

# Genetic effects on gene expression across human tissue

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Cracking the regulatory code. <i>Nature</i> , 2017, 550, 190-191.	13.7	18
2	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
3	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	13.7	229
4	Enhancing GTEx by bridging the gaps between genotype, gene expression, and disease. <i>Nature Genetics</i> , 2017, 49, 1664-1670.	9.4	179
5	Identifying <i>cis</i> -mediators for <i>trans</i> -eQTLs across many human tissues using genomic mediation analysis. <i>Genome Research</i> , 2017, 27, 1859-1871.	2.4	72
6	Co-expression networks reveal the tissue-specific regulation of transcription and splicing. <i>Genome Research</i> , 2017, 27, 1843-1858.	2.4	139
7	Quantifying the regulatory effect size of <i>cis</i> -acting genetic variation using allelic fold change. <i>Genome Research</i> , 2017, 27, 1872-1884.	2.4	114
8	Estimating the causal tissues for complex traits and diseases. <i>Nature Genetics</i> , 2017, 49, 1676-1683.	9.4	166
10	Principles of gene regulation across tissues. <i>Nature Reviews Genetics</i> , 2017, 18, 701-701.	7.7	7
11	Molecular Epidemiology of Heart Failure. <i>JACC Basic To Translational Science</i> , 2017, 2, 757-769.	1.9	25
12	Unexplored therapeutic opportunities in the human genome. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 317-332.	21.5	263
13	The importance of cohort studies in the post-GWAS era. <i>Nature Genetics</i> , 2018, 50, 322-328.	9.4	60
14	Co-occurring expression and methylation QTLs allow detection of common causal variants and shared biological mechanisms. <i>Nature Communications</i> , 2018, 9, 804.	5.8	66
15	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	5.8	126
16	From gene networks to drugs: systems pharmacology approaches for AUD. <i>Psychopharmacology</i> , 2018, 235, 1635-1662.	1.5	15
17	2017 Presidential Address: Checking, Balancing, and Celebrating Diversity: Celebrating Some of the Women Who Paved the Way. <i>American Journal of Human Genetics</i> , 2018, 102, 342-349.	2.6	1
18	Advancing translational research and precision medicine with targeted proteomics. <i>Journal of Proteomics</i> , 2018, 189, 1-10.	1.2	72
19	Rare variants in axonogenesis genes connect three families with soundâ€™ color synesthesia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3168-3173.	3.3	34

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20	Cardiomyocytes have mosaic patterns of protein expression. <i>Cardiovascular Pathology</i> , 2018, 34, 50-57.	0.7	18
21	Single nucleotide variant counts computed from RNA sequencing and cellular traffic into human kidney allografts. <i>American Journal of Transplantation</i> , 2018, 18, 2429-2442.	2.6	11
22	Functional Assays to Screen and Dissect Genomic Hits. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002178.	1.6	18
23	Dissecting the sources of gene expression variation in a pan-cancer analysis identifies novel regulatory mutations. <i>Nucleic Acids Research</i> , 2018, 46, 4370-4381.	6.5	40
24	Widespread Enhancer Activity from Core Promoters. <i>Trends in Biochemical Sciences</i> , 2018, 43, 452-468.	3.7	54
25	Genetic variants in mRNA untranslated regions. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1474.	3.2	118
26	High-throughput mouse phenomics for characterizing mammalian gene function. <i>Nature Reviews Genetics</i> , 2018, 19, 357-370.	7.7	78
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28	Selection in the Introgressed Regions of the Chimpanzee Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 1132-1138.	1.1	13
29	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018, 50, 572-580.	9.4	143
30	Environmental microbiology: Too much food for thought? " An argument for reductionism. <i>Environmental Microbiology</i> , 2018, 20, 1929-1935.	1.8	2
31	The Extending Spectrum of NPC1-Related Human Disorders: From Niemann-Pick C1 Disease to Obesity. <i>Endocrine Reviews</i> , 2018, 39, 192-220.	8.9	32
32	Patterns of shared signatures of recent positive selection across human populations. <i>Nature Ecology and Evolution</i> , 2018, 2, 713-720.	3.4	63
33	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , 2018, 9, 490.	5.8	198
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35	Cloud computing for genomic data analysis and collaboration. <i>Nature Reviews Genetics</i> , 2018, 19, 208-219.	7.7	205
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39	The chromatin basis of neurodevelopmental disorders: Rethinking dysfunction along the molecular and temporal axes. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2018, 84, 306-327.	2.5	73
40	Gene and MicroRNA Perturbations of Cellular Response to Pemetrexed Implicate Biological Networks and Enable Imputation of Response in Lung Adenocarcinoma. <i>Scientific Reports</i> , 2018, 8, 733.	1.6	12
41	Asparagine bioavailability governs metastasis in a model of breast cancer. <i>Nature</i> , 2018, 554, 378-381.	13.7	362
42	The complex genetics of human insulin-like growth factor 2 are not reflected in public databases. <i>Journal of Biological Chemistry</i> , 2018, 293, 4324-4333.	1.6	21
43	Brain Transcriptome Databases: A User's Guide. <i>Journal of Neuroscience</i> , 2018, 38, 2399-2412.	1.7	68
44	GTEx project maps wide range of normal human genetic variation. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 263-264.	0.7	6
46	Bacterial genomics of plant adaptation. <i>Nature Genetics</i> , 2018, 50, 2-4.	9.4	1
47	Mapping regulatory variants in hiPSC models. <i>Nature Genetics</i> , 2018, 50, 1-2.	9.4	33
48	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. <i>BioEssays</i> , 2018, 40, 1700148.	1.2	71
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56	RNaseq analysis of bronchial epithelial cells to identify COPD-associated genes and SNPs. <i>BMC Pulmonary Medicine</i> , 2018, 18, 42.	0.8	20
57	Effects on gene expression and behavior of untagged short tandem repeats: the case of arginine vasopressin receptor 1a (AVPR1a) and externalizing behaviors. <i>Translational Psychiatry</i> , 2018, 8, 72.	2.4	11

