Andrew E Teschendorff

List of Publications by Year
in descending order

149 papers	20,044 citations	11608 70 h-index	12233 133 g-index
166 all docs	166 docs citations	166 times ranked	29839 citing authors

#	Article	IF	Citations
1	International Multicenter Study of Clinical Outcomes of Sinonasal Melanoma Shows Survival Benefit for Patients Treated with Immune Checkpoint Inhibitors and Potential Improvements to the Current TNM Staging System. Journal of Neurological Surgery, Part B: Skull Base, 2023, 84, 307-319.	0.4	10
2	A comparison of epithelial cell content of oral samples estimated using cytology and DNA methylation. Epigenetics, 2022, 17, 327-334.	1.3	11
3	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. Genome Biology, 2022, 23, 13.	3.8	19
4	Clinical outcomes, Kadish-INSICA staging and therapeutic targeting of somatostatin receptor 2 in olfactory neuroblastoma. European Journal of Cancer, 2022, 162, 221-236.	1.3	22
5	Novel epigenetic network biomarkers for early detection of esophageal cancer. Clinical Epigenetics, 2022, 14, 23.	1.8	11
6	Multicenter Analysis of Clinical Outcomes of Sinonasal Mucosal Melanoma. Journal of Neurological Surgery, Part B: Skull Base, 2022, 83, .	0.4	0
7	Cell-type heterogeneity: Why we should adjust for it in epigenome and biomarker studies. Clinical Epigenetics, 2022, 14, 31.	1.8	18
8	A pan-tissue DNA methylation atlas enables in silico decomposition of human tissue methylomes at cell-type resolution. Nature Methods, 2022, 19, 296-306.	9.0	46
9	Making sense of the ageing methylome. Nature Reviews Genetics, 2022, 23, 585-605.	7.7	86
10	Computational Identification of Preneoplastic Cells Displaying High Stemness and Risk of Cancer Progression. Cancer Research, 2022, 82, 2520-2537.	0.4	9
11	dbDEMC 3.0: Functional Exploration of Differentially Expressed miRNAs in Cancers of Human and Model Organisms. Genomics, Proteomics and Bioinformatics, 2022, 20, 446-454.	3.0	32
12	Inference of age-associated transcription factor regulatory activity changes in single cells. Nature Aging, 2022, 2, 548-561.	5.3	15
13	Ultra-fast scalable estimation of single-cell differentiation potency from scRNA-Seq data. Bioinformatics, 2021, 37, 1528-1534.	1.8	13
14	Statistical mechanics meets single-cell biology. Nature Reviews Genetics, 2021, 22, 459-476.	7.7	65
15	Pan-cancer characterization of long non-coding RNA and DNA methylation mediated transcriptional dysregulation. EBioMedicine, 2021, 68, 103399.	2.7	25
16	EpiDISH web server: Epigenetic Dissection of Intra-Sample-Heterogeneity with online GUI. Bioinformatics, 2020, 36, 1950-1951.	1.8	40
17	Improved detection of tumor suppressor events in single-cell RNA-Seq data. Npj Genomic Medicine, 2020, 5, 43.	1.7	15
18	EPISCORE: cell type deconvolution of bulk tissue DNA methylomes from single-cell RNA-Seq data. Genome Biology, 2020, 21, 221.	3.8	58

