones. *Applied Immunohistochemistry & Molecular Morphology*. 2015;23(3):178-187. Exclude: No outcome of interest.
725. Kim C, Paik S. Gene-expression-based prognostic assays for breast cancer. *Nature Reviews Clinical Oncology*. 2010;7(6):340-347. Exclude: Publication type-not systematic review.
726. Kim C, Tang G, Pogue-Geile KL, et al. Estrogen receptor (ESR1) mRNA expression and benefit from tamoxifen in the treatment and prevention of estrogen receptor-positive breast cancer. *Journal of Clinical Oncology*. 2011;29(31):4160-4167. Exclude: Not intervention of interest.
727. Kim HS, Moon HG, Han W, et al. COX2 overexpression is a prognostic marker for Stage III breast cancer. *Breast Cancer Research & Treatment*. 2012;132(1):51-59. Exclude: Not intervention of interest.
728. Kim HS, Umbricht CB, Illei PB, et al. Optimizing the Use of Gene Expression Profiling in Early-Stage Breast Cancer. *Journal of Clinical Oncology*. 2016;34(36):4390-4397. Exclude: No outcome of interest.
729. Kim JH, Bossuyt V, Ponn T, Lannin D, Haffty BG. Cyclooxygenase-2 expression in postmastectomy chest wall relapse. *Clinical Cancer Research*. 2005;11(14):5199-5205. Exclude: Date.
730. Kim S, Lin CW, Tseng GC. MetaKTSP: a meta-analytic top scoring pair method for robust cross-study validation of omics prediction analysis. *Bioinformatics*. 2016;32(13):1966-1973. Exclude: Not intervention of interest.
731. Kim S, Nam H, Lee D. Exploring molecular links between lymph node invasion and cancer prognosis in human breast cancer. *BMC Systems Biology*. 2011;5 Suppl 2:S4. Exclude: Not intervention of interest.
732. Kim SY, Kim YS. A gene sets approach for identifying prognostic gene signatures for outcome prediction. *BMC Genomics*. 2008;9:177. Exclude: No outcome of interest.
733. Kim YR, Lee BK, Park RY, et al. Differential CARM1 expression in prostate and colorectal cancers. *BMC Cancer*. 2010;10:197. Exclude: Not intervention of interest.
734. Kimbung S, Johansson I, Danielsson A, et al. Transcriptional Profiling of Breast Cancer Metastases Identifies Liver Metastasis-Selective Genes Associated with Adverse Outcome in Luminal A Primary Breast Cancer. *Clinical Cancer Research*. 2016;22(1):146-157. Exclude: Not intervention of interest.

735. Kimbung S, Kovacs A, Bendahl PO, et al. Claudin-2 is an independent negative prognostic factor in breast cancer and specifically predicts early liver recurrences. *Molecular Oncology*. 2014;8(1):119-128. Exclude: Not intervention of interest.
736. Kimbung S, Kovacs A, Danielsson A, et al. Contrasting breast cancer molecular subtypes across serial tumor progression stages: biological and prognostic implications. *Oncotarget*. 2015;6(32):33306-33318. Exclude: No outcome of interest.
737. King TA, Lyman JP, Gonen M, et al. Prognostic Impact of 21-Gene Recurrence Score in Patients With Stage IV Breast Cancer: TBCRC 013. *Journal of Clinical Oncology*. 2016;34(20):2359-2365. Exclude: No outcome of interest.
738. Kip M, Monteban H, Steuten L. Long-term cost-effectiveness of Oncotype DX versus current clinical practice from a Dutch cost perspective. *Journal of Comparative Effectiveness Research*. 2015;4(5):433-445. Exclude: In included systematic review.
739. Kirk R. Risk factors. Oncotype DX assay predicts local recurrence in breast cancer. *Nature Reviews Clinical Oncology*. 2010;7(6):300. Exclude: No outcome of interest.
740. Kirmizis A, Bartley SM, Farnham PJ. Identification of the polycomb group protein SU(Z)12 as a potential molecular target for human cancer therapy. *Molecular Cancer Therapeutics*. 2003;2(1):113-121. Exclude: Date.
741. Kittaneh M, Montero AJ, Gluck S. Molecular profiling for breast cancer: a comprehensive review. *Biomarkers in Cancer*. 2013;5:61-70. Exclude: Publication type-not systematic review.
742. Kizy S, Huang JL, Marmor S, Tuttle TM, Hui JYC. Impact of the 21-gene recurrence score on outcome in patients with invasive lobular carcinoma of the breast. *Breast Cancer Research & Treatment*. 2017;165(3):757-763. Exclude: No outcome of interest.
743. Klajic J, Busato F, Edvardsen H, et al. DNA methylation status of key cell-cycle regulators such as CDKN2A/p16 and CCNA1 correlates with treatment response to doxorubicin and 5-fluorouracil in locally advanced breast tumors. *Clinical Cancer Research*. 2014;20(24):6357-6366. Exclude: Not intervention of interest.
744. Klang SH, Hammerman A, Liebermann N, Efrat N, Doberne J, Hornberger J. Economic implications of 21-gene breast cancer risk assay from the perspective of an Israeli-managed health-care organization. *Value Health*. 2010;13(4):381-387. Exclude: In included systematic review.
745. Klein ME, Dabbs DJ, Shuai Y, et al. Prediction of the Oncotype DX recurrence score: use of pathology-generated equations derived by linear regression analysis. *Modern Pathology*. 2013;26(5):658-664. Exclude: No outcome of interest.
746. Kleivi Sahlberg K, Bottai G, Naume B, et al. A serum microRNA signature predicts tumor relapse and survival in triple-negative breast cancer patients. *Clinical Cancer Research*. 2015;21(5):1207-1214. Exclude: Not intervention of interest.
747. Knauer M, Cardoso F, Wesseling J, et al. Identification of a low-risk subgroup of HER-2-positive breast cancer by the 70-gene prognosis signature. *British Journal of Cancer*. 2010;103(12):1788-1793. Exclude: No outcome of interest.
748. Knauer M, Filipits M, Dubsky P. Late recurrences in early breast cancer: for whom and how long is endocrine therapy beneficial? *Breast Care*. 2014;9(2):97-100. Exclude: Publication type-commentary.

749. Knauer M, Mook S, Rutgers EJ, et al. The predictive value of the 70-gene signature for adjuvant chemotherapy in early breast cancer. *Breast Cancer Research & Treatment*. 2010;120(3):655-661. Exclude: No outcome of interest.
750. Knopfmacher A, Fox J, Lo Y, Shapiro N, Fineberg S. Correlation of histopathologic features of ductal carcinoma in situ of the breast with the oncotype DX DCIS score. *Modern Pathology*. 2015;28(9):1167-1173. Exclude: No outcome of interest.
751. Knudsen ES, Witkiewicz AK. Defining the transcriptional and biological response to CDK4/6 inhibition in relation to ER+/HER2- breast cancer. *Oncotarget*. 2016;7(43):69111-69123. Exclude: Not intervention of interest.
752. Koch A, De Meyer T, Jeschke J, Van Criekinge W. MEXPRESS: visualizing expression, DNA methylation and clinical TCGA data. *BMC Genomics*. 2015;16:636. Exclude: Not intervention of interest.
753. Kohli-Laven N, Bourret P, Keating P, Cambrosio A. Cancer clinical trials in the era of genomic signatures: biomedical innovation, clinical utility, and regulatory-scientific hybrids. *Social Studies of Science*. 2011;41(4):487-513. Exclude: Publication type-commentary.
754. Kok M, Koornstra RH, Mook S, et al. Additional value of the 70-gene signature and levels of ER and PR for the prediction of outcome in tamoxifen-treated ER-positive breast cancer. *Breast*. 2012;21(6):769-778. Exclude: No outcome of interest.
755. Kok M, Linn SC, Van Laar RK, et al. Comparison of gene expression profiles predicting progression in breast cancer patients treated with tamoxifen. *Breast Cancer Research & Treatment*. 2009;113(2):275-283. Exclude: No outcome of interest.
756. Koleck TA, Conley YP. Identification and prioritization of candidate genes for symptom variability in breast cancer survivors based on disease characteristics at the cellular level. *Breast Cancer Targets and Therap*. 2016;8:29-37. Exclude: Not intervention of interest.
757. Kondo M, Hoshi SL, Ishiguro H, Toi M. Economic evaluation of the 70-gene prognosis-signature (MammaPrint) in hormone receptor-positive, lymph node-negative, human epidermal growth factor receptor type 2-negative early stage breast cancer in Japan. *Breast Cancer Research & Treatment*. 2012;133(2):759-768. Exclude: In included systematic review.
758. Kondo M, Hoshi SL, Ishiguro H, Yoshiyayashi H, Toi M. Economic evaluation of 21-gene reverse transcriptase-polymerase chain reaction assay in lymph-node-negative, estrogen-receptor-positive, early-stage breast cancer in Japan. *Breast Cancer Res Treat*. 2008;112(1):175-187. Exclude: In included systematic review.
759. Kondo M, Hoshi SL, Yamanaka T, Ishiguro H, Toi M. Economic evaluation of the 21-gene signature (Oncotype DX) in lymph node-negative/positive, hormone receptor-positive early-stage breast cancer based on Japanese validation study (JBCRG-TR03). *Breast Cancer Res Treat*. 2011;127(3):739-749. Exclude: In included systematic review.
760. Koo JS, Jung W, Yang WI. HER-2 protein overexpressing breast cancer without gene amplification shows higher hormone receptor expression than HER-2 protein overexpressing breast cancer with gene amplification. *International Journal of Surgical Pathology*. 2011;19(4):425-432. Exclude: Not intervention of interest.
761. Korde LA, Lusa L, McShane L, et al. Gene expression pathway analysis to predict response to neoadjuvant docetaxel and capecitabine for breast cancer. *Breast Cancer Research & Treatment*. 2010;119(3):685-699. Exclude: No outcome of interest.

762. Korkola JE, Blaveri E, DeVries S, et al. Identification of a robust gene signature that predicts breast cancer outcome in independent data sets. *BMC Cancer*. 2007;7:61. Exclude: No outcome of interest.
763. Kos Z, Nielsen TO. Developing a new generation of breast cancer clinical gene expression tests. *Breast Cancer Research*. 2014;16(4):103. Exclude: Publication type-commentary.
764. Kosaka Y, Kataoka A, Yamaguchi H, et al. Vascular endothelial growth factor receptor-1 mRNA overexpression in peripheral blood as a useful prognostic marker in breast cancer. *Breast Cancer Research*. 2012;14(5):R140. Exclude: Not intervention of interest.
765. Koscielny S. Critical review of microarray-based prognostic tests and trials in breast cancer. *Curr Opin Obstet Gynecol*. 2008;20(1):47-50. Exclude: Publication type-not systematic review.
766. Kozick Z, Hashmi A, Dove J, et al. Disparities in compliance with the Oncotype DX breast cancer test in the United States: A National Cancer Data Base assessment. *American Journal of Surgery*. 2017. Exclude: No outcome of interest.
767. Kraus JA, Dabbs DJ, Beriwal S, Bhargava R. Semi-quantitative immunohistochemical assay versus oncotype DX() qRT-PCR assay for estrogen and progesterone receptors: an independent quality assurance study. *Modern Pathology*. 2012;25(6):869-876. Exclude: No outcome of interest.
768. Kreike B, Halfwerk H, Armstrong N, et al. Local recurrence after breast-conserving therapy in relation to gene expression patterns in a large series of patients. *Clinical Cancer Research*. 2009;15(12):4181-4190. Exclude: No outcome of interest.
769. Kreike B, Halfwerk H, Kristel P, et al. Gene expression profiles of primary breast carcinomas from patients at high risk for local recurrence after breast-conserving therapy. *Clinical Cancer Research*. 2006;12(19):5705-5712. Exclude: Date.
770. Kreike B, Hart G, Bartelink H, van de Vijver MJ. Analysis of breast cancer related gene expression using natural splines and the Cox proportional hazard model to identify prognostic associations. *Breast Cancer Research & Treatment*. 2010;122(3):711-720. Exclude: No outcome of interest.
771. Krijgsman O, Roepman P, Zwart W, et al. A diagnostic gene profile for molecular subtyping of breast cancer associated with treatment response. *Breast Cancer Research & Treatment*. 2012;133(1):37-47. Exclude: Not intervention of interest.
772. Krishnamurti U, Wetherilt CS, Yang J, Peng L, Li X. Tumor-infiltrating lymphocytes are significantly associated with better overall survival and disease-free survival in triple-negative but not estrogen receptor-positive breast cancers. *Human Pathology*. 2017;64:7-12. Exclude: Not intervention of interest.
773. Kristyanto H, Utomo AR. Pharmacogenetic application in personalized cancer treatment. *Acta Medica Indonesiana*. 2010;42(2):109-115. Exclude: Not intervention of interest.
774. Kroenke CH, Sweeney C, Kwan ML, et al. Race and breast cancer survival by intrinsic subtype based on PAM50 gene expression. *Breast Cancer Res Treat*. 2014;144(3):689-699. Exclude: No outcome of interest.
775. Kronenwett R, Bohmann K, Prinzler J, et al. Decentral gene expression analysis: analytical validation of the Endopredict genomic multianalyte breast cancer prognosis test. *BMC Cancer*. 2012;12:456. Exclude: No outcome of interest.
776. Krop I, Ismaila N, Andre F, et al. Use of Biomarkers to Guide Decisions on Adjuvant Systemic Therapy for Women With Early-Stage Invasive Breast Cancer: American Society of Clinical Oncology Clinical Practice Guideline Focused Update. *Journal of Clinical Oncology*. 2017;35(24):2838-2847. Exclude: Publication type-not systematic review.

777. Krop I, Johnston S, Mayer IA, et al. The FERGI phase II study of the PI3K inhibitor pictilisib (GDC-0941) plus fulvestrant vs fulvestrant plus placebo in patients with ER+, aromatase inhibitor (AI)-resistant advanced or metastatic breast cancer - Part I results. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
778. Krystel-Whittemore M, Brogi E, Bowser ZL, Dickler M, Hudis C, Wen HY. Distant metastases in breast cancer patients with oncotype Dx recurrence score lower than 18. *Laboratory investigation*. 2016;96(12). Exclude: No outcome of interest.
779. Kuchel A, Robinson T, Comins C, et al. The impact of the 21-gene assay on adjuvant treatment decisions in oestrogen receptor-positive early breast cancer: a prospective study. *Br J Cancer*. 2016;114(7):731-736. Exclude: In included systematic review.
780. Kuderer NM, Lyman GH. Gene expression profile assays as predictors of distant recurrence-free survival in early-stage breast cancer. *Cancer Investigation*. 2009;27(9):885-890. Exclude: No outcome of interest.
781. Kuijter A, Drukker CA, Elias SG, et al. Changes over time in the impact of gene-expression profiles on the administration of adjuvant chemotherapy in estrogen receptor positive early stage breast cancer patients: A nationwide study. *International Journal of Cancer*. 2016;139(4):769-775. Exclude: Ecological study.
782. Kuijter A, Straver M, Elias S, et al. Concordance of local immunohistochemistry with TargetPrint microarray based assessment of ER, PR and Her2 and Blueprint molecular subtyping in the Symphony Triple A study. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
783. Kuijter A, Straver M, Elias S, et al. Impact of 70-gene signature use on adjuvant chemotherapy decisions in early breast cancer patients: results of the prospective symphony triple A study. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
784. Kuniyoshi RK, Gehrke Fde S, Alves BC, et al. Gene profiling and circulating tumor cells as biomarker to prognostic of patients with locoregional breast cancer. *Tumour Biology*. 2015;36(10):8075-8083. Exclude: No outcome of interest.
785. Kunz G. Use of a genomic test (MammaPrint™) in daily clinical practice to assist in risk stratification of young breast cancer patients. *Archives of Gynecology & Obstetrics*. 2011;283(3):597-602. Exclude: No outcome of interest.
786. Kurian AW, Friese CR, Bondarenko I, et al. Second Opinions From Medical Oncologists for Early-Stage Breast Cancer: Prevalence, Correlates, and Consequences. *JAMA Oncology*. 2017;3(3):391-397. Exclude: No outcome of interest.
787. Kurono S, Kaneko Y, Matsuura N, et al. Identification of potential breast cancer markers in nipple discharge by protein profile analysis using two-dimensional nano-liquid chromatography/nanoelectrospray ionization-mass spectrometry. *Proteomics Clinical Applications*. 2016;10(5):605-613. Exclude: Not intervention of interest.
788. Kwan ML, Bernard PS, Kroenke CH, et al. Breastfeeding, PAM50 tumor subtype, and breast cancer prognosis and survival. *Journal of the National Cancer Institute*. 2015;107(7). Exclude: No outcome of interest.

789. Kwan ML, Kroenke CH, Sweeney C, et al. Association of high obesity with PAM50 breast cancer intrinsic subtypes and gene expression. *BMC Cancer*. 2015;15:278. Exclude: No outcome of interest.
790. Kwan ML, Quesenberry CP, Jr., Caan BJ. RE: Body Mass Index, PAM50 Subtype, and Outcomes in Node-Positive Breast Cancer: CALGB 9741. *Journal of the National Cancer Institute*. 2016;108(1). Exclude: No outcome of interest.
791. Lacal JC. How molecular biology can improve clinical management: the MammaPrint experience. *Clinical & Translational Oncology: Official Publication of the Federation of Spanish Oncology Societies & of the National Cancer Institute of Mexico*. 2007;9(4):203. Exclude: Cannot be found.
792. Lafleur EA, Jia SF, Worth LL, Zhou Z, Owen-Schaub LB, Kleinerman ES. Interleukin (IL)-12 and IL-12 gene transfer up-regulate Fas expression in human osteosarcoma and breast cancer cells. *Cancer Research*. 2001;61(10):4066-4071. Exclude: Date.
793. Lagios MD, Silverstein MJ. Risk of recurrence of ductal carcinoma in situ by oncotype Dx technology: some concerns. *Cancer*. 2014;120(7):1085. Exclude: No outcome of interest.
794. Lai MS, Yen MF, Kuo HS, Koong SL, Chen TH, Duffy SW. Efficacy of breast-cancer screening for female relatives of breast-cancer-index cases: Taiwan multicentre cancer screening (TAMCAS). *International Journal of Cancer*. 1998;78(1):21-26. Exclude: Date.
795. Lal S, McCart Reed AE, de Luca XM, Simpson PT. Molecular signatures in breast cancer. *Methods (Duluth)*. 2017;131:135-146. Exclude: No outcome of interest.
796. Lalani N, Rakovitch E. Improving Therapeutic Ratios with the Oncotype DX Ductal Carcinoma In Situ (DCIS) Score. *Cureus*. 2017;9(4):e1185. Exclude: No outcome of interest.
797. Lamond NW, Skedgel C, Rayson D, Lethbridge L, Younis T. Cost-utility of the 21-gene recurrence score assay in node-negative and node-positive breast cancer. *Breast Cancer Res Treat*. 2012;133(3):1115-1123. Exclude: In included systematic review.
798. Lamond NW, Skedgel C, Younis T. Is the 21-gene recurrence score a cost-effective assay in endocrine-sensitive node-negative breast cancer? *Expert Rev Pharmacoecon Outcomes Res*. 2013;13(2):243-250. Exclude: Publication type-older systematic review.
799. Lamy PJ, Fina F, Bascoul-Mollevi C, et al. Quantification and clinical relevance of gene amplification at chromosome 17q12-q21 in human epidermal growth factor receptor 2-amplified breast cancers. *Breast Cancer Research*. 2011;13(1):R15. Exclude: Not intervention of interest.
800. Lancashire LJ, Powe DG, Reis-Filho JS, et al. A validated gene expression profile for detecting clinical outcome in breast cancer using artificial neural networks. *Breast Cancer Research & Treatment*. 2010;120(1):83-93. Exclude: No outcome of interest.
801. Landemaine T, Jackson A, Bellahcene A, et al. A six-gene signature predicting breast cancer lung metastasis. *Cancer Research*. 2008;68(15):6092-6099. Exclude: Not intervention of interest.
802. Landmark-Hoyvik H, Reinertsen KV, Loge JH, Fossa SD, Borresen-Dale AL, Dumeaux V. Alterations of gene expression in blood cells associated with chronic fatigue in breast cancer survivors. *Pharmacogenomics Journal*. 2009;9(5):333-340. Exclude: Not intervention of interest.
803. Lang K, Hao Y, Huang H, Lin I, Rogerio JW, Menzin J. Treatment patterns among elderly patients with stage IV breast cancer treated with HER-2-targeted therapy. *Journal of Comparative Effectiveness Research*. 2014;3(5):481-490. Exclude: Not intervention of interest.

804. Langerod A, Zhao H, Borgan O, et al. TP53 mutation status and gene expression profiles are powerful prognostic markers of breast cancer. *Breast Cancer Research*. 2007;9(3):R30. Exclude: Not intervention of interest.
805. Laronga C, Harness JK, Dixon M, Borgen PI. The role of the breast cancer surgeon in personalized cancer care: clinical utility of the 21-gene assay. *American Journal of Surgery*. 2012;203(6):751-758. Exclude: Publication type-commentary.
806. Laurberg T, Tramm T, Gelmon K, et al. In two independent randomized trials young high risk breast cancer patients with luminal A tumors had benefit from postmastectomy radiation therapy. *European journal of cancer*. 2013;49(27). Exclude: Not intervention of interest.
807. Lawler K, Papouli E, Naceur-Lombardelli C, et al. Gene expression modules in primary breast cancers as risk factors for organotropic patterns of first metastatic spread: a case control study. *Breast Cancer Research*. 2017;19(1):113. Exclude: No outcome of interest.
808. Le Du F, Gonzalez-Angulo AM, Park M, Liu DD, Hortobagyi GN, Ueno NT. Effect of 21-gene RT-PCR assay on adjuvant therapy and outcomes in patients with stage I breast cancer. *Clinical Breast Cancer*. 2015;15(6):458-466. Exclude: No comparator.
809. Lebeau A, Kreipe H, Dietel M, Schlake W, Kreienberg R. [Breast cancer: current recommendations for pathologists on the basis of the S3 guidelines]. *Pathologe*. 2013;34(4):293-302; quiz 303-294. Exclude: Not English.
810. Lee HH, Lim CA, Cheong YT, Singh M, Gam LH. Comparison of protein expression profiles of different stages of lymph nodes metastasis in breast cancer. *International Journal of Biological Sciences [Electronic Resource]*. 2012;8(3):353-362. Exclude: Not intervention of interest.
811. Lee HJ, Lee JJ, Song IH, et al. Prognostic and predictive value of NanoString-based immune-related gene signatures in a neoadjuvant setting of triple-negative breast cancer: relationship to tumor-infiltrating lymphocytes. *Breast Cancer Research & Treatment*. 2015;151(3):619-627. Exclude: No outcome of interest.
812. Lee J, Kim HH, Ro SM, Yang JH. Capecitabine and cisplatin (XP) combination systemic chemotherapy in heavily pre-treated HER2 negative metastatic breast cancer. *PLoS ONE [Electronic Resource]*. 2017;12(2):e0171605. Exclude: Not intervention of interest.
813. Lee JJ, Shen J. Is the Oncotype DX assay necessary in strongly estrogen receptor-positive breast cancers? *American Surgeon*. 2011;77(10):1364-1367. Exclude: No outcome of interest.
814. Lee JK, Coutant C, Kim YC, et al. Prospective comparison of clinical and genomic multivariate predictors of response to neoadjuvant chemotherapy in breast cancer. *Clinical Cancer Research*. 2010;16(2):711-718. Exclude: No outcome of interest.
815. Lee JS, Kim GE, Park MH, Yoon JH. Up-regulation of SPARC is associated with breast tumor progression and epithelial SPARC expression is correlated with poor survival and MMP-2 expression in patients with breast carcinoma. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
816. Lee JY, Park K, Lee E, et al. Gene Expression Profiling of Breast Cancer Brain Metastasis. *Scientific Reports*. 2016;6:28623. Exclude: No outcome of interest.
817. Lee LH, Swanson PE, Tang PA, Bigras G, Yang H. Association Between Phosphorylated Histone H3 and Oncotype DX Recurrence Scores in Breast Cancer. *Applied Immunohistochemistry & Molecular Morphology*. 2017;25(1):25-31. Exclude: No outcome of interest.

818. Lee M, Beggs SM, Gildea D, et al. Necdin is a breast cancer metastasis suppressor that regulates the transcription of c-Myc. *Oncotarget*. 2015;6(31):31557-31568. Exclude: Not intervention of interest.
819. Lee MH, Han W, Lee JE, et al. The clinical impact of 21-gene recurrence score on treatment decisions for patients with hormone receptor-positive early breast cancer in Korea. *Cancer Res Treat*. 2015;47(2):208-214. Exclude: In included systematic review.
820. Lee SC, Xu X, Chng WJ, et al. Post-treatment tumor gene expression signatures are more predictive of treatment outcomes than baseline signatures in breast cancer. *Pharmacogenetics and Genomics*. 2009;19(11):833-842. Exclude: No outcome of interest.
821. Lee SG, Orel SG, Woo IJ, et al. MR imaging screening of the contralateral breast in patients with newly diagnosed breast cancer: preliminary results. *Radiology*. 2003;226(3):773-778. Exclude: Date.
822. Lee SH, Ha S, An HJ, et al. Association between partial-volume corrected SUVmax and Oncotype DX recurrence score in early-stage, ER-positive/HER2-negative invasive breast cancer. *European Journal of Nuclear Medicine & Molecular Imaging*. 2016;43(9):1574-1584. Exclude: No outcome of interest.
823. Lee U, Frankenberger C, Yun J, et al. A prognostic gene signature for metastasis-free survival of triple negative breast cancer patients. *PLoS ONE [Electronic Resource]*. 2013;8(12):e82125. Exclude: No outcome of interest.
824. Legare S, Cavallone L, Mamo A, et al. The Estrogen Receptor Cofactor SPEN Functions as a Tumor Suppressor and Candidate Biomarker of Drug Responsiveness in Hormone-Dependent Breast Cancers. *Cancer Research*. 2015;75(20):4351-4363. Exclude: Not intervention of interest.
825. Leggett LE, Lorenzetti DL, Noseworthy T, Tiwana S, Mackean G, Clement F. Experiences and attitudes toward risk of recurrence testing in women with breast cancer: a systematic review. *Breast Cancer Res Treat*. 2014;144(3):457-465. Exclude: No outcome of interest.
826. Lehmann BD, Ding Y, Viox DJ, et al. Evaluation of public cancer datasets and signatures identifies TP53 mutant signatures with robust prognostic and predictive value. *BMC Cancer*. 2015;15:179. Exclude: Not intervention of interest.
827. Lehmann BD, Jovanovic B, Chen X, et al. Refinement of Triple-Negative Breast Cancer Molecular Subtypes: Implications for Neoadjuvant Chemotherapy Selection. *PLoS ONE [Electronic Resource]*. 2016;11(6):e0157368. Exclude: No outcome of interest.
828. Lei B, Zhang XY, Zhou JP, et al. Transcriptome sequencing of HER2-positive breast cancer stem cells identifies potential prognostic marker. *Tumour Biology*. 2016;37(11):14757-14764. Exclude: Not intervention of interest.
829. Lemee F, Bergoglio V, Fernandez-Vidal A, et al. DNA polymerase theta up-regulation is associated with poor survival in breast cancer, perturbs DNA replication, and promotes genetic instability. *Proceedings of the National Academy of Sciences of the United States of America*. 2010;107(30):13390-13395. Exclude: Not intervention of interest.
830. Lemler DJ, Lynch ML, Tesfay L, et al. DCYTB is a predictor of outcome in breast cancer that functions via iron-independent mechanisms. *Breast Cancer Research*. 2017;19(1):25. Exclude: Not intervention of interest.
831. Leonard C, Lei R, Antell A, et al. A comparison of models (physician, the Van Nuys prognostic index, the Memorial-Sloan-Kettering Cancer Center DCIS nomogram) to predict ipsilateral breast events in patients with ductal carcinoma in situ (DCIS) of the breast after breast-conserving surgery failed to replicate results of the oncotype DCIS recurrence score. *Cancer research Conference: 39th annual CTRC*

AACR san antonio breast cancer symposium United states. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

832. Leoni F, Colnaghi MI, Canevari S, et al. Glycolipids carrying Le(y) are preferentially expressed on small-cell lung cancer cells as detected by the monoclonal antibody MLuCl. *International Journal of Cancer*. 1992;51(2):225-231. Exclude: Date.

833. Leung RC, Yau TC, Chan MC, et al. The impact of the Oncotype DX Breast Cancer Assay on treatment decisions for women with estrogen receptor-positive, node-negative breast carcinoma in Hong Kong. *Clinical Breast Cancer*. 2016;16(5):372-378. Exclude: In included systematic review.

834. Levine MN, Julian JA, Bedard PL, et al. Prospective evaluation of the 21-gene recurrence score assay for breast cancer decision-making in Ontario. *J Clin Oncol*. 2016;34(10):1065-1071. Exclude: In included systematic review.

835. Li D, Yu H, Xu TF, Li JH, Sun YF, Zhang WQ. Interleukin-12 gene modification exerts anti-tumor effects on murine mammary sarcoma cell line in vivo. *Cellular & Molecular Immunology*. 2008;5(3):225-230. Exclude: Not intervention of interest.

836. Li H, Zhu Y, Burnside ES, et al. MR Imaging Radiomics Signatures for Predicting the Risk of Breast Cancer Recurrence as Given by Research Versions of MammaPrint, Oncotype DX, and PAM50 Gene Assays. *Radiology*. 2016;281(2):382-391. Exclude: No outcome of interest.

837. Li J, Humphreys K, Darabi H, et al. A genome-wide association scan on estrogen receptor-negative breast cancer. *Breast Cancer Research*. 2010;12(6):R93. Exclude: No outcome of interest.

838. Li J, Ivansson E, Klevebring D, et al. Molecular Differences between Screen-Detected and Interval Breast Cancers Are Largely Explained by PAM50 Subtypes. *Clinical Cancer Research*. 2017;23(10):2584-2592. Exclude: No outcome of interest.

839. Li JY, Zhang Y, Zhang WH, Jia S, Kang Y, Tian R. Effects of differential distribution of microvessel density, possibly regulated by miR-374a, on breast cancer prognosis. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2013;14(3):1715-1720. Exclude: Not intervention of interest.

840. Li JY, Zhang Y, Zhang WH, Jia S, Kang Y, Zhu XY. Differential distribution of miR-20a and miR-20b may underly metastatic heterogeneity of breast cancers. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2012;13(5):1901-1906. Exclude: Not intervention of interest.

841. Li LF, Xu XJ, Zhao Y, et al. Integrated gene expression profile predicts prognosis of breast cancer patients. *Breast Cancer Research & Treatment*. 2009;113(2):231-237. Exclude: No outcome of interest.

842. Li Q, Eklund AC, Birkbak NJ, et al. Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. *BMC Bioinformatics*. 2011;12:310. Exclude: Not intervention of interest.

843. Li Q, Eklund AC, Juul N, et al. Minimising immunohistochemical false negative ER classification using a complementary 23 gene expression signature of ER status. *PLoS ONE [Electronic Resource]*. 2010;5(12):e15031. Exclude: Not intervention of interest.

844. Li R, Campos J, Iida J. A Gene Regulatory Program in Human Breast Cancer. *Genetics*. 2015;201(4):1341-1348. Exclude: Not intervention of interest.

845. Li Y, Arellano AR, Bare LA, Bender RA, Strom CM, Devlin JJ. A Multigene Test Could Cost-Effectively Help Extend Life Expectancy for Women at Risk of Hereditary Breast Cancer. *Value in Health*. 2017;20(4):547-555. Exclude: Not intervention of interest.

846. Li Y, Guo M, Fu Z, et al. Immunoglobulin superfamily genes are novel prognostic biomarkers for breast cancer. *Oncotarget*. 2017;8(2):2444-2456. Exclude: Not intervention of interest.
847. Li Y, Wang X, Vural S, Mishra NK, Cowan KH, Guda C. Exome analysis reveals differentially mutated gene signatures of stage, grade and subtype in breast cancers. *PLoS ONE [Electronic Resource]*. 2015;10(3):e0119383. Exclude: Not intervention of interest.
848. Ligibel JA, Cirrincione CT, Liu M, et al. Body Mass Index, PAM50 Subtype, and Outcomes in Node-Positive Breast Cancer: CALGB 9741 (Alliance). *Journal of the National Cancer Institute*. 2015;107(9). Exclude: No outcome of interest.
849. Lillie SE, Brewer NT, O'Neill SC, et al. Retention and use of breast cancer recurrence risk information from genomic tests: the role of health literacy. *Cancer Epidemiology, Biomarkers & Prevention*. 2007;16(2):249-255. Exclude: No outcome of interest.
850. Lim S, Park Y, Hur B, Kim M, Han W, Kim S. Protein interaction network (PIN)-based breast cancer subsystem identification and activation measurement for prognostic modeling. *Methods (Duluth)*. 2016;110:81-89. Exclude: Not intervention of interest.
851. Lin CH, Chen IC, Huang CS, et al. TP53 Mutational Analysis Enhances the Prognostic Accuracy of IHC4 and PAM50 Assays. *Scientific Reports*. 2015;5:17879. Exclude: No outcome of interest.
852. Lin Z, Li JW, Wang Y, et al. Abnormal miRNA-30e Expression is Associated with Breast Cancer Progression. *Clinical Laboratory*. 2016;62(1-2):121-128. Exclude: Not intervention of interest.
853. Lindstrom LS, Benz CC, Yau C, van't Veer LJ, Thompson CK, Esserman LJ. MammaPrint accurately predicts long-term survival (25 years) and adjuvant tamoxifen therapy benefit in lymph node negative patients. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
854. Lindstrom LS, Yau C, Czene K, et al. Intra-tumor heterogeneity of the estrogen receptor predicts less benefit from tamoxifen therapy and poor long-term breast cancer patient survival-Retrospective analyses of the STO-3 randomized trial. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
855. Lipkus IM, Vadaparampil ST, Jacobsen PB, Miree CA. Knowledge about genomic recurrence risk testing among breast cancer survivors. *Journal of Cancer Education*. 2011;26(4):664-669. Exclude: No outcome of interest.
856. Lips EH, Mukhtar RA, Yau C, et al. Lobular histology and response to neoadjuvant chemotherapy in invasive breast cancer. *Breast Cancer Research & Treatment*. 2012;136(1):35-43. Exclude: Not intervention of interest.
857. List M, Hauschild AC, Tan Q, et al. Classification of breast cancer subtypes by combining gene expression and DNA methylation data. *Journal of Integrative Bioinformatics*. 2014;11(2):236. Exclude: No outcome of interest.
858. listed Na. MammaPrint Reduces Breast Cancer Overtreatment. *Cancer Discov*. 2016;6(6):Of4. Exclude: Publication type-commentary.
859. Litviakov NV, Cherdyntseva NV, Tsyganov MM, et al. Deletions of multidrug resistance gene loci in breast cancer leads to the down-regulation of its expression and predict tumor response to neoadjuvant chemotherapy. *Oncotarget*. 2016;7(7):7829-7841. Exclude: Not intervention of interest.

860. Liu J, Campen A, Huang S, et al. Identification of a gene signature in cell cycle pathway for breast cancer prognosis using gene expression profiling data. *BMC Medical Genomics [Electronic Resource]*. 2008;1:39. Exclude: Not intervention of interest.
861. Liu L, Li XR, Hu YH, Zhang J. [Relevance between TOP2A, EGFR gene expression and efficacy of docetaxel plus epirubicin as neoadjuvant chemotherapy in triple negative breast cancer patients]. *Chung-Hua i Hsueh Tsa Chih [Chinese Medical Journal]*. 2016;96(12):940-943. Exclude: Not intervention of interest.
862. Liu LY, Chang LY, Kuo WH, Hwa HL, Chang KJ, Hsieh FJ. A supervised network analysis on gene expression profiles of breast tumors predicts a 41-gene prognostic signature of the transcription factor MYB across molecular subtypes. *Computational & Mathematical Methods in Medicine*. 2014;2014:813067. Exclude: Not intervention of interest.
863. Liu MC, Pitcher BN, Mardis ER, et al. PAM50 gene signatures and breast cancer prognosis with adjuvant anthracycline- and taxane-based chemotherapy: correlative analysis of C9741 (Alliance). *NPJ Breast Cancer*. 2016;2. Exclude: No outcome of interest.
864. Liu NQ, Stingl C, Look MP, et al. Comparative proteome analysis revealing an 11-protein signature for aggressive triple-negative breast cancer. *Journal of the National Cancer Institute*. 2014;106(2):djt376. Exclude: Not intervention of interest.
865. Liu R, Zhang W, Liu ZQ, Zhou HH. Gene modules associated with breast cancer distant metastasis-free survival in the PAM50 molecular subtypes. *Oncotarget*. 2016;7(16):21686-21698. Exclude: No outcome of interest.
866. Liu RZ, Graham K, Glubrecht DD, Lai R, Mackey JR, Godbout R. A fatty acid-binding protein 7/RXRbeta pathway enhances survival and proliferation in triple-negative breast cancer. *Journal of Pathology*. 2012;228(3):310-321. Exclude: Not intervention of interest.
867. Liu S, Chapman JA, Burnell MJ, et al. Prognostic and predictive investigation of PAM50 intrinsic subtypes in the NCIC CTG MA.21 phase III chemotherapy trial. *Breast Cancer Research & Treatment*. 2015;149(2):439-448. Exclude: No outcome of interest.
868. Liu X, Zhao B, Wang H, et al. Aberrant expression of Arpin in human breast cancer and its clinical significance. *Journal of Cellular & Molecular Medicine*. 2016;20(3):450-458. Exclude: Not intervention of interest.
869. Liu Y, Lv DL, Duan JJ, et al. ALDH1A1 expression correlates with clinicopathologic features and poor prognosis of breast cancer patients: a systematic review and meta-analysis. *BMC Cancer*. 2014;14:444. Exclude: Not intervention of interest.
870. Llombart A, Cortes J, Ciruelos E, et al. A phase II, randomized study of T-DM1 versus T-DM1 plus short induction with docetaxel in first line treatment for locally advanced or metastatic HER2+ breast cancer (SOLTI-1203). *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
871. Llombart-Cussac A, Cortes J, Pare L, et al. HER2-enriched subtype as a predictor of pathological complete response following trastuzumab and lapatinib without chemotherapy in early-stage HER2-positive breast cancer (PAMELA): an open-label, single-group, multicentre, phase 2 trial. *Lancet Oncology*. 2017;18(4):545-554. Exclude: Not intervention of interest.
872. Lo LC, Cheng TL, Chiang JY, Damdinsuren N. Breast cancer index: a perspective on tongue diagnosis in traditional chinese medicine. *Journal of Traditional & Complementary Medicine*. 2013;3(3):194-203. Exclude: No outcome of interest.

873. Lo SS, Mumby PB, Norton J, et al. Prospective multicenter study of the impact of the 21-gene recurrence score assay on medical oncologist and patient adjuvant breast cancer treatment selection. *J Clin Oncol*. 2010;28(10):1671-1676. Exclude: In included systematic review.
874. Lo WC, Li W, Jones EF, et al. Effect of Imaging Parameter Thresholds on MRI Prediction of Neoadjuvant Chemotherapy Response in Breast Cancer Subtypes. *PLoS ONE [Electronic Resource]*. 2016;11(2):e0142047. Exclude: Not intervention of interest.
875. Loi S, Haibe-Kains B, Desmedt C, et al. Definition of clinically distinct molecular subtypes in estrogen receptor-positive breast carcinomas through genomic grade.[Erratum appears in *J Clin Oncol*. 2007 Aug 20;25(24):3790]. *Journal of Clinical Oncology*. 2007;25(10):1239-1246. Exclude: No outcome of interest.
876. Loi S, Haibe-Kains B, Desmedt C, et al. Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. *BMC Genomics*. 2008;9:239. Exclude: No outcome of interest.
877. Loi S, Michiels S, Lambrechts D, et al. Somatic mutation profiling and associations with prognosis and trastuzumab benefit in early breast cancer. *Journal of the National Cancer Institute*. 2013;105(13):960-967. Exclude: Not intervention of interest.
878. Loman N, Bladstrom A, Johannsson O, Borg A, Olsson H. Cancer incidence in relatives of a population-based set of cases of early-onset breast cancer with a known BRCA1 and BRCA2 mutation status. *Breast Cancer Research*. 2003;5(6):R175-186. Exclude: Date.
879. Lomnytska M, Dubrovskaya A, Hellman U, Volodko N, Souchelnyskyi S. Increased expression of cSHMT, Tbx3 and utrophin in plasma of ovarian and breast cancer patients. *International Journal of Cancer*. 2006;118(2):412-421. Exclude: Date.
880. Lonning PE. Poor-prognosis estrogen receptor- positive disease: present and future clinical solutions. *Therapeutic Advances in Medical Oncology*. 2012;4(3):127-137. Exclude: Not intervention of interest.
881. Lonning PE, Sorlie T, Perou CM, Brown PO, Botstein D, Borresen-Dale AL. Microarrays in primary breast cancer--lessons from chemotherapy studies. *Endocrine-Related Cancer*. 2001;8(3):259-263. Exclude: Date.
882. Lopes N, Sousa B, Martins D, et al. Alterations in Vitamin D signalling and metabolic pathways in breast cancer progression: a study of VDR, CYP27B1 and CYP24A1 expression in benign and malignant breast lesions. *BMC Cancer*. 2010;10:483. Exclude: Not intervention of interest.
883. Lopez Ruiz JA, Zabalza Estevez I, Mieza Arana JA. Breast cancer: determining the genetic profile from ultrasound-guided percutaneous biopsy specimens obtained during the diagnostic workups. *Radiologia*. 2016;58(3):214-220. Exclude: No outcome of interest.
884. Lopez-Tarruella S, Martin M. Recent advances in systemic therapy: advances in adjuvant systemic chemotherapy of early breast cancer. *Breast Cancer Research*. 2009;11(2):204. Exclude: Publication type-commentary.
885. Losk K, Vaz-Luis I, Camuso K, et al. Factors Associated With Delays in Chemotherapy Initiation Among Patients With Breast Cancer at a Comprehensive Cancer Center. *Journal of the National Comprehensive Cancer Network*. 2016;14(12):1519-1526. Exclude: Not intervention of interest.
886. Lou L, Cong XL, Yu GF, Li JC, Ma YX. US findings of bilateral primary breast cancer: retrospective study. *European Journal of Radiology*. 2007;61(1):154-157. Exclude: Not intervention of interest.
887. Lu Z, Liu M, Stribinskis V, et al. MicroRNA-21 promotes cell transformation by targeting the programmed cell death 4 gene. *Oncogene*. 2008;27(31):4373-4379. Exclude: Not intervention of interest.

888. Luan Y, Li H. Group additive regression models for genomic data analysis. *Biostatistics*. 2008;9(1):100-113. Exclude: No outcome of interest.
889. Lund MJ, Mosunjac M, Davis KM, et al. 21-Gene recurrence scores: racial differences in testing, scores, treatment, and outcome. *Cancer*. 2012;118(3):788-796. Exclude: No outcome of interest.
890. Luo J, Liu S, Leung S, et al. An mRNA Gene Expression-Based Signature to Identify FGFR1-Amplified Estrogen Receptor-Positive Breast Tumors. *Journal of Molecular Diagnostics*. 2017;19(1):147-161. Exclude: Not intervention of interest.
891. Luporsi E, Bellocq JP, Barriere J, et al. [uPA/PAI-1, Oncotype DXTM, MammaPrint(). Prognosis and predictive values for clinical utility in breast cancer management]. *Bulletin du Cancer*. 2015;102(9):719-729. Exclude: No outcome of interest.
892. Lyman GH, Cosler LE, Kuderer NM, Hornberger J. Impact of a 21-gene RT-PCR assay on treatment decisions in early-stage breast cancer: an economic analysis based on prognostic and predictive validation studies. *Cancer*. 2007;109(6):1011-1018. Exclude: Date.
893. Lyman GH, Kuderer NM. Gene expression profile assays as predictors of recurrence-free survival in early-stage breast cancer: a metaanalysis. *Clinical Breast Cancer*. 2006;7(5):372-379. Exclude: Date.
894. Lynch JA, Berse B, Coomer N, Kautter J. 21-Gene recurrence score testing among Medicare beneficiaries with breast cancer in 2010-2013. *Genetics in Medicine*. 2017;19(10):1134-1143. Exclude: No outcome of interest.
895. Lynch JA, Berse B, Petkov V, et al. Implementation of the 21-gene recurrence score test in the United States in 2011. *Genetics in Medicine*. 2016;18(10):982-990. Exclude: No outcome of interest.
896. Lyng MB, Kodahl AR, Binder H, Ditzel HJ. Prospective validation of a blood-based 9-miRNA profile for early detection of breast cancer in a cohort of women examined by clinical mammography. *Molecular Oncology*. 2016;10(10):1621-1626. Exclude: Not intervention of interest.
897. Ma C, Sastry KS, Flore M, et al. CrossLink: a novel method for cross-condition classification of cancer subtypes. *BMC Genomics*. 2016;17 Suppl 7:549. Exclude: Not intervention of interest.
898. Ma CX, Bose R, Ellis MJ. Prognostic and predictive biomarkers of endocrine responsiveness for estrogen receptor positive breast cancer. *Advances in Experimental Medicine and Biology*. 2016;882:125-154. Exclude: No outcome of interest.
899. Ma H, Lu Y, Marchbanks PA, et al. Quantitative measures of estrogen receptor expression in relation to breast cancer-specific mortality risk among white women and black women. *Breast Cancer Research*. 2013;15(5):R90. Exclude: Not intervention of interest.
900. Ma S, Huang J, Xie Y, Yi N. Identification of breast cancer prognosis markers using integrative sparse boosting. *Methods of Information in Medicine*. 2012;51(2):152-161. Exclude: Not intervention of interest.
901. Ma S, Huang Y, Huang J, Fang K. Gene network-based cancer prognosis analysis with sparse boosting. *Genetical research*. 2012;94(4):205-221. Exclude: No outcome of interest.
902. Ma S, Kosorok MR. Detection of gene pathways with predictive power for breast cancer prognosis. *BMC Bioinformatics*. 2010;11:1. Exclude: No outcome of interest.
903. Ma W, Deng Y, Zhou L. The prognostic value of adhesion molecule CD44v6 in women with primary breast carcinoma: a clinicopathologic study. *Clinical Oncology (Royal College of Radiologists)*. 2005;17(4):258-263. Exclude: Date.

904. Ma XJ, Salunga R, Dahiya S, et al. A five-gene molecular grade index and HOXB13:IL17BR are complementary prognostic factors in early stage breast cancer. *Clinical Cancer Research*. 2008;14(9):2601-2608. Exclude: Not intervention of interest.
905. MacKenzie TA, Schwartz GN, Calderone HM, et al. Stromal expression of miR-21 identifies high-risk group in triple-negative breast cancer. *American Journal of Pathology*. 2014;184(12):3217-3225. Exclude: Not intervention of interest.
906. Madaras L, Balint N, Gyorffy B, et al. BRCA Mutation-Related and Claudin-Low Breast Cancer: Blood Relatives or Stepsisters. *Pathobiology*. 2016;83(1):1-12. Exclude: Not intervention of interest.
907. Madden SF, Clarke C, Gaule P, et al. BreastMark: an integrated approach to mining publicly available transcriptomic datasets relating to breast cancer outcome. *Breast Cancer Research*. 2013;15(4):R52. Exclude: No outcome of interest.
908. Magbanua MJ, Wolf DM, Yau C, et al. Serial expression analysis of breast tumors during neoadjuvant chemotherapy reveals changes in cell cycle and immune pathways associated with recurrence and response. *Breast Cancer Research*. 2015;17:73. Exclude: No outcome of interest.
909. Makama M, Drukker CA, Rutgers EJT, et al. An association study of established breast cancer reproductive and lifestyle risk factors with tumour subtype defined by the prognostic 70-gene expression signature (MammaPrint[®]). *European Journal of Cancer*. 2017;75:5-13. Exclude: No outcome of interest.
910. Malamou-Mitsi V, Gogas H, Dafni U, et al. Evaluation of the prognostic and predictive value of p53 and Bcl-2 in breast cancer patients participating in a randomized study with dose-dense sequential adjuvant chemotherapy. *Annals of Oncology*. 2006;17(10):1504-1511. Exclude: Date.
911. Malinowski DP. Multiple biomarkers in molecular oncology. II. Molecular diagnostics applications in breast cancer management. *Expert Review of Molecular Diagnostics*. 2007;7(3):269-280. Exclude: No outcome of interest.
912. Mamounas EP, Budd GT, Miller KD. Incorporating the Oncotype DX breast cancer assay into community practice: an expert Q&A and case study sampling. *Clinical Advances in Hematology & Oncology*. 2008;6(2 Suppl 3):1-8. Exclude: Publication type-commentary.
913. Mamounas EP, Liu Q, Paik S, et al. 21-Gene Recurrence Score and Locoregional Recurrence in Node-Positive/ER-Positive Breast Cancer Treated With Chemo-Endocrine Therapy. *Journal of the National Cancer Institute*. 2017;109(4):01. Exclude: No outcome of interest.
914. Mamounas EP, Tang G, Fisher B, et al. Association between the 21-gene recurrence score assay and risk of locoregional recurrence in node-negative, estrogen receptor-positive breast cancer: results from NSABP B-14 and NSABP B-20. *Journal of Clinical Oncology*. 2010;28(10):1677-1683. Exclude: Publication type-commentary.
915. Mamounas EP, Tang G, Paik S, et al. Association between the 21-gene recurrence score (RS) and benefit from adjuvant paclitaxel (Pac) in node-positive (N+), ER-positive breast cancer patients (pts): Results from NSABP B-28 5. *Cancer Research*. 2012;72(24 Supplement):Abstract no: S1-10. Exclude: Publication type-conference abstract.
916. Manders JB, Kuerer HM, Smith BD, et al. Clinical utility of the 12-Gene DCIS score assay: Impact on radiotherapy recommendations for patients with ductal carcinoma in situ. *Annals of Surgical Oncology*. 2017;24(3):660-668. Exclude: Not intervention of interest.

917. Manjili MH, Najarian K, Wang XY. Signatures of tumor-immune interactions as biomarkers for breast cancer prognosis. *Future Oncology*. 2012;8(6):703-711. Exclude: No outcome of interest.
918. Mannelqvist M, Wik E, Stefansson IM, Akslen LA. An 18-gene signature for vascular invasion is associated with aggressive features and reduced survival in breast cancer. *PLoS ONE [Electronic Resource]*. 2014;9(6):e98787. Exclude: Not intervention of interest.
919. Manso L, Mouron S, Tress M, et al. Analysis of Paired Primary-Metastatic Hormone-Receptor Positive Breast Tumors (HRPBC) Uncovers Potential Novel Drivers of Hormonal Resistance. *PLoS ONE [Electronic Resource]*. 2016;11(5):e0155840. Exclude: Not intervention of interest.
920. Mantha MM. [Oncotype DX. Treating breast cancer with or without chemotherapy. Deciding which is best]. *Perspective infirmiere: Revue Officielle de l'Ordre des Infirmieres et Infirmiers du Quebec*. 2012;9(5):59-60. Exclude: Not English.
921. Mao XY, Lee MJ, Zhu J, Zhu C, Law SM, Snijders AM. Genome-wide screen identifies a novel prognostic signature for breast cancer survival. *Oncotarget*. 2017;8(8):14003-14016. Exclude: Not intervention of interest.
922. Mao Y, Chen XS, Liang Y, et al. [Effect of 21-gene recurrence score on chemotherapy decisions for patients with estrogen receptor-positive, epidermal growth factor receptor 2-negative and lymph node-negative early stage-breast cancer]. *Zhonghua Zhong Liu Za Zhi*. 2017;39(7):502-508. Exclude: Not English.
923. Mar-Aguilar F, Mendoza-Ramirez JA, Malagon-Santiago I, et al. Serum circulating microRNA profiling for identification of potential breast cancer biomarkers. *Disease Markers*. 2013;34(3):163-169. Exclude: Not intervention of interest.
924. Marchenko GN, Marchenko ND, Strongin AY. The structure and regulation of the human and mouse matrix metalloproteinase-21 gene and protein. *Biochemical Journal*. 2003;372(Pt 2):503-515. Exclude: Date.
925. Marchio C, Geyer FC, Ng CK, et al. The genetic landscape of breast carcinomas with neuroendocrine differentiation. *Journal of Pathology*. 2017;241(3):405-419. Exclude: Not intervention of interest.
926. Marchionni L, Afsari B, Geman D, Leek JT. A simple and reproducible breast cancer prognostic test. *BMC Genomics*. 2013;14:336. Exclude: No outcome of interest.
927. Marchionni L, Wilson RF, Marinopoulos SS, et al. Impact of gene expression profiling tests on breast cancer outcomes. *Evidence Report/Technology Assessment*. 2007(160):1-105. Exclude: No outcome of interest.
928. Marchionni L, Wilson RF, Wolff AC, et al. Systematic review: gene expression profiling assays in early-stage breast cancer. *Ann Intern Med*. 2008;148(5):358-369. Exclude: Publication type-older systematic review.
929. Marcinkowski EF, Ottesen R, Niland J, Vito C. Acceptance of adjuvant chemotherapy recommendations in early-stage hormone-positive breast cancer. *Journal of Surgical Research*. 2017;214:79-85. Exclude: No outcome of interest.
930. Marino P, Siani C, Bertucci F, et al. Economic issues involved in integrating genomic testing into clinical care: the case of genomic testing to guide decision-making about chemotherapy for breast cancer patients. *Breast Cancer Research & Treatment*. 2011;129(2):401-409. Exclude: Not intervention of interest.
931. Mark KMK, Varn FS, Ung MH, Qian F, Cheng C. The E2F4 prognostic signature predicts pathological response to neoadjuvant chemotherapy in breast cancer patients. *BMC Cancer*. 2017;17(1):306. Exclude: Not intervention of interest.

932. Markopoulos C. Overview of the use of Oncotype DX() as an additional treatment decision tool in early breast cancer. *Expert Review of Anticancer Therapy*. 2013;13(2):179-194. Exclude: Publication type-commentary.
933. Markopoulos C, van de Velde C, Zarca D, Ozmen V, Masetti R. Clinical evidence supporting genomic tests in early breast cancer: Do all genomic tests provide the same information? *European Journal of Surgical Oncology*. 2017;43(5):909-920. Exclude: Publication type-not systematic review.
934. Markopoulos C, Xepapadakis G, Venizelos V, et al. Clinical experience of using Oncotype DX as an additional treatment decision tool in early breast cancer - a retrospective analysis from 5 Greek institutions. *European Journal of Surgical Oncology*. 2012;38(5):413-419. Exclude: No outcome of interest.
935. Markowski DN, Huhle S, Nimzyk R, Stenman G, Loning T, Bullerdiel J. MED12 mutations occurring in benign and malignant mammalian smooth muscle tumors. *Genes, Chromosomes & Cancer*. 2013;52(3):297-304. Exclude: Not intervention of interest.
936. Marks JR, Humphrey PA, Wu K, et al. Overexpression of p53 and HER-2/neu proteins as prognostic markers in early stage breast cancer. *Annals of Surgery*. 1994;219(4):332-341. Exclude: Date.
937. Maroni P, Matteucci E, Luzzati A, Perrucchini G, Bendinelli P, Desiderio MA. Nuclear co-localization and functional interaction of COX-2 and HIF-1alpha characterize bone metastasis of human breast carcinoma. *Breast Cancer Research & Treatment*. 2011;129(2):433-450. Exclude: Not intervention of interest.
938. Marrakchi R, Ouerhani S, Benammar S, et al. Detection of cytokeratin 19 mRNA and CYFRA 21-1 (cytokeratin 19 fragments) in blood of Tunisian women with breast cancer. *International Journal of Biological Markers*. 2008;23(4):238-243. Exclude: Not intervention of interest.
939. Marrone M, Stewart A, Dotson WD. Clinical utility of gene-expression profiling in women with early breast cancer: an overview of systematic reviews. *Genet Med*. 2015;17(7):519-532. Exclude: Publication type-not systematic review.
940. Martel S, Prady C, Simon R, Matte C. OncotypeDX for breast cancer: a multigene assay that makes a difference? *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
941. Martin DN, Boersma BJ, Yi M, et al. Differences in the tumor microenvironment between African-American and European-American breast cancer patients. *PLoS ONE [Electronic Resource]*. 2009;4(2):e4531. Exclude: Not intervention of interest.
942. Martin M, Brase JC, Calvo L, et al. Clinical validation of the EndoPredict test in node-positive, chemotherapy-treated ER+/HER2- breast cancer patients: results from the GEICAM 9906 trial. *Breast Cancer Research*. 2014;16(2):R38. Exclude: No outcome of interest.
943. Martin M, Brase JC, Ruiz A, et al. Prognostic ability of EndoPredict compared to research-based versions of the PAM50 risk of recurrence (ROR) scores in node-positive, estrogen receptor-positive, and HER2-negative breast cancer. A GEICAM/9906 sub-study. *Breast Cancer Research & Treatment*. 2016;156(1):81-89. Exclude: No outcome of interest.
944. Martin M, Gonzalez Palacios F, Cortes J, de la Haba J, Schneider J. Prognostic and predictive factors and genetic analysis of early breast cancer. *Clinical & Translational Oncology: Official Publication of the Federation of Spanish Oncology Societies & of the National Cancer Institute of Mexico*. 2009;11(10):634-642. Exclude: No outcome of interest.