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59	Genetics in multiple sclerosis: Updates in the era of big data. <i>Clinical and Experimental Neuroimmunology</i> , 2018, 9, 19-24.	0.5	3
60	Sequential regulatory activity prediction across chromosomes with convolutional neural networks. <i>Genome Research</i> , 2018, 28, 739-750.	2.4	324
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62	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
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67	Genetic regulation of <i>IL1RL1</i> methylation and <i>IL1RL1</i> -a protein levels in asthma. <i>European Respiratory Journal</i> , 2018, 51, 1701377.	3.1	24
68	A screen for deeply conserved non-coding GWAS SNPs uncovers a <i>MIR-9-2</i> functional mutation associated to retinal vasculature defects in human. <i>Nucleic Acids Research</i> , 2018, 46, 3517-3531.	6.5	33
69	Clinical and biological significance of a <i>73A&gt;A</i> variation in the <i>CDH1</i> promoter of patients with sporadic gastric carcinoma. <i>Gastric Cancer</i> , 2018, 21, 606-616.	2.7	4
70	Genetic architecture: the shape of the genetic contribution to human traits and disease. <i>Nature Reviews Genetics</i> , 2018, 19, 110-124.	7.7	335
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74	InDePTH: detection of hub genes for developing gene expression networks under anticancer drug treatment. <i>Oncotarget</i> , 2018, 9, 29097-29111.	0.8	8
75	Novel disease syndromes unveiled by integrative multiscale network analysis of diseases sharing molecular effectors and comorbidities. <i>BMC Medical Genomics</i> , 2018, 11, 112.	0.7	8
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92	Highâ€resolution mapping of cancer cell networks using coâ€functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	3.2	61
93	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018, 14, e1007755.	1.5	30
94	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. <i>F1000Research</i> , 2018, 7, 952.	0.8	87