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19	A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. Nature Communications, 2020, 11, 4779.	5.8	32
20	A comparison of epigenetic mitotic-like clocks for cancer risk prediction. Genome Medicine, 2020, 12, 56.	3.6	56
21	Detection of Epigenetic Field Defects Using a Weighted Epigenetic Distance-Based Method. Methods in Molecular Biology, 2020, 2117, 109-131.	0.4	0
22	Single-cell landscape in mammary epithelium reveals bipotent-like cells associated with breast cancer risk and outcome. Communications Biology, 2019, 2, 306.	2.0	41
23	Appraising the causal relevance of DNA methylation for risk of lung cancer. International Journal of Epidemiology, 2019, 48, 1493-1504.	0.9	53
24	ebGSEA: an improved Gene Set Enrichment Analysis method for Epigenome-Wide-Association Studies. Bioinformatics, 2019, 35, 3514-3516.	1.8	15
25	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. Bioinformatics, 2019, 35, 4767-4769.	1.8	84
26	Estimating Differentiation Potency of Single Cells Using Single-Cell Entropy (SCENT). Methods in Molecular Biology, 2019, 1935, 125-139.	0.4	12
27	DNA methylation aging clocks: challenges and recommendations. Genome Biology, 2019, 20, 249.	3.8	552
28	Avoiding common pitfalls in machine learning omic data science. Nature Materials, 2019, 18, 422-427.	13.3	83
29	Detection of epigenetic field defects using a weighted epigenetic distance-based method. Nucleic Acids Research, 2019, 47, e6-e6.	6.5	9
30	Accounting for differential variability in detecting differentially methylated regions. Briefings in Bioinformatics, 2019, 20, 47-57.	3.2	10
31	Epigenome-based cancer risk prediction: rationale, opportunities and challenges. Nature Reviews Clinical Oncology, 2018, 15, 292-309.	12.5	129
32	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. Human Molecular Genetics, 2018, 27, 1301-1308.	1.4	102
33	A novel cell-type deconvolution algorithm reveals substantial contamination by immune cells in saliva, buccal and cervix. Epigenomics, 2018, 10, 925-940.	1.0	116
34	Tumor origin detection with tissue-specific miRNA and DNA methylation markers. Bioinformatics, 2018, 34, 398-406.	1.8	308
35	Roadmap for investigating epigenome deregulation and environmental origins of cancer. International Journal of Cancer, 2018, 142, 874-882.	2.3	64
36	Statistical and integrative system-level analysis of DNA methylation data. Nature Reviews Genetics, 2018, 19, 129-147.	7.7	228

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37	Identification of differentially methylated cell types in epigenome-wide association studies. Nature Methods, 2018, 15, 1059-1066.	9.0	166
38	Quantifying Waddingtonâ€™s epigenetic landscape: a comparison of single-cell potency measures. Briefings in Bioinformatics, 2018, , .	3.2	33
39	Tensorial blind source separation for improved analysis of multi-omic data. Genome Biology, 2018, 19, 76.	3.8	20
40	DNA Methylation Patterns in Normal Tissue Correlate more Strongly with Breast Cancer Status than Copy-Number Variants. EBioMedicine, 2018, 31, 243-252.	2.7	27
41	Epigenetic clocks galore: a new improved clock predicts age-acceleration in Hutchinson Gilford Progeria Syndrome patients. Aging, 2018, 10, 1799-1800.	1.4	4
42	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. Aging, 2018, 10, 3541-3557.	1.4	42
43	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. Nature Methods, 2017, 14, 216-217.	9.0	59
44	DNA methylome analysis reveals distinct epigenetic patterns of ascending aortic dissection and bicuspid aortic valve. Cardiovascular Research, 2017, 113, 692-704.	1.8	33
45	Single-cell entropy for accurate estimation of differentiation potency from a cellâ€™s transcriptome. Nature Communications, 2017, 8, 15599.	5.8	230
46	Cell-type deconvolution in epigenome-wide association studies: a review and recommendations. Epigenomics, 2017, 9, 757-768.	1.0	131
47	dbDEMC 2.0: updated database of differentially expressed miRNAs in human cancers. Nucleic Acids Research, 2017, 45, D812-D818.	6.5	296
48	ChAMP: updated methylation analysis pipeline for Illumina BeadChips. Bioinformatics, 2017, 33, 3982-3984.	1.8	572
49	Are objective measures of physical capability related to accelerated epigenetic age? Findings from a British birth cohort. BMJ Open, 2017, 7, e016708.	0.8	36
50	A comparison of reference-based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies. BMC Bioinformatics, 2017, 18, 105.	1.2	297
51	Epigenetic and genetic deregulation in cancer target distinct signaling pathway domains. Nucleic Acids Research, 2017, 45, 583-596.	6.5	18
52	Systems-epigenomics inference of transcription factor activity implicates aryl-hydrocarbon-receptor inactivation as a key event in lung cancer development. Genome Biology, 2017, 18, 236.	3.8	46
53	The potential of circulating tumor DNA methylation analysis for the early detection and management of ovarian cancer. Genome Medicine, 2017, 9, 116.	3.6	122
54	Aberrant regulation of RANKL/OPG in women at high risk of developing breast cancer. Oncotarget, 2017, 8, 3811-3825.	0.8	45

