



BRECT collaborative publications 2010-present

Original research publications (319)

2020

1. Eriksson, M., Czene, K., Strand, F., Zackrisson, S., Lindholm, P., et al., 2020. Identification of Women at High Risk of Breast Cancer Who Need Supplemental Screening. *Radiology* 201620. <https://doi.org/10.1148/radiol.2020201620>
2. Ugalde-Morales, E., Grassmann, F., Humphreys, K., Li, J., Eriksson, M., et al., 2020. Association between breast cancer risk and disease aggressiveness: Characterizing underlying gene expression patterns. *Int. J. Cancer*. <https://doi.org/10.1002/ijc.33270>
3. Gabrielson, M., Azam, S., Hardell, E., Holm, M., Ubhayasekera, K.A., et al., 2020a. Hormonal determinants of mammographic density and density change. *Breast Cancer Res.* 22, 95. <https://doi.org/10.1186/s13058-020-01332-4>
4. Yang, H., Holowko, N., Grassmann, F., Eriksson, M., Hall, P., et al., 2020. Hyperthyroidism is associated with breast cancer risk and mammographic and genetic risk predictors. *BMC Med* 18, 225. <https://doi.org/10.1186/s12916-020-01690-y>
5. Rainey, L., Eriksson, M., Trinh, T., Czene, K., Broeders, M.J.M., et al., 2020. The impact of alcohol consumption and physical activity on breast cancer: The role of breast cancer risk. *Int. J. Cancer* 147, 931–939. <https://doi.org/10.1002/ijc.32846>
6. Edman Kessler, L., Wiklander, O., Hamberg, E., Bergh, J., Foukakis, T., et al., 2020a. Efficacy and safety of cyclin dependent kinases 4/6 inhibitors in the treatment of metastatic breast cancer: a real-world experience. *Acta Oncol* 1–6. <https://doi.org/10.1080/0284186X.2020.1804613>
7. Lundberg, A., Lindström, L.S., Parker, J.S., Löverli, E., Perou, C.M., et al., 2020. A pan-cancer analysis of the frequency of DNA alterations across cell cycle activity levels. *Oncogene* 39, 5430–5440. <https://doi.org/10.1038/s41388-020-1367-4>
8. Thorén, L., Lindh, J.D., Ackehed, G., Kringen, M.K., Hall, P., et al., 2020. Impairment of endoxifen formation in tamoxifen-treated premenopausal breast cancer patients carrying reduced-function CYP2D6 alleles. *Br J Clin Pharmacol*. <https://doi.org/10.1111/bcp.14500>
9. Kho, P.-F., Amant, F., Annibaldi, D., Ashton, K., Attia, J., et al., 2020. Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. *Int. J. Cancer*. <https://doi.org/10.1002/ijc.33206>
10. Tamborero, D., Dienstmann, R., Rachid, M.H., Boekel, J., Baird, R., et al., 2020. Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. *Nat. Med.* 26, 992–994. <https://doi.org/10.1038/s41591-020-0969-2>
11. Feng, H., Gusev, A., Pasaniuc, B., Wu, L., Long, J., et al., 2020. Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genet. Epidemiol.* 44, 442–468. <https://doi.org/10.1002/gepi.22288>



12. Liu, J., Prager-van der Smissen, W.J.C., Collée, J.M., Bolla, M.K., Wang, Q., et al., 2020. Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Sci Rep* 10, 9688. <https://doi.org/10.1038/s41598-020-65665-y>
13. Giardiello, D., Hauptmann, M., Steyerberg, E.W., Adank, M.A., Akdeniz, D., et al., 2020. Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. *Breast Cancer Res. Treat.* 181, 423–434. <https://doi.org/10.1007/s10549-020-05611-8>
14. Edman Kessler, L., Sigfridsson, J., Hatzidaki, D., Bergh, J., Foukakis, T., et al., 2020b. Chemotherapy use near the end-of-life in patients with metastatic breast cancer. *Breast Cancer Res. Treat.* 181, 645–651. <https://doi.org/10.1007/s10549-020-05663-w>
15. Kapoor, P.M., Mavaddat, N., Choudhury, P.P., Wilcox, A.N., Lindström, S., et al., 2020. Combined associations of a polygenic risk score and classical risk factors with breast cancer risk. *J. Natl. Cancer Inst.* <https://doi.org/10.1093/jnci/djaa056>
16. Brandberg, Y., Johansson, H., Hellström, M., Gnant, M., Möbus, V., et al., 2020. Long-term (up to 16 months) health-related quality of life after adjuvant tailored dose-dense chemotherapy vs. standard three-weekly chemotherapy in women with high-risk early breast cancer. *Breast Cancer Res. Treat.* 181, 87–96. <https://doi.org/10.1007/s10549-020-05602-9>
17. Holowko, N., Eriksson, M., Kuja-Halkola, R., Azam, S., He, W., et al., 2020. Heritability of Mammographic Breast Density, Density Change, Microcalcifications, and Masses. *Cancer Res.* 80, 1590–1600. <https://doi.org/10.1158/0008-5472.CAN-19-2455>
18. Papakonstantinou, A., Matikas, A., Bengtsson, N.O., Malmström, P., Hedayati, E., et al., 2020a. Efficacy and safety of tailored and dose-dense adjuvant chemotherapy and trastuzumab for resected HER2-positive breast cancer: Results from the phase 3 PANTHER trial. *Cancer* 126, 1175–1182. <https://doi.org/10.1002/cncr.32653>
19. Neo, S.Y., Yang, Y., Record, J., Ma, R., Chen, X., et al., 2020. CD73 immune checkpoint defines regulatory NK cells within the tumor microenvironment. *J. Clin. Invest.* 130, 1185–1198. <https://doi.org/10.1172/JCI128895>
20. Papakonstantinou, A., Hedayati, E., Hellström, M., Johansson, H., Gnant, M., et al., 2020b. Neutropenic complications in the PANTHER phase III study of adjuvant tailored dose-dense chemotherapy in early breast cancer. *Acta Oncol* 59, 75–81. <https://doi.org/10.1080/0284186X.2019.1670353>
21. Zhang, H., Ahearn, T.U., Lecarpentier, J., Barnes, D., Beesley, J., et al., 2020. Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nat. Genet.* 52, 572–581. <https://doi.org/10.1038/s41588-020-0609-2>
22. Zerdes, I., Sifakis, E.G., Matikas, A., Chrétien, S., Tobin, N.P., et al., 2020. Programmed death-ligand 1 gene expression is a prognostic marker in early breast cancer and provides additional prognostic value to 21-gene and 70-gene signatures in estrogen receptor-positive disease. *Mol Oncol* 14, 951–963. <https://doi.org/10.1002/1878-0261.12654>



23. Azam, S., Eriksson, M., Sjölander, A., Hellgren, R., Gabrielson, M., et al., 2020. Mammographic Density Change and Risk of Breast Cancer. *J. Natl. Cancer Inst.* 112, 391–399. <https://doi.org/10.1093/jnci/djz149>
24. Gabrielson, M., Ubhayasekera, K.A., Acharya, S.R., Franko, M.A., Eriksson, M., et al., 2020b. Inclusion of Endogenous Plasma Dehydroepiandrosterone Sulfate and Mammographic Density in Risk Prediction Models for Breast Cancer. *Cancer Epidemiol. Biomarkers Prev.* 29, 574–581. <https://doi.org/10.1158/1055-9965.EPI-19-1120>
25. Schmid, P., Cortes, J., Pusztai, L., McArthur, H., Kümmel, S., et al., 2020. Pembrolizumab for Early Triple-Negative Breast Cancer. *N. Engl. J. Med.* 382, 810–821. <https://doi.org/10.1056/NEJMoa1910549>
26. Mega, A., Hartmark Nilsen, M., Leiss, L.W., Tobin, N.P., Miletic, H., et al., 2020. Astrocytes enhance glioblastoma growth. *Glia* 68, 316–327. <https://doi.org/10.1002/glia.23718>
27. He, W., Grassmann, F., Eriksson, M., Eliasson, E., Margolin, S., et al., 2020. CYP2D6 Genotype Predicts Tamoxifen Discontinuation and Prognosis in Patients With Breast Cancer. *J. Clin. Oncol.* 38, 548–557. <https://doi.org/10.1200/JCO.19.01535>
28. Fachal, L., Aschard, H., Beesley, J., Barnes, D.R., Allen, J., et al., 2020. Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nat. Genet.* 52, 56–73. <https://doi.org/10.1038/s41588-019-0537-1>
29. Escala-Garcia, M., Abraham, J., Andrulis, I.L., Anton-Culver, H., Arndt, V., et al., 2020. A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nat Commun* 11, 312. <https://doi.org/10.1038/s41467-019-14100-6>

2019

30. Hellgren, R.J., Sundbom, A.E., Czene, K., Izhaky, D., Hall, P., et al., 2019. Does three-dimensional functional infrared imaging improve breast cancer detection based on digital mammography in women with dense breasts? *Eur Radiol* 29, 6227–6235. <https://doi.org/10.1007/s00330-019-06248-y>
31. Zerdes, I., Wallerius, M., Sifakis, E.G., Wallmann, T., Betts, S., et al., 2019. STAT3 Activity Promotes Programmed-Death Ligand 1 Expression and Suppresses Immune Responses in Breast Cancer. *Cancers (Basel)* 11. <https://doi.org/10.3390/cancers11101479>
32. Svedlund, J., Strell, C., Qian, X., Zilkens, K.J.C., Tobin, N.P., et al., 2019. Generation of in situ sequencing based OncoMaps to spatially resolve gene expression profiles of diagnostic and prognostic markers in breast cancer. *EBioMedicine* 48, 212–223. <https://doi.org/10.1016/j.ebiom.2019.09.009>
33. Yu, N.Y., Iftimi, A., Yau, C., Tobin, N.P., van 't Veer, L., et al., 2019. Assessment of Long-term Distant Recurrence-Free Survival Associated With Tamoxifen Therapy in Postmenopausal Patients With Luminal A or Luminal B Breast Cancer. *JAMA Oncol.* <https://doi.org/10.1001/jamaoncol.2019.1856>