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96	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
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104	Computational Methods for the Pharmacogenetic Interpretation of Next Generation Sequencing Data. <i>Frontiers in Pharmacology</i> , 2018, 9, 1437.	1.6	62
105	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018, 9, 5269.	5.8	331
106	A C6orf10/LOC101929163 locus is associated with age of onset in C9orf72 carriers. <i>Brain</i> , 2018, 141, 2895-2907.	3.7	39
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115	Individual variations in cardiovascular-disease-related protein levels are driven by genetics and gut microbiome. <i>Nature Genetics</i> , 2018, 50, 1524-1532.	9.4	97
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118	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	1.8	15
119	Genome-wide association studies of brain imaging phenotypes in UK Biobank. <i>Nature</i> , 2018, 562, 210-216.	13.7	551
120	Defining the molecular signatures of Achilles tendinopathy and anterior cruciate ligament ruptures: A whole-exome sequencing approach. <i>PLoS ONE</i> , 2018, 13, e0205860.	1.1	16
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125	Taking genomics research to the next level: The Genotype-tissue expression project. <i>Movement Disorders</i> , 2018, 33, 1097-1097.	2.2	2
126	A comparative study of endoderm differentiation in humans and chimpanzees. <i>Genome Biology</i> , 2018, 19, 162.	3.8	32
127	Genetic determinants of childhood and adult height associated with osteosarcoma risk. <i>Cancer</i> , 2018, 124, 3742-3752.	2.0	20
128	Cell-type-specific eQTL of primary melanocytes facilitates identification of melanoma susceptibility genes. <i>Genome Research</i> , 2018, 28, 1621-1635.	2.4	67
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130	The genetics of neuropsychiatric disorders. <i>Brain and Neuroscience Advances</i> , 2018, 2, 239821281879927.	1.8	53
131	Deciphering the Emerging Complexities of Molecular Mechanisms at GWAS Loci. <i>American Journal of Human Genetics</i> , 2018, 103, 637-653.	2.6	93



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134	Exome sequencing study in patients with multiple sclerosis reveals variants associated with disease course. <i>Journal of Neuroinflammation</i> , 2018, 15, 265.	3.1	25
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138	L1 retrotransposition in the soma: a field jumping ahead. <i>Mobile DNA</i> , 2018, 9, 22.	1.3	63
139	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , 2018, 9, 280.	1.1	11
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141	Functionally distinct ERAP1 and ERAP2 are a hallmark of HLA-A29-(Birdshot) Uveitis. <i>Human Molecular Genetics</i> , 2018, 27, 4333-4343.	1.4	42
142	Transethnic and race-stratified genome-wide association study of fibroid characteristics in African American and European American women. <i>Fertility and Sterility</i> , 2018, 110, 737-745.e34.	0.5	12
143	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. <i>PLoS Genetics</i> , 2018, 14, e1007650.	1.5	43
144	Reduced monocyte and macrophage TNFSF15/TL1A expression is associated with susceptibility to inflammatory bowel disease. <i>PLoS Genetics</i> , 2018, 14, e1007458.	1.5	30
145	Decoding the non-coding genome: Opportunities and challenges of genomic and epigenomic consortium data. <i>Current Opinion in Systems Biology</i> , 2018, 11, 82-90.	1.3	4
146	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <i>Nature Genetics</i> , 2018, 50, 1483-1493.	9.4	55
147	Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. <i>Nature Genetics</i> , 2018, 50, 1359-1365.	9.4	93
148	Variable Clinical Manifestations of Xia-Gibbs syndrome: Findings of Consecutively Identified Cases at a Single Children's Hospital. <i>American Journal of Medical Genetics, Part A</i> , 2018, 176, 1890-1896.	0.7	20
149	GWAS with Heterogeneous Data: Estimating the Fraction of Phenotypic Variation Mediated by Gene Expression Data. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3059-3068.	0.8	28

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151	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	2.6	128
152	From genome-wide associations to candidate causal variants by statistical fine-mapping. <i>Nature Reviews Genetics</i> , 2018, 19, 491-504.	7.7	611
153	Rare-Variant Studies to Complement Genome-Wide Association Studies. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 97-112.	2.5	34
154	Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. <i>Cell</i> , 2018, 173, 1796-1809.e17.	13.5	165
155	Genetic-Driven Druggable Target Identification and Validation. <i>Trends in Genetics</i> , 2018, 34, 558-570.	2.9	44
156	A joint view on genetic variants for adiposity differentiates subtypes with distinct metabolic implications. <i>Nature Communications</i> , 2018, 9, 1946.	5.8	33
157	GWAS4D: multidimensional analysis of context-specific regulatory variant for human complex diseases and traits. <i>Nucleic Acids Research</i> , 2018, 46, W114-W120.	6.5	69
158	Genetics of Resistant Hypertension: the Missing Heritability and Opportunities. <i>Current Hypertension Reports</i> , 2018, 20, 48.	1.5	9
159	Large-Scale Analysis of Genetic and Clinical Patient Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 263-274.	2.8	13
160	Genomic approaches for the elucidation of genes and gene networks underlying cardiovascular traits. <i>Biophysical Reviews</i> , 2018, 10, 1053-1060.	1.5	5
161	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018, 50, 956-967.	9.4	389
162	Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. <i>Nature Genetics</i> , 2018, 50, 1041-1047.	9.4	154
163	Immune differences between porcine ileal and jejunal Peyer's patches revealed by global transcriptome sequencing of gut-associated lymphoid tissues. <i>Scientific Reports</i> , 2018, 8, 9077.	1.6	12
164	Sex-specific genetic predictors of Alzheimer's disease biomarkers. <i>Acta Neuropathologica</i> , 2018, 136, 857-872.	3.9	87
165	A non-coding CRHR2 SNP rs255105, a cis-eQTL for a downstream lincRNA AC005154.6, is associated with heroin addiction. <i>PLoS ONE</i> , 2018, 13, e0199951.	1.1	11
166	Natural Selection Has Differentiated the Progesterone Receptor among Human Populations. <i>American Journal of Human Genetics</i> , 2018, 103, 45-57.	2.6	30
167	Transposable elements generate regulatory novelty in a tissue-specific fashion. <i>BMC Genomics</i> , 2018, 19, 468.	1.2	86