945. Martin M, Gonzalez-Rivera M, Morales S, et al. Prospective study of the impact of the Prosigna assay on adjuvant clinical decision-making in unselected patients with estrogen receptor positive, human epidermal growth factor receptor negative, node negative early-stage breast cancer. *Curr Med Res Opin.* 2015;31(6):1129-1137. Exclude: In included systematic review.
946. Martin M, Muller K, Cadenas C, et al. ERBB2 overexpression triggers transient high mechanoactivity of breast tumor cells. *Cytoskeleton.* 2012;69(5):267-277. Exclude: Not intervention of interest.
947. Martin M, Prat A, Rodriguez-Lescure A, et al. PAM50 proliferation score as a predictor of weekly paclitaxel benefit in breast cancer. *Breast Cancer Research & Treatment.* 2013;138(2):457-466. Exclude: No outcome of interest.
948. Martinet O, Divino CM, Zang Y, et al. T cell activation with systemic agonistic antibody versus local 4-1BB ligand gene delivery combined with interleukin-12 eradicate liver metastases of breast cancer. *Gene Therapy.* 2002;9(12):786-792. Exclude: Date.
949. Maslikowski BM, Neel BD, Wu Y, et al. Cellular processes of v-Src transformation revealed by gene profiling of primary cells--implications for human cancer. *BMC Cancer.* 2010;10:41. Exclude: Not intervention of interest.
950. Masuda H, Baggerly KA, Wang Y, et al. Differential response to neoadjuvant chemotherapy among 7 triple-negative breast cancer molecular subtypes. *Clinical Cancer Research.* 2013;19(19):5533-5540. Exclude: Not intervention of interest.
951. Masuda H, Qi Y, Liu S, et al. Reverse phase protein array identification of triple-negative breast cancer subtypes and comparison with mRNA molecular subtypes. *Oncotarget.* 2017;8(41):70481-70495. Exclude: Not intervention of interest.
952. Masuda TA, Kataoka A, Ohno S, et al. Detection of occult cancer cells in peripheral blood and bone marrow by quantitative RT-PCR assay for cytokeratin-7 in breast cancer patients. *International Journal of Oncology.* 2005;26(3):721-730. Exclude: Date.
953. Matboli M, Eissa S, Said H. Evaluation of histidine-rich glycoprotein tissue RNA and serum protein as novel markers for breast cancer. *Medical Oncology.* 2014;31(4):897. Exclude: Not intervention of interest.
954. Mathieu MC, Mazouni C, Kesty NC, et al. Breast Cancer Index predicts pathological complete response and eligibility for breast conserving surgery in breast cancer patients treated with neoadjuvant chemotherapy. *Ann Oncol.* 2012;23(8):2046-2052. Exclude: No outcome of interest.
955. Matkovic B, Juretic A, Separovic V, et al. Immunohistochemical analysis of ER, PR, HER-2, CK 5/6, p63 and EGFR antigen expression in medullary breast cancer. *Tumori.* 2008;94(6):838-844. Exclude: Not intervention of interest.
956. Matsuda N, Lim B, Wang Y, et al. Identification of frequent somatic mutations in inflammatory breast cancer. *Breast Cancer Research & Treatment.* 2017;163(2):263-272. Exclude: Not intervention of interest.
957. Mattes MD, Mann JM, Ashamalla H, Tejwani A. Routine histopathologic characteristics can predict oncotype DX(TM) recurrence score in subsets of breast cancer patients. *Cancer Investigation.* 2013;31(9):604-606. Exclude: No outcome of interest.
958. Maxhimer JB, Pesce CE, Stewart RA, Gattuso P, Prinz RA, Xu X. Ductal carcinoma in situ of the breast and heparanase-1 expression: a molecular explanation for more aggressive subtypes. *Journal of the American College of Surgeons.* 2005;200(3):328-335. Exclude: Date.
959. Mayer EL, Vaz-Luis I, Richardson AL, et al. TBCRC030: A randomized, phase II study of preoperative cisplatin versus paclitaxel in patients (pts) with BRCA1/2-proficient triple-negative breast cancer (TNBC)-

- Evaluating the homologous recombination deficiency (HRD) biomarker. *Journal of clinical oncology*. 2014;32(15 SUPPL. 1):CONFERENCE START: 2014 May 2030 CONFERENCE END: 2014 Jun 2013. Exclude: Not intervention of interest.
960. Mazzotta A, Partipilo G, De Summa S, Giotta F, Simone G, Mangia A. Nuclear PARP1 expression and its prognostic significance in breast cancer patients. *Tumour Biology*. 2016;37(5):6143-6153. Exclude: Not intervention of interest.
961. Mazzucchelli S, Fiandra L, Bellini M, et al. H-ferritin allows nanometronomic treatment of breast cancer with doxorubicin preventing drug resistance and circumventing cardiotoxicity. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
962. McCarthy MM, Sznol M, DiVito KA, Camp RL, Rimm DL, Kluger HM. Evaluating the expression and prognostic value of TRAIL-R1 and TRAIL-R2 in breast cancer. *Clinical Cancer Research*. 2005;11(14):5188-5194. Exclude: Date.
963. McDermott AM, Kerin MJ, Miller N. Identification and validation of miRNAs as endogenous controls for RQ-PCR in blood specimens for breast cancer studies. *PLoS ONE [Electronic Resource]*. 2013;8(12):e83718. Exclude: Not intervention of interest.
964. McGuire A, Brown JA, Kerin MJ. Metastatic breast cancer: the potential of miRNA for diagnosis and treatment monitoring. *Cancer & Metastasis Reviews*. 2015;34(1):145-155. Exclude: Not intervention of interest.
965. McVeigh TP, Hughes LM, Miller N, et al. The impact of Oncotype DX testing on breast cancer management and chemotherapy prescribing patterns in a tertiary referral centre. *European Journal of Cancer*. 2014;50(16):2763-2770. Exclude: No comparator.
966. McVeigh TP, Kerin MJ. Clinical use of the Oncotype DX genomic test to guide treatment decisions for patients with invasive breast cancer. *Breast Cancer Targets and Therap*. 2017;9:393-400. Exclude: Publication type-not systematic review.
967. Medimegh I, Omrane I, Privat M, et al. MicroRNAs expression in triple negative vs non triple negative breast cancer in Tunisia: interaction with clinical outcome. *PLoS ONE [Electronic Resource]*. 2014;9(11):e111877. Exclude: Not intervention of interest.
968. Mehra R, Varambally S, Ding L, et al. Identification of GATA3 as a breast cancer prognostic marker by global gene expression meta-analysis. *Cancer Research*. 2005;65(24):11259-11264. Exclude: Date.
969. Mehta R, Jain RK, Badve S. Personalized medicine: the road ahead. *Clinical Breast Cancer*. 2011;11(1):20-26. Exclude: Publication type-commentary.
970. Meijer D, Jansen MP, Look MP, et al. TSC22D1 and PSAP predict clinical outcome of tamoxifen treatment in patients with recurrent breast cancer. *Breast Cancer Research & Treatment*. 2009;113(2):253-260. Exclude: Not intervention of interest.
971. Meleth S, Reeder-Hayes K, Ashok M, et al. AHRQ Technology Assessments. In: *Technology Assessment of Molecular Pathology Testing for the Estimation of Prognosis for Common Cancers*. Rockville (MD): Agency for Healthcare Research and Quality (US); 2014.
972. Menard S, Casalini P, Campiglio M, Pupa SM, Tagliabue E. Role of HER2/neu in tumor progression and therapy. *Cellular & Molecular Life Sciences*. 2004;61(23):2965-2978. Exclude: Date.

973. Meng J, Li P, Zhang Q, Yang Z, Fu S. A four-long non-coding RNA signature in predicting breast cancer survival. *Journal of Experimental & Clinical Cancer Research*. 2014;33:84. Exclude: Not intervention of interest.
974. Mercaldo ND, Lau KF, Zhou XH. Confidence intervals for predictive values with an emphasis to case-control studies. *Statistics in Medicine*. 2007;26(10):2170-2183. Exclude: No outcome of interest.
975. Meshkat M, Tanha HM, Naeini MM, et al. Functional SNP in stem of mir-146a affects Her2 status and breast cancer survival. *Cancer Biomarkers: Section A of Disease Markers*. 2016;17(2):213-222. Exclude: Not intervention of interest.
976. Mettu RK, Wan YW, Habermann JK, Ried T, Guo NL. A 12-gene genomic instability signature predicts clinical outcomes in multiple cancer types. *International Journal of Biological Markers*. 2010;25(4):219-228. Exclude: No outcome of interest.
977. Meunier-Carpentier S, Dales JP, Djemli A, et al. Comparison of the prognosis indication of VEGFR-1 and VEGFR-2 and Tie2 receptor expression in breast carcinoma. *International Journal of Oncology*. 2005;26(4):977-984. Exclude: Date.
978. Meyers MO, Klauber-Demore N, Ollila DW, et al. Impact of breast cancer molecular subtypes on locoregional recurrence in patients treated with neoadjuvant chemotherapy for locally advanced breast cancer. *Annals of Surgical Oncology*. 2011;18(10):2851-2857. Exclude: Not intervention of interest.
979. Michishita S, Kim SJ, Shimazu K, et al. Prediction of pathological complete response to neoadjuvant chemotherapy by magnetic resonance imaging in breast cancer patients. *Breast*. 2015;24(2):159-165. Exclude: Not intervention of interest.
980. Miecznikowski JC, Wang D, Liu S, Sucheston L, Gold D. Comparative survival analysis of breast cancer microarray studies identifies important prognostic genetic pathways. *BMC Cancer*. 2010;10:573. Exclude: No outcome of interest.
981. Mikulova V, Cabinakova M, Janatkova I, Mestek O, Zima T, Tesarova P. Detection of circulating tumor cells during follow-up of patients with early breast cancer: Clinical utility for monitoring of therapy efficacy. *Scandinavian Journal of Clinical & Laboratory Investigation*. 2014;74(2):132-142. Exclude: Not intervention of interest.
982. Milano G. Highlight on DPYD gene polymorphisms and treatment by capecitabine (.). *Scandinavian Journal of Clinical and Laboratory Investigation Supplement*. 2016;245:S30-33. Exclude: Not intervention of interest.
983. Milburn M, Rosman M, Mylander C, Tafral L. Is oncotype DX recurrence score (RS) of prognostic value once HER2-positive and low-ER expression patients are removed? *Breast Journal*. 2013;19(4):357-364. Exclude: No outcome of interest.
984. Milde-Langosch K, Karn T, Muller V, et al. Validity of the proliferation markers Ki67, TOP2A, and RacGAP1 in molecular subgroups of breast cancer. *Breast Cancer Research & Treatment*. 2013;137(1):57-67. Exclude: Not intervention of interest.
985. Milioli HH, Vimieiro R, Riveros C, Tishchenko I, Berretta R, Moscato P. The Discovery of Novel Biomarkers Improves Breast Cancer Intrinsic Subtype Prediction and Reconciles the Labels in the METABRIC Data Set. *PLoS ONE [Electronic Resource]*. 2015;10(7):e0129711. Exclude: No outcome of interest.

986. Milioli HH, Vimieiro R, Tishchenko I, Riveros C, Berretta R, Moscato P. Iteratively refining breast cancer intrinsic subtypes in the METABRIC dataset. *BioData Mining [electronic resource]*. 2016;9:2. Exclude: No outcome of interest.
987. Miller DP, Petkov VI, Shak S. The performance of the 21-gene assay standard cutpoints of 18 and 31 in HR+, HER2-invasive breast cancer (BC), while waiting for TAILORx mid-range recurrence score results. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
988. Miller WR, Larionov A, Anderson TJ, Evans DB, Dixon JM. Sequential changes in gene expression profiles in breast cancers during treatment with the aromatase inhibitor, letrozole. *Pharmacogenomics Journal*. 2012;12(1):10-21. Exclude: Not intervention of interest.
989. Mina L, Soule SE, Badve S, et al. Predicting response to primary chemotherapy: gene expression profiling of paraffin-embedded core biopsy tissue. *Breast Cancer Research & Treatment*. 2007;103(2):197-208. Exclude: No outcome of interest.
990. Mirnezami AH, Pickard K, Zhang L, Primrose JN, Packham G. MicroRNAs: key players in carcinogenesis and novel therapeutic targets. *European Journal of Surgical Oncology*. 2009;35(4):339-347. Exclude: Not intervention of interest.
991. Miron L, Marinca A, Marinca M, Miron I. [Triple-negative breast cancer--towards a new entity]. *Revista Medico-Chirurgicala a Societatii de Medici Si Naturalisti Din Iasi*. 2008;112(1):51-58. Exclude: Not intervention of interest.
992. Mislick K, Schonfeld W, Bodnar C, Tong KB. Cost-effectiveness analysis of Mammostrat compared with Oncotype DX to inform the treatment of breast cancer. *Clinicoeconomics & Outcomes Research*. 2014;6:37-47. Exclude: In included systematic review.
993. Mitsuhashi M, Liu J, Cao S, Shi X, Ma X. Regulation of interleukin-12 gene expression and its anti-tumor activities by prostaglandin E2 derived from mammary carcinomas. *Journal of Leukocyte Biology*. 2004;76(2):322-332. Exclude: Date.
994. Mittempergher L, de Ronde JJ, Nieuwland M, et al. Gene expression profiles from formalin fixed paraffin embedded breast cancer tissue are largely comparable to fresh frozen matched tissue. *PLoS ONE [Electronic Resource]*. 2011;6(2):e17163. Exclude: No outcome of interest.
995. Mittempergher L, Saghatchian M, Wolf DM, et al. A gene signature for late distant metastasis in breast cancer identifies a potential mechanism of late recurrences. *Molecular Oncology*. 2013;7(5):987-999. Exclude: Not intervention of interest.
996. Miyoshi Y, Shien T, Ogiya A, et al. Differences in expression of the cancer stem cell marker aldehyde dehydrogenase 1 among estrogen receptor-positive/human epidermal growth factor receptor type 2-negative breast cancer cases with early, late, and no recurrence. *Breast Cancer Research*. 2016;18(1):73. Exclude: Not intervention of interest.
997. Mobasheri MB, Shirkoohi R, Zendejdel K, et al. Transcriptome analysis of the cancer/testis genes, DAZ1, AURKC, and TEX101, in breast tumors and six breast cancer cell lines. *Tumour Biology*. 2015;36(10):8201-8206. Exclude: Not intervention of interest.
998. Modlich O, Bojar H. Can a 70-gene signature provide useful prognostic information in patients with node-negative breast cancer? *Nature Clinical Practice Oncology*. 2007;4(4):216-217. Exclude: No outcome of interest.

999. Mokbel K, Wazir U, El Hage Chehade H, et al. A Comparison of the Performance of EndoPredict Clinical and NHS PREDICT in 120 Patients Treated for ER-positive Breast Cancer. *Anticancer Research*. 2017;37(12):6863-6869. Exclude: No outcome of interest.
1000. Mollerstrom E, Delle U, Danielsson A, et al. High-resolution genomic profiling to predict 10-year overall survival in node-negative breast cancer. *Cancer Genetics & Cytogenetics*. 2010;198(2):79-89. Exclude: No outcome of interest.
1001. Molloy TJ, Roepman P, Naume B, van't Veer LJ. A prognostic gene expression profile that predicts circulating tumor cell presence in breast cancer patients. *PLoS ONE [Electronic Resource]*. 2012;7(2):e32426. Exclude: No outcome of interest.
1002. Monahan DA, Wang J, Lee O, et al. Cytologic atypia in the contralateral unaffected breast is related to parity and estrogen-related genes. *Surgical Oncology*. 2016;25(4):449-456. Exclude: Not intervention of interest.
1003. Montemurro F, Prat A, Rossi V, et al. Potential biomarkers of long-term benefit from single-agent trastuzumab or lapatinib in HER2-positive metastatic breast cancer. *Cancer research*. 2013;73(24 SUPPL. 1):CONFERENCE START: 2013 Dec 2010 CONFERENCE END: 2013 Dec 2014. Exclude: Publication type-conference abstract.
1004. Montemurro F, Prat A, Rossi V, et al. Potential biomarkers of long-term benefit from single-agent trastuzumab or lapatinib in HER2-positive metastatic breast cancer. *Molecular Oncology*. 2014;8(1):20-26. Exclude: No outcome of interest.
1005. Montenegro MF, Sanchez-Del-Campo L, Gonzalez-Guerrero R, et al. Tumor suppressor SET9 guides the epigenetic plasticity of breast cancer cells and serves as an early-stage biomarker for predicting metastasis. *Oncogene*. 2016;35(47):6143-6152. Exclude: Not intervention of interest.
1006. Montes de Oca R, Gurard-Levin ZA, Berger F, et al. The histone chaperone HJURP is a new independent prognostic marker for luminal A breast carcinoma. *Molecular Oncology*. 2015;9(3):657-674. Exclude: Not intervention of interest.
1007. Mook S, Bonnefoi H, Pruneri G, et al. Daily clinical practice of fresh tumour tissue freezing and gene expression profiling; logistics pilot study preceding the MINDACT trial. *European Journal of Cancer*. 2009;45(7):1201-1208. Exclude: No outcome of interest.
1008. Mook S, Knauer M, Bueno-de-Mesquita JM, et al. Metastatic potential of T1 breast cancer can be predicted by the 70-gene MammaPrint signature. *Annals of Surgical Oncology*. 2010;17(5):1406-1413. Exclude: No outcome of interest.
1009. Mook S, Schmidt MK, Viale G, et al. The 70-gene prognosis-signature predicts disease outcome in breast cancer patients with 1-3 positive lymph nodes in an independent validation study. *Breast Cancer Research & Treatment*. 2009;116(2):295-302. Exclude: No outcome of interest.
1010. Mook S, Schmidt MK, Weigelt B, et al. The 70-gene prognosis signature predicts early metastasis in breast cancer patients between 55 and 70 years of age. *Annals of Oncology*. 2010;21(4):717-722. Exclude: No outcome of interest.
1011. Mook S, Van't Veer LJ, Rutgers EJ, Piccart-Gebhart MJ, Cardoso F. Individualization of therapy using Mammprint: from development to the MINDACT Trial. *Cancer Genomics & Proteomics*. 2007;4(3):147-155. Exclude: No outcome of interest.

1012. Moran O, Nikitina D, Royer R, et al. Revisiting breast cancer patients who previously tested negative for BRCA mutations using a 12-gene panel. *Breast Cancer Research & Treatment*. 2017;161(1):135-142. Exclude: No outcome of interest.
1013. Morandi A, Martin LA, Gao Q, et al. GDNF-RET signaling in ER-positive breast cancers is a key determinant of response and resistance to aromatase inhibitors. *Cancer Research*. 2013;73(12):3783-3795. Exclude: Not intervention of interest.
1014. Morini M, Albini A, Lorusso G, et al. Prevention of angiogenesis by naked DNA IL-12 gene transfer: angioprevention by immunogene therapy. *Gene Therapy*. 2004;11(3):284-291. Exclude: Date.
1015. Morris SR, Carey LA. Gene expression profiling in breast cancer. *Current Opinion in Oncology*. 2007;19(6):547-551. Exclude: Publication type-not systematic review.
1016. Morris SR, Carey LA. Molecular profiling in breast cancer. *Reviews in Endocrine & Metabolic Disorders*. 2007;8(3):185-198. Exclude: Publication type-not systematic review.
1017. Mortara L, Giuliani L, De Lerma Barbaro A, Accolla RS, Noonan DM. Experimental therapeutic approaches to adenocarcinoma: the potential of tumor cells engineered to express MHC class II molecules combined with naked DNA interleukin-12 gene transfer. *Surgical Oncology*. 2007;16 Suppl 1:S33-36. Exclude: Not intervention of interest.
1018. Mostert B, Sieuwerts AM, Kraan J, et al. Gene expression profiles in circulating tumor cells to predict prognosis in metastatic breast cancer patients. *Annals of Oncology*. 2015;26(3):510-516. Exclude: Not intervention of interest.
1019. Motakis E, Ivshina AV, Kuznetsov VA. Data-driven approach to predict survival of cancer patients: estimation of microarray genes' prediction significance by Cox proportional hazard regression model. *IEEE Engineering in Medicine & Biology Magazine*. 2009;28(4):58-66. Exclude: No outcome of interest.
1020. Moulder S, Yan K, Huang F, et al. Development of candidate genomic markers to select breast cancer patients for dasatinib therapy. *Molecular Cancer Therapeutics*. 2010;9(5):1120-1127. Exclude: No outcome of interest.
1021. Mu L, Tuck D, Katsaros D, et al. Favorable outcome associated with an IGF-1 ligand signature in breast cancer. *Breast Cancer Research & Treatment*. 2012;133(1):321-331. Exclude: Not intervention of interest.
1022. Muller BM, Brase JC, Haufe F, et al. Comparison of the RNA-based EndoPredict multigene test between core biopsies and corresponding surgical breast cancer sections. *Journal of Clinical Pathology*. 2012;65(7):660-662. Exclude: No outcome of interest.
1023. Muller BM, Keil E, Lehmann A, et al. The EndoPredict gene-expression assay in clinical practice - performance and impact on clinical decisions. *PLoS One*. 2013;8(6):e68252. Exclude: In included systematic review.
1024. Muller KE, Marotti JD, de Abreu FB, et al. Targeted next-generation sequencing detects a high frequency of potentially actionable mutations in metastatic breast cancers. *Experimental & Molecular Pathology*. 2016;100(3):421-425. Exclude: Not intervention of interest.
1025. Muller V, Witzel I, Luck HJ, et al. Prognostic and predictive impact of the HER-2/ neu extracellular domain (ECD) in the serum of patients treated with chemotherapy for metastatic breast cancer. *Breast Cancer Research & Treatment*. 2004;86(1):9-18. Exclude: Date.

1026. Munzone E, Nole F, Goldhirsch A, et al. Changes of HER2 status in circulating tumor cells compared with the primary tumor during treatment for advanced breast cancer. *Clinical Breast Cancer*. 2010;10(5):392-397. Exclude: Not intervention of interest.
1027. Muranen TA, Blomqvist C, Dork T, et al. Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. *Breast Cancer Research*. 2016;18(1):98. Exclude: No outcome of interest.
1028. Mushlin AI. To (genetic) test or not to test, that is the question. *Journal of Comparative Effectiveness Research*. 2015;4(5):429-431. Exclude: Publication type-commentary.
1029. Muss HB. Adjuvant chemotherapy in older women with breast cancer: who and what? *Journal of Clinical Oncology*. 2014;32(19):1996-2000. Exclude: Publication type-case report.
1030. Mustacchi G, Sormani MP, Bruzzi P, et al. Identification and validation of a new set of five genes for prediction of risk in early breast cancer. *International Journal of Molecular Sciences*. 2013;14(5):9686-9702. Exclude: Not intervention of interest.
1031. Muthukaruppan A, Lasham A, Blenkiron C, et al. Gene expression profiling of breast tumours from New Zealand patients. *New Zealand Medical Journal*. 2017;130(1464):40-56. Exclude: No outcome of interest.
1032. Myburgh EJ, Langenhoven L, Grant KA, van der Merwe L, Kotze MJ. Clinical Overestimation of HER2 Positivity in Early Estrogen and Progesterone Receptor-Positive Breast Cancer and the Value of Molecular Subtyping Using BluePrint. *Journal of Global Oncology*. 2017;3(4):314-322. Exclude: Not intervention of interest.
1033. Myers MB. Targeted therapies with companion diagnostics in the management of breast cancer: current perspectives. *Pharmacogenomics & Personalized Medicine*. 2016;9:7-16. Exclude: Publication type-commentary.
1034. Myhre S, Lingjaerde OC, Hennessy BT, et al. Influence of DNA copy number and mRNA levels on the expression of breast cancer related proteins. *Molecular Oncology*. 2013;7(3):704-718. Exclude: Not intervention of interest.
1035. Na KY, Kim KS, Lee JE, et al. The 70-gene prognostic signature for korean breast cancer patients. *Journal of Breast Cancer*. 2011;14(1):33-38. Exclude: No outcome of interest.
1036. Naderi A, Teschendorff AE, Barbosa-Morais NL, et al. A gene-expression signature to predict survival in breast cancer across independent data sets. *Oncogene*. 2007;26(10):1507-1516. Exclude: No outcome of interest.
1037. Nagaraj G, Ma CX. Adjuvant chemotherapy decisions in clinical practice for early-stage node-negative, estrogen receptor-positive, HER2-negative breast cancer: challenges and considerations. *Journal of the National Comprehensive Cancer Network*. 2013;11(3):246-250; quiz 251. Exclude: Publication type-commentary.
1038. Nagarajan R, Upreti M. An approach for deciphering patient-specific variations with application to breast cancer molecular expression profiles. *Journal of Biomedical Informatics*. 2016;63:120-130. Exclude: No outcome of interest.
1039. Nagashima T, Suzuki T, Kondo S, et al. Integrative genome-wide expression analysis bears evidence of estrogen receptor-independent transcription in heregulin-stimulated MCF-7 cells. *PLoS ONE [Electronic Resource]*. 2008;3(3):e1803. Exclude: Not intervention of interest.

1040. Nakamura H, Bai J, Nishinaka Y, et al. Expression of thioredoxin and glutaredoxin, redox-regulating proteins, in pancreatic cancer. *Cancer Detection & Prevention*. 2000;24(1):53-60. Exclude: Date.
1041. Nakano K, Miki Y, Hata S, et al. Identification of androgen-responsive microRNAs and androgen-related genes in breast cancer. *Anticancer Research*. 2013;33(11):4811-4819. Exclude: Not intervention of interest.
1042. Nakauchi C, Naoi Y, Shimazu K, et al. Development of a prediction model for lymph node metastasis in luminal A subtype breast cancer: the possibility to omit sentinel lymph node biopsy. *Cancer Letters*. 2014;353(1):52-58. Exclude: Not intervention of interest.
1043. Nakopoulou LL, Alexiadou A, Theodoropoulos GE, Lazaris AC, Tzonou A, Keramopoulos A. Prognostic significance of the co-expression of p53 and c-erbB-2 proteins in breast cancer. *Journal of Pathology*. 1996;179(1):31-38. Exclude: Date.
1044. Nam K, Nam HY, Kim PH, Kim SW. Paclitaxel-conjugated PEG and arginine-grafted bio-reducible poly (disulfide amine) micelles for co-delivery of drug and gene. *Biomaterials*. 2012;33(32):8122-8130. Exclude: Not intervention of interest.
1045. Naoi Y, Kishi K, Tanei T, et al. Prediction of pathologic complete response to sequential paclitaxel and 5-fluorouracil/epirubicin/cyclophosphamide therapy using a 70-gene classifier for breast cancers. *Cancer*. 2011;117(16):3682-3690. Exclude: No outcome of interest.
1046. Naoi Y, Kishi K, Tsunashima R, et al. Comparison of efficacy of 95-gene and 21-gene classifier (Oncotype DX) for prediction of recurrence in ER-positive and node-negative breast cancer patients. *Breast Cancer Research & Treatment*. 2013;140(2):299-306. Exclude: No outcome of interest.
1047. Naoi Y, Noguchi S. Multi-gene classifiers for prediction of recurrence in breast cancer patients. *Breast Cancer*. 2016;23(1):12-18. Exclude: No outcome of interest.
1048. Naoi Y, Tanei T, Kishi K, et al. 70-Gene classifier for differentiation between paclitaxel- and docetaxel-sensitive breast cancers. *Cancer Letters*. 2012;314(2):206-212. Exclude: Publication type-letter.
1049. Nathan B, Gusterson B, Jadayel D, et al. Expression of BCL-2 in primary breast cancer and its correlation with tumour phenotype. For the International (Ludwig) Breast Cancer Study Group. *Annals of Oncology*. 1994;5(5):409-414. Exclude: Date.
1050. Natoli C, Vici P, Sperduti I, et al. Effectiveness of neoadjuvant trastuzumab and chemotherapy in HER2-overexpressing breast cancer. *Journal of Cancer Research & Clinical Oncology*. 2013;139(7):1229-1240. Exclude: Not intervention of interest.
1051. Natowicz R, Incitti R, Horta EG, et al. Prediction of the outcome of preoperative chemotherapy in breast cancer using DNA probes that provide information on both complete and incomplete responses. *BMC Bioinformatics*. 2008;9:149. Exclude: Not intervention of interest.
1052. Natrajan R, Sailem H, Mardakheh FK, et al. Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histology-Genomic Integration Analysis. *PLoS Medicine / Public Library of Science*. 2016;13(2):e1001961. Exclude: Not intervention of interest.
1053. Naume B, Zhao X, Synnestvedt M, et al. Presence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancer.[Erratum appears in Mol Oncol. 2010 Apr;4(2):169]. *Molecular Oncology*. 2007;1(2):160-171. Exclude: Not intervention of interest.
1054. Nayak SR, Harrington E, Boone D, et al. A Role for Histone H2B Variants in Endocrine-Resistant Breast Cancer. *Hormones & Cancer*. 2015;6(5-6):214-224. Exclude: Not intervention of interest.

1055. Neapolitan RE, Jiang X. Study of integrated heterogeneous data reveals prognostic power of gene expression for breast cancer survival. *PLoS ONE [Electronic Resource]*. 2015;10(2):e0117658. Exclude: No outcome of interest.
1056. Need EF, Selth LA, Trotta AP, et al. The unique transcriptional response produced by concurrent estrogen and progesterone treatment in breast cancer cells results in upregulation of growth factor pathways and switching from a Luminal A to a Basal-like subtype. *BMC Cancer*. 2015;15:791. Exclude: Not intervention of interest.
1057. Nerich V, Curtit E, Bazan F, et al. [Economic assessment of the routine use of Oncotype DX assay for early breast cancer in Franche-Comte region]. *Bulletin du Cancer*. 2014;101(7-8):681-689. Exclude: In included systematic review.
1058. Netanel D, Avraham A, Ben-Baruch A, Evron E, Shamir R. Expression and methylation patterns partition luminal-A breast tumors into distinct prognostic subgroups.[Erratum appears in Breast Cancer Res. 2016 Nov 28;18(1):117; PMID: 27894324]. *Breast Cancer Research*. 2016;18(1):74. Exclude: No outcome of interest.
1059. Neumeister V, Agarwal S, Bordeaux J, Camp RL, Rimm DL. In situ identification of putative cancer stem cells by multiplexing ALDH1, CD44, and cytokeratin identifies breast cancer patients with poor prognosis. *American Journal of Pathology*. 2010;176(5):2131-2138. Exclude: Not intervention of interest.
1060. Ngoi N, Lee SC, Hartman M, Khin LW, Wong A. Interest and attitudes of patients, cancer physicians, medical students and cancer researchers towards a spectrum of genetic tests relevant to breast cancer patients. *Breast*. 2013;22(1):47-52. Exclude: No outcome of interest.
1061. Nguyen B, Cusumano PG, Deck K, et al. Comparison of molecular subtyping with BluePrint, MammaPrint, and TargetPrint to local clinical subtyping in breast cancer patients. *Annals of Surgical Oncology*. 2012;19(10):3257-3263. Exclude: No outcome of interest.
1062. Nguyen MT, Stessin A, Nagar H, et al. Impact of oncotype DX recurrence score in the management of breast cancer cases. *Clinical Breast Cancer*. 2014;14(3):182-190. Exclude: No outcome of interest.
1063. Nicolini A, Ferrari P, Fallahi P, Antonelli A. An iron regulatory gene signature in breast cancer: more than a prognostic genetic profile? *Future Oncology*. 2012;8(2):131-134. Exclude: Not intervention of interest.
1064. Nicoll G, Crichton DN, McDowell HE, Kernohan N, Hupp TR, Thompson AM. Expression of the Hypermethylated in Cancer gene (HIC-1) is associated with good outcome in human breast cancer. *British Journal of Cancer*. 2001;85(12):1878-1882. Exclude: Date.
1065. Nielsen T, Wallden B, Schaper C, et al. Analytical validation of the PAM50-based Prosigna Breast Cancer Prognostic Gene Signature Assay and nCounter Analysis System using formalin-fixed paraffin-embedded breast tumor specimens. *BMC Cancer*. 2014;14:177. Exclude: No outcome of interest.
1066. Nielsen TO, Parker JS, Leung S, et al. A comparison of PAM50 intrinsic subtyping with immunohistochemistry and clinical prognostic factors in tamoxifen-treated estrogen receptor-positive breast cancer. *Clinical Cancer Research*. 2010;16(21):5222-5232. Exclude: No outcome of interest.
1067. Niikura N, Iwamoto T, Masuda S, et al. Immunohistochemical Ki67 labeling index has similar proliferation predictive power to various gene signatures in breast cancer. *Cancer Science*. 2012;103(8):1508-1512. Exclude: No outcome of interest.

1068. Nikolenyi A, Sukosd F, Kaizer L, et al. Tumor topoisomerase II alpha status and response to anthracycline-based neoadjuvant chemotherapy in breast cancer. *Oncology*. 2011;80(3-4):269-277. Exclude: Not intervention of interest.
1069. Nishio M, Naoi Y, Tsunashima R, et al. 72-gene classifier for predicting prognosis of estrogen receptor-positive and node-negative breast cancer patients using formalin-fixed, paraffin-embedded tumor tissues. *Clinical Breast Cancer*. 2014;14(3):e73-80. Exclude: Not intervention of interest.
1070. Nitz U, Gluz O, Christgen M, et al. Reducing chemotherapy use in clinically high-risk, genomically low-risk pN0 and pN1 early breast cancer patients: five-year data from the prospective, randomised phase 3 West German Study Group (WSG) PlanB trial. *Breast Cancer Research & Treatment*. 2017;165(3):573-583. Exclude: No outcome of interest.
1071. Nitz U, Gluz O, Kates RE, et al. Prognostic impact of discordance between different risk assessment tools in early breast cancer (recurrence score, central grade, Ki67): Early outcome analysis from the prospective phase III WSG-PlanB trial. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
1072. Niu Y, Fu X, Lv A, Fan Y, Wang Y. Potential markers predicting distant metastasis in axillary node-negative breast carcinoma. *International Journal of Cancer*. 2002;98(5):754-760. Exclude: Date.
1073. Nofech-Mozes S, Vella ET, Dhesy-Thind S, et al. Systematic review on hormone receptor testing in breast cancer. *Applied Immunohistochemistry & Molecular Morphology*. 2012;20(3):214-263. Exclude: Not intervention of interest.
1074. Noguchi M, Ohta N, Thomas M, et al. A retrospective study on the clinical and biological prediction of axillary lymph node metastasis in breast cancer. *Surgery Today*. 1993;23(7):573-579. Exclude: Date.
1075. Noman AS, Uddin M, Rahman MZ, et al. Overexpression of sonic hedgehog in the triple negative breast cancer: clinicopathological characteristics of high burden breast cancer patients from Bangladesh. *Scientific Reports*. 2016;6:18830. Exclude: Not intervention of interest.
1076. Noordermeer SM, Wennemers M, Bergevoet SM, et al. Expression of the BRCA1 complex member BRE predicts disease free survival in breast cancer. *Breast Cancer Research & Treatment*. 2012;135(1):125-133. Exclude: Not intervention of interest.
1077. Novak P, Stampfer MR, Munoz-Rodriguez JL, et al. Cell-type specific DNA methylation patterns define human breast cellular identity. *PLoS ONE [Electronic Resource]*. 2012;7(12):e52299. Exclude: Not intervention of interest.
1078. Nunes RA, Wray L, Mete M, et al. Genomic profiling of breast cancer in African-American women using MammaPrint. *Breast Cancer Res Treat*. 2016;159(3):481-488. Exclude: No outcome of interest.
1079. Nuyten DS, Hastie T, Chi JT, Chang HY, van de Vijver MJ. Combining biological gene expression signatures in predicting outcome in breast cancer: An alternative to supervised classification. *European Journal of Cancer*. 2008;44(15):2319-2329. Exclude: No outcome of interest.
1080. Nuyten DS, Kreike B, Hart AA, et al. Predicting a local recurrence after breast-conserving therapy by gene expression profiling. *Breast Cancer Research*. 2006;8(5):R62. Exclude: Date.
1081. Nygard S, Borgan O, Lingjaerde OC, Stovold HL. Partial least squares Cox regression for genome-wide data. *Lifetime Data Analysis*. 2008;14(2):179-195. Exclude: Not intervention of interest.
1082. Oakman C, Bessi S, Zafarana E, Galardi F, Biganzoli L, Di Leo A. Recent advances in systemic therapy: new diagnostics and biological predictors of outcome in early breast cancer. *Breast Cancer Research*. 2009;11(2):205. Exclude: No outcome of interest.

1083. Oakman C, Santarpia L, Di Leo A. Breast cancer assessment tools and optimizing adjuvant therapy. *Nature Reviews Clinical Oncology*. 2010;7(12):725-732. Exclude: No outcome of interest.
1084. Obermayr E, Sanchez-Cabo F, Tea MK, et al. Assessment of a six gene panel for the molecular detection of circulating tumor cells in the blood of female cancer patients. *BMC Cancer*. 2010;10:666. Exclude: Not intervention of interest.
1085. O'Brien MA, Dhesy-Thind S, Charles C, Hammond Mobilio M, Leighl NB, Grunfeld E. Uptake of a 21-gene expression assay in breast cancer practice: views of academic and community-based oncologists. *Current Oncology*. 2017;24(2):e138-e145. Exclude: No outcome of interest.
1086. O'Brien SL, Fagan A, Fox EJ, et al. CENP-F expression is associated with poor prognosis and chromosomal instability in patients with primary breast cancer. *International Journal of Cancer*. 2007;120(7):1434-1443. Exclude: Not intervention of interest.
1087. Ocana Fernandez A, Templeton AJ, Casas M, et al. Prognostic role for derived neutrophil-to-lymphocyte ratio in early breast cancer. *Annals of oncology Conference: 41st european society for medical oncology congress, ESMO*. 2016;27(no pagination). Exclude: Publication type-conference abstract.
1088. O'Connor SM, Beriwal S, Dabbs DJ, Bhargava R. Concordance between semiquantitative immunohistochemical assay and oncotype DX RT-PCR assay for estrogen and progesterone receptors. *Applied Immunohistochemistry & Molecular Morphology*. 2010;18(3):268-272. Exclude: No outcome of interest.
1089. Oestreicher N, Ramsey SD, Linden HM, et al. Gene expression profiling and breast cancer care: what are the potential benefits and policy implications? *Genetics in Medicine*. 2005;7(6):380-389. Exclude: Date.
1090. Ohnstad HO, Borgen E, Falk RS, et al. Prognostic value of PAM50 and risk of recurrence score in patients with early-stage breast cancer with long-term follow-up. *Breast Cancer Research*. 2017;19(1):120. Exclude: No outcome of interest.
1091. Ojo D, Seliman M, Tang D. Signatures derived from increase in SHARPIN gene copy number are associated with poor prognosis in patients with breast cancer. *BBA Clinical*. 2017;8:56-65. Exclude: Not intervention of interest.
1092. Okuma HS, Koizumi F, Hirakawa A, et al. Clinical and microarray analysis of breast cancers of all subtypes from two prospective preoperative chemotherapy studies. *British Journal of Cancer*. 2016;115(4):411-419. Exclude: Not intervention of interest.
1093. O'Neill SC, DeFrank JT, Vegella P, et al. Engaging in health behaviors to lower risk for breast cancer recurrence. *PLoS ONE [Electronic Resource]*. 2013;8(1):e53607. Exclude: Not intervention of interest.
1094. Onody P, Bertrand F, Muzeau F, Bieche I, Lidereau R. Fluorescence in situ hybridization and immunohistochemical assays for HER-2/neu status determination: application to node-negative breast cancer. *Archives of Pathology & Laboratory Medicine*. 2001;125(6):746-750. Exclude: Date.
1095. Onstenk W, Sieuwerts AM, Weekhout M, et al. Gene expression profiles of circulating tumor cells versus primary tumors in metastatic breast cancer. *Cancer Letters*. 2015;362(1):36-44. Exclude: Not intervention of interest.
1096. Ontario HQ. Gene expression profiling for guiding adjuvant chemotherapy decisions in women with early breast cancer: an evidence-based and economic analysis. *Ont Health Technol Assess Ser*. 2010;10(23):1-57. Exclude: In included systematic review.

1097. Oratz R, Kim B, Chao C, et al. Physician survey of the effect of the 21-gene recurrence score assay results on treatment recommendations for patients with lymph node-positive, estrogen receptor-positive breast cancer. *J Oncol Pract.* 2011;7(2):94-99. Exclude: Cross-sectional design.
1098. Oratz R, Paul D, Cohn AL, Sedlacek SM. Impact of a commercial reference laboratory test recurrence score on decision making in early-stage breast cancer. *J Oncol Pract.* 2007;3(4):182-186. Exclude: In included systematic review.
1099. Orucevic A, Bell JL, McNabb AP, Heidel RE. Oncotype DX breast cancer recurrence score can be predicted with a novel nomogram using clinicopathologic data. *Breast Cancer Research & Treatment.* 2017;163(1):51-61. Exclude: No outcome of interest.
1100. O'Sullivan DE, Johnson KC, Skinner L, Koestler DC, Christensen BC. Epigenetic and genetic burden measures are associated with tumor characteristics in invasive breast carcinoma. *Epigenetics: Official Journal of the DNA Methylation Society.* 2016;11(5):344-353. Exclude: No outcome of interest.
1101. Ota D, Mimori K, Yokobori T, et al. Identification of recurrence-related microRNAs in the bone marrow of breast cancer patients. *International Journal of Oncology.* 2011;38(4):955-962. Exclude: Not intervention of interest.
1102. O'Toole SA, Selinger CI, Millar EK, Lum T, Beith JM. Molecular assays in breast cancer pathology. *Pathology.* 2011;43(2):116-127. Exclude: Publication type-not systematic review.
1103. Overmoyer B, Regan M, Schlosnagle E, et al. Phase I study of the JAK 1/2 inhibitor ruxolitinib with weekly paclitaxel for the treatment of HER2 negative metastatic breast cancer (MBC). *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states.* 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1104. Ozmen V, Atasoy A, Gokmen E, et al. Impact of Oncotype DX recurrence score on treatment decisions: results of a prospective multicenter study in Turkey. *Cureus.* 2016;8(3):e522. Exclude: In included systematic review.
1105. Ozmen V, Atasoy A, Gokmen E, et al. Correlations Between Oncotype DX Recurrence Score and Classic Risk Factors in Early Breast Cancer: Results of A Prospective Multicenter Study in Turkey. *Meme Saglg Dergisi.* 2016;12(3):107-111. Exclude: No outcome of interest.
1106. Paik S. Development and clinical utility of a 21-gene recurrence score prognostic assay in patients with early breast cancer treated with tamoxifen. *Oncologist.* 2007;12(6):631-635. Exclude: No outcome of interest.
1107. Paik S. Is gene array testing to be considered routine now? *Breast.* 2011;20 Suppl 3:S87-91. Exclude: Publication type-commentary.
1108. Paik S, Shak S, Tang G, et al. A multigene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. *New England Journal of Medicine.* 2004;351(27):2817-2826. Exclude: Date.
1109. Paik S, Shak S, Tang G, et al. Expression of the 21 genes in the Recurrence Score assay and tamoxifen clinical benefit in the NSABP study B-14 of node negative, estrogen receptor positive breast cancer. *Journal of Clinical Oncology.* 2005;23(16_suppl):510. Exclude: Date.
1110. Paik S, Tang G, Shak S, et al. Gene expression and benefit of chemotherapy in women with node-negative, estrogen receptor-positive breast cancer. *Journal of Clinical Oncology.* 2006;24(23):3726-3734. Exclude: Date.
1111. Pal SK, Mortimer J. Adjuvant systemic therapy for older adults with early-stage breast cancer. *Women's health.* 2009;5(3):251-262. Exclude: Not intervention of interest.

1112. Palmer K, Hitt M, Emtage PC, Gyorffy S, Gaudie J. Combined CXC chemokine and interleukin-12 gene transfer enhances antitumor immunity. *Gene Therapy*. 2001;8(4):282-290. Exclude: Date.
1113. Paluch-Shimon S, Ben-Baruch N, Wolf I, et al. Hormone receptor expression is associated with a unique pattern of metastatic spread and increased survival among HER2-overexpressing breast cancer patients. *American Journal of Clinical Oncology*. 2009;32(5):504-508. Exclude: Not intervention of interest.
1114. Pan D, Kocherginsky M, Conzen SD. Activation of the glucocorticoid receptor is associated with poor prognosis in estrogen receptor-negative breast cancer. *Cancer Research*. 2011;71(20):6360-6370. Exclude: Not intervention of interest.
1115. Pan Z, Jing W, He K, Zhang L, Long X. SATB1 is Correlated with Progression and Metastasis of Breast Cancers: A Meta-Analysis. *Cellular Physiology & Biochemistry*. 2016;38(5):1975-1983. Exclude: Not intervention of interest.
1116. Panis C, Pizzatti L, Herrera AC, Cecchini R, Abdelhay E. Putative circulating markers of the early and advanced stages of breast cancer identified by high-resolution label-free proteomics. *Cancer Letters*. 2013;330(1):57-66. Exclude: Not intervention of interest.
1117. Panousis D, Ntasiou P, Grosomanidis D, et al. Impact of Oncotype DX on chemotherapy assignment: a retrospective single-center study on female breast cancer patients. *Journal of BUOn*. 2017;22(5):1199-1208. Exclude: Not appropriate comparator.
1118. Panse J, Friedrichs K, Marx A, et al. Chemokine CXCL13 is overexpressed in the tumour tissue and in the peripheral blood of breast cancer patients. *British Journal of Cancer*. 2008;99(6):930-938. Exclude: Not intervention of interest.
1119. Papadakis ES, Reeves T, Robson NH, Maishman T, Packham G, Cutress RI. BAG-1 as a biomarker in early breast cancer prognosis: a systematic review with meta-analyses. *British Journal of Cancer*. 2017;116(12):1585-1594. Exclude: Not intervention of interest.
1120. Paquet ER, Hallett MT. Absolute assignment of breast cancer intrinsic molecular subtype. *Journal of the National Cancer Institute*. 2015;107(1):357. Exclude: No outcome of interest.
1121. Parisi F, Gonzalez AM, Nadler Y, et al. Benefits of biomarker selection and clinico-pathological covariate inclusion in breast cancer prognostic models. *Breast Cancer Research*. 2010;12(5):R66. Exclude: No outcome of interest.
1122. Park ES, Lee JS, Woo HG, et al. Heterologous tissue culture expression signature predicts human breast cancer prognosis. *PLoS ONE [Electronic Resource]*. 2007;2(1):e145. Exclude: No outcome of interest.
1123. Park IH, Kang JH, Lee KS, Nam S, Ro J, Kim JH. Identification and clinical implications of circulating microRNAs for estrogen receptor-positive breast cancer. *Tumour Biology*. 2014;35(12):12173-12180. Exclude: Not intervention of interest.
1124. Park J, Hur B, Rhee S, et al. Information theoretic sub-network mining characterizes breast cancer subtypes in terms of cancer core mechanisms. *Journal of Bioinformatics & Computational Biology*. 2016;14(5):1644002. Exclude: No outcome of interest.
1125. Park JW, Liu MC, Yee D, et al. Adaptive Randomization of Neratinib in Early Breast Cancer. *New England Journal of Medicine*. 2016;375(1):11-22. Exclude: Not intervention of interest.
1126. Park K, Han S, Shin E, Kim HJ, Kim JY. EGFR gene and protein expression in breast cancers. *European Journal of Surgical Oncology*. 2007;33(8):956-960. Exclude: Not intervention of interest.

1127. Park MM, Ebel JJ, Zhao W, Zynger DL. ER and PR immunohistochemistry and HER2 FISH versus oncotype DX: implications for breast cancer treatment. *Breast Journal*. 2014;20(1):37-45. Exclude: No outcome of interest.
1128. Parker BS, Ciocca DR, Bidwell BN, et al. Primary tumour expression of the cysteine cathepsin inhibitor Stefin A inhibits distant metastasis in breast cancer. *Journal of Pathology*. 2008;214(3):337-346. Exclude: Not intervention of interest.
1129. Parker J, Mullins M, Cheang MC, et al. A supervised risk predictor of breast cancer based on biological subtypes. *Journal of Clinical Oncology*. 2008;26(15_suppl):11008. Exclude: No outcome of interest.
1130. Parker JS, Mullins M, Cheang MC, et al. Supervised risk predictor of breast cancer based on intrinsic subtypes. *Journal of Clinical Oncology*. 2009;27(8):1160-1167. Exclude: No outcome of interest.
1131. Partin JF, Mamounas EP. Impact of the 21-gene recurrence score assay compared with standard clinicopathologic guidelines in adjuvant therapy selection for node-negative, estrogen receptor-positive breast cancer. *Annals of Surgical Oncology*. 2011;18(12):3399-3406. Exclude: In included systematic review.
1132. Patsialou A, Wang Y, Lin J, et al. Selective gene-expression profiling of migratory tumor cells in vivo predicts clinical outcome in breast cancer patients. *Breast Cancer Research*. 2012;14(5):R139. Exclude: No outcome of interest.
1133. Paulden M, Franek J, Pham B, Bedard PL, Trudeau M, Krahn M. Cost-effectiveness of the 21-gene assay for guiding adjuvant chemotherapy decisions in early breast cancer. *Value Health*. 2013;16(5):729-739. Exclude: In included systematic review.
1134. Pauletti G, Dandekar S, Rong H, et al. Assessment of methods for tissue-based detection of the HER-2/neu alteration in human breast cancer: a direct comparison of fluorescence in situ hybridization and immunohistochemistry. *Journal of Clinical Oncology*. 2000;18(21):3651-3664. Exclude: Date.
1135. Pavlou MP, Dimitromanolakis A, Martinez-Morillo E, Smid M, Foekens JA, Diamandis EP. Integrating meta-analysis of microarray data and targeted proteomics for biomarker identification: application in breast cancer. *Journal of Proteome Research*. 2014;13(6):2897-2909. Exclude: Not intervention of interest.
1136. Pawitan Y, Bjohle J, Amler L, et al. Gene expression profiling spares early breast cancer patients from adjuvant therapy: derived and validated in two population-based cohorts. *Breast Cancer Research*. 2005;7(6):R953-964. Exclude: Date.
1137. Pawitan Y, Bjohle J, Wedren S, et al. Gene expression profiling for prognosis using Cox regression. *Statistics in Medicine*. 2004;23(11):1767-1780. Exclude: Date.
1138. Peeters DJ, Brouwer A, Van den Eynden GG, et al. Circulating tumour cells and lung microvascular tumour cell retention in patients with metastatic breast and cervical cancer. *Cancer Letters*. 2015;356(2 Pt B):872-879. Exclude: Not intervention of interest.
1139. Peethambaram PP, Hoskin TL, Day CN, Goetz MP, Habermann EB, Boughey JC. Use of 21-gene recurrence score assay to individualize adjuvant chemotherapy recommendations in ER+/HER2- node positive breast cancer-A National Cancer Database study. *NPJ Breast Cancer*. 2017;3:41. Exclude: No outcome of interest.
1140. Peinado H, Moreno-Bueno G, Hardisson D, et al. Lysyl oxidase-like 2 as a new poor prognosis marker of squamous cell carcinomas. *Cancer Research*. 2008;68(12):4541-4550. Exclude: Not intervention of interest.

1141. Pelaez-Garcia A, Yebenes L, Berjon A, et al. Comparison of risk classification between EndoPredict and MammaPrint in ER-positive/HER2-negative primary invasive breast cancer. *PLoS ONE [Electronic Resource]*. 2017;12(9):e0183452. Exclude: No outcome of interest.
1142. Pelkonen M, Luostari K, Tengstrom M, et al. Low expression levels of hepsin and TMPRSS3 are associated with poor breast cancer survival. *BMC Cancer*. 2015;15:431. Exclude: Not intervention of interest.
1143. Penault-Llorca F, Kwiatkowski F, Grenier J, et al. UCBG 2-14: a prospective multicenter non-randomized trial evaluating the effect of EndoPredict (EPclin) clinico-genomic test on treatment decision making among patients with intermediate clinical risk. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1144. Pentheroudakis G, Batistatou A, Kalogeras KT, et al. Prognostic utility of beta-tubulin isotype III and correlations with other molecular and clinicopathological variables in patients with early breast cancer: a translational Hellenic Cooperative Oncology Group (HeCOG) study. *Breast Cancer Research & Treatment*. 2011;127(1):179-193. Exclude: Not intervention of interest.
1145. Pentheroudakis G, Kalogeras KT, Wirtz RM, et al. Gene expression of estrogen receptor, progesterone receptor and microtubule-associated protein Tau in high-risk early breast cancer: a quest for molecular predictors of treatment benefit in the context of a Hellenic Cooperative Oncology Group trial. *Breast Cancer Research & Treatment*. 2009;116(1):131-143. Exclude: Not intervention of interest.
1146. Pentheroudakis G, Spector Y, Krikelis D, et al. Global microRNA profiling in favorable prognosis subgroups of cancer of unknown primary (CUP) demonstrates no significant expression differences with metastases of matched known primary tumors. *Clinical & Experimental Metastasis*. 2013;30(4):431-439. Exclude: Not intervention of interest.
1147. Penzvalto Z, Mihaly Z, Gyorffy B. [Gene expression based multigene prognostic and predictive tests in breast cancer]. *Magyar Onkologia*. 2009;53(4):351-359. Exclude: No outcome of interest.
1148. Pepin F, Bertos N, Laferriere J, et al. Gene-expression profiling of microdissected breast cancer microvasculature identifies distinct tumor vascular subtypes. *Breast Cancer Research*. 2012;14(4):R120. Exclude: No outcome of interest.
1149. Peppone LJ, Rickles AS, Janelins MC, Insalaco MR, Skinner KA. The association between breast cancer prognostic indicators and serum 25-OH vitamin D levels. *Annals of Surgical Oncology*. 2012;19(8):2590-2599. Exclude: No outcome of interest.
1150. Pera E, Kaemmerer E, Milevskiy MJG, et al. The voltage gated Ca(2+)-channel Cav3.2 and therapeutic responses in breast cancer. *Cancer Cell International*. 2016;16:24. Exclude: Not intervention of interest.
1151. Perez EA, Baehner FL, Butler SM, et al. The relationship between quantitative human epidermal growth factor receptor 2 gene expression by the 21-gene reverse transcriptase polymerase chain reaction assay and adjuvant trastuzumab benefit in Alliance N9831. *Breast Cancer Research*. 2015;17(1):133. Exclude: No outcome of interest.
1152. Perez EA, Ballman KV, Mashadi-Hosseini A, et al. Intrinsic Subtype and Therapeutic Response Among HER2-Positive Breast Tumors from the NCCTG (Alliance) N9831 Trial. *Journal of the National Cancer Institute*. 2017;109(2):02. Exclude: Not intervention of interest.

1153. Perez EA, Thompson EA, Ballman KV, et al. Genomic analysis reveals that immune function genes are strongly linked to clinical outcome in the North Central Cancer Treatment Group n9831 Adjuvant Trastuzumab Trial. *Journal of Clinical Oncology*. 2015;33(7):701-708. Exclude: Not intervention of interest.
1154. Perou CM, Borresen-Dale AL. Systems biology and genomics of breast cancer. *Cold Spring Harbor perspectives in biology*. 2011;3(2):01. Exclude: Publication type-commentary.
1155. Perreard L, Fan C, Quackenbush JF, et al. Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. *Breast Cancer Research*. 2006;8(2):R23. Exclude: Date.
1156. Perren TJ. c-erbB-2 oncogene as a prognostic marker in breast cancer. *British Journal of Cancer*. 1991;63(3):328-332. Exclude: Date.
1157. Pervez A, Riaz SK, Mehmood A, Rashid R, Arshad Malik MF. Expression analysis of human epidermal growth factor receptor type 2 transcripts in breast cancer cohort and its association with clinical features. *Journal of Cancer Research & Therapeutics*. 2016;12(2):1036-1039. Exclude: Not intervention of interest.
1158. Petkov VI, Miller DP, Howlader N, et al. Breast-cancer-specific mortality in patients treated based on the 21-gene assay: a SEER population-based study. *NPJ Breast Cancer*. 2016;2:16017. Exclude: No comparator.
1159. Petrillo LA, Wolf DM, Kapoun AM, et al. Xenografts faithfully recapitulate breast cancer-specific gene expression patterns of parent primary breast tumors. *Breast Cancer Research & Treatment*. 2012;135(3):913-922. Exclude: No outcome of interest.
1160. Piccart M, Bogaerts J, Cardoso F, et al. The EORTC 10041/BIG 03-04 MINDACT (Microarray in Node Negative and 1 to 3 Positive Lymph Node Disease May Avoid ChemoTherapy) trial: Patients' baseline characteristics and logistics aspects after a successful accrual. *European journal of cancer*. 2011;47(7). Exclude: Publication type-conference abstract.
1161. Piccart M, Rutgers E, Van't Veer L, et al. Primary analysis of the EORTC 10041/ BIG 3-04 MINDACT study: a prospective, randomized study evaluating the clinical utility of the 70-gene signature (MammaPrint) combined with common clinical-pathological criteria for selection of patients for adjuvant chemotherapy in breast cancer with 0 to 3 positive nodes. *Cancer research Conference: 107th annual meeting of the american association for cancer research, AACR*. 2016;76(14 Supplement). Exclude: Publication type-conference abstract.
1162. Pich A, Margaria E, Chiusa L. Oncogenes and male breast carcinoma: c-erbB-2 and p53 coexpression predicts a poor survival. *Journal of Clinical Oncology*. 2000;18(16):2948-2956. Exclude: Date.
1163. Pietilainen T, Lipponen P, Aaltomaa S, Eskelinen M, Kosma VM, Syrjanen K. Expression of p53 protein has no independent prognostic value in breast cancer. *Journal of Pathology*. 1995;177(3):225-232. Exclude: Date.
1164. Pillai SG, Dasgupta N, Siddappa CM, et al. Paired-like Homeodomain Transcription factor 2 expression by breast cancer bone marrow disseminated tumor cells is associated with early recurrent disease development. *Breast Cancer Research & Treatment*. 2015;153(3):507-517. Exclude: Not intervention of interest.
1165. Pittman J, Huang E, Dressman H, et al. Integrated modeling of clinical and gene expression information for personalized prediction of disease outcomes. *Proceedings of the National Academy of Sciences of the United States of America*. 2004;101(22):8431-8436. Exclude: Date.