34. Sjöberg, E., Meyrath, M., Milde, L., Herrera, M., Lövrot, J., et al., 2019. A Novel ACKR2-Dependent Role of Fibroblast-Derived CXCL14 in Epithelial-to-Mesenchymal Transition and Metastasis of Breast Cancer. *Clin. Cancer Res.* 25, 3702–3717. <https://doi.org/10.1158/1078-0432.CCR-18-1294>
35. Tsagozis, P., Augsten, M., Zhang, Y., Li, T., Hesla, A., et al., 2019. An immunosuppressive macrophage profile attenuates the prognostic impact of CD20-positive B cells in human soft tissue sarcoma. *Cancer Immunol. Immunother.* 68, 927–936. <https://doi.org/10.1007/s00262-019-02322-y>
36. Chrétien, S., Zerdes, I., Bergh, J., Matikas, A., Foukakis, T., 2019. Beyond PD-1/PD-L1 Inhibition: What the Future Holds for Breast Cancer Immunotherapy. *Cancers (Basel)* 11. <https://doi.org/10.3390/cancers11050628>
37. Early Breast Cancer Trialists' Collaborative Group (EBCTCG), 2019. Increasing the dose intensity of chemotherapy by more frequent administration or sequential scheduling: a patient-level meta-analysis of 37 298 women with early breast cancer in 26 randomised trials. *Lancet* 393, 1440–1452. [https://doi.org/10.1016/S0140-6736\(18\)33137-4](https://doi.org/10.1016/S0140-6736(18)33137-4)
38. Alsheh Ali, M., Eriksson, M., Czene, K., Hall, P., Humphreys, K., 2019a. Detection of potential microcalcification clusters using multivendor for-presentation digital mammograms for short-term breast cancer risk estimation. *Med Phys* 46, 1938–1946. <https://doi.org/10.1002/mp.13450>
39. Azam, S., Sjölander, A., Eriksson, M., Gabrielson, M., Czene, K., et al., 2019. Determinants of Mammographic Density Change. *JNCI Cancer Spectr* 3, pkz004. <https://doi.org/10.1093/jncics/pkz004>
40. Langebäck, A., Bacanu, S., Laursen, H., Mout, L., Seki, T., et al., 2019. CETSA-based target engagement of taxanes as biomarkers for efficacy and resistance. *Sci Rep* 9, 19384. <https://doi.org/10.1038/s41598-019-55526-8>
41. Giardiello, D., Steyerberg, E.W., Hauptmann, M., Adank, M.A., Akdeniz, D., et al., 2019. Prediction and clinical utility of a contralateral breast cancer risk model. *Breast Cancer Res.* 21, 144. <https://doi.org/10.1186/s13058-019-1221-1>
42. Grassmann, F., He, W., Eriksson, M., Gabrielson, M., Hall, P., et al., 2019. Interval breast cancer is associated with other types of tumors. *Nat Commun* 10, 4648. <https://doi.org/10.1038/s41467-019-12652-1>
43. Alsheh Ali, M., Czene, K., Hall, P., Humphreys, K., 2019b. Association of Microcalcification Clusters with Short-term Invasive Breast Cancer Risk and Breast Cancer Risk Factors. *Sci Rep* 9, 14604. <https://doi.org/10.1038/s41598-019-51186-w>
44. Strell, C., Paulsson, J., Jin, S.-B., Tobin, N.P., Mezheyeuski, A., et al., 2019. Impact of Epithelial-Stromal Interactions on Peritumoral Fibroblasts in Ductal Carcinoma in Situ. *J. Natl. Cancer Inst.* 111, 983–995. <https://doi.org/10.1093/jnci/djy234>
45. Matikas, Alexios, Zerdes, I., Lövrot, J., Richard, F., Sotiriou, C., et al., 2019. Prognostic Implications of PD-L1 Expression in Breast Cancer: Systematic Review and Meta-analysis of Immunohistochemistry and Pooled Analysis of Transcriptomic Data. *Clin. Cancer Res.* 25, 5717–5726. <https://doi.org/10.1158/1078-0432.CCR-19-1131>



46. Yang, H., Pawitan, Y., He, W., Eriksson, L., Holowko, N., et al., 2019. Disease trajectories and mortality among women diagnosed with breast cancer. *Breast Cancer Res.* 21, 95. <https://doi.org/10.1186/s13058-019-1181-5>
47. Sandri, B.J., Masvidal, L., Murie, C., Bartish, M., Avdulov, S., et al., 2019. Distinct Cancer-Promoting Stromal Gene Expression Depending on Lung Function. *Am. J. Respir. Crit. Care Med.* 200, 348–358. <https://doi.org/10.1164/rccm.201801-0080OC>
48. Dörk, T., Peterlongo, P., Mannermaa, A., Bolla, M.K., Wang, Q., et al., 2019. Two truncating variants in FANCC and breast cancer risk. *Sci Rep* 9, 12524. <https://doi.org/10.1038/s41598-019-48804-y>
49. Costa, T.D.F., Zhuang, T., Lorent, J., Turco, E., Olofsson, H., et al., 2019. PAK4 suppresses RELB to prevent senescence-like growth arrest in breast cancer. *Nat Commun* 10, 3589. <https://doi.org/10.1038/s41467-019-11510-4>
50. Matikas, A., Foukakis, T., Swain, S., Bergh, J., 2019a. Avoiding over- and undertreatment in patients with resected node-positive breast cancer with the use of gene expression signatures: are we there yet? *Ann. Oncol.* 30, 1044–1050. <https://doi.org/10.1093/annonc/mdz126>
51. Shu, X., Wu, L., Khankari, N.K., Shu, X.-O., Wang, T.J., et al., 2019. Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *Int J Epidemiol* 48, 795–806. <https://doi.org/10.1093/ije/dyy201>
52. Ooi, B.N.S., Loh, H., Ho, P.J., Milne, R.L., Giles, G., et al., 2019. The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. *Int J Epidemiol* 48, 781–794. <https://doi.org/10.1093/ije/dyz124>
53. Vachon, C.M., Scott, C.G., Tamimi, R.M., Thompson, D.J., Fasching, P.A., et al., 2019. Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. *Breast Cancer Res.* 21, 68. <https://doi.org/10.1186/s13058-019-1138-8>
54. Prakash, V., Carson, B.B., Feenstra, J.M., Dass, R.A., Sekyrova, P., et al., 2019. Ribosome biogenesis during cell cycle arrest fuels EMT in development and disease. *Nat Commun* 10, 2110. <https://doi.org/10.1038/s41467-019-10100-8>
55. Matikas, A., Foukakis, T., Bergh, J., 2019b. Minimally invasive tissue access as a tool for delivering personalized medicine - with focus on oncology. *J. Intern. Med.* 285, 395–397. <https://doi.org/10.1111/joim.12860>
56. Ferreira, M.A., Gamazon, E.R., Al-Ejeh, F., Aittomäki, K., Andrulis, I.L., et al., 2019. Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nat Commun* 10, 1741. <https://doi.org/10.1038/s41467-018-08053-5>
57. Li, J., Wen, W.X., Eklund, M., Kvist, A., Eriksson, M., et al., 2019. Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. *Int. J. Cancer* 144, 1195–1204. <https://doi.org/10.1002/ijc.31841>



58. Ho, P.J., Tan, C.S., Shawon, S.R., Eriksson, M., Lim, L.Y., et al., 2019. Comparison of self-reported and register-based hospital medical data on comorbidities in women. *Sci Rep* 9, 3527. <https://doi.org/10.1038/s41598-019-40072-0>
59. Escala-Garcia, M., Guo, Q., Dörk, T., Canisius, S., Keeman, R., et al., 2019. Genome-wide association study of germline variants and breast cancer-specific mortality. *Br. J. Cancer* 120, 647–657. <https://doi.org/10.1038/s41416-019-0393-x>
60. Alzubi, M.A., Turner, T.H., Olex, A.L., Sohal, S.S., Tobin, N.P., et al., 2019. Separation of breast cancer and organ microenvironment transcriptomes in metastases. *Breast Cancer Res.* 21, 36. <https://doi.org/10.1186/s13058-019-1123-2>
61. Lundberg, A., Lindström, L.S., Li, J., Harrell, J.C., Darai-Ramqvist, E., et al., 2019. The long-term prognostic and predictive capacity of cyclin D1 gene amplification in 2305 breast tumours. *Breast Cancer Res.* 21, 34. <https://doi.org/10.1186/s13058-019-1121-4>
62. Strand, F., Azavedo, E., Hellgren, R., Humphreys, K., Eriksson, M., et al., 2019. Localized mammographic density is associated with interval cancer and large breast cancer: a nested case-control study. *Breast Cancer Res.* 21, 8. <https://doi.org/10.1186/s13058-019-1099-y>
63. Mavaddat, N., Michailidou, K., Dennis, J., Lush, M., Fachal, L., et al., 2019. Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *Am. J. Hum. Genet.* 104, 21–34. <https://doi.org/10.1016/j.ajhg.2018.11.002>
64. Matikas, A., Foukakis, T., Moebus, V., Greil, R., Bengtsson, N.-O., et al., 2019c. Dose tailoring of adjuvant chemotherapy for breast cancer based on hematologic toxicities: further results from the prospective PANTHER study with focus on obese patients. *Ann. Oncol.* 30, 109–114. <https://doi.org/10.1093/annonc/mdy475>
65. Jiang, X., Finucane, H.K., Schumacher, F.R., Schmit, S.L., Tyrer, J.P., et al., 2019. Shared heritability and functional enrichment across six solid cancers. *Nat Commun* 10, 431. <https://doi.org/10.1038/s41467-018-08054-4>
66. He, W., Eriksson, L., Törnberg, S., Strand, F., Hall, P., et al., 2019. Discontinuation of adjuvant hormone therapy among breast cancer patients not previously attending mammography screening. *BMC Med* 17, 24. <https://doi.org/10.1186/s12916-019-1252-6>
67. Figlioli, G., Bogliolo, M., Catucci, I., Caleca, L., Lasheras, S.V., et al., 2019. The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *NPJ Breast Cancer* 5, 38. <https://doi.org/10.1038/s41523-019-0127-5>

2018

68. Falato, C., Taylor, S.K., Szulkin, R., Nordblom, A., Eriksson, L., et al., 2018. Prognosis in patients diagnosed with loco-regional failure of breast cancer: 34 years longitudinal data from the Stockholm-Gotland cancer registry. *Breast Cancer Res. Treat.* 172, 703–712. <https://doi.org/10.1007/s10549-018-4936-2>



69. Wallmann, T., Zhang, X.-M., Wallerius, M., Bolin, S., Joly, A.-L., et al., 2018. Microglia Induce PDGFRB Expression in Glioma Cells to Enhance Their Migratory Capacity. *iScience* 9, 71–83. <https://doi.org/10.1016/j.isci.2018.10.011>
70. Gabrielson, M., Ubhayasekera, K., Ek, B., Andersson Franko, M., Eriksson, M., et al., 2018a. Inclusion of Plasma Prolactin Levels in Current Risk Prediction Models of Premenopausal and Postmenopausal Breast Cancer. *JNCI Cancer Spectr* 2, pky055. <https://doi.org/10.1093/jncics/pky055>
71. Eriksson, L., He, W., Eriksson, M., Humphreys, K., Bergh, J., et al., 2018a. Adjuvant Therapy and Mammographic Density Changes in Women With Breast Cancer. *JNCI Cancer Spectr* 2, pky071. <https://doi.org/10.1093/jncics/pky071>
72. Robertson, S., Stålhammar, G., Darai-Ramqvist, E., Rantalainen, M., Tobin, N.P., et al., 2018. Prognostic value of Ki67 analysed by cytology or histology in primary breast cancer. *J. Clin. Pathol.* 71, 787–794. <https://doi.org/10.1136/jclinpath-2017-204976>
73. Gabrielson, M., Chiesa, F., Behmer, C., Rönnow, K., Czene, K., et al., 2018b. Association of reproductive history with breast tissue characteristics and receptor status in the normal breast. *Breast Cancer Res. Treat.* 170, 487–497. <https://doi.org/10.1007/s10549-018-4768-0>
74. Li, J., Humphreys, K., Ho, P.J., Eriksson, M., Darai-Ramqvist, E., et al., 2018a. Family History, Reproductive, and Lifestyle Risk Factors for Fibroadenoma and Breast Cancer. *JNCI Cancer Spectr* 2, pky051. <https://doi.org/10.1093/jncics/pky051>
75. Eriksson, M., Li, J., Leifland, K., Czene, K., Hall, P., 2018. A comprehensive tool for measuring mammographic density changes over time. *Breast Cancer Res. Treat.* 169, 371–379. <https://doi.org/10.1007/s10549-018-4690-5>
76. Stålhammar, G., Robertson, S., Wedlund, L., Lippert, M., Rantalainen, M., et al., 2018. Digital image analysis of Ki67 in hot spots is superior to both manual Ki67 and mitotic counts in breast cancer. *Histopathology* 72, 974–989. <https://doi.org/10.1111/his.13452>
77. Matikas, A., Margolin, S., Hellström, M., Johansson, H., Bengtsson, N.-O., et al., 2018a. Long-term safety and survival outcomes from the Scandinavian Breast Group 2004-1 randomized phase II trial of tailored dose-dense adjuvant chemotherapy for early breast cancer. *Breast Cancer Res. Treat.* 168, 349–355. <https://doi.org/10.1007/s10549-017-4599-4>
78. Mutvei, A.P., Landor, S.K.-J., Fox, R., Braune, E.-B., Tsoi, Y.L., et al., 2018. Notch signaling promotes a HIF2 α -driven hypoxic response in multiple tumor cell types. *Oncogene* 37, 6083–6095. <https://doi.org/10.1038/s41388-018-0400-3>
79. Matikas, A., Foukakis, T., Bergh, J., 2018b. RE: Receptor Conversion in Distant Breast Cancer Metastases: A Systematic Review and Meta-analysis. *J. Natl. Cancer Inst.* 110, 1280–1281. <https://doi.org/10.1093/jnci/djy046>
80. Li, J., Ugalde-Morales, E., Wen, W.X., Decker, B., Eriksson, M., et al., 2018b. Differential Burden of Rare and Common Variants on Tumor Characteristics, Survival, and Mode of Detection in Breast Cancer. *Cancer Res.* 78, 6329–6338. <https://doi.org/10.1158/0008-5472.CAN-18-1018>