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169	Casein kinase 1 $\alpha$ : biological mechanisms and theranostic potential. <i>Cell Communication and Signaling</i> , 2018, 16, 23.	2.7	78
170	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
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1080	Proinflammatory Signaling Pathways and Genomic Signatures in Head and Neck Cancers. , 2021, , 143-184.		2
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1138	Potential biomarkers and lncRNA-mRNA regulatory networks in invasive growth hormone-secreting pituitary adenomas. <i>Journal of Endocrinological Investigation</i> , 2021, 44, 1947-1959.	1.8	9
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1171	Single cell eQTL analysis identifies cell type-specific genetic control of gene expression in fibroblasts and reprogrammed induced pluripotent stem cells. <i>Genome Biology</i> , 2021, 22, 76.	3.8	58
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1174	Advances in bulk and single-cell multi-omics approaches for systems biology and precision medicine. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	31
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1386	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. <i>Nature Communications</i> , 2021, 12, 4178.	5.8	20
1388	Genetic Variants Associated With Intraparenchymal Hemorrhage Progression After Traumatic Brain Injury. <i>JAMA Network Open</i> , 2021, 4, e2116839.	2.8	11
1390	Investigation of convergent and divergent genetic influences underlying schizophrenia and alcohol use disorder. <i>Psychological Medicine</i> , 2023, 53, 1196-1204.	2.7	7
1391	Mendelian randomization analysis identified genes potentially pleiotropically associated with periodontitis. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 4089-4095.	1.8	4
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1393	Enhancers with tissue-specific activity are enriched in intronic regions. <i>Genome Research</i> , 2021, 31, 1325-1336.	2.4	21
1395	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. <i>Nature Communications</i> , 2021, 12, 4496.	5.8	28
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1407	Effect of sex chromosomes versus hormones in neonatal lung injury. <i>JCI Insight</i> , 2021, 6, .	2.3	18
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1411	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR-FlowFISH. <i>Nature Genetics</i> , 2021, 53, 1166-1176.	9.4	36
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1567	Shared genetic pathways contribute to risk of hypertrophic and dilated cardiomyopathies with opposite directions of effect. <i>Nature Genetics</i> , 2021, 53, 128-134.	9.4	155
1568	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	13.7	89
1569	Proteome-wide Systems Genetics to Identify Functional Regulators of Complex Traits. <i>Cell Systems</i> , 2021, 12, 5-22.	2.9	19
1571	Making Biological Sense of Genetic Studies of Age-Related Macular Degeneration. <i>Advances in Experimental Medicine and Biology</i> , 2021, 1256, 201-219.	0.8	2
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1580	Multi-tissue transcriptome-wide association studies. <i>Genetic Epidemiology</i> , 2021, 45, 324-337.	0.6	8
1581	AutoPVS1: An automatic classification tool for PVS1 interpretation of null variants. <i>Human Mutation</i> , 2020, 41, 1488-1498.	1.1	34
1582	Introductory Methods for eQTL Analyses. <i>Methods in Molecular Biology</i> , 2020, 2082, 3-14.	0.4	4
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1587	The Shared Genetic Basis of Hyperuricemia, Gout, and Kidney Function. <i>Seminars in Nephrology</i> , 2020, 40, 586-599.	0.6	10
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1880	False positives in trans-eQTL and co-expression analyses arising from RNA-sequencing alignment errors. <i>F1000Research</i> , 2018, 7, 1860.	0.8	45
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