1166. Pivot X, Mansi L, Chaigneau L, et al. In the era of genomics, should tumor size be reconsidered as a criterion for neoadjuvant chemotherapy? *Oncologist*. 2015;20(4):344-350. Exclude: Not intervention of interest.
1167. Pockaj BA, Basu GD, Pathangey LB, et al. Reduced T-cell and dendritic cell function is related to cyclooxygenase-2 overexpression and prostaglandin E2 secretion in patients with breast cancer. *Annals of Surgical Oncology*. 2004;11(3):328-339. Exclude: Date.
1168. Pogue-Geile KL, Kim C, Jeong JH, et al. Predicting degree of benefit from adjuvant trastuzumab in NSABP trial B-31. *Journal of the National Cancer Institute*. 2013;105(23):1782-1788. Exclude: Not intervention of interest.
1169. Pogue-Geile KL, Song N, Jeong JH, et al. Intrinsic subtypes, PIK3CA mutation, and the degree of benefit from adjuvant trastuzumab in the NSABP B-31 trial. *Journal of Clinical Oncology*. 2015;33(12):1340-1347. Exclude: Not intervention of interest.
1170. Pohl G, Rudas M, Taucher S, et al. Expression of cell cycle regulatory proteins in breast carcinomas before and after preoperative chemotherapy. *Breast Cancer Research & Treatment*. 2003;78(1):97-103. Exclude: Date.
1171. Pohl H, Kotze MJ, Grant KA, et al. Impact of MammaPrint on clinical decision-making in South African patients with early-stage breast cancer. *Breast Journal*. 2016;22(4):442-446. Exclude: In included systematic review.
1172. Poltinnikov IM, Rudoler SB, Tymofyeyev Y, Kennedy J, Anne PR, Curran WJ, Jr. Impact of Her-2 Neu overexpression on outcome of elderly women treated with wide local excision and breast irradiation for early stage breast cancer: an exploratory analysis. *American Journal of Clinical Oncology*. 2006;29(1):71-79. Exclude: Date.
1173. Pommier SJ, Hernandez A, Han E, et al. Fresh surgical specimens yield breast stem/progenitor cells and reveal their oncogenic abnormalities. *Annals of Surgical Oncology*. 2012;19(2):527-535. Exclude: Not intervention of interest.
1174. Poorhosseini SM, Hashemi M, Alipour Olyaei N, et al. New Gene Profiling in Determination of Breast Cancer Recurrence and Prognosis in Iranian Women. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2016;17(S3):155-160. Exclude: Not intervention of interest.
1175. Poremba C, Uhlendorff J, Pfitzner BM, et al. Preanalytical variables and performance of diagnostic RNA-based gene expression analysis in breast cancer. *Virchows Archiv*. 2014;465(4):409-417. Exclude: No outcome of interest.
1176. Potosky AL, O'Neill SC, Isaacs C, et al. Population-based study of the effect of gene expression profiling on adjuvant chemotherapy use in breast cancer patients under the age of 65 years. *Cancer*. 2015;121(22):4062-4070. Exclude: In included systematic review.
1177. Prabhakaran S, Rizk VT, Ma Z, et al. Evaluation of invasive breast cancer samples using a 12-chemokine gene expression score: correlation with clinical outcomes. *Breast Cancer Research*. 2017;19(1):71. Exclude: Not intervention of interest.
1178. Prat A, Bianchini G, Thomas M, et al. Research-based PAM50 subtype predictor identifies higher responses and improved survival outcomes in HER2-positive breast cancer in the NOAH study. *Clinical Cancer Research*. 2014;20(2):511-521. Exclude: No outcome of interest.

1179. Prat A, Cheang MC, Galvan P, et al. Prognostic Value of Intrinsic Subtypes in Hormone Receptor-Positive Metastatic Breast Cancer Treated With Letrozole With or Without Lapatinib. *JAMA Oncology*. 2016;2(10):1287-1294. Exclude: No outcome of interest.
1180. Prat A, Cheang MC, Martin M, et al. Prognostic significance of progesterone receptor-positive tumor cells within immunohistochemically defined luminal A breast cancer. *Journal of Clinical Oncology*. 2013;31(2):203-209. Exclude: Not intervention of interest.
1181. Prat A, Cruz C, Hoadley KA, Diez O, Perou CM, Balmana J. Molecular features of the basal-like breast cancer subtype based on BRCA1 mutation status. *Breast Cancer Research & Treatment*. 2014;147(1):185-191. Exclude: No outcome of interest.
1182. Prat A, Galvan P, Jimenez B, et al. Prediction of Response to Neoadjuvant Chemotherapy Using Core Needle Biopsy Samples with the Prosigna Assay. *Clinical Cancer Research*. 2016;22(3):560-566. Exclude: No outcome of interest.
1183. Prat A, Lluch A, Turnbull AK, et al. A PAM50-Based Chemoendocrine Score for Hormone Receptor-Positive Breast Cancer with an Intermediate Risk of Relapse. *Clinical Cancer Research*. 2017;23(12):3035-3044. Exclude: No outcome of interest.
1184. Prat A, Ortega V, Villagrasa P, et al. Efficacy and gene expression results from SOLTI1007 NEOERIBULIN phase II clinical trial in HER2-negative early breast cancer. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1185. Prat A, Parker JS, Fan C, et al. Concordance among gene expression-based predictors for ER-positive breast cancer treated with adjuvant tamoxifen. *Annals of Oncology*. 2012;23(11):2866-2873. Exclude: No outcome of interest.
1186. Prat A, Parker JS, Fan C, Perou CM. PAM50 assay and the three-gene model for identifying the major and clinically relevant molecular subtypes of breast cancer. *Breast Cancer Research & Treatment*. 2012;135(1):301-306. Exclude: No outcome of interest.
1187. Prat A, Pineda E, Adamo B, et al. Clinical implications of the intrinsic molecular subtypes of breast cancer. *Breast*. 2015;24 Suppl 2:S26-35. Exclude: Publication type-commentary.
1188. Priedigkeit N, Hartmaier RJ, Chen Y, et al. Intrinsic Subtype Switching and Acquired ERBB2/HER2 Amplifications and Mutations in Breast Cancer Brain Metastases. *JAMA Oncology*. 2017;3(5):666-671. Exclude: Not intervention of interest.
1189. Puhalla SL, Davidson NE. Breast cancer: The 21-gene recurrence score - biology remains at the forefront. *Nature Reviews Clinical Oncology*. 2016;13(8):470-472. Exclude: Publication type-letter.
1190. Puisieux I, Odin L, Poujol D, et al. Canarypox virus-mediated interleukin 12 gene transfer into murine mammary adenocarcinoma induces tumor suppression and long-term antitumoral immunity. *Human Gene Therapy*. 1998;9(17):2481-2492. Exclude: Date.
1191. Pula B, Olbromski M, Owczarek T, et al. Nogo-B receptor expression correlates negatively with malignancy grade and ki-67 antigen expression in invasive ductal breast carcinoma. *Anticancer Research*. 2014;34(9):4819-4828. Exclude: Not intervention of interest.
1192. Pusztai L, Hatzis C, Cardoso F, et al. Combined use of genomic prognostic and treatment response predictors in breast cancer. *Journal of Clinical Oncology*. 2008;26(15_suppl):527. Exclude: Publication type-conference abstract.

1193. Qi H, Li YH, Zheng SB. [Oral gene therapy via live attenuated Salmonella leads to tumor regression and survival prolongation in mice]. *Nan Fang Yi Ke Da Xue Xue Bao = Journal of Southern Medical University*. 2006;26(12):1738-1741. Exclude: Date.
1194. Quan C, Huang N, Yang B, et al. A single-center report of 125 cases of incidental internal mammary lymph node biopsy in free abdominal flap breast reconstruction. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1195. Quddus RM, Sung JC, Zhang C, Pasqueriello T, Eklund M, Steinhoff MM. HER-2/neu expression in locally advanced breast carcinomas: pre-and post-neoadjuvant chemotherapy. *Breast Cancer*. 2005;12(4):294-298. Exclude: Date.
1196. Quigley D, Silwal-Pandit L, Dannenfelser R, et al. Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type TP53. *Molecular Cancer Research: MCR*. 2015;13(3):493-501. Exclude: Not intervention of interest.
1197. Quiroz-Zarate A, Harshfield BJ, Hu R, et al. Expression Quantitative Trait loci (QTL) in tumor adjacent normal breast tissue and breast tumor tissue. *PLoS ONE [Electronic Resource]*. 2017;12(2):e0170181. Exclude: Not intervention of interest.
1198. Radke I, Gotte M, Kersting C, Mattsson B, Kiesel L, Wulfing P. Expression and prognostic impact of the protein tyrosine phosphatases PRL-1, PRL-2, and PRL-3 in breast cancer. *British Journal of Cancer*. 2006;95(3):347-354. Exclude: Date.
1199. Rahilly-Tierney C, Walton SM. Cost-effectiveness of the 70-gene signature versus adjuvant! Online and systematic chemotherapy for risk stratification of patients with node-negative breast cancer: does accuracy matter? *J Clin Oncol*. 2015;33(14):1628-1629. Exclude: Publication type-letter.
1200. Rahko E, Blanco G, Bloigu R, Soini Y, Talvensaari-Mattila A, Jukkola A. Adverse outcome and resistance to adjuvant antiestrogen therapy in node-positive postmenopausal breast cancer patients-The role of p53. *Breast*. 2006;15(1):69-75. Exclude: Date.
1201. Rajput AB, Hu N, Varma S, et al. Immunohistochemical Assessment of Expression of Centromere Protein-A (CENPA) in Human Invasive Breast Cancer. *Cancers*. 2011;3(4):4212-4227. Exclude: Not intervention of interest.
1202. Rakha EA, Agarwal D, Green AR, et al. Prognostic stratification of oestrogen receptor-positive HER2-negative lymph node-negative class of breast cancer. *Histopathology*. 2017;70(4):622-631. Exclude: Not intervention of interest.
1203. Rakhmievich AL, Hooper AT, Hicklin DJ, Sondel PM. Treatment of experimental breast cancer using interleukin-12 gene therapy combined with anti-vascular endothelial growth factor receptor-2 antibody. *Molecular Cancer Therapeutics*. 2004;3(8):969-976. Exclude: Date.
1204. Rakhmievich AL, Janssen K, Hao Z, Sondel PM, Yang NS. Interleukin-12 gene therapy of a weakly immunogenic mouse mammary carcinoma results in reduction of spontaneous lung metastases via a T-cell-independent mechanism. *Cancer Gene Therapy*. 2000;7(6):826-838. Exclude: Date.
1205. Rakovitch E, Nofech-Mozes S, Hanna W, et al. A population-based validation study of the DCIS Score predicting recurrence risk in individuals treated by breast-conserving surgery alone. *Breast Cancer Research & Treatment*. 2015;152(2):389-398. Exclude: No outcome of interest.

1206. Raldow AC, Sher D, Chen AB, Recht A, Punglia RS. Cost Effectiveness of the Oncotype DX DCIS Score for Guiding Treatment of Patients With Ductal Carcinoma In Situ. *J Clin Oncol*. 2016. Exclude: Not intervention of interest.
1207. Ramsey SD, Barlow WE, Gonzalez-Angulo AM, et al. Integrating comparative effectiveness design elements and endpoints into a phase III, randomized clinical trial (SWOG S1007) evaluating oncotypedX-guided management for women with breast cancer involving lymph nodes. *Contemporary Clinical Trials*. 2013;34(1):1-9. Exclude: No outcome of interest.
1208. Rathnagiriswaran S, Wan YW, Abraham J, Castranova V, Qian Y, Guo NL. A population-based gene signature is predictive of breast cancer survival and chemoresponse. *International Journal of Oncology*. 2010;36(3):607-616. Exclude: Not intervention of interest.
1209. Ray D, Murphy KR, Gal S. The DNA binding and accumulation of p53 from breast cancer cell lines and the link with serine 15 phosphorylation. *Cancer Biology & Therapy*. 2012;13(10):848-857. Exclude: Not intervention of interest.
1210. Rayhanabad JA, Difronzo LA, Haigh PI, Romero L. Changing paradigms in breast cancer management: introducing molecular genetics into the treatment algorithm. *American Surgeon*. 2008;74(10):887-890. Exclude: In included systematic review.
1211. Reed SD, Dinan MA, Schulman KA, Lyman GH. Cost-effectiveness of the 21-gene recurrence score assay in the context of multifactorial decision making to guide chemotherapy for early-stage breast cancer. *Genet Med*. 2013;15(3):203-211. Exclude: In included systematic review.
1212. Ren H, Bouliskas T, Lundstrom K, Soling A, Warnke PC, Rainov NG. Immunogene therapy of recurrent glioblastoma multiforme with a liposomally encapsulated replication-incompetent Semliki forest virus vector carrying the human interleukin-12 gene--a phase I/II clinical protocol.[Erratum appears in J Neurooncol. 2003 Nov;65(2):191]. *Journal of Neuro-Oncology*. 2003;64(1-2):147-154. Exclude: Date.
1213. Retel VP, Bueno-de-Mesquita JM, Hummel MJ, et al. Constructive Technology Assessment (CTA) as a tool in coverage with evidence development: the case of the 70-gene prognosis signature for breast cancer diagnostics. *International Journal of Technology Assessment in Health Care*. 2009;25(1):73-83. Exclude: No outcome of interest.
1214. Retel VP, Groothuis-Oudshoorn CG, Aaronson NK, Brewer NT, Rutgers EJ, van Harten WH. Association between genomic recurrence risk and well-being among breast cancer patients. *BMC Cancer*. 2013;13:295. Exclude: Not appropriate comparator.
1215. Retel VP, Grutters JP, van Harten WH, Joore MA. Value of research and value of development in early assessments of new medical technologies. *Value in Health*. 2013;16(5):720-728. Exclude: No outcome of interest.
1216. Retel VP, Joore MA, Drukker CA, et al. Prospective cost-effectiveness analysis of genomic profiling in breast cancer. *Eur J Cancer*. 2013;49(18):3773-3779. Exclude: In included systematic review.
1217. Retel VP, Joore MA, Knauer M, Linn SC, Hauptmann M, Harten WH. Cost-effectiveness of the 70-gene signature versus St. Gallen guidelines and Adjuvant Online for early breast cancer. *Eur J Cancer*. 2010;46(8):1382-1391. Exclude: In included systematic review.
1218. Retel VP, Joore MA, Linn SC, Rutgers EJ, van Harten WH. Scenario drafting to anticipate future developments in technology assessment. *BMC Research Notes*. 2012;5:442. Exclude: No outcome of interest.

1219. Retel VP, Joore MA, van Harten WH. Head-to-head comparison of the 70-gene signature versus the 21-gene assay: cost-effectiveness and the effect of compliance. *Breast Cancer Res Treat.* 2012;131(2):627-636. Exclude: In included systematic review.
1220. Reyat F, Bollet MA, Caly M, et al. Respective prognostic value of genomic grade and histological proliferation markers in early stage (pN0) breast carcinoma.[Erratum appears in PLoS One. 2012;7(7). doi: 10.1371/annotation/46dc7048-61b1-45bd-b4cd-a3b80a2f3f5a]. *PLoS ONE [Electronic Resource]*. 2012;7(4):e35184. Exclude: Not intervention of interest.
1221. Reyat F, van Vliet MH, Armstrong NJ, et al. A comprehensive analysis of prognostic signatures reveals the high predictive capacity of the proliferation, immune response and RNA splicing modules in breast cancer. *Breast Cancer Research.* 2008;10(6):R93. Exclude: No outcome of interest.
1222. Rhee DK, Park SH, Jang YK. Molecular signatures associated with transformation and progression to breast cancer in the isogenic MCF10 model. *Genomics.* 2008;92(6):419-428. Exclude: No outcome of interest.
1223. Riaz SK, Ye L, Sahar NE, et al. Transcriptional Profiling of Sonic Hedgehog in a Prospective Cohort of Breast Cancer in a Pakistani Population. *Anticancer Research.* 2017;37(8):4449-4454. Exclude: Not intervention of interest.
1224. Ribnikar D, Ribeiro JM, Pinto D, et al. Breast cancer under age 40: a different approach. *Current Treatment Options in Oncology.* 2015;16(4):16. Exclude: Publication type-commentary.
1225. Richman AR, Tzeng JP, Carey LA, Retel VP, Brewer NT. Knowledge of genomic testing among early-stage breast cancer patients. *Psycho-Oncology.* 2011;20(1):28-35. Exclude: No outcome of interest.
1226. Ricks-Santi LJ, McDonald JT. Low utility of Oncotype DX in the clinic. *Cancer Medicine.* 2017;6(3):501-507. Exclude: No outcome of interest.
1227. Ricks-Santi LJ, McDonald JT. Low utility of Oncotype DX(R) in the clinic. *Cancer Medicine.* 2017;6(3):501-507. Exclude: No outcome of interest.
1228. Ring BZ, Seitz RS, Beck R, et al. Novel prognostic immunohistochemical biomarker panel for estrogen receptor-positive breast cancer. *Journal of Clinical Oncology.* 2006;24(19):3039-3047. Exclude: Date.
1229. Roberts MC, Bryson A, Weinberger M, et al. Oncologists' Barriers and Facilitators for Oncotype Dx Use: Qualitative Study. *International Journal of Technology Assessment in Health Care.* 2016;32(5):355-361. Exclude: No outcome of interest.
1230. Roberts MC, Bryson A, Weinberger M, et al. Patient-Centered Communication for Discussing Oncotype DX Testing. *Cancer Investigation.* 2016;34(5):205-212. Exclude: No outcome of interest.
1231. Roberts MC, Miller DP, Shak S, Petkov VI. Breast cancer-specific survival in patients with lymph node-positive hormone receptor-positive invasive breast cancer and Oncotype DX Recurrence Score results in the SEER database. *Breast Cancer Research & Treatment.* 2017;163(2):303-310. Exclude: No outcome of interest.
1232. Roberts MC, Weinberger M, Dusetzina SB, et al. Racial Variation in the Uptake of Oncotype DX Testing for Early-Stage Breast Cancer. *J Clin Oncol.* 2016;34(2):130-138. Exclude: No outcome of interest.
1233. Roberts MC, Weinberger M, Dusetzina SB, et al. Racial variation in adjuvant chemotherapy initiation among breast cancer patients receiving oncotype DX testing. *Breast Cancer Res Treat.* 2015;153(1):191-200. Exclude: No outcome of interest.

1234. Robertson JFR, Noguchi S, Shao Z, Grinsted LM, Fazal M, Ellis MJ. Progression-free survival results in patient subgroups from a Phase 3 randomized trial of fulvestrant 500 mg vs anastrozole for hormone receptor-positive advanced breast cancer (FALCON). *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1235. Robison JE, Perreard L, Bernard PS. State of the science: molecular classifications of breast cancer for clinical diagnostics. *Clinical Biochemistry*. 2004;37(7):572-578. Exclude: Date.
1236. Rodriguez CA, Garcia-Munoz M, Sancho M, et al. Impact of the Prosigna (PAM50) assay on adjuvant clinical decision making in patients with early stage breast cancer: results of a prospective multicenter public program. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
1237. Rody A, Karn T, Gatje R, et al. Gene expression profiles of breast cancer obtained from core cut biopsies before neoadjuvant docetaxel, adriamycin, and cyclophosphamide chemotherapy correlate with routine prognostic markers and could be used to identify predictive signatures. *Zentralblatt für Gynakologie*. 2006;128(2):76-81. Exclude: Date.
1238. Rojas PA, May M, Sequeira GR, et al. Progesterone Receptor Isoform Ratio: A Breast Cancer Prognostic and Predictive Factor for Antiprogesterin Responsiveness. *Journal of the National Cancer Institute*. 2017;109(7):01. Exclude: Not intervention of interest.
1239. Romero A, Martin M, Oliva B, et al. Glutathione S-transferase P1 c.313A > G polymorphism could be useful in the prediction of doxorubicin response in breast cancer patients. *Annals of Oncology*. 2012;23(7):1750-1756. Exclude: Not intervention of interest.
1240. Romero A, Prat A, Garcia-Saenz JA, et al. Assignment of tumor subtype by genomic testing and pathologic-based approximations: implications on patient's management and therapy selection. *Clinical & Translational Oncology: Official Publication of the Federation of Spanish Oncology Societies & of the National Cancer Institute of Mexico*. 2014;16(4):386-394. Exclude: Not intervention of interest.
1241. Romo-Bucheli D, Janowczyk A, Gilmore H, Romero E, Madabhushi A. Automated Tubule Nuclei Quantification and Correlation with Oncotype DX risk categories in ER+ Breast Cancer Whole Slide Images. *Scientific Reports*. 2016;6:32706. Exclude: No outcome of interest.
1242. Romo-Bucheli D, Janowczyk A, Gilmore H, Romero E, Madabhushi A. A deep learning based strategy for identifying and associating mitotic activity with gene expression derived risk categories in estrogen receptor positive breast cancers. *Cytometry Part A: The Journal of the International Society for Analytical Cytology*. 2017;91(6):566-573. Exclude: Not intervention of interest.
1243. Rosa M. Advances in the Molecular Analysis of Breast Cancer: Pathway Toward Personalized Medicine. *Cancer Control*. 2015;22(2):211-219. Exclude: Publication type-commentary.
1244. Rosman M, Mylander WC, Tafral L. What is the value of the 21 gene recurrence score in HER2-negative patients? *Journal of Clinical Oncology*. 2010;28(31):e647; author reply e648. Exclude: Publication type-commentary.
1245. Ross JS. Multigene classifiers, prognostic factors, and predictors of breast cancer clinical outcome. *Advances in Anatomic Pathology*. 2009;16(4):204-215. Exclude: No outcome of interest.
1246. Ross JS. A 50-gene intrinsic subtype classifier for prognosis and prediction of benefit from adjuvant tamoxifen. *Breast Diseases*. 2013;24(3):264-265. Exclude: No outcome of interest.

1247. Ross JS, Hatzis C, Symmans WF, Pusztai L, Hortobagyi GN. Commercialized multigene predictors of clinical outcome for breast cancer. *Oncologist*. 2008;13(5):477-493. Exclude: No outcome of interest.
1248. Roukos DH, Ziogas DE, Katsios C. Multigene assays and isolated tumor cells for early breast cancer treatment: time for bionetworks. *Expert Review of Anticancer Therapy*. 2010;10(8):1187-1195. Exclude: Publication type-commentary.
1249. Rouzier R, Bonneau C, Cayre A, et al. Evaluation of intra-tumor heterogeneity, test reproducibility and their impact in breast cancer samples assessed by Prosigna™: results from a decision impact prospective study and a matched case-control study. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1250. Rouzier R, Pronzato P, Chereau E, Carlson J, Hunt B, Valentine WJ. Multigene assays and molecular markers in breast cancer: systematic review of health economic analyses. *Breast Cancer Res Treat*. 2013;139(3):621-637. Exclude: Publication type-older systematic review.
1251. Rouzier R, Roulot A, Jeiranian AH, et al. Denaturing fixatives are compatible with the NanoString nCounter[®] platform and the Prosigna[®] assay. *New Biotechnology*. 2017;36:37-41. Exclude: No outcome of interest.
1252. Royce ME, Xia W, Sahin AA, et al. STK15/Aurora-A expression in primary breast tumors is correlated with nuclear grade but not with prognosis. *Cancer*. 2004;100(1):12-19. Exclude: Date.
1253. Roylance R, Endesfelder D, Gorman P, et al. Relationship of extreme chromosomal instability with long-term survival in a retrospective analysis of primary breast cancer. *Cancer Epidemiology, Biomarkers & Prevention*. 2011;20(10):2183-2194. Exclude: Not intervention of interest.
1254. Ruckhaberle E, Karn T, Engels K, et al. Prognostic impact of thymidine phosphorylase expression in breast cancer--comparison of microarray and immunohistochemical data. *European Journal of Cancer*. 2010;46(3):549-557. Exclude: Not intervention of interest.
1255. Rugo HS, Olopade OI, DeMichele A, et al. Adaptive Randomization of Veliparib-Carboplatin Treatment in Breast Cancer. *New England Journal of Medicine*. 2016;375(1):23-34. Exclude: Not intervention of interest.
1256. Ruiz Martin J, Perez Sanchez C, de las Heras Camino A. Three molecular classifications surrogate to four immunohistochemical markers in 374 invasive breast carcinomas with long follow-up: which is better? *Pathology, Research & Practice*. 2013;209(6):337-344. Exclude: Not intervention of interest.
1257. Runnak MA, Hazha MA, Hemin HA, Wasan AA, Rekawt RM, Michael HD. A population-based study of Kurdish breast cancer in northern Iraq: hormone receptor and HER2 status. A comparison with Arabic women and United States SEER data. *BMC Women's Health*. 2012;12:16. Exclude: Not intervention of interest.
1258. Rusin M, Zientek H, Krzesniak M, et al. Intronic polymorphism (1541-1542delGT) of the constitutive heat shock protein 70 gene has functional significance and shows evidence of association with lung cancer risk. *Molecular Carcinogenesis*. 2004;39(3):155-163. Exclude: Date.
1259. Rutgers E, Piccart-Gebhart MJ, Bogaerts J, et al. Baseline results of the EORTC 10041/MINDACT TRIAL (Microarray in Node 0-3 positive Disease may Avoid ChemoTherapy). *European journal of cancer*. 2013;49(27). Exclude: Publication type-conference abstract.

1260. Rutgers E, Piccart-Gebhart MJ, Bogaerts J, et al. The EORTC 10041/BIG 03-04 MINDACT trial is feasible: results of the pilot phase. *European Journal of Cancer*. 2011;47(18):2742-2749. Exclude: No outcome of interest.
1261. Rutter CE, Lester-Coll NH, Evans SB. (S029) evaluating the role of a 21-gene expression assay in directing adjuvant radiotherapy decisions for elderly women with early-stage breast cancer. *Oncology*. 2015;29(4 Suppl 1):21. Exclude: Publication type-conference abstract.
1262. Rutter CE, Yao X, Mancini BR, et al. Influence of a 21-gene recurrence score assay on chemotherapy delivery in breast cancer. *Clinical Breast Cancer*. 2016;16(1):59-62. Exclude: No comparator.
1263. Sabatier R, Finetti P, Mamessier E, et al. Prognostic and predictive value of PDL1 expression in breast cancer. *Oncotarget*. 2015;6(7):5449-5464. Exclude: Not intervention of interest.
1264. Sabatier R, Finetti P, Mamessier E, et al. Kinome expression profiling and prognosis of basal breast cancers. *Molecular Cancer*. 2011;10:86. Exclude: Not intervention of interest.
1265. Saghatchian M, Mook S, Pruneri G, et al. Additional prognostic value of the 70-gene signature (MammaPrint()) among breast cancer patients with 4-9 positive lymph nodes. *Breast*. 2013;22(5):682-690. Exclude: No outcome of interest.
1266. Sahebjam S, Aloyz R, Pilavdzic D, et al. Ki 67 is a major, but not the sole determinant of Oncotype Dx recurrence score. *British Journal of Cancer*. 2011;105(9):1342-1345. Exclude: No outcome of interest.
1267. Sakata S, Cronk M. The financial burden of using Oncotype Dx for patients with lymph node-negative and estrogen receptor-positive breast cancer in Australia. *Asia Pac J Clin Oncol*. 2014;10(1):94-95. Exclude: Publication type-letter.
1268. Salhia B, Kiefer J, Ross JT, et al. Integrated genomic and epigenomic analysis of breast cancer brain metastasis. *PLoS ONE [Electronic Resource]*. 2014;9(1):e85448. Exclude: Not intervention of interest.
1269. Sanchez-Forbach ER, Carpinteyro-Espin U, Aleman-Aviles JA, Sanchez-Basurto C. [Validation and clinical application of MammaPrint in patients with breast cancer]. *Cirugia y Cirujanos*. 2017;85(4):320-324. Exclude: Not English.
1270. Sanchez-Forbach ER, Carpinteyro-Espin U, Aleman-Aviles JA, Sanchez-Basurto C. [Validation and clinical application of MammaPrint(R) in patients with breast cancer]. *Cir Cir*. 2017;85(4):320-324. Exclude: Not English.
1271. Sanchez-Navarro I, Gamez-Pozo A, Pinto A, et al. An 8-gene qRT-PCR-based gene expression score that has prognostic value in early breast cancer. *BMC Cancer*. 2010;10:336. Exclude: Not intervention of interest.
1272. Sanger N, Ruckhaberle E, Bianchini G, et al. OPG and PgR show similar cohort specific effects as prognostic factors in ER positive breast cancer. *Molecular Oncology*. 2014;8(7):1196-1207. Exclude: Not intervention of interest.
1273. Santagata S, Thakkar A, Ergonul A, et al. Taxonomy of breast cancer based on normal cell phenotype predicts outcome. *Journal of Clinical Investigation*. 2014;124(2):859-870. Exclude: Not intervention of interest.
1274. Sapino A, Roepman P, Linn SC, et al. MammaPrint molecular diagnostics on formalin-fixed, paraffin-embedded tissue. *Journal of Molecular Diagnostics*. 2014;16(2):190-197. Exclude: No outcome of interest.
1275. Sato-Tadano A, Suzuki T, Amari M, et al. Hexokinase II in breast carcinoma: a potent prognostic factor associated with hypoxia-inducible factor-1alpha and Ki-67. *Cancer Science*. 2013;104(10):1380-1388. Exclude: Not intervention of interest.

1276. Sauer T, Furu I, Beraki K, Jebsen PW, Ormerod E, Naess O. nm23 protein expression in fine-needle aspirates from breast carcinoma: inverse correlation with cytologic grading, lymph node status, and ploidy. *Cancer*. 1998;84(2):109-114. Exclude: Date.
1277. Sauerbrei W, Royston P. Exaggeration of the prognostic effect of Mammostrat: a consequence of poor reporting? *Journal of Clinical Oncology*. 2013;31(21):2760-2761. Exclude: No outcome of interest.
1278. Schindlbeck C, Kampik T, Janni W, et al. Prognostic relevance of disseminated tumor cells in the bone marrow and biological factors of 265 primary breast carcinomas. *Breast Cancer Research*. 2005;7(6):R1174-1185. Exclude: Date.
1279. Schmid P, Pinder SE, Wheatley D, et al. Preoperative window of opportunity study of the PI3K inhibitor pictilisib (GDC-0941) plus anastrozole vs anastrozole alone in patients with ER+, HER2-negative operable breast cancer (OPPORTUNE study). *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
1280. Schmidt C. Mammaprint Reveals Who Can Skip Chemotherapy for Breast Cancer. *Journal of the National Cancer Institute*. 2016;108(8). Exclude: Publication type-commentary.
1281. Schmidt KT, Chau CH, Price DK, Figg WD. Precision Oncology Medicine: The Clinical Relevance of Patient-Specific Biomarkers Used to Optimize Cancer Treatment. *Journal of Clinical Pharmacology*. 2016;56(12):1484-1499. Exclude: Publication type-not systematic review.
1282. Schmidt M, Bohm D, von Torne C, et al. The humoral immune system has a key prognostic impact in node-negative breast cancer. *Cancer Research*. 2008;68(13):5405-5413. Exclude: Not intervention of interest.
1283. Schmidt M, Hellwig B, Hammad S, et al. A comprehensive analysis of human gene expression profiles identifies stromal immunoglobulin kappa C as a compatible prognostic marker in human solid tumors. *Clinical Cancer Research*. 2012;18(9):2695-2703. Exclude: Not intervention of interest.
1284. Schmidt M, Lewark B, Kohlschmidt N, et al. Long-term prognostic significance of HER-2/neu in untreated node-negative breast cancer depends on the method of testing. *Breast Cancer Research*. 2005;7(2):R256-266. Exclude: Date.
1285. Schmidt M, Petry IB, Bohm D, et al. Ep-CAM RNA expression predicts metastasis-free survival in three cohorts of untreated node-negative breast cancer. *Breast Cancer Research & Treatment*. 2011;125(3):637-646. Exclude: Not intervention of interest.
1286. Schmidt M, Thomssen C, Untch M. Intrinsic Subtypes of Primary Breast Cancer--Gene Expression Analysis. *Oncology Research and Treatment*. 2016;39(3):102-110. Exclude: No outcome of interest.
1287. Schneeweiss A, Lauschner I, Ruiz A, et al. Doxorubicin/pemetrexed followed by docetaxel versus doxorubicin/ cyclophosphamide followed by docetaxel as neoadjuvant treatment for early-stage breast cancer: a randomized phase II trial. *Clinical breast cancer*. 2007;7(7):555-558. Exclude: Not intervention of interest.
1288. Schneider JG, Khalil DN. Why does Oncotype DX recurrence score reduce adjuvant chemotherapy use? *Breast Cancer Research & Treatment*. 2012;134(3):1125-1132. Exclude: No outcome of interest.
1289. Schondorf T, Eisele L, Gohring UJ, et al. The V109G polymorphism of the p27 gene CDKN1B indicates a worse outcome in node-negative breast cancer patients. *Tumour Biology*. 2004;25(5-6):306-312. Exclude: Date.
1290. Schroder C, Schumacher U, Fogel M, et al. Expression and prognostic value of L1-CAM in breast cancer. *Oncology Reports*. 2009;22(5):1109-1117. Exclude: Not intervention of interest.

1291. Schroeder B, Zhang Y, Stal O, et al. Risk stratification with Breast Cancer Index for late distant recurrence in patients with clinically low-risk (T1N0) estrogen receptor-positive breast cancer. *NPJ Breast Cancer*. 2017;3:28. Exclude: No outcome of interest.
1292. Schroeder BE, Zhang Y, Stal O, et al. Prognostic impact of genomic risk stratification with breast cancer index in patients with clinically low risk, hormone receptor-positive, node-negative, T1 breast cancer. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1293. Schroth W, Winter S, Buttner F, et al. Clinical outcome and global gene expression data support the existence of the estrogen receptor-negative/progesterone receptor-positive invasive breast cancer phenotype. *Breast Cancer Research & Treatment*. 2016;155(1):85-97. Exclude: No outcome of interest.
1294. Schummer M, Green A, Beatty JD, et al. Comparison of breast cancer to healthy control tissue discovers novel markers with potential for prognosis and early detection.[Erratum appears in PLoS One. 2010;5(4). doi: 10.1371/annotation/632c5ae8-271b-4d19-8509-dc3b2eefe6a4]. *PLoS ONE [Electronic Resource]*. 2010;5(2):e9122. Exclude: Not intervention of interest.
1295. Schuster SR, Pockaj BA, Bothe MR, David PS, Northfelt DW. Clinical utility of gene expression profiling data for clinical decision-making regarding adjuvant therapy in early stage, node-negative breast cancer: a case report. *Journal of Personalized Medicine*. 2012;2(3):71-76. Exclude: Publication type-case report.
1296. Schwartz GF, Bartelink H, Burstein HJ, et al. Adjuvant therapy in stage I carcinoma of the breast: the influence of multigene analyses and molecular phenotyping. *Breast Journal*. 2012;18(4):303-311. Exclude: Publication type-not systematic review.
1297. Scott A, Ambannavar R, Jeong J, Liu ML, Cronin MT. RT-PCR-based gene expression profiling for cancer biomarker discovery from fixed, paraffin-embedded tissues. *Methods in Molecular Biology*. 2011;724:239-257. Exclude: No outcome of interest.
1298. Segui MA, Crespo C, Cortes J, et al. In response: Genomic profile of breast cancer. *Expert Review of Pharmacoeconomics & Outcomes Research*. 2015;15(3):395-397. Exclude: Publication type-letter.
1299. Segui MA, Crespo C, Cortes J, et al. Genomic profile of breast cancer: cost-effectiveness analysis from the Spanish National Healthcare System perspective. *Expert Rev Pharmacoecon Outcomes Res*. 2014;14(6):889-899. Exclude: In included systematic review.
1300. Sellers TA, Anderson VE, Potter JD, et al. Epidemiologic and genetic follow-up study of 544 Minnesota breast cancer families: design and methods. *Genetic Epidemiology*. 1995;12(4):417-429. Exclude: Date.
1301. Senkus E, Kyriakides S, Ohno S, et al. Primary breast cancer: ESMO Clinical Practice Guidelines for diagnosis, treatment and follow-up. *Ann Oncol*. 2015;26 Suppl 5:v8-30. Exclude: Publication type-not systematic review.
1302. Seong MK, Lee JY, Byeon J, et al. Bcl-2 is a highly significant prognostic marker of hormone-receptor-positive, human epidermal growth factor receptor-2-negative breast cancer. *Breast Cancer Research & Treatment*. 2015;150(1):141-148. Exclude: Not intervention of interest.
1303. Servant N, Bollet MA, Halfwerk H, et al. Search for a gene expression signature of breast cancer local recurrence in young women. *Clinical Cancer Research*. 2012;18(6):1704-1715. Exclude: No outcome of interest.

1304. Sestak I, Cuzick J, Dowsett M, et al. Prediction of late distant recurrence after 5 years of endocrine treatment: a combined analysis of patients from the Austrian breast and colorectal cancer study group 8 and arimidex, tamoxifen alone or in combination randomized trials using the PAM50 risk of recurrence score. *Journal of Clinical Oncology*. 2015;33(8):916-922. Exclude: No outcome of interest.
1305. Sestak I, Dowsett M, Zabaglo L, et al. Factors predicting late recurrence for estrogen receptor-positive breast cancer. *Journal of the National Cancer Institute*. 2013;105(19):1504-1511. Exclude: No outcome of interest.
1306. Sestak I, Zhang Y, Schroeder BE, et al. Cross-Stratification and Differential Risk by Breast Cancer Index and Recurrence Score in Women with Hormone Receptor-Positive Lymph Node-Negative Early-Stage Breast Cancer. *Clinical Cancer Research*. 2016;22(20):5043-5048. Exclude: No outcome of interest.
1307. Sgroi D, Hameed O, Hattab E, et al. Comparison of risk stratification of ER-positive, node-negative breast cancer patients by Oncotype DX versus molecular grade index and HOXB13/IL17BR ratio. *Journal of Clinical Oncology*. 2008;26(15_suppl):22061. Exclude: No outcome of interest.
1308. Sgroi DC, Chapman JA, Badovinac-Crnjevic T, et al. Assessment of the prognostic and predictive utility of the Breast Cancer Index (BCI): an NCIC CTG MA.14 study. *Breast Cancer Research*. 2016;18(1):1. Exclude: No outcome of interest.
1309. Sgroi DC, Sestak I, Cuzick J, et al. Prediction of late distant recurrence in patients with oestrogen-receptor-positive breast cancer: a prospective comparison of the breast-cancer index (BCI) assay, 21-gene recurrence score, and IHC4 in the TransATAC study population. *Lancet Oncology*. 2013;14(11):1067-1076. Exclude: No outcome of interest.
1310. Shagisultanova EI, Novikova IA, Sidorenko YS, Marchenko GN, Strongin AY, Malkhosyan SR. The matrix metalloproteinase-21 gene 572C/T polymorphism and the risk of breast cancer. *Anticancer Research*. 2004;24(1):199-201. Exclude: Date.
1311. Shah PD, Patil S, Dickler MN, Offit K, Hudis CA, Robson ME. Twenty-one-gene recurrence score assay in BRCA-associated versus sporadic breast cancers: Differences based on germline mutation status. *Cancer*. 2016;122(8):1178-1184. Exclude: No outcome of interest.
1312. Shah SH, Miller P, Garcia-Contreras M, et al. Hierarchical paracrine interaction of breast cancer associated fibroblasts with cancer cells via hMAPK-microRNAs to drive ER-negative breast cancer phenotype. *Cancer Biology & Therapy*. 2015;16(11):1671-1681. Exclude: Not intervention of interest.
1313. Shaheed SU, Rustogi N, Scally A, et al. Identification of stage-specific breast markers using quantitative proteomics. *Journal of Proteome Research*. 2013;12(12):5696-5708. Exclude: Not intervention of interest.
1314. Shchurov MF, Voloshyna NM, Pogorila TY. [Factors of Prognosis in Patients with Early Cancer of Mammary Gland]. *Klinicheskaya Khirurgiya*. 2015(12):38-40. Exclude: Not intervention of interest.
1315. Sheffield BS, Kos Z, Asleh-Aburaya K, et al. Molecular subtype profiling of invasive breast cancers weakly positive for estrogen receptor. *Breast Cancer Research & Treatment*. 2016;155(3):483-490. Exclude: No outcome of interest.
1316. Shen K, Qi Y, Song N, et al. Cell line derived multi-gene predictor of pathologic response to neoadjuvant chemotherapy in breast cancer: a validation study on US Oncology 02-103 clinical trial. *BMC Medical Genomics [Electronic Resource]*. 2012;5:51. Exclude: Not intervention of interest.

1317. Shen K, Song N, Kim Y, et al. A systematic evaluation of multi-gene predictors for the pathological response of breast cancer patients to chemotherapy. *PLoS ONE [Electronic Resource]*. 2012;7(11):e49529. Exclude: No outcome of interest.
1318. Sheppard VB, O'Neill SC, Dilawari A, Horton S, Hirpa FA, Isaacs C. Patterns of 21-gene assay testing and chemotherapy use in black and white breast cancer patients. *Clin Breast Cancer*. 2015;15(2):e83-92. Exclude: No outcome of interest.
1319. Shetty A, Loddo M, Fanshawe T, et al. DNA replication licensing and cell cycle kinetics of normal and neoplastic breast. *British Journal of Cancer*. 2005;93(11):1295-1300. Exclude: Date.
1320. Shi L, Campbell G, Jones WD, et al. The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. *Nature Biotechnology*. 2010;28(8):827-838. Exclude: No outcome of interest.
1321. Shi L, Dong B, Li Z, et al. Expression of ER- α 36, a novel variant of estrogen receptor α , and resistance to tamoxifen treatment in breast cancer. *Journal of Clinical Oncology*. 2009;27(21):3423-3429. Exclude: Not intervention of interest.
1322. Shi M, DeRoo LA, Sandler DP, Weinberg CR. Migraine and possible etiologic heterogeneity for hormone-receptor-negative breast cancer.[Erratum appears in Sci Rep. 2016;6:17238; PMID: 26740285]. *Scientific Reports*. 2015;5:14943. Exclude: Not intervention of interest.
1323. Shi M, Zhang B. Semi-supervised learning improves gene expression-based prediction of cancer recurrence. *Bioinformatics*. 2011;27(21):3017-3023. Exclude: No outcome of interest.
1324. Shibata MA, Ito Y, Morimoto J, Kusakabe K, Yoshinaka R, Otsuki Y. In vivo electrogene transfer of interleukin-12 inhibits tumor growth and lymph node and lung metastases in mouse mammary carcinomas. *Journal of Gene Medicine*. 2006;8(3):335-352. Exclude: Date.
1325. Shigemizu D, Iwase T, Yoshimoto M, et al. The prediction models for postoperative overall survival and disease-free survival in patients with breast cancer. *Cancer Medicine*. 2017;6(7):1627-1638. Exclude: Not intervention of interest.
1326. Shih J, Bashir B, Gustafson KS, et al. Cancer Signature Investigation: ERBB2 (HER2)-Activating Mutation and Amplification-Positive Breast Carcinoma Mimicking Lung Primary. *Journal of the National Comprehensive Cancer Network*. 2015;13(8):947-952. Exclude: Not intervention of interest.
1327. Shimizu H, Horimoto Y, Arakawa A, et al. Application of a 70-Gene Expression Profile to Japanese Breast Cancer Patients. *Breast Care*. 2015;10(2):118-122. Exclude: Publication type-letter.
1328. Shin A, Cai Q, Shu XO, Gao YT, Zheng W. Genetic polymorphisms in the matrix metalloproteinase 12 gene (MMP12) and breast cancer risk and survival: the Shanghai Breast Cancer Study. *Breast Cancer Research*. 2005;7(4):R506-512. Exclude: Date.
1329. Shivers SC, Russell S, Blumencranz L, et al. Long-term follow-up of early stage breast cancer patients with results of MammaPrint, Oncotype DX and MammoStrat risk classification assays. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1330. Shkurnikov MY, Galatenko VV, Lebedev AE, Podol'skii VE, Tonevitskii EA, Mal'tseva DV. On statistical relationship between ADRA2A expression and the risk of breast cancer relapse. *Bulletin of Experimental Biology & Medicine*. 2014;157(4):454-458. Exclude: Not intervention of interest.
1331. Shkurnikov MY, Nechaev IN, Khaustova NA, et al. Expression profile of inflammatory breast cancer. *Bulletin of Experimental Biology & Medicine*. 2013;155(5):667-672. Exclude: Not intervention of interest.

1332. Shomali M, Cheng J, Koundinya M, et al. Identification of SAR439859, an orally bioavailable selective estrogen receptor degrader (SERD) that has strong antitumor activity in wild-type and mutant ER+ breast cancer models. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1333. Short SM, Yoder BJ, Tarr SM, et al. The expression of the cytoskeletal focal adhesion protein paxillin in breast cancer correlates with HER2 overexpression and may help predict response to chemotherapy: a retrospective immunohistochemical study. *Breast Journal*. 2007;13(2):130-139. Exclude: Not intervention of interest.
1334. Siamakpour-Reihani S, Owzar K, Jiang C, et al. Genomic profiling in locally advanced and inflammatory breast cancer and its link to DCE-MRI and overall survival. *International Journal of Hyperthermia*. 2015;31(4):386-395. Exclude: No outcome of interest.
1335. Sicking I, Edlund K, Wesbuer E, et al. Prognostic influence of pre-operative C-reactive protein in node-negative breast cancer patients. *PLoS ONE [Electronic Resource]*. 2014;9(10):e111306. Exclude: Not intervention of interest.
1336. Siddiqui RA, Harvey KA, Walker C, et al. Characterization of synergistic anti-cancer effects of docosahexaenoic acid and curcumin on DMBA-induced mammary tumorigenesis in mice. *BMC Cancer*. 2013;13:418. Exclude: Not intervention of interest.
1337. Siddiqui SF, Pawelek J, Handerson T, et al. Coexpression of beta1,6-N-acetylglucosaminyltransferase V glycoprotein substrates defines aggressive breast cancers with poor outcome. *Cancer Epidemiology, Biomarkers & Prevention*. 2005;14(11 Pt 1):2517-2523. Exclude: Date.
1338. Sidiropoulos KG, Ding Q, Pampalakis G, et al. KLK6-regulated miRNA networks activate oncogenic pathways in breast cancer subtypes. *Molecular Oncology*. 2016;10(7):993-1007. Exclude: Not intervention of interest.
1339. Siegelmann-Danieli N, Silverman B, Zick A, Beit-Or A, Katzir I, Porath A. The impact of the Oncotype DX Recurrence Score on treatment decisions and clinical outcomes in patients with early breast cancer: the Maccabi Healthcare Services experience with a unified testing policy. *Ecancermedicalscience*. 2013;7:380. Exclude: No comparator.
1340. Siegelmann-Danieli N, Stein ME, Wallach N. [Molecular portrait of breast cancer with sub-classification of breast tumor]. *Harefuah*. 2007;146(1):48-52, 77-48. Exclude: Not English.
1341. Siegfried JM, Lin Y, Diergaarde B, et al. Expression of PAM50 Genes in Lung Cancer: Evidence that Interactions between Hormone Receptors and HER2/HER3 Contribute to Poor Outcome. *Neoplasia (New York)*. 2015;17(11):817-825. Exclude: Not intervention of interest.
1342. Sieuwerts AM, Ansems M, Look MP, et al. Clinical significance of the nuclear receptor co-regulator DC-SCRIPT in breast cancer: an independent retrospective validation study. *Breast Cancer Research*. 2010;12(6):R103. Exclude: Not intervention of interest.
1343. Sieuwerts AM, Meijer-van Gelder ME, Timmermans M, et al. How ADAM-9 and ADAM-11 differentially from estrogen receptor predict response to tamoxifen treatment in patients with recurrent breast cancer: a retrospective study. *Clinical Cancer Research*. 2005;11(20):7311-7321. Exclude: Date.
1344. Silverstein MJ, Recht A, Lagios MD, et al. Special report: Consensus conference III. Image-detected breast cancer: state-of-the-art diagnosis and treatment. *Journal of the American College of Surgeons*. 2009;209(4):504-520. Exclude: Not intervention of interest.

1345. Silwal-Pandit L, Vollan HK, Chin SF, et al. TP53 mutation spectrum in breast cancer is subtype specific and has distinct prognostic relevance.[Erratum appears in Clin Cancer Res. 2015 Mar 15;21(6):1502; PMID: 25770298]. *Clinical Cancer Research*. 2014;20(13):3569-3580. Exclude: Not intervention of interest.
1346. Simchoni S, Friedman E, Kaufman B, et al. Familial clustering of site-specific cancer risks associated with BRCA1 and BRCA2 mutations in the Ashkenazi Jewish population. *Proceedings of the National Academy of Sciences of the United States of America*. 2006;103(10):3770-3774. Exclude: Date.
1347. Singh R, Gupta S, Pawar SB, Pawar RS, Gandham SV, Prabhudesai S. Evaluation of ER, PR and HER-2 receptor expression in breast cancer patients presenting to a semi urban cancer centre in Western India. *Journal of Cancer Research & Therapeutics*. 2014;10(1):26-28. Exclude: Not intervention of interest.
1348. Sinn BV, von Minckwitz G, Denkert C, et al. Evaluation of Mucin-1 protein and mRNA expression as prognostic and predictive markers after neoadjuvant chemotherapy for breast cancer. *Annals of Oncology*. 2013;24(9):2316-2324. Exclude: Not intervention of interest.
1349. Sinn P, Aulmann S, Wirtz R, et al. Multigene Assays for Classification, Prognosis, and Prediction in Breast Cancer: a Critical Review on the Background and Clinical Utility. *Geburtshilfe Frauenheilkd*. 2013;73(9):932-940. Exclude: Publication type-not systematic review.
1350. Sircoulomb F, Bekhouche I, Finetti P, et al. Genome profiling of ERBB2-amplified breast cancers. *BMC Cancer*. 2010;10:539. Exclude: Not intervention of interest.
1351. Skelthorne-Gross G, Reid AL, Apostoli AJ, et al. Stromal adipocyte PPARgamma protects against breast tumorigenesis. *Carcinogenesis*. 2012;33(7):1412-1420. Exclude: Not intervention of interest.
1352. Slodkowska EA, Ross JS. MammaPrint 70-gene signature: another milestone in personalized medical care for breast cancer patients. *Expert Review of Molecular Diagnostics*. 2009;9(5):417-422. Exclude: Publication type-commentary.
1353. Smith IE, Yeo B, Schiavon G. The optimal duration and selection of adjuvant endocrine therapy for breast cancer: how long is enough? *American Society of Clinical Oncology Educational Book*. 2014:e16-24. Exclude: Publication type-commentary.
1354. Smyth L, Watson G, Walsh EM, et al. Economic impact of 21-gene recurrence score testing on early-stage breast cancer in Ireland. *Breast Cancer Res Treat*. 2015;153(3):573-582. Exclude: In included systematic review.
1355. Sninsky J, Wang A, Gray K, et al. Predictive value of a proliferation score (MS) in postmenopausal women with endocrine-responsive breast cancer: Results from International Breast Cancer Study Group (IBCSG) Trial IX. *Cancer research*. 2012;72(24 SUPPL. 3):CONFERENCE START: 2012 Dec 2014 CONFERENCE END: 2012 Dec 2018. Exclude: Publication type-conference abstract.
1356. Solin LJ, Gray R, Baehner FL, et al. A multigene expression assay to predict local recurrence risk for ductal carcinoma in situ of the breast. *Journal of the National Cancer Institute*. 2013;105(10):701-710. Exclude: No outcome of interest.
1357. Solin LJ, Gray R, Goldstein LJ, et al. Prognostic value of biologic subtype and the 21-gene recurrence score relative to local recurrence after breast conservation treatment with radiation for early stage breast carcinoma: results from the Eastern Cooperative Oncology Group E2197 study. *Breast Cancer Res Treat*. 2012;134(2):683-692. Exclude: No outcome of interest.

1358. Somlo G, Chu P, Frankel P, et al. Molecular profiling including epidermal growth factor receptor and p21 expression in high-risk breast cancer patients as indicators of outcome. *Annals of Oncology*. 2008;19(11):1853-1859. Exclude: Not intervention of interest.
1359. Somlo G, Lau S, Frankel P, et al. Basal-, Luminal-, and HER2- Molecular Subtype, and the MammaPrint 70-Gene Signature as Predictors of Response to Neoadjuvant Chemotherapy (NCT) with Docetaxel, Doxorubicin, Cyclophosphamide (TAC), or AC and Nab-Paclitaxel and Carboplatin +/- Trastuzumab in Patients (Pts) with Stage II-III and Inflammatory Breast Cancer (BC). 2010. Exclude: No outcome of interest.
1360. Soncini D, Caffa I, Zoppoli G, et al. Nicotinamide phosphoribosyltransferase promotes epithelial-to-mesenchymal transition as a soluble factor independent of its enzymatic activity. *Journal of Biological Chemistry*. 2014;289(49):34189-34204. Exclude: Not intervention of interest.
1361. Song Q, Huang R, Li J, et al. The diverse distribution of risk factors between breast cancer subtypes of ER, PR and HER2: a 10-year retrospective multi-center study in China. *PLoS ONE [Electronic Resource]*. 2013;8(8):e72175. Exclude: Not intervention of interest.
1362. Sonnenblick A, Brohee S, Fumagalli D, et al. Integrative proteomic and gene expression analysis identify potential biomarkers for adjuvant trastuzumab resistance: analysis from the Fin-her phase III randomized trial. *Oncotarget*. 2015;6(30):30306-30316. Exclude: Not intervention of interest.
1363. Soond SM, Smith PG, Wahl L, et al. Novel WWP2 ubiquitin ligase isoforms as potential prognostic markers and molecular targets in cancer. *Biochimica et Biophysica Acta*. 2013;1832(12):2127-2135. Exclude: Not intervention of interest.
1364. Soran A, Bhargava R, Johnson R, et al. The impact of Oncotype DX recurrence score of paraffin-embedded core biopsy tissues in predicting response to neoadjuvant chemotherapy in women with breast cancer. *Breast Disease*. 2016;36(2-3):65-71. Exclude: No outcome of interest.
1365. Sorlie T, Perou CM, Fan C, et al. Gene expression profiles do not consistently predict the clinical treatment response in locally advanced breast cancer. *Molecular Cancer Therapeutics*. 2006;5(11):2914-2918. Exclude: Date.
1366. Sota Y, Naoi Y, Tsunashima R, et al. Construction of novel immune-related signature for prediction of pathological complete response to neoadjuvant chemotherapy in human breast cancer. *Annals of Oncology*. 2014;25(1):100-106. Exclude: Not intervention of interest.
1367. Sotiriou C, Powles TJ, Dowsett M, et al. Gene expression profiles derived from fine needle aspiration correlate with response to systemic chemotherapy in breast cancer. *Breast Cancer Research*. 2002;4(3):R3. Exclude: Date.
1368. Sparano JA. A 21-Gene Expression Assay in Breast Cancer. *New England Journal of Medicine*. 2016;374(14):1387. Exclude: Publication type-letter.
1369. Sparano JA, Goldstein LJ, Davidson NE, Sledge GW, Jr., Gray R. TOP2A RNA expression and recurrence in estrogen receptor-positive breast cancer. *Breast Cancer Research & Treatment*. 2012;134(2):751-757. Exclude: Not intervention of interest.
1370. Sparano JA, Gray R, Oktay MH, et al. A metastasis biomarker (MetaSite Breast™ Score) is associated with distant recurrence in hormone receptor-positive, HER2-negative early-stage breast cancer. *NPJ Breast Cancer*. 2017;3:42. Exclude: Not intervention of interest.
1371. Sparano JA, Gray RJ, Makower DF, et al. Prospective Validation of a 21-Gene Expression Assay in Breast Cancer. *N Engl J Med*. 2015;373(21):2005-2014. Exclude: No outcome of interest.