81. Adam, H., Docherty Skogh, A.C., Edsander Nord, Å., Schultz, I., Gahm, J., et al., 2018. Risk of recurrence and death in patients with breast cancer after delayed deep inferior epigastric perforator flap reconstruction. *Br J Surg* 105, 1435–1445. <https://doi.org/10.1002/bjs.10866>
82. Eriksson, L., Bergh, J., Humphreys, K., Wärnberg, F., Törnberg, S., et al., 2018b. Time from breast cancer diagnosis to therapeutic surgery and breast cancer prognosis: A population-based cohort study. *Int. J. Cancer* 143, 1093–1104. <https://doi.org/10.1002/ijc.31411>
83. Zerdes, I., Matikas, A., Bergh, J., Rassidakis, G.Z., Foukakis, T., 2018. Genetic, transcriptional and post-translational regulation of the programmed death protein ligand 1 in cancer: biology and clinical correlations. *Oncogene* 37, 4639–4661. <https://doi.org/10.1038/s41388-018-0303-3>
84. O'Mara, T.A., Glubb, D.M., Amant, F., Annibaldi, D., Ashton, K., et al., 2018. Identification of nine new susceptibility loci for endometrial cancer. *Nat Commun* 9, 3166. <https://doi.org/10.1038/s41467-018-05427-7>
85. Borgquist, S., Rosendahl, A.H., Czene, K., Bhoo-Pathy, N., Dorkhan, M., et al., 2018. Long-term exposure to insulin and volumetric mammographic density: observational and genetic associations in the Karma study. *Breast Cancer Res.* 20, 93. <https://doi.org/10.1186/s13058-018-1026-7>
86. Wu, L., Shi, W., Long, J., Guo, X., Michailidou, K., et al., 2018. A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nat. Genet.* 50, 968–978. <https://doi.org/10.1038/s41588-018-0132-x>
87. Sjöström, M., Staaf, J., Edén, P., Wärnberg, F., Bergh, J., et al., 2018. Identification and validation of single-sample breast cancer radiosensitivity gene expression predictors. *Breast Cancer Res.* 20, 64. <https://doi.org/10.1186/s13058-018-0978-y>
88. Lindström, L.S., Yau, C., Czene, K., Thompson, C.K., Hoadley, K.A., et al., 2018. Intratumor Heterogeneity of the Estrogen Receptor and the Long-term Risk of Fatal Breast Cancer. *J. Natl. Cancer Inst.* 110, 726–733. <https://doi.org/10.1093/jnci/djx270>
89. Delcoigne, B., Hagenbuch, N., Schelin, M.E., Salim, A., Lindström, L.S., et al., 2018. Feasibility of reusing time-matched controls in an overlapping cohort. *Stat Methods Med Res* 27, 1818–1829. <https://doi.org/10.1177/0962280216669744>
90. Painter, J.N., O'Mara, T.A., Morris, A.P., Cheng, T.H.T., Gorman, M., et al., 2018. Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Med* 7, 1978–1987. <https://doi.org/10.1002/cam4.1445>
91. Kim, C., Gao, R., Sei, E., Brandt, R., Hartman, J., et al., 2018. Chemoresistance Evolution in Triple-Negative Breast Cancer Delineated by Single-Cell Sequencing. *Cell* 173, 879–893.e13. <https://doi.org/10.1016/j.cell.2018.03.041>
92. Colombo, M., Lòpez-Perolio, I., Meeks, H.D., Caleca, L., Parsons, M.T., et al., 2018. The BRCA2 c.68-7T > A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Hum. Mutat.* 39, 729–741. <https://doi.org/10.1002/humu.23411>



93. Ullah, I., Karthik, G.-M., Alkodsí, A., Kjällquist, U., Stålhammar, G., et al., 2018. Evolutionary history of metastatic breast cancer reveals minimal seeding from axillary lymph nodes. *J. Clin. Invest.* 128, 1355–1370. <https://doi.org/10.1172/JCI96149>
94. Strand, F., Humphreys, K., Holm, J., Eriksson, M., Törnberg, S., et al., 2018. Long-term prognostic implications of risk factors associated with tumor size: a case study of women regularly attending screening. *Breast Cancer Res.* 20, 31. <https://doi.org/10.1186/s13058-018-0962-6>
95. Rudolph, A., Song, M., Brook, M.N., Milne, R.L., Mavaddat, N., et al., 2018. Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. *Int J Epidemiol* 47, 526–536. <https://doi.org/10.1093/ije/dyx242>
96. Ghousaini, M., Edwards, S.L., Michailidou, K., Nord, S., Cowper-Sal Lari, R., et al., 2018. Publisher Correction: Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nat Commun* 9, 16193. <https://doi.org/10.1038/ncomms16193>
97. Brand, J.S., Humphreys, K., Li, J., Karlsson, R., Hall, P., et al., 2018. Common genetic variation and novel loci associated with volumetric mammographic density. *Breast Cancer Res.* 20, 30. <https://doi.org/10.1186/s13058-018-0954-6>
98. Kjällquist, U., Erlandsson, R., Tobin, N.P., Alkodsí, A., Ullah, I., et al., 2018. Exome sequencing of primary breast cancers with paired metastatic lesions reveals metastasis-enriched mutations in the A-kinase anchoring protein family (AKAPs). *BMC Cancer* 18, 174. <https://doi.org/10.1186/s12885-018-4021-6>
99. Foukakis, T., Lövrot, J., Matikas, A., Zerdes, I., Lorent, J., et al., 2018. Immune gene expression and response to chemotherapy in advanced breast cancer. *Br. J. Cancer* 118, 480–488. <https://doi.org/10.1038/bjc.2017.446>
100. Byström, S., Eklund, M., Hong, M.-G., Fredolini, C., Eriksson, M., et al., 2018. Affinity proteomic profiling of plasma for proteins associated to area-based mammographic breast density. *Breast Cancer Res.* 20, 14. <https://doi.org/10.1186/s13058-018-0940-z>
101. Yang, H., He, W., Eriksson, M., Li, J., Holowko, N., et al., 2018. Inherited factors contribute to an inverse association between preeclampsia and breast cancer. *Breast Cancer Res.* 20, 6. <https://doi.org/10.1186/s13058-017-0930-6>
102. Tanaka, N., Kanatani, S., Tomer, R., Sahlgren, C., Kronqvist, P., et al., 2018. Publisher Correction: Whole-tissue biopsy phenotyping of three-dimensional tumours reveals patterns of cancer heterogeneity. *Nat Biomed Eng* 2, 48. <https://doi.org/10.1038/s41551-017-0162-1>
103. Matikas, A., Lövrot, J., Ramberg, A., Eriksson, M., Lindsten, T., et al., 2018c. Dynamic evaluation of the immune infiltrate and immune function genes as predictive markers for neoadjuvant chemotherapy in hormone receptor positive, HER2 negative breast cancer. *Oncoimmunology* 7, e1466017. <https://doi.org/10.1080/2162402X.2018.1466017>



2017

104. Lundberg, A., Lindström, L.S., Harrell, J.C., Falato, C., Carlson, J.W., et al., 2017. Gene Expression Signatures and Immunohistochemical Subtypes Add Prognostic Value to Each Other in Breast Cancer Cohorts. *Clin. Cancer Res.* 23, 7512–7520. <https://doi.org/10.1158/1078-0432.CCR-17-1535>
105. Tobin, N.P., Lundberg, A., Lindström, L.S., Harrell, J.C., Foukakis, T., et al., 2017. PAM50 Provides Prognostic Information When Applied to the Lymph Node Metastases of Advanced Breast Cancer Patients. *Clin. Cancer Res.* 23, 7225–7231. <https://doi.org/10.1158/1078-0432.CCR-17-2301>
106. Milne, R.L., Kuchenbaecker, K.B., Michailidou, K., Beesley, J., Kar, S., et al., 2017. Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nat. Genet.* 49, 1767–1778. <https://doi.org/10.1038/ng.3785>
107. Karthik, G.-M., Rantalainen, M., Stålhammar, G., Lövrot, J., Ullah, I., et al., 2017. Intra-tumor heterogeneity in breast cancer has limited impact on transcriptomic-based molecular profiling. *BMC Cancer* 17, 802. <https://doi.org/10.1186/s12885-017-3815-2>
108. Jiao, X., Aravidis, C., Marikkannu, R., Rantala, J., Picelli, S., et al., 2017. PHIP - a novel candidate breast cancer susceptibility locus on 6q14.1. *Oncotarget* 8, 102769–102782. <https://doi.org/10.18632/oncotarget.21800>
109. Brouckaert, O., Rudolph, A., Laenen, A., Keeman, R., Bolla, M.K., et al., 2017. Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Res.* 19, 119. <https://doi.org/10.1186/s13058-017-0909-3>
110. Esserman, L.J., Yau, C., Thompson, C.K., van 't Veer, L.J., Borowsky, A.D., et al., 2017. Use of Molecular Tools to Identify Patients With Indolent Breast Cancers With Ultralow Risk Over 2 Decades. *JAMA Oncol* 3, 1503–1510. <https://doi.org/10.1001/jamaoncol.2017.1261>
111. Andersson, T.M.-L., Crowther, M.J., Czene, K., Hall, P., Humphreys, K., 2017. Mammographic Density Reduction as a Prognostic Marker for Postmenopausal Breast Cancer: Results Using a Joint Longitudinal-Survival Modeling Approach. *Am. J. Epidemiol.* 186, 1065–1073. <https://doi.org/10.1093/aje/kwx178>
112. Ali, M.A., Czene, K., Eriksson, L., Hall, P., Humphreys, K., 2017. Breast Tissue Organisation and its Association with Breast Cancer Risk. *Breast Cancer Res.* 19, 103. <https://doi.org/10.1186/s13058-017-0894-6>
113. Day, F.R., Thompson, D.J., Helgason, H., Chasman, D.I., Finucane, H., et al., 2017. Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nat. Genet.* 49, 834–841. <https://doi.org/10.1038/ng.3841>
114. Li, J., Ivansson, E., Klevebring, D., Tobin, N.P., Lindström, L.S., et al., 2017a. Molecular Differences between Screen-Detected and Interval Breast Cancers Are Largely Explained by PAM50 Subtypes. *Clin. Cancer Res.* 23, 2584–2592. <https://doi.org/10.1158/1078-0432.CCR-16-0967>