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55	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. Nature Communications, 2016, 7, 13555.	5.8	142
56	Epigenetic drift, epigenetic clocks and cancer risk. Epigenomics, 2016, 8, 705-719.	1.0	101
57	Correlation of an epigenetic mitotic clock with cancer risk. Genome Biology, 2016, 17, 205.	3.8	197
58	The multi-omic landscape of transcription factor inactivation in cancer. Genome Medicine, 2016, 8, 89.	3.6	26
59	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
60	The lncRNA HOTAIR impacts on mesenchymal stem cellsviatriple helix formation. Nucleic Acids Research, 2016, 44, 10631-10643.	6.5	141
61	Menopause accelerates biological aging. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 9327-9332.	3.3	363
62	Tissue-independent and tissue-specific patterns of DNA methylation alteration in cancer. Epigenetics and Chromatin, 2016, 9, 10.	1.8	40
63	Stochastic epigenetic outliers can define field defects in cancer. BMC Bioinformatics, 2016, 17, 178.	1.2	36
64	DNA methylation outliers in normal breast tissue identify field defects that are enriched in cancer. Nature Communications, 2016, 7, 10478.	5.8	195
65	The integrative epigenomic-transcriptomic landscape of ER positive breast cancer. Clinical Epigenetics, 2015, 7, 126.	1.8	24
66	Increased signaling entropy in cancer requires the scale-free property of proteininteraction networks. Scientific Reports, 2015, 5, 9646.	1.6	59
67	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. Genome Medicine, 2015, 7, 108.	3.6	138
68	Î² - catenin is central to DUX4 -driven network rewiring in facioscapulohumeral muscular dystrophy. Journal of the Royal Society Interface, 2015, 12, 20140797.	1.5	52
69	An Integrative Multi-scale Analysis of the Dynamic DNA Methylation Landscape in Aging. PLoS Genetics, 2015, 11, e1004996.	1.5	132
70	A General Strategy for Inter-sample Variability Assessment and Normalisation. Translational Bioinformatics, 2015, , 51-68.	0.0	0
71	Systems Epigenomics and Applications to Ageing and Cancer. Translational Bioinformatics, 2015, , 161-185.	0.0	0
72	Intra-Tumour Signalling Entropy Determines Clinical Outcome in Breast and Lung Cancer. PLoS Computational Biology, 2015, 11, e1004115.	1.5	62

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73	Denoising perturbation signatures reveal an actionable AKT-signaling gene module underlying a poor clinical outcome in endocrine-treated ER+ breast cancer. Genome Biology, 2015, 16, 61.	3.8	5
74	Correlation of Smoking-Associated DNA Methylation Changes in Buccal Cells With DNA Methylation Changes in Epithelial Cancer. JAMA Oncology, 2015, 1, 476.	3.4	177
75	Glioblastoma Stem Cells Respond to Differentiation Cues but Fail to Undergo Commitment and Terminal Cell-Cycle Arrest. Stem Cell Reports, 2015, 5, 829-842.	2.3	93
76	Epigenetic dysregulation and poorer prognosis in DAXX-deficient pancreatic neuroendocrine tumours. Endocrine-Related Cancer, 2015, 22, L13-L18.	1.6	50
77	An integrative pan-cancer-wide analysis of epigenetic enzymes reveals universal patterns of epigenomic deregulation in cancer. Genome Biology, 2015, 16, 140.	3.8	60
78	Variational Bayesian Matrix Factorization for Bounded Support Data. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 876-889.	9.7	151
79	Expression profiling of nuclear receptors in breast cancer identifies TLX as a mediator of growth and invasion in triple-negative breast cancer. Oncotarget, 2015, 6, 21685-21703.	0.8	24
80	JAK2-Centered Interactome Hotspot Identified by an Integrative Network Algorithm in Acute Stanford Type A Aortic Dissection. PLoS ONE, 2014, 9, e89406.	1.1	19
81	The Dynamics of DNA Methylation Covariation Patterns in Carcinogenesis. PLoS Computational Biology, 2014, 10, e1003709.	1.5	52
82	Comparisons of Non-Gaussian Statistical Models in DNA Methylation Analysis. International Journal of Molecular Sciences, 2014, 15, 10835-10854.	1.8	6
83	A BRCA1-mutation associated DNA methylation signature in blood cells predicts sporadic breast cancer incidence and survival. Genome Medicine, 2014, 6, 47.	3.6	53
84	Using high-density DNA methylation arrays to profile copy number alterations. Genome Biology, 2014, 15, R30.	13.9	113
85	ChAMP: 450k Chip Analysis Methylation Pipeline. Bioinformatics, 2014, 30, 428-430.	1.8	757
86	Signalling entropy: A novel network-theoretical framework for systems analysis and interpretation of functional omic data. Methods, 2014, 67, 282-293.	1.9	67
87	Genome-wide age-related changes in DNA methylation and gene expression in human PBMCs. Age, 2014, 36, 9648.	3.0	135
88	A systems-level integrative framework for genome-wide DNA methylation and gene expression data identifies differential gene expression modules under epigenetic control. Bioinformatics, 2014, 30, 2360-2366.	1.8	148
89	Supervised Normalization of Large-Scale Omic Datasets Using Blind Source Separation. Signals and Communication Technology, 2014, , 465-497.	0.4	0
90	Identification and functional validation of HPV-mediated hypermethylation in head and neck squamous cell carcinoma. Genome Medicine, 2013, 5, 15.	3.6	118