1372. Sparano JA, Paik S. Development of the 21-gene assay and its application in clinical practice and clinical trials. *Journal of Clinical Oncology*. 2008;26(5):721-728. Exclude: No outcome of interest.
1373. Spears M, Yousif F, Lyttle N, et al. A four gene signature predicts benefit from anthracyclines: evidence from the BR9601 and MA.5 clinical trials. *Oncotarget*. 2015;6(31):31693-31701. Exclude: Not intervention of interest.
1374. Specht K, Harbeck N, Smida J, et al. Expression profiling identifies genes that predict recurrence of breast cancer after adjuvant CMF-based chemotherapy. *Breast Cancer Research & Treatment*. 2009;118(1):45-56. Exclude: No outcome of interest.
1375. Spellman E, Sulayman N, Eggly S, et al. Conveying genomic recurrence risk estimates to patients with early-stage breast cancer: oncologist perspectives. *Psycho-Oncology*. 2013;22(9):2110-2116. Exclude: No outcome of interest.
1376. Spizzo G, Went P, Dirnhofer S, et al. High Ep-CAM expression is associated with poor prognosis in node-positive breast cancer. *Breast Cancer Research & Treatment*. 2004;86(3):207-213. Exclude: Date.
1377. Stal O, Jerevall P, Ma X, et al. Validation of Prognostic Utility of HOXB13:IL17BR and Molecular Grade Index in Early Stage Breast Cancer. 2010. Exclude: Not intervention of interest.
1378. Stal O, Sullivan S, Wingren S, et al. c-erbB-2 expression and benefit from adjuvant chemotherapy and radiotherapy of breast cancer. *European Journal of Cancer*. 1995;31A(13-14):2185-2190. Exclude: Date.
1379. Stalhammar G, Fuentes Martinez N, Lippert M, et al. Digital image analysis outperforms manual biomarker assessment in breast cancer. *Modern Pathology*. 2016;29(4):318-329. Exclude: No outcome of interest.
1380. Stanley J, Klepczyk L, Keene K, et al. PARP1 and phospho-p65 protein expression is increased in human HER2-positive breast cancers. *Breast Cancer Research & Treatment*. 2015;150(3):569-579. Exclude: Not intervention of interest.
1381. Staren ED, Braun D, Tan B, et al. Initial experience with genomic profiling of heavily pretreated breast cancers. *Annals of Surgical Oncology*. 2014;21(10):3216-3222. Exclude: Not intervention of interest.
1382. Starmans MH, Lieuwes NG, Span PN, et al. Independent and functional validation of a multi-tumour-type proliferation signature. *British Journal of Cancer*. 2012;107(3):508-515. Exclude: Not intervention of interest.
1383. Stathopoulou A, Mavroudis D, Perraki M, et al. Molecular detection of cancer cells in the peripheral blood of patients with breast cancer: comparison of CK-19, CEA and maspin as detection markers. *Anticancer Research*. 2003;23(2C):1883-1890. Exclude: Date.
1384. Stearns V, Jacobs LK, Fackler M, et al. Biomarker modulation following short-term vorinostat in women with newly diagnosed primary breast cancer. *Clinical Cancer Research*. 2013;19(14):4008-4016. Exclude: No outcome of interest.
1385. Stefansson OA, Moran S, Gomez A, et al. A DNA methylation-based definition of biologically distinct breast cancer subtypes. *Molecular Oncology*. 2015;9(3):555-568. Exclude: Not intervention of interest.
1386. Stein GY, Yosef N, Reichman H, et al. Met kinetic signature derived from the response to HGF/SF in a cellular model predicts breast cancer patient survival. *PLoS ONE [Electronic Resource]*. 2012;7(9):e45969. Exclude: Not intervention of interest.
1387. Stein R, Makris A, Hughes-Davies L, et al. OPTIMA prelim: Optimal personalized treatment of early breast cancer using multiparameter tests. *Journal of clinical oncology*. 2013;31(15 SUPPL. 1):CONFERENCE START: 2013 May 2031 CONFERENCE END: 2013 Jun 2014. Exclude: Publication type-conference abstract.

1388. Stein R, Makris A, Hughes-Davies L, et al. OPTIMA: a prospective randomised trial to validate the predictive utility and cost-effectiveness of gene expression test directed chemotherapy decisions. *European journal of surgical oncology*. 2016;Conference: joint BASO-ACS annual scientific conference and NCRI cancer conference. 2016. United kingdom. Conference start: 20161106. Conference end: 20161109 42(11):S229. Exclude: Publication type-conference abstract.
1389. Stein R, Makris A, Luke HD, et al. OPTIMA prelim: Optimal personalized treatment of early breast cancer using multiparameter analysis: Preliminary study. *Journal of clinical oncology*. 2012;30(15 SUPPL. 1):CONFERENCE START: 2012 Jun 2011 CONFERENCE END: 2012 Jun 2015. Exclude: Publication type-conference abstract.
1390. Stein RC, Dunn JA, Bartlett JM, et al. OPTIMA prelim: a randomised feasibility study of personalised care in the treatment of women with early breast cancer. *Health Technology Assessment (Winchester, England)*. 2016;20(10):xxiii-xxix, 1-201. Exclude: No outcome of interest.
1391. Stein RC, Makris A, Hughes-Davies L, et al. Results of the OPTIMA (Optimal Personalized Treatment of early breast cancer using Multi-parameter Analysis) prelim study. *European Journal of Cancer*. 2015;51(25). Exclude: Publication type-conference abstract.
1392. Stein RC, Marshall A, Hall PS, et al. OPTIMA (optimal personalised treatment of early breast cancer using multi-parameter analysis), a prospective trial to validate the predictive utility and cost-effectiveness of gene expression test-directed chemotherapy decisions. *Cancer research*. 2015;76(4 SUPPL. 1) (no pagination):CONFERENCE START: 2015 Dec 2018 CONFERENCE END: 2015 Dec 2012. Exclude: Publication type-conference abstract.
1393. Stemmer SM, Klang SH, Ben-Baruch N, et al. The impact of the 21-gene Recurrence Score assay on clinical decision-making in node-positive (up to 3 positive nodes) estrogen receptor-positive breast cancer patients. *Breast Cancer Res Treat*. 2013;140(1):83-92. Exclude: Date.
1394. Stemmer SM, Steiner M, Rizel S, et al. First prospectively-designed outcome study in estrogen receptor (ER)+ breast cancer (BC) patients (pts) with N1mi or 1-3 positive nodes in whom treatment decisions in clinical practice incorporated the 21-gene recurrence score (RS) result. *Annals of oncology Conference: 41st european society for medical oncology congress, ESMO*. 2016;27(no pagination). Exclude: Publication type-conference abstract.
1395. Stemmer SM, Steiner M, Rizel S, et al. Clinical outcomes in patients with node-negative breast cancer treated based on the recurrence score results: Evidence from a large prospectively designed registry. *NPJ Breast Cancer*. 2017;3:33. Exclude: No comparator.
1396. Stephen J, Murray G, Cameron DA, et al. Time dependence of biomarkers: non-proportional effects of immunohistochemical panels predicting relapse risk in early breast cancer. *British Journal of Cancer*. 2014;111(12):2242-2247. Exclude: No outcome of interest.
1397. Stickeler E, Pils D, Klar M, et al. Basal-like molecular subtype and HER4 up-regulation and response to neoadjuvant chemotherapy in breast cancer. *Oncology Reports*. 2011;26(4):1037-1045. Exclude: Not intervention of interest.
1398. Stover DG, Coloff JL, Barry WT, Brugge JS, Winer EP, Selfors LM. The Role of Proliferation in Determining Response to Neoadjuvant Chemotherapy in Breast Cancer: A Gene Expression-Based Meta-Analysis. *Clinical Cancer Research*. 2016;22(24):6039-6050. Exclude: No outcome of interest.

1399. Straver ME, Glas AM, Hannemann J, et al. The 70-gene signature as a response predictor for neoadjuvant chemotherapy in breast cancer. *Breast Cancer Research & Treatment*. 2010;119(3):551-558. Exclude: No outcome of interest.
1400. Stricker TP, Brown CD, Bandlamudi C, et al. Robust stratification of breast cancer subtypes using differential patterns of transcript isoform expression. *PLoS Genetics*. 2017;13(3):e1006589. Exclude: Not intervention of interest.
1401. Strom T, Harrison LB, Giuliano AR, et al. Tumour radiosensitivity is associated with immune activation in solid tumours. *European Journal of Cancer*. 2017;84:304-314. Exclude: Not intervention of interest.
1402. Strunz K, Deissler H, Kreienberg R, Sauer G. [Predicting response to therapy in breast cancer]. *Gynakologisch-Geburtshilfliche Rundschau*. 2008;48(3):113-117. Exclude: Not English.
1403. Su KW, Hall J, Soulos PR, et al. Association of 21-gene recurrence score assay and adjuvant chemotherapy use in the medicare population, 2008-2011. *Journal of Geriatric Oncology*. 2016;7(1):15-23. Exclude: In included systematic review.
1404. Subramanian J, Simon R. What should physicians look for in evaluating prognostic gene-expression signatures? *Nature Reviews Clinical Oncology*. 2010;7(6):327-334. Exclude: No outcome of interest.
1405. Suh DH, Kim M, Kim HJ, Lee KH, Kim JW. Major clinical research advances in gynecologic cancer in 2015. *Journal of Gynecologic Oncology*. 2016;27(6):e53. Exclude: Publication type-not systematic review.
1406. Suh EJ, Kabir MH, Kang UB, et al. Comparative profiling of plasma proteome from breast cancer patients reveals thrombospondin-1 and BRWD3 as serological biomarkers. *Experimental & Molecular Medicine*. 2012;44(1):36-44. Exclude: Not intervention of interest.
1407. Sulayman N, Spellman E, Graves KD, et al. Psychosocial and Quality of Life in Women Receiving the 21-Gene Recurrence Score Assay: The Impact of Decision Style in Women with Intermediate RS. *J Cancer Epidemiol*. 2012;2012:728290. Exclude: No comparator.
1408. Sun B, Zhang F, Wu SK, et al. Gene expression profiling for breast cancer prognosis in Chinese populations. *Breast Journal*. 2011;17(2):172-179. Exclude: No outcome of interest.
1409. Sun JM, Han W, Im SA, et al. A combination of HER-2 status and the St. Gallen classification provides useful information on prognosis in lymph node-negative breast carcinoma. *Cancer*. 2004;101(11):2516-2522. Exclude: Date.
1410. Sun X, Gierach GL, Sandhu R, et al. Relationship of mammographic density and gene expression: analysis of normal breast tissue surrounding breast cancer. *Clinical Cancer Research*. 2013;19(18):4972-4982. Exclude: No outcome of interest.
1411. Sun Y, Goodison S, Li J, Liu L, Farmerie W. Improved breast cancer prognosis through the combination of clinical and genetic markers. *Bioinformatics*. 2007;23(1):30-37. Exclude: No outcome of interest.
1412. Sun Y, Urquidí V, Goodison S. Derivation of molecular signatures for breast cancer recurrence prediction using a two-way validation approach. *Breast Cancer Research & Treatment*. 2010;119(3):593-599. Exclude: Not intervention of interest.
1413. Sun Z, Prat A, Cheang MC, Gelber RD, Perou CM. Chemotherapy benefit for 'ER-positive' breast cancer and contamination of nonluminal subtypes-waiting for TAILORx and RxPONDER. *Annals of Oncology*. 2015;26(1):70-74. Exclude: No outcome of interest.

1414. Sundaramurthy G, Eghbalnia HR. A probabilistic approach for automated discovery of perturbed genes using expression data from microarray or RNA-Seq. *Computers in Biology & Medicine*. 2015;67:29-40. Exclude: Not intervention of interest.
1415. Suo C, Hrydziusko O, Lee D, et al. Integration of somatic mutation, expression and functional data reveals potential driver genes predictive of breast cancer survival. *Bioinformatics*. 2015;31(16):2607-2613. Exclude: No outcome of interest.
1416. Suo Z, Risberg B, Kallsson MG, et al. EGFR family expression in breast carcinomas. c-erbB-2 and c-erbB-4 receptors have different effects on survival. *Journal of Pathology*. 2002;196(1):17-25. Exclude: Date.
1417. Supernat A, Markiewicz A, Welnicka-Jaskiewicz M, et al. CD73 expression as a potential marker of good prognosis in breast carcinoma. *Applied Immunohistochemistry & Molecular Morphology*. 2012;20(2):103-107. Exclude: Not intervention of interest.
1418. Sutton EJ, Oh JH, Dashevsky BZ, et al. Breast cancer subtype intertumor heterogeneity: MRI-based features predict results of a genomic assay. *Journal of Magnetic Resonance Imaging*. 2015;42(5):1398-1406. Exclude: No outcome of interest.
1419. Suzuki S, Takagi K, Miki Y, et al. Nucleobindin 2 in human breast carcinoma as a potent prognostic factor. *Cancer Science*. 2012;103(1):136-143. Exclude: Not intervention of interest.
1420. Swain SM, Nunes R, Yoshizawa C, Rothney M, Sing AP. Quantitative Gene Expression by Recurrence Score in ER-Positive Breast Cancer, by Age. *Advances in Therapy*. 2015;32(12):1222-1236. Exclude: No outcome of interest.
1421. Sweeney C, Bernard PS, Factor RE, et al. Intrinsic subtypes from PAM50 gene expression assay in a population-based breast cancer cohort: differences by age, race, and tumor characteristics. *Cancer Epidemiol Biomarkers Prev*. 2014;23(5):714-724. Exclude: No outcome of interest.
1422. Szasz AM, Li Q, Eklund AC, et al. The CIN4 chromosomal instability qPCR classifier defines tumor aneuploidy and stratifies outcome in grade 2 breast cancer. *PLoS ONE [Electronic Resource]*. 2013;8(2):e56707. Exclude: Not intervention of interest.
1423. Tabarestani S, Ghaderian SM, Rezvani H, Mirfakhraie R. Expression profiling of breast cancer patients treated with tamoxifen: prognostic or predictive significance. *Medical Oncology*. 2014;31(4):896. Exclude: No outcome of interest.
1424. Takahashi H, Kobayashi T, Honda H. Construction of robust prognostic predictors by using projective adaptive resonance theory as a gene filtering method. *Bioinformatics*. 2005;21(2):179-186. Exclude: Date.
1425. Talvinen K, Tuikkala J, Nykanen M, et al. Altered expression of p120catenin predicts poor outcome in invasive breast cancer. *Journal of Cancer Research & Clinical Oncology*. 2010;136(9):1377-1387. Exclude: Not intervention of interest.
1426. Tamimi RM, Baer HJ, Marotti J, et al. Comparison of molecular phenotypes of ductal carcinoma in situ and invasive breast cancer. *Breast Cancer Research*. 2008;10(4):R67. Exclude: Not intervention of interest.
1427. Tan BK, Tan LK, Yu K, et al. Clinical validation of a customized multiple signature microarray for breast cancer. *Clinical Cancer Research*. 2008;14(2):461-469. Exclude: Not intervention of interest.
1428. Tang G, Cuzick J, Costantino JP, et al. Risk of recurrence and chemotherapy benefit for patients with node-negative, estrogen receptor-positive breast cancer: recurrence score alone and integrated with

pathologic and clinical factors. *Journal of Clinical Oncology*. 2011;29(33):4365-4372. Exclude: No outcome of interest.

1429. Tang G, Shak S, Paik S, et al. Comparison of the prognostic and predictive utilities of the 21-gene Recurrence Score assay and Adjuvant! for women with node-negative, ER-positive breast cancer: results from NSABP B-14 and NSABP B-20. *Breast Cancer Research & Treatment*. 2011;127(1):133-142. Exclude: No outcome of interest.

1430. Tang P, Wang J, Hicks DG, et al. A lower Allred score for progesterone receptor is strongly associated with a higher recurrence score of 21-gene assay in breast cancer. *Cancer Investigation*. 2010;28(9):978-982. Exclude: Publication type-commentary.

1431. Tang Y, Zhou X, Ji J, et al. High expression levels of miR-21 and miR-210 predict unfavorable survival in breast cancer: a systemic review and meta-analysis. *International Journal of Biological Markers*. 2015;30(4):e347-358. Exclude: Not intervention of interest.

1432. Tanioka M, Fan C, Carey LA, et al. Integrated analysis of multidimensional genomic data on CALGB 40601 (Alliance), a randomized neoadjuvant phase III trial of weekly paclitaxel (T) and trastuzumab (H) with or without lapatinib (L) for HER2-positive breast cancer. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

1433. Teig B. [Genomic signature in breast cancer: Oncotype DX()]. *Annales de Pathologie*. 2013;33(3):225-228. Exclude: Not English.

1434. Tellaroli P, Bazzi M, Donato M, Brazzale AR, Draghici S. Cross-Clustering: A Partial Clustering Algorithm with Automatic Estimation of the Number of Clusters. *PLoS ONE [Electronic Resource]*. 2016;11(3):e0152333. Exclude: Not intervention of interest.

1435. Teschendorff AE, Caldas C. A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. *Breast Cancer Research*. 2008;10(4):R73. Exclude: Not intervention of interest.

1436. Teschendorff AE, Gomez S, Arenas A, et al. Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. *BMC Cancer*. 2010;10:604. Exclude: Not intervention of interest.

1437. Teschendorff AE, Naderi A, Barbosa-Morais NL, et al. A consensus prognostic gene expression classifier for ER positive breast cancer. *Genome Biology*. 2006;7(10):R101. Exclude: Date.

1438. Teschendorff AE, Severini S. Increased entropy of signal transduction in the cancer metastasis phenotype. *BMC Systems Biology*. 2010;4:104. Exclude: Not intervention of interest.

1439. Thaker NG, Hoffman KE, Stauder MC, et al. The 21-gene recurrence score complements IBTR! Estimates in early-stage, hormone receptor-positive, HER2-normal, lymph node-negative breast cancer. *Springerplus*. 2015;4:36. Exclude: No outcome of interest.

1440. Thomassen M, Tan Q, Eiriksdottir F, Bak M, Cold S, Kruse TA. Prediction of metastasis from low-malignant breast cancer by gene expression profiling. *International Journal of Cancer*. 2007;120(5):1070-1075. Exclude: No outcome of interest.

1441. Thorat MA, Marchio C, Morimiya A, et al. Forkhead box A1 expression in breast cancer is associated with luminal subtype and good prognosis. *Journal of Clinical Pathology*. 2008;61(3):327-332. Exclude: Not intervention of interest.

1442. Thuerigen O, Schneeweiss A, Toedt G, et al. Gene expression signature predicting pathologic complete response with gemcitabine, epirubicin, and docetaxel in primary breast cancer. *Journal of Clinical Oncology*. 2006;24(12):1839-1845. Exclude: Date.
1443. Tian S, Roepman P, Van't Veer LJ, Bernards R, de Snoo F, Glas AM. Biological functions of the genes in the mammaprint breast cancer profile reflect the hallmarks of cancer. *Biomark Insights*. 2010;5:129-138. Exclude: No outcome of interest.
1444. Tiberi D, Masucci L, Shedid D, et al. Limitations of Personalized Medicine and Gene Assays for Breast Cancer. *Cureus*. 2017;9(3):e1100. Exclude: Publication type-case report.
1445. Titus AJ, Way GP, Johnson KC, Christensen BC. Deconvolution of DNA methylation identifies differentially methylated gene regions on 1p36 across breast cancer subtypes. *Scientific Reports*. 2017;7(1):11594. Exclude: Not intervention of interest.
1446. Tobin NP, Harrell JC, Lovrot J, et al. Molecular subtype and tumor characteristics of breast cancer metastases as assessed by gene expression significantly influence patient post-relapse survival. *Annals of Oncology*. 2015;26(1):81-88. Exclude: No outcome of interest.
1447. Tobin NP, Lindstrom LS, Carlson JW, Bjohle J, Bergh J, Wennmalm K. Multi-level gene expression signatures, but not binary, outperform Ki67 for the long term prognostication of breast cancer patients.[Erratum appears in Mol Oncol. 2014 Sep 12;8(6):1159]. *Molecular Oncology*. 2014;8(3):741-752. Exclude: No outcome of interest.
1448. Tobin NP, Wennmalm K, Lindstrom LS, et al. An Endothelial Gene Signature Score Predicts Poor Outcome in Patients with Endocrine-Treated, Low Genomic Grade Breast Tumors. *Clinical Cancer Research*. 2016;22(10):2417-2426. Exclude: No outcome of interest.
1449. Toi M, Iwata H, Yamanaka T, et al. Clinical significance of the 21-gene signature (Oncotype DX) in hormone receptor-positive early stage primary breast cancer in the Japanese population. *Cancer*. 2010;116(13):3112-3118. Exclude: No outcome of interest.
1450. Toi M, Tominaga T, Osaki A, Toge T. Role of epidermal growth factor receptor expression in primary breast cancer: results of a biochemical study and an immunocytochemical study. *Breast Cancer Research & Treatment*. 1994;29(1):51-58. Exclude: Date.
1451. Tokunaga E, Kimura Y, Oki E, et al. Akt is frequently activated in HER2/neu-positive breast cancers and associated with poor prognosis among hormone-treated patients. *International Journal of Cancer*. 2006;118(2):284-289. Exclude: Date.
1452. Tolaney SM, Barry WT, Guo H, et al. Seven-year (yr) follow-up of adjuvant paclitaxel (T) and trastuzumab (H) (APT trial) for node-negative, HER2-positive breast cancer (BC). *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
1453. Tolaney SM, Boucher Y, Duda DG, et al. Role of vascular density and normalization in response to neoadjuvant bevacizumab and chemotherapy in breast cancer patients. *Proceedings of the National Academy of Sciences of the United States of America*. 2015;112(46):14325-14330. Exclude: Not intervention of interest.
1454. Tomida S, Yanagisawa K, Koshikawa K, et al. Identification of a metastasis signature and the DLX4 homeobox protein as a regulator of metastasis by combined transcriptome approach. *Oncogene*. 2007;26(31):4600-4608. Exclude: Not intervention of interest.
1455. Toole MJ, Kidwell KM, Van Poznak C. Oncotype dx results in multiple primary breast cancers. *Breast Cancer*. 2014;8:1-6. Exclude: No outcome of interest.

1456. Toribio MG, Mar J, Galve E, et al. Budget impact analysis of the 21-gene assay (Oncotype DX breast cancer) for the breast cancer treatment in the Basque country. *Annals of oncology Conference: 41st european society for medical oncology congress, ESMO*. 2016;27(no pagination). Exclude: Publication type-conference abstract.
1457. Torres-Roca JF, Fulp WJ, Caudell JJ, et al. Integration of a Radiosensitivity Molecular Signature Into the Assessment of Local Recurrence Risk in Breast Cancer. *International Journal of Radiation Oncology, Biology, Physics*. 2015;93(3):631-638. Exclude: Not intervention of interest.
1458. Torrisi R, Garcia-Etienne CA, Losurdo A, et al. Potential impact of the 70-gene signature in the choice of adjuvant systemic treatment for ER positive, HER2 negative tumors: a single institution experience. *Breast*. 2013;22(4):419-424. Exclude: No outcome of interest.
1459. Tramm T, Mohammed H, Myhre S, et al. Development and validation of a gene profile predicting benefit of postmastectomy radiotherapy in patients with high-risk breast cancer: a study of gene expression in the DBCG82bc cohort. *Clinical Cancer Research*. 2014;20(20):5272-5280. Exclude: No outcome of interest.
1460. Tripathy D, Chien AJ, Hylton N, et al. Adaptively randomized trial of neoadjuvant chemotherapy with or without the Akt inhibitor MK-2206: Graduation results from the I-SPY 2 Trial. *Journal of clinical oncology*. 2015;33(15 SUPPL. 1):CONFERENCE START: 2015 May 2029 CONFERENCE END: 2015 Jun 2012. Exclude: Not intervention of interest.
1461. Triulzi T, De Cecco L, Sandri M, et al. Whole-transcriptome analysis links trastuzumab sensitivity of breast tumors to both HER2 dependence and immune cell infiltration. *Oncotarget*. 2015;6(29):28173-28182. Exclude: Not intervention of interest.
1462. Troester MA, Sun X, Allott EH, et al. Racial Differences in PAM50 Subtypes in the Carolina Breast Cancer Study. *Journal of the National Cancer Institute*. 2018;110(2):01. Exclude: No outcome of interest.
1463. Troester MA, Sun X, Allott EH, et al. Race and age differences in PAM50 biomarker status in the Carolina breast cancer study. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1464. Trosman JR, Van Bebber SL, Phillips KA. Coverage policy development for personalized medicine: private payer perspectives on developing policy for the 21-gene assay. *Journal of oncology practice/American Society of Clinical Oncology*. 2010;6(5):238-242. Exclude: Publication type-commentary.
1465. Tsai ML, Lillemoe TJ, Finkelstein MJ, et al. Utility of Oncotype DX Risk Assessment in Patients With Invasive Lobular Carcinoma. *Clinical Breast Cancer*. 2016;16(1):45-50. Exclude: No outcome of interest.
1466. Tsoi DT, Inoue M, Kelly CM, Verma S, Pritchard KI. Cost-effectiveness analysis of recurrence score-guided treatment using a 21-gene assay in early breast cancer. *Oncologist*. 2010;15(5):457-465. Exclude: In included systematic review.
1467. Tsuchida Y, Hayashi N, Omata F, Yamauchi H. Clinicopathological predictors for low risk recurrence distinguished by 21-gene recurrence score in estrogen receptor-positive invasive breast cancer patients. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1468. Tsunashima R, Naoi Y, Kishi K, et al. Estrogen receptor positive breast cancer identified by 95-gene classifier as at high risk for relapse shows better response to neoadjuvant chemotherapy. *Cancer Letters*. 2012;324(1):42-47. Exclude: Not intervention of interest.

1469. Tsutsui S, Yasuda K, Higashi H, et al. Prognostic implication of p53 protein expression in relation to nuclear pleomorphism and the MIB-1 counts in breast cancer. *Breast Cancer*. 2004;11(2):160-168. Exclude: Date.
1470. Tuma RS. Multiple gene signatures aim to qualify risk in breast cancer. *Journal of the National Cancer Institute*. 2005;97(5):332. Exclude: Date.
1471. Tuma RS. Trial and error: prognostic gene signature study design altered. *Journal of the National Cancer Institute*. 2005;97(5):331-333. Exclude: Date.
1472. Tung N. What is the optimal endocrine therapy for postmenopausal women with hormone receptor-positive early breast cancer? *Journal of Clinical Oncology*. 2013;31(11):1391-1397. Exclude: Publication type-case report.
1473. Tung N, Lin NU, Kidd J, et al. Frequency of Germline Mutations in 25 Cancer Susceptibility Genes in a Sequential Series of Patients With Breast Cancer. *Journal of Clinical Oncology*. 2016;34(13):1460-1468. Exclude: Not intervention of interest.
1474. Turaga K, Acs G, Laronga C. Gene expression profiling in breast cancer. *Cancer Control*. 2010;17(3):177-182. Exclude: Publication type-not systematic review.
1475. Turashvili G, Brogi E, Morrow M, et al. The 21-gene recurrence score in special histologic subtypes of breast cancer with favorable prognosis. *Breast Cancer Research & Treatment*. 2017;165(1):65-76. Exclude: No outcome of interest.
1476. Turashvili G, Chou JF, Brogi E, et al. 21-Gene recurrence score and locoregional recurrence in lymph node-negative, estrogen receptor-positive breast cancer. *Breast Cancer Research & Treatment*. 2017;166(1):69-76. Exclude: No outcome of interest.
1477. Turnbull AK, Arthur LM, Renshaw L, et al. Accurate Prediction and Validation of Response to Endocrine Therapy in Breast Cancer. *Journal of Clinical Oncology*. 2015;33(20):2270-2278. Exclude: Not intervention of interest.
1478. Turner B, Tang P, Hicks D. The value of algorithms predicting the Oncotype DX recurrence score should not be underestimated! *Breast Cancer Res Treat*. 2017;164(1):249-250. Exclude: Publication type-letter.
1479. Turner BM, Skinner KA, Tang P, et al. Use of modified Magee equations and histologic criteria to predict the Oncotype DX recurrence score. *Modern Pathology*. 2015;28(7):921-931. Exclude: No outcome of interest.
1480. Tzeng JP, Mayer D, Richman AR, et al. Women's experiences with genomic testing for breast cancer recurrence risk. *Cancer*. 2010;116(8):1992-2000. Exclude: No outcome of interest.
1481. Ueda S, Saeki T, Takeuchi H, et al. Genomic profiling shows increased glucose metabolism in luminal B breast cancer. *Journal of Breast Cancer*. 2013;16(3):342-344. Exclude: No outcome of interest.
1482. Ueno T, Masuda N, Yamanaka T, et al. Evaluating the 21-gene assay Recurrence Score as a predictor of clinical response to 24 weeks of neoadjuvant exemestane in estrogen receptor-positive breast cancer. *International Journal of Clinical Oncology*. 2014;19(4):607-613. Exclude: No outcome of interest.
1483. Usmani A, Shoro AA, Memon Z, Hussain M, Rehman R. Diagnostic, prognostic and predictive value of MicroRNA-21 in breast cancer patients, their daughters and healthy individuals. *American Journal of Cancer Research*. 2015;5(8):2484-2490. Exclude: Not intervention of interest.
1484. Vacirca JL, Agajanian R, Papai Z, et al. Sustained efficacy of eflapegrastim in breast cancer patients in a phase 2, open-label, doseranging study. *Cancer research Conference: 39th annual CTRC AACR san*

antonio breast cancer symposium United states. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

1485. Valet F, de Cremoux P, Spyrtos F, et al. Challenging single- and multi-probesets gene expression signatures of pathological complete response to neoadjuvant chemotherapy in breast cancer: experience of the REMAGUS 02 phase II trial. *Breast*. 2013;22(6):1052-1059. Exclude: Not intervention of interest.

1486. van Agthoven T, Sieuwerts AM, Veldscholte J, et al. CITED2 and NCOR2 in anti-oestrogen resistance and progression of breast cancer. *British Journal of Cancer*. 2009;101(11):1824-1832. Exclude: Not intervention of interest.

1487. van de Vijver MJ, He YD, van't Veer LJ, et al. A gene-expression signature as a predictor of survival in breast cancer. *New England Journal of Medicine*. 2002;347(25):1999-2009. Exclude: Date.

1488. van den Broek AJ, Broeks A, Horlings HM, et al. Association of the germline TP53 R72P and MDM2 SNP309 variants with breast cancer survival in specific breast tumor subgroups. *Breast Cancer Research & Treatment*. 2011;130(2):599-608. Exclude: Not intervention of interest.

1489. Van den Eynden GG, Van der Auwera I, Van Laere SJ, et al. Comparison of molecular determinants of angiogenesis and lymphangiogenesis in lymph node metastases and in primary tumours of patients with breast cancer. *Journal of Pathology*. 2007;213(1):56-64. Exclude: Not intervention of interest.

1490. Van der Auwera I, Yu W, Suo L, et al. Array-based DNA methylation profiling for breast cancer subtype discrimination. *PLoS ONE [Electronic Resource]*. 2010;5(9):e12616. Exclude: Not intervention of interest.

1491. van der Hage JA, van den Broek LJ, Legrand C, et al. Overexpression of P70 S6 kinase protein is associated with increased risk of locoregional recurrence in node-negative premenopausal early breast cancer patients. *British Journal of Cancer*. 2004;90(8):1543-1550. Exclude: Date.

1492. van der Hoeven JJ. [70-Gene signature as an aid to treatment decisions in early-stage breast cancer]. *Ned Tijdschr Geneesk*. 2017;161(0):D1369. Exclude: Not English.

1493. van der Velden BHM, Elias SG, Bismeyer T, et al. Complementary Value of Contralateral Parenchymal Enhancement on DCE-MRI to Prognostic Models and Molecular Assays in High-risk ER⁺/HER2⁻ Breast Cancer. *Clinical Cancer Research*. 2017;23(21):6505-6515. Exclude: Not intervention of interest.

1494. Van Grembergen O, Bizet M, de Bony EJ, et al. Portraying breast cancers with long noncoding RNAs. *Science Advances*. 2016;2(9):e1600220. Exclude: No outcome of interest.

1495. Van Laar RK. Design and multiseres validation of a web-based gene expression assay for predicting breast cancer recurrence and patient survival. *Journal of Molecular Diagnostics*. 2011;13(3):297-304. Exclude: Not intervention of interest.

1496. Van Laere S, Beissbarth T, Van der Auwera I, et al. Relapse-free survival in breast cancer patients is associated with a gene expression signature characteristic for inflammatory breast cancer. *Clinical Cancer Research*. 2008;14(22):7452-7460. Exclude: No outcome of interest.

1497. Van Laere SJ, Ueno NT, Finetti P, et al. Uncovering the molecular secrets of inflammatory breast cancer biology: an integrated analysis of three distinct affymetrix gene expression datasets. *Clinical Cancer Research*. 2013;19(17):4685-4696. Exclude: No outcome of interest.

1498. van Nes JG, de Kruijf EM, Putter H, et al. Co-expression of SNAIL and TWIST determines prognosis in estrogen receptor-positive early breast cancer patients. *Breast Cancer Research & Treatment*. 2012;133(1):49-59. Exclude: Not intervention of interest.

1499. van Schooneveld E, Wildiers H, Vergote I, Vermeulen PB, Dirix LY, Van Laere SJ. Dysregulation of microRNAs in breast cancer and their potential role as prognostic and predictive biomarkers in patient management. *Breast Cancer Research*. 2015;17:21. Exclude: Not intervention of interest.
1500. van 't Veer LJ, Yau C, Yu NY, et al. Tamoxifen therapy benefit for patients with 70-gene signature high and low risk. *Breast Cancer Research & Treatment*. 2017;166(2):593-601. Exclude: No comparator.
1501. Vandergrift JL, Niland JC, Theriault RL, et al. Time to adjuvant chemotherapy for breast cancer in National Comprehensive Cancer Network institutions. *Journal of the National Cancer Institute*. 2013;105(2):104-112. Exclude: No outcome of interest.
1502. Vanderlaan BF, Broder MS, Chang EY, Oratz R, Bentley TG. Cost-effectiveness of 21-gene assay in node-positive, early-stage breast cancer. *Am J Manag Care*. 2011;17(7):455-464. Exclude: In included systematic review.
1503. Vanneschi L, Farinaccio A, Mauri G, Antoniotti M, Provero P, Giacobini M. A comparison of machine learning techniques for survival prediction in breast cancer. *BioData Mining [electronic resource]*. 2011;4:12. Exclude: Not intervention of interest.
1504. Varadan V, Gilmore H, Miskimen KL, et al. Immune Signatures Following Single Dose Trastuzumab Predict Pathologic Response to Preoperative Trastuzumab and Chemotherapy in HER2-Positive Early Breast Cancer. *Clinical Cancer Research*. 2016;22(13):3249-3259. Exclude: No outcome of interest.
1505. Varadan V, Kamalakaran S, Gilmore H, et al. Brief-exposure to preoperative bevacizumab reveals a TGF-beta signature predictive of response in HER2-negative breast cancers. *International Journal of Cancer*. 2016;138(3):747-757. Exclude: Not intervention of interest.
1506. Varga Z, Sinn P, Fritzsche F, et al. Comparison of EndoPredict and Oncotype DX test results in hormone receptor positive invasive breast cancer.[Erratum appears in PLoS One. 2013;8(10). doi:10.1371/annotation/f715f38e-7aee-4d2b-8bbf-da0411dc6ef3]. *PLoS ONE [Electronic Resource]*. 2013;8(3):e58483. Exclude: No outcome of interest.
1507. Varn FS, Ung MH, Lou SK, Cheng C. Integrative analysis of survival-associated gene sets in breast cancer. *BMC Medical Genomics [Electronic Resource]*. 2015;8:11. Exclude: Not intervention of interest.
1508. Vataire AL, Laas E, Aballea S, Gligorov J, Rouzier R, Chereau E. [Cost-effectiveness of a chemotherapy predictive test]. *Bull Cancer*. 2012;99(10):907-914. Exclude: In included systematic review.
1509. Vegue LB, Rojo F, Hardisson D, et al. Comparison of molecular analysis and histopathology for axillary lymph node staging in primary breast cancer: results of the B-CLOSER-I study. *Diagnostic Molecular Pathology*. 2012;21(2):69-76. Exclude: Not intervention of interest.
1510. Vendrell JA, Robertson KE, Ravel P, et al. A candidate molecular signature associated with tamoxifen failure in primary breast cancer. *Breast Cancer Research*. 2008;10(5):R88. Exclude: Not intervention of interest.
1511. Vera-Badillo FE, Chang MC, Kuruzar G, et al. Association between androgen receptor expression, Ki-67 and the 21-gene recurrence score in non-metastatic, lymph node-negative, estrogen receptor-positive and HER2-negative breast cancer. *Journal of Clinical Pathology*. 2015;68(10):839-843. Exclude: No outcome of interest.
1512. Viale G, Slaets L, Bogaerts J, et al. High concordance of protein (by IHC), gene (by FISH; HER2 only), and microarray readout (by TargetPrint) of ER, PgR, and HER2: results from the EORTC 10041/BIG 03-04 MINDACT trial. *Annals of Oncology*. 2014;25(4):816-823. Exclude: Not intervention of interest.

1513. Viale G, Slaets L, de Snoo FA, et al. Discordant assessment of tumor biomarkers by histopathological and molecular assays in the EORTC randomized controlled 10041/BIG 03-04 MINDACT trial breast cancer : Intratumoral heterogeneity and DCIS or normal tissue components are unlikely to be the cause of discordance. *Breast Cancer Research & Treatment*. 2016;155(3):463-469. Exclude: No outcome of interest.
1514. Viale G, Slaets L, De Snoo FA, et al. Pathological assessment of discordant cases for molecular (BluePrint and MammaPrint) vs clinical subtypes for breast cancer, among 6,694 patients from the EORTC 10041/BIG 3-04 (MINDACT) trial. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
1515. Vidal M, Peg V, Galvan P, et al. Gene expression-based classifications of fibroadenomas and phyllodes tumours of the breast. *Molecular Oncology*. 2015;9(6):1081-1090. Exclude: No outcome of interest.
1516. Vilquin P, Donini CF, Villedieu M, et al. MicroRNA-125b upregulation confers aromatase inhibitor resistance and is a novel marker of poor prognosis in breast cancer. *Breast Cancer Research*. 2015;17:13. Exclude: Not intervention of interest.
1517. Volinia S, Croce CM. Prognostic microRNA/mRNA signature from the integrated analysis of patients with invasive breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*. 2013;110(18):7413-7417. Exclude: Not intervention of interest.
1518. Volla HK, Rueda OM, Chin SF, et al. A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. *Molecular Oncology*. 2015;9(1):115-127. Exclude: Not intervention of interest.
1519. Vuaroqueaux V, Urban P, Labuhn M, et al. Low E2F1 transcript levels are a strong determinant of favorable breast cancer outcome. *Breast Cancer Research*. 2007;9(3):R33. Exclude: Publication type-commentary.
1520. Waddell N, Arnold J, Cocciardi S, et al. Subtypes of familial breast tumours revealed by expression and copy number profiling. *Breast Cancer Research & Treatment*. 2010;123(3):661-677. Exclude: Not intervention of interest.
1521. Wagner LI, Gray RJ, Sledge GW, et al. Patient-reported cognitive impairments among women with breast cancer randomly assigned to hormonal therapy (HT) alone versus chemotherapy followed by hormonal therapy (C+HT): Results from the Trial Assigning Individualized Options for Treatment (TAILORx). *Journal of clinical oncology*. 2012;30(15 SUPPL. 1):CONFERENCE START: 2012 Jun 2011 CONFERENCE END: 2012 Jun 2015. Exclude: Publication type-conference abstract.
1522. Wallden B, Storhoff J, Nielsen T, et al. Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. *BMC Medical Genomics [Electronic Resource]*. 2015;8:54. Exclude: No outcome of interest.
1523. Wan F, Dong L, Zhang F, et al. Clinical study of the relationship between gamma-synuclein and the response of neoadjuvant chemotherapy in breast cancer. *Journal of International Medical Research*. 2013;41(3):743-753. Exclude: Not intervention of interest.
1524. Wan YW, Qian Y, Rathnagiriswaran S, Castranova V, Guo NL. A breast cancer prognostic signature predicts clinical outcomes in multiple tumor types. *Oncology Reports*. 2010;24(2):489-494. Exclude: Not intervention of interest.

1525. Wang DY, Done SJ, Mc Cready DR, Leong WL. Validation of the prognostic gene portfolio, ClinicoMolecular Triad Classification, using an independent prospective breast cancer cohort and external patient populations. *Breast Cancer Research*. 2014;16(4):R71. Exclude: No outcome of interest.
1526. Wang DY, Done SJ, McCready DR, Boerner S, Kulkarni S, Leong WL. A new gene expression signature, the ClinicoMolecular Triad Classification, may improve prediction and prognostication of breast cancer at the time of diagnosis. *Breast Cancer Research*. 2011;13(5):R92. Exclude: Not intervention of interest.
1527. Wang H, Sun Q, Zhao W, et al. Individual-level analysis of differential expression of genes and pathways for personalized medicine. *Bioinformatics*. 2015;31(1):62-68. Exclude: Not intervention of interest.
1528. Wang H, Wang J, Yu P, et al. Identification of antibiotic resistance genes in the multidrug-resistant *Acinetobacter baumannii* strain, MDR-SHH02, using whole-genome sequencing. *International Journal of Molecular Medicine*. 2017;39(2):364-372. Exclude: Not intervention of interest.
1529. Wang J, Yang X, Chen H, et al. A high-throughput method to detect RNA profiling by integration of RT-MLPA with next generation sequencing technology. *Oncotarget*. 2017;8(28):46071-46080. Exclude: Not intervention of interest.
1530. Wang M, Bao YL, Wu Y, et al. Identification and characterization of the human testes-specific protease 50 gene promoter. *DNA & Cell Biology*. 2008;27(6):307-314. Exclude: Not intervention of interest.
1531. Wang SL, Li YX, Song YW, et al. Triple-negative or HER2-positive status predicts higher rates of locoregional recurrence in node-positive breast cancer patients after mastectomy. *International Journal of Radiation Oncology, Biology, Physics*. 2011;80(4):1095-1101. Exclude: Not intervention of interest.
1532. Wang X, Chao L, Ma G, et al. Increased expression of osteopontin in patients with triple-negative breast cancer. *European Journal of Clinical Investigation*. 2008;38(6):438-446. Exclude: Not intervention of interest.
1533. Wang X, Ring BZ, Seitz RS, et al. Expression of α -Tocopherol-Associated protein (TAP) is associated with clinical outcome in breast cancer patients. *BMC Clinical Pathology*. 2015;15:21. Exclude: Not intervention of interest.
1534. Wang Y, Klijn J, Zhang Y, Atkins D, Foekens J. Gene expression profiles and prognostic markers for primary breast cancer. *Methods in Molecular Biology*. 2007;377:131-138. Exclude: No outcome of interest.
1535. Wang YZ, Han YS, Ma YS, et al. Differential gene expression of Wnt signaling pathway in benign, premalignant, and malignant human breast epithelial cells. *Tumour Biology*. 2012;33(6):2317-2327. Exclude: Not intervention of interest.
1536. Wang Z, Dahiya S, Provencher H, et al. The prognostic biomarkers HOXB13, IL17BR, and CHDH are regulated by estrogen in breast cancer. *Clinical Cancer Research*. 2007;13(21):6327-6334. Exclude: Not intervention of interest.
1537. Ward S, Scope A, Rafia R, et al. Gene expression profiling and expanded immunohistochemistry tests to guide the use of adjuvant chemotherapy in breast cancer management: a systematic review and cost-effectiveness analysis. *Health Technol Assess*. 2013;17(44):1-302. Exclude: In included systematic review.
1538. Warf MB, Rajamani S, Krappmann K, et al. Analytical validation of a 12-gene molecular test for the prediction of distant recurrence in breast cancer. *Future Science OA*. 2017;3(3):FSO221. Exclude: No outcome of interest.

1539. Watson RG, McLeod HL. Pharmacogenomic contribution to drug response. *Cancer Journal*. 2011;17(2):80-88. Exclude: Not intervention of interest.
1540. Webster LR, Lee SF, Ringland C, et al. Poor-prognosis estrogen receptor-positive breast cancer identified by histopathologic subclassification. *Clinical Cancer Research*. 2008;14(20):6625-6633. Exclude: Not intervention of interest.
1541. Weigelt B, Hu Z, He X, et al. Molecular portraits and 70-gene prognosis signature are preserved throughout the metastatic process of breast cancer. *Cancer Research*. 2005;65(20):9155-9158. Exclude: Date.
1542. Weigelt B, Ng CK, Shen R, et al. Metaplastic breast carcinomas display genomic and transcriptomic heterogeneity [corrected]. [Erratum appears in Mod Pathol. 2015 Apr;28(4):607; PMID: 25836989]. *Modern Pathology*. 2015;28(3):340-351. Exclude: No outcome of interest.
1543. Weigelt B, Wessels LF, Bosma AJ, et al. No common denominator for breast cancer lymph node metastasis. *British Journal of Cancer*. 2005;93(8):924-932. Exclude: Date.
1544. Welsh AW, Harigopal M, Wimberly H, Prasad M, Rimm DL. Quantitative analysis of estrogen receptor expression shows SP1 antibody is more sensitive than 1D5. *Applied Immunohistochemistry & Molecular Morphology*. 2013;21(2):139-147. Exclude: Not intervention of interest.
1545. Wen HY, Krystel-Whittemore M, Patil S, et al. Breast carcinoma with an Oncotype Dx recurrence score <18: Rate of distant metastases in a large series with clinical follow-up. *Cancer*. 2017;123(1):131-137. Exclude: No outcome of interest.
1546. West NR, Milne K, Truong PT, Macpherson N, Nelson BH, Watson PH. Tumor-infiltrating lymphocytes predict response to anthracycline-based chemotherapy in estrogen receptor-negative breast cancer. *Breast Cancer Research*. 2011;13(6):R126. Exclude: Not intervention of interest.
1547. Whitworth P, Beatty J, Baron P, et al. Functional subtyping with Blueprint 80-gene profile identifies two distinct triple positive subtypes with and without trastuzumab/chemo-sensitivity: Implications for treatment from the NBRST registry. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
1548. Whitworth P, Beitsch P, Mislowsky A, et al. Chemosensitivity and Endocrine Sensitivity in Clinical Luminal Breast Cancer Patients in the Prospective Neoadjuvant Breast Registry Symphony Trial (NBRST) Predicted by Molecular Subtyping. *Annals of Surgical Oncology*. 2017;24(3):669-675. Exclude: Not intervention of interest.
1549. Whitworth P, Stork-Sloots L, de Snoo FA, et al. Chemosensitivity predicted by Blueprint 80-gene functional subtype and MammaPrint in the Prospective Neoadjuvant Breast Registry Symphony Trial (NBRST). *Annals of Surgical Oncology*. 2014;21(10):3261-3267. Exclude: No outcome of interest.
1550. Wiesner FG, Magener A, Fasching PA, et al. Ki-67 as a prognostic molecular marker in routine clinical use in breast cancer patients. *Breast*. 2009;18(2):135-141. Exclude: Not intervention of interest.
1551. Williams DJ, Cohen C, Darrow M, Page AJ, Chastain B, Adams AL. Proliferation (Ki-67 and phosphohistone H3) and oncotype DX recurrence score in estrogen receptor-positive breast cancer. *Applied Immunohistochemistry & Molecular Morphology*. 2011;19(5):431-436. Exclude: No outcome of interest.
1552. Williams PD, Cheon S, Havaleshko DM, et al. Concordant gene expression signatures predict clinical outcomes of cancer patients undergoing systemic therapy. *Cancer Research*. 2009;69(21):8302-8309. Exclude: No outcome of interest.

1553. Wilsher MJ, Owens TW, Allcock RJ. Next generation sequencing of the nidus of early (adenosquamous proliferation rich) radial sclerosing lesions of the breast reveals evidence for a neoplastic precursor lesion. *The Journal of Pathology Clinical Research*. 2017;3(2):115-122. Exclude: Not intervention of interest.
1554. Wilson TR, Yu J, Lu X, et al. The molecular landscape of high-risk early breast cancer: comprehensive biomarker analysis of a phase III adjuvant population. *NPJ Breast Cancer*. 2016;2:16022. Exclude: No outcome of interest.
1555. Wirapati P, Sotiriou C, Kunkel S, et al. Meta-analysis of gene expression profiles in breast cancer: toward a unified understanding of breast cancer subtyping and prognosis signatures. *Breast Cancer Research*. 2008;10(4):R65. Exclude: No outcome of interest.
1556. Wirtz RM, Scheffen I, Marme F, et al. Predictive value of ultra-high ESR1 mRNA expression in early breast cancer. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1557. Wittner BS, Sgroi DC, Ryan PD, et al. Analysis of the MammaPrint breast cancer assay in a predominantly postmenopausal cohort. *Clinical Cancer Research*. 2008;14(10):2988-2993. Exclude: No outcome of interest.
1558. Wolf DM, Lenburg ME, Yau C, Boudreau A, van 't Veer LJ. Gene co-expression modules as clinically relevant hallmarks of breast cancer diversity. *PLoS ONE [Electronic Resource]*. 2014;9(2):e88309. Exclude: No outcome of interest.
1559. Wolf DM, Yau C, Sanil A, et al. Combining sensitivity markers to identify triple-negative breast cancer patients most responsive to veliparib/carboplatin: results from the I-SPY 2 TRIAL. *Cancer research Conference: 107th annual meeting of the american association for cancer research, AACR*. 2016;76(14 Supplement). Exclude: Publication type-conference abstract.
1560. Wolf DM, Yau C, Sanil A, et al. MammaPrint High1/High2 risk class as a biomarker of response to veliparib/carboplatin plus standard neoadjuvant therapy for breast cancer in the I-SPY 2 TRIAL. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
1561. Wolf DM, Yau C, Sanil A, et al. DNA repair deficiency biomarkers and the 70-gene ultra-high risk signature as predictors of veliparib/carboplatin response in the I-SPY 2 breast cancer trial. *NPJ Breast Cancer*. 2017;3:31. Exclude: No outcome of interest.
1562. Wolf I, Ben-Baruch N, Shapira-Frommer R, et al. Association between standard clinical and pathologic characteristics and the 21-gene recurrence score in breast cancer patients: a population-based study. *Cancer*. 2008;112(4):731-736. Exclude: No outcome of interest.
1563. Wolff AC, Berry D, Carey LA, et al. Research issues affecting preoperative systemic therapy for operable breast cancer. *Journal of Clinical Oncology*. 2008;26(5):806-813. Exclude: Not intervention of interest.
1564. Wolmark N, Mamounas EP, Baehner FL, et al. Prognostic Impact of the Combination of Recurrence Score and Quantitative Estrogen Receptor Expression (ESR1) on Predicting Late Distant Recurrence Risk in Estrogen Receptor-Positive Breast Cancer After 5 Years of Tamoxifen: Results From NRG Oncology/National Surgical Adjuvant Breast and Bowel Project B-28 and B-14. *Journal of Clinical Oncology*. 2016;34(20):2350-2358. Exclude: No outcome of interest.

1565. Woltmann A, Chen B, Lascorz J, et al. Systematic pathway enrichment analysis of a genome-wide association study on breast cancer survival reveals an influence of genes involved in cell adhesion and calcium signaling on the patients' clinical outcome. *PLoS ONE [Electronic Resource]*. 2014;9(6):e98229. Exclude: No outcome of interest.
1566. Won JR, Gao D, Chow C, et al. A survey of immunohistochemical biomarkers for basal-like breast cancer against a gene expression profile gold standard. *Modern Pathology*. 2013;26(11):1438-1450. Exclude: Not intervention of interest.
1567. Wong DJ, Nuyten DS, Regev A, et al. Revealing targeted therapy for human cancer by gene module maps. *Cancer Research*. 2008;68(2):369-378. Exclude: Not intervention of interest.
1568. Wong WB, Ramsey SD, Barlow WE, Garrison LP, Jr., Veenstra DL. The value of comparative effectiveness research: projected return on investment of the RxPONDER trial (SWOG S1007). *Contemp Clin Trials*. 2012;33(6):1117-1123. Exclude: No outcome of interest.
1569. Wood WC, Alvarado M, Buchholz DJ, et al. The current clinical value of the DCIS Score. *Oncology (Williston Park)*. 2014;28 Suppl 2:C2, 1-8, C3. Exclude: Publication type-commentary.
1570. Wu J, Fang Y, Lin L, et al. Distribution patterns of 21-gene recurrence score in 980 Chinese estrogen receptor-positive, HER2-negative early breast cancer patients. *Oncotarget*. 2017;8(24):38706-38716. Exclude: No outcome of interest.
1571. Wu J, Zhang S, Shan J, et al. Elevated HMGA2 expression is associated with cancer aggressiveness and predicts poor outcome in breast cancer. *Cancer Letters*. 2016;376(2):284-292. Exclude: Not intervention of interest.
1572. Wu JY, Fang Y, Lin L, et al. [Clinical utility study of 21-gene assay in 927 Chinese patients with early breast cancer]. *Zhonghua Zhong Liu Za Zhi*. 2017;39(9):668-675. Exclude: Not English.
1573. Wu K, Weng Z, Tao Q, et al. Stage-specific expression of breast cancer-specific gene gamma-synuclein. *Cancer Epidemiology, Biomarkers & Prevention*. 2003;12(9):920-925. Exclude: Date.
1574. Wu SG, He ZY, Li Q, et al. Prognostic value of metastatic axillary lymph node ratio for Chinese breast cancer patients. *PLoS ONE [Electronic Resource]*. 2013;8(4):e61410. Exclude: Not intervention of interest.
1575. Wu T, Wang X, Li J, et al. Identification of Personalized Chemoresistance Genes in Subtypes of Basal-Like Breast Cancer Based on Functional Differences Using Pathway Analysis. *PLoS ONE [Electronic Resource]*. 2015;10(6):e0131183. Exclude: Not intervention of interest.
1576. Wu YM, Hu W, Wang Y, et al. Exploring novel targets of basal-like breast carcinoma by comparative gene profiling and mechanism analysis. *Breast Cancer Research & Treatment*. 2013;141(1):23-32. Exclude: No outcome of interest.
1577. Wuerstlein R, Gluz O, Kates R, et al. Results of multigene assay (MammaPrint) and molecular subtyping (BluePrint) substantially impact treatment decision making in early breast cancer: final analysis of the WSG PRIME decision impact study. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1578. Wuerstlein R, Prat A, Ortega V, et al. Efficacy and gene expression results from SOLT1007, a phase II study evaluating neoadjuvant eribulin in hormone receptor (HR)-positive/HER2-negative breast cancer. *Oncology research and treatment Conference: jahrestagung der deutschen, osterreichischen und schweizerischen gesellschaften fur hamatologie und medizinische onkologie*. 2016;39:182-183. Exclude: Publication type-conference abstract.

1579. Wurstlein R, Sotlar K, Gluz O, et al. WSG BCIST study: Prosigna results impact on adjuvant decision making in early breast cancer (EBC). *Oncology Research and Treatment Conference*. 2016;39(49). Exclude: Publication type-conference abstract.
1580. Xiang YJ, Guo MM, Zhou CJ, et al. Absence of gamma-interferon-inducible lysosomal thiol reductase (GILT) is associated with poor disease-free survival in breast cancer patients.[Erratum appears in PLoS One. 2015;10(1):e0117653; PMID: 25629608]. *PLoS ONE [Electronic Resource]*. 2014;9(10):e109449. Exclude: Not intervention of interest.
1581. Xin L, Liu YH, Martin TA, Jiang WG. The Era of Multigene Panels Comes? The Clinical Utility of Oncotype DX and MammaPrint. *World Journal of Oncology*. 2017;8(2):34-40. Exclude: Publication type-not systematic review.
1582. Xing L, Salas M, Zhang H, et al. Creation and characterization of BAC-transgenic mice with physiological overexpression of epitope-tagged RCAN1 (DSCR1). *Mammalian Genome*. 2013;24(1-2):30-43. Exclude: Not intervention of interest.
1583. Xu B, Williams C, De P, et al. Differential mutation pattern between neoadjuvant and metastatic settings in breast cancer patients. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1584. Xu L, Fengji L, Changning L, et al. Comparison of the Prognostic Utility of the Diverse Molecular Data among lncRNA, DNA Methylation, microRNA, and mRNA across Five Human Cancers.[Erratum appears in PLoS One. 2016;11(3):e0152631; PMID: 27010936]. *PLoS ONE [Electronic Resource]*. 2015;10(11):e0142433. Exclude: Not intervention of interest.
1585. Xu L, Tan AC, Winslow RL, Geman D. Merging microarray data from separate breast cancer studies provides a robust prognostic test. *BMC Bioinformatics*. 2008;9:125. Exclude: No outcome of interest.
1586. Xu W, Jia G, Cai N, et al. A 16 Yin Yang gene expression ratio signature for ER+/node- breast cancer. *International Journal of Cancer*. 2017;140(6):1413-1424. Exclude: Not intervention of interest.
1587. Yamamoto S, Ibusuki M, Yamamoto Y, et al. Clinical relevance of Ki67 gene expression analysis using formalin-fixed paraffin-embedded breast cancer specimens. *Breast Cancer*. 2013;20(3):262-270. Exclude: Not intervention of interest.
1588. Yamamoto-Ibusuki M, Yamamoto Y, Yamamoto S, et al. Comparison of prognostic values between combined immunohistochemical score of estrogen receptor, progesterone receptor, human epidermal growth factor receptor 2, Ki-67 and the corresponding gene expression score in breast cancer. *Modern Pathology*. 2013;26(1):79-86. Exclude: No outcome of interest.
1589. Yamauchi H, Nakagawa C, Takei H, et al. Prospective study of the effect of the 21-gene assay on adjuvant clinical decision-making in Japanese women with estrogen receptor-positive, node-negative, and node-positive breast cancer. *Clin Breast Cancer*. 2014;14(3):191-197. Exclude: In included systematic review.
1590. Yamauchi H, Nakagawa C, Yamashige S, et al. Societal cost-effectiveness analysis of the 21-gene assay in estrogen-receptor-positive, lymph-node-negative early-stage breast cancer in Japan. *BMC Health Serv Res*. 2014;14:372. Exclude: In included systematic review.
1591. Yan L, Tian L, Liu S. Combining large number of weak biomarkers based on AUC. *Statistics in Medicine*. 2015;34(29):3811-3830. Exclude: No outcome of interest.