115. Fagerholm, R., Khan, S., Schmidt, M.K., García-Closas, M., Heikkilä, P., et al., 2017. TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. *Oncotarget* 8, 18381–18398. <https://doi.org/10.18632/oncotarget.15110>
116. Delcoigne, B., Colzani, E., Prochazka, M., Gagliardi, G., Hall, P., et al., 2017. Breaking the matching in nested case-control data offered several advantages for risk estimation. *J Clin Epidemiol* 82, 79–86. <https://doi.org/10.1016/j.jclinepi.2016.11.014>
117. Strand, F., Humphreys, K., Eriksson, M., Li, J., Andersson, T.M.L., et al., 2017. Longitudinal fluctuation in mammographic percent density differentiates between interval and screen-detected breast cancer. *Int. J. Cancer* 140, 34–40. <https://doi.org/10.1002/ijc.30427>
118. Paulsson, J., Rydén, L., Strell, C., Frings, O., Tobin, N.P., et al., 2017. High expression of stromal PDGFR β is associated with reduced benefit of tamoxifen in breast cancer. *J Pathol Clin Res* 3, 38–43. <https://doi.org/10.1002/cjp2.56>
119. Li, J., Eriksson, M., He, W., Hall, P., Czene, K., 2017b. Associations between childhood body size and seventeen adverse outcomes: analysis of 65,057 European women. *Sci Rep* 7, 16917. <https://doi.org/10.1038/s41598-017-17258-5>
120. Guo, Q., Burgess, S., Turman, C., Bolla, M.K., Wang, Q., et al., 2017. Body mass index and breast cancer survival: a Mendelian randomization analysis. *Int J Epidemiol* 46, 1814–1822. <https://doi.org/10.1093/ije/dyx131>
121. Gabrielson, M., Eriksson, M., Hammarström, M., Borgquist, S., Leifland, K., et al., 2017. Cohort Profile: The Karolinska Mammography Project for Risk Prediction of Breast Cancer (KARMA). *Int J Epidemiol* 46, 1740–1741g. <https://doi.org/10.1093/ije/dyw357>
122. Pan, H., Gray, R., Braybrooke, J., Davies, C., Taylor, C., et al., 2017. 20-Year Risks of Breast-Cancer Recurrence after Stopping Endocrine Therapy at 5 Years. *N. Engl. J. Med.* 377, 1836–1846. <https://doi.org/10.1056/NEJMoa1701830>
123. Michailidou, K., Lindström, S., Dennis, J., Beesley, J., Hui, S., et al., 2017. Association analysis identifies 65 new breast cancer risk loci. *Nature* 551, 92–94. <https://doi.org/10.1038/nature24284>
124. Barrdahl, M., Rudolph, A., Hopper, J.L., Southey, M.C., Broeks, A., et al., 2017. Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *Int. J. Cancer* 141, 1830–1840. <https://doi.org/10.1002/ijc.30859>
125. He, W., Smedby, K.E., Fang, F., Olsson, H., Margolin, S., et al., 2017a. Treatment Restarting After Discontinuation of Adjuvant Hormone Therapy in Breast Cancer Patients. *J. Natl. Cancer Inst.* 109. <https://doi.org/10.1093/jnci/djx041>
126. Feng, Y.-C.A., Cho, K., Lindstrom, S., Kraft, P., Cormack, J., et al., 2017. Investigating the genetic relationship between Alzheimer's disease and cancer using GWAS summary statistics. *Hum. Genet.* 136, 1341–1351. <https://doi.org/10.1007/s00439-017-1831-6>



127. Yang, H., Brand, J.S., Li, J., Ludvigsson, J.F., Ugalde-Morales, E., et al., 2017a. Risk and predictors of psoriasis in patients with breast cancer: a Swedish population-based cohort study. *BMC Med* 15, 154. <https://doi.org/10.1186/s12916-017-0915-4>
128. Ugalde-Morales, E., Li, J., Humphreys, K., Ludvigsson, J.F., Yang, H., et al., 2017. Common shared genetic variation behind decreased risk of breast cancer in celiac disease. *Sci Rep* 7, 5942. <https://doi.org/10.1038/s41598-017-06287-9>
129. Holm, J., Eriksson, L., Ploner, A., Eriksson, M., Rantalainen, M., et al., 2017. Assessment of Breast Cancer Risk Factors Reveals Subtype Heterogeneity. *Cancer Res.* 77, 3708–3717. <https://doi.org/10.1158/0008-5472.CAN-16-2574>
130. Shimelis, H., Mesman, R.L.S., Von Nicolai, C., Ehlen, A., Guidugli, L., et al., 2017. BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Res.* 77, 2789–2799. <https://doi.org/10.1158/0008-5472.CAN-16-2568>
131. He, W., Sofie Lindström, L., Hall, P., Czene, K., 2017b. Cause-specific mortality in women with breast cancer in situ. *Int. J. Cancer* 140, 2414–2421. <https://doi.org/10.1002/ijc.30413>
132. Krüger, K., Wik, E., Knutsvik, G., Nalwoga, H., Klingen, T.A., et al., 2017. Expression of Nestin associates with BRCA1 mutations, a basal-like phenotype and aggressive breast cancer. *Sci Rep* 7, 1089. <https://doi.org/10.1038/s41598-017-00862-w>
133. Eriksson, M., Czene, K., Pawitan, Y., Leifland, K., Darabi, H., et al., 2017. A clinical model for identifying the short-term risk of breast cancer. *Breast Cancer Res.* 19, 29. <https://doi.org/10.1186/s13058-017-0820-y>
134. Yang, H., Brand, J.S., Fang, F., Chiesa, F., Johansson, A.L.V., et al., 2017b. Time-dependent risk of depression, anxiety, and stress-related disorders in patients with invasive and in situ breast cancer. *Int. J. Cancer* 140, 841–852. <https://doi.org/10.1002/ijc.30514>
135. Brand, J.S., Hedayati, E., Bhoo-Pathy, N., Bergh, J., Hall, P., et al., 2017. Time-dependent risk and predictors of venous thromboembolism in breast cancer patients: A population-based cohort study. *Cancer* 123, 468–475. <https://doi.org/10.1002/cncr.30364>
136. Rajaram, N., Mariapun, S., Eriksson, M., Tapia, J., Kwan, P.Y., et al., 2017. Differences in mammographic density between Asian and Caucasian populations: a comparative analysis. *Breast Cancer Res. Treat.* 161, 353–362. <https://doi.org/10.1007/s10549-016-4054-y>

2016

137. Hamdi, Y., Soucy, P., Adoue, V., Michailidou, K., Canisius, S., et al., 2016. Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. *Oncotarget* 7, 80140–80163. <https://doi.org/10.18632/oncotarget.12818>



138. Colzani, E., Clements, M., Johansson, A.L.V., Liljegren, A., He, W., et al., 2016. Risk of hospitalisation and death due to bone fractures after breast cancer: a registry-based cohort study. *Br. J. Cancer* 115, 1400–1407. <https://doi.org/10.1038/bjc.2016.314>
139. Brand, J.S., Hedayati, E., Humphreys, K., Ludvigsson, J.F., Johansson, A.L.V., et al., 2016a. Chemotherapy, Genetic Susceptibility, and Risk of Venous Thromboembolism in Breast Cancer Patients. *Clin. Cancer Res.* 22, 5249–5255. <https://doi.org/10.1158/1078-0432.CCR-16-1110>
140. Ghousaini, M., French, J.D., Michailidou, K., Nord, S., Beesley, J., et al., 2016. Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. *Am. J. Hum. Genet.* 99, 903–911. <https://doi.org/10.1016/j.ajhg.2016.07.017>
141. Shi, J., Zhang, Y., Zheng, W., Michailidou, K., Ghousaini, M., et al., 2016. Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *Int. J. Cancer* 139, 1303–1317. <https://doi.org/10.1002/ijc.30150>
142. Zhao, Z., Wen, W., Michailidou, K., Bolla, M.K., Wang, Q., et al., 2016. Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes Control* 27, 679–693. <https://doi.org/10.1007/s10552-016-0741-6>
143. Lundberg, F.E., Johansson, A.L.V., Rodriguez-Wallberg, K., Brand, J.S., Czene, K., et al., 2016. Association of infertility and fertility treatment with mammographic density in a large screening-based cohort of women: a cross-sectional study. *Breast Cancer Res.* 18, 36. <https://doi.org/10.1186/s13058-016-0693-5>
144. Stålhammar, G., Fuentes Martinez, N., Lippert, M., Tobin, N.P., Mølholm, I., et al., 2016. Digital image analysis outperforms manual biomarker assessment in breast cancer. *Mod. Pathol.* 29, 318–329. <https://doi.org/10.1038/modpathol.2016.34>
145. Falato, C., Tobin, N.P., Lorent, J., Lindström, L.S., Bergh, J., et al., 2016. Intrinsic subtypes and genomic signatures of primary breast cancer and prognosis after systemic relapse. *Mol Oncol* 10, 517–525. <https://doi.org/10.1016/j.molonc.2015.11.004>
146. Dunning, A.M., Michailidou, K., Kuchenbaecker, K.B., Thompson, D., French, J.D., et al., 2016. Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nat. Genet.* 48, 374–386. <https://doi.org/10.1038/ng.3521>
147. Petridis, C., Brook, M.N., Shah, V., Kohut, K., Gorman, P., et al., 2016. Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Res.* 18, 22. <https://doi.org/10.1186/s13058-016-0675-7>
148. Thompson, D.J., O'Mara, T.A., Glubb, D.M., Painter, J.N., Cheng, T., et al., 2016. CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocr. Relat. Cancer* 23, 77–91. <https://doi.org/10.1530/ERC-15-0386>
149. Meeks, H.D., Song, H., Michailidou, K., Bolla, M.K., Dennis, J., et al., 2016. BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *J. Natl. Cancer Inst.* 108. <https://doi.org/10.1093/jnci/djv315>



150. Holm, J., Li, J., Darabi, H., Eklund, M., Eriksson, M., et al., 2016. Associations of Breast Cancer Risk Prediction Tools With Tumor Characteristics and Metastasis. *J. Clin. Oncol.* 34, 251–258. <https://doi.org/10.1200/JCO.2015.63.0624>
151. Lei, J., Rudolph, A., Moysich, K.B., Behrens, S., Goode, E.L., et al., 2016. Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. *Hum. Genet.* 135, 137–154. <https://doi.org/10.1007/s00439-015-1616-8>
152. Southey, M.C., Goldgar, D.E., Winqvist, R., Pylkäs, K., Couch, F., et al., 2016. PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *J. Med. Genet.* 53, 800–811. <https://doi.org/10.1136/jmedgenet-2016-103839>
153. Li, Jingmei, Humphreys, K., Eriksson, M., Dar, H., Brandberg, Y., et al., 2016a. Worse quality of life in young and recently diagnosed breast cancer survivors compared with female survivors of other cancers: A cross-sectional study. *Int. J. Cancer* 139, 2415–2425. <https://doi.org/10.1002/ijc.30370>
154. Li, Jingmei, Eriksson, M., Czene, K., Hall, P., Rodriguez-Wallberg, K.A., 2016b. Common diseases as determinants of menopausal age. *Hum. Reprod.* 31, 2856–2864. <https://doi.org/10.1093/humrep/dew264>
155. Rantalainen, M., Klevebring, D., Lindberg, J., Ivansson, E., Rosin, G., et al., 2016. Sequencing-based breast cancer diagnostics as an alternative to routine biomarkers. *Sci Rep* 6, 38037. <https://doi.org/10.1038/srep38037>
156. Painter, J.N., O'Mara, T.A., Marquart, L., Webb, P.M., Attia, J., et al., 2016. Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. *Cancer Epidemiol. Biomarkers Prev.* 25, 1503–1510. <https://doi.org/10.1158/1055-9965.EPI-16-0147>
157. Liu, J., Lončar, I., Collée, J.M., Bolla, M.K., Dennis, J., et al., 2016. rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. *Sci Rep* 6, 36874. <https://doi.org/10.1038/srep36874>
158. Fredholm, H., Magnusson, K., Lindström, L.S., Garmo, H., Fält, S.E., et al., 2016. Long-term outcome in young women with breast cancer: a population-based study. *Breast Cancer Res. Treat.* 160, 131–143. <https://doi.org/10.1007/s10549-016-3983-9>
159. Strand, F., Humphreys, K., Cheddad, A., Törnberg, S., Azavedo, E., et al., 2016. Novel mammographic image features differentiate between interval and screen-detected breast cancer: a case-case study. *Breast Cancer Res.* 18, 100. <https://doi.org/10.1186/s13058-016-0761-x>
160. Sackey, H., Hui, M., Czene, K., Verkooijen, H., Edgren, G., et al., 2016. The impact of in situ breast cancer and family history on risk of subsequent breast cancer events and mortality - a population-based study from Sweden. *Breast Cancer Res.* 18, 105. <https://doi.org/10.1186/s13058-016-0764-7>
161. Muranen, T.A., Blomqvist, C., Dörk, T., Jakubowska, A., Heikkilä, P., et al., 2016. Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. *Breast Cancer Res.* 18, 98. <https://doi.org/10.1186/s13058-016-0758-5>