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91	Distinctive topology of age-associated epigenetic drift in the human interactome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14138-14143.	3.3	49
92	Epigenetics makes its mark on women-specific cancersâ€"an opportunity to redefine oncological approaches?. Gynecologic Oncology, 2013, 128, 134-143.	0.6	13
93	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. Bioinformatics, 2013, 29, 189-196.	1.8	1,295
94	Age-associated epigenetic drift: implications, and a case of epigenetic thrift?. Human Molecular Genetics, 2013, 22, R7-R15.	1.4	261
95	Meta-analysis of IDH-mutant cancers identifies EBF1 as an interaction partner for TET2. Nature Communications, 2013, 4, 2166.	5.8	152
96	Role of DNA Methylation and Epigenetic Silencing of HAND2 in Endometrial Cancer Development. PLoS Medicine, 2013, 10, e1001551.	3.9	135
97	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. Epigenetics, 2013, 8, 333-346.	1.3	192
98	A VARIATIONAL BAYES BETA MIXTURE MODEL FOR FEATURE SELECTION IN DNA METHYLATION STUDIES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1350005.	0.3	17
99	An integrative network algorithm identifies age-associated differential methylation interactome hotspots targeting stem-cell differentiation pathways. Scientific Reports, 2013, 3, 1630.	1.6	88
100	Cellular network entropy as the energy potential in Waddington's differentiation landscape. Scientific Reports, 2013, 3, 3039.	1.6	129
101	A Network Systems Approach to Identify Functional Epigenetic Drivers in Cancer. Translational Bioinformatics, 2013, , 131-152.	0.0	1
102	Corruption of the Intra-Gene DNA Methylation Architecture Is a Hallmark of Cancer. PLoS ONE, 2013, 8, e68285.	1.1	19
103	Epigenetic aging: insights from network biology. Aging, 2013, 5, 719-720.	1.4	8
104	The Dynamics and Prognostic Potential of DNA Methylation Changes at Stem Cell Gene Loci in Women's Cancer. PLoS Genetics, 2012, 8, e1002517.	1.5	111
105	Differential network entropy reveals cancer system hallmarks. Scientific Reports, 2012, 2, 802.	1.6	154
106	Differential variability improves the identification of cancer risk markers in DNA methylation studies profiling precursor cancer lesions. Bioinformatics, 2012, 28, 1487-1494.	1.8	119
107	A functional methylome map of ulcerative colitis. Genome Research, 2012, 22, 2130-2137.	2.4	116
108	Phenotypic and functional characterisation of the luminal cell hierarchy of the mammary gland. Breast Cancer Research, 2012, 14, R134.	2.2	260