1592. Yang D, Chen MB, Wang LQ, Yang L, Liu CY, Lu PH. Bcl-2 expression predicts sensitivity to chemotherapy in breast cancer: a systematic review and meta-analysis. *Journal of Experimental & Clinical Cancer Research*. 2013;32:105. Exclude: Not intervention of interest.
1593. Yang J, Xing T, Hu R. [Expression of C-erbB-2 protein in breast cancer and its clinical significance]. *Hua-Hsi i Ko Ta Hsueh Hsueh Pao [Journal of West China University of Medical Sciences]*. 1999;30(1):75-76. Exclude: Date.
1594. Yang L, Shen Y, Yuan X, Zhang J, Wei J. Analysis of breast cancer subtypes by AP-ISA biclustering. *BMC Bioinformatics*. 2017;18(1):481. Exclude: Not intervention of interest.
1595. Yang M, Rajan S, Issa AM. Cost effectiveness of gene expression profiling for early stage breast cancer: a decision-analytic model. *Cancer*. 2012;118(20):5163-5170. Exclude: In included systematic review.
1596. Yang X, Bentink S, Scheid S, Spang R. Similarities of ordered gene lists. *Journal of Bioinformatics & Computational Biology*. 2006;4(3):693-708. Exclude: Date.
1597. Yang X, Vasudevan P, Parekh V, Penev A, Cunningham JM. Bridging cancer biology with the clinic: relative expression of a GRHL2-mediated gene-set pair predicts breast cancer metastasis. *PLoS ONE [Electronic Resource]*. 2013;8(2):e56195. Exclude: Not intervention of interest.
1598. Yao F, Zhang C, Du W, Liu C, Xu Y. Identification of Gene-Expression Signatures and Protein Markers for Breast Cancer Grading and Staging. *PLoS ONE [Electronic Resource]*. 2015;10(9):e0138213. Exclude: No outcome of interest.
1599. Yao K, Goldschmidt R, Turk M, et al. Molecular subtyping improves diagnostic stratification of patients with primary breast cancer into prognostically defined risk groups. *Breast Cancer Research & Treatment*. 2015;154(1):81-88. Exclude: No outcome of interest.
1600. Yardley DA, Peacock NW, Shastry M, et al. A phase II trial of ixabepilone and cyclophosphamide as neoadjuvant therapy for patients with HER2-negative breast cancer: correlation of pathologic complete response with the 21-gene recurrence score. *Breast Cancer Research & Treatment*. 2015;154(2):299-308. Exclude: No comparator.
1601. Yasojima H, Shimomura A, Naoi Y, et al. Association between c-myc amplification and pathological complete response to neoadjuvant chemotherapy in breast cancer. *European Journal of Cancer*. 2011;47(12):1779-1788. Exclude: Not intervention of interest.
1602. Yau C, Fedele V, Roydasgupta R, et al. Aging impacts transcriptomes but not genomes of hormone-dependent breast cancers. *Breast Cancer Research*. 2007;9(5):R59. Exclude: Not intervention of interest.
1603. Yau C, Wolf DM, Sanil A, et al. MammaPrint High1/High2 risk class as a biomarker of response to neratinib plus standard neoadjuvant therapy for breast cancer in the I-SPY 2 TRIAL. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.
1604. Yau TK, Soong IS, Chan K, et al. Evaluation of the prognostic value of 2005 St Gallen risk categories for operated breast cancers in Hong Kong. *Breast*. 2008;17(1):58-63. Exclude: Not intervention of interest.
1605. Yee D, Paoloni M, Van't Veer L, et al. The evaluation of ganitumab/metformin plus standard neoadjuvant therapy in high-risk breast cancer: results from the ISPY 2 trial. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.

1606. Yeh YT, Hou MF, Chung YF, et al. Decreased expression of phosphorylated JNK in breast infiltrating ductal carcinoma is associated with a better overall survival. *International Journal of Cancer*. 2006;118(11):2678-2684. Exclude: Date.
1607. Yepes MM, Romilly AP, Collado-Mesa F, et al. Can mammographic and sonographic imaging features predict the Oncotype DXTM recurrence score in T1 and T2, hormone receptor positive, HER2 negative and axillary lymph node negative breast cancers? *Breast Cancer Research & Treatment*. 2014;148(1):117-123. Exclude: No outcome of interest.
1608. Yerushalmi R, Gelmon KA, Leung S, et al. Insulin-like growth factor receptor (IGF-1R) in breast cancer subtypes. *Breast Cancer Research & Treatment*. 2012;132(1):131-142. Exclude: Not intervention of interest.
1609. Yi M, Buchholz TA, Meric-Bernstam F, et al. Classification of ipsilateral breast tumor recurrences after breast conservation therapy can predict patient prognosis and facilitate treatment planning. *Annals of Surgery*. 2011;253(3):572-579. Exclude: Not intervention of interest.
1610. Yin ZQ, Liu JJ, Xu YC, et al. A 41-gene signature derived from breast cancer stem cells as a predictor of survival. *Journal of Experimental & Clinical Cancer Research*. 2014;33:49. Exclude: Not intervention of interest.
1611. Yokoyama J, Kobayashi T, Nakamura T, Nakajima Y. [A case of male breast cancer in which oncotype DX was used to determine the therapeutic strategy]. *Gan to Kagaku Ryoho [Japanese Journal of Cancer & Chemotherapy]*. 2012;39(12):2057-2059. Exclude: Not English.
1612. Yorozyua K, Takeuchi T, Yoshida M, et al. Evaluation of Oncotype DX Recurrence Score as a prognostic factor in Japanese women with estrogen receptor-positive, node-negative primary Stage I or IIA breast cancer. *Journal of Cancer Research & Clinical Oncology*. 2010;136(6):939-944. Exclude: No outcome of interest.
1613. You Y, Deng J, Zheng J, et al. IL-21 gene polymorphism is associated with the prognosis of breast cancer in Chinese populations. *Breast Cancer Research & Treatment*. 2013;137(3):893-901. Exclude: Not intervention of interest.
1614. Yu CP, Yu JC, Sun CA, Tzao C, Ho JY, Yen AM. Tumor susceptibility and prognosis of breast cancer associated with the G870A polymorphism of CCND1. *Breast Cancer Research & Treatment*. 2008;107(1):95-102. Exclude: Not intervention of interest.
1615. Yu KD, Jiang YZ, Hao S, Shao ZM. Molecular essence and endocrine responsiveness of estrogen receptor-negative, progesterone receptor-positive, and HER2-negative breast cancer. *BMC Medicine*. 2015;13:254. Exclude: No outcome of interest.
1616. Yu KD, Zhu R, Zhan M, et al. Identification of prognosis-relevant subgroups in patients with chemoresistant triple-negative breast cancer. *Clinical Cancer Research*. 2013;19(10):2723-2733. Exclude: Not intervention of interest.
1617. Yuan X, Zhang M, Wu H, et al. Expression of Notch1 Correlates with Breast Cancer Progression and Prognosis. *PLoS ONE [Electronic Resource]*. 2015;10(6):e0131689. Exclude: Not intervention of interest.
1618. Yuan Y, Leszczynska M, Konstantinovskiy S, Trope CG, Reich R, Davidson B. Netrin-4 is upregulated in breast carcinoma effusions compared to corresponding solid tumors. *Diagnostic Cytopathology*. 2011;39(8):562-566. Exclude: Not intervention of interest.
1619. Yun J, Frankenberger CA, Kuo WL, et al. Signalling pathway for RKIP and Let-7 regulates and predicts metastatic breast cancer. *EMBO Journal*. 2011;30(21):4500-4514. Exclude: Not intervention of interest.

1620. Zanotti L, Bottini A, Rossi C, Generali D, Cappelletti MR. Diagnostic tests based on gene expression profile in breast cancer: from background to clinical use. *Tumour Biology*. 2014;35(9):8461-8470. Exclude: Publication type-commentary.
1621. Zbytek B, Cohen C, Wang J, Page A, Williams DJ, Adams AL. Nottingham-defined mitotic score: comparison with visual and image cytometric phosphohistone H3 labeling indices and correlation with Oncotype DX recurrence score. *Applied Immunohistochemistry & Molecular Morphology*. 2013;21(1):48-53. Exclude: No outcome of interest.
1622. Zelnak AB, O'Regan RM. Genomic subtypes in choosing adjuvant therapy for breast cancer. *Oncology (Williston Park)*. 2013;27(3):204-210. Exclude: Publication type-commentary.
1623. Zemmour C, Bertucci F, Finetti P, et al. Prediction of early breast cancer metastasis from DNA microarray data using high-dimensional cox regression models. *Cancer Informatics [Electronic Resource]*. 2015;14(Suppl 2):129-138. Exclude: No outcome of interest.
1624. Zeng T, Liu J. Mixture classification model based on clinical markers for breast cancer prognosis. *Artificial Intelligence in Medicine*. 2010;48(2-3):129-137. Exclude: No outcome of interest.
1625. Zeng Y, Li Q, Qin T, et al. Impact of a 21-Gene Recurrence Score Test on the Choice of Adjuvant Chemotherapy for Hormone Receptor-positive Early-stage Breast Cancer: A Prospective Study. *Anticancer Res*. 2017;37(8):4539-4547. Exclude: No comparator.
1626. Zhang K, Luo Z, Zhang Y, et al. Circulating lncRNA H19 in plasma as a novel biomarker for breast cancer. *Cancer Biomarkers: Section A of Disease Markers*. 2016;17(2):187-194. Exclude: Not intervention of interest.
1627. Zhang K, Wang YW, Wang YY, et al. Identification of microRNA biomarkers in the blood of breast cancer patients based on microRNA profiling. *Gene*. 2017;619:10-20. Exclude: Not intervention of interest.
1628. Zhang K, Zhao S, Wang Q, Yang HS, Zhu J, Ma R. Identification of microRNAs in Nipple Discharge as Potential Diagnostic Biomarkers for Breast Cancer. *Annals of Surgical Oncology*. 2015;22 Suppl 3:S536-544. Exclude: Not intervention of interest.
1629. Zhang L, Xu Y, Jin X, et al. A circulating miRNA signature as a diagnostic biomarker for non-invasive early detection of breast cancer. *Breast Cancer Research & Treatment*. 2015;154(2):423-434. Exclude: Not intervention of interest.
1630. Zhang Y, Jerevall PL, Schroeder BE, et al. Impact of treatment history on prognostic ability of breast cancer index (BCI): subset analysis from a validation study of patients with hormone receptor-positive (HR+) breast cancer with 1-3 positive nodes. *Cancer research Conference: 39th annual CTRC AACR san antonio breast cancer symposium United states*. 2017;77(4 Supplement 1). Exclude: Publication type-conference abstract.
1631. Zhang Y, Schnabel CA, Schroeder BE, et al. Breast cancer index identifies early-stage estrogen receptor-positive breast cancer patients at risk for early- and late-distant recurrence. *Clinical Cancer Research*. 2013;19(15):4196-4205. Exclude: No outcome of interest.
1632. Zhang Y, Schroeder BE, Jannok PL, et al. Prediction of benefit from endocrine therapy in ER+ early stage breast cancer: Correlative studies of the breast cancer index HoxB13/IL17BR (H/I) ratio, ER, PR, and HER2 expression in the randomized Stockholm trial. *Cancer research*. 2014;75(9 SUPPL. 1):CONFERENCE START: 2014 Dec 2019 CONFERENCE END: 2014 Dec 2013. Exclude: Publication type-conference abstract.

1633. Zhang YN, Zhou YD, Mao F, Sun Q. Impact of the 21-Gene Recurrence Score Assay in adjuvant chemotherapy selection for node-negative, hormone receptor-positive breast cancer in the Chinese population. *Neoplasia*. 2015;62(4):658-665. Exclude: In included systematic review.
1634. Zhang Z, Chen D, Fenstermacher DA. Integrated analysis of independent gene expression microarray datasets improves the predictability of breast cancer outcome. *BMC Genomics*. 2007;8:331. Exclude: No outcome of interest.
1635. Zhang Z, Yamashita H, Toyama T, et al. HDAC6 expression is correlated with better survival in breast cancer. *Clinical Cancer Research*. 2004;10(20):6962-6968. Exclude: Date.
1636. Zhao HY, Huang H, Hu ZH, et al. Evaluations of biomarkers associated with sensitivity to 5-fluorouracil and taxanes for recurrent/advanced breast cancer patients treated with capecitabine-based first-line chemotherapy. *Anti-Cancer Drugs*. 2012;23(5):534-542. Exclude: Not intervention of interest.
1637. Zhao SD, Parmigiani G, Huttenhower C, Waldron L. Mas-o-menos: a simple sign averaging method for discrimination in genomic data analysis. *Bioinformatics*. 2014;30(21):3062-3069. Exclude: Not intervention of interest.
1638. Zhao SG, Shilkrot M, Speers C, et al. Development and validation of a novel platform-independent metastasis signature in human breast cancer. *PLoS ONE [Electronic Resource]*. 2015;10(5):e0126631. Exclude: Not intervention of interest.
1639. Zhao X, Mirza S, Alshareeda A, et al. Overexpression of a novel cell cycle regulator ecdysoneless in breast cancer: a marker of poor prognosis in HER2/neu-overexpressing breast cancer patients. *Breast Cancer Research & Treatment*. 2012;134(1):171-180. Exclude: Not intervention of interest.
1640. Zhao X, Rodland EA, Sorlie T, et al. Systematic assessment of prognostic gene signatures for breast cancer shows distinct influence of time and ER status. *BMC Cancer*. 2014;14:211. Exclude: No outcome of interest.
1641. Zhao X, Rodland EA, Tibshirani R, Plevritis S. Molecular subtyping for clinically defined breast cancer subgroups. *Breast Cancer Research*. 2015;17:29. Exclude: No outcome of interest.
1642. Zheng M, Zhou Y, Yang X, et al. High GINS2 transcript level predicts poor prognosis and correlates with high histological grade and endocrine therapy resistance through mammary cancer stem cells in breast cancer patients. *Breast Cancer Research & Treatment*. 2014;148(2):423-436. Exclude: Not intervention of interest.
1643. Zhi F, Dong H, Jia X, et al. Functionalized graphene oxide mediated adriamycin delivery and miR-21 gene silencing to overcome tumor multidrug resistance in vitro. *PLoS ONE [Electronic Resource]*. 2013;8(3):e60034. Exclude: Not intervention of interest.
1644. Zhong Z, Shan M, Wang J, Liu T, Shi Q, Pang D. Decreased Wnt5a Expression is a Poor Prognostic Factor in Triple-Negative Breast Cancer. *Medical Science Monitor*. 2016;22:1-7. Exclude: Not intervention of interest.
1645. Zhou S, Wang GP, Liu C, Zhou M. Eukaryotic initiation factor 4E (eIF4E) and angiogenesis: prognostic markers for breast cancer. *BMC Cancer*. 2006;6:231. Exclude: Date.
1646. Zhou W, Jirstrom K, Amini RM, et al. Molecular subtypes in ductal carcinoma in situ of the breast and their relation to prognosis: a population-based cohort study. *BMC Cancer*. 2013;13:512. Exclude: Not intervention of interest.

1647. Zhou X, Tan M, Stone Hawthorne V, et al. Activation of the Akt/mammalian target of rapamycin/4E-BP1 pathway by ErbB2 overexpression predicts tumor progression in breast cancers. *Clinical Cancer Research*. 2004;10(20):6779-6788. Exclude: Date.
1648. Zhou X, Wang X, Huang Z, Xu L, Zhu W, Liu P. An ER-associated miRNA signature predicts prognosis in ER-positive breast cancer. *Journal of Experimental & Clinical Cancer Research*. 2014;33:94. Exclude: Not intervention of interest.
1649. Zhou YH, Barry WT, Wright FA. Empirical pathway analysis, without permutation. *Biostatistics*. 2013;14(3):573-585. Exclude: Not intervention of interest.
1650. Zhu M, Liu CC, Cheng C. REACTIN: regulatory activity inference of transcription factors underlying human diseases with application to breast cancer. *BMC Genomics*. 2013;14:504. Exclude: Not intervention of interest.
1651. Zhu X, Dent S, Paquet L, Zhang T, Graham N, Song X. Factors influencing Oncotype DX use in the management of early breast cancer: a single centre experience. *European Journal of Cancer*. 2014;50(15):2544-2549. Exclude: No outcome of interest.
1652. Zuckerman NS, Yu H, Simons DL, et al. Altered local and systemic immune profiles underlie lymph node metastasis in breast cancer patients. *International Journal of Cancer*. 2013;132(11):2537-2547. Exclude: Not intervention of interest.
1653. Zujewski JA, Kamin L. Trial assessing individualized options for treatment for breast cancer: the TAILORx trial. *Future Oncol*. 2008;4(5):603-610. Exclude: No outcome of interest.

Prostate Cancer

1. Alshalalfa M, Crisan A, Vergara IA, et al. Clinical and genomic analysis of metastatic prostate cancer progression with a background of postoperative biochemical recurrence. *BJU International*. 2015;116(4):556-567. Exclude: Not intervention of interest.
2. Alshalalfa M, Schliekelman M, Shin H, Erho N, Davicioni E. Evolving transcriptomic fingerprint based on genome-wide data as prognostic tools in prostate cancer. *Biology of the Cell*. 2015;107(7):232-244. Exclude: Not intervention of interest.
3. Alshalalfa M, Verhaegh GW, Gibb EA, et al. Low PCA3 expression is a marker of poor differentiation in localized prostate tumors: exploratory analysis from 12,076 patients. *Oncotarget*. 2017;8(31):50804-50813. Exclude: Not intervention of interest.
4. Amaro A, Esposito AI, Gallina A, et al. Validation of proposed prostate cancer biomarkers with gene expression data: a long road to travel. *Cancer & Metastasis Reviews*. 2014;33(2-3):657-671. Exclude: Publication type-commentary.
5. Ashida S, Orloff MS, Bebek G, et al. Integrated analysis reveals critical genomic regions in prostate tumor microenvironment associated with clinicopathologic phenotypes. *Clinical Cancer Research*. 2012;18(6):1578-1587. Exclude: Not intervention of interest.
6. Assikis VJ, Do KA, Wen S, et al. Clinical and biomarker correlates of androgen-independent, locally aggressive prostate cancer with limited metastatic potential. *Clinical Cancer Research*. 2004;10(20):6770-6778. Exclude: Date.
7. Ayubi E, Safiri S. Re: R. Jeffrey Karnes, Voleak Choeurng, Ashley E. Ross, et al. Validation of a Genomic Risk Classifier to Predict Prostate Cancer-specific Mortality in Men with Adverse Pathologic Features. *Eur*

- Urol. In press. <https://doi.org/10.1016/j.eururo.2017.03.036>. *Eur Urol*. 2017. Exclude: Publication type-letter.
8. Badani KK, Thompson DJ, Brown G, et al. Effect of a genomic classifier test on clinical practice decisions for patients with high-risk prostate cancer after surgery. *BJU Int*. 2015;115(3):419-429. Exclude: hypothetical or scenario-based outcome.
9. Baetke SC, Adriaens ME, Seigneuric R, Evelo CT, Eijssen LM. Molecular pathways involved in prostate carcinogenesis: insights from public microarray datasets. *PLoS ONE [Electronic Resource]*. 2012;7(11):e49831. Exclude: Not intervention of interest.
10. Bakshi S, Zhang X, Godoy-Tundidor S, et al. Transcriptome analyses in normal prostate epithelial cells exposed to low-dose cadmium: oncogenic and immunomodulations involving the action of tumor necrosis factor. *Environmental Health Perspectives*. 2008;116(6):769-776. Exclude: Not intervention of interest.
11. Bedia C, Dalmau N, Jaumot J, Tauler R. Phenotypic malignant changes and untargeted lipidomic analysis of long-term exposed prostate cancer cells to endocrine disruptors. *Environmental Research*. 2015;140:18-31. Exclude: Not intervention of interest.
12. Bee A, Ke Y, Forootan S, et al. Ribosomal protein l19 is a prognostic marker for human prostate cancer. *Clinical Cancer Research*. 2006;12(7 Pt 1):2061-2065. Exclude: Date.
13. Beer M, Montani M, Gerhardt J, et al. Profiling gastrin-releasing peptide receptor in prostate tissues: clinical implications and molecular correlates. *Prostate*. 2012;72(3):318-325. Exclude: Not intervention of interest.
14. Berthois Y, Bourrie B, Galiegue S, et al. SR31747A is a sigma receptor ligand exhibiting antitumoural activity both in vitro and in vivo. *British Journal of Cancer*. 2003;88(3):438-446. Exclude: Date.
15. Bettuzzi S. The new anti-oncogene clusterin and the molecular profiling of prostate cancer progression and prognosis. *Acta Bio-Medica de l Ateneo Parmense*. 2003;74(2):101-104. Exclude: Date.
16. Bettuzzi S, Scaltriti M, Caporali A, et al. Successful prediction of prostate cancer recurrence by gene profiling in combination with clinical data: a 5-year follow-up study. *Cancer Research*. 2003;63(13):3469-3472. Exclude: Date.
17. Bian XL, Wang CZ, Wang Y, Li YN, Zhang LZ, Liu L. Analysis of postoperative PSA changes after ultrasound-guided permanent [125I] seed implantation for the treatment of prostate cancer. *Genetics & Molecular Research*. 2015;14(2):7142-7150. Exclude: Not intervention of interest.
18. Bienkowska JR, Dalgin GS, Batliwalla F, et al. Convergent Random Forest predictor: methodology for predicting drug response from genome-scale data applied to anti-TNF response. *Genomics*. 2009;94(6):423-432. Exclude: Not intervention of interest.
19. Borque A, Esteban LM, Sanz G, Rubio-Briones J, Gil Sanz MJ. [Usefulness of clinical nomograms and predictive models for pca. Predictive clinical factors of tumor aggressiveness]. *Archivos Espanoles de Urologia*. 2015;68(3):267-281. Exclude: Publication type-not systematic review.
20. Bostrom PJ, Bjartell AS, Catto JW, et al. Genomic Predictors of Outcome in Prostate Cancer. *Eur Urol*. 2015;68(6):1033-1044. Exclude: No outcome of interest.
21. Brand TC, Zhang N, Crager MR, et al. Patient-specific Meta-analysis of 2 Clinical Validation Studies to Predict Pathologic Outcomes in Prostate Cancer Using the 17-Gene Genomic Prostate Score. *Urology*. 2016;89:69-75. Exclude: No outcome of interest.

22. Carvalho L, Yu J, Schwartzmann G, McLeod HL, Fleshman JW. RNA expression of the molecular signature genes for metastasis in colorectal cancer. *Oncology Reports*. 2011;25(5):1321-1327. Exclude: Not intervention of interest.
23. Castellucci P, Jadvar H. PET/CT in prostate cancer: non-choline radiopharmaceuticals. *The Quarterly Journal of Nuclear Medicine & Molecular Imaging*. 2012;56(4):367-374. Exclude: Not intervention of interest.
24. Chan JM, Weinberg V, Magbanua MJ, et al. Nutritional supplements, COX-2 and IGF-1 expression in men on active surveillance for prostate cancer. *Cancer Causes & Control*. 2011;22(1):141-150. Exclude: Not intervention of interest.
25. Chan SW, Nguyen PN, Violette P, et al. Early detection of clinically significant prostate cancer at diagnosis: a prospective study using a novel panel of TMPRSS2:ETS fusion gene markers. *Cancer Medicine*. 2013;2(1):63-75. Exclude: Not intervention of interest.
26. Chen JL, Espinosa I, Lin AY, Liao OY, van de Rijn M, West RB. Stromal responses among common carcinomas correlated with clinicopathologic features. *Clinical Cancer Research*. 2013;19(18):5127-5135. Exclude: Not intervention of interest.
27. Cheville JC, Karnes RJ, Therneau TM, et al. Gene panel model predictive of outcome in men at high-risk of systemic progression and death from prostate cancer after radical retropubic prostatectomy. *Journal of Clinical Oncology*. 2008;26(24):3930-3936. Exclude: Not intervention of interest.
28. Colicchia M, Morlacco A, Cheville JC, Karnes RJ. Genomic tests to guide prostate cancer management following diagnosis. *Expert Review of Molecular Diagnostics*. 2017;17(4):367-377. Exclude: Publication type-not systematic review.
29. Cooperberg MR, Davicioni E, Crisan A, Jenkins RB, Ghadessi M, Karnes RJ. Combined value of validated clinical and genomic risk stratification tools for predicting prostate cancer mortality in a high-risk prostatectomy cohort. *European Urology*. 2015;67(2):326-333. Exclude: No outcome of interest.
30. Cucchiarra V, Cooperberg MR, Dall'Era M, et al. Genomic Markers in Prostate Cancer Decision Making. *Eur Urol*. 2017. Exclude: Publication type-not systematic review.
31. Cullen J, Rosner IL, Brand TC, et al. A biopsy-based 17-gene genomic prostate score predicts recurrence after radical prostatectomy and adverse surgical pathology in a racially diverse population of men with clinically low- and intermediate-risk prostate cancer. *Eur Urol*. 2015;68(1):123-131. Exclude: No outcome of interest.
32. Cuzick J, Swanson GP, Fisher G, et al. Prognostic value of an RNA expression signature derived from cell cycle proliferation genes in patients with prostate cancer: a retrospective study. *Lancet Oncology*. 2011;12(3):245-255. Exclude: Not intervention of interest.
33. Dagliyan O, Uney-Yuksektepe F, Kavakli IH, Turkay M. Optimization based tumor classification from microarray gene expression data. *PLoS ONE [Electronic Resource]*. 2011;6(2):e14579. Exclude: Not intervention of interest.
34. Dalela D, Loppenberg B, Sood A, Sammon J, Abdollah F. Contemporary Role of the Decipher(R) Test in Prostate Cancer Management: Current Practice and Future Perspectives. *Rev Urol*. 2016;18(1):1-9. Exclude: Publication type-not systematic review.
35. Dalela D, Santiago-Jimenez M, Yousefi K, et al. Genomic Classifier Augments the Role of Pathological Features in Identifying Optimal Candidates for Adjuvant Radiation Therapy in Patients With Prostate

- Cancer: Development and Internal Validation of a Multivariable Prognostic Model. *Journal of Clinical Oncology*. 2017;35(18):1982-1990. Exclude: No outcome of interest.
36. Dalmau N, Jaumot J, Tauler R, Bedia C. Epithelial-to-mesenchymal transition involves triacylglycerol accumulation in DU145 prostate cancer cells. *Molecular Biosystems*. 2015;11(12):3397-3406. Exclude: Not intervention of interest.
37. Danila DC, Fleisher M, Scher HI. Circulating tumor cells as biomarkers in prostate cancer. *Clinical Cancer Research*. 2011;17(12):3903-3912. Exclude: Not intervention of interest.
38. Debiais-Delpech C, Godet J, Pedretti N, et al. Expression patterns of candidate susceptibility genes HNF1beta and CtBP2 in prostate cancer: association with tumor progression. *Urologic Oncology*. 2014;32(4):426-432. Exclude: Not intervention of interest.
39. Demark-Wahnefried W, Rais-Bahrami S, Desmond RA, et al. Presurgical weight loss affects tumour traits and circulating biomarkers in men with prostate cancer. *British Journal of Cancer*. 2017;117(9):1303-1313. Exclude: No outcome of interest.
40. Di Lorenzo G, De Placido S, Autorino R, et al. Expression of biomarkers modulating prostate cancer progression: implications in the treatment of the disease. *Prostate Cancer & Prostatic Diseases*. 2005;8(1):54-59. Exclude: Date.
41. Domhan S, Schwager C, Wei Q, et al. Deciphering the systems biology of mTOR inhibition by integrative transcriptome analysis. *Current Pharmaceutical Design*. 2014;20(1):88-100. Exclude: Not intervention of interest.
42. Du Z, Fei T, Verhaak RG, et al. Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer. *Nature Structural & Molecular Biology*. 2013;20(7):908-913. Exclude: Not intervention of interest.
43. Duarte AH, Colli S, Alves-Pereira JL, Martins MP, Sampaio FJ, Ramos CF. Collagen I and III and metalloproteinase gene and protein expression in prostate cancer in relation to Gleason score. *International Braz J Urol*. 2012;38(3):341-354; discussion 354-345. Exclude: Not intervention of interest.
44. Ebot EM, Gerke T, Labbe DP, et al. Gene expression profiling of prostate tissue identifies chromatin regulation as a potential link between obesity and lethal prostate cancer. *Cancer*. 2017;123(21):4130-4138. Exclude: No outcome of interest.
45. Eguchi FC, Faria EF, Scapulatempo Neto C, et al. The role of TMPRSS2:ERG in molecular stratification of PCa and its association with tumor aggressiveness: a study in Brazilian patients. *Scientific Reports*. 2014;4:5640. Exclude: Not intervention of interest.
46. Endzelins E, Melne V, Kalnina Z, et al. Diagnostic, prognostic and predictive value of cell-free miRNAs in prostate cancer: a systematic review. *Molecular Cancer*. 2016;15(1):41. Exclude: Not intervention of interest.
47. Erho N, Crisan A, Vergara IA, et al. Discovery and validation of a prostate cancer genomic classifier that predicts early metastasis following radical prostatectomy. *PLoS ONE [Electronic Resource]*. 2013;8(6):e66855. Exclude: No outcome of interest.
48. Evans JR, Zhao SG, Chang SL, et al. Patient-Level DNA Damage and Repair Pathway Profiles and Prognosis After Prostatectomy for High-Risk Prostate Cancer. *JAMA Oncology*. 2016;2(4):471-480. Exclude: Not intervention of interest.

49. Faisal FA, Sundi D, Tosoian JJ, et al. Racial Variations in Prostate Cancer Molecular Subtypes and Androgen Receptor Signaling Reflect Anatomic Tumor Location. *European Urology*. 2016;70(1):14-17. Exclude: Not intervention of interest.
50. Falzarano SM, Ferro M, Bollito E, Klein EA, Carrieri G, Magi-Galluzzi C. Novel biomarkers and genomic tests in prostate cancer: a critical analysis. *Minerva Urologica e Nefrologica*. 2015;67(3):211-231. Exclude: Publication type-not systematic review.
51. Febbo PG, Sellers WR. Use of expression analysis to predict outcome after radical prostatectomy. *Journal of Urology*. 2003;170(6 Pt 2):S11-19; discussion S19-20. Exclude: Date.
52. Flores IE, Sierra-Fonseca JA, Davalos O, et al. Stress alters the expression of cancer-related genes in the prostate. *BMC Cancer*. 2017;17(1):621. Exclude: Not intervention of interest.
53. Forootan SS, Foster CS, Aachi VR, et al. Prognostic significance of osteopontin expression in human prostate cancer. *International Journal of Cancer*. 2006;118(9):2255-2261. Exclude: Date.
54. Fussel S, Unversucht S, Meye A, et al. [Comparative evaluation of expression patterns of established and new prostate carcinoma associated genes with reference to suitability for molecular biologic diagnostic and prognostic factors]. *Urologe (Auszg A)*. 2007;46(9):1088-1089. Exclude: Not intervention of interest.
55. Gayyed MF, El-Maqsoud NM, Tawfik ER, El Gelany SA, Rahman MF. A comprehensive analysis of CDC20 overexpression in common malignant tumors from multiple organs: its correlation with tumor grade and stage. *Tumour Biology*. 2016;37(1):749-762. Exclude: Not intervention of interest.
56. Gerke TA, Martin NE, Ding Z, et al. Evaluating a 4-marker signature of aggressive prostate cancer using time-dependent AUC. *Prostate*. 2015;75(16):1926-1933. Exclude: Not intervention of interest.
57. Gevensleben H, Dietrich D, Golletz C, et al. The Immune Checkpoint Regulator PD-L1 Is Highly Expressed in Aggressive Primary Prostate Cancer. *Clinical Cancer Research*. 2016;22(8):1969-1977. Exclude: Not intervention of interest.
58. Geybels MS, Wright JL, Bibikova M, et al. Epigenetic signature of Gleason score and prostate cancer recurrence after radical prostatectomy. *Clinical Epigenetics*. 2016;8:97. Exclude: Not intervention of interest.
59. Giangreco AA, Vaishnav A, Wagner D, et al. Tumor suppressor microRNAs, miR-100 and -125b, are regulated by 1,25-dihydroxyvitamin D in primary prostate cells and in patient tissue. *Cancer Prevention Research*. 2013;6(5):483-494. Exclude: Not intervention of interest.
60. Giesing M, Suchy B, Driesel G, Molitor D. Clinical utility of antioxidant gene expression levels in circulating cancer cell clusters for the detection of prostate cancer in patients with prostate-specific antigen levels of 4-10 ng/mL and disease prognostication after radical prostatectomy. *BJU International*. 2010;105(7):1000-1010. Exclude: Not intervention of interest.
61. Ginsburg S, Ali S, Lee G, Basavanahally A, Madabhushi A. Variable importance in nonlinear kernels (VINK): classification of digitized histopathology. *Medical Image Computing & Computer-Assisted Intervention: MICCAI*. 2013;16(Pt 2):238-245. Exclude: Not intervention of interest.
62. Glass AG, Leo MC, Haddad Z, et al. Validation of a Genomic Classifier for Predicting Post-Prostatectomy Recurrence in a Community Based Health Care Setting. *Journal of Urology*. 2016;195(6):1748-1753. Exclude: No outcome of interest.

63. Glowa C, Peschke P, Brons S, et al. Carbon ion radiotherapy: impact of tumor differentiation on local control in experimental prostate carcinomas. *Radiation Oncology*. 2017;12(1):174. Exclude: Not intervention of interest.
64. Goh LK, Liem N, Vijayaraghavan A, et al. Diagnostic and prognostic utility of a DNA hypermethylated gene signature in prostate cancer. *PLoS ONE [Electronic Resource]*. 2014;9(3):e91666. Exclude: No outcome of interest.
65. Gomez CR, Kosari F, Munz JM, et al. Prognostic value of discs large homolog 7 transcript levels in prostate cancer. *PLoS ONE [Electronic Resource]*. 2013;8(12):e82833. Exclude: Not intervention of interest.
66. Gore JL, Du Plessis M, Santiago-Jimenez M, et al. Decipher test impacts decision-making among patients considering adjuvant and salvage treatment following radical prostatectomy: interim results from the multicenter prospective pro-impact study. *Journal of urology*. 2017;Conference: 112th annual meeting of the american urological association, AUA. 2017. United states 197(4 Supplement 1):e1355. Exclude: Publication type: conference abstract.
67. Goswami S, Sharma-Walia N. Osteoprotegerin secreted by inflammatory and invasive breast cancer cells induces aneuploidy, cell proliferation and angiogenesis. *BMC Cancer*. 2015;15:935. Exclude: Not intervention of interest.
68. Gourdeau H, McAlpine JB, Ranger M, et al. Identification, characterization and potent antitumor activity of ECO-4601, a novel peripheral benzodiazepine receptor ligand.[Erratum appears in Cancer Chemother Pharmacol. 2009 Feb;63(3):569], [Erratum appears in Cancer Chemother Pharmacol. 2008 Oct 22. doi: 10.1007/s00280-008-0848-x Note: Farnet, Chris M [added]]. *Cancer Chemotherapy & Pharmacology*. 2008;61(6):911-921. Exclude: Not intervention of interest.
69. Grasso YZ, Gupta MK, Levin HS, Zippe CD, Klein EA. Combined nested RT-PCR assay for prostate-specific antigen and prostate-specific membrane antigen in prostate cancer patients: correlation with pathological stage. *Cancer Research*. 1998;58(7):1456-1459. Exclude: Date.
70. Grindel B, Li Q, Arnold R, et al. Perlecan/HSPG2 and matrilysin/MMP-7 as indices of tissue invasion: tissue localization and circulating perlecan fragments in a cohort of 288 radical prostatectomy patients. *Oncotarget*. 2016;7(9):10433-10447. Exclude: Not intervention of interest.
71. Guo S, Skala W, Magdolen V, et al. A Single Glycan at the 99-Loop of Human Kallikrein-related Peptidase 2 Regulates Activation and Enzymatic Activity. *Journal of Biological Chemistry*. 2016;291(2):593-604. Exclude: Not intervention of interest.
72. Guzey M, Jukic D, Arlotti J, Acquafondata M, Dhir R, Getzenberg RH. Increased apoptosis of periprostatic adipose tissue in VDR null mice. *Journal of Cellular Biochemistry*. 2004;93(1):133-141. Exclude: Date.
73. Hurt EM, Kawasaki BT, Klarmann GJ, Thomas SB, Farrar WL. CD44+ CD24(-) prostate cells are early cancer progenitor/stem cells that provide a model for patients with poor prognosis. *British Journal of Cancer*. 2008;98(4):756-765. Exclude: Not intervention of interest.
74. Hwang JE, Joung JY, Shin SP, et al. Ad5/35E1aPSESE4: A novel approach to marking circulating prostate tumor cells with a replication competent adenovirus controlled by PSA/PSMA transcription regulatory elements. *Cancer Letters*. 2016;372(1):57-64. Exclude: Not intervention of interest.
75. Jalava SE, Urbanucci A, Latonen L, et al. Androgen-regulated miR-32 targets BTG2 and is overexpressed in castration-resistant prostate cancer. *Oncogene*. 2012;31(41):4460-4471. Exclude: Not intervention of interest.

76. Jia Z, Rahmatpanah FB, Chen X, et al. Expression changes in the stroma of prostate cancer predict subsequent relapse.[Erratum appears in PLoS One. 2012;7(9). doi: 10.1371/annotation/7de63575-e5c9-4f1d-bb45-fc6420e92c71]. *PLoS ONE [Electronic Resource]*. 2012;7(8):e41371. Exclude: Not intervention of interest.
77. Johnson IR, Parkinson-Lawrence EJ, Keegan H, et al. Endosomal gene expression: a new indicator for prostate cancer patient prognosis? *Oncotarget*. 2015;6(35):37919-37929. Exclude: Not intervention of interest.
78. Jordan VC. A century of deciphering the control mechanisms of sex steroid action in breast and prostate cancer: the origins of targeted therapy and chemoprevention. *Cancer Research*. 2009;69(4):1243-1254. Exclude: Not intervention of interest.
79. Kachroo N, Valencia T, Warren AY, Gnanapragasam VJ. Evidence for downregulation of the negative regulator SPRED2 in clinical prostate cancer. *British Journal of Cancer*. 2013;108(3):597-601. Exclude: Not intervention of interest.
80. Kachroo N, Warren AY, Gnanapragasam VJ. Multi-transcript profiling in archival diagnostic prostate cancer needle biopsies to evaluate biomarkers in non-surgically treated men. *BMC Cancer*. 2014;14:673. Exclude: Not intervention of interest.
81. Kallifatidis G, Munoz D, Singh RK, Salazar N, Hoy JJ, Lokeshwar BL. beta-Arrestin-2 Counters CXCR7-Mediated EGFR Transactivation and Proliferation. *Molecular Cancer Research: MCR*. 2016;14(5):493-503. Exclude: Not intervention of interest.
82. Kandasamy S, Khalid AF, Majid U, Vanstone M. Prostate cancer patient perspectives on the use of information in treatment decision-making: a systematic review and qualitative meta-synthesis. *Ontario Health Technology Assessment Series*. 2017;17(7):1-32. Exclude: No outcome of interest.
83. Karyala P, Namsa ND, Chilakalapudi DR. Translational up-regulation and high-level protein expression from plasmid vectors by mTOR activation via different pathways in PC3 and 293T cells. *PLoS ONE [Electronic Resource]*. 2010;5(12):e14408. Exclude: Not intervention of interest.
84. Kaushal V, Mukunyadzi P, Dennis RA, Siegel ER, Johnson DE, Kohli M. Stage-specific characterization of the vascular endothelial growth factor axis in prostate cancer: expression of lymphangiogenic markers is associated with advanced-stage disease. *Clinical Cancer Research*. 2005;11(2 Pt 1):584-593. Exclude: Date.
85. Kela I, Harmelin A, Waks T, Orr-Urtreger A, Domany E, Eshhar Z. Interspecies comparison of prostate cancer gene-expression profiles reveals genes associated with aggressive tumors. *Prostate*. 2009;69(10):1034-1044. Exclude: Not intervention of interest.
86. Khandelwal A, Gediya L, Njar V. MS-275 synergistically enhances the growth inhibitory effects of RAMBA VN/66-1 in hormone-insensitive PC-3 prostate cancer cells and tumours. *British Journal of Cancer*. 2008;98(7):1234-1243. Exclude: Not intervention of interest.
87. Khanim FL, Gommersall LM, Wood VH, et al. Altered SMRT levels disrupt vitamin D3 receptor signalling in prostate cancer cells. *Oncogene*. 2004;23(40):6712-6725. Exclude: Date.
88. Khor LY, Bae K, Paulus R, et al. MDM2 and Ki-67 predict for distant metastasis and mortality in men treated with radiotherapy and androgen deprivation for prostate cancer: RTOG 92-02. *Journal of Clinical Oncology*. 2009;27(19):3177-3184. Exclude: Not intervention of interest.
89. Khor LY, Moughan J, Al-Saleem T, et al. Bcl-2 and Bax expression predict prostate cancer outcome in men treated with androgen deprivation and radiotherapy on radiation therapy oncology group protocol 92-02. *Clinical Cancer Research*. 2007;13(12):3585-3590. Exclude: Not intervention of interest.

90. Kim EA, Kim YH, Kang HW, et al. Lower Levels of Human MOB3B Are Associated with Prostate Cancer Susceptibility and Aggressive Clinicopathological Characteristics. *Journal of Korean Medical Science*. 2015;30(7):937-942. Exclude: Not intervention of interest.
91. Kim H, Kalchman I, Santiago-Jimenez M, et al. Transcriptome evaluation of the relation between body mass index and prostate cancer outcomes. *Cancer*. 2017;123(12):2240-2247. Exclude: Not intervention of interest.
92. Kim YR, Lee BK, Park RY, et al. Differential CARM1 expression in prostate and colorectal cancers. *BMC Cancer*. 2010;10:197. Exclude: Not intervention of interest.
93. Kinoshita M, Nakagawa T, Shimizu A, Katsuoka Y. Differently regulated androgen receptor transcriptional complex in prostate cancer compared with normal prostate. *International Journal of Urology*. 2005;12(4):390-397. Exclude: Date.
94. Klein EA, Cooperberg MR, Carroll PR. Reply to Yuri Tolkach, Markus Kuczyk, Florian Imkamp's letter to the editor re: Eric A. Klein, Matthew R. Cooperberg, Cristina Magi-Galluzzi, et al. A 17-gene assay to predict prostate cancer aggressiveness in the context of gleason grade heterogeneity, tumor multifocality, and biopsy undersampling. *Eur urol* 2014;66:550-60. *Eur Urol*. 2014;66(6):e117-118. Exclude: Publication type-letter.
95. Klein EA, Cooperberg MR, Magi-Galluzzi C, et al. A 17-gene assay to predict prostate cancer aggressiveness in the context of Gleason grade heterogeneity, tumor multifocality, and biopsy undersampling. *Eur Urol*. 2014;66(3):550-560. Exclude: No outcome of interest.
96. Klein EA, Haddad Z, Yousefi K, et al. Decipher Genomic Classifier Measured on Prostate Biopsy Predicts Metastasis Risk. *Urology*. 2016;90:148-152. Exclude: No outcome of interest.
97. Klein EA, Santiago-Jimenez M, Yousefi K, et al. Molecular Analysis of Low Grade Prostate Cancer Using a Genomic Classifier of Metastatic Potential. *Journal of Urology*. 2017;197(1):122-128. Exclude: Not intervention of interest.
98. Klein EA, Yousefi K, Haddad Z, et al. A genomic classifier improves prediction of metastatic disease within 5 years after surgery in node-negative high-risk prostate cancer patients managed by radical prostatectomy without adjuvant therapy. *European Urology*. 2015;67(4):778-786. Exclude: No outcome of interest.
99. Knezevic D, Goddard AD, Natraj N, et al. Analytical validation of the Oncotype DX prostate cancer assay - a clinical RT-PCR assay optimized for prostate needle biopsies. *BMC Genomics*. 2013;14:690. Exclude: No outcome of interest.
100. Knudsen BS, Kim HL, Erho N, et al. Application of a Clinical Whole-Transcriptome Assay for Staging and Prognosis of Prostate Cancer Diagnosed in Needle Core Biopsy Specimens. *Journal of Molecular Diagnostics*. 2016;18(3):395-406. Exclude: Not intervention of interest.
101. Koh CM, Gurel B, Sutcliffe S, et al. Alterations in nucleolar structure and gene expression programs in prostatic neoplasia are driven by the MYC oncogene. *American Journal of Pathology*. 2011;178(4):1824-1834. Exclude: Not intervention of interest.
102. Koo KM, Wee EJ, Trau M. High-speed biosensing strategy for non-invasive profiling of multiple cancer fusion genes in urine. *Biosensors & Bioelectronics*. 2017;89(Pt 2):715-720. Exclude: Not intervention of interest.
103. Kosari F, Munz JM, Savci-Heijink CD, et al. Identification of prognostic biomarkers for prostate cancer. *Clinical Cancer Research*. 2008;14(6):1734-1743. Exclude: Not intervention of interest.

104. Kovtun IV, Cheville JC, Murphy SJ, et al. Lineage relationship of Gleason patterns in Gleason score 7 prostate cancer. *Cancer Research*. 2013;73(11):3275-3284. Exclude: Not intervention of interest.
105. Krajewska M, Krajewski S, Banares S, et al. Elevated expression of inhibitor of apoptosis proteins in prostate cancer. *Clinical Cancer Research*. 2003;9(13):4914-4925. Exclude: Date.
106. Kretschmer A, Tolkach Y, Ellinger J, Kristiansen G. [Molecular biomarkers and prognostic factors for prostate cancer]. *Urologe (Auszg A)*. 2017;56(7):933-944. Exclude: No outcome of interest.
107. Kristensen H, Haldrup C, Strand S, et al. Hypermethylation of the GABRE~miR-452~miR-224 promoter in prostate cancer predicts biochemical recurrence after radical prostatectomy. *Clinical Cancer Research*. 2014;20(8):2169-2181. Exclude: Not intervention of interest.
108. Kuefer R, Hofer MD, Zorn CS, et al. Assessment of a fragment of e-cadherin as a serum biomarker with predictive value for prostate cancer. *British Journal of Cancer*. 2005;92(11):2018-2023. Exclude: Date.
109. Lalonde E, Ishkanian AS, Sykes J, et al. Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study. *Lancet Oncology*. 2014;15(13):1521-1532. Exclude: Not intervention of interest.
110. Lam HM, Ouyang B, Chen J, et al. Targeting GPR30 with G-1: a new therapeutic target for castration-resistant prostate cancer. *Endocrine-Related Cancer*. 2014;21(6):903-914. Exclude: Not intervention of interest.
111. Lapointe J, Li C, Higgins JP, et al. Gene expression profiling identifies clinically relevant subtypes of prostate cancer. *Proceedings of the National Academy of Sciences of the United States of America*. 2004;101(3):811-816. Exclude: Date.
112. Leapman MS, Westphalen AC, Ameli N, et al. Association between a 17-gene genomic prostate score and multi-parametric prostate MRI in men with low and intermediate risk prostate cancer (PCa). *PLoS ONE [Electronic Resource]*. 2017;12(10):e0185535. Exclude: No outcome of interest.
113. Lee CT, Capodici P, Osman I, et al. Overexpression of the cyclin-dependent kinase inhibitor p16 is associated with tumor recurrence in human prostate cancer. *Clinical Cancer Research*. 1999;5(5):977-983. Exclude: Date.
114. Lee HJ, Yousefi K, Haddad Z, et al. Evaluation of a genomic classifier in radical prostatectomy patients with lymph node metastasis. *Research & Reports in Urology*. 2016;8:77-84. Exclude: No outcome of interest.
115. Lehmusvaara S, Erkkila T, Urbanucci A, et al. Chemical castration and anti-androgens induce differential gene expression in prostate cancer. *Journal of Pathology*. 2012;227(3):336-345. Exclude: Not intervention of interest.
116. Leite KR, Sousa-Canavez JM, Reis ST, et al. Change in expression of miR-let7c, miR-100, and miR-218 from high grade localized prostate cancer to metastasis. *Urologic Oncology*. 2011;29(3):265-269. Exclude: Not intervention of interest.
117. Lin B, Utleg AG, Gravdal K, et al. WDR19 expression is increased in prostate cancer compared with normal cells, but low-intensity expression in cancers is associated with shorter time to biochemical failures and local recurrence. *Clinical Cancer Research*. 2008;14(5):1397-1406. Exclude: Not intervention of interest.
118. Liong ML, Lim CR, Yang H, et al. Blood-based biomarkers of aggressive prostate cancer. *PLoS ONE [Electronic Resource]*. 2012;7(9):e45802. Exclude: Not intervention of interest.
119. Loeb S, Ross AE. Genomic testing for localized prostate cancer: where do we go from here? *Current Opinion in Urology*. 2017;27(5):495-499. Exclude: Publication type-commentary.

120. Long Q, Johnson BA, Osunkoya AO, et al. Protein-coding and microRNA biomarkers of recurrence of prostate cancer following radical prostatectomy. *American Journal of Pathology*. 2011;179(1):46-54. Exclude: Not intervention of interest.
121. Loubeau G, Boudra R, Maquaire S, et al. NPM1 silencing reduces tumour growth and MAPK signalling in prostate cancer cells. *PLoS ONE [Electronic Resource]*. 2014;9(5):e96293. Exclude: Not intervention of interest.
122. Loukola A, Chadha M, Penn SG, et al. Comprehensive evaluation of the association between prostate cancer and genotypes/haplotypes in CYP17A1, CYP3A4, and SRD5A2. *European Journal of Human Genetics*. 2004;12(4):321-332. Exclude: Date.
123. Luo JH, Yu YP, Cieply K, et al. Gene expression analysis of prostate cancers. *Molecular Carcinogenesis*. 2002;33(1):25-35. Exclude: Date.
124. Lynch J, Rothney M, Salup R, et al. A multi-center analysis of prostate cancer (PCA) treatment among veterans following introduction of the 17-gene genomic prostate score (GPS) assay. *Journal of urology*. 2017;Conference: 112th annual meeting of the american urological association, AUA. 2017. United states 197(4 Supplement 1):e1162-e1163. Exclude: No outcome of interest.
125. Magi-Galluzzi C, Maddala T, Falzarano SM, et al. Gene expression in normal-appearing tissue adjacent to prostate cancers are predictive of clinical outcome: evidence for a biologically meaningful field effect. *Oncotarget*. 2016;7(23):33855-33865. Exclude: Not intervention of interest.
126. Marin-Aguilera M, Reig O, Lozano JJ, et al. Molecular profiling of peripheral blood is associated with circulating tumor cells content and poor survival in metastatic castration-resistant prostate cancer.[Erratum appears in *Oncotarget*. 2017 Apr 18;8(16):27673; PMID: 28460489]. *Oncotarget*. 2015;6(12):10604-10616. Exclude: Not intervention of interest.
127. Marrone M, Potosky AL, Penson D, Freedman AN. A 22 Gene-expression Assay, Decipher (GenomeDx Biosciences) to Predict Five-year Risk of Metastatic Prostate Cancer in Men Treated with Radical Prostatectomy. *PLoS currents*. 2015;7:17. Exclude: No outcome of interest.
128. Mecklenburg I, Weckermann D, Zippelius A, et al. A multimarker real-time RT-PCR for MAGE-A gene expression allows sensitive detection and quantification of the minimal systemic tumor load in patients with localized cancer. *Journal of Immunological Methods*. 2007;323(2):180-193. Exclude: Not intervention of interest.
129. Mengual L, Ars E, Lozano JJ, et al. Gene expression profiles in prostate cancer: identification of candidate non-invasive diagnostic markers. *Actas Urologicas Espanolas*. 2014;38(3):143-149. Exclude: Not intervention of interest.
130. Menon R, Deng M, Ruenauver K, et al. Somatic copy number alterations by whole-exome sequencing implicates YWHAZ and PTK2 in castration-resistant prostate cancer.[Erratum appears in *J Pathol*. 2014 May;233(1):101 Note: Pfeifer, Martin [corrected to Peifer, Martin]]. *Journal of Pathology*. 2013;231(4):505-516. Exclude: Not intervention of interest.
131. Miakhil I, Macneal P, Sadien I, et al. Predictive value of multiparametric MRI (MP-MRI) for the detection of prostate cancer using 12-core trus-guided prostate biopsy-a United Kingdom multicenter study. *Journal of urology*. 2017;Conference: 112th annual meeting of the american urological association, AUA. 2017. United states 197(4 Supplement 1):e484-e485. Exclude: Not intervention of interest.

132. Mirnezami AH, Pickard K, Zhang L, Primrose JN, Packham G. MicroRNAs: key players in carcinogenesis and novel therapeutic targets. *European Journal of Surgical Oncology*. 2009;35(4):339-347. Exclude: Not intervention of interest.
133. Mortensen MM, Hoyer S, Lynnerup AS, et al. Expression profiling of prostate cancer tissue delineates genes associated with recurrence after prostatectomy. *Scientific Reports*. 2015;5:16018. Exclude: Not intervention of interest.
134. Mortensen MM, Hoyer S, Orntoft TF, Sorensen KD, Dyrskjot L, Borre M. High miR-449b expression in prostate cancer is associated with biochemical recurrence after radical prostatectomy. *BMC Cancer*. 2014;14:859. Exclude: Not intervention of interest.
135. Moschini M, Spahn M, Mattei A, Cheville J, Karnes RJ. Incorporation of tissue-based genomic biomarkers into localized prostate cancer clinics. *BMC Medicine*. 2016;14:67. Exclude: Publication type-not systematic review.
136. Moustafa AA, Ziada M, Elshaikh A, et al. Identification of microRNA signature and potential pathway targets in prostate cancer. *Experimental Biology & Medicine*. 2017;242(5):536-546. Exclude: Not intervention of interest.
137. Mucci LA, Pawitan Y, Demichelis F, et al. Testing a multigene signature of prostate cancer death in the Swedish Watchful Waiting Cohort. *Cancer Epidemiology, Biomarkers & Prevention*. 2008;17(7):1682-1688. Exclude: Not intervention of interest.
138. Mucci LA, Pawitan Y, Demichelis F, et al. Nine-gene molecular signature is not associated with prostate cancer death in a watchful waiting cohort. *Cancer Epidemiology, Biomarkers & Prevention*. 2008;17(1):249-251. Exclude: Not intervention of interest.
139. Na R, Wu Y, Ding Q, Xu J. Clinically available RNA profiling tests of prostate tumors: utility and comparison. *Asian Journal of Andrology*. 2016;18(4):575-579. Exclude: Publication type-not systematic review.
140. Nakagawa T, Kollmeyer TM, Morlan BW, et al. A tissue biomarker panel predicting systemic progression after PSA recurrence post-definitive prostate cancer therapy. *PLoS ONE [Electronic Resource]*. 2008;3(5):e2318. Exclude: No outcome of interest.
141. Nanni S, Priolo C, Grasselli A, et al. Epithelial-restricted gene profile of primary cultures from human prostate tumors: a molecular approach to predict clinical behavior of prostate cancer. *Molecular Cancer Research: MCR*. 2006;4(2):79-92. Exclude: Date.
142. Nariculam J, Freeman A, Bott S, et al. Utility of tissue microarrays for profiling prognostic biomarkers in clinically localized prostate cancer: the expression of BCL-2, E-cadherin, Ki-67 and p53 as predictors of biochemical failure after radical prostatectomy with nested control for clinical and pathological risk factors. *Asian Journal of Andrology*. 2009;11(1):109-118. Exclude: Not intervention of interest.
143. Nguyen HG, Welty CJ, Cooperberg MR. Diagnostic associations of gene expression signatures in prostate cancer tissue. *Current Opinion in Urology*. 2015;25(1):65-70. Exclude: No outcome of interest.
144. Nguyen PL, Haddad Z, Ross AE, et al. Ability of a Genomic Classifier to Predict Metastasis and Prostate Cancer-specific Mortality after Radiation or Surgery based on Needle Biopsy Specimens. *European Urology*. 2017;72(5):845-852. Exclude: No outcome of interest.
145. Nguyen PL, Shin H, Yousefi K, et al. Impact of a genomic classifier of metastatic risk on postprostatectomy treatment recommendations by radiation oncologists and urologists. *Urology*. 2015;86(1):35-40. Exclude: hypothetical or scenario-based outcome.