162. Wyszynski, A., Hong, C.-C., Lam, K., Michailidou, K., Lytle, C., et al., 2016. An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. *Hum. Mol. Genet.* 25, 3863–3876. <https://doi.org/10.1093/hmg/ddw223>
163. Lawrenson, K., Kar, S., McCue, K., Kuchenbaecker, K., Michailidou, K., et al., 2016. Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nat Commun* 7, 12675. <https://doi.org/10.1038/ncomms12675>
164. Kar, S.P., Beesley, J., Amin Al Olama, A., Michailidou, K., Tyrer, J., et al., 2016. Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. *Cancer Discov* 6, 1052–1067. <https://doi.org/10.1158/2159-8290.CD-15-1227>
165. Fehring, G., Kraft, P., Pharoah, P.D., Eeles, R.A., Chatterjee, N., et al., 2016. Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. *Cancer Res.* 76, 5103–5114. <https://doi.org/10.1158/0008-5472.CAN-15-2980>
166. Darabi, H., Beesley, J., Droit, A., Kar, S., Nord, S., et al., 2016. Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). *Sci Rep* 6, 32512. <https://doi.org/10.1038/srep32512>
167. Schmidt, M.K., Hogervorst, F., van Hien, R., Cornelissen, S., Broeks, A., et al., 2016. Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *J. Clin. Oncol.* 34, 2750–2760. <https://doi.org/10.1200/JCO.2016.66.5844>
168. Guo, Y., Warren Andersen, S., Shu, X.-O., Michailidou, K., Bolla, M.K., et al., 2016. Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. *PLoS Med.* 13, e1002105. <https://doi.org/10.1371/journal.pmed.1002105>
169. Becker, J., Haas, S.L., Mokrowiecka, A., Wasilica-Berger, J., Ateeb, Z., et al., 2016. The HLA-DQB1 insertion is a strong achalasia risk factor and displays a geospatial north-south gradient among Europeans. *Eur. J. Hum. Genet.* 24, 1228–1231. <https://doi.org/10.1038/ejhg.2015.262>
170. Gabrielson, M., Chiesa, F., Paulsson, J., Strell, C., Behmer, C., et al., 2016. Amount of stroma is associated with mammographic density and stromal expression of oestrogen receptor in normal breast tissues. *Breast Cancer Res. Treat.* 158, 253–261. <https://doi.org/10.1007/s10549-016-3877-x>
171. Zeng, C., Guo, X., Long, J., Kuchenbaecker, K.B., Droit, A., et al., 2016. Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. *Breast Cancer Res.* 18, 64. <https://doi.org/10.1186/s13058-016-0718-0>
172. Wallerius, M., Wallmann, T., Bartish, M., Östling, J., Mezheyski, A., et al., 2016. Guidance Molecule SEMA3A Restricts Tumor Growth by Differentially Regulating



- the Proliferation of Tumor-Associated Macrophages. *Cancer Res.* 76, 3166–3178. <https://doi.org/10.1158/0008-5472.CAN-15-2596>
173. Li, J., Holm, J., Bergh, J., Eriksson, M., Darabi, H., et al., 2016. Breast cancer genetic risk profile is differentially associated with interval and screen-detected breast cancers. *Ann. Oncol.* 27, 1181. <https://doi.org/10.1093/annonc/mdw096>
174. de la Hoya, M., Soukarieh, O., López-Perolio, I., Vega, A., Walker, L.C., et al., 2016. Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. *Hum. Mol. Genet.* 25, 2256–2268. <https://doi.org/10.1093/hmg/ddw094>
175. Cheng, T.H., Thompson, D.J., O'Mara, T.A., Painter, J.N., Glubb, D.M., et al., 2016. Five endometrial cancer risk loci identified through genome-wide association analysis. *Nat. Genet.* 48, 667–674. <https://doi.org/10.1038/ng.3562>
176. Brand, J.S., Colzani, E., Johansson, A.L.V., Giesecke, J., Clements, M., et al., 2016b. Infection-related hospitalizations in breast cancer patients: Risk and impact on prognosis. *J. Infect.* 72, 650–658. <https://doi.org/10.1016/j.jinf.2016.04.003>
177. Tobin, N.P., Wennmalm, K., Lindström, L.S., Foukakis, T., He, L., et al., 2016. An Endothelial Gene Signature Score Predicts Poor Outcome in Patients with Endocrine-Treated, Low Genomic Grade Breast Tumors. *Clin. Cancer Res.* 22, 2417–2426. <https://doi.org/10.1158/1078-0432.CCR-15-1691>
178. Sjöberg, E., Augsten, M., Bergh, J., Jirström, K., Östman, A., 2016. Expression of the chemokine CXCL14 in the tumour stroma is an independent marker of survival in breast cancer. *Br. J. Cancer* 114, 1117–1124. <https://doi.org/10.1038/bjc.2016.104>
179. Ovarian Cancer Association Consortium, Breast Cancer Association Consortium, and Consortium of Modifiers of BRCA1 and BRCA2, Hollestelle, A., van der Baan, F.H., Berchuck, A., Johnatty, S.E., et al., 2016. No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecol. Oncol.* 141, 386–401. <https://doi.org/10.1016/j.ygyno.2015.04.034>
180. Easton, D.F., Lesueur, F., Decker, B., Michailidou, K., Li, J., et al., 2016. No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *J. Med. Genet.* 53, 298–309. <https://doi.org/10.1136/jmedgenet-2015-103529>
181. Couch, F.J., Kuchenbaecker, K.B., Michailidou, K., Mendoza-Fandino, G.A., Nord, S., et al., 2016. Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nat Commun* 7, 11375. <https://doi.org/10.1038/ncomms11375>
182. Pelttari, L.M., Khan, S., Vuorela, M., Kiiski, J.I., Vilske, S., et al., 2016. RAD51B in Familial Breast Cancer. *PLoS ONE* 11, e0153788. <https://doi.org/10.1371/journal.pone.0153788>
183. Koitsalu, M., Sprangers, M.A.G., Eklund, M., Czene, K., Hall, P., et al., 2016. Public interest in and acceptability of the prospect of risk-stratified screening for breast and prostate cancer. *Acta Oncol* 55, 45–51. <https://doi.org/10.3109/0284186X.2015.1043024>



184. Horne, H.N., Chung, C.C., Zhang, H., Yu, K., Prokunina-Olsson, L., et al., 2016. Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE* 11, e0160316. <https://doi.org/10.1371/journal.pone.0160316>

2015

185. Tobin, N.P., Foukakis, T., De Petris, L., Bergh, J., 2015a. The importance of molecular markers for diagnosis and selection of targeted treatments in patients with cancer. *J. Intern. Med.* 278, 545–570. <https://doi.org/10.1111/joim.12429>
186. Jamshidi, M., Fagerholm, R., Khan, S., Aittomäki, K., Czene, K., et al., 2015. SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. *Oncotarget* 6, 37979–37994. <https://doi.org/10.18632/oncotarget.4991>
187. Zhang, B., Shu, X.-O., Delahanty, R.J., Zeng, C., Michailidou, K., et al., 2015. Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *J. Natl. Cancer Inst.* 107. <https://doi.org/10.1093/jnci/djv219>
188. Guo, X., Long, J., Zeng, C., Michailidou, K., Ghoussaini, M., et al., 2015. Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiol. Biomarkers Prev.* 24, 1680–1691. <https://doi.org/10.1158/1055-9965.EPI-15-0363>
189. Day, F.R., Ruth, K.S., Thompson, D.J., Lunetta, K.L., Pervjakova, N., et al., 2015. Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nat. Genet.* 47, 1294–1303. <https://doi.org/10.1038/ng.3412>
190. Kimbung, S., Kovács, A., Danielsson, A., Bendahl, P.-O., Lövgren, K., et al., 2015. Contrasting breast cancer molecular subtypes across serial tumor progression stages: biological and prognostic implications. *Oncotarget* 6, 33306–33318. <https://doi.org/10.18632/oncotarget.5089>
191. Vilhjálmsson, B.J., Yang, J., Finucane, H.K., Gusev, A., Lindström, S., et al., 2015. Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *Am. J. Hum. Genet.* 97, 576–592. <https://doi.org/10.1016/j.ajhg.2015.09.001>
192. O'Mara, T.A., Glubb, D.M., Painter, J.N., Cheng, T., Dennis, J., et al., 2015. Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. *Endocr. Relat. Cancer* 22, 851–861. <https://doi.org/10.1530/ERC-15-0319>
193. Hong, J., Tobin, N.P., Rundqvist, H., Li, T., Lavergne, M., et al., 2015. Role of Tumor Pericytes in the Recruitment of Myeloid-Derived Suppressor Cells. *J. Natl. Cancer Inst.* 107. <https://doi.org/10.1093/jnci/djv209>
194. Abrahamsson, L., Czene, K., Hall, P., Humphreys, K., 2015. Breast cancer tumour growth modelling for studying the association of body size with tumour growth rate and symptomatic detection using case-control data. *Breast Cancer Res.* 17, 116. <https://doi.org/10.1186/s13058-015-0614-z>



195. Rudolph, A., Fasching, P.A., Behrens, S., Eilber, U., Bolla, M.K., et al., 2015a. A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. *Breast Cancer Res.* 17, 110. <https://doi.org/10.1186/s13058-015-0625-9>
196. He, W., Fang, F., Varnum, C., Eriksson, M., Hall, P., et al., 2015. Predictors of Discontinuation of Adjuvant Hormone Therapy in Patients With Breast Cancer. *J. Clin. Oncol.* 33, 2262–2269. <https://doi.org/10.1200/JCO.2014.59.3673>
197. Darabi, H., McCue, K., Beesley, J., Michailidou, K., Nord, S., et al., 2015. Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. *Am. J. Hum. Genet.* 97, 22–34. <https://doi.org/10.1016/j.ajhg.2015.05.002>
198. Trinh, T., Christensen, S.E., Brand, J.S., Cuzick, J., Czene, K., et al., 2015. Background risk of breast cancer influences the association between alcohol consumption and mammographic density. *Br. J. Cancer* 113, 159–165. <https://doi.org/10.1038/bjc.2015.185>
199. Stone, J., Thompson, D.J., Dos Santos Silva, I., Scott, C., Tamimi, R.M., et al., 2015. Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. *Cancer Res.* 75, 2457–2467. <https://doi.org/10.1158/0008-5472.CAN-14-2012>
200. Brand, J.S., Li, J., Humphreys, K., Karlsson, R., Eriksson, M., et al., 2015. Identification of two novel mammographic density loci at 6Q25.1. *Breast Cancer Res.* 17, 75. <https://doi.org/10.1186/s13058-015-0591-2>
201. Klevebring, D., Lindberg, J., Rockberg, J., Hilliges, C., Hall, P., et al., 2015. Exome sequencing of contralateral breast cancer identifies metastatic disease. *Breast Cancer Res. Treat.* 151, 319–324. <https://doi.org/10.1007/s10549-015-3403-6>
202. Cheddad, A., Czene, K., Hall, P., Humphreys, K., 2015. Pectoral muscle attenuation as a marker for breast cancer risk in full-field digital mammography. *Cancer Epidemiol. Biomarkers Prev.* 24, 985–991. <https://doi.org/10.1158/1055-9965.EPI-14-1362>
203. Orr, N., Dudbridge, F., Dryden, N., Maguire, S., Novo, D., et al., 2015. Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Hum. Mol. Genet.* 24, 2966–2984. <https://doi.org/10.1093/hmg/ddv035>
204. Schoormans, D., Czene, K., Hall, P., Brandberg, Y., 2015. The impact of co-morbidity on health-related quality of life in breast cancer survivors and controls. *Acta Oncol* 54, 727–734. <https://doi.org/10.3109/0284186X.2014.998277>
205. Mavaddat, N., Pharoah, P.D.P., Michailidou, K., Tyrer, J., Brook, M.N., et al., 2015. Prediction of breast cancer risk based on profiling with common genetic variants. *J. Natl. Cancer Inst.* 107. <https://doi.org/10.1093/jnci/djv036>
206. Guo, Q., Schmidt, M.K., Kraft, P., Canisius, S., Chen, C., et al., 2015. Identification of novel genetic markers of breast cancer survival. *J. Natl. Cancer Inst.* 107. <https://doi.org/10.1093/jnci/djv081>



