

# Association analysis identifies 65 new breast cancer risk

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
2	The use of panel testing in familial breast and ovarian cancer. <i>Clinical Medicine</i> , 2017, 17, 568-572.	0.8	6
3	Update Breast Cancer 2017 – Implementation of Novel Therapies. <i>Geburtshilfe Und Frauenheilkunde</i> , 2017, 77, 1281-1290.	0.8	19
4	Breast Cancer Risk Model Requirements for Counseling, Prevention, and Screening. <i>Journal of the National Cancer Institute</i> , 2018, 110, 994-1002.	3.0	46
5	Disentangling the determinants of interest and willingness-to-pay for breast cancer susceptibility testing in the general population: a cross-sectional Web-based survey among women of Québec (Canada). <i>BMJ Open</i> , 2018, 8, e016662.	0.8	9
7	Frequency of pathogenic germline mutations in cancer susceptibility genes in breast cancer patients. <i>Medical Oncology</i> , 2018, 35, 81.	1.2	7
8	Towards Prevention of Breast Cancer: What Are the Clinical Challenges?. <i>Cancer Prevention Research</i> , 2018, 11, 255-264.	0.7	15
9	Should breast cancer screening programs routinely measure mammographic density?. <i>Journal of Medical Imaging and Radiation Oncology</i> , 2018, 62, 151-158.	0.9	3
10	Human individual radiation sensitivity and prospects for prediction. <i>Annals of the ICRP</i> , 2018, 47, 126-141.	3.0	41
11	An esophageal adenocarcinoma susceptibility locus at 9q22 also confers risk to esophageal squamous cell carcinoma by regulating the function of BARX1. <i>Cancer Letters</i> , 2018, 421, 103-111.	3.2	13
12	Common Genetic Variation and Breast Cancer Risk – Past, Present, and Future. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 380-394.	1.1	108
13	Genome-Wide Association Studies in Glioma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 418-428.	1.1	34
14	Genetic insights into the morass of metastatic heterogeneity. <i>Nature Reviews Cancer</i> , 2018, 18, 211-223.	12.8	140
15	Exome sequencing and case-control analyses identify <i>RCC1</i> as a candidate breast cancer susceptibility gene. <i>International Journal of Cancer</i> , 2018, 142, 2512-2517.	2.3	17
16	Assessment of a FBXW8 frameshift mutation, c.1312_1313delGT, in breast cancer patients and controls from Central Europe. <i>Cancer Genetics</i> , 2018, 220, 38-43.	0.2	1
17	Complex HLA association in paraneoplastic cerebellar ataxia with anti-Yo antibodies. <i>Journal of Neuroimmunology</i> , 2018, 315, 28-32.	1.1	17
18	Breast cancer: The translation of big genomic data to cancer precision medicine. <i>Cancer Science</i> , 2018, 109, 497-506.	1.7	92
19	A Comprehensive cis-eQTL Analysis Revealed Target Genes in Breast Cancer Susceptibility Loci Identified in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2018, 102, 890-903.	2.6	72

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20	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomics. <i>American Journal of Human Genetics</i> , 2018, 102, 904-919.	2.6	30
21	Are VNTRs co-localizing with breast cancer-associated SNPs?. <i>Breast Cancer Research and Treatment</i> , 2018, 168, 277-281.	1.1	2
22	Personalized prevention in high risk individuals: Managing hormones and beyond. <i>Breast</i> , 2018, 39, 139-147.	0.9	18
23	Update Breast Cancer 2018 (Part 2) â€“ Advanced Breast Cancer, Quality of Life and Prevention. <i>Geburtshilfe Und Frauenheilkunde</i> , 2018, 78, 246-259.	0.8	23
25	Breast Cancer Family History and Contralateral Breast Cancer Risk in Young Women: An Update From the Womenâ€™s Environmental Cancer and Radiation Epidemiology Study. <i>Journal of Clinical Oncology</i> , 2018, 36, 1513-1520.	0.8	44
26	Leveraging Human Genetics to Guide Cancer Drug Development. <i>JCO Clinical Cancer Informatics</i> , 2018, 2, 1-11.	1.0	3
27	Model for Predicting Breast Cancer Risk in Women With Atypical Hyperplasia. <i>Journal of Clinical Oncology</i> , 2018, 36, 1840-1846.	0.8	22
28	Expression reflects population structure. <i>PLoS Genetics</i> , 2018, 14, e1007841.	1.5	27
29	Recursive Feature Elimination by Sensitivity Testing. , 2018, 2018, 40-47.		18
30	Cirrus: An Automated Mammography-Based Measure of Breast Cancer Risk Based on Textural Features. <i>JNCI Cancer Spectrum</i> , 2018, 2, pky057.	1.4	24
31	Non-Coding Variants in BRCA1 and BRCA2 Genes: Potential Impact on Breast and Ovarian Cancer Predisposition. <i>Cancers</i> , 2018, 10, 453.	1.7	14
32	Update Breast Cancer 2018 (Part 3) â€“ Genomics, Individualized Medicine and Immune Therapies â€“ in the Middle of a New Era: Prevention and Treatment Strategies for Early Breast Cancer. <i>Geburtshilfe Und Frauenheilkunde</i> , 2018, 78, 1110-1118.	0.8	8
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34	Machine learning identifies interacting genetic variants contributing to breast cancer risk: A case study in Finnish cases and controls. <i>Scientific Reports</i> , 2018, 8, 13149.	1.6	58