146. Nnabugwu, II, Ugwumba FO, Enivwenae OA, Udeh EI, Otene CO, Nnabugwu CA. Serum total prostate-specific antigen values in men with symptomatic prostate enlargement in Nigeria: role in clinical decision-making. *Clinical Interventions In Aging*. 2015;10:89-93. Exclude: Not intervention of interest.
147. Oderda M, Cozzi G, Daniele L, et al. Cell-cycle Progression-score Might Improve the Current Risk Assessment in Newly Diagnosed Prostate Cancer Patients. *Urology*. 2017;102:73-78. Exclude: No outcome of interest.
148. Ohara S, Oue N, Matsubara A, et al. Reg IV is an independent prognostic factor for relapse in patients with clinically localized prostate cancer. *Cancer Science*. 2008;99(8):1570-1577. Exclude: Not intervention of interest.
149. Olmos D, Brewer D, Clark J, et al. Prognostic value of blood mRNA expression signatures in castration-resistant prostate cancer: a prospective, two-stage study. *Lancet Oncology*. 2012;13(11):1114-1124. Exclude: Not intervention of interest.
150. Pang C, Liu M, Fang W, et al. MiR-139-5p is Increased in the Peripheral Blood of Patients with Prostate Cancer. *Cellular Physiology & Biochemistry*. 2016;39(3):1111-1117. Exclude: Not intervention of interest.
151. Pasqualini R, Arap W, McDonald DM. Probing the structural and molecular diversity of tumor vasculature. *Trends in Molecular Medicine*. 2002;8(12):563-571. Exclude: Date.
152. Perry AS, Liyanage H, Lawler M, Woodson K. Discovery of DNA hypermethylation using a DHPLC screening strategy. *Epigenetics: Official Journal of the DNA Methylation Society*. 2007;2(1):43-49. Exclude: Not intervention of interest.
153. Piao G, Wu J. Mining featured biomarkers associated with prostatic carcinoma based on bioinformatics. *Biomarkers*. 2013;18(7):580-586. Exclude: Not intervention of interest.
154. Pickel B, Drew DP, Manczak T, Weitzel C, Simonsen HT, Ro DK. Identification and characterization of a kunzeaol synthase from *Thapsia garganica*: implications for the biosynthesis of the pharmaceutical thapsigargin. *Biochemical Journal*. 2012;448(2):261-271. Exclude: Not intervention of interest.
155. Prabhakaran K, Ramasamy G, Doraisamy U, Mannu J, K R, Murugesan JR. Polyketide Natural Products, Acetogenins from *Graviola* (*Annona muricata* L), its Biochemical, Cytotoxic Activity and Various Analyses Through Computational and Bio-Programming Methods. *Current Pharmaceutical Design*. 2016;22(34):5204-5210. Exclude: Not intervention of interest.
156. Prensner JR, Zhao S, Erho N, et al. RNA biomarkers associated with metastatic progression in prostate cancer: a multi-institutional high-throughput analysis of SChLAP1. *Lancet Oncology*. 2014;15(13):1469-1480. Exclude: Not intervention of interest.
157. Reis ST, Antunes AA, Pontes-Junior J, et al. Underexpression of MMP-2 and its regulators, TIMP2, MT1-MMP and IL-8, is associated with prostate cancer. *International Braz J Urol*. 2012;38(2):167-174. Exclude: Not intervention of interest.
158. Reiter RE. Risk stratification of prostate cancer 2016. *Scandinavian Journal of Clinical and Laboratory Investigation Supplement*. 2016;245:S54-59. Exclude: No outcome of interest.
159. Renard Penna R, Cancel-Tassin G, Comperat E, et al. Apparent diffusion coefficient value is a strong predictor of unsuspected aggressiveness of prostate cancer before radical prostatectomy. *World Journal of Urology*. 2016;34(10):1389-1395. Exclude: Not intervention of interest.

160. Rishi I, Baidouri H, Abbasi JA, et al. Prostate cancer in African American men is associated with downregulation of zinc transporters.[Erratum appears in *Appl Immunohistochem Mol Morphol*. 2006 Sep;14(3):368]. *Applied Immunohistochemistry & Molecular Morphology*. 2003;11(3):253-260. Exclude: Date.
161. Rodriguez S, Al-Ghamdi OA, Guthrie PA, et al. Frequency of KLK3 gene deletions in the general population. *Annals of Clinical Biochemistry*. 2017;54(4):472-480. Exclude: Not intervention of interest.
162. Ross AE, D'Amico AV, Freedland SJ. Which, when and why? Rational use of tissue-based molecular testing in localized prostate cancer. *Prostate Cancer & Prostatic Diseases*. 2016;19(1):1-6. Exclude: Publication type-not systematic review.
163. Ross AE, Den RB, Yousefi K, et al. Efficacy of post-operative radiation in a prostatectomy cohort adjusted for clinical and genomic risk. *Prostate Cancer & Prostatic Diseases*. 2016;19(3):277-282. Exclude: No outcome of interest.
164. Ross AE, Feng FY, Ghadessi M, et al. A genomic classifier predicting metastatic disease progression in men with biochemical recurrence after prostatectomy. *Prostate Cancer & Prostatic Diseases*. 2014;17(1):64-69. Exclude: No outcome of interest.
165. Ross AE, Johnson MH, Yousefi K, et al. Tissue-based Genomics Augments Post-prostatectomy Risk Stratification in a Natural History Cohort of Intermediate- and High-Risk Men. *European Urology*. 2016;69(1):157-165. Exclude: No outcome of interest.
166. Ross-Adams H, Lamb AD, Dunning MJ, et al. Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study. *EBioMedicine*. 2015;2(9):1133-1144. Exclude: Not intervention of interest.
167. Rubin MA, Bismar TA, Andren O, et al. Decreased alpha-methylacyl CoA racemase expression in localized prostate cancer is associated with an increased rate of biochemical recurrence and cancer-specific death. *Cancer Epidemiology, Biomarkers & Prevention*. 2005;14(6):1424-1432. Exclude: Date.
168. Sanati S, Watson MA, Salavaggione AL, Humphrey PA. Gene expression profiles of ductal versus acinar adenocarcinoma of the prostate. *Modern Pathology*. 2009;22(10):1273-1279. Exclude: Not intervention of interest.
169. Sartori DA, Chan DW. Biomarkers in prostate cancer: what's new? *Current Opinion in Oncology*. 2014;26(3):259-264. Exclude: Publication type-not systematic review.
170. Schoenborn JR, Nelson P, Fang M. Genomic profiling defines subtypes of prostate cancer with the potential for therapeutic stratification. *Clinical Cancer Research*. 2013;19(15):4058-4066. Exclude: No outcome of interest.
171. Schubert M, Spahn M, Kneitz S, et al. Distinct microRNA expression profile in prostate cancer patients with early clinical failure and the impact of let-7 as prognostic marker in high-risk prostate cancer. *PLoS ONE [Electronic Resource]*. 2013;8(6):e65064. Exclude: Not intervention of interest.
172. Schulz WA, Alexa A, Jung V, et al. Factor interaction analysis for chromosome 8 and DNA methylation alterations highlights innate immune response suppression and cytoskeletal changes in prostate cancer. *Molecular Cancer*. 2007;6:14. Exclude: Not intervention of interest.
173. Seiden MV, Kantoff PW, Krithivas K, et al. Detection of circulating tumor cells in men with localized prostate cancer. *Journal of Clinical Oncology*. 1994;12(12):2634-2639. Exclude: Date.
174. Shore N, Concepcion R, Saltzstein D, et al. Clinical utility of a biopsy-based cell cycle gene expression assay in localized prostate cancer. *Curr Med Res Opin*. 2014;30(4):547-553. Exclude: No comparator.

175. Shukla S, Zhang X, Niknafs YS, et al. Identification and Validation of PCAT14 as Prognostic Biomarker in Prostate Cancer. *Neoplasia (New York)*. 2016;18(8):489-499. Exclude: Not intervention of interest.
176. Sommariva S, Tarricone R, Lazzeri M, Ricciardi W, Montorsi F. Prognostic Value of the Cell Cycle Progression Score in Patients with Prostate Cancer: A Systematic Review and Meta-analysis. *Eur Urol*. 2016;69(1):107-115. Exclude: Individual studies from systematic review are included.
177. Sommer A, Haendler B. Androgen receptor and prostate cancer: molecular aspects and gene expression profiling. *Current Opinion in Drug Discovery & Development*. 2003;6(5):702-711. Exclude: Date.
178. Soond SM, Smith PG, Wahl L, et al. Novel WWP2 ubiquitin ligase isoforms as potential prognostic markers and molecular targets in cancer. *Biochimica et Biophysica Acta*. 2013;1832(12):2127-2135. Exclude: Not intervention of interest.
179. Spratt DE, Yousefi K, Deheshi S, et al. Individual Patient-Level Meta-Analysis of the Performance of the Decipher Genomic Classifier in High-Risk Men After Prostatectomy to Predict Development of Metastatic Disease. *J Clin Oncol*. 2017;35(18):1991-1998. Exclude: No outcome of interest.
180. Stegeman S, Amankwah E, Klein K, et al. A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. *Cancer Discovery*. 2015;5(4):368-379. Exclude: Not intervention of interest.
181. Stuopelyte K, Daniunaite K, Bakavicius A, Lazutka JR, Jankevicius F, Jarmalaite S. The utility of urine-circulating miRNAs for detection of prostate cancer. *British Journal of Cancer*. 2016;115(6):707-715. Exclude: Not intervention of interest.
182. Sugie S, Mukai S, Yamasaki K, Kamibeppu T, Tsukino H, Kamoto T. Significant Association of Caveolin-1 and Caveolin-2 with Prostate Cancer Progression. *Cancer Genomics & Proteomics*. 2015;12(6):391-396. Exclude: Not intervention of interest.
183. Sun Y, Goodison S. Optimizing molecular signatures for predicting prostate cancer recurrence. *Prostate*. 2009;69(10):1119-1127. Exclude: Not intervention of interest.
184. Tajtakova M, Pidanicova A, Valansky L, et al. Serum level of IGFBP3 and IGF1/IGFBP3 molar ratio in addition to PSA and single nucleotide polymorphism in PSA and CYP17 gene may contribute to early diagnostics of prostate cancer. *Neoplasma*. 2010;57(2):118-122. Exclude: Not intervention of interest.
185. Tamboli P, Amin MB, Xu HJ, Linden MD. Immunohistochemical expression of retinoblastoma and p53 tumor suppressor genes in prostatic intraepithelial neoplasia: comparison with prostatic adenocarcinoma and benign prostate. *Modern Pathology*. 1998;11(3):247-252. Exclude: Date.
186. Taneja SS. Re: A biopsy-based 17-gene genomic prostate score predicts recurrence after radical prostatectomy and adverse surgical pathology in a racially diverse population of men with clinically low- and intermediate-risk prostate cancer. *J Urol*. 2015;193(5):1541. Exclude: Publication type-commentary.
187. Tei H, Miyake H, Harada K, Fujisawa M. Expression profile of CD44s, CD44v6, and CD44v10 in localized prostate cancer: effect on prognostic outcomes following radical prostatectomy. *Urologic Oncology*. 2014;32(5):694-700. Exclude: Not intervention of interest.
188. Theurillat JP, Udeshi ND, Errington WJ, et al. Prostate cancer. Ubiquitylome analysis identifies dysregulation of effector substrates in SPOP-mutant prostate cancer. *Science*. 2014;346(6205):85-89. Exclude: Not intervention of interest.
189. Thorsen K, Sorensen KD, Brems-Eskildsen AS, et al. Alternative splicing in colon, bladder, and prostate cancer identified by exon array analysis. *Molecular & Cellular Proteomics*. 2008;7(7):1214-1224. Exclude: Not intervention of interest.

190. Timofeeva OA, Zhang X, Ransom HW, et al. Enhanced expression of SOS1 is detected in prostate cancer epithelial cells from African-American men. *International Journal of Oncology*. 2009;35(4):751-760. Exclude: Not intervention of interest.
191. Tolkach Y, Kuczyk M, Imkamp F. Re: Eric A. Klein, Matthew R. Cooperberg, Cristina Magi-Galluzzi, et al. A 17-gene assay to predict prostate cancer aggressiveness in the context of gleason grade heterogeneity, tumor multifocality, and biopsy undersampling. *Eur urol* 2014;66:550-60. *Eur Urol*. 2014;66(6):e115-116. Exclude: Publication type-letter.
192. Tolkach Y, Merseburger A, Herrmann T, Kuczyk M, Serth J, Imkamp F. Signatures of Adverse Pathological Features, Androgen Insensitivity and Metastatic Potential in Prostate Cancer. *Anticancer Research*. 2015;35(10):5443-5451. Exclude: Not intervention of interest.
193. Tomlins SA, Alshalalfa M, Davicioni E, et al. Characterization of 1577 primary prostate cancers reveals novel biological and clinicopathologic insights into molecular subtypes. *European Urology*. 2015;68(4):555-567. Exclude: No outcome of interest.
194. Tomlins SA, Rhodes DR, Yu J, et al. The role of SPINK1 in ETS rearrangement-negative prostate cancers. *Cancer Cell*. 2008;13(6):519-528. Exclude: Not intervention of interest.
195. Torres A, Alshalalfa M, Tomlins SA, et al. Comprehensive Determination of Prostate Tumor ETS Gene Status in Clinical Samples Using the CLIA Decipher Assay. *Journal of Molecular Diagnostics*. 2017;19(3):475-484. Exclude: No outcome of interest.
196. Trock BJ, Karnes RJ. Reply to Erfan Ayubi and Saeid Safiri's Letter to the Editor re: R. Jeffrey Karnes, Voleak Choeurng, Ashley E. Ross, et al. Validation of a Genomic Risk Classifier to Predict Prostate Cancer-specific Mortality in Men with Adverse Pathologic Features. *Eur Urol*. In press. <https://doi.org/10.1016/j.eururo.2017.03.036>: Methodological Issues. *Eur Urol*. 2017. Exclude: Publication type-letter.
197. Tsuchiyama K, Ito H, Taga M, et al. Expression of microRNAs associated with Gleason grading system in prostate cancer: miR-182-5p is a useful marker for high grade prostate cancer. *Prostate*. 2013;73(8):827-834. Exclude: Not intervention of interest.
198. Varambally S, Yu J, Laxman B, et al. Integrative genomic and proteomic analysis of prostate cancer reveals signatures of metastatic progression. *Cancer Cell*. 2005;8(5):393-406. Exclude: Date.
199. Vesalainen SL, Lipponen PK, Talja MT, Alhava EM, Syrjanen KJ. Proliferating cell nuclear antigen and p53 expression as prognostic factors in T1-2M0 prostatic adenocarcinoma. *International Journal of Cancer*. 1994;58(2):303-308. Exclude: Date.
200. Wang L, Yu J, Xu J, Zheng C, Li X, Du J. The analysis of microRNA-34 family expression in human cancer studies comparing cancer tissues with corresponding pericarcinous tissues. *Gene*. 2015;554(1):1-8. Exclude: Not intervention of interest.
201. Wang N, Gerling GJ, Krupski TL, Childress RM, Martin ML. Using a prostate exam simulator to decipher palpation techniques that facilitate the detection of abnormalities near clinical limits. *Simulation in Healthcare: The Journal of The Society for Medical Simulation*. 2010;5(3):152-160. Exclude: Not intervention of interest.
202. Wang Q, Zhang JG, Wang W. Expression and significance of S100P, CD147, and OCT4 in different prostate cancer tissue TNM stages. *Genetics & Molecular Research*. 2015;14(2):6844-6851. Exclude: Not intervention of interest.

203. Wei L, Wang J, Lampert E, et al. Intratumoral and Intertumoral Genomic Heterogeneity of Multifocal Localized Prostate Cancer Impacts Molecular Classifications and Genomic Prognosticators. *European Urology*. 2017;71(2):183-192. Exclude: Not intervention of interest.
204. Went P, Vasei M, Bubendorf L, et al. Frequent high-level expression of the immunotherapeutic target Ep-CAM in colon, stomach, prostate and lung cancers. *British Journal of Cancer*. 2006;94(1):128-135. Exclude: Date.
205. Whitaker HC, Shiong LL, Kay JD, et al. N-acetyl-L-aspartyl-L-glutamate peptidase-like 2 is overexpressed in cancer and promotes a pro-migratory and pro-metastatic phenotype. *Oncogene*. 2014;33(45):5274-5287. Exclude: Not intervention of interest.
206. Wilson S, Fan L, Sahgal N, Qi J, Filipp FV. The histone demethylase KDM3A regulates the transcriptional program of the androgen receptor in prostate cancer cells. *Oncotarget*. 2017;8(18):30328-30343. Exclude: Not intervention of interest.
207. Xiao K, Guo J, Zhang X, et al. Use of two gene panels for prostate cancer diagnosis and patient risk stratification. *Tumour Biology*. 2016;37(8):10115-10122. Exclude: No outcome of interest.
208. Xiaoli Z, Yawei W, Lianna L, Haifeng L, Hui Z. Screening of Target Genes and Regulatory Function of miRNAs as Prognostic Indicators for Prostate Cancer. *Medical Science Monitor*. 2015;21:3748-3759. Exclude: Not intervention of interest.
209. Yang X, Bentink S, Scheid S, Spang R. Similarities of ordered gene lists. *Journal of Bioinformatics & Computational Biology*. 2006;4(3):693-708. Exclude: Date.
210. Yap WN, Chang PN, Han HY, et al. Gamma-tocotrienol suppresses prostate cancer cell proliferation and invasion through multiple-signalling pathways. *British Journal of Cancer*. 2008;99(11):1832-1841. Exclude: Not intervention of interest.
211. Yu C, Gong AY, Chen D, Solelo Leon D, Young CY, Chen XM. Phenethyl isothiocyanate inhibits androgen receptor-regulated transcriptional activity in prostate cancer cells through suppressing PCAF. *Molecular Nutrition & Food Research*. 2013;57(10):1825-1833. Exclude: Not intervention of interest.
212. Yu J, Cao Q, Mehra R, et al. Integrative genomics analysis reveals silencing of beta-adrenergic signaling by polycomb in prostate cancer. *Cancer Cell*. 2007;12(5):419-431. Exclude: Not intervention of interest.
213. Yu YP, Ding Y, Chen Z, et al. Novel fusion transcripts associate with progressive prostate cancer. *American Journal of Pathology*. 2014;184(10):2840-2849. Exclude: Not intervention of interest.
214. Zedan AH, Blavnsfeldt SG, Hansen TF, et al. Heterogeneity of miRNA expression in localized prostate cancer with clinicopathological correlations. *PLoS ONE [Electronic Resource]*. 2017;12(6):e0179113. Exclude: Not intervention of interest.
215. Zhang L, Guo F, Gao X, Wu Y. Golgi phosphoprotein 3 expression predicts poor prognosis in patients with prostate cancer undergoing radical prostatectomy. *Molecular Medicine Reports*. 2015;12(1):1298-1304. Exclude: Not intervention of interest.
216. Zhang T, Song B, Zhu W, et al. An ileal Crohn's disease gene signature based on whole human genome expression profiles of disease unaffected ileal mucosal biopsies. *PLoS ONE [Electronic Resource]*. 2012;7(5):e37139. Exclude: Not intervention of interest.
217. Zhao H, Logothetis CJ, Gorlov IP. Usefulness of the top-scoring pairs of genes for prediction of prostate cancer progression. *Prostate Cancer & Prostatic Diseases*. 2010;13(3):252-259. Exclude: Not intervention of interest.

218. Zhao SG, Chang SL, Spratt DE, et al. Development and validation of a 24-gene predictor of response to postoperative radiotherapy in prostate cancer: a matched, retrospective analysis. *Lancet Oncology*. 2016;17(11):1612-1620. Exclude: No outcome of interest.
219. Zhao SG, Evans JR, Kothari V, et al. The Landscape of Prognostic Outlier Genes in High-Risk Prostate Cancer. *Clinical Cancer Research*. 2016;22(7):1777-1786. Exclude: Not intervention of interest.
220. Zhao SG, Jackson WC, Kothari V, et al. High-throughput transcriptomic analysis nominates proteasomal genes as age-specific biomarkers and therapeutic targets in prostate cancer. *Prostate Cancer & Prostatic Diseases*. 2015;18(3):229-236. Exclude: Not intervention of interest.
221. Zhuang L, Johnson MT. How precisely can prostate cancer be managed? *International neuourology journal*. 2016;20(Suppl 2):S120-130. Exclude: Publication type-commentary.

Colon Cancer

1. Adris S, Chuluyan E, Bravo A, et al. Mice vaccination with interleukin 12-transduced colon cancer cells potentiates rejection of syngeneic non-organ-related tumor cells. *Cancer Research*. 2000;60(23):6696-6703. Exclude: Not intervention of interest.
2. Agesen TH, Sveen A, Merok MA, et al. ColoGuideEx: a robust gene classifier specific for stage II colorectal cancer prognosis. *Gut*. 2012;61(11):1560-1567. Exclude: Not intervention of interest.
3. Agostini M, Janssen KP, Kim JJ, et al. An integrative approach for the identification of prognostic and predictive biomarkers in rectal cancer. *Oncotarget*. 2015;6(32):32561-32574. Exclude: Not intervention of interest.
4. Agrawal D, Chen T, Irby R, et al. Osteopontin identified as lead marker of colon cancer progression, using pooled sample expression profiling. *Journal of the National Cancer Institute*. 2002;94(7):513-521. Exclude: Date.
5. Ahmed FE, Ahmed NC, Vos PW, et al. Diagnostic microRNA markers to screen for sporadic human colon cancer in stool: I. Proof of principle. *Cancer Genomics & Proteomics*. 2013;10(3):93-113. Exclude: Not intervention of interest.
6. Alhadheq AM, Purusottapatnam Shaik J, Alamri A, et al. The Effect of Poly(ADP-ribose) Polymerase-1 Gene 3'Untranslated Region Polymorphism in Colorectal Cancer Risk among Saudi Cohort. *Disease Markers*. 2016;2016:8289293. Exclude: Not intervention of interest.
7. Allen WL, Jithesh PV, Oliver GR, et al. The colorectal cancer disease-specific transcriptome may facilitate the discovery of more biologically and clinically relevant information. *BMC Cancer*. 2010;10:687. Exclude: Not intervention of interest.
8. Al-Mulla F, Hagan S, Behbehani AI, et al. Raf kinase inhibitor protein expression in a survival analysis of colorectal cancer patients. *Journal of Clinical Oncology*. 2006;24(36):5672-5679. Exclude: Date.
9. Alves A, Vibert E, Trajcevski S, et al. Adjuvant interleukin-12 gene therapy for the management of colorectal liver metastases. *Cancer Gene Therapy*. 2004;11(12):782-789. Exclude: Not intervention of interest.
10. An N, Shi X, Zhang Y, et al. Discovery of a Novel Immune Gene Signature with Profound Prognostic Value in Colorectal Cancer: A Model of Cooperativity Disorientation Created in the Process from Development to Cancer. *PLoS ONE [Electronic Resource]*. 2015;10(9):e0137171. Exclude: No outcome of interest.

11. Angelopoulou K, Spiropoulou T, Stathopoulou A, et al. Development of a highly sensitive RT-PCR luminometric hybridization assay for human telomerase reverse-transcriptase beta-plus transcript. *Anticancer Research*. 2003;23(6C):4821-4829. Exclude: Date.
12. Anjomshoaa A, Lin YH, Black MA, et al. Reduced expression of a gene proliferation signature is associated with enhanced malignancy in colon cancer. *British Journal of Cancer*. 2008;99(6):966-973. Exclude: Not intervention of interest.
13. Aprile G, Casagrande M, De Maglio G, et al. Comparison of the molecular profile of brain metastases from colorectal cancer and corresponding primary tumors. *Future Oncology*. 2017;13(2):135-144. Exclude: Not intervention of interest.
14. Arfaoui AT, Kriaa LB, El Hadj Oel A, et al. Association of a p73 exon 2 GC/AT polymorphism with colorectal cancer risk and survival in Tunisian patients. *Virchows Archiv*. 2010;457(3):359-368. Exclude: Not intervention of interest.
15. Aschele C, Debernardis D, Lonardi S, et al. Deleted in colon cancer protein expression in colorectal cancer metastases: a major predictor of survival in patients with unresectable metastatic disease receiving palliative fluorouracil-based chemotherapy. *Journal of Clinical Oncology*. 2004;22(18):3758-3765. Exclude: Date.
16. Astrosini C, Roefzaad C, Dai YY, Dieckgraefe BK, Jons T, Kemmner W. REG1A expression is a prognostic marker in colorectal cancer and associated with peritoneal carcinomatosis. *International Journal of Cancer*. 2008;123(2):409-413. Exclude: Not intervention of interest.
17. Auman JT, Church R, Lee SY, Watson MA, Fleshman JW, McLeod HL. Celecoxib pre-treatment in human colorectal adenocarcinoma patients is associated with gene expression alterations suggestive of diminished cellular proliferation. *European Journal of Cancer*. 2008;44(12):1754-1760. Exclude: Not intervention of interest.
18. Baba H, Baba Y, Uemoto S, et al. Changes in expression levels of ERCC1, DPYD, and VEGFA mRNA after first-line chemotherapy of metastatic colorectal cancer: results of a multicenter study.[Erratum appears in *Oncotarget*. 2015 Nov 17;6(36):39384]. *Oncotarget*. 2015;6(32):34004-34013. Exclude: Not intervention of interest.
19. Balcerczak M, Balcerczak E, Pasz-Walczak G, Kordek R, Mirowski M. Expression of the p65 gene in patients with colorectal cancer: comparison with some histological typing, grading and clinical staging. *European Journal of Surgical Oncology*. 2004;30(3):266-270. Exclude: Date.
20. Bandres E, Malumbres R, Cubedo E, et al. A gene signature of 8 genes could identify the risk of recurrence and progression in Dukes' B colon cancer patients. *Oncology Reports*. 2007;17(5):1089-1094. Exclude: Not intervention of interest.
21. Banerjea A, Feakins RM, Nickols CD, et al. Immunogenic hsp-70 is overexpressed in colorectal cancers with high-degree microsatellite instability. *Diseases of the Colon & Rectum*. 2005;48(12):2322-2328. Exclude: Date.
22. Barrett MT, Anderson KS, Lenkiewicz E, et al. Genomic amplification of 9p24.1 targeting JAK2, PD-L1, and PD-L2 is enriched in high-risk triple negative breast cancer. *Oncotarget*. 2015;6(28):26483-26493. Exclude: Not intervention of interest.
23. Barrier A, Boelle PY, Lemoine A, Flahault A, Dudoit S, Huguier M. [Gene expression profiling in colon cancer]. *Bulletin de l'Academie Nationale de Medecine*. 2007;191(6):1091-1101; discussion 1102-1093. Exclude: Not intervention of interest.

24. Barrier A, Boelle PY, Lemoine A, et al. Gene expression profiling of nonneoplastic mucosa may predict clinical outcome of colon cancer patients. *Diseases of the Colon & Rectum*. 2005;48(12):2238-2248. Exclude: Date.
25. Barrier A, Boelle PY, Roser F, et al. Stage II colon cancer prognosis prediction by tumor gene expression profiling. *Journal of Clinical Oncology*. 2006;24(29):4685-4691. Exclude: Date.
26. Barrier A, Lemoine A, Boelle PY, et al. Colon cancer prognosis prediction by gene expression profiling. *Oncogene*. 2005;24(40):6155-6164. Exclude: Date.
27. Barrier A, Roser F, Boelle PY, et al. Prognosis of stage II colon cancer by non-neoplastic mucosa gene expression profiling. *Oncogene*. 2007;26(18):2642-2648. Exclude: Not intervention of interest.
28. Bennett JJ, Malhotra S, Wong RJ, et al. Interleukin 12 secretion enhances antitumor efficacy of oncolytic herpes simplex viral therapy for colorectal cancer. *Annals of Surgery*. 2001;233(6):819-826. Exclude: Not intervention of interest.
29. Berdiel-Acer M, Berenguer A, Sanz-Pamplona R, et al. A 5-gene classifier from the carcinoma-associated fibroblast transcriptomic profile and clinical outcome in colorectal cancer. *Oncotarget*. 2014;5(15):6437-6452. Exclude: Not intervention of interest.
30. Berstein LM, Iyevleva AG, Vasilyev D, Poroshina TE, Imyaninov EN. Genetic polymorphisms potentially associated with response to metformin in postmenopausal diabetics suffering and not suffering with cancer. *Cell Cycle*. 2013;12(23):3681-3688. Exclude: Not intervention of interest.
31. Bhushan A, Singh A, Kapur S, et al. Identification and Validation of Fibroblast Growth Factor 12 Gene as a Novel Potential Biomarker in Esophageal Cancer Using Cancer Genomic Datasets. *Omics a Journal of Integrative Biology*. 2017;21(10):616-631. Exclude: Not intervention of interest.
32. Bigagli E, De Filippo C, Castagnini C, et al. DNA copy number alterations, gene expression changes and disease-free survival in patients with colorectal cancer: a 10 year follow-up. *Cellular Oncology*. 2016;39(6):545-558. Exclude: No outcome of interest.
33. Bilchik AJ, Wainberg ZA, Nissan A, et al. Value of primary tumor gene signatures in colon cancer when national quality standards are adhered to: preliminary results of an international prospective multicenter trial. *Annals of Surgical Oncology*. 2015;22(2):535-542. Exclude: Not intervention of interest.
34. Bjerrum JT, Nielsen OH, Riis LB, et al. Transcriptional analysis of left-sided colitis, pancolitis, and ulcerative colitis-associated dysplasia. *Inflammatory Bowel Diseases*. 2014;20(12):2340-2352. Exclude: Not intervention of interest.
35. Breccia M, Diverio D, Pane F, et al. Discontinuation of imatinib therapy after achievement of complete molecular response in a Ph(+) CML patient treated while in long lasting complete cytogenetic remission (CCR) induced by interferon. *Leukemia Research*. 2006;30(12):1577-1579. Exclude: Date.
36. Brett D, Kemmner W, Koch G, Roefzaad C, Gross S, Schlag PM. A rapid bioinformatic method identifies novel genes with direct clinical relevance to colon cancer. *Oncogene*. 2001;20(33):4581-4585. Exclude: Date.
37. Brettingham-Moore KH, Duong CP, Greenawalt DM, et al. Pretreatment transcriptional profiling for predicting response to neoadjuvant chemoradiotherapy in rectal adenocarcinoma. *Clinical Cancer Research*. 2011;17(9):3039-3047. Exclude: Not intervention of interest.
38. Budinska E, Popovici V, Tejpar S, et al. Gene expression patterns unveil a new level of molecular heterogeneity in colorectal cancer. *Journal of Pathology*. 2013;231(1):63-76. Exclude: Not intervention of interest.

39. Buhl IK, Gerster S, Delorenzi M, et al. Cell Line Derived 5-FU and Irinotecan Drug-Sensitivity Profiles Evaluated in Adjuvant Colon Cancer Trial Data. *PLoS ONE [Electronic Resource]*. 2016;11(5):e0155123. Exclude: Not intervention of interest.
40. Byeon JS, Jeong JY, Kim MJ, et al. Adiponectin and adiponectin receptor in relation to colorectal cancer progression. *International Journal of Cancer*. 2010;127(12):2758-2767. Exclude: Not intervention of interest.
41. Carlson B. Putting a lid on chemotherapy costs. *Biotechnology Healthcare*. 2011;8(2):15-18. Exclude: Publication type-news story.
42. Carmona FJ, Esteller M. Moving closer to a prognostic DNA methylation signature in colon cancer. *Clinical Cancer Research*. 2011;17(6):1215-1217. Exclude: Not intervention of interest.
43. Cartwright T, Chao C, Lee M, et al. Effect of the 12-gene colon cancer assay results on adjuvant treatment recommendations in patients with stage II colon cancer. *Current Medical Research & Opinion*. 2014;30(2):321-328. Exclude: Not appropriate study design.
44. Caruso M, Pham-Nguyen K, Kwong YL, et al. Adenovirus-mediated interleukin-12 gene therapy for metastatic colon carcinoma. *Proceedings of the National Academy of Sciences of the United States of America*. 1996;93(21):11302-11306. Exclude: Not intervention of interest.
45. Carvalho TI, Novais PC, Lizarte FSN, et al. Analysis of gene expression EGFR and KRAS, microRNA-21 and microRNA-203 in patients with colon and rectal cancer and correlation with clinical outcome and prognostic factors. *Acta Cirurgica Brasileira*. 2017;32(3):243-250. Exclude: Not intervention of interest.
46. Casado E, Garcia VM, Sanchez JJ, et al. Upregulation of trefoil factor 3 (TFF3) after rectal cancer chemoradiotherapy is an adverse prognostic factor and a potential therapeutic target. *International Journal of Radiation Oncology, Biology, Physics*. 2012;84(5):1151-1158. Exclude: Not intervention of interest.
47. Cesaroni M, Powell J, Sapienza C. Validation of methylation biomarkers that distinguish normal colon mucosa of cancer patients from normal colon mucosa of patients without cancer. *Cancer Prevention Research*. 2014;7(7):717-726. Exclude: Not intervention of interest.
48. Chang W, Gao X, Han Y, et al. Gene expression profiling-derived immunohistochemistry signature with high prognostic value in colorectal carcinoma. *Gut*. 2014;63(9):1457-1467. Exclude: Not intervention of interest.
49. Chang YT, Huang MY, Yeh YS, et al. A Prospective Study of Comparing Multi-Gene Biomarker Chip and Serum Carcinoembryonic Antigen in the Postoperative Surveillance for Patients with Stage I-III Colorectal Cancer. *PLoS ONE [Electronic Resource]*. 2016;11(10):e0163264. Exclude: Not intervention of interest.
50. Chen J, Liu XS, Wang F, et al. [Construction of a RU486 inducible recombinant adenoviral vector carrying murine interleukin-12 gene and experimental treatment of colonic carcinoma]. *Chung-Hua i Hsueh Tsa Chih [Chinese Medical Journal]*. 2009;89(20):1372-1376. Exclude: Not intervention of interest.
51. Chen J, Wang W, Zhang Y, Chen Y, Hu T. Predicting distant metastasis and chemoresistance using plasma miRNAs. *Medical Oncology*. 2014;31(1):799. Exclude: Not intervention of interest.
52. Chen JL, Espinosa I, Lin AY, Liao OY, van de Rijn M, West RB. Stromal responses among common carcinomas correlated with clinicopathologic features. *Clinical Cancer Research*. 2013;19(18):5127-5135. Exclude: Not intervention of interest.
53. Chen Q, Xia HW, Ge XJ, Zhang YC, Tang QL, Bi F. Serum miR-19a predicts resistance to FOLFOX chemotherapy in advanced colorectal cancer cases. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2013;14(12):7421-7426. Exclude: Not intervention of interest.

54. Chen SH, Pham-Nguyen KB, Martinet O, et al. Rejection of disseminated metastases of colon carcinoma by synergism of IL-12 gene therapy and 4-1BB costimulation. *Molecular Therapy: the Journal of the American Society of Gene Therapy*. 2000;2(1):39-46. Exclude: Not intervention of interest.
55. Chen X, Su Z, Wang S, Xu H. Clinical and prognostic significance of Arl4c expression in colorectal cancer. *Cancer Biomarkers: Section A of Disease Markers*. 2016;16(2):253-257. Exclude: Not intervention of interest.
56. Chen Z, He X, Xia W, et al. Prognostic value and clinicopathological differences of HIFs in colorectal cancer: evidence from meta-analysis. *PLoS ONE [Electronic Resource]*. 2013;8(12):e80337. Exclude: Not intervention of interest.
57. Chikkanna-Gowda CP, Sheahan BJ, Fleeton MN, Atkins GJ. Regression of mouse tumours and inhibition of metastases following administration of a Semliki Forest virus vector with enhanced expression of IL-12. *Gene Therapy*. 2005;12(16):1253-1263. Exclude: Date.
58. Choi YW, Song YS, Lee H, et al. MicroRNA Expression Signatures Associated With BRAF-Mutated Versus KRAS-Mutated Colorectal Cancers. *Medicine*. 2016;95(15):e3321. Exclude: Not intervention of interest.
59. Chow YH, Chiang BL, Lee YL, et al. Development of Th1 and Th2 populations and the nature of immune responses to hepatitis B virus DNA vaccines can be modulated by codelivery of various cytokine genes. *Journal of Immunology*. 1998;160(3):1320-1329. Exclude: Not intervention of interest.
60. Chowdary D, Lathrop J, Skelton J, et al. Prognostic gene expression signatures can be measured in tissues collected in RNAlater preservative. *Journal of Molecular Diagnostics*. 2006;8(1):31-39. Exclude: Date.
61. Chung C, Christianson M. Predictive and prognostic biomarkers with therapeutic targets in breast, colorectal, and non-small cell lung cancers: a systemic review of current development, evidence, and recommendation. *Journal of Oncology Pharmacy Practice*. 2014;20(1):11-28. Exclude: Publication type-not systematic review.
62. Cilloni D, Messa F, Gottardi E, et al. Sensitivity to imatinib therapy may be predicted by testing Wilms tumor gene expression and colony growth after a short in vitro incubation. *Cancer*. 2004;101(5):979-988. Exclude: Date.
63. Ciurea RN, Rogoveanu I, Pirici D, et al. B2 adrenergic receptors and morphological changes of the enteric nervous system in colorectal adenocarcinoma. *World Journal of Gastroenterology*. 2017;23(7):1250-1261. Exclude: Not intervention of interest.
64. Clark-Langone KM, Sangli C, Krishnakumar J, Watson D. Translating tumor biology into personalized treatment planning: analytical performance characteristics of the Oncotype DX Colon Cancer Assay. *BMC Cancer*. 2010;10:691. Exclude: No outcome of interest.
65. Coget J, Borrini F, Susman S, Sabourin JC. Colorectal carcinomas in 2013: the search for powerful prognostic markers is still on the go! *Cancer Biomarkers: Section A of Disease Markers*. 2014;14(2-3):145-150. Exclude: Publication type-commentary.
66. Colombo MP, Vagliani M, Spreafico F, et al. Amount of interleukin 12 available at the tumor site is critical for tumor regression. *Cancer Research*. 1996;56(11):2531-2534. Exclude: Not intervention of interest.
67. Croner RS, Fortsch T, Bruckl WM, et al. Molecular signature for lymphatic metastasis in colorectal carcinomas. *Annals of Surgery*. 2008;247(5):803-810. Exclude: Not intervention of interest.

68. Csiszar A, Szentes T, Haraszti B, Balazs A, Petranyi GG, Pocsik E. The pattern of cytokine gene expression in human colorectal carcinoma. *Pathology Oncology Research*. 2004;10(2):109-116. Exclude: Date.
69. Dalerba P, Sahoo D, Paik S, et al. CDX2 as a Prognostic Biomarker in Stage II and Stage III Colon Cancer. *New England Journal of Medicine*. 2016;374(3):211-222. Exclude: Not intervention of interest.
70. Dancik GM, Ru Y, Owens CR, Theodorescu D. A framework to select clinically relevant cancer cell lines for investigation by establishing their molecular similarity with primary human cancers. *Cancer Research*. 2011;71(24):7398-7409. Exclude: Not intervention of interest.
71. D'Arrigo A, Belluco C, Ambrosi A, et al. Metastatic transcriptional pattern revealed by gene expression profiling in primary colorectal carcinoma. *International Journal of Cancer*. 2005;115(2):256-262. Exclude: Date.
72. Datta S, Datta S. Empirical Bayes screening of many p-values with applications to microarray studies. *Bioinformatics*. 2005;21(9):1987-1994. Exclude: Date.
73. Dawod MAI, Sui JSY, Kelly D, et al. Clinical utility of Oncotype DX in early stage colon cancer. *Journal of clinical oncology Conference*. 2017;35(15 Supplement 1). Exclude: Publication type-conference abstract.
74. Dekervel J, Hompes D, van Malenstein H, et al. Hypoxia-driven gene expression is an independent prognostic factor in stage II and III colon cancer patients. *Clinical Cancer Research*. 2014;20(8):2159-2168. Exclude: Not intervention of interest.
75. Demirbas S, Sucullu I, Yildirim S, Celenk T. Influence of the c-erb B-2, nm23, bcl-2 and p53 protein markers on colorectal cancer. *Turkish Journal of Gastroenterology*. 2006;17(1):13-19. Exclude: Date.
76. Demirkol S, Gomceli I, Isbilen M, et al. A Combined ULBP2 and SEMA5A Expression Signature as a Prognostic and Predictive Biomarker for Colon Cancer. *Journal of Cancer*. 2017;8(7):1113-1122. Exclude: No outcome of interest.
77. Deverka PA, Schully SD, Ishibe N, et al. Stakeholder assessment of the evidence for cancer genomic tests: insights from three case studies.[Erratum appears in Genet Med. 2013 Jan;15(1):91]. *Genetics in Medicine*. 2012;14(7):656-662. Exclude: No outcome of interest.
78. Di Nicolantonio F, Martini M, Molinari F, et al. Wild-type BRAF is required for response to panitumumab or cetuximab in metastatic colorectal cancer. *Journal of Clinical Oncology*. 2008;26(35):5705-5712. Exclude: Not intervention of interest.
79. Diaz Z, Aguilar-Mahecha A, Paquet ER, et al. Next-generation biobanking of metastases to enable multidimensional molecular profiling in personalized medicine. *Modern Pathology*. 2013;26(11):1413-1424. Exclude: Not intervention of interest.
80. Dietmaier W, Bettstetter M, Wild PJ, et al. Nuclear Maspin expression is associated with response to adjuvant 5-fluorouracil based chemotherapy in patients with stage III colon cancer. *International Journal of Cancer*. 2006;118(9):2247-2254. Exclude: Date.
81. Donehower LA, Creighton CJ, Schultz N, et al. MLH1-silenced and non-silenced subgroups of hypermutated colorectal carcinomas have distinct mutational landscapes. *Journal of Pathology*. 2013;229(1):99-110. Exclude: Not intervention of interest.
82. Dotan E, Cohen SJ. Challenges in the management of stage II colon cancer. *Seminars in Oncology*. 2011;38(4):511-520. Exclude: Not intervention of interest.

83. Dry JR, Pavey S, Pratilas CA, et al. Transcriptional pathway signatures predict MEK addiction and response to selumetinib (AZD6244). *Cancer Research*. 2010;70(6):2264-2273. Exclude: Not intervention of interest.
84. Du C, Yao Y, Xue W, Zhu WG, Peng Y, Gu J. The expression of chemokine receptors CXCR3 and CXCR4 in predicting postoperative tumour progression in stages I-II colon cancer: a retrospective study. *BMJ Open*. 2014;4(8):e005012. Exclude: Not intervention of interest.
85. Du XM, Wang LH, Chen XW, Li YX, Li YC, Cao YW. Prognostic value of Sox2 expression in digestive tract cancers: A meta-analysis. *Journal of Huazhong University of Science and Technology Medical Sciences*. 2016;36(3):305-312. Exclude: Not intervention of interest.
86. Duchrow M, Hasemeyer S, Broll R, Bruch HP, Windhovel U. Assessment of proliferative activity in colorectal carcinomas by quantitative reverse transcriptase-polymerase chain reaction (RT-PCR). *Cancer Investigation*. 2001;19(6):588-596. Exclude: Date.
87. Duchrow M, Ziemann T, Windhovel U, Bruch HP, Broll R. Colorectal carcinomas with high MIB-1 labelling indices but low pKi67 mRNA levels correlate with better prognostic outcome. *Histopathology*. 2003;42(6):566-574. Exclude: Date.
88. Eguchi J, Hiroishi K, Ishii S, Mitamura K. Interferon-alpha and interleukin-12 gene therapy of cancer: interferon-alpha induces tumor-specific immune responses while interleukin-12 stimulates non-specific killing. *Cancer Immunology, Immunotherapy*. 2003;52(6):378-386. Exclude: Date.
89. Eslahi NK, Muller S, Nguyen L, et al. Fusogenic activity of vesicular stomatitis virus glycoprotein plasmid in tumors as an enhancer of IL-12 gene therapy. *Cancer Gene Therapy*. 2001;8(1):55-62. Exclude: Not intervention of interest.
90. Fan J, Yan D, Teng M, et al. Digital transcript profile analysis with aRNA-LongSAGE validates FERMT1 as a potential novel prognostic marker for colon cancer. *Clinical Cancer Research*. 2011;17(9):2908-2918. Exclude: Not intervention of interest.
91. Fang WJ, Zheng Y, Wu LM, et al. Genome-wide analysis of aberrant DNA methylation for identification of potential biomarkers in colorectal cancer patients. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2012;13(5):1917-1921. Exclude: Not intervention of interest.
92. Farshidfar F, Weljie AM, Kopciuk KA, et al. A validated metabolomic signature for colorectal cancer: exploration of the clinical value of metabolomics. *British Journal of Cancer*. 2016;115(7):848-857. Exclude: Not intervention of interest.
93. Favis R, Huang J, Gerry NP, et al. Harmonized microarray/mutation scanning analysis of TP53 mutations in undissected colorectal tumors. *Human Mutation*. 2004;24(1):63-75. Exclude: Date.
94. Fehlker M, Huska MR, Jons T, Andrade-Navarro MA, Kemmner W. Concerted down-regulation of immune-system related genes predicts metastasis in colorectal carcinoma. *BMC Cancer*. 2014;14:64. Exclude: Not intervention of interest.
95. Fensterer H, Radlwimmer B, Strater J, et al. Matrix-comparative genomic hybridization from multicenter formalin-fixed paraffin-embedded colorectal cancer tissue blocks. *BMC Cancer*. 2007;7:58. Exclude: Not intervention of interest.
96. Fernandez-Marcelo T, Moran A, de Juan C, et al. Differential expression of senescence and cell death factors in non-small cell lung and colorectal tumors showing telomere attrition. *Oncology*. 2012;82(3):153-164. Exclude: Not intervention of interest.

97. Fodor IK, Hutchins GG, Espiritu C, Quirke P, Jubb AM. Prognostic and predictive significance of proliferation in 867 colorectal cancers. *Journal of Clinical Pathology*. 2012;65(11):989-995. Exclude: Not intervention of interest.
98. Fossar N, Chaouche M, Prochasson P, Rousset M, Brison O. Deregulated expression of the keratin 18 gene in human colon carcinoma cells. *Somatic Cell & Molecular Genetics*. 1999;25(4):223-235. Exclude: Not intervention of interest.
99. Friederichs J, Rosenberg R, Mages J, et al. Gene expression profiles of different clinical stages of colorectal carcinoma: toward a molecular genetic understanding of tumor progression. *International Journal of Colorectal Disease*. 2005;20(5):391-402. Exclude: Date.
100. Fritzmann J, Morkel M, Besser D, et al. A colorectal cancer expression profile that includes transforming growth factor beta inhibitor BAMBI predicts metastatic potential. *Gastroenterology*. 2009;137(1):165-175. Exclude: Not intervention of interest.
101. Furumoto K, Ariei S, Yamasaki S, et al. Spleen-derived dendritic cells engineered to enhance interleukin-12 production elicit therapeutic antitumor immune responses. *International Journal of Cancer*. 2000;87(5):665-672. Exclude: Not intervention of interest.
102. Gaedcke J, Leha A, Claus R, et al. Identification of a DNA methylation signature to predict disease-free survival in locally advanced rectal cancer. *Oncotarget*. 2014;5(18):8123-8135. Exclude: Not intervention of interest.
103. Galon J, Costes A, Sanchez-Cabo F, et al. Type, density, and location of immune cells within human colorectal tumors predict clinical outcome. *Science*. 2006;313(5795):1960-1964. Exclude: Date.
104. Gao M, Zhu X, Wu L, Qiu L. Cationic Polyphosphazene Vesicles for Cancer Immunotherapy by Efficient in Vivo Cytokine IL-12 Plasmid Delivery. *Biomacromolecules*. 2016;17(6):2199-2209. Exclude: Not intervention of interest.
105. Gao S, Tibiche C, Zou J, et al. Identification and Construction of Combinatory Cancer Hallmark-Based Gene Signature Sets to Predict Recurrence and Chemotherapy Benefit in Stage II Colorectal Cancer. *JAMA Oncology*. 2016;2(1):37-45. Exclude: Not intervention of interest.
106. Garcia V, Garcia JM, Pena C, et al. Thymidylate synthase messenger RNA expression in plasma from patients with colon cancer: prognostic potential. *Clinical Cancer Research*. 2006;12(7 Pt 1):2095-2100. Exclude: Date.
107. Garcia-Alfonso P, Salazar R, Garcia-Foncillas J, et al. Guidelines for biomarker testing in colorectal carcinoma (CRC): a national consensus of the Spanish Society of Pathology (SEAP) and the Spanish Society of Medical Oncology (SEOM). *Clinical & Translational Oncology: Official Publication of the Federation of Spanish Oncology Societies & of the National Cancer Institute of Mexico*. 2012;14(10):726-739. Exclude: Publication type-not systematic review.
108. Garrity MM, Burgart LJ, Mahoney MR, et al. Prognostic value of proliferation, apoptosis, defective DNA mismatch repair, and p53 overexpression in patients with resected Dukes' B2 or C colon cancer: a North Central Cancer Treatment Group Study. *Journal of Clinical Oncology*. 2004;22(9):1572-1582. Exclude: Date.
109. Gayyed MF, El-Maqsoud NM, Tawfik ER, El Gelany SA, Rahman MF. A comprehensive analysis of CDC20 overexpression in common malignant tumors from multiple organs: its correlation with tumor grade and stage. *Tumour Biology*. 2016;37(1):749-762. Exclude: Not intervention of interest.

110. Gelmini S, Poggesi M, Pinzani P, et al. Distribution of Tankyrase-1 mRNA expression in colon cancer and its prospective correlation with progression stage. *Oncology Reports*. 2006;16(6):1261-1266. Exclude: Date.
111. Ghadimi BM, Grade M, Difilippantonio MJ, et al. Effectiveness of gene expression profiling for response prediction of rectal adenocarcinomas to preoperative chemoradiotherapy. *Journal of Clinical Oncology*. 2005;23(9):1826-1838. Exclude: Date.
112. Ghanbari R, Mosakhani N, Asadi J, et al. Decreased expression of fecal miR-4478 and miR-1295b-3p in early-stage colorectal cancer. *Cancer Biomarkers: Section A of Disease Markers*. 2015;15(2):189-195. Exclude: Not intervention of interest.
113. Giralt J, de las Heras M, Cerezo L, et al. The expression of epidermal growth factor receptor results in a worse prognosis for patients with rectal cancer treated with preoperative radiotherapy: a multicenter, retrospective analysis. *Radiotherapy & Oncology*. 2005;74(2):101-108. Exclude: Date.
114. Goel G. Evolving role of gene expression signatures as biomarkers in early-stage colon cancer. *Journal of Gastrointestinal Cancer*. 2014;45(4):399-404. Exclude: Publication type-commentary.
115. Gonzalez-Vallinas M, Vargas T, Moreno-Rubio J, et al. Clinical relevance of the differential expression of the glycosyltransferase gene GCNT3 in colon cancer. *European Journal of Cancer*. 2015;51(1):1-8. Exclude: Not intervention of interest.
116. Goossens-Beumer IJ, Benard A, van Hoesel AQ, et al. Age-dependent clinical prognostic value of histone modifications in colorectal cancer. *Translational Research: The Journal Of Laboratory & Clinical Medicine*. 2015;165(5):578-588. Exclude: Not intervention of interest.
117. Gosens MJ, van Kempen LC, van de Velde CJ, van Krieken JH, Nagtegaal ID. Loss of membranous Ep-CAM in budding colorectal carcinoma cells. *Modern Pathology*. 2007;20(2):221-232. Exclude: Not intervention of interest.
118. Govindarajan R, Posey J, Chao CY, et al. A comparison of 12-gene colon cancer assay gene expression in African American and Caucasian patients with stage II colon cancer. *BMC Cancer*. 2016;16:368. Exclude: No outcome of interest.
119. Gray RG, Quirke P, Handley K, et al. Validation study of a quantitative multigene reverse transcriptase-polymerase chain reaction assay for assessment of recurrence risk in patients with stage II colon cancer. *Journal of Clinical Oncology*. 2011;29(35):4611-4619. Exclude: No outcome of interest.
120. Gunther M, Frebourg T, Laithier M, et al. An Sp1 binding site and the minimal promoter contribute to overexpression of the cytokeratin 18 gene in tumorigenic clones relative to that in nontumorigenic clones of a human carcinoma cell line. *Molecular & Cellular Biology*. 1995;15(5):2490-2499. Exclude: Date.
121. Guo JY, Qin AQ, Li RK, et al. [Association of the IL-18 gene polymorphism with susceptibility to colorectal cancer]. *Zhonghua Weichang Waiké Zazhi*. 2012;15(4):400-403. Exclude: Not intervention of interest.
122. Gyorffy B, Serra V, Jurchott K, et al. Prediction of doxorubicin sensitivity in breast tumors based on gene expression profiles of drug-resistant cell lines correlates with patient survival. *Oncogene*. 2005;24(51):7542-7551. Exclude: Date.
123. Haghshenas MR, Hosseini SV, Mahmoudi M, Saberi-Firozi M, Farjadian S, Ghaderi A. IL-18 serum level and IL-18 promoter gene polymorphism in Iranian patients with gastrointestinal cancers. *Journal of Gastroenterology & Hepatology*. 2009;24(6):1119-1122. Exclude: Not intervention of interest.

124. Hainsworth JD, Schnabel CA, Erlander MG, Haines DW, 3rd, Greco FA. A retrospective study of treatment outcomes in patients with carcinoma of unknown primary site and a colorectal cancer molecular profile. *Clinical Colorectal Cancer*. 2012;11(2):112-118. Exclude: Not intervention of interest.
125. Hamm A, Prenen H, Van Delm W, et al. Tumour-educated circulating monocytes are powerful candidate biomarkers for diagnosis and disease follow-up of colorectal cancer. *Gut*. 2016;65(6):990-1000. Exclude: Not intervention of interest.
126. Han MY, Liu Q, Peng JP. [Changes of tumorigenicity induced by interleukin-18 gene transduction and its anti-tumor effect on human colon cancer SW480 cells]. *Chung-Hua Chung Liu Tsa Chih [Chinese Journal of Oncology]*. 2007;29(2):105-106. Exclude: Not intervention of interest.
127. Han SS, Sue LY, Berndt SI, et al. Associations between genes in the one-carbon metabolism pathway and advanced colorectal adenoma risk in individuals with low folate intake. *Cancer Epidemiology, Biomarkers & Prevention*. 2012;21(3):417-427. Exclude: Not intervention of interest.
128. Hansen TF, Kjaer-Frifeldt S, Christensen RD, et al. Redefining high-risk patients with stage II colon cancer by risk index and microRNA-21: results from a population-based cohort. *British Journal of Cancer*. 2014;111(7):1285-1292. Exclude: Not intervention of interest.
129. Health Quality O. Gene expression profiling for guiding adjuvant chemotherapy decisions in women with early breast cancer: an evidence-based and economic analysis. *Ontario Health Technology Assessment Series*. 2010;10(23):1-57. Exclude: Not intervention of interest.
130. Hernandez JM, Farma JM, Coppola D, et al. Expression of the antiapoptotic protein survivin in colon cancer. *Clinical Colorectal Cancer*. 2011;10(3):188-193. Exclude: Not intervention of interest.
131. Higashidani Y, Tamura S, Morita T, et al. Analysis of K-ras codon 12 mutation in flat and nodular variants of serrated adenoma in the colon. *Diseases of the Colon & Rectum*. 2003;46(3):327-332. Exclude: Not intervention of interest.
132. Hu L, Chen HY, Han T, et al. Downregulation of DHRS9 expression in colorectal cancer tissues and its prognostic significance. *Tumour Biology*. 2016;37(1):837-845. Exclude: Not intervention of interest.
133. Huang ZQ, Wang JL, Pan GG, Wei YS. Association of single nucleotide polymorphisms in IL-12 and IL-27 genes with colorectal cancer risk. *Clinical Biochemistry*. 2012;45(1-2):54-59. Exclude: Not intervention of interest.
134. Hughes R, Parry J, Beynon J, Jenkins G. Molecular changes consistent with increased proliferation and invasion are common in rectal cancer. *Clinical & Translational Oncology: Official Publication of the Federation of Spanish Oncology Societies & of the National Cancer Institute of Mexico*. 2011;13(10):753-759. Exclude: Not intervention of interest.
135. Huh JW, Kim HR, Lee JH, Kim YJ. Comparison of cyclooxygenase-2 and CD44 mRNA expression in colorectal cancer and its relevance for prognosis. *Virchows Archiv*. 2009;454(4):381-387. Exclude: Not intervention of interest.
136. Hur H, Tulina I, Cho MS, et al. Biomarker-Based Scoring System for Prediction of Tumor Response After Preoperative Chemoradiotherapy in Rectal Cancer by Reverse Transcriptase Polymerase Chain Reaction Analysis. *Diseases of the Colon & Rectum*. 2016;59(12):1174-1182. Exclude: Not intervention of interest.
137. Hur K, Toiyama Y, Okugawa Y, et al. Circulating microRNA-203 predicts prognosis and metastasis in human colorectal cancer. *Gut*. 2017;66(4):654-665. Exclude: Not intervention of interest.

138. Hur K, Toiyama Y, Schetter AJ, et al. Identification of a metastasis-specific MicroRNA signature in human colorectal cancer. *Journal of the National Cancer Institute*. 2015;107(3). Exclude: Not intervention of interest.
139. Ieta K, Tanaka F, Yokobori T, et al. Clinicopathological significance of stanniocalcin 2 gene expression in colorectal cancer. *International Journal of Cancer*. 2009;125(4):926-931. Exclude: Not intervention of interest.
140. Inoue Y, Shirane M, Miki C, et al. Gene expression profiles of colorectal carcinoma in response to neo-adjuvant chemotherapy. *International Journal of Oncology*. 2004;25(6):1641-1649. Exclude: Date.
141. Irshad S, Bansal M, Guarnieri P, et al. Bone morphogenetic protein and Notch signalling crosstalk in poor-prognosis, mesenchymal-subtype colorectal cancer. *Journal of Pathology*. 2017;242(2):178-192. Exclude: Not intervention of interest.
142. Itaya T, Judde JG, Hunt B, Frost P. Genotypic and phenotypic evidence of clonal interactions in murine tumor cells. *Journal of the National Cancer Institute*. 1989;81(9):664-668. Exclude: Date.
143. Ito H, Mo Q, Qin LX, et al. Gene expression profiles accurately predict outcome following liver resection in patients with metastatic colorectal cancer. *PLoS ONE*. 2013;8(12). Exclude: No outcome of interest.
144. Iwatani Y, Shimada Y, Seima Y, Yamazaki T, Miyazaki N. The biological and clinicopathological characteristics of right-sided colon cancer. *Oncology Reports*. 2000;7(5):991-994. Exclude: Date.
145. Jeong DH, Kim WR, Min BS, Kim YW, Song MK, Kim NK. Validation of a quantitative 12-multigene expression assay (Oncotype DX) Colon Cancer Assay) in Korean patients with stage II colon cancer: implication of ethnic differences contributing to differences in gene expression. *OncoTargets and therapy*. 2015;8:3817-3825. Exclude: No outcome of interest.
146. Jepsen RK, Novotny GW, Klarskov LL, Christensen IJ, Hogdall E, Riis LB. Investigating intra-tumor heterogeneity and expression gradients of miR-21, miR-92a and miR-200c and their potential of predicting lymph node metastases in early colorectal cancer. *Experimental & Molecular Pathology*. 2016;101(2):187-196. Exclude: Not intervention of interest.
147. Jernvall P, Makinen MJ, Karttunen TJ, Makela J, Vihko P. Morphological and genetic abnormalities in prediction of recurrence in radically operated colorectal cancer. *Anticancer Research*. 1999;19(2B):1357-1362. Exclude: Date.
148. Joensuu EI, Abdel-Rahman WM, Ollikainen M, Ruosaari S, Knuutila S, Peltomaki P. Epigenetic signatures of familial cancer are characteristic of tumor type and family category. *Cancer Research*. 2008;68(12):4597-4605. Exclude: Not intervention of interest.
149. Kalady MF, DeJulius K, Church JM, Lavery IC, Fazio VW, Ishwaran H. Gene signature is associated with early stage rectal cancer recurrence. *Journal of the American College of Surgeons*. 2010;211(2):187-195. Exclude: Not intervention of interest.
150. Kalina U, Koyama N, Hosoda T, et al. Enhanced production of IL-18 in butyrate-treated intestinal epithelium by stimulation of the proximal promoter region. *European Journal of Immunology*. 2002;32(9):2635-2643. Exclude: Not intervention of interest.
151. Kang HJ, Kim EJ, Kim BG, et al. Quantitative analysis of cancer-associated gene methylation connected to risk factors in Korean colorectal cancer patients.[Erratum appears in J Prev Med Public Health. 2012;45(5):333]. *Journal of Preventive Medicine & Public Health / Yebang Uihakhoe Chi*. 2012;45(4):251-258. Exclude: Not intervention of interest.