207. Pirie, A., Guo, Q., Kraft, P., Canisius, S., Eccles, D.M., et al., 2015. Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Res.* 17, 58. <https://doi.org/10.1186/s13058-015-0570-7>
208. Fagerholm, R., Schmidt, M.K., Khan, S., Rafiq, S., Tapper, W., et al., 2015. The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. *Oncotarget* 6, 7390–7407. <https://doi.org/10.18632/oncotarget.3506>
209. Trinh, Thang, Eriksson, M., Darabi, H., Bonn, S.E., Brand, J.S., et al., 2015. Background risk of breast cancer and the association between physical activity and mammographic density. *Breast Cancer Res.* 17, 50. <https://doi.org/10.1186/s13058-015-0565-4>
210. Michailidou, K., Beesley, J., Lindstrom, S., Canisius, S., Dennis, J., et al., 2015. Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nat. Genet.* 47, 373–380. <https://doi.org/10.1038/ng.3242>
211. Holm, J., Humphreys, K., Li, J., Ploner, A., Cheddad, A., et al., 2015. Risk factors and tumor characteristics of interval cancers by mammographic density. *J. Clin. Oncol.* 33, 1030–1037. <https://doi.org/10.1200/JCO.2014.58.9986>
212. Rudolph, A., Milne, R.L., Truong, T., Knight, J.A., Seibold, P., et al., 2015b. Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. *Int. J. Cancer* 136, E685–696. <https://doi.org/10.1002/ijc.29188>
213. Painter, J.N., O'Mara, T.A., Batra, J., Cheng, T., Lose, F.A., et al., 2015. Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. *Hum. Mol. Genet.* 24, 1478–1492. <https://doi.org/10.1093/hmg/ddu552>
214. Kabisch, M., Lorenzo Bermejo, J., Dünnebier, T., Ying, S., Michailidou, K., et al., 2015. Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. *Carcinogenesis* 36, 256–271. <https://doi.org/10.1093/carcin/bgu326>
215. Carvajal-Carmona, L.G., O'Mara, T.A., Painter, J.N., Lose, F.A., Dennis, J., et al., 2015. Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. *Hum. Genet.* 134, 231–245. <https://doi.org/10.1007/s00439-014-1515-4>
216. Glubb, D.M., Maranian, M.J., Michailidou, K., Pooley, K.A., Meyer, K.B., et al., 2015. Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. *Am. J. Hum. Genet.* 96, 5–20. <https://doi.org/10.1016/j.ajhg.2014.11.009>
217. Lin, W.-Y., Camp, N.J., Ghousaini, M., Beesley, J., Michailidou, K., et al., 2015. Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Hum. Mol. Genet.* 24, 285–298. <https://doi.org/10.1093/hmg/ddu431>



218. Tobin, N.P., Harrell, J.C., Lötvrot, J., Egyhazi Brage, S., Frostvik Stolt, M., et al., 2015b. Molecular subtype and tumor characteristics of breast cancer metastases as assessed by gene expression significantly influence patient post-relapse survival. *Ann. Oncol.* 26, 81–88. <https://doi.org/10.1093/annonc/mdu498>
219. Cheng, T.H.T., Thompson, D., Painter, J., O'Mara, T., Gorman, M., et al., 2015. Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. *Sci Rep* 5, 17369. <https://doi.org/10.1038/srep17369>
220. Lei, J., Rudolph, A., Moysich, K.B., Rafiq, S., Behrens, S., et al., 2015. Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. *Breast Cancer Res.* 17, 18. <https://doi.org/10.1186/s13058-015-0522-2>
221. Johansson, H.J., Sanchez, B.C., Forshed, J., Stål, O., Fohlin, H., et al., 2015. Proteomics profiling identify CAPS as a potential predictive marker of tamoxifen resistance in estrogen receptor positive breast cancer. *Clin Proteomics* 12, 8. <https://doi.org/10.1186/s12014-015-9080-y>

2014

222. Spurdle, A.B., Couch, F.J., Parsons, M.T., McGuffog, L., Barrowdale, D., et al., 2014. Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. *Breast Cancer Res.* 16, 3419. <https://doi.org/10.1186/s13058-014-0474-y>
223. Brand, J.S., Humphreys, K., Thompson, D.J., Li, J., Eriksson, M., et al., 2014a. Volumetric mammographic density: heritability and association with breast cancer susceptibility loci. *J. Natl. Cancer Inst.* 106. <https://doi.org/10.1093/jnci/dju334>
224. Purrington, K.S., Slettedahl, S., Bolla, M.K., Michailidou, K., Czene, K., et al., 2014. Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. *Hum. Mol. Genet.* 23, 6034–6046. <https://doi.org/10.1093/hmg/ddu300>
225. Milne, R.L., Burwinkel, B., Michailidou, K., Arias-Perez, J.-I., Zamora, M.P., et al., 2014a. Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Hum. Mol. Genet.* 23, 6096–6111. <https://doi.org/10.1093/hmg/ddu311>
226. Lindström, S., Thompson, D.J., Paterson, A.D., Li, J., Gierach, G.L., et al., 2014. Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. *Nat Commun* 5, 5303. <https://doi.org/10.1038/ncomms6303>
227. Perry, J.R., Day, F., Elks, C.E., Sulem, P., Thompson, D.J., et al., 2014. Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature* 514, 92–97. <https://doi.org/10.1038/nature13545>
228. Lindström, L.S., Li, J., Lee, M., Einbeigi, Z., Hartman, M., et al., 2014. Prognostic information of a previously diagnosed sister is an independent prognosticator for a



- newly diagnosed sister with breast cancer. *Ann. Oncol.* 25, 1966–1972. <https://doi.org/10.1093/annonc/mdu270>
229. Ghossaini, M., Edwards, S.L., Michailidou, K., Nord, S., Cowper-Sal Lari, R., et al., 2014. Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nat Commun* 4, 4999. <https://doi.org/10.1038/ncomms5999>
230. Brand, J.S., Czene, K., Shepherd, J.A., Leifland, K., Heddson, B., et al., 2014b. Automated measurement of volumetric mammographic density: a tool for widespread breast cancer risk assessment. *Cancer Epidemiol. Biomarkers Prev.* 23, 1764–1772. <https://doi.org/10.1158/1055-9965.EPI-13-1219>
231. Rosin, G., de Boniface, J., Karthik, G.M., Frisell, J., Bergh, J., et al., 2014. Oestrogen receptors $\beta 1$ and βx have divergent roles in breast cancer survival and lymph node metastasis. *Br. J. Cancer* 111, 918–926. <https://doi.org/10.1038/bjc.2014.398>
232. Klevebring, D., Rosin, G., Ma, R., Lindberg, J., Czene, K., et al., 2014a. Sequencing of breast cancer stem cell populations indicates a dynamic conversion between differentiation states in vivo. *Breast Cancer Res.* 16, R72. <https://doi.org/10.1186/bcr3687>
233. Cheddad, A., Czene, K., Shepherd, J.A., Li, J., Hall, P., et al., 2014a. Enhancement of mammographic density measures in breast cancer risk prediction. *Cancer Epidemiol. Biomarkers Prev.* 23, 1314–1323. <https://doi.org/10.1158/1055-9965.EPI-13-1240>
234. Li, J., Lindström, L.S., Foo, J.N., Rafiq, S., Schmidt, M.K., et al., 2014. 2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. *Nat Commun* 5, 4051. <https://doi.org/10.1038/ncomms5051>
235. Pettersson, A., Graff, R.E., Ursin, G., Santos Silva, I.D., McCormack, V., et al., 2014. Mammographic density phenotypes and risk of breast cancer: a meta-analysis. *J. Natl. Cancer Inst.* 106. <https://doi.org/10.1093/jnci/dju078>
236. Perry, J.R.B., Hsu, Y.-H., Chasman, D.I., Johnson, A.D., Elks, C., et al., 2014. DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. *Hum. Mol. Genet.* 23, 2490–2497. <https://doi.org/10.1093/hmg/ddt620>
237. Tobin, N.P., Lindström, L.S., Carlson, J.W., Bjöhle, J., Bergh, J., et al., 2014. Multi-level gene expression signatures, but not binary, outperform Ki67 for the long term prognostication of breast cancer patients. *Mol Oncol* 8, 741–752. <https://doi.org/10.1016/j.molonc.2014.02.007>
238. Sovio, U., Li, J., Aitken, Z., Humphreys, K., Czene, K., et al., 2014. Comparison of fully and semi-automated area-based methods for measuring mammographic density and predicting breast cancer risk. *Br. J. Cancer* 110, 1908–1916. <https://doi.org/10.1038/bjc.2014.82>
239. Milne, R.L., Herranz, J., Michailidou, K., Dennis, J., Tyrer, J.P., et al., 2014b. A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46,450 cases and 42,461 controls from the breast cancer association consortium. *Hum. Mol. Genet.* 23, 1934–1946. <https://doi.org/10.1093/hmg/ddt581>



240. Ahsan, H., Halpern, J., Kibriya, M.G., Pierce, B.L., Tong, L., et al., 2014. A genome-wide association study of early-onset breast cancer identifies PFKM as a novel breast cancer gene and supports a common genetic spectrum for breast cancer at any age. *Cancer Epidemiol. Biomarkers Prev.* 23, 658–669. <https://doi.org/10.1158/1055-9965.EPI-13-0340>
241. Colzani, E., Johansson, A.L.V., Liljegren, A., Foukakis, T., Clements, M., et al., 2014. Time-dependent risk of developing distant metastasis in breast cancer patients according to treatment, age and tumour characteristics. *Br. J. Cancer* 110, 1378–1384. <https://doi.org/10.1038/bjc.2014.5>
242. Agarwal, D., Pineda, S., Michailidou, K., Herranz, J., Pita, G., et al., 2014. FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. *Br. J. Cancer* 110, 1088–1100. <https://doi.org/10.1038/bjc.2013.769>
243. Justenhoven, C., Pentimalli, D., Rabstein, S., Harth, V., Lotz, A., et al., 2014. CYP2B6*6 is associated with increased breast cancer risk. *Int. J. Cancer* 134, 426–430. <https://doi.org/10.1002/ijc.28356>
244. Schoeps, A., Rudolph, A., Seibold, P., Dunning, A.M., Milne, R.L., et al., 2014. Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. *Genet. Epidemiol.* 38, 84–93. <https://doi.org/10.1002/gepi.21771>
245. Sawyer, E., Roylance, R., Petridis, C., Brook, M.N., Nowinski, S., et al., 2014. Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genet.* 10, e1004285. <https://doi.org/10.1371/journal.pgen.1004285>
246. Klevebring, D., Neiman, M., Sundling, S., Eriksson, L., Darai Ramqvist, E., et al., 2014b. Evaluation of exome sequencing to estimate tumor burden in plasma. *PLoS ONE* 9, e104417. <https://doi.org/10.1371/journal.pone.0104417>
247. Khan, S., Greco, D., Michailidou, K., Milne, R.L., Muranen, T.A., et al., 2014. MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE* 9, e109973. <https://doi.org/10.1371/journal.pone.0109973>
248. Cheddad, A., Czene, K., Eriksson, M., Li, J., Easton, D., et al., 2014b. Area and volumetric density estimation in processed full-field digital mammograms for risk assessment of breast cancer. *PLoS ONE* 9, e110690. <https://doi.org/10.1371/journal.pone.0110690>