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109	TGFÎ² induces the formation of tumour-initiating cells in claudinlow breast cancer. Nature Communications, 2012, 3, 1055.	5.8	95
110	A comparison of feature selection and classification methods in DNA methylation studies using the Illumina Infinium platform. BMC Bioinformatics, 2012, 13, 59.	1.2	95
111	Comments on: Interpretation of genome-wide infinium methylation data from ligated DNA in formalin-fixed paraffin-embedded paired tumor and normal tissue. BMC Research Notes, 2012, 5, 631.	0.6	2
112	Approximate entropy of network parameters. Physical Review E, 2012, 85, 046111.	0.8	12
113	Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. Nature, 2012, 481, 389-393.	13.7	1,655
114	Epigenetic variability in cells of normal cytology is associated with the risk of future morphological transformation. Genome Medicine, 2012, 4, 24.	3.6	162
115	DART: Denoising Algorithm based on Relevance network Topology improves molecular pathway activity inference. BMC Bioinformatics, 2011, 12, 403.	1.2	26
116	Comparative methylome analysis of benign and malignant peripheral nerve sheath tumors. Genome Research, 2011, 21, 515-524.	2.4	94
117	Independent surrogate variable analysis to deconvolve confounding factors in large-scale microarray profiling studies. Bioinformatics, 2011, 27, 1496-1505.	1.8	232
118	Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. BMC Cancer, 2010, 10, 604.	1.1	144
119	Increased entropy of signal transduction in the cancer metastasis phenotype. BMC Systems Biology, 2010, 4, 104.	3.0	91
120	Genome-wide DNA methylation analysis for diabetic nephropathy in type 1 diabetes mellitus. BMC Medical Genomics, 2010, 3, 33.	0.7	261
121	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. PLoS ONE, 2010, 5, e14040.	1.1	215
122	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. Science Translational Medicine, 2010, 2, 38ra47.	5.8	138
123	Prognostic gene network modules in breast cancer hold promise. Breast Cancer Research, 2010, 12, 317.	2.2	0
124	Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.	1.4	68
125	Genomic gain of 5p15 leads to over-expression of Misu (NSUN2) in breast cancer. Cancer Letters, 2010, 289, 71-80.	3.2	80
126	Genome-wide DNA methylation analysis of archival formalin-fixed paraffin-embedded tissue using the Illumina Infinium HumanMethylation27 BeadChip. Methods, 2010, 52, 248-254.	1.9	92

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127	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. Genome Research, 2010, 20, 440-446.	2.4	740
128	Common germline polymorphisms in COMT, CYP19A1, ESR1, PGR, SULT1E1 and STS and survival after a diagnosis of breast cancer. International Journal of Cancer, 2009, 125, 2687-2696.	2.3	34
129	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	13.7	984
130	The breast cancer somatic 'muta-ome': tackling the complexity. Breast Cancer Research, 2009, 11, 301.	2.2	27
131	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. PLoS ONE, 2009, 4, e8274.	1.1	291
132	ESR1 gene amplification in breast cancer: a common phenomenon?. Nature Genetics, 2008, 40, 806-807.	9.4	62
133	A comprehensive analysis of prognostic signatures reveals the high predictive capacity of the Proliferation, Immune response and RNA splicing modules in breast cancer. Breast Cancer Research, 2008, 10, R93.	2.2	113
134	A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. Breast Cancer Research, 2008, 10, R73.	2.2	87
135	Allele-Specific Up-Regulation of FGFR2 Increases Susceptibility to Breast Cancer. PLoS Biology, 2008, 6, e108.	2.6	254
136	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. PLoS Computational Biology, 2007, 3, e161.	1.5	108
137	BEX2 Is Overexpressed in a Subset of Primary Breast Cancers and Mediates Nerve Growth Factor/Nuclear Factor-ºB Inhibition of Apoptosis in Breast Cancer Cell Lines. Cancer Research, 2007, 67, 6725-6736.	0.4	81
138	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. Genome Biology, 2007, 8, R215.	13.9	275
139	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. Genome Biology, 2007, 8, R214.	13.9	828
140	An immune response gene expression module identifies a good prognosis subtype in estrogen receptor negative breast cancer. Genome Biology, 2007, 8, R157.	13.9	433
141	Co-amplification of 8p12 and 11q13 in breast cancers is not the result of a single genomic event. Genes Chromosomes and Cancer, 2007, 46, 427-439.	1.5	27
142	A consensus prognostic gene expression classifier for ER positive breast cancer. Genome Biology, 2006, 7, R101.	13.9	82
143	Distribution of breakpoints on chromosome 18 in breast, colorectal, and pancreatic carcinoma cell lines. Cancer Genetics and Cytogenetics, 2006, 164, 97-109.	1.0	17
144	Differential expression of selected histone modifier genes in human solid cancers. BMC Genomics, 2006, 7, 90.	1.2	209

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145	Interferon-Â treatment of cervical keratinocytes naturally infected with human papillomavirus 16 episomes promotes rapid reduction in episome numbers and emergence of latent integrants. Carcinogenesis, 2006, 27, 2341-2353.	1.3	100
146	PACK: Profile Analysis using Clustering and Kurtosis to find molecular classifiers in cancer. Bioinformatics, 2006, 22, 2269-2275.	1.8	61
147	A 1â€‰Mb minimal amplicon at 8p11â€“12 in breast cancer identifies new candidate oncogenes. Oncogene, 2005, 24, 5235-5245.	2.6	146
148	A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. Bioinformatics, 2005, 21, 3025-3033.	1.8	73
149	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. PLoS Computational Biology, 2005, preprint, e161.	1.5	0