152. Karpinski P, Walter M, Szmida E, et al. Intermediate- and low-methylation epigenotypes do not correspond to CpG island methylator phenotype (low and -zero) in colorectal cancer. *Cancer Epidemiology, Biomarkers & Prevention*. 2013;22(2):201-208. Exclude: Not intervention of interest.
153. Katoh S, Goi T, Naruse T, et al. Cancer stem cell marker in circulating tumor cells: expression of CD44 variant exon 9 is strongly correlated to treatment refractoriness, recurrence and prognosis of human colorectal cancer. *Anticancer Research*. 2015;35(1):239-244. Exclude: Not intervention of interest.
154. Katzenmaier EM, Andre S, Kopitz J, Gabius HJ. Impact of sodium butyrate on the network of adhesion/growth-regulatory galectins in human colon cancer in vitro. *Anticancer Research*. 2014;34(10):5429-5438. Exclude: Not intervention of interest.
155. Kelley RK, Van Bebber SL, Phillips KA, Venook AP. Personalized medicine and oncology practice guidelines: a case study of contemporary biomarkers in colorectal cancer. *Journal of the National Comprehensive Cancer Network*. 2011;9(1):13-25. Exclude: Publication type-not systematic review.
156. Kelley RK, Venook AP. Prognostic and predictive markers in stage II colon cancer: is there a role for gene expression profiling? *Clinical Colorectal Cancer*. 2011;10(2):73-80. Exclude: Publication type-not systematic review.
157. Kemmner W, Roefzaad C, Haensch W, Schlag PM. Glycosyltransferase expression in human colonic tissue examined by oligonucleotide arrays. *Biochimica et Biophysica Acta*. 2003;1621(3):272-279. Exclude: Date.
158. Kennedy RD, Bylesjo M, Kerr P, et al. Development and independent validation of a prognostic assay for stage II colon cancer using formalin-fixed paraffin-embedded tissue. *Journal of Clinical Oncology*. 2011;29(35):4620-4626. Exclude: Not intervention of interest.
159. Kijima T, Hazama S, Tsunedomi R, et al. MicroRNA-6826 and -6875 in plasma are valuable non-invasive biomarkers that predict the efficacy of vaccine treatment against metastatic colorectal cancer. *Oncology Reports*. 2017;37(1):23-30. Exclude: Not intervention of interest.
160. Killian A, Di Fiore F, Le Pessot F, et al. A simple method for the routine detection of somatic quantitative genetic alterations in colorectal cancer. *Gastroenterology*. 2007;132(2):645-653. Exclude: Not intervention of interest.
161. Kim DH, Park YS, Park CJ, et al. Expression of the HMGI(Y) gene in human colorectal cancer. *International Journal of Cancer*. 1999;84(4):376-380. Exclude: Date.
162. Kim IJ, Lim SB, Kang HC, et al. Microarray gene expression profiling for predicting complete response to preoperative chemoradiotherapy in patients with advanced rectal cancer. *Diseases of the Colon & Rectum*. 2007;50(9):1342-1353. Exclude: Not intervention of interest.
163. Kim MY, Yim SH, Kwon MS, et al. Recurrent genomic alterations with impact on survival in colorectal cancer identified by genome-wide array comparative genomic hybridization. *Gastroenterology*. 2006;131(6):1913-1924. Exclude: Date.
164. Kim YR, Lee BK, Park RY, et al. Differential CARM1 expression in prostate and colorectal cancers. *BMC Cancer*. 2010;10:197. Exclude: Not intervention of interest.
165. Kirmizis A, Bartley SM, Farnham PJ. Identification of the polycomb group protein SU(Z)12 as a potential molecular target for human cancer therapy. *Molecular Cancer Therapeutics*. 2003;2(1):113-121. Exclude: Not intervention of interest.

166. Koga Y, Yamazaki N, Takizawa S, et al. Gene expression analysis using a highly sensitive DNA microarray for colorectal cancer screening. *Anticancer Research*. 2014;34(1):169-176. Exclude: Not intervention of interest.
167. Kohonen-Corish MR, Daniel JJ, Chan C, et al. Low microsatellite instability is associated with poor prognosis in stage C colon cancer. *Journal of Clinical Oncology*. 2005;23(10):2318-2324. Exclude: Date.
168. Kopetz S, Tabernero J, Rosenberg R, et al. Genomic classifier ColoPrint predicts recurrence in stage II colorectal cancer patients more accurately than clinical factors. *Oncologist*. 2015;20(2):127-133. Exclude: No outcome of interest.
169. Kotti A, Holmqvist A, Albertsson M, Sun XF. SPARCL1 expression increases with preoperative radiation therapy and predicts better survival in rectal cancer patients. *International Journal of Radiation Oncology, Biology, Physics*. 2014;88(5):1196-1202. Exclude: Not intervention of interest.
170. Koumariou A, Tzeveleki I, Mekras D, et al. Prognostic markers in early-stage colorectal cancer: significance of TYMS mRNA expression. *Anticancer Research*. 2014;34(9):4949-4962. Exclude: Not intervention of interest.
171. Kraus S, Nabiochtchikov I, Shapira S, Arber N. Recent advances in personalized colorectal cancer research. *Cancer Letters*. 2014;347(1):15-21. Exclude: Publication type-not systematic review.
172. Krieg A, Werner TA, Verde PE, Stoecklein NH, Knoefel WT. Prognostic and clinicopathological significance of survivin in colorectal cancer: a meta-analysis. *PLoS ONE [Electronic Resource]*. 2013;8(6):e65338. Exclude: Not intervention of interest.
173. Kropotova ES, Zinovieva OL, Zyryanova AF, et al. Altered expression of multiple genes involved in retinoic acid biosynthesis in human colorectal cancer. *Pathology Oncology Research*. 2014;20(3):707-717. Exclude: Not intervention of interest.
174. Kuramochi H, Nakamura A, Nakajima G, et al. PTEN mRNA expression is less pronounced in left- than right-sided colon cancer: a retrospective observational study. *BMC Cancer*. 2016;16:366. Exclude: Not intervention of interest.
175. Lacunza E, Canzoneri R, Rabassa ME, et al. RHBDD2: a 5-fluorouracil responsive gene overexpressed in the advanced stages of colorectal cancer. *Tumour Biology*. 2012;33(6):2393-2399. Exclude: Not intervention of interest.
176. Lascorz J, Bevier M, Schonfels WV, et al. Polymorphisms in the mitochondrial oxidative phosphorylation chain genes as prognostic markers for colorectal cancer. *BMC Medical Genetics*. 2012;13:31. Exclude: Not intervention of interest.
177. Lascorz J, Chen B, Hemminki K, Forsti A. Consensus pathways implicated in prognosis of colorectal cancer identified through systematic enrichment analysis of gene expression profiling studies. *PLoS ONE [Electronic Resource]*. 2011;6(4):e18867. Exclude: No outcome of interest.
178. Laurell H, Bouisson M, Berthelemy P, et al. Identification of biomarkers of human pancreatic adenocarcinomas by expression profiling and validation with gene expression analysis in endoscopic ultrasound-guided fine needle aspiration samples. *World Journal of Gastroenterology*. 2006;12(21):3344-3351. Exclude: Date.
179. Le Rolle AF, Klempner SJ, Garrett CR, et al. Identification and characterization of RET fusions in advanced colorectal cancer. *Oncotarget*. 2015;6(30):28929-28937. Exclude: Not intervention of interest.
180. Lee BP, Rushlow WJ, Chakraborty C, Lala PK. Differential gene expression in premalignant human trophoblast: role of IGFBP-5. *International Journal of Cancer*. 2001;94(5):674-684. Exclude: Date.

181. Lee SC, Wu CJ, Wu PY, Huang YL, Wu CW, Tao MH. Inhibition of established subcutaneous and metastatic murine tumors by intramuscular electroporation of the interleukin-12 gene. *Journal of Biomedical Science*. 2003;10(1):73-86. Exclude: Date.
182. Lenehan PF, Boardman LA, Riegert-Johnson D, et al. Generation and external validation of a tumor-derived 5-gene prognostic signature for recurrence of lymph node-negative, invasive colorectal carcinoma. *Cancer*. 2012;118(21):5234-5244. Exclude: Not intervention of interest.
183. Leng J, Zhang L, Yao H, Cao X. Antitumor effects of interleukin-18 gene-modified hepatocyte cell line on implanted liver carcinoma. *Chinese Medical Journal*. 2003;116(10):1475-1479. Exclude: Date.
184. Letellier E, Schmitz M, Baig K, et al. Identification of SOCS2 and SOCS6 as biomarkers in human colorectal cancer. *British Journal of Cancer*. 2014;111(4):726-735. Exclude: Not intervention of interest.
185. Levine EA, Blazer DG, 3rd, Kim MK, et al. Gene expression profiling of peritoneal metastases from appendiceal and colon cancer demonstrates unique biologic signatures and predicts patient outcomes. *Journal of the American College of Surgeons*. 2012;214(4):599-606; discussion 606-597. Exclude: Not intervention of interest.
186. Li M, Yuan YH, Han Y, et al. Expression profile of cancer-testis genes in 121 human colorectal cancer tissue and adjacent normal tissue. *Clinical Cancer Research*. 2005;11(5):1809-1814. Exclude: Date.
187. Li Q, Wang Y, Lai Y, Xu P, Yang Z. HspB5 correlates with poor prognosis in colorectal cancer and prompts epithelial-mesenchymal transition through ERK signaling. *PLoS ONE [Electronic Resource]*. 2017;12(8):e0182588. Exclude: Not intervention of interest.
188. Li S, Lu X, Chi P, Pan J. Identification of Nkx2-3 and TGFB11 expression levels as potential biomarkers to predict the effects of FOLFOX4 chemotherapy. *Cancer Biology & Therapy*. 2012;13(6):443-449. Exclude: Not intervention of interest.
189. Li W, Wang R, Yan Z, Bai L, Sun Z. High accordance in prognosis prediction of colorectal cancer across independent datasets by multi-gene module expression profiles.[Erratum appears in PLoS One. 2012;9(7). doi:10.1371/annotation/59a30e2e-76cf-4b51-9489-5bf0c2394afb]. *PLoS ONE [Electronic Resource]*. 2012;7(3):e33653. Exclude: Not intervention of interest.
190. Liersch T, Grade M, Gaedcke J, et al. Preoperative chemoradiotherapy in locally advanced rectal cancer: correlation of a gene expression-based response signature with recurrence. *Cancer Genetics & Cytogenetics*. 2009;190(2):57-65. Exclude: Not intervention of interest.
191. Liesenfeld DB, Grapov D, Fahrman JF, et al. Metabolomics and transcriptomics identify pathway differences between visceral and subcutaneous adipose tissue in colorectal cancer patients: the ColoCare study. *American Journal of Clinical Nutrition*. 2015;102(2):433-443. Exclude: Not intervention of interest.
192. Lin AY, Chua MS, Choi YL, et al. Comparative profiling of primary colorectal carcinomas and liver metastases identifies LEF1 as a prognostic biomarker. *PLoS ONE [Electronic Resource]*. 2011;6(2):e16636. Exclude: Not intervention of interest.
193. Lin HH, Wei NC, Chou TY, et al. Building personalized treatment plans for early-stage colorectal cancer patients. *Oncotarget*. 2017;8(8):13805-13817. Exclude: No outcome of interest.
194. Ling L, Zhao P, Yan G, et al. The frequency of Th17 and Th22 cells in patients with colorectal cancer at pre-operation and post-operation. *Immunological Investigations*. 2015;44(1):56-69. Exclude: Not intervention of interest.
195. Little AS, Balmain K, Sale MJ, et al. A correction to the research article titled: "Amplification of the driving oncogene, KRAS or BRAF, underpins acquired resistance to MEK1/2 inhibitors in colorectal cancer

- cells" by A. S. Little, K. Balmanno, M. J. Sale, S. Newman, J. R. Dry, M. Hampson, P. A. W. Edwards, P. D. Smith, S. J. Cook.[Republished from *Sci Signal*. 2011;4(166):ra17; PMID: 21447798]. *Science Signaling [Electronic Resource]*. 2011;4(170):er2. Exclude: Not intervention of interest.
196. Little AS, Balmanno K, Sale MJ, et al. Amplification of the driving oncogene, KRAS or BRAF, underpins acquired resistance to MEK1/2 inhibitors in colorectal cancer cells.[Erratum appears in *Sci Signal*. 2011;4(170). doi:10.1126/scisignal.4170er2], [Republished in *Sci Signal*. 2011;4(170):er2; PMID: 21674991]. *Science Signaling [Electronic Resource]*. 2011;4(166):ra17. Exclude: Not intervention of interest.
197. Liu F, Ye P, Bi T, et al. COLORECTAL Polymeric Immunoglobulin Receptor Expression is Correlated with Hepatic Metastasis and Poor Prognosis in Colon Carcinoma Patients with Hepatic Metastasis. *Hepato-Gastroenterology*. 2014;61(131):652-659. Exclude: Not intervention of interest.
198. Liu YJ, Zhang S, Hou K, et al. Analysis of key genes and pathways associated with colorectal cancer with microarray technology. *Asian Pacific Journal of Cancer Prevention: Apjcp*. 2013;14(3):1819-1823. Exclude: Not intervention of interest.
199. Lopez NE, Weiss AC, Robles J, Fanta P, Ramamoorthy SL. A systematic review of clinically available gene expression profiling assays for stage II colorectal cancer: initial steps toward genetic staging. *American Journal of Surgery*. 2016;212(4):700-714. Exclude: Not clinical utility.
200. Low YS, Blocker C, McPherson JR, et al. A formalin-fixed paraffin-embedded (FFPE)-based prognostic signature to predict metastasis in clinically low risk stage I/II microsatellite stable colorectal cancer. *Cancer Letters*. 2017;403:13-20. Exclude: Not intervention of interest.
201. Lu AT, Salpeter SR, Reeve AE, et al. Gene expression profiles as predictors of poor outcomes in stage II colorectal cancer: A systematic review and meta-analysis. *Clinical Colorectal Cancer*. 2009;8(4):207-214. Exclude: No outcome of interest.
202. Lu J, Pei H, Kaeck M, Thompson HJ. Gene expression changes associated with chemically induced rat mammary carcinogenesis. *Molecular Carcinogenesis*. 1997;20(2):204-215. Exclude: Not intervention of interest.
203. Luna-Perez P, Segura J, Alvarado I, Labastida S, Santiago-Payan H, Quintero A. Specific c-K-ras gene mutations as a tumor-response marker in locally advanced rectal cancer treated with preoperative chemoradiotherapy. *Annals of Surgical Oncology*. 2000;7(10):727-731. Exclude: Date.
204. Luo M, Liang X, Luo ST, et al. Folate-Modified Lipoplexes Delivering the Interleukin-12 Gene for Targeting Colon Cancer Immunogene Therapy. *Journal of Biomedical Nanotechnology*. 2015;11(11):2011-2023. Exclude: Not intervention of interest.
205. Lv S, Yang Y, Kwon S, et al. The association of CXCR4 expression with prognosis and clinicopathological indicators in colorectal carcinoma patients: a meta-analysis.[Erratum appears in *Histopathology*. 2014 Jun;64(7):1047]. *Histopathology*. 2014;64(5):701-712. Exclude: Not intervention of interest.
206. Maak M, Simon I, Nitsche U, et al. Independent validation of a prognostic genomic signature (ColoPrint) for patients with stage II colon cancer. *Annals of Surgery*. 2013;257(6):1053-1058. Exclude: No outcome of interest.
207. Mahato RI, Lee M, Han S, Maheshwari A, Kim SW. Intratumoral delivery of p2CMVmIL-12 using water-soluble lipopolymers. *Molecular Therapy: the Journal of the American Society of Gene Therapy*. 2001;4(2):130-138. Exclude: Date.

208. Majima T, Ichikura T, Chochi K, et al. Exploitation of interleukin-18 by gastric cancers for their growth and evasion of host immunity. *International Journal of Cancer*. 2006;118(2):388-395. Exclude: Date.
209. Marisa L, de Reynies A, Duval A, et al. Gene expression classification of colon cancer into molecular subtypes: characterization, validation, and prognostic value. *PLoS Medicine / Public Library of Science*. 2013;10(5):e1001453. Exclude: No outcome of interest.
210. Marisa L, Svrcek M, Collura A, et al. The Balance Between Cytotoxic T-cell Lymphocytes and Immune Checkpoint Expression in the Prognosis of Colon Tumors. *Journal of the National Cancer Institute*. 2018;110(1):01. Exclude: Not intervention of interest.
211. Maus MK, Hanna DL, Stephens CL, et al. Distinct gene expression profiles of proximal and distal colorectal cancer: implications for cytotoxic and targeted therapy. *Pharmacogenomics Journal*. 2015;15(4):354-362. Exclude: Not intervention of interest.
212. Mayor R, Casadome L, Azuara D, et al. Long-range epigenetic silencing at 2q14.2 affects most human colorectal cancers and may have application as a non-invasive biomarker of disease. *British Journal of Cancer*. 2009;100(10):1534-1539. Exclude: Not intervention of interest.
213. Mazzolini G, Narvaiza I, Bustos M, et al. Alpha(v)beta(3) integrin-mediated adenoviral transfer of interleukin-12 at the periphery of hepatic colon cancer metastases induces VCAM-1 expression and T-cell recruitment. *Molecular Therapy: the Journal of the American Society of Gene Therapy*. 2001;3(5 Pt 1):665-672. Exclude: Not intervention of interest.
214. Mazzolini G, Qian C, Xie X, et al. Regression of colon cancer and induction of antitumor immunity by intratumoral injection of adenovirus expressing interleukin-12. *Cancer Gene Therapy*. 1999;6(6):514-522. Exclude: Not intervention of interest.
215. McCleary NJ, Sato K, Nishihara R, et al. Prognostic Utility of Molecular Factors by Age at Diagnosis of Colorectal Cancer. *Clinical Cancer Research*. 2016;22(6):1489-1498. Exclude: Not intervention of interest.
216. Medina-Echeverez J, Fioravanti J, Zabala M, Ardaiz N, Prieto J, Berraondo P. Successful colon cancer eradication after chemoimmunotherapy is associated with profound phenotypic change of intratumoral myeloid cells. *Journal of Immunology*. 2011;186(2):807-815. Exclude: Not intervention of interest.
217. Meleth S, Reeder-Hayes K, Ashok M, et al. AHRQ Technology Assessments. In: *Technology Assessment of Molecular Pathology Testing for the Estimation of Prognosis for Common Cancers*. Rockville (MD): Agency for Healthcare Research and Quality (US); 2014.
218. Mendiratta SK, Quezada A, Matar M, et al. Combination of interleukin 12 and interferon alpha gene therapy induces a synergistic antitumor response against colon and renal cell carcinoma. *Human Gene Therapy*. 2000;11(13):1851-1862. Exclude: Not intervention of interest.
219. Mendiratta SK, Quezada A, Matar M, et al. Intratumoral delivery of IL-12 gene by polyvinyl polymeric vector system to murine renal and colon carcinoma results in potent antitumor immunity. *Gene Therapy*. 1999;6(5):833-839. Exclude: Not intervention of interest.
220. Meropol NJ, Lyman GH, Chien R, Hornberger JC. Use of a multigene prognostic assay for selection of adjuvant chemotherapy in patients with stage II colon cancer: Impact on quality-adjusted life expectancy and costs. *Journal of clinical oncology*. 2011;29(4 SUPPL. 1):CONFERENCE START: 2011 Jan 2020 CONFERENCE END: 2011 Jan 2022. Exclude: Publication type-conference abstract.
221. Mettu RK, Wan YW, Habermann JK, Ried T, Guo NL. A 12-gene genomic instability signature predicts clinical outcomes in multiple cancer types. *International Journal of Biological Markers*. 2010;25(4):219-228. Exclude: Not intervention of interest.

222. Miller G, Bleier JI, Antonescu C, et al. Natural killer cell depletion confounds the antitumor mechanism of endogenous IL-12 overexpression. *International Journal of Cancer*. 2004;110(3):395-402. Exclude: Date.
223. Millino C, Maretto I, Pacchioni B, et al. Gene and MicroRNA Expression Are Predictive of Tumor Response in Rectal Adenocarcinoma Patients Treated With Preoperative Chemoradiotherapy. *Journal of Cellular Physiology*. 2017;232(2):426-435. Exclude: Not intervention of interest.
224. Mirnezami AH, Pickard K, Zhang L, Primrose JN, Packham G. MicroRNAs: key players in carcinogenesis and novel therapeutic targets. *European Journal of Surgical Oncology*. 2009;35(4):339-347. Exclude: Not intervention of interest.
225. Mlecnik B, Bindea G, Angell HK, et al. Integrative Analyses of Colorectal Cancer Show Immunoscore Is a Stronger Predictor of Patient Survival Than Microsatellite Instability. *Immunity*. 2016;44(3):698-711. Exclude: Not intervention of interest.
226. Motoyama K, Inoue H, Takatsuno Y, et al. Over- and under-expressed microRNAs in human colorectal cancer. *International Journal of Oncology*. 2009;34(4):1069-1075. Exclude: Not intervention of interest.
227. Mullany LE, Herrick JS, Wolff RK, Stevens JR, Slattey ML. Association of cigarette smoking and microRNA expression in rectal cancer: Insight into tumor phenotype. *Cancer Epidemiology*. 2016;45:98-107. Exclude: Not intervention of interest.
228. Munoz-Bellvis L, Fontanillo C, Gonzalez-Gonzalez M, et al. Unique genetic profile of sporadic colorectal cancer liver metastasis versus primary tumors as defined by high-density single-nucleotide polymorphism arrays. *Modern Pathology*. 2012;25(4):590-601. Exclude: Not intervention of interest.
229. Nakamori M, Iwahashi M, Nakamura M, Ueda K, Zhang X, Yamaue H. Intensification of antitumor effect by T helper 1-dominant adoptive immunogene therapy for advanced orthotopic colon cancer. *Clinical Cancer Research*. 2003;9(6):2357-2365. Exclude: Not intervention of interest.
230. Nakanishi R, Kitao H, Fujinaka Y, et al. FANCI expression predicts the response to 5-fluorouracil-based chemotherapy in MLH1-proficient colorectal cancer. *Annals of Surgical Oncology*. 2012;19(11):3627-3635. Exclude: Not intervention of interest.
231. Nebiker CA, Han J, Eppenberger-Castori S, et al. GM-CSF Production by Tumor Cells Is Associated with Improved Survival in Colorectal Cancer. *Clinical Cancer Research*. 2014;20(12):3094-3106. Exclude: Not intervention of interest.
232. Negri FV, Bozzetti C, Lagrasta CA, et al. PTEN status in advanced colorectal cancer treated with cetuximab. *British Journal of Cancer*. 2010;102(1):162-164. Exclude: Not intervention of interest.
233. Nguyen MN, Choi TG, Nguyen DT, et al. CRC-113 gene expression signature for predicting prognosis in patients with colorectal cancer. *Oncotarget*. 2015;6(31):31674-31692. Exclude: Not intervention of interest.
234. Nie Y, Zhang ZR, He B, Gu Z. Investigation of PEG-PLGA-PEG nanoparticles-based multipolyplexes for IL-18 gene delivery. *Journal of Biomaterials Applications*. 2012;26(8):893-916. Exclude: Not intervention of interest.
235. Niedzwiecki D, Frankel WL, Venook AP, et al. Association Between Results of a Gene Expression Signature Assay and Recurrence-Free Interval in Patients With Stage II Colon Cancer in Cancer and Leukemia Group B 9581 (Alliance). *Journal of Clinical Oncology*. 2016;34(25):3047-3053. Exclude: Not intervention of interest.

236. Ning Y, Hanna DL, Zhang W, et al. Cytokeratin-20 and Survivin-Expressing Circulating Tumor Cells Predict Survival in Metastatic Colorectal Cancer Patients by a Combined Immunomagnetic qRT-PCR Approach. *Molecular Cancer Therapeutics*. 2015;14(10):2401-2408. Exclude: Not intervention of interest.
237. Noshio K, Yamamoto H, Taniguchi H, et al. Interplay of insulin-like growth factor-II, insulin-like growth factor-I, insulin-like growth factor-I receptor, COX-2, and matrix metalloproteinase-7, play key roles in the early stage of colorectal carcinogenesis. *Clinical Cancer Research*. 2004;10(23):7950-7957. Exclude: Date.
238. Ogino S, Noshio K, Irahara N, et al. A cohort study of cyclin D1 expression and prognosis in 602 colon cancer cases. *Clinical Cancer Research*. 2009;15(13):4431-4438. Exclude: Not intervention of interest.
239. Oh SC, Park YY, Park ES, et al. Prognostic gene expression signature associated with two molecularly distinct subtypes of colorectal cancer. *Gut*. 2012;61(9):1291-1298. Exclude: Not intervention of interest.
240. Ohta K, Yamaguchi Y, Shimizu K, Miyahara E, Toge T. Novel system for generating cytotoxic effector lymphocytes using carcinoembryonic antigen (CEA) peptide and cultured dendritic cells. *Anticancer Research*. 2002;22(5):2597-2606. Exclude: Not intervention of interest.
241. Ojima T, Iwahashi M, Nakamura M, et al. Successful cancer vaccine therapy for carcinoembryonic antigen (CEA)-expressing colon cancer using genetically modified dendritic cells that express CEA and T helper-type 1 cytokines in CEA transgenic mice. *International Journal of Cancer*. 2007;120(3):585-593. Exclude: Not intervention of interest.
242. Omolo B, Yang M, Lo FY, et al. Adaptation of a RAS pathway activation signature from FF to FFPE tissues in colorectal cancer. *BMC Medical Genomics [Electronic Resource]*. 2016;9(1):65. Exclude: No outcome of interest.
243. Onodera H, Nagayama S, Tachibana T, Fujimoto A, Imamura M. Brain metastasis from colorectal cancer. *International Journal of Colorectal Disease*. 2005;20(1):57-61. Exclude: Date.
244. Ozcan O, Kara M, Yumrutas O, Bozgeyik E, Bozgeyik I, Celik OI. MTUS1 and its targeting miRNAs in colorectal carcinoma: significant associations. *Tumour Biology*. 2016;37(5):6637-6645. Exclude: Not intervention of interest.
245. Pan PY, Gu P, Li Q, Xu D, Weber K, Chen SH. Regulation of dendritic cell function by NK cells: mechanisms underlying the synergism in the combination therapy of IL-12 and 4-1BB activation. *Journal of Immunology*. 2004;172(8):4779-4789. Exclude: Not intervention of interest.
246. Pancione M, Remo A, Zanella C, et al. The chromatin remodelling component SMARCB1/INI1 influences the metastatic behavior of colorectal cancer through a gene signature mapping to chromosome 22. *Journal of Translational Medicine*. 2013;11:297. Exclude: Not intervention of interest.
247. Pang R, Law WL, Chu AC, et al. A subpopulation of CD26+ cancer stem cells with metastatic capacity in human colorectal cancer. *Cell Stem Cell*. 2010;6(6):603-615. Exclude: Not intervention of interest.
248. Paquet ER, Cui J, Davidson D, et al. A 12-gene signature to distinguish colon cancer patients with better clinical outcome following treatment with 5-fluorouracil or FOLFIRI. *The Journal of Pathology Clinical Research*. 2015;1(3):160-172. Exclude: Not intervention of interest.
249. Parikh AR, Keating NL, Liu PH, et al. Oncologists' selection of genetic and molecular testing in the evolving landscape of stage II colorectal cancer. *Journal of oncology practice/American Society of Clinical Oncology*. 2016;12(3):e308-319, 259-360. Exclude: Publication type-commentary.
250. Park YY, Lee SS, Lim JY, et al. Comparison of prognostic genomic predictors in colorectal cancer. *PLoS ONE [Electronic Resource]*. 2013;8(4):e60778. Exclude: No outcome of interest.

251. Patai AV, Bartak BK, Peterfia B, et al. Comprehensive DNA Methylation and Mutation Analyses Reveal a Methylation Signature in Colorectal Sessile Serrated Adenomas. *Pathology Oncology Research*. 2017;23(3):589-594. Exclude: No outcome of interest.
252. Pentheroudakis G, Raptou G, Kotoula V, et al. Immune response gene expression in colorectal cancer carries distinct prognostic implications according to tissue, stage and site: a prospective retrospective translational study in the context of a hellenic cooperative oncology group randomised trial. *PLoS ONE [Electronic Resource]*. 2015;10(5):e0124612. Exclude: Not intervention of interest.
253. Pham-Nguyen KB, Yang W, Saxena R, Thung SN, Woo SL, Chen SH. Role of NK and T cells in IL-12-induced anti-tumor response against hepatic colon carcinoma. *International Journal of Cancer*. 1999;81(5):813-819. Exclude: Not intervention of interest.
254. Pommier AJ, Farren M, Patel B, et al. Leptin, BMI, and a Metabolic Gene Expression Signature Associated with Clinical Outcome to VEGF Inhibition in Colorectal Cancer. *Cell Metabolism*. 2016;23(1):77-93. Exclude: Not intervention of interest.
255. Powell AG, Ferguson J, Al-Mulla F, et al. The relationship between genetic profiling, clinicopathological factors and survival in patients undergoing surgery for node-negative colorectal cancer: 10-year follow-up. *Journal of Cancer Research & Clinical Oncology*. 2013;139(12):2013-2020. Exclude: Not intervention of interest.
256. Prochasson P, Delouis C, Brison O. Transcriptional deregulation of the keratin 18 gene in human colon carcinoma cells results from an altered acetylation mechanism. *Nucleic Acids Research*. 2002;30(15):3312-3322. Exclude: Not intervention of interest.
257. Prochasson P, Gunther M, Laithier M, Fossar N, Lavalie C, Brison O. Transcriptional mechanisms responsible for the overexpression of the keratin 18 gene in cells of a human colon carcinoma cell line. *Experimental Cell Research*. 1999;248(1):243-259. Exclude: Not intervention of interest.
258. Qiao J, Chen SH, Pham-Nguyen KB, Mandeli J, Woo SL. Construction and characterization of a recombinant adenoviral vector expressing human interleukin-12. *Cancer Gene Therapy*. 1999;6(4):373-379. Exclude: Date.
259. Qiu Y, Cai G, Zhou B, et al. A distinct metabolic signature of human colorectal cancer with prognostic potential. *Clinical Cancer Research*. 2014;20(8):2136-2146. Exclude: Not intervention of interest.
260. Rambau PF, Odida M, Wabinga H. p53 expression in colorectal carcinoma in relation to histopathological features in Ugandan patients. *African Health Sciences*. 2008;8(4):234-238. Exclude: Not intervention of interest.
261. Reimers MS, Bastiaannet E, Langley RE, et al. Expression of HLA class I antigen, aspirin use, and survival after a diagnosis of colon cancer. *JAMA Internal Medicine*. 2014;174(5):732-739. Exclude: Not intervention of interest.
262. Reimers MS, Kuppen PJ, Lee M, et al. Validation of the 12-gene colon cancer recurrence score as a predictor of recurrence risk in stage II and III rectal cancer patients. *Journal of the National Cancer Institute*. 2014;106(11). Exclude: Not intervention of interest.
263. Reimers MS, Kuppen PJK, Lee M, et al. Validation of the 12-gene colon cancer recurrence score assay as a predictor of recurrence risk in stage II and III rectal cancer patients. *European journal of cancer*. 2013;49(27). Exclude: Not intervention of interest.

264. Reimers MS, Zeestraten EC, Kuppen PJ, Liefers GJ, van de Velde CJ. Biomarkers in precision therapy in colorectal cancer. *Gastroenterology Report*. 2013;1(3):166-183. Exclude: Publication type-not systematic review.
265. Rihova B, Etrych T, Pechar M, et al. Doxorubicin bound to a HPMA copolymer carrier through hydrazone bond is effective also in a cancer cell line with a limited content of lysosomes. *Journal of Controlled Release*. 2001;74(1-3):225-232. Exclude: Date.
266. Rihova B, Jelinkova M, Strohalm J, et al. Antiproliferative effect of a lectin- and anti-Thy-1.2 antibody-targeted HPMA copolymer-bound doxorubicin on primary and metastatic human colorectal carcinoma and on human colorectal carcinoma transfected with the mouse Thy-1.2 gene. *Bioconjugate Chemistry*. 2000;11(5):664-673. Exclude: Date.
267. Rimkus C, Friederichs J, Rosenberg R, Holzmann B, Siewert JR, Janssen KP. Expression of the mitotic checkpoint gene MAD2L2 has prognostic significance in colon cancer. *International Journal of Cancer*. 2007;120(1):207-211. Exclude: Not intervention of interest.
268. Rossowska J, Pajtasz-Piasecka E, Szyda A, Krawczenko A, Zietara N, Dus D. Tumour antigen-loaded mouse dendritic cells maturing in the presence of inflammatory cytokines are potent activators of immune response in vitro but not in vivo. *Oncology Reports*. 2009;21(6):1539-1549. Exclude: Not intervention of interest.
269. Rozenberg P, Kocsis J, Saar M, Prohaszka Z, Fust G, Fishelson Z. Elevated levels of mitochondrial mortalin and cytosolic HSP70 in blood as risk factors in patients with colorectal cancer. *International Journal of Cancer*. 2013;133(2):514-518. Exclude: Not intervention of interest.
270. Rubie C, Kollmar O, Frick VO, et al. Differential CXCR receptor expression in colorectal carcinomas. *Scandinavian Journal of Immunology*. 2008;68(6):635-644. Exclude: Not intervention of interest.
271. Russo AL, Borger DR, Szymonifka J, et al. Mutational analysis and clinical correlation of metastatic colorectal cancer. *Cancer*. 2014;120(10):1482-1490. Exclude: Not intervention of interest.
272. Ruzzo A, Graziano F, Loupakakis F, et al. Pharmacogenetic profiling in patients with advanced colorectal cancer treated with first-line FOLFIRI chemotherapy. *Pharmacogenomics Journal*. 2008;8(4):278-288. Exclude: Not intervention of interest.
273. Saigusa S, Tanaka K, Toiyama Y, et al. Gene expression profiles of tumor regression grade in locally advanced rectal cancer after neoadjuvant chemoradiotherapy. *Oncology Reports*. 2012;28(3):855-861. Exclude: Not intervention of interest.
274. Saigusa S, Toiyama Y, Tanaka K, et al. Prognostic significance of glucose transporter-1 (GLUT1) gene expression in rectal cancer after preoperative chemoradiotherapy. *Surgery Today*. 2012;42(5):460-469. Exclude: Not intervention of interest.
275. Salazar R, Roepman P, Capella G, et al. Gene expression signature to improve prognosis prediction of stage II and III colorectal cancer. *Journal of Clinical Oncology*. 2011;29(1):17-24. Exclude: No outcome of interest.
276. Sanz-Pamplona R, Berenguer A, Cordero D, et al. Clinical value of prognosis gene expression signatures in colorectal cancer: a systematic review. *PLoS ONE [Electronic Resource]*. 2012;7(11):e48877. Exclude: No outcome of interest.
277. Sato N, Hayashi N, Imamura Y, et al. Usefulness of transcription-reverse transcription concerted reaction method for detecting circulating tumor cells in patients with colorectal cancer. *Annals of Surgical Oncology*. 2012;19(6):2060-2065. Exclude: Not intervention of interest.

278. Satoh Y, Esche C, Gambotto A, et al. Local administration of IL-12-transfected dendritic cells induces antitumor immune responses to colon adenocarcinoma in the liver in mice. *Journal of Experimental Therapeutics & Oncology*. 2002;2(6):337-349. Exclude: Not intervention of interest.
279. Schetter AJ, Nguyen GH, Bowman ED, et al. Association of inflammation-related and microRNA gene expression with cancer-specific mortality of colon adenocarcinoma. *Clinical Cancer Research*. 2009;15(18):5878-5887. Exclude: Not intervention of interest.
280. Schmidt M, Hellwig B, Hammad S, et al. A comprehensive analysis of human gene expression profiles identifies stromal immunoglobulin kappa C as a compatible prognostic marker in human solid tumors. *Clinical Cancer Research*. 2012;18(9):2695-2703. Exclude: Not intervention of interest.
281. Seo AN, Kwak Y, Kim DW, et al. HER2 status in colorectal cancer: its clinical significance and the relationship between HER2 gene amplification and expression. *PLoS ONE [Electronic Resource]*. 2014;9(5):e98528. Exclude: Not intervention of interest.
282. Shi M, Zhang B. Semi-supervised learning improves gene expression-based prediction of cancer recurrence. *Bioinformatics*. 2011;27(21):3017-3023. Exclude: No outcome of interest.
283. Shih W, Chetty R, Tsao MS. Expression profiling by microarrays in colorectal cancer (Review). *Oncology Reports*. 2005;13(3):517-524. Exclude: Date.
284. Shimodaira K, Nakayama J, Nakamura N, Hasebe O, Katsuyama T, Fukuda M. Carcinoma-associated expression of core 2 beta-1,6-N-acetylglucosaminyltransferase gene in human colorectal cancer: role of O-glycans in tumor progression. *Cancer Research*. 1997;57(23):5201-5206. Exclude: Date.
285. Singh T, Levine AP, Smith PJ, Smith AM, Segal AW, Barrett JC. Characterization of expression quantitative trait loci in the human colon. *Inflammatory Bowel Diseases*. 2015;21(2):251-256. Exclude: Not intervention of interest.
286. Sipos F, Germann TM, Wichmann B, et al. MMP3 and CXCL1 are potent stromal protein markers of dysplasia-carcinoma transition in sporadic colorectal cancer. *European Journal of Cancer Prevention*. 2014;23(5):336-343. Exclude: Not intervention of interest.
287. Slattery ML, Herrick JS, Mullany LE, et al. An evaluation and replication of miRNAs with disease stage and colorectal cancer-specific mortality. *International Journal of Cancer*. 2015;137(2):428-438. Exclude: Not intervention of interest.
288. Smith FM, Reynolds JV, Miller N, Stephens RB, Kennedy MJ. Pathological and molecular predictors of the response of rectal cancer to neoadjuvant radiochemotherapy. *European Journal of Surgical Oncology*. 2006;32(1):55-64. Exclude: Date.
289. Snipstad K, Fenton CG, Kjaeve J, Cui G, Anderssen E, Paulssen RH. New specific molecular targets for radio-chemotherapy of rectal cancer. *Molecular Oncology*. 2010;4(1):52-64. Exclude: Not intervention of interest.
290. Snoeren N, van Hooff SR, Adam R, et al. Exploring gene expression signatures for predicting disease free survival after resection of colorectal cancer liver metastases. *PLoS ONE [Electronic Resource]*. 2012;7(11):e49442. Exclude: No outcome of interest.
291. Son HJ, Kim JS. Therapeutic efficacy of DNA-loaded PLGA microspheres in tumor-bearing mice. *Archives of Pharmacal Research*. 2007;30(8):1047-1050. Exclude: Not intervention of interest.
292. Song N, Pogue-Geile KL, Gavin PG, et al. Clinical Outcome From Oxaliplatin Treatment in Stage II/III Colon Cancer According to Intrinsic Subtypes: Secondary Analysis of NSABP C-07/NRG Oncology Randomized Clinical Trial. *JAMA Oncology*. 2016;2(9):1162-1169. Exclude: Not intervention of interest.

293. Sugamura K, Makino M, Kaibara N. Apoptosis as a prognostic factor in colorectal carcinoma. *Surgery Today*. 1998;28(2):145-150. Exclude: Date.
294. Sun Y, Shen S, Tang H, et al. miR-429 identified by dynamic transcriptome analysis is a new candidate biomarker for colorectal cancer prognosis. *Omics a Journal of Integrative Biology*. 2014;18(1):54-64. Exclude: Not intervention of interest.
295. Sveen A, Nesbakken A, Agesen TH, et al. Anticipating the clinical use of prognostic gene expression-based tests for colon cancer stage II and III: is Godot finally arriving? *Clinical Cancer Research*. 2013;19(24):6669-6677. Exclude: Publication type-not systematic review.
296. Svoboda M, Sana J, Fabian P, et al. MicroRNA expression profile associated with response to neoadjuvant chemoradiotherapy in locally advanced rectal cancer patients. *Radiation Oncology*. 2012;7:195. Exclude: Not intervention of interest.
297. Tada H, Kishida T, Fujiwara H, et al. Reprogrammed chondrocytes engineered to produce IL-12 provide novel ex vivo immune-gene therapy for cancer. *Immunotherapy*. 2017;9(3):239-248. Exclude: Not intervention of interest.
298. Tahara K, Mimori K, Iinuma H, et al. Serum matrix-metalloproteinase-1 is a bona fide prognostic marker for colorectal cancer. *Annals of Surgical Oncology*. 2010;17(12):3362-3369. Exclude: Not intervention of interest.
299. Takahashi Y, Sawada G, Sato T, et al. Microarray analysis reveals that high mobility group A1 is involved in colorectal cancer metastasis. *Oncology Reports*. 2013;30(3):1488-1496. Exclude: Not intervention of interest.
300. Takatsuno Y, Mimori K, Yamamoto K, et al. The rs6983267 SNP is associated with MYC transcription efficiency, which promotes progression and worsens prognosis of colorectal cancer. *Annals of Surgical Oncology*. 2013;20(4):1395-1402. Exclude: Not intervention of interest.
301. Tamura T, Nishi T, Goto T, et al. Intratumoral delivery of interleukin 12 expression plasmids with in vivo electroporation is effective for colon and renal cancer. *Human Gene Therapy*. 2001;12(10):1265-1276. Exclude: Not intervention of interest.
302. Tan IB, Tan P. Genetics: an 18-gene signature (ColoPrint) for colon cancer prognosis. *Nature Reviews Clinical Oncology*. 2011;8(3):131-133. Exclude: Publication type-news story.
303. Tasaki K, Yoshida Y, Maeda T, et al. Protective immunity is induced in murine colon carcinoma cells by the expression of interleukin-12 or interleukin-18, which activate type 1 helper T cells. *Cancer Gene Therapy*. 2000;7(2):247-254. Exclude: Not intervention of interest.
304. Tavangar SM, Sharifabrizi A, Soroush AR. Her-2/neu over-expression correlates with more advanced disease in Iranian colorectal cancer patients. *Medical Science Monitor*. 2005;11(3):CR123-126. Exclude: Date.
305. Thorsen K, Sorensen KD, Brems-Eskildsen AS, et al. Alternative splicing in colon, bladder, and prostate cancer identified by exon array analysis. *Molecular & Cellular Proteomics*. 2008;7(7):1214-1224. Exclude: Not intervention of interest.
306. Tosolini M, Kirilovsky A, Mlecnik B, et al. Clinical impact of different classes of infiltrating T cytotoxic and helper cells (Th1, th2, treg, th17) in patients with colorectal cancer.[Erratum appears in Cancer Res. 2011 Jul 1;71(13):4732]. *Cancer Research*. 2011;71(4):1263-1271. Exclude: Not intervention of interest.

307. Toth K, Galamb O, Spisak S, et al. The influence of methylated septin 9 gene on RNA and protein level in colorectal cancer. *Pathology Oncology Research*. 2011;17(3):503-509. Exclude: Not intervention of interest.
308. Troncone G, Malapelle U, Cozzolino I, Palombini L. KRAS mutation analysis on cytological specimens of metastatic colo-rectal cancer. *Diagnostic Cytopathology*. 2010;38(12):869-873. Exclude: Not intervention of interest.
309. Tros De Ilarduya C, Bunuales M, Qian C, Duzgunes N. Antitumoral activity of transferrin-lipoplexes carrying the IL-12 gene in the treatment of colon cancer. *Journal of Drug Targeting*. 2006;14(8):527-535. Exclude: Not intervention of interest.
310. Tunca B, Tezcan G, Cecener G, et al. Overexpression of CK20, MAP3K8 and EIF5A correlates with poor prognosis in early-onset colorectal cancer patients. *Journal of Cancer Research & Clinical Oncology*. 2013;139(4):691-702. Exclude: Not intervention of interest.
311. Ubink I, Elias SG, Moelans CB, et al. A Novel Diagnostic Tool for Selecting Patients With Mesenchymal-Type Colon Cancer Reveals Intratumor Subtype Heterogeneity. *Journal of the National Cancer Institute*. 2017;109(8):01. Exclude: Not intervention of interest.
312. Uemura A, Takehara T, Miyagi T, et al. Natural killer cell is a major producer of interferon gamma that is critical for the IL-12-induced anti-tumor effect in mice. *Cancer Immunology, Immunotherapy*. 2010;59(3):453-463. Exclude: Not intervention of interest.
313. Uemura M, Yamamoto H, Takemasa I, et al. Jumonji domain containing 1A is a novel prognostic marker for colorectal cancer: in vivo identification from hypoxic tumor cells. *Clinical Cancer Research*. 2010;16(18):4636-4646. Exclude: Not intervention of interest.
314. Uner A, Ebinc FA, Akyurek N, Unsal D, Montes BB, Dursun A. Vascular endothelial growth factor, c-erbB-2 and c-erbB-3 expression in colorectal adenoma and adenocarcinoma. *Experimental Oncology*. 2005;27(3):225-228. Exclude: Date.
315. Uratani R, Toiyama Y, Kitajima T, et al. Diagnostic Potential of Cell-Free and Exosomal MicroRNAs in the Identification of Patients with High-Risk Colorectal Adenomas. *PLoS ONE [Electronic Resource]*. 2016;11(10):e0160722. Exclude: Not intervention of interest.
316. van der Stok EP, Smid M, Sieuwerts AM, et al. mRNA expression profiles of colorectal liver metastases as a novel biomarker for early recurrence after partial hepatectomy. *Molecular Oncology*. 2016;10(10):1542-1550. Exclude: Not intervention of interest.
317. Vargas T, Moreno-Rubio J, Herranz J, et al. ColoLipidGene: signature of lipid metabolism-related genes to predict prognosis in stage-II colon cancer patients. *Oncotarget*. 2015;6(9):7348-7363. Exclude: Not intervention of interest.
318. Varghese S, Burness M, Xu H, Beresnev T, Pingpank J, Alexander HR. Site-specific gene expression profiles and novel molecular prognostic factors in patients with lower gastrointestinal adenocarcinoma diffusely metastatic to liver or peritoneum. *Annals of Surgical Oncology*. 2007;14(12):3460-3471. Exclude: Not intervention of interest.
319. Venook AP, Niedzwiecki D, Lopatin M, et al. Biologic determinants of tumor recurrence in stage II colon cancer: validation study of the 12-gene recurrence score in cancer and leukemia group B (CALGB) 9581. *Journal of Clinical Oncology*. 2013;31(14):1775-1781. Exclude: No outcome of interest.
320. Wang L, Shen X, Wang Z, et al. A molecular signature for the prediction of recurrence in colorectal cancer. *Molecular Cancer*. 2015;14:22. Exclude: Not intervention of interest.

321. Wang L, Yu J, Xu J, Zheng C, Li X, Du J. The analysis of microRNA-34 family expression in human cancer studies comparing cancer tissues with corresponding pericarcinous tissues. *Gene*. 2015;554(1):1-8. Exclude: Not intervention of interest.
322. Wang S, Zhou J, Wang XY, et al. Down-regulated expression of SATB2 is associated with metastasis and poor prognosis in colorectal cancer. *Journal of Pathology*. 2009;219(1):114-122. Exclude: Not intervention of interest.
323. Wang X, Wang J, Ma H, Zhang J, Zhou X. Downregulation of miR-195 correlates with lymph node metastasis and poor prognosis in colorectal cancer. *Medical Oncology*. 2012;29(2):919-927. Exclude: Not intervention of interest.
324. Wang Y, Jatko T, Zhang Y, et al. Gene expression profiles and molecular markers to predict recurrence of Dukes' B colon cancer. *Journal of Clinical Oncology*. 2004;22(9):1564-1571. Exclude: Date.
325. Wang Y, Zeng TT. Clinical significance of neutrophil gelatinase-associated lipocalin (NGAL) in colorectal cancer: a meta-analysis. *Genetics & Molecular Research*. 2014;13(3):7102-7112. Exclude: Not intervention of interest.
326. Watanabe T, Kobunai T, Akiyoshi T, Matsuda K, Ishihara S, Nozawa K. Prediction of response to preoperative chemoradiotherapy in rectal cancer by using reverse transcriptase polymerase chain reaction analysis of four genes. *Diseases of the Colon & Rectum*. 2014;57(1):23-31. Exclude: Not intervention of interest.
327. Watanabe T, Kobunai T, Yamamoto Y, et al. Gene expression of vascular endothelial growth factor A, thymidylate synthase, and tissue inhibitor of metalloproteinase 3 in prediction of response to bevacizumab treatment in colorectal cancer patients. *Diseases of the Colon & Rectum*. 2011;54(8):1026-1035. Exclude: Not intervention of interest.
328. Watson NF, Ramage JM, Madjd Z, et al. Immunosurveillance is active in colorectal cancer as downregulation but not complete loss of MHC class I expression correlates with a poor prognosis. *International Journal of Cancer*. 2006;118(1):6-10. Exclude: Date.
329. Webber EM, Lin JS, Evelyn PW. Oncotype DX tumor gene expression profiling in stage II colon cancer. Application: prognostic, risk prediction. *PLoS currents*. 2010;2:02. Exclude: Publication type-not systematic review.
330. Went P, Vasei M, Bubendorf L, et al. Frequent high-level expression of the immunotherapeutic target Ep-CAM in colon, stomach, prostate and lung cancers. *British Journal of Cancer*. 2006;94(1):128-135. Exclude: Date.
331. Wielenga VJ, Heider KH, Offerhaus GJ, et al. Expression of CD44 variant proteins in human colorectal cancer is related to tumor progression. *Cancer Research*. 1993;53(20):4754-4756. Exclude: Date.
332. Wilson PM, Yang D, Azuma M, et al. Intratumoral expression profiling of genes involved in angiogenesis in colorectal cancer patients treated with chemotherapy plus the VEGFR inhibitor PTK787/ZK 222584 (vatalanib). *Pharmacogenomics Journal*. 2013;13(5):410-416. Exclude: Not intervention of interest.
333. Wong JC, Chan SK, Schaeffer DF, et al. Absence of MMP2 expression correlates with poor clinical outcomes in rectal cancer, and is distinct from MMP1-related outcomes in colon cancer. *Clinical Cancer Research*. 2011;17(12):4167-4176. Exclude: Not intervention of interest.
334. Wong NA, Malcomson RD, Jodrell DI, Groome NP, Harrison DJ, Saunders PT. ERbeta isoform expression in colorectal carcinoma: an in vivo and in vitro study of clinicopathological and molecular correlates. *Journal of Pathology*. 2005;207(1):53-60. Exclude: Date.

335. Wu D, Li Q, Song G, Lu J. Identification of disrupted pathways in ulcerative colitis-related colorectal carcinoma by systematic tracking the dysregulated modules. *Journal of BUOn*. 2016;21(2):366-374. Exclude: Not intervention of interest.
336. Wu X, Li S, Xu X, et al. The potential value of miR-1 and miR-374b as biomarkers for colorectal cancer. *International Journal of Clinical & Experimental Pathology*. 2015;8(3):2840-2851. Exclude: Not intervention of interest.
337. Wulff H, Krieger T, Kruger K, et al. Cloning and characterization of an adenoviral vector for highly efficient and doxycycline-suppressible expression of bioactive human single-chain interleukin 12 in colon cancer. *BMC Biotechnology*. 2007;7:35. Exclude: Not intervention of interest.
338. Xi Y, Formentini A, Nakajima G, Kornmann M, Ju J. Validation of biomarkers associated with 5-fluorouracil and thymidylate synthase in colorectal cancer. *Oncology Reports*. 2008;19(1):257-262. Exclude: Not intervention of interest.
339. Xia X, Yang B, Zhai X, et al. Prognostic role of microRNA-21 in colorectal cancer: a meta-analysis. *PLoS ONE [Electronic Resource]*. 2013;8(11):e80426. Exclude: Not intervention of interest.
340. Xu DP, Sauter BV, Huang TG, Meseck M, Woo SL, Chen SH. The systemic administration of Ig-4-1BB ligand in combination with IL-12 gene transfer eradicates hepatic colon carcinoma. *Gene Therapy*. 2005;12(20):1526-1533. Exclude: Not intervention of interest.
341. Xu L, Fengji L, Changning L, et al. Comparison of the Prognostic Utility of the Diverse Molecular Data among lncRNA, DNA Methylation, microRNA, and mRNA across Five Human Cancers.[Erratum appears in PLoS One. 2016;11(3):e0152631; PMID: 27010936]. *PLoS ONE [Electronic Resource]*. 2015;10(11):e0142433. Exclude: Not intervention of interest.
342. Xu L, Li M, Wang M, Yan D, Feng G, An G. The expression of microRNA-375 in plasma and tissue is matched in human colorectal cancer. *BMC Cancer*. 2014;14:714. Exclude: Not intervention of interest.
343. Xu L, Ziegelbauer J, Wang R, et al. Distinct Profiles for Mitochondrial t-RNAs and Small Nucleolar RNAs in Locally Invasive and Metastatic Colorectal Cancer. *Clinical Cancer Research*. 2016;22(3):773-784. Exclude: Not intervention of interest.
344. Xu Y, Xu Q, Yang L, et al. Identification and validation of a blood-based 18-gene expression signature in colorectal cancer. *Clinical Cancer Research*. 2013;19(11):3039-3049. Exclude: No outcome of interest.
345. Yamanaka T, Oki E, Yamazaki K, et al. 12-gene recurrence score assay stratifies the recurrence risk in stage II/III colon cancer with surgery alone: the SUNRISE study. *Journal of Clinical Oncology*. 2016;34(24):2906-2913. Exclude: No outcome of interest.
346. Yamasaki M, Takemasa I, Komori T, et al. The gene expression profile represents the molecular nature of liver metastasis in colorectal cancer. *International Journal of Oncology*. 2007;30(1):129-138. Exclude: Not intervention of interest.
347. Yao J, Li ZH, Li YX, et al. Association between the -607 C > A polymorphism in interleukin-18 gene promoter with gastrointestinal cancer risk: a meta-analysis. *Genetics & Molecular Research*. 2015;14(4):16880-16887. Exclude: Not intervention of interest.
348. Yarom N, Marginean C, Moyana T, et al. EGFR expression variance in paired colorectal cancer primary and metastatic tumors. *Cancer Biology & Therapy*. 2010;10(5):416-421. Exclude: Not intervention of interest.

349. Yasuno M, Mori T, Koike M, et al. Importance of thymidine phosphorylase expression in tumor stroma as a prognostic factor in patients with advanced colorectal carcinoma. *Oncology Reports*. 2005;13(3):405-412. Exclude: Date.
350. Yau TO, Wu CW, Dong Y, et al. microRNA-221 and microRNA-18a identification in stool as potential biomarkers for the non-invasive diagnosis of colorectal carcinoma. *British Journal of Cancer*. 2014;111(9):1765-1771. Exclude: Not intervention of interest.
351. Yoneda K, Iida H, Endo H, et al. Identification of Cystatin SN as a novel tumor marker for colorectal cancer. *International Journal of Oncology*. 2009;35(1):33-40. Exclude: Not intervention of interest.
352. Yoshida T, Kobayashi T, Itoda M, et al. Clinical omics analysis of colorectal cancer incorporating copy number aberrations and gene expression data. *Cancer Informatics [Electronic Resource]*. 2010;9:147-161. Exclude: Not intervention of interest.
353. Yothers G, O'Connell MJ, Lee M, et al. Validation of the 12-gene colon cancer recurrence score in NSABP C-07 as a predictor of recurrence in patients with stage II and III colon cancer treated with fluorouracil and leucovorin (FU/LV) and FU/LV plus oxaliplatin.[Erratum appears in J Clin Oncol. 2014 Mar 10;32(8):866]. *Journal of Clinical Oncology*. 2013;31(36):4512-4519. Exclude: No outcome of interest.
354. You YN, Rustin RB, Sullivan JD. Oncotype DX() colon cancer assay for prediction of recurrence risk in patients with stage II and III colon cancer: A review of the evidence. *Surgical Oncology*. 2015;24(2):61-66. Exclude: Publication type-not systematic review.
355. Yu J, Shannon WD, Watson MA, McLeod HL. Gene expression profiling of the irinotecan pathway in colorectal cancer. *Clinical Cancer Research*. 2005;11(5):2053-2062. Exclude: Date.
356. Yuan D, Li K, Zhu K, Yan R, Dang C. Plasma miR-183 predicts recurrence and prognosis in patients with colorectal cancer. *Cancer Biology & Therapy*. 2015;16(2):268-275. Exclude: Not intervention of interest.
357. Yun K, Merrie AE, Gunn J, Phillips LV, McCall JL. Keratin 20 is a specific marker of submicroscopic lymph node metastases in colorectal cancer: validation by K-RAS mutations. *Journal of Pathology*. 2000;191(1):21-26. Exclude: Date.
358. Zhang W, Azuma M, Lurje G, et al. Molecular predictors of combination targeted therapies (cetuximab, bevacizumab) in irinotecan-refractory colorectal cancer (BOND-2 study). *Anticancer research*. 2010;30(10):4209-4217. Exclude: Not intervention of interest.
359. Zhang Y, Zhang M, Yu F, et al. Karyopherin alpha 2 is a novel prognostic marker and a potential therapeutic target for colon cancer. *Journal of Experimental & Clinical Cancer Research*. 2015;34:145. Exclude: Not intervention of interest.
360. Zhao M, Liang F, Zhang B, Yan W, Zhang J. The impact of osteopontin on prognosis and clinicopathology of colorectal cancer patients: a systematic meta-analysis. *Scientific Reports*. 2015;5:12713. Exclude: Not intervention of interest.
361. Zheng G, Du L, Yang X, et al. Serum microRNA panel as biomarkers for early diagnosis of colorectal adenocarcinoma. *British Journal of Cancer*. 2014;111(10):1985-1992. Exclude: Not intervention of interest.
362. Zheng S, Xiao ZX, Pan YL, Han MY, Dong Q. Continuous release of interleukin 12 from microencapsulated engineered cells for colon cancer therapy. *World Journal of Gastroenterology*. 2003;9(5):951-955. Exclude: Not intervention of interest.

363. Zhu JS, Guo H, Song MQ, Chen GQ, Sun Q, Zhang Q. Gene profiles between non-invasive and invasive colon cancer using laser microdissection and polypeptide analysis. *World Journal of Gastroenterology*. 2008;14(38):5887-5892. Exclude: Not intervention of interest.
364. Zhu L, Chen H, Zhou D, et al. MicroRNA-9 up-regulation is involved in colorectal cancer metastasis via promoting cell motility. *Medical Oncology*. 2012;29(2):1037-1043. Exclude: Not intervention of interest.
365. Ziskin JL, Dunlap D, Yaylaoglu M, et al. In situ validation of an intestinal stem cell signature in colorectal cancer. *Gut*. 2013;62(7):1012-1023. Exclude: Not intervention of interest.
366. Zochbauer S, Wallner J, Haider K, Depisch D, Huber H, Pirker R. MDR1 RNA transcripts do not indicate long-term prognosis in colorectal carcinomas. *European Journal of Cancer*. 1997;33(9):1516-1518. Exclude: Date.

Multiple Myeloma

1. Abramenko IV, Belous NI, Kriachok IA, et al. [Expression of PRAME gene in multiple myeloma]. *Terapevticheskii Arkhiv*. 2004;76(7):77-81. Exclude: Date.
2. Agnelli L, Forcato M, Ferrari F, et al. The reconstruction of transcriptional networks reveals critical genes with implications for clinical outcome of multiple myeloma. *Clinical Cancer Research*. 2011;17(23):7402-7412. Exclude: Not intervention of interest.
3. Ahmad N, Haider S, Jagannathan S, Anaissie E, Driscoll JJ. MicroRNA theragnostics for the clinical management of multiple myeloma. *Leukemia*. 2014;28(4):732-738. Exclude: Not intervention of interest.
4. Ailawadhi S, Miecznikowski J, Gaile DP, et al. Bortezomib mitigates adverse prognosis conferred by Bcl-2 overexpression in patients with relapsed/refractory multiple myeloma. *Leukemia & Lymphoma*. 2012;53(6):1174-1182. Exclude: Not intervention of interest.
5. Alapat D, Coviello-Malle J, Owens R, et al. Diagnostic usefulness and prognostic impact of CD200 expression in lymphoid malignancies and plasma cell myeloma. *American Journal of Clinical Pathology*. 2012;137(1):93-100. Exclude: Not intervention of interest.
6. Anaissie Elias J, van Rhee F, Hoering A, et al. Comparing toxicities and survival outcomes with total therapy 4 (TT4) for 70-gene (R70)-defined low-risk multiple myeloma (MM) to results obtained with total therapy 3 protocols TT3a and TT3b [Abstract No. 368]. *Blood*. 2010;116(21). Exclude: Publication type-conference abstract.
7. Andersen MN, Andersen NF, Rodgaard-Hansen S, Hokland M, Abildgaard N, Moller HJ. The novel biomarker of alternative macrophage activation, soluble mannose receptor (sMR/sCD206): Implications in multiple myeloma. *Leukemia Research*. 2015;39(9):971-975. Exclude: Not intervention of interest.
8. Anderson KC, Shaughnessy JD, Jr., Barlogie B, Harousseau JL, Roodman GD. Multiple myeloma. *Hematology*. 2002:214-240. Exclude: Date.
9. Andrade VC, Vettore AL, Panepucci RA, et al. Number of expressed cancer/testis antigens identifies focal adhesion pathway genes as possible targets for multiple myeloma therapy. *Leukemia & Lymphoma*. 2010;51(8):1543-1549. Exclude: Not intervention of interest.
10. Anguiano A, Tuchman SA, Acharya C, et al. Gene expression profiles of tumor biology provide a novel approach to prognosis and may guide the selection of therapeutic targets in multiple myeloma.[Erratum appears in J Clin Oncol. 2012 Apr 20;30(12):1398]. *Journal of Clinical Oncology*. 2009;27(25):4197-4203. Exclude: Not intervention of interest.

11. Aref S, Azmy E, El-Gilany AH. Upregulation of CD200 is associated with regulatory T cell expansion and disease progression in multiple myeloma. *Hematological Oncology*. 2017;35(1):51-57. Exclude: Not intervention of interest.
12. Armellini A, Sarasquete ME, Garcia-Sanz R, et al. Low expression of ZHX2, but not RCBTB2 or RAN, is associated with poor outcome in multiple myeloma. *British Journal of Haematology*. 2008;141(2):212-215. Exclude: Not intervention of interest.
13. Bagratuni T, Wu P, Gonzalez de Castro D, et al. XBP1s levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. *Blood*. 2010;116(2):250-253. Exclude: Not intervention of interest.
14. Barille-Nion S, Barlogie B, Bataille R, et al. Advances in biology and therapy of multiple myeloma. *Hematology*. 2003:248-278. Exclude: Date.
15. Barlogie B, Mitchell A, van Rhee F, Epstein J, Morgan GJ, Crowley J. Curing myeloma at last: defining criteria and providing the evidence. *Blood*. 2014;124(20):3043-3051. Exclude: Not intervention of interest.
16. Barlogie B, Shaughnessy J, Tricot G, et al. Treatment of multiple myeloma. *Blood*. 2004;103(1):20-32. Exclude: Date.
17. Bhutani M, Landgren O, Usmani SZ. Multiple myeloma: is it time for biomarker-driven therapy? *American Society of Clinical Oncology Educational Book*. 2015:e493-503. Exclude: Publication type-commentary.
18. Bi C, Chung TH, Huang G, et al. Genome-wide pharmacologic unmasking identifies tumor suppressive microRNAs in multiple myeloma. *Oncotarget*. 2015;6(28):26508-26518. Exclude: Not intervention of interest.
19. Bogsted M, Bilgrau AE, Wardell CP, et al. Proof of the concept to use a malignant B cell line drug screen strategy for identification and weight of melphalan resistance genes in multiple myeloma. *PLoS ONE [Electronic Resource]*. 2013;8(12):e83252. Exclude: Not intervention of interest.
20. Bolonsky A, Hose D, Schreder M, et al. Insulin like growth factor binding protein 7 (IGFBP7) expression is linked to poor prognosis but may protect from bone disease in multiple myeloma. *Journal of hematology & oncology*. 2015;8:10. Exclude: Not intervention of interest.
21. Bolonsky A, Hubl W, Spada S, et al. IKAROS expression in distinct bone marrow cell populations as a candidate biomarker for outcome with lenalidomide-dexamethasone therapy in multiple myeloma. *American Journal of Hematology*. 2017;92(3):269-278. Exclude: Not intervention of interest.
22. Boyd KD, Ross FM, Walker BA, et al. Mapping of chromosome 1p deletions in myeloma identifies FAM46C at 1p12 and CDKN2C at 1p32.3 as being genes in regions associated with adverse survival. *Clinical Cancer Research*. 2011;17(24):7776-7784. Exclude: Not intervention of interest.
23. Boyd KD, Walker BA, Wardell CP, et al. High expression levels of the mammalian target of rapamycin inhibitor DEPTOR are predictive of response to thalidomide in myeloma. *Leukemia & Lymphoma*. 2010;51(11):2126-2129. Exclude: Not intervention of interest.
24. Braggio E, Albarracin Garramuno F. [Genetic tools for risk-stratification in multiple myeloma]. *Medicina*. 2013;73(4):369-375. Exclude: Not intervention of interest.
25. Bret C, Hose D, Reme T, et al. Expression of genes encoding for proteins involved in heparan sulphate and chondroitin sulphate chain synthesis and modification in normal and malignant plasma cells. *British Journal of Haematology*. 2009;145(3):350-368. Exclude: Not intervention of interest.

26. Brown CO, Schibler J, Fitzgerald MP, et al. Scavenger receptor class A member 3 (SCARA3) in disease progression and therapy resistance in multiple myeloma. *Leukemia Research*. 2013;37(8):963-969. Exclude: Not intervention of interest.
27. Broyl A, Corthals SL, Jongen JL, et al. Mechanisms of peripheral neuropathy associated with bortezomib and vincristine in patients with newly diagnosed multiple myeloma: a prospective analysis of data from the HOVON-65/GMMG-HD4 trial. *Lancet Oncology*. 2010;11(11):1057-1065. Exclude: Not intervention of interest.
28. Burington B, Barlogie B, Zhan F, Crowley J, Shaughnessy JD, Jr. Tumor cell gene expression changes following short-term in vivo exposure to single agent chemotherapeutics are related to survival in multiple myeloma. *Clinical Cancer Research*. 2008;14(15):4821-4829. Exclude: Not intervention of interest.
29. Cagnetta A, Cea M, Calimeri T, et al. Intracellular NAD⁺ depletion enhances bortezomib-induced anti-myeloma activity. *Blood*. 2013;122(7):1243-1255. Exclude: Not intervention of interest.
30. Campo S, Allegra A, D'Ascola A, et al. MiRNome expression is deregulated in the peripheral lymphoid compartment of multiple myeloma. *British Journal of Haematology*. 2014;165(6):801-813. Exclude: Not intervention of interest.
31. Carrasco DR, Tonon G, Huang Y, et al. High-resolution genomic profiles define distinct clinico-pathogenetic subgroups of multiple myeloma patients. *Cancer Cell*. 2006;9(4):313-325. Exclude: Date.
32. Chavan SS, Bauer MA, Peterson EA, Heuck CJ, Johann DJ, Jr. Towards the integration, annotation and association of historical microarray experiments with RNA-seq. *BMC Bioinformatics*. 2013;14 Suppl 14:S4. Exclude: No outcome of interest.
33. Chen T, Berno T, Zangari M. Low-risk identification in multiple myeloma using a new 14-gene model. *European Journal of Haematology*. 2012;89(1):28-36. Exclude: No outcome of interest.
34. Chng WJ, Braggio E, Mulligan G, et al. The centrosome index is a powerful prognostic marker in myeloma and identifies a cohort of patients that might benefit from aurora kinase inhibition. *Blood*. 2008;111(3):1603-1609. Exclude: Not intervention of interest.
35. Chng WJ, Chung TH, Kumar S, et al. Gene signature combinations improve prognostic stratification of multiple myeloma patients. *Leukemia*. 2016;30(5):1071-1078. Exclude: No outcome of interest.
36. Chng WJ, Fonseca R. Genomics in multiple myeloma: biology and clinical implications. *Pharmacogenomics*. 2005;6(6):563-573. Exclude: Date.
37. Chng WJ, Glebov O, Bergsagel PL, Kuehl WM. Genetic events in the pathogenesis of multiple myeloma. *Bailliere's Best Practice in Clinical Haematology*. 2007;20(4):571-596. Exclude: Not intervention of interest.
38. Chng WJ, Gualberto A, Fonseca R. IGF-1R is overexpressed in poor-prognostic subtypes of multiple myeloma. *Leukemia*. 2006;20(1):174-176. Exclude: Date.
39. Chng WJ, Huang GF, Chung TH, et al. Clinical and biological implications of MYC activation: a common difference between MGUS and newly diagnosed multiple myeloma. *Leukemia*. 2011;25(6):1026-1035. Exclude: Not intervention of interest.
40. Chng WJ, Kuehl WM, Bergsagel PL, Fonseca R. Translocation t(4;14) retains prognostic significance even in the setting of high-risk molecular signature.[Erratum appears in *Leukemia*. 2008 Feb;22(2):462]. *Leukemia*. 2008;22(2):459-461. Exclude: Not intervention of interest.
41. Chng WJ, Kumar S, Vanwier S, et al. Molecular dissection of hyperdiploid multiple myeloma by gene expression profiling. *Cancer Research*. 2007;67(7):2982-2989. Exclude: Not intervention of interest.

42. Cho SF, Chang YC, Chang CS, et al. MALAT1 long non-coding RNA is overexpressed in multiple myeloma and may serve as a marker to predict disease progression. *BMC Cancer*. 2014;14:809. Exclude: Not intervention of interest.
43. Chung TH, Mulligan G, Fonseca R, Chng WJ. A novel measure of chromosome instability can account for prognostic difference in multiple myeloma. *PLoS ONE [Electronic Resource]*. 2013;8(6):e66361. Exclude: Not intervention of interest.
44. Claudio JO, Masih-Khan E, Stewart AK. Insights from the gene expression profiling of multiple myeloma. *Current Hematology Reports*. 2004;3(1):67-73. Exclude: Date.
45. Condomines M, Hose D, Raynaud P, et al. Cancer/testis genes in multiple myeloma: expression patterns and prognosis value determined by microarray analysis. *Journal of Immunology*. 2007;178(5):3307-3315. Exclude: Not intervention of interest.
46. Cottini F, Hideshima T, Suzuki R, et al. Synthetic Lethal Approaches Exploiting DNA Damage in Aggressive Myeloma. *Cancer Discovery*. 2015;5(9):972-987. Exclude: Not intervention of interest.
47. Decaux O, Lode L, Magrangeas F, et al. Prediction of survival in multiple myeloma based on gene expression profiles reveals cell cycle and chromosomal instability signatures in high-risk patients and hyperdiploid signatures in low-risk patients: a study of the Intergroupe Francophone du Myelome. *Journal of Clinical Oncology*. 2008;26(29):4798-4805. Exclude: Not intervention of interest.
48. Dementyeva E, Kryukov F, Kubickova L, et al. Clinical implication of centrosome amplification and expression of centrosomal functional genes in multiple myeloma. *Journal of Translational Medicine*. 2013;11:77. Exclude: Not intervention of interest.
49. Dhodapkar MV, Sexton R, Waheed S, et al. Clinical, genomic, and imaging predictors of myeloma progression from asymptomatic monoclonal gammopathies (SWOG S0120). *Blood*. 2014;123(1):78-85. Exclude: No outcome of interest.
50. Dickens NJ, Walker BA, Leone PE, et al. Homozygous deletion mapping in myeloma samples identifies genes and an expression signature relevant to pathogenesis and outcome. *Clinical Cancer Research*. 2010;16(6):1856-1864. Exclude: Not intervention of interest.
51. Durie BG, Van Ness B, Ramos C, et al. Genetic polymorphisms of EPHX1, Gsk3beta, TNFSF8 and myeloma cell DKK-1 expression linked to bone disease in myeloma. *Leukemia*. 2009;23(10):1913-1919. Exclude: Not intervention of interest.
52. Duru AD, Sutlu T, Wallblom A, et al. Deletion of Chromosomal Region 8p21 Confers Resistance to Bortezomib and Is Associated with Upregulated Decoy TRAIL Receptor Expression in Patients with Multiple Myeloma. *PLoS ONE [Electronic Resource]*. 2015;10(9):e0138248. Exclude: Not intervention of interest.
53. Egan P, Drain S, Conway C, Bjourson AJ, Alexander HD. Towards Stratified Medicine in Plasma Cell Myeloma. *International Journal of Molecular Sciences*. 2016;17(10):21. Exclude: Not intervention of interest.
54. Felix RS, Colleoni GW, Caballero OL, et al. SAGE analysis highlights the importance of p53csv, ddx5, mapkapk2 and ranbp2 to multiple myeloma tumorigenesis. *Cancer Letters*. 2009;278(1):41-48. Exclude: Not intervention of interest.
55. Fernandez de Larrea C, Martin-Antonio B, Cibeira MT, et al. Impact of global and gene-specific DNA methylation pattern in relapsed multiple myeloma patients treated with bortezomib. *Leukemia Research*. 2013;37(6):641-646. Exclude: Not intervention of interest.

56. Folkman J, Rogers MS. Thalidomide for multiple myeloma. *New England Journal of Medicine*. 2006;354(22):2389-2390; author reply 2389-2390. Exclude: Date.
57. Fonseca R, Bergsagel PL, Drach J, et al. International Myeloma Working Group molecular classification of multiple myeloma: spotlight review. *Leukemia*. 2009;23(12):2210-2221. Exclude: Publication type-not systematic review.
58. Fonseca R, Monge J. Myeloma: classification and risk assessment. *Seminars in Oncology*. 2013;40(5):554-566. Exclude: Not intervention of interest.
59. Fonseca R, Monge J, Dimopoulos MA. Staging and prognostication of multiple myeloma. *Expert Review of Hematology*. 2014;7(1):21-31. Exclude: Not intervention of interest.
60. Girnius S, Munshi NC. Individualized therapy in multiple myeloma: are we there? *Seminars in Oncology*. 2013;40(5):567-576. Exclude: Not intervention of interest.
61. Giuliani N, Ferretti M, Bolzoni M, et al. Increased osteocyte death in multiple myeloma patients: role in myeloma-induced osteoclast formation. *Leukemia*. 2012;26(6):1391-1401. Exclude: Not intervention of interest.
62. Gravitz L. Diagnostics: The early bird. *Nature*. 2011;480(7377):S36-37. Exclude: Not intervention of interest.
63. Gu C, Feng L, Peng H, Yang H, Feng Z, Yang Y. MTDH is an oncogene in multiple myeloma, which is suppressed by Bortezomib treatment. *Oncotarget*. 2016;7(4):4559-4569. Exclude: Not intervention of interest.
64. Haessler J, Shaughnessy JD, Jr., Zhan F, et al. Benefit of complete response in multiple myeloma limited to high-risk subgroup identified by gene expression profiling. *Clinical Cancer Research*. 2007;13(23):7073-7079. Exclude: No outcome of interest.
65. Hanamura I, Stewart JP, Huang Y, et al. Frequent gain of chromosome band 1q21 in plasma-cell dyscrasias detected by fluorescence in situ hybridization: incidence increases from MGUS to relapsed myeloma and is related to prognosis and disease progression following tandem stem-cell transplantation. *Blood*. 2006;108(5):1724-1732. Exclude: Date.
66. Hao M, Zang M, Wendlandt E, et al. Low serum miR-19a expression as a novel poor prognostic indicator in multiple myeloma. *International Journal of Cancer*. 2015;136(8):1835-1844. Exclude: Not intervention of interest.
67. Hermansen NE, Borup R, Andersen MK, et al. Gene expression risk signatures maintain prognostic power in multiple myeloma despite microarray probe set translation. *International Journal of Laboratory Hematology*. 2016;38(3):298-307. Exclude: No outcome of interest.
68. Herold T, Mulaw MA, Jurinovic V, et al. High expression of MZB1 predicts adverse prognosis in chronic lymphocytic leukemia, follicular lymphoma and diffuse large B-cell lymphoma and is associated with a unique gene expression signature. *Leukemia & Lymphoma*. 2013;54(8):1652-1657. Exclude: Not intervention of interest.
69. Heuck CJ, Qu P, van Rhee F, et al. Five gene probes carry most of the discriminatory power of the 70-gene risk model in multiple myeloma. *Leukemia*. 2014;28(12):2410-2413. Exclude: Not intervention of interest.
70. Hose D, Reme T, Hielscher T, et al. Proliferation is a central independent prognostic factor and target for personalized and risk-adapted treatment in multiple myeloma. *Haematologica*. 2011;96(1):87-95. Exclude: Not intervention of interest.

71. Hose D, Reme T, Meissner T, et al. Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. *Blood*. 2009;113(18):4331-4340. Exclude: Not intervention of interest.
72. Hose D, Seckinger A, Jauch A, et al. The role of fluorescence in situ hybridization and gene expression profiling in myeloma risk stratification. *Srpski Arhiv Za Celokupno Lekarstvo*. 2011;139 Suppl 2:84-89. Exclude: Not intervention of interest.
73. Hu AX, Huang ZY, Zhang L, Shen J. Potential prognostic long non-coding RNA identification and their validation in predicting survival of patients with multiple myeloma. *Tumour Biology*. 2017;39(4):1010428317694563. Exclude: Not intervention of interest.
74. Huang J, Zhou Y, Thomas GS, et al. NEDD8 Inhibition Overcomes CKS1B-Induced Drug Resistance by Upregulation of p21 in Multiple Myeloma. *Clinical Cancer Research*. 2015;21(24):5532-5542. Exclude: Not intervention of interest.
75. Huang SY, Lin CW, Lin HH, et al. Expression of cereblon protein assessed by immunohistochemicalstaining in myeloma cells is associated with superior response of thalidomide- and lenalidomide-based treatment, but not bortezomib-based treatment, in patients with multiple myeloma. *Annals of Hematology*. 2014;93(8):1371-1380. Exclude: Not intervention of interest.
76. Hussain S, Bedekovics T, Chesi M, Bergsagel PL, Galardy PJ. UCHL1 is a biomarker of aggressive multiple myeloma required for disease progression. *Oncotarget*. 2015;6(38):40704-40718. Exclude: Not intervention of interest.
77. Jenner MW, Leone PE, Walker BA, et al. Gene mapping and expression analysis of 16q loss of heterozygosity identifies WWOX and CYLD as being important in determining clinical outcome in multiple myeloma. *Blood*. 2007;110(9):3291-3300. Exclude: Not intervention of interest.
78. Jethava Y, Mitchell A, Zangari M, et al. Dose-dense and less dose-intense Total Therapy 5 for gene expression profiling-defined high-risk multiple myeloma. *Blood Cancer Journal*. 2016;6(7):e453. Exclude: No outcome of interest.
79. Jethava YS, Mitchell A, Epstein J, et al. Adverse Metaphase Cytogenetics Can Be Overcome by Adding Bortezomib and Thalidomide to Fractionated Melphalan Transplants. *Clinical Cancer Research*. 2017;23(11):2665-2672. Exclude: Not intervention of interest.
80. Johnson SK, Heuck CJ, Albino AP, et al. The use of molecular-based risk stratification and pharmacogenomics for outcome prediction and personalized therapeutic management of multiple myeloma. *International Journal of Hematology*. 2011;94(4):321-333. Exclude: Publication type-not systematic review.
81. Jourdan M, Reme T, Goldschmidt H, et al. Gene expression of anti- and pro-apoptotic proteins in malignant and normal plasma cells. *British Journal of Haematology*. 2009;145(1):45-58. Exclude: Not intervention of interest.
82. Kaiser MF, Johnson DC, Wu P, et al. Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. *Blood*. 2013;122(2):219-226. Exclude: Not intervention of interest.
83. Kassambara A, Hose D, Moreaux J, et al. Identification of pluripotent and adult stem cell genes unrelated to cell cycle and associated with poor prognosis in multiple myeloma. *PLoS ONE [Electronic Resource]*. 2012;7(7):e42161. Exclude: Not intervention of interest.

84. Kassambara A, Hose D, Moreaux J, et al. Genes with a spike expression are clustered in chromosome (sub)bands and spike (sub)bands have a powerful prognostic value in patients with multiple myeloma. *Haematologica*. 2012;97(4):622-630. Exclude: Not intervention of interest.
85. Kassambara A, Schoenhals M, Moreaux J, et al. Inhibition of DEPDC1A, a bad prognostic marker in multiple myeloma, delays growth and induces mature plasma cell markers in malignant plasma cells. *PLoS ONE [Electronic Resource]*. 2013;8(4):e62752. Exclude: Not intervention of interest.
86. Keutgens A, Foguene J, Gothot A, Tassin F. Atypical plasma cells with coexpression of myeloid markers and bundles of Auer rod-like inclusions. *International Journal of Laboratory Hematology*. 2015;37(4):e85-86. Exclude: Not intervention of interest.
87. Kowalski J, Dwivedi B, Newman S, et al. Gene integrated set profile analysis: a context-based approach for inferring biological endpoints. *Nucleic Acids Research*. 2016;44(7):e69. Exclude: Not intervention of interest.
88. Kristensen IB, Christensen JH, Lyng MB, et al. Expression of osteoblast and osteoclast regulatory genes in the bone marrow microenvironment in multiple myeloma: only up-regulation of Wnt inhibitors SFRP3 and DKK1 is associated with lytic bone disease. *Leukemia & Lymphoma*. 2014;55(4):911-919. Exclude: Not intervention of interest.
89. Kryukov F, Nemec P, Dementyeva E, et al. Molecular heterogeneity and centrosome-associated genes in multiple myeloma. *Leukemia & Lymphoma*. 2013;54(9):1982-1988. Exclude: Not intervention of interest.
90. Kryukov F, Nemec P, Radova L, et al. Centrosome associated genes pattern for risk sub-stratification in multiple myeloma. *Journal of Translational Medicine*. 2016;14(1):150. Exclude: Not intervention of interest.
91. Kubiczkova L, Kryukov F, Slaby O, et al. Circulating serum microRNAs as novel diagnostic and prognostic biomarkers for multiple myeloma and monoclonal gammopathy of undetermined significance. *Haematologica*. 2014;99(3):511-518. Exclude: Not intervention of interest.
92. Kuhn DJ, Berkova Z, Jones RJ, et al. Targeting the insulin-like growth factor-1 receptor to overcome bortezomib resistance in preclinical models of multiple myeloma. *Blood*. 2012;120(16):3260-3270. Exclude: Not intervention of interest.
93. Kuiper R, Broyl A, de Knecht Y, et al. A gene expression signature for high-risk multiple myeloma.[Erratum appears in *Leukemia*. 2014 May;28(5):1178-80. doi: 10.1038/leu.2014.53.]. *Leukemia*. 2012;26(11):2406-2413. Exclude: No outcome of interest.
94. Kuiper R, van Duin M, van Vliet MH, et al. Prediction of high- and low-risk multiple myeloma based on gene expression and the International Staging System. *Blood*. 2015;126(17):1996-2004. Exclude: No outcome of interest.
95. Kumar SK, Uno H, Jacobus SJ, et al. Impact of gene expression profiling-based risk stratification in patients with myeloma receiving initial therapy with lenalidomide and dexamethasone. *Blood*. 2011;118(16):4359-4362. Exclude: No outcome of interest.
96. Li Y, Li D, Yan Z, et al. Potential relationship and clinical significance of miRNAs and Th17 cytokines in patients with multiple myeloma. *Leukemia Research*. 2014;38(9):1130-1135. Exclude: Not intervention of interest.
97. Li Y, Wang X, Zheng H, et al. Classify hyperdiploidy status of multiple myeloma patients using gene expression profiles. *PLoS ONE [Electronic Resource]*. 2013;8(3):e58809. Exclude: Not intervention of interest.

98. Liapis K, Kastritis E, Bagratouni T, et al. Early tumor-cell gene expression changes may predict the response to first-line bortezomib-based therapy in patients with newly diagnosed multiple myeloma. *Journal of BUOn*. 2015;20(5):1314-1321. Exclude: Not intervention of interest.
99. Lionetti M, Barbieri M, Todoerti K, et al. A compendium of DIS3 mutations and associated transcriptional signatures in plasma cell dyscrasias. *Oncotarget*. 2015;6(28):26129-26141. Exclude: Not intervention of interest.
100. Liu J, Gu Z, Yang Y, Wendlandt E, Xu H. A subset of CD20(+) MM patients without the t(11;14) are associated with poor prognosis and a link to aberrant expression of Wnt signaling. *Hematological Oncology*. 2014;32(4):215-217. Exclude: Not intervention of interest.
101. Liu Q, Sung AH, Chen Z, Liu J, Huang X, Deng Y. Feature selection and classification of MAQC-II breast cancer and multiple myeloma microarray gene expression data. *PLoS ONE [Electronic Resource]*. 2009;4(12):e8250. Exclude: Not intervention of interest.
102. Lopez-Corral L, Mateos MV, Corchete LA, et al. Genomic analysis of high-risk smoldering multiple myeloma. *Haematologica*. 2012;97(9):1439-1443. Exclude: Not intervention of interest.
103. Lopez-Girona A, Heintel D, Zhang LH, et al. Lenalidomide downregulates the cell survival factor, interferon regulatory factor-4, providing a potential mechanistic link for predicting response. *British Journal of Haematology*. 2011;154(3):325-336. Exclude: Not intervention of interest.
104. Maes K, De Smedt E, Kassambara A, et al. In vivo treatment with epigenetic modulating agents induces transcriptional alterations associated with prognosis and immunomodulation in multiple myeloma. *Oncotarget*. 2015;6(5):3319-3334. Exclude: Not intervention of interest.
105. Mahtouk K, Moreaux J, Hose D, et al. Growth factors in multiple myeloma: a comprehensive analysis of their expression in tumor cells and bone marrow environment using Affymetrix microarrays. *BMC Cancer*. 2010;10:198. Exclude: Not intervention of interest.
106. Manier S, Powers JT, Sacco A, et al. The LIN28B/let-7 axis is a novel therapeutic pathway in multiple myeloma. *Leukemia*. 2017;31(4):853-860. Exclude: Not intervention of interest.
107. Mansoor A, Akhter A, Pournazari P, et al. Protein Expression for Novel Prognostic Markers (Cyclins D1, D2, D3, B1, B2, ITGbeta7, FGFR3, PAX5) Correlate With Previously Reported Gene Expression Profile Patterns in Plasma Cell Myeloma. *Applied Immunohistochemistry & Molecular Morphology*. 2015;23(5):327-333. Exclude: No outcome of interest.
108. Mattioli M, Agnelli L, Fabris S, et al. Gene expression profiling of plasma cell dyscrasias reveals molecular patterns associated with distinct IGH translocations in multiple myeloma. *Oncogene*. 2005;24(15):2461-2473. Exclude: Date.
109. McDonald JE, Kessler MM, Gardner MW, et al. Assessment of Total Lesion Glycolysis by ¹⁸F FDG PET/CT Significantly Improves Prognostic Value of GEP and ISS in Myeloma. *Clinical Cancer Research*. 2017;23(8):1981-1987. Exclude: Not intervention of interest.
110. McMillin DW, Jacobs HM, Delmore JE, et al. Molecular and cellular effects of NEDD8-activating enzyme inhibition in myeloma. *Molecular Cancer Therapeutics*. 2012;11(4):942-951. Exclude: Not intervention of interest.
111. Mehta J. Total therapy 2 in treatment of multiple myeloma: questions about gene expression profiling and treatment-related mortality. *Journal of Clinical Oncology*. 2011;29(5):e124; author reply e125-126. Exclude: Not intervention of interest.

112. Meisner T, Seckinger A, Hemminki K, et al. Profound impact of sample processing delay on gene expression of multiple myeloma plasma cells. *BMC Medical Genomics [Electronic Resource]*. 2015;8:85. Exclude: No outcome of interest.
113. Meissner T, Seckinger A, Reme T, et al. Gene expression profiling in multiple myeloma--reporting of entities, risk, and targets in clinical routine. *Clinical Cancer Research*. 2011;17(23):7240-7247. Exclude: Not intervention of interest.
114. Misra RR, Pinsky PF, Srivastava S. Prognostic factors for hematologic cancers. *Hematology - Oncology Clinics of North America*. 2000;14(4):907-924, ix-x. Exclude: Date.
115. Mitsiades CS, Ocio EM, Pandiella A, et al. Aplidin, a marine organism-derived compound with potent antitumor activity in vitro and in vivo. *Cancer Research*. 2008;68(13):5216-5225. Exclude: Not intervention of interest.
116. Moehler TM, Seckinger A, Hose D, et al. The glycome of normal and malignant plasma cells. *PLoS ONE [Electronic Resource]*. 2013;8(12):e83719. Exclude: Not intervention of interest.
117. Moreaux J, Cremer FW, Reme T, et al. The level of TACI gene expression in myeloma cells is associated with a signature of microenvironment dependence versus a plasmablastic signature. *Blood*. 2005;106(3):1021-1030. Exclude: Date.
118. Moreaux J, Hose D, Bonnefond A, et al. MYEOV is a prognostic factor in multiple myeloma. *Experimental Hematology*. 2010;38(12):1189-1198.e1183. Exclude: Not intervention of interest.
119. Moreaux J, Hose D, Reme T, et al. CD200 is a new prognostic factor in multiple myeloma.[Erratum appears in Blood. 2007 Apr 1;109(7):2717]. *Blood*. 2006;108(13):4194-4197. Exclude: Date.
120. Moreaux J, Klein B, Bataille R, et al. A high-risk signature for patients with multiple myeloma established from the molecular classification of human myeloma cell lines. *Haematologica*. 2011;96(4):574-582. Exclude: Not intervention of interest.
121. Moreaux J, Reme T, Leonard W, et al. Development of gene expression-based score to predict sensitivity of multiple myeloma cells to DNA methylation inhibitors. *Molecular Cancer Therapeutics*. 2012;11(12):2685-2692. Exclude: Not intervention of interest.
122. Moreaux J, Reme T, Leonard W, et al. Gene expression-based prediction of myeloma cell sensitivity to histone deacetylase inhibitors. *British Journal of Cancer*. 2013;109(3):676-685. Exclude: Not intervention of interest.
123. Mulligan G, Mitsiades C, Bryant B, et al. Gene expression profiling and correlation with outcome in clinical trials of the proteasome inhibitor bortezomib. *Blood*. 2007;109(8):3177-3188. Exclude: Not intervention of interest.
124. Munshi NC, Anderson KC, Bergsagel PL, et al. Consensus recommendations for risk stratification in multiple myeloma: report of the International Myeloma Workshop Consensus Panel 2. *Blood*. 2011;117(18):4696-4700. Exclude: Not intervention of interest.
125. Nair B, Shaughnessy JD, Jr., Zhou Y, et al. Gene expression profiling of plasma cells at myeloma relapse from tandem transplantation trial Total Therapy 2 predicts subsequent survival. *Blood*. 2009;113(26):6572-6575. Exclude: Not intervention of interest.
126. Nair B, van Rhee F, Shaughnessy JD, Jr., et al. Superior results of Total Therapy 3 (2003-33) in gene expression profiling-defined low-risk multiple myeloma confirmed in subsequent trial 2006-66 with VRD maintenance. *Blood*. 2010;115(21):4168-4173. Exclude: No outcome of interest.

127. Neri P, Kumar S, Fulciniti MT, et al. Neutralizing B-cell activating factor antibody improves survival and inhibits osteoclastogenesis in a severe combined immunodeficient human multiple myeloma model. *Clinical Cancer Research*. 2007;13(19):5903-5909. Exclude: Not intervention of interest.
128. Noll JE, Vandyke K, Hewett DR, et al. PTTG1 expression is associated with hyperproliferative disease and poor prognosis in multiple myeloma. *Journal of hematology & oncology*. 2015;8:106. Exclude: Not intervention of interest.
129. Paiva B, Corchete LA, Vidriales MB, et al. Phenotypic and genomic analysis of multiple myeloma minimal residual disease tumor cells: a new model to understand chemoresistance. *Blood*. 2016;127(15):1896-1906. Exclude: Not intervention of interest.
130. Paiva B, Puig N, Cedena MT, et al. Differentiation stage of myeloma plasma cells: biological and clinical significance. *Leukemia*. 2017;31(2):382-392. Exclude: Not intervention of interest.
131. Panero J, Stanganelli C, Arbelbide J, et al. Expression profile of shelterin components in plasma cell disorders. Clinical significance of POT1 overexpression. *Blood Cells Molecules & Diseases*. 2014;52(2-3):134-139. Exclude: Not intervention of interest.
132. Papanikolaou X, Alapat D, Rosenthal A, et al. The flow cytometry-defined light chain cytoplasmic immunoglobulin index and an associated 12-gene expression signature are independent prognostic factors in multiple myeloma. *Leukemia*. 2015;29(8):1713-1720. Exclude: Not intervention of interest.
133. Parker H, Cheung KL, Robinson HM, Harrison CJ, Strefford JC. Cytogenetic and genomic characterization of cell line ARH77. *Cancer Genetics & Cytogenetics*. 2008;181(1):40-45. Exclude: Not intervention of interest.
134. Pineda-Roman M, Zangari M, Haessler J, et al. Sustained complete remissions in multiple myeloma linked to bortezomib in total therapy 3: comparison with total therapy 2. *British Journal of Haematology*. 2008;140(6):625-634. Exclude: Not intervention of interest.
135. Prasad HK, Zhan F, Shaughnessy J. Smoldering multiple myeloma. *New England Journal of Medicine*. 2007;357(10):1048; author reply 1049-1050. Exclude: Not intervention of interest.
136. Qi CF, Zhou JX, Lee CH, et al. Anaplastic, plasmablastic, and plasmacytic plasmacytomas of mice: relationships to human plasma cell neoplasms and late-stage differentiation of normal B cells. *Cancer Research*. 2007;67(6):2439-2447. Exclude: Not intervention of interest.
137. Qu P, Barlogie B, Crowley J. Using a latent class model to refine risk stratification in multiple myeloma. *Statistics in Medicine*. 2015;34(21):2971-2980. Exclude: No outcome of interest.
138. Rajpal R, Dowling P, Meiller J, et al. A novel panel of protein biomarkers for predicting response to thalidomide-based therapy in newly diagnosed multiple myeloma patients. *Proteomics*. 2011;11(8):1391-1402. Exclude: Not intervention of interest.
139. Reme T, Hose D, Theillet C, Klein B. Modeling risk stratification in human cancer. *Bioinformatics*. 2013;29(9):1149-1157. Exclude: Not intervention of interest.
140. Richardson PG. Towards a better understanding of treatment-related peripheral neuropathy in multiple myeloma. *Lancet Oncology*. 2010;11(11):1014-1016. Exclude: Not intervention of interest.
141. Riz I, Hawley TS, Hawley RG. KLF4-SQSTM1/p62-associated prosurvival autophagy contributes to carfilzomib resistance in multiple myeloma models. *Oncotarget*. 2015;6(17):14814-14831. Exclude: Not intervention of interest.

142. Robillard N, Wulleme S, Lode L, Magrangeas F, Minvielle S, Avet-Loiseau H. CD33 is expressed on plasma cells of a significant number of myeloma patients, and may represent a therapeutic target. *Leukemia*. 2005;19(11):2021-2022. Exclude: Date.
143. Roccaro AM, Sacco A, Thompson B, et al. MicroRNAs 15a and 16 regulate tumor proliferation in multiple myeloma. *Blood*. 2009;113(26):6669-6680. Exclude: Not intervention of interest.
144. Roy M, Liang L, Xiao X, et al. Lycorine Downregulates HMGB1 to Inhibit Autophagy and Enhances Bortezomib Activity in Multiple Myeloma. *Theranostics*. 2016;6(12):2209-2224. Exclude: Not intervention of interest.
145. Saini N, Mahindra A. Therapeutic strategies for the treatment of multiple myeloma. *Discovery Medicine*. 2013;15(83):251-258. Exclude: Not intervention of interest.
146. San-Miguel J, Mateos MV, Gutierrez NC. Risk stratification in the era of novel therapies. *Cancer Journal*. 2009;15(6):457-464. Exclude: Not intervention of interest.
147. Sarasquete ME, Martinez-Lopez J, Chillon MC, et al. Evaluating gene expression profiling by quantitative polymerase chain reaction to develop a clinically feasible test for outcome prediction in multiple myeloma. *British Journal of Haematology*. 2013;163(2):223-234. Exclude: Not intervention of interest.
148. Sawyer JR. The prognostic significance of cytogenetics and molecular profiling in multiple myeloma. *Cancer Genetics*. 2011;204(1):3-12. Exclude: Not intervention of interest.
149. Seckinger A, Meisner T, Moreaux J, et al. miRNAs in multiple myeloma--a survival relevant complex regulator of gene expression. *Oncotarget*. 2015;6(36):39165-39183. Exclude: Not intervention of interest.
150. Seckinger A, Meissner T, Moreaux J, et al. Bone morphogenic protein 6: a member of a novel class of prognostic factors expressed by normal and malignant plasma cells inhibiting proliferation and angiogenesis. *Oncogene*. 2009;28(44):3866-3879. Exclude: Not intervention of interest.
151. Sehgal K, Das R, Zhang L, et al. Clinical and pharmacodynamic analysis of pomalidomide dosing strategies in myeloma: impact of immune activation and cereblon targets. *Blood*. 2015;125(26):4042-4051. Exclude: Not intervention of interest.
152. Shaughnessy J, Jr. Primer on medical genomics. Part IX: scientific and clinical applications of DNA microarrays--multiple myeloma as a disease model. *Mayo Clinic Proceedings*. 2003;78(9):1098-1109. Exclude: Date.
153. Shaughnessy J. Amplification and overexpression of CKS1B at chromosome band 1q21 is associated with reduced levels of p27Kip1 and an aggressive clinical course in multiple myeloma. *Hematology*. 2005;10 Suppl 1:117-126. Exclude: Date.
154. Shaughnessy J, Jr., Zhan F, Barlogie B, Stewart AK. Gene expression profiling and multiple myeloma. *Bailliere's Best Practice in Clinical Haematology*. 2005;18(4):537-552. Exclude: Date.
155. Shaughnessy JD, Jr., Haessler J, van Rhee F, et al. Testing standard and genetic parameters in 220 patients with multiple myeloma with complete data sets: superiority of molecular genetics. *British Journal of Haematology*. 2007;137(6):530-536. Exclude: No outcome of interest.
156. Shaughnessy JD, Jr., Qu P, Usmani S, et al. Pharmacogenomics of bortezomib test-dosing identifies hyperexpression of proteasome genes, especially PSMD4, as novel high-risk feature in myeloma treated with Total Therapy 3. *Blood*. 2011;118(13):3512-3524. Exclude: Not intervention of interest.

157. Shaughnessy JD, Jr., Zhan F, Burington BE, et al. A validated gene expression model of high-risk multiple myeloma is defined by deregulated expression of genes mapping to chromosome 1. *Blood*. 2007;109(6):2276-2284. Exclude: No outcome of interest.
158. Sherborne AL, Begum DB, Price A, et al. Identifying ultra-high risk myeloma by integrated molecular genetic and gene expression profiling. *Blood Conference: 58th annual meeting of the american society of hematology, ASH*. 2016;128(22). Exclude: No outcome of interest.
159. Shi L, Campbell G, Jones WD, et al. The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. *Nature Biotechnology*. 2010;28(8):827-838. Exclude: Not intervention of interest.
160. Shiratori S, Kondo T, Kubota K, et al. [Loss of CD20 expression following rituximab-combined chemotherapy in CD20-positive and CyclinD1-positive multiple myeloma]. *Rinsho Ketsueki - Japanese Journal of Clinical Hematology*. 2008;49(11):1536-1540. Exclude: Not intervention of interest.
161. Sirohi B, Powles R. Multiple myeloma. *Lancet*. 2004;363(9412):875-887. Exclude: Date.
162. Sive JI, Ambrose JC, Yong KL, et al. RNA sequencing of newly diagnosed multiple myeloma to identify a predictive signature for proteasome inhibitor-based therapy. *Blood Conference: 58th annual meeting of the american society of hematology, ASH*. 2016;128(22). Exclude: Not intervention of interest.
163. Smith D, Yong K. Advances in understanding prognosis in myeloma. *British Journal of Haematology*. 2016;175(3):367-380. Exclude: Publication type-not systematic review.
164. Stella F, Pedrazzini E, Baialardo E, Fantl DB, Schutz N, Slavutsky I. Quantitative analysis of CKS1B mRNA expression and copy number gain in patients with plasma cell disorders. *Blood Cells Molecules & Diseases*. 2014;53(3):110-117. Exclude: Not intervention of interest.
165. Stephens OW, Zhang Q, Qu P, et al. An intermediate-risk multiple myeloma subgroup is defined by sIL-6r: levels synergistically increase with incidence of SNP rs2228145 and 1q21 amplification. *Blood*. 2012;119(2):503-512. Exclude: No outcome of interest.
166. Stewart AK, Fonseca R. Prognostic and therapeutic significance of myeloma genetics and gene expression profiling. *Journal of Clinical Oncology*. 2005;23(26):6339-6344. Exclude: Date.
167. Sukhdeo K, Mani M, Zhang Y, et al. Targeting the beta-catenin/TCF transcriptional complex in the treatment of multiple myeloma. *Proceedings of the National Academy of Sciences of the United States of America*. 2007;104(18):7516-7521. Exclude: Not intervention of interest.
168. Terragna C, Remondini D, Martello M, et al. The genetic and genomic background of multiple myeloma patients achieving complete response after induction therapy with bortezomib, thalidomide and dexamethasone (VTD). *Oncotarget*. 2016;7(9):9666-9679. Exclude: Not intervention of interest.
169. Terragna C, Renzulli M, Remondini D, et al. Correlation between eight-gene expression profiling and response to therapy of newly diagnosed multiple myeloma patients treated with thalidomide-dexamethasone incorporated into double autologous transplantation. *Annals of Hematology*. 2013;92(9):1271-1280. Exclude: Not intervention of interest.
170. Tian Z, Zhao JJ, Tai YT, et al. Investigational agent MLN9708/2238 targets tumor-suppressor miR33b in MM cells. *Blood*. 2012;120(19):3958-3967. Exclude: Not intervention of interest.
171. Tillinghast GW. Microarrays in the clinic. *Nature Biotechnology*. 2010;28(8):810-812. Exclude: Not intervention of interest.

172. Todoerti K, Agnelli L, Fabris S, et al. Transcriptional characterization of a prospective series of primary plasma cell leukemia revealed signatures associated with tumor progression and poorer outcome. *Clinical Cancer Research*. 2013;19(12):3247-3258. Exclude: Not intervention of interest.
173. Tricot G. Prognostic factors in multiple myeloma. *Clinical Advances in Hematology & Oncology*. 2005;3(3):167-168. Exclude: Date.
174. Usmani SZ, Heuck C, Mitchell A, et al. Extramedullary disease portends poor prognosis in multiple myeloma and is over-represented in high-risk disease even in the era of novel agents. *Haematologica*. 2012;97(11):1761-1767. Exclude: Not intervention of interest.
175. Usmani SZ, Hoering A, Sexton R, et al. SWOG 1211: A randomized phase I/II study of optimal induction therapy for newly diagnosed high-risk multiple myeloma (HRMM). *Journal of clinical oncology*. 2014;32(15 SUPPL. 1):CONFERENCE START: 2014 May 2030 CONFERENCE END: 2014 Jun 2013. Exclude: Not intervention of interest.
176. Usmani SZ, Mitchell A, Waheed S, et al. Prognostic implications of serial 18-fluoro-deoxyglucose emission tomography in multiple myeloma treated with total therapy 3. *Blood*. 2013;121(10):1819-1823. Exclude: Not intervention of interest.
177. Usmani SZ, Nair B, Qu P, et al. Primary plasma cell leukemia: clinical and laboratory presentation, gene-expression profiling and clinical outcome with Total Therapy protocols. *Leukemia*. 2012;26(11):2398-2405. Exclude: Not intervention of interest.
178. Usmani SZ, Rodriguez-Otero P, Bhutani M, Mateos MV, Miguel JS. Defining and treating high-risk multiple myeloma. *Leukemia*. 2015;29(11):2119-2125. Exclude: Publication type-not systematic review.
179. Usmani SZ, Rosenthal A, Sexton R, et al. Secondary myelodysplasia-associated metaphase cytogenetic abnormalities in newly diagnosed multiple myeloma treated on total therapies 2 & 3- influence of cumulative dosing of maintenance drugs. *Blood*. 2012;120(21):324. Exclude: Not intervention of interest.
180. van Beers EH, van Vliet MH, Kuiper R, et al. Prognostic Validation of SKY92 and Its Combination With ISS in an Independent Cohort of Patients With Multiple Myeloma. *Clinical Lymphoma, Myeloma & Leukemia*. 2017;17(9):555-562. Exclude: No outcome of interest.
181. van de Donk NW, Sonneveld P. Diagnosis and risk stratification in multiple myeloma. *Hematology - Oncology Clinics of North America*. 2014;28(5):791-813. Exclude: Not intervention of interest.
182. van Laar R, Flinchum R, Brown N, et al. Translating a gene expression signature for multiple myeloma prognosis into a robust high-throughput assay for clinical use. *BMC Medical Genomics [Electronic Resource]*. 2014;7:25. Exclude: No outcome of interest.
183. van Rhee F, Szmania SM, Zhan F, et al. NY-ESO-1 is highly expressed in poor-prognosis multiple myeloma and induces spontaneous humoral and cellular immune responses. *Blood*. 2005;105(10):3939-3944. Exclude: Date.
184. Vangsted AJ, Helm-Petersen S, Cowland JB, et al. Drug response prediction in high-risk multiple myeloma. *Gene*. 2017. Exclude: Not intervention of interest.
185. Viziteu E, Grandmougin C, Goldschmidt H, et al. Chetomin, targeting HIF-1 α /p300 complex, exhibits antitumour activity in multiple myeloma. *British Journal of Cancer*. 2016;114(5):519-523. Exclude: Not intervention of interest.

186. Wagner V, Hose D, Seckinger A, et al. Preclinical efficacy of sepantronium bromide (YM155) in multiple myeloma is conferred by down regulation of Mcl-1. *Oncotarget*. 2014;5(21):10237-10250. Exclude: Not intervention of interest.
187. Waheed S, Mitchell A, Usmani S, et al. Standard and novel imaging methods for multiple myeloma: correlates with prognostic laboratory variables including gene expression profiling data. *Haematologica*. 2013;98(1):71-78. Exclude: Not intervention of interest.
188. Waheed S, Shaughnessy JD, van Rhee F, et al. International staging system and metaphase cytogenetic abnormalities in the era of gene expression profiling data in multiple myeloma treated with total therapy 2 and 3 protocols.[Erratum appears in *Cancer*. 2011 Jul 1;117(13):3060]. *Cancer*. 2011;117(5):1001-1009. Exclude: Not intervention of interest.
189. Walker BA, Wardell CP, Murison A, et al. APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. *Nature communications*. 2015;6:6997. Exclude: Not intervention of interest.
190. Wang S, Tricot G, Shi L, et al. RARalpha2 expression is associated with disease progression and plays a crucial role in efficacy of ATRA treatment in myeloma. *Blood*. 2009;114(3):600-607. Exclude: Not intervention of interest.
191. Weinhold N, Ashby C, Rasche L, et al. Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. *Blood*. 2016;128(13):1735-1744. Exclude: Not intervention of interest.
192. Weinhold N, Heuck CJ, Rosenthal A, et al. Clinical value of molecular subtyping multiple myeloma using gene expression profiling. *Leukemia*. 2016;30(2):423-430. Exclude: No outcome of interest.
193. Wester R, Van Der Holt B, Asselbergs E, et al. Phase 2 study of carfilzomib, thalidomide, and low-dose dexamethasone as induction/consolidation in newly diagnosed, transplant eligible patients with multiple myeloma, the carthadex trial. *Blood Conference: 58th annual meeting of the american society of hematology, ASH*. 2016;128(22). Exclude: Not intervention of interest.
194. Wu P, Agnelli L, Walker BA, et al. Improved risk stratification in myeloma using a microRNA-based classifier. *British Journal of Haematology*. 2013;162(3):348-359. Exclude: Not intervention of interest.
195. Xiao R, Cerny J, Devitt K, et al. MYC protein expression is detected in plasma cell myeloma but not in monoclonal gammopathy of undetermined significance (MGUS). *American Journal of Surgical Pathology*. 2014;38(6):776-783. Exclude: Not intervention of interest.
196. Yaccoby S, Pennisi A, Li X, et al. Atacicept (TACI-Ig) inhibits growth of TACI(high) primary myeloma cells in SCID-hu mice and in coculture with osteoclasts. *Leukemia*. 2008;22(2):406-413. Exclude: Not intervention of interest.
197. Yaccoby S, Qu P, Mehdi S, et al. Signatures of mesenchymal cell lineages and microenvironment factors are dysregulated in high risk myeloma. *Blood Conference: 58th annual meeting of the american society of hematology, ASH*. 2016;128(22). Exclude: Not intervention of interest.
198. Yang Y, Gu C, Luo C, Li F, Wang M. BUB1B promotes multiple myeloma cell proliferation through CDC20/CCNB axis. *Medical Oncology*. 2015;32(3):81. Exclude: Not intervention of interest.
199. Yang Y, Shi J, Tolomelli G, et al. RARalpha2 expression confers myeloma stem cell features. *Blood*. 2013;122(8):1437-1447. Exclude: Not intervention of interest.

200. Yee AJ, Hari P, Marcheselli R, et al. Outcomes in patients with relapsed or refractory multiple myeloma in a phase I study of everolimus in combination with lenalidomide. *British Journal of Haematology*. 2014;166(3):401-409. Exclude: Not intervention of interest.
201. Zent CS, Zhan F, Schichman SA, et al. The distinct gene expression profiles of chronic lymphocytic leukemia and multiple myeloma suggest different anti-apoptotic mechanisms but predict only some differences in phenotype. *Leukemia Research*. 2003;27(9):765-774. Exclude: Date.
202. Zhan F, Barlogie B, Arzoumanian V, et al. Gene-expression signature of benign monoclonal gammopathy evident in multiple myeloma is linked to good prognosis. *Blood*. 2007;109(4):1692-1700. Exclude: Not intervention of interest.
203. Zhan F, Barlogie B, Shaughnessy J, Jr. Toward the identification of distinct molecular and clinical entities of multiple myeloma using global gene expression profiling. *Seminars in Hematology*. 2003;40(4):308-320. Exclude: Date.
204. Zhan F, Hardin J, Kordsmeier B, et al. Global gene expression profiling of multiple myeloma, monoclonal gammopathy of undetermined significance, and normal bone marrow plasma cells. *Blood*. 2002;99(5):1745-1757. Exclude: Date.
205. Zhan F, Huang Y, Colla S, et al. The molecular classification of multiple myeloma. *Blood*. 2006;108(6):2020-2028. Exclude: Date.
206. Zhang J, Xiao X, Liu J. The role of circulating miRNAs in multiple myeloma. *Science China Life sciences*. 2015;58(12):1262-1269. Exclude: Not intervention of interest.
207. Zhang XD, Baladandayuthapani V, Lin H, et al. Tight Junction Protein 1 Modulates Proteasome Capacity and Proteasome Inhibitor Sensitivity in Multiple Myeloma via EGFR/JAK1/STAT3 Signaling. *Cancer Cell*. 2016;29(5):639-652. Exclude: Not intervention of interest.
208. Zhao A, Kong F, Liu CJ, et al. Tumor Cell-Derived Microvesicles Induced Not Epithelial-Mesenchymal Transition but Apoptosis in Human Proximal Tubular (HK-2) Cells: Implications for Renal Impairment in Multiple Myeloma. *International Journal of Molecular Sciences*. 2017;18(3):27. Exclude: Not intervention of interest.
209. Zhao C, Shi L, Tong W, et al. Maximum predictive power of the microarray-based models for clinical outcomes is limited by correlation between endpoint and gene expression profile. *BMC Genomics*. 2011;12 Suppl 5:S3. Exclude: Not intervention of interest.
210. Zhou M, Zhao H, Wang Z, et al. Identification and validation of potential prognostic lncRNA biomarkers for predicting survival in patients with multiple myeloma. *Journal of Experimental & Clinical Cancer Research*. 2015;34:102. Exclude: No outcome of interest.
211. Zhou W, Yang Y, Xia J, et al. NEK2 induces drug resistance mainly through activation of efflux drug pumps and is associated with poor prognosis in myeloma and other cancers. *Cancer Cell*. 2013;23(1):48-62. Exclude: Not intervention of interest.
212. Zhou Y, Barlogie B, Shaughnessy JD, Jr. The molecular characterization and clinical management of multiple myeloma in the post-genome era. *Leukemia*. 2009;23(11):1941-1956. Exclude: Publication type-not systematic review.
213. Zhou Y, Chen L, Barlogie B, et al. High-risk myeloma is associated with global elevation of miRNAs and overexpression of EIF2C2/AGO2. *Proceedings of the National Academy of Sciences of the United States of America*. 2010;107(17):7904-7909. Exclude: Not intervention of interest.

214. Zhou Y, Nair B, Shaughnessy JD, Jr., et al. Cytogenetic abnormalities in multiple myeloma: poor prognosis linked to concomitant detection in random and focal lesion bone marrow samples and associated with high-risk gene expression profile. *British Journal of Haematology*. 2009;145(5):637-641.

Exclude: Not intervention of interest.

215. Zhou Y, Zhang Q, Stephens O, et al. Prediction of cytogenetic abnormalities with gene expression profiles. *Blood*. 2012;119(21):e148-150. Exclude: Not intervention of interest.