2013

249. Meyer, K.B., O'Reilly, M., Michailidou, K., Carlebur, S., Edwards, S.L., et al., 2013. Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. *Am. J. Hum. Genet.* 93, 1046–1060. <https://doi.org/10.1016/j.ajhg.2013.10.026>
250. Rudolph, A., Hein, R., Lindström, S., Beckmann, L., Behrens, S., et al., 2013. Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a



- genome-wide interaction study. *Endocr. Relat. Cancer* 20, 875–887. <https://doi.org/10.1530/ERC-13-0349>
251. Milosevic, J., Klinge, J., Borg, A.-L., Foukakis, T., Bergh, J., et al., 2013. Clinical instability of breast cancer markers is reflected in long-term in vitro estrogen deprivation studies. *BMC Cancer* 13, 473. <https://doi.org/10.1186/1471-2407-13-473>
252. Li, J., Foo, J.N., Schoof, N., Varghese, J.S., Fernandez-Navarro, P., et al., 2013a. Large-scale genotyping identifies a new locus at 22q13.2 associated with female breast size. *J. Med. Genet.* 50, 666–673. <https://doi.org/10.1136/jmedgenet-2013-101708>
253. Li, J., Humphreys, K., Eriksson, L., Edgren, G., Czene, K., et al., 2013b. Mammographic density reduction is a prognostic marker of response to adjuvant tamoxifen therapy in postmenopausal patients with breast cancer. *J. Clin. Oncol.* 31, 2249–2256. <https://doi.org/10.1200/JCO.2012.44.5015>
254. Eriksson, L., Czene, K., Rosenberg, L.U., Törnberg, S., Humphreys, K., et al., 2013a. Mammographic density and survival in interval breast cancers. *Breast Cancer Res.* 15, R48. <https://doi.org/10.1186/bcr3440>
255. Frings, O., Augsten, M., Tobin, N.P., Carlson, J., Paulsson, J., et al., 2013. Prognostic significance in breast cancer of a gene signature capturing stromal PDGF signaling. *Am. J. Pathol.* 182, 2037–2047. <https://doi.org/10.1016/j.ajpath.2013.02.018>
256. Sandberg, M.E.C., Alkner, S., Hartman, M., Eloranta, S., Rydén, L., et al., 2013a. Influence of radiotherapy for the first tumor on aggressiveness of contralateral breast cancer. *Int. J. Cancer* 132, 2388–2394. <https://doi.org/10.1002/ijc.27890>
257. French, J.D., Ghossaini, M., Edwards, S.L., Meyer, K.B., Michailidou, K., et al., 2013. Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. *Am. J. Hum. Genet.* 92, 489–503. <https://doi.org/10.1016/j.ajhg.2013.01.002>
258. Michailidou, K., Hall, P., Gonzalez-Neira, A., Ghossaini, M., Dennis, J., et al., 2013. Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nat. Genet.* 45, 353–361, 361e1-2. <https://doi.org/10.1038/ng.2563>
259. Hein, R., Flesch-Janys, D., Dahmen, N., Beckmann, L., Lindström, S., et al., 2013. A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. *Breast Cancer Res. Treat.* 138, 529–542. <https://doi.org/10.1007/s10549-013-2443-z>
260. Garcia-Closas, M., Couch, F.J., Lindstrom, S., Michailidou, K., Schmidt, M.K., et al., 2013. Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nat. Genet.* 45, 392–398, 398e1-2. <https://doi.org/10.1038/ng.2561>
261. Bojesen, S.E., Pooley, K.A., Johnatty, S.E., Beesley, J., Michailidou, K., et al., 2013. Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nat. Genet.* 45, 371–384, 384e1-2. <https://doi.org/10.1038/ng.2566>



262. Sandberg, M.E.C., Li, J., Hall, P., Hartman, M., dos-Santos-Silva, I., et al., 2013b. Change of mammographic density predicts the risk of contralateral breast cancer--a case-control study. *Breast Cancer Res.* 15, R57. <https://doi.org/10.1186/bcr3451>
263. Li, J., Czene, K., Brauch, H., Schroth, W., Saladores, P., et al., 2013c. Association of CYP2D6 metabolizer status with mammographic density change in response to tamoxifen treatment. *Breast Cancer Res.* 15, R93. <https://doi.org/10.1186/bcr3495>
264. Eriksson, L., Czene, K., Rosenberg, L., Humphreys, K., Hall, P., 2013b. Possible influence of mammographic density on local and locoregional recurrence of breast cancer. *Breast Cancer Res.* 15, R56. <https://doi.org/10.1186/bcr3450>
265. Brand, J.S., Czene, K., Eriksson, L., Trinh, T., Bhoo-Pathy, N., et al., 2013. Influence of lifestyle factors on mammographic density in postmenopausal women. *PLoS ONE* 8, e81876. <https://doi.org/10.1371/journal.pone.0081876>

2012

266. Siddiq, A., Couch, F.J., Chen, G.K., Lindström, S., Eccles, D., et al., 2012. A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. *Hum. Mol. Genet.* 21, 5373–5384. <https://doi.org/10.1093/hmg/dds381>
267. Weischer, M., Nordestgaard, B.G., Pharoah, P., Bolla, M.K., Nevanlinna, H., et al., 2012. CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *J. Clin. Oncol.* 30, 4308–4316. <https://doi.org/10.1200/JCO.2012.42.7336>
268. Warren, H., Dudbridge, F., Fletcher, O., Orr, N., Johnson, N., et al., 2012. 9q31.2-rs865686 as a susceptibility locus for estrogen receptor-positive breast cancer: evidence from the Breast Cancer Association Consortium. *Cancer Epidemiol. Biomarkers Prev.* 21, 1783–1791. <https://doi.org/10.1158/1055-9965.EPI-12-0526>
269. Fasching, P.A., Pharoah, P.D.P., Cox, A., Nevanlinna, H., Bojesen, S.E., et al., 2012. The role of genetic breast cancer susceptibility variants as prognostic factors. *Hum. Mol. Genet.* 21, 3926–3939. <https://doi.org/10.1093/hmg/dds159>
270. Tobin, N.P., Bergh, J., 2012. Analysis of Cyclin D1 in Breast Cancer: A Call to Arms. *Curr Breast Cancer Rep* 4, 171–173. <https://doi.org/10.1007/s12609-012-0083-7>
271. Li, J., Szekely, L., Eriksson, L., Hedden, B., Sundbom, A., et al., 2012. High-throughput mammographic-density measurement: a tool for risk prediction of breast cancer. *Breast Cancer Res.* 14, R114. <https://doi.org/10.1186/bcr3238>
272. Stevens, K.N., Lindstrom, S., Scott, C.G., Thompson, D., Sellers, T.A., et al., 2012a. Identification of a novel percent mammographic density locus at 12q24. *Hum. Mol. Genet.* 21, 3299–3305. <https://doi.org/10.1093/hmg/dds158>
273. Vachon, C.M., Scott, C.G., Fasching, P.A., Hall, P., Tamimi, R.M., et al., 2012a. Common breast cancer susceptibility variants in LSP1 and RAD51L1 are associated with mammographic density measures that predict breast cancer risk. *Cancer*



- Epidemiol. Biomarkers Prev. 21, 1156–1166. <https://doi.org/10.1158/1055-9965.EPI-12-0066>
274. Sandberg, M.E.C., Hartman, M., Klevebring, D., Eloranta, S., Ploner, A., et al., 2012a. Prognostic implications of estrogen receptor pattern of both tumors in contralateral breast cancer. *Breast Cancer Res. Treat.* 134, 793–800. <https://doi.org/10.1007/s10549-012-2096-3>
275. Lambrechts, D., Truong, T., Justenhoven, C., Humphreys, M.K., Wang, J., et al., 2012. 11q13 is a susceptibility locus for hormone receptor positive breast cancer. *Hum. Mutat.* 33, 1123–1132. <https://doi.org/10.1002/humu.22089>
276. Eriksson, Louise, Czene, K., Rosenberg, L., Humphreys, K., Hall, P., 2012. The influence of mammographic density on breast tumor characteristics. *Breast Cancer Res. Treat.* 134, 859–866. <https://doi.org/10.1007/s10549-012-2127-0>
277. Eriksson, L., Hall, P., Czene, K., Dos Santos Silva, I., McCormack, V., et al., 2012. Mammographic density and molecular subtypes of breast cancer. *Br. J. Cancer* 107, 18–23. <https://doi.org/10.1038/bjc.2012.234>
278. Eloranta, S., Lambert, P.C., Andersson, T.M.L., Czene, K., Hall, P., et al., 2012. Partitioning of excess mortality in population-based cancer patient survival studies using flexible parametric survival models. *BMC Med Res Methodol* 12, 86. <https://doi.org/10.1186/1471-2288-12-86>
279. Stevens, K.N., Fredericksen, Z., Vachon, C.M., Wang, X., Margolin, S., et al., 2012b. 19p13.1 is a triple-negative-specific breast cancer susceptibility locus. *Cancer Res.* 72, 1795–1803. <https://doi.org/10.1158/0008-5472.CAN-11-3364>
280. Varghese, J.S., Thompson, D.J., Michailidou, K., Lindström, S., Turnbull, C., et al., 2012. Mammographic breast density and breast cancer: evidence of a shared genetic basis. *Cancer Res.* 72, 1478–1484. <https://doi.org/10.1158/0008-5472.CAN-11-3295>
281. Ghousaini, M., Fletcher, O., Michailidou, K., Turnbull, C., Schmidt, M.K., et al., 2012. Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nat. Genet.* 44, 312–318. <https://doi.org/10.1038/ng.1049>
282. Rosin, G., Hannelius, U., Lindström, L., Hall, P., Bergh, J., et al., 2012. The dyslexia candidate gene *DYX1C1* is a potential marker of poor survival in breast cancer. *BMC Cancer* 12, 79. <https://doi.org/10.1186/1471-2407-12-79>
283. Darabi, H., Czene, K., Zhao, W., Liu, J., Hall, P., et al., 2012. Breast cancer risk prediction and individualised screening based on common genetic variation and breast density measurement. *Breast Cancer Res.* 14, R25. <https://doi.org/10.1186/bcr3110>
284. Vachon, C.M., Li, J., Scott, C.G., Hall, P., Czene, K., et al., 2012b. No evidence for association of inherited variation in genes involved in mitosis and percent mammographic density. *Breast Cancer Res.* 14, R7. <https://doi.org/10.1186/bcr3088>
285. Sandberg, M.E.C., Hall, P., Hartman, M., Johansson, A.L.V., Eloranta, S., et al., 2012b. Estrogen receptor status in relation to risk of contralateral breast cancer—a population-based cohort study. *PLoS ONE* 7, e46535. <https://doi.org/10.1371/journal.pone.0046535>



286. Neiman, M., Sundling, S., Grönberg, H., Hall, P., Czene, K., et al., 2012. Library preparation and multiplex capture for massive parallel sequencing applications made efficient and easy. *PLoS ONE* 7, e48616. <https://doi.org/10.1371/journal.pone.0048616>
287. Li, Y., Low, H.-Q., Foo, J.N., Darabi, H., Einarsdóttir, K., et al., 2012. Genetic variants in ER cofactor genes and endometrial cancer risk. *PLoS ONE* 7, e42445. <https://doi.org/10.1371/journal.pone.0042445>
288. Hein, R., Maranian, M., Hopper, J.L., Kapuscinski, M.K., Southey, M.C., et al., 2012. Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). *PLoS ONE* 7, e42380. <https://doi.org/10.1371/journal.pone.0042380>

2011

289. Figueroa, J.D., Garcia-Closas, M., Humphreys, M., Platte, R., Hopper, J.L., et al., 2011. Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. *Hum. Mol. Genet.* 20, 4693–4706. <https://doi.org/10.1093/hmg/ddr368>
290. Biesheuvel, C., Czene, K., Orgeás, C.C., Hall, P., 2011. The role of mammography screening attendance and detection mode in predicting breast cancer survival—is there added prognostic value? *Cancer Epidemiol* 35, 545–550. <https://doi.org/10.1016/j.canep.2011.02.008>
291. Early Breast Cancer Trialists' Collaborative Group (EBCTCG), Darby, S., McGale, P., Correa, C., Taylor, C., et al., 2011a. Effect of radiotherapy after breast-conserving surgery on 10-year recurrence and 15-year breast cancer death: meta-analysis of individual patient data for 10,801 women in 17 randomised trials. *Lancet* 378, 1707–1716. [https://doi.org/10.1016/S0140-6736\(11\)61629-2](https://doi.org/10.1016/S0140-6736(11)61629-2)
292. Colzani, E., Liljegren, A., Johansson, A.L.V., Adolfsson, J., Hellborg, H., et al., 2011. Prognosis of patients with breast cancer: causes of death and effects of time since diagnosis, age, and tumor characteristics. *J. Clin. Oncol.* 29, 4014–4021. <https://doi.org/10.1200/JCO.2010.32.6462>
293. Milne, R.L., Lorenzo-Bermejo, J., Burwinkel, B., Malats, N., Arias, J.I., et al., 2011. 7q21-rs6964587 and breast cancer risk: an extended case-control study by the Breast Cancer Association Consortium. *J. Med. Genet.* 48, 698–702. <https://doi.org/10.1136/jmedgenet-2011-100303>
294. Broeks, A., Schmidt, M.K., Sherman, M.E., Couch, F.J., Hopper, J.L., et al., 2011. Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. *Hum. Mol. Genet.* 20, 3289–3303. <https://doi.org/10.1093/hmg/ddr228>
295. Darabi, H., Czene, K., Wedrén, S., Li, Y., Liu, J., et al., 2011. Genetic variation in the androgen estrogen conversion pathway in relation to breast cancer prognosticators. *Breast Cancer Res. Treat.* 127, 503–509. <https://doi.org/10.1007/s10549-010-1218-z>



296. Li, J., Seibold, P., Chang-Claude, J., Flesch-Janys, D., Liu, J., et al., 2011a. Coffee consumption modifies risk of estrogen-receptor negative breast cancer. *Breast Cancer Res.* 13, R49. <https://doi.org/10.1186/bcr2879>
297. Spurdle, A.B., Thompson, D.J., Ahmed, S., Ferguson, K., Healey, C.S., et al., 2011. Genome-wide association study identifies a common variant associated with risk of endometrial cancer. *Nat. Genet.* 43, 451–454. <https://doi.org/10.1038/ng.812>
298. Inaki, K., Hillmer, A.M., Ukil, L., Yao, F., Woo, X.Y., et al., 2011. Transcriptional consequences of genomic structural aberrations in breast cancer. *Genome Res.* 21, 676–687. <https://doi.org/10.1101/gr.113225.110>
299. Hillmer, A.M., Yao, F., Inaki, K., Lee, W.H., Ariyaratne, P.N., et al., 2011. Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. *Genome Res.* 21, 665–675. <https://doi.org/10.1101/gr.113555.110>
300. Li, J., Humphreys, K., Heikkinen, T., Aittomäki, K., Blomqvist, C., et al., 2011b. A combined analysis of genome-wide association studies in breast cancer. *Breast Cancer Res. Treat.* 126, 717–727. <https://doi.org/10.1007/s10549-010-1172-9>
301. O'Mara, T.A., Fahey, P., Ferguson, K., Marquart, L., Lambrechts, D., et al., 2011. Progesterone receptor gene variants and risk of endometrial cancer. *Carcinogenesis* 32, 331–335. <https://doi.org/10.1093/carcin/bgq263>
302. Lindström, S., Vachon, C.M., Li, J., Varghese, J., Thompson, D., et al., 2011. Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. *Nat. Genet.* 43, 185–187. <https://doi.org/10.1038/ng.760>
303. Salmela, E., Lappalainen, T., Liu, J., Sistonen, P., Andersen, P.M., et al., 2011. Swedish population substructure revealed by genome-wide single nucleotide polymorphism data. *PLoS ONE* 6, e16747. <https://doi.org/10.1371/journal.pone.0016747>
304. Yang, X.R., Chang-Claude, J., Goode, E.L., Couch, F.J., Nevanlinna, H., et al., 2011. Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. *J. Natl. Cancer Inst.* 103, 250–263. <https://doi.org/10.1093/jnci/djq526>
305. Li, Y., Li, Yi, Wedrén, S., Li, G., Charn, T.H., et al., 2011. Genetic variation of ESR1 and its co-activator PPARGC1B is synergistic in augmenting the risk of estrogen receptor-positive breast cancer. *Breast Cancer Res.* 13, R10. <https://doi.org/10.1186/bcr2817>
306. Early Breast Cancer Trialists' Collaborative Group (EBCTCG), Davies, C., Godwin, J., Gray, R., Clarke, M., et al., 2011b. Relevance of breast cancer hormone receptors and other factors to the efficacy of adjuvant tamoxifen: patient-level meta-analysis of randomised trials. *Lancet* 378, 771–784. [https://doi.org/10.1016/S0140-6736\(11\)60993-8](https://doi.org/10.1016/S0140-6736(11)60993-8)



2010

307. Mahmoudi, S., Henriksson, S., Weibrecht, I., Smith, S., Söderberg, O., et al., 2010. WRAP53 is essential for Cajal body formation and for targeting the survival of motor neuron complex to Cajal bodies. *PLoS Biol.* 8, e1000521. <https://doi.org/10.1371/journal.pbio.1000521>
308. Fletcher, O., Johnson, N., dos Santos Silva, I., Orr, N., Ashworth, A., et al., 2010. Missense variants in ATM in 26,101 breast cancer cases and 29,842 controls. *Cancer Epidemiol. Biomarkers Prev.* 19, 2143–2151. <https://doi.org/10.1158/1055-9965.EPI-10-0374>
309. Sandberg, M.E.C., Hartman, M., Edgren, G., Eloranta, S., Ploner, A., et al., 2010. Diagnostic work-up of contralateral breast cancers has not improved over calendar period. *Breast Cancer Res. Treat.* 122, 889–895. <https://doi.org/10.1007/s10549-010-0748-8>
310. Low, Y.L., Li, Yuqing, Humphreys, K., Thalamuthu, A., Li, Yi, et al., 2010. Multi-variant pathway association analysis reveals the importance of genetic determinants of estrogen metabolism in breast and endometrial cancer susceptibility. *PLoS Genet.* 6, e1001012. <https://doi.org/10.1371/journal.pgen.1001012>
311. Tennis, M., Singh, B., Hjerpe, A., Prochazka, M., Czene, K., et al., 2010. Pathological confirmation of primary lung cancer following breast cancer. *Lung Cancer* 69, 40–45. <https://doi.org/10.1016/j.lungcan.2009.08.018>
312. Azzato, E.M., Tyrer, J., Fasching, P.A., Beckmann, M.W., Ekici, A.B., et al., 2010. Association between a germline OCA2 polymorphism at chromosome 15q13.1 and estrogen receptor-negative breast cancer survival. *J. Natl. Cancer Inst.* 102, 650–662. <https://doi.org/10.1093/jnci/djq057>
313. Tamimi, R.M., Lagiou, P., Czene, K., Liu, J., Ekblom, A., et al., 2010a. Birth weight, breast cancer susceptibility loci, and breast cancer risk. *Cancer Causes Control* 21, 689–696. <https://doi.org/10.1007/s10552-009-9496-7>
314. Khoshnoud, R., He, Q., Sylván, M., Khoshnoud, A., Ivarsson, M., et al., 2010. The impact of RNA standardization and heterogeneous gene expression on the results of cDNA array of human breast carcinoma. *Int. J. Mol. Med.* 25, 735–741. https://doi.org/10.3892/ijmm_00000399
315. Tamimi, R.M., Eriksson, L., Lagiou, P., Czene, K., Ekblom, A., et al., 2010b. Birth weight and mammographic density among postmenopausal women in Sweden. *Int. J. Cancer* 126, 985–991. <https://doi.org/10.1002/ijc.24786>
316. Milne, R.L., Gaudet, M.M., Spurdle, A.B., Fasching, P.A., Couch, F.J., et al., 2010. Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. *Breast Cancer Res.* 12, R110. <https://doi.org/10.1186/bcr2797>
317. Li, J., Humphreys, K., Eriksson, L., Czene, K., Liu, J., et al., 2010a. Effects of childhood body size on breast cancer tumour characteristics. *Breast Cancer Res.* 12, R23. <https://doi.org/10.1186/bcr2564>



318. Li, J., Humphreys, K., Darabi, H., Rosin, G., Hannelius, U., et al., 2010b. A genome-wide association scan on estrogen receptor-negative breast cancer. *Breast Cancer Res.* 12, R93. <https://doi.org/10.1186/bcr2772>
319. Li, J., Eriksson, L., Humphreys, K., Czene, K., Liu, J., et al., 2010c. Genetic variation in the estrogen metabolic pathway and mammographic density as an intermediate phenotype of breast cancer. *Breast Cancer Res.* 12, R19. <https://doi.org/10.1186/bcr2488>

Reviews and book chapters (8)

1. Saeed, A.A., Genové, G., Li, T., Hülshorst, F., Betsholtz, C., et al., 2015. Increased flux of the plant sterols campesterol and sitosterol across a disrupted blood brain barrier. *Steroids* 99, 183–188. <https://doi.org/10.1016/j.steroids.2015.02.005>
2. Bergh, J., Hall, P., Östman, A., Toftgård, R., 2013. Breast cancer biology and the future of tailored therapies. Introduction. *J. Intern. Med.* 274, 102–104. <https://doi.org/10.1111/joim.12101>
3. Ostman, A., Pietras, K., 2013. Introduction to tumor-stroma interactions. *Exp. Cell Res.* 319, 1595. <https://doi.org/10.1016/j.yexcr.2013.05.026>
4. Weiland, A., Roswall, P., Hatzihristidis, T.C., Pietras, K., Ostman, A., et al., 2012. Fibroblast-dependent regulation of the stem cell properties of cancer cells. *Neoplasma* 59, 719–727. https://doi.org/10.4149/neo_2012_091
5. Early Breast Cancer Trialists' Collaborative Group (EBCTCG), Darby, S., McGale, P., Correa, C., Taylor, C., et al., 2011. Effect of radiotherapy after breast-conserving surgery on 10-year recurrence and 15-year breast cancer death: meta-analysis of individual patient data for 10,801 women in 17 randomised trials. *Lancet* 378, 1707–1716. [https://doi.org/10.1016/S0140-6736\(11\)61629-2](https://doi.org/10.1016/S0140-6736(11)61629-2)
6. Armulik, A., Genové, G., Betsholtz, C., 2011. Pericytes: developmental, physiological, and pathological perspectives, problems, and promises. *Dev. Cell* 21, 193–215. <https://doi.org/10.1016/j.devcel.2011.07.001>
7. Pietras, K., Ostman, A., 2010. Hallmarks of cancer: interactions with the tumor stroma. *Exp. Cell Res.* 316, 1324–1331. <https://doi.org/10.1016/j.yexcr.2010.02.045>
8. Early Breast Cancer Trialists' Collaborative Group (EBCTCG), Correa, C., McGale, P., Taylor, C., Wang, Y., et al., 2010. Overview of the randomized trials of radiotherapy in ductal carcinoma in situ of the breast. *J. Natl. Cancer Inst. Monographs* 2010, 162–177. <https://doi.org/10.1093/jncimonographs/lgq039>