35	Ept7, a quantitative trait locus that controls estrogen-induced pituitary lactotroph hyperplasia in rat, is orthologous to a locus in humans that has been associated with numerous cancer types and common diseases. <i>PLoS ONE</i> , 2018, 13, e0204727.	1.1	2
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40	Interactions Between ABCB1 Genotype and Preoperative Statin Use Impact Clinical Outcomes Among Breast Cancer Patients. <i>Frontiers in Oncology</i> , 2018, 8, 428.	1.3	8
41	Camptothecin@HMSNs/thermosensitive hydrogel composite for applications in preventing local breast cancer recurrence. <i>Chinese Chemical Letters</i> , 2018, 29, 1819-1823.	4.8	19
42	Personalised medicine and population health: breast and ovarian cancer. <i>Human Genetics</i> , 2018, 137, 769-778.	1.8	36
43	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. <i>Nature Communications</i> , 2018, 9, 3636.	5.8	74
44	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , 2018, 9, 280.	1.1	11
45	<i>BRCA1</i> and <i>BRCA2</i> 5' noncoding region variants identified in breast cancer patients alter promoter activity and protein binding. <i>Human Mutation</i> , 2018, 39, 2025-2039.	1.1	15
46	Cancer genetics, precision prevention and a call to action. <i>Nature Genetics</i> , 2018, 50, 1212-1218.	9.4	94
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50	Transcriptome-wide association studies accounting for colocalization using Egger regression. <i>Genetic Epidemiology</i> , 2018, 42, 418-433.	0.6	59
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52	Complex polymorphisms in endocytosis genes suggest alpha-cyclodextrin as a treatment for breast cancer. <i>PLoS ONE</i> , 2018, 13, e0199012.	1.1	17
54	Using whole genome scores to compare three clinical phenotyping methods in complex diseases. <i>Scientific Reports</i> , 2018, 8, 11360.	1.6	9
55	Enhancer mapping uncovers phenotypic heterogeneity and evolution in patients with luminal breast cancer. <i>Nature Medicine</i> , 2018, 24, 1469-1480.	15.2	98
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57	Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians. <i>BMJ: British Medical Journal</i> , 2018, 362, k601.	2.4	1,880
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65	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178
66	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. <i>Nature Genetics</i> , 2018, 50, 1219-1224.	9.4	2,111
67	Vitamin D and overall cancer risk and cancer mortality: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2018, 27, 4315-4322.	1.4	49
68	Moderate-Penetrance Predisposition to Breast Cancer. <i>Current Breast Cancer Reports</i> , 2018, 10, 232-239.	0.5	0
69	Rat models of 17 $\beta$ -estradiol-induced mammary cancer reveal novel insights into breast cancer etiology and prevention. <i>Physiological Genomics</i> , 2018, 50, 215-234.	1.0	33
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73	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	9.4	184
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75	Transmission of breast cancer polygenic risk based on single nucleotide polymorphisms. <i>Breast</i> , 2018, 41, 14-18.	0.9	4
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77	Insight into genetic predisposition to chronic lymphocytic leukemia from integrative epigenomics. <i>Nature Communications</i> , 2019, 10, 3615.	5.8	32
78	Polygenic Risk Scores in Breast Cancer. <i>Current Breast Cancer Reports</i> , 2019, 11, 117-122.	0.5	0
79	Pleiotropy Complicates Human Gene Editing: CCR5 <sup>Δ32</sup> and Beyond. <i>Frontiers in Genetics</i> , 2019, 10, 669.	1.1	13
80	Identifying Putative Susceptibility Genes and Evaluating Their Associations with Somatic Mutations in Human Cancers. <i>American Journal of Human Genetics</i> , 2019, 105, 477-492.	2.6	27
81	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
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86	Breast Cancer Susceptibility—Towards Individualised Risk Prediction. <i>Current Genetic Medicine Reports</i> , 2019, 7, 124-135.	1.9	4
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88	A Splice Site Variant of CDK12 and Breast Cancer in Three Eurasian Populations. <i>Frontiers in Oncology</i> , 2019, 9, 493.	1.3	4
89	The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 781-794.	0.9	37
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100	Update Breast Cancer 2019 Part 4 “ Diagnostic and Therapeutic Challenges of New, Personalised Therapies for Patients with Early Breast Cancer. <i>Geburtshilfe Und Frauenheilkunde</i> , 2019, 79, 1079-1089.	0.8	18
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105	Analysis of Promoter-Associated Chromatin Interactions Reveals Biologically Relevant Candidate Target Genes at Endometrial Cancer Risk Loci. <i>Cancers</i> , 2019, 11, 1440.	1.7	29
106	Editorial: Accomplishments, Collaborative Projects and Future Initiatives in Breast Cancer Genetic Predisposition. <i>Frontiers in Oncology</i> , 2019, 9, 841.	1.3	0
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109	Association Analysis Among Treatment Modalities and Comorbidity for Prostate Cancer. , 2019, , .		0
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113	Genome-wide association study of peripheral blood DNA methylation and conventional mammographic density measures. <i>International Journal of Cancer</i> , 2019, 145, 1768-1773.	2.3	17
114	Hereditary Breast and Hereditary Ovarian Cancer: Implications for the Oncology Nurse. <i>Seminars in Oncology Nursing</i> , 2019, 35, 47-57.	0.7	4
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119	Update Breast Cancer 2019 Part 1 – Implementation of Study Results of Novel Study Designs in Clinical Practice in Patients with Early Breast Cancer. <i>Geburtshilfe Und Frauenheilkunde</i> , 2019, 79, 256-267.	0.8	17
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121	REQUITE: A prospective multicentre cohort study of patients undergoing radiotherapy for breast, lung or prostate cancer. <i>Radiotherapy and Oncology</i> , 2019, 138, 59-67.	0.3	53
125	Sex hormone binding globulin and risk of breast cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2019, 48, 807-816.	0.9	50
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137	Centromeric Satellite DNAs: Hidden Sequence Variation in the Human Population. <i>Genes</i> , 2019, 10, 352.	1.0	75
138	Polygenic prediction via Bayesian regression and continuous shrinkage priors. <i>Nature Communications</i> , 2019, 10, 1776.	5.8	832
139	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019, 51, 815-823.	9.4	89
140	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
141	Common matrix metalloproteinase-2 gene variants and altered susceptibility to breast cancer and associated features in Tunisian women. <i>Tumor Biology</i> , 2019, 41, 101042831984574.	0.8	13
142	Mendelian randomization analysis using mixture models for robust and efficient estimation of causal effects. <i>Nature Communications</i> , 2019, 10, 1941.	5.8	118
143	A functional single nucleotide polymorphism in <i>ABCC11</i> , rs17822931, is associated with the risk of breast cancer in Japanese. <i>Carcinogenesis</i> , 2019, 40, 537-543.	1.3	7
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147	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. <i>PLoS Genetics</i> , 2019, 15, e1007530.	1.5	35
148	Interactions of <i>PVT1</i> and <i>CASC11</i> on Prostate Cancer Risk in African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1067-1075.	1.1	14
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150	Recurrent moderate-risk mutations in Finnish breast and ovarian cancer patients. <i>International Journal of Cancer</i> , 2019, 145, 2692-2700.	2.3	19
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152	Breast cancer pathology and stage are better predicted by risk stratification models that include mammographic density and common genetic variants. <i>Breast Cancer Research and Treatment</i> , 2019, 176, 141-148.	1.1	56
153	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52

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155	Molecular comparison of interval and screen-detected breast cancers. <i>Journal of Pathology</i> , 2019, 248, 243-252.	2.1	15
156	The association between weight at birth and breast cancer risk revisited using Mendelian randomisation. <i>European Journal of Epidemiology</i> , 2019, 34, 591-600.	2.5	16
157	<i>RECQL5</i> : Another DNA helicase potentially involved in hereditary breast cancer susceptibility. <i>Human Mutation</i> , 2019, 40, 566-577.	1.1	16
158	Genetic Epidemiology of Breast Cancer in Latin America. <i>Genes</i> , 2019, 10, 153.	1.0	34
159	MCF-7 as a Model for Functional Analysis of Breast Cancer Risk Variants. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1735-1745.	1.1	7
162	Impact of glycemic traits, type 2 diabetes and metformin use on breast and prostate cancer risk: a Mendelian randomization study. <i>BMJ Open Diabetes Research and Care</i> , 2019, 7, e000872.	1.2	34
163	Making the Most of Clumping and Thresholding for Polygenic Scores. <i>American Journal of Human Genetics</i> , 2019, 105, 1213-1221.	2.6	123
164	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019, 575, 652-657.	13.7	198
166	Prediction and clinical utility of a contralateral breast cancer risk model. <i>Breast Cancer Research</i> , 2019, 21, 144.	2.2	24
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