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Integrating common and rare genetic variation in diverse human populations

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2343	Connecting the Human Variome Project to nutrigenomics. 2010 , 5, 275-283		4
2342	Real-Time SNP Analysis in Secondary-Structure-Folded Nucleic Acids. 2010 , 122, 9134-9137		11
2341	Real-time SNP analysis in secondary-structure-folded nucleic acids. 2010 , 49, 8950-3		50
2340	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
2339	Genomics: The search for association. <i>Nature</i> , 2010 , 467, 1135-8	50.4	17
2338	Expanding HapMap. 2010 , 7, 780-1		2
2337	In Brief. 2010 , 11, 671-671		
2336	Multiethnic genetic association studies improve power for locus discovery. 2010 , 5, e12600		44
2335	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. 2010 , 20, 1344-51		40
2334	The Wire. 2010 , 21, 1223-1225		
2333	Deep resequencing reveals excess rare recent variants consistent with explosive population growth. 2010 , 1, 131		183
2332	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation. 2010 , 330, 1551-7		884
2331	Genetic diversity in India and the inference of Eurasian population expansion. 2010 , 11, R113		47
2330	The \$1,000 genome, the \$100,000 analysis?. 2010 , 2, 84		195
2329	. 2011 ,		3

2328	A world in a grain of sand: human history from genetic data. 2011 , 12, 234	7
2327	Mapping of disease-associated variants in admixed populations. 2011 , 12, 223	47
2326	Identification of cis-regulatory sequence variations in individual genome sequences. 2011 , 3, 65	13
2325	'Big' science: genome regulatory networks and novel molecular tools to improve health. 2011 , 11, 123-6	18
2324	Schizophrenia Key Essays. 2011 , 5-273	
2323	Overview of Genotyping. 2011 , 1-23	3
2322	Extensive genomic and transcriptional diversity identified through massively parallel DNA and RNA sequencing of eighteen Korean individuals. 2011 , 43, 745-52	110
2321	Genomics of cardiovascular disease. 2011 , 365, 2098-109	194
2320	Genome-wide association study identifies five new schizophrenia loci. 2011 , 43, 969-76	1508
2319	Genetic influences on social cognition. 2011 , 69, 85R-91R	66
2318	An X-linked haplotype of Neandertal origin is present among all non-African populations. 2011 , 28, 1957-62	78
2317	Comparing strategies to fine-map the association of common SNPs at chromosome 9p21 with type 2 diabetes and myocardial infarction. 2011 , 43, 801-5	75
2316	Mouse models for Down syndrome-associated developmental cognitive disabilities. 2011 , 33, 404-13	44
2315	Sperm methylation profiles reveal features of epigenetic inheritance and evolution in primates. 2011 , 146, 1029-41	280
2314	Clan genomics and the complex architecture of human disease. 2011 , 147, 32-43	268
2313	Perspectives on human population structure at the cusp of the sequencing era. 2011 , 12, 245-74	58
2312	Next generation genome-wide association tool: design and coverage of a high-throughput European-optimized SNP array. 2011 , 98, 79-89	154
2311	Gene set analysis of genome-wide association studies: methodological issues and perspectives. 2011 , 98, 1-8	162

2310	Design and coverage of high throughput genotyping arrays optimized for individuals of East Asian, African American, and Latino race/ethnicity using imputation and a novel hybrid SNP selection algorithm. 2011 , 98, 422-30	121
2309	A genome-wide linkage study of mammographic density, a risk factor for breast cancer. 2011 , 13, R132	7
2308	Computational and statistical approaches to analyzing variants identified by exome sequencing. 2011 , 12, 227	104
2307	The functional spectrum of low-frequency coding variation. 2011 , 12, R84	161
2306	A comparative analysis of exome capture. 2011 , 12, R97	99
2305	The Genetic Makeup of Azoreans Versus Mainland Portugal Population. 2011 ,	
2304	Accurate estimation of homologue-specific DNA concentration-ratios in cancer samples allows long-range haplotyping. 2011 ,	12
2303	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. 2011 ,	
2302	The importance of global studies of the genetics of type 2 diabetes. 2011 , 35, 91-100	12
2301	Psychiatric genetics in South Africa: cutting a rough diamond. 2011 , 14, 355-66	1
2300	Population genetics of GYPB and association study between GYPB*S/s polymorphism and susceptibility to <i>P. falciparum</i> infection in the Brazilian Amazon. 2011 , 6, e16123	27
2299	Swedish population substructure revealed by genome-wide single nucleotide polymorphism data. 2011 , 6, e16747	28
2298	Similarity in recombination rate estimates highly correlates with genetic differentiation in humans. 2011 , 6, e17913	13
2297	Integrated analyses of copy number variations and gene expression in lung adenocarcinoma. 2011 , 6, e24829	55
2296	Performance of genotype imputation for rare variants identified in exons and flanking regions of genes. 2011 , 6, e24945	46
2295	Protein characterization of a candidate mechanism SNP for Crohn's disease: the macrophage stimulating protein R689C substitution. 2011 , 6, e27269	22
2294	Genetics of osteoarthritis. 2011 , 23, 479-83	30
2293	Selection for translation efficiency on synonymous polymorphisms in recent human evolution. 2011 , 3, 749-61	37

2292	Pharmacogenomic Research in South Africa: Lessons Learned and Future Opportunities in the Rainbow Nation. 2011 , 9, 191-207	49
2291	The UCSC Genome Browser. 2011 , Chapter 18, Unit18.6	31
2290	Effective population size of current human population. 2011 , 93, 105-14	21
2289	Human genetics and genomics a decade after the release of the draft sequence of the human genome. 2011 , 5, 577-622	65
2288	Assessing the patterns of linkage disequilibrium in genic regions of the human genome. 2011 , 278, 3748-55	13
2287	MMP-8 -799 C>T genetic polymorphism is associated with the susceptibility to chronic and aggressive periodontitis in Taiwanese. 2011 , 38, 1078-84	12
2286	Discovery and genotyping of genome structural polymorphism by sequencing on a population scale. 2011 , 43, 269-76	250
2285	From expression QTLs to personalized transcriptomics. 2011 , 12, 277-82	122
2284	Haplotype phasing: existing methods and new developments. 2011 , 12, 703-14	406
2283	Does the new HapMap throw the baby out with the bath water?. 2011 , 19, 733-4	1
2282	Imputation of low-frequency variants using the HapMap3 benefits from large, diverse reference sets. 2011 , 19, 662-6	34
2281	Investigating population stratification and admixture using eigenanalysis of dense genotypes. 2011 , 107, 413-20	25
2280	A genome-wide association study on common SNPs and rare CNVs in anorexia nervosa. 2011 , 16, 949-59	159
2279	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4 833
2278	Charting a course for genomic medicine from base pairs to bedside. <i>Nature</i> , 2011 , 470, 204-13	50.4 677
2277	A decade's perspective on DNA sequencing technology. <i>Nature</i> , 2011 , 470, 198-203	50.4 605
2276	Haplotype-resolved genome sequencing of a Gujarati Indian individual. 2011 , 29, 59-63	194
2275	Phylomedicine: an evolutionary telescope to explore and diagnose the universe of disease mutations. 2011 , 27, 377-86	61

2274	SNPs in ADAMTS13. 2011 , 12, 1147-60	8
2273	DASH: a method for identical-by-descent haplotype mapping uncovers association with recent variation. 2011 , 88, 706-717	60
2272	Indian Siddis: African descendants with Indian admixture. 2011 , 89, 154-61	38
2271	Genome-wide comparison of African-ancestry populations from CARE and other cohorts reveals signals of natural selection. 2011 , 89, 368-81	63
2270	Denisova admixture and the first modern human dispersals into Southeast Asia and Oceania. 2011 , 89, 516-28	390
2269	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. 2011 , 89, 619-27	145
2268	Genome-wide association of copy-number variation reveals an association between short stature and the presence of low-frequency genomic deletions. 2011 , 89, 751-9	52
2267	Shared and unique components of human population structure and genome-wide signals of positive selection in South Asia. 2011 , 89, 731-44	125
2266	Transcriptional control of the human glucocorticoid receptor: identification and analysis of alternative promoter regions. 2011 , 129, 533-43	46
2265	Fine mapping the KLK3 locus on chromosome 19q13.33 associated with prostate cancer susceptibility and PSA levels. 2011 , 129, 675-85	41
2264	Revisiting Mendelian disorders through exome sequencing. 2011 , 129, 351-70	183
2263	Genomic medicine and neurological disease. 2011 , 130, 103-21	12
2262	Current status of genome-wide association studies in cancer. 2011 , 130, 59-78	142
2261	An efficient multiplex genotyping approach for detecting the major worldwide human Y-chromosome haplogroups. 2011 , 125, 879-85	31
2260	Overview of the development of personalized genomic medicine and surgery. 2011 , 35, 1693-9	13
2259	Meta-analysis of 8q24 for seven cancers reveals a locus between NOV and ENPP2 associated with cancer development. 2011 , 12, 156	26
2258	ParaHaplo 3.0: A program package for imputation and a haplotype-based whole-genome association study using hybrid parallel computing. 2011 , 6, 10	2
2257	Different approaches for dealing with rare variants in family-based genetic studies: application of a Genetic Analysis Workshop 17 problem. 2011 , 5 Suppl 9, S78	1

2256	A Monte Carlo test of linkage disequilibrium for single nucleotide polymorphisms. 2011 , 4, 124	1
2255	Enhancements to the ADMIXTURE algorithm for individual ancestry estimation. 2011 , 12, 246	483
2254	Genotyping common and rare variation using overlapping pool sequencing. 2011 , 12 Suppl 6, S2	3
2253	Implication of next-generation sequencing on association studies. 2011 , 12, 322	18
2252	Detecting genetic interactions for quantitative traits with U-statistics. 2011 , 35, 457-68	18
2251	Haplotype variation and genotype imputation in African populations. 2011 , 35, 766-80	31
2250	Transethnic meta-analysis of genomewide association studies. 2011 , 35, 809-22	218
2249	Impact of patatin-like phospholipase-3 (rs738409 C>G) polymorphism on fibrosis progression and steatosis in chronic hepatitis C. 2011 , 54, 60-9	146
2248	Evolutionary genetics evidence of an essential, nonredundant role of the IFN- γ pathway in protective immunity. 2011 , 32, 633-42	20
2247	WAVE: web analysis of the variome. 2011 , 32, 729-34	18
2246	dbNSFP: a lightweight database of human nonsynonymous SNPs and their functional predictions. 2011 , 32, 894-9	529
2245	Racial differences in gene-specific DNA methylation levels are present at birth. 2011 , 91, 728-36	117
2244	Preventing familial breast and ovarian cancer: major research advances with little implication. 2011 , 7, 135-8	0
2243	Gene inactivation and its implications for annotation in the era of personal genomics. 2011 , 25, 1-10	23
2242	A method for identifying haplotypes carrying the causative allele in positive natural selection and genome-wide association studies. 2011 , 27, 822-8	6
2241	Impact of intra- and interspecies variation of occludin on its function as coreceptor for authentic hepatitis C virus particles. 2011 , 85, 7613-21	39
2240	Using human demographic history to infer natural selection reveals contrasting patterns on different families of immune genes. 2011 , 278, 1587-94	6
2239	Archaic human ancestry in East Asia. 2011 , 108, 18301-6	113

2238	Progress and promise of genome-wide association studies for human complex trait genetics. 2011 , 187, 367-83	406
2237	Analysis of genomic variation in non-coding elements using population-scale sequencing data from the 1000 Genomes Project. 2011 , 39, 7058-76	58
2236	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. 2011 , 20, 2869-78	39
2235	Genetic determinants of coronary heart disease: new discoveries and insights from genome-wide association studies. 2011 , 97, 1463-73	17
2234	ICSNPathway: identify candidate causal SNPs and pathways from genome-wide association study by one analytical framework. 2011 , 39, W437-43	62
2233	Global patterns of genetic diversity and signals of natural selection for human ADME genes. 2011 , 20, 528-40	66
2232	Africa: the next frontier for human disease gene discovery?. 2011 , 20, R214-20	22
2231	The landscape of recombination in African Americans. <i>Nature</i> , 2011 , 476, 170-5	50.4 243
2230	A powerful and flexible statistical framework for testing hypotheses of allele-specific gene expression from RNA-seq data. 2011 , 21, 1728-37	132
2229	Genetics of infectious diseases: hidden etiologies and common pathways. 2011 , 49, 1427-37	10
2228	SNP detection and genotyping from low-coverage sequencing data on multiple diploid samples. 2011 , 21, 952-60	117
2227	Human population dispersal "Out of Africa" estimated from linkage disequilibrium and allele frequencies of SNPs. 2011 , 21, 821-9	111
2226	Identification of metabolic modifiers that underlie phenotypic variations in energy-balance regulation. 2011 , 60, 726-34	9
2225	Distinct signatures of diversifying selection revealed by genome analysis of respiratory tract and invasive bacterial populations. 2011 , 108, 5039-44	76
2224	The TERT-CLPTM1L locus for lung cancer predisposes to bronchial obstruction and emphysema. 2011 , 38, 924-31	23
2223	Association of known loci with lipid levels among children and prediction of dyslipidemia in adults. 2011 , 4, 673-80	33
2222	Personalizing prophylactic surgery in cancer: current practice and future perspectives from new genome-wide association studies. 2011 , 11, 813-6	1
2221	Copy number polymorphisms in new HapMap III and Singapore populations. 2011 , 56, 552-60	1

2220	A population-based study of copy number variants and regions of homozygosity in healthy Swedish individuals. 2011 , 56, 524-33	9
2219	Evolutionary genetic dissection of human interferons. 2011 , 208, 2747-59	118
2218	Missing heritability, next-generation genome-wide association studies and primary cancer prevention: an Atlantean illusion?. 2011 , 7, 477-80	3
2217	Genetic variants in CYP (-1A2, -2C9, -2C19, -3A4 and -3A5), VKORC1 and ABCB1 genes in a black South African population: a window into diversity. 2011 , 12, 1663-70	50
2216	Evidence for hitchhiking of deleterious mutations within the human genome. 2011 , 7, e1002240	59
2215	Encyclopedia of Schizophrenia. 2011 ,	2
2214	Single-tissue and cross-tissue heritability of gene expression via identity-by-descent in related or unrelated individuals. 2011 , 7, e1001317	138
2213	Enhanced statistical tests for GWAS in admixed populations: assessment using African Americans from CARE and a Breast Cancer Consortium. 2011 , 7, e1001371	86
2212	Signatures of environmental genetic adaptation pinpoint pathogens as the main selective pressure through human evolution. 2011 , 7, e1002355	349
2211	Breast cancer susceptibility polymorphisms and endometrial cancer risk: a Collaborative Endometrial Cancer Study. 2011 , 32, 1862-6	4
2210	A genome-wide metabolic QTL analysis in Europeans implicates two loci shaped by recent positive selection. 2011 , 7, e1002270	109
2209	Genotype imputation with thousands of genomes. 2011 , 1, 457-70	719
2208	Reconstruction of genealogical relationships with applications to Phase III of HapMap. 2011 , 27, i333-41	12
2207	Identification, replication, and fine-mapping of Loci associated with adult height in individuals of african ancestry. 2011 , 7, e1002298	77
2206	Sequencing of high-complexity DNA pools for identification of nucleotide and structural variants in regions associated with complex traits. 2012 , 20, 77-83	9
2205	Genome-wide detection of natural selection in African Americans pre- and post-admixture. 2012 , 22, 519-27	60
2204	A discovery resource of rare copy number variations in individuals with autism spectrum disorder. 2012 , 2, 1665-85	132
2203	"Why do we have to learn this stuff?"--a new genetics for 21st century students. 2012 , 10, e1001356	43

2202	Genomic tools for evolution and conservation in the chimpanzee: <i>Pan troglodytes ellioti</i> is a genetically distinct population. 2012 , 8, e1002504	45
2201	A quantitative comparison of the similarity between genes and geography in worldwide human populations. 2012 , 8, e1002886	83
2200	Interpretation of the consequences of mutations in protein kinases: combined use of bioinformatics and text mining. 2012 , 3, 323	7
2199	RHOA is a modulator of the cholesterol-lowering effects of statin. 2012 , 8, e1003058	24
2198	Development of a panel of genome-wide ancestry informative markers to study admixture throughout the Americas. 2012 , 8, e1002554	176
2197	Genomic ancestry of North Africans supports back-to-Africa migrations. 2012 , 8, e1002397	219
2196	Knowledge-driven analysis identifies a gene-gene interaction affecting high-density lipoprotein cholesterol levels in multi-ethnic populations. 2012 , 8, e1002714	55
2195	Population structure of Hispanics in the United States: the multi-ethnic study of atherosclerosis. 2012 , 8, e1002640	65
2194	Predicting signatures of "synthetic associations" and "natural associations" from empirical patterns of human genetic variation. 2012 , 8, e1002600	13
2193	Chapter 11: Genome-wide association studies. 2012 , 8, e1002822	708
2192	The metabochip, a custom genotyping array for genetic studies of metabolic, cardiovascular, and anthropometric traits. 2012 , 8, e1002793	395
2191	Consanguinity in Centre d'Étude du Polymorphisme Humain (CEPH) pedigrees. 2012 , 20, 657-67	6
2190	Exact coalescent simulation of new haplotype data from existing reference haplotypes. 2012 , 28, 838-44	1
2189	Efficiency and power as a function of sequence coverage, SNP array density, and imputation. 2012 , 8, e1002604	17
2188	Exome sequencing identifies 2 rare variants for low high-density lipoprotein cholesterol in an extended family. 2012 , 5, 538-46	17
2187	Genomic variation and its impact on gene expression in <i>Drosophila melanogaster</i> . 2012 , 8, e1003055	85
2186	Type 2 diabetes risk alleles demonstrate extreme directional differentiation among human populations, compared to other diseases. 2012 , 8, e1002621	95
2185	Distinguishing between selective sweeps from standing variation and from a de novo mutation. 2012 , 8, e1003011	134

2184	A British approach to sampling. 2012 , 20, 129-30	7
2183	Mapping of the UGT1A locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. 2012 , 21, 1918-30	58
2182	The search for genetic modifiers of disease severity in the Hemoglobinopathies. 2012 , 2,	40
2181	Population genetics models of local ancestry. 2012 , 191, 607-19	186
2180	Limited evidence for classic selective sweeps in African populations. 2012 , 192, 1049-64	56
2179	Human population structure and the adaptive response to pathogen-induced selection pressures. 2012 , 367, 878-86	36
2178	Genomewide pharmacogenetics of bisphosphonate-induced osteonecrosis of the jaw: the role of RBMS3. 2012 , 17, 279-87	84
2177	Random forest Gini importance favours SNPs with large minor allele frequency: impact, sources and recommendations. 2012 , 13, 292-304	65
2176	Worldwide variation in human drug-metabolism enzyme genes CYP2B6 and UGT2B7: implications for HIV/AIDS treatment. 2012 , 13, 555-70	53
2175	VARIANT: Command Line, Web service and Web interface for fast and accurate functional characterization of variants found by Next-Generation Sequencing. 2012 , 40, W54-8	36
2174	BioQ: tracing experimental origins in public genomic databases using a novel data provenance model. 2012 , 28, 1189-91	11
2173	Fine mapping and conditional analysis identify a new mutation in the autoimmunity susceptibility gene BLK that leads to reduced half-life of the BLK protein. 2012 , 71, 1219-26	28
2172	Estimation of alternative splicing variability in human populations. 2012 , 22, 528-38	49
2171	Lymphoblastoid cell lines in pharmacogenomic discovery and clinical translation. 2012 , 13, 55-70	82
2170	Efficiency of trans-ethnic genome-wide meta-analysis and fine-mapping. 2012 , 20, 1300-7	20
2169	Psoriasis and other complex trait dermatoses: from Loci to functional pathways. 2012 , 132, 915-22	68
2168	The linkage disequilibrium pattern of the angiotensin converting enzyme gene in Arabic and Asian population groups. 2012 , 39, 538-40	2
2167	WT1 mutations and single nucleotide polymorphism rs16754 analysis of patients with pediatric acute myeloid leukemia in a Chinese population. 2012 , 53, 2195-204	10

2166	iSNP: An integrated, automatically updated SNP database. 2012,	
2165	Why personalized medicine will fail if we stay the course. 2012, 9, 839-847	27
2164	Optimized filtering reduces the error rate in detecting genomic variants by short-read sequencing. 2011, 30, 61-8	163
2163	Comprehensive evaluation of imputation performance in African Americans. 2012, 57, 411-21	11
2162	Genome-wide association study of serious blistering skin rash caused by drugs. 2012, 12, 96-104	28
2161	cn.MOPS: mixture of Poissons for discovering copy number variations in next-generation sequencing data with a low false discovery rate. 2012, 40, e69	284
2160	GWASdb: a database for human genetic variants identified by genome-wide association studies. 2012, 40, D1047-54	143
2159	Common genetic variants in the PSCA gene influence gene expression and bladder cancer risk. 2012, 109, 4974-9	69
2158	Ethnic differences in genetic predisposition to hypertension. 2012, 35, 574-81	41
2157	HapZipper: sharing HapMap populations just got easier. 2012, 40, e159	1
2156	EnigmaVis: online interactive visualization of genome-wide association studies of the Enhancing NeuroImaging Genetics through Meta-Analysis (ENIGMA) consortium. 2012, 15, 414-8	27
2155	Alzheimer's disease risk gene, GAB2, is associated with regional brain volume differences in 755 young healthy twins. 2012, 15, 286-95	15
2154	Relationship of a variant in the NTRK1 gene to white matter microstructure in young adults. 2012, 32, 5964-72	34
2153	Epigenetic effects on eye diseases. 2012, 7, 127-134	4
2152	Donor ABCB1 variant associates with increased risk for kidney allograft failure. 2012, 23, 1891-9	58
2151	Simultaneous Analysis of Common and Rare Variants in Complex Traits: Application to SNPs (SCARVAsnp). 2012, 6, 177-85	5
2150	Combining markers into haplotypes can improve population structure inference. 2012, 190, 159-74	31
2149	ADHDgene: a genetic database for attention deficit hyperactivity disorder. 2012, 40, D1003-9	50

2148	CellBase, a comprehensive collection of RESTful web services for retrieving relevant biological information from heterogeneous sources. 2012 , 40, W609-14	24
2147	Mining the unknown: a systems approach to metabolite identification combining genetic and metabolic information. 2012 , 8, e1003005	126
2146	The gene in its natural habitat: the importance of gene-trait interactions. 2012 , 24, 1307-18	22
2145	Investigation of the genetic association between quantitative measures of psychosis and schizophrenia: a polygenic risk score analysis. 2012 , 7, e37852	53
2144	A systematic characterization of genes underlying both complex and Mendelian diseases. 2012 , 21, 1611-24	27
2143	DECIPHER: web-based, community resource for clinical interpretation of rare variants in developmental disorders. 2012 , 21, R37-44	55
2142	The chromosome 2p21 region harbors a complex genetic architecture for association with risk for renal cell carcinoma. 2012 , 21, 1190-200	33
2141	Interleukin-1 β gene variants influence bone mineral density and the risk of osteoporotic hip fractures in elderly Slovenian people. 2012 , 50, 1379-85	10
2140	Performance of genotype imputations using data from the 1000 Genomes Project. 2012 , 73, 18-25	31
2139	Improved eigenanalysis of discrete subpopulations and admixture using the minimum average partial test. 2012 , 73, 73-83	10
2138	Eotaxin/CCL11 in idiopathic retroperitoneal fibrosis. 2012 , 27, 3875-84	24
2137	DETECTING HIGHLY DIFFERENTIATED COPY-NUMBER VARIANTS FROM POOLED POPULATION SEQUENCING. 2012 ,	1
2136	The expanding role of epigenetics. 2012 , 2012, 7	9
2135	A coalescent model for genotype imputation. 2012 , 191, 1239-55	18
2134	A comparison of gene region simulation methods. 2012 , 7, e40925	3
2133	African ancestry and innate immunity contribute to the incidence of multicentric Castleman's disease in HIV-1/Kaposi's sarcoma herpesvirus-coinfected individuals. 2012 , 7, 729-734	3
2132	VWF sequence variants: innocent until proven guilty. 2012 , 119, 1959-60	1
2131	Effect of MHC and non-MHC donor/recipient genetic disparity on the outcome of allogeneic HCT. 2012 , 120, 2796-806	65

2130	NetView: a high-definition network-visualization approach to detect fine-scale population structures from genome-wide patterns of variation. 2012 , 7, e48375	73
2129	An atlas of the Epstein-Barr virus transcriptome and epigenome reveals host-virus regulatory interactions. 2012 , 12, 233-45	175
2128	Changes in genome content generated via segregation of non-allelic homologs. 2012 , 72, 390-9	21
2127	Individual differences in amygdala-medial prefrontal anatomy link negative affect, impaired social functioning, and polygenic depression risk. 2012 , 32, 18087-100	223
2126	Highly penetrant alterations of a critical region including BDNF in human psychopathology and obesity. 2012 , 69, 1238-46	16
2125	Molecular diagnosis of infantile mitochondrial disease with targeted next-generation sequencing. 2012 , 4, 118ra10	362
2124	The transcriptional landscape and mutational profile of lung adenocarcinoma. 2012 , 22, 2109-19	435
2123	Reconstructing the population history of European Romani from genome-wide data. 2012 , 22, 2342-9	73
2122	Population-specificity of human DNA methylation. 2012 , 13, R8	203
2121	Human pigmentation genes under environmental selection. 2012 , 13, 248	120
2120	Next generation deep sequencing and vaccine design: today and tomorrow. 2012 , 30, 443-52	48
2119	Use of support vector machines for disease risk prediction in genome-wide association studies: concerns and opportunities. 2012 , 33, 1708-18	28
2118	Zukünftige Entwicklung der gynkologischen Onkologie. 2012 , 45, 678-683	
2117	Meiotic recombinations within major histocompatibility complex of human embryos. 2012 , 64, 839-44	5
2116	Copy number variation in the cattle genome. 2012 , 12, 609-24	38
2115	Systems genetics of metabolism: the use of the BXD murine reference panel for multiscalar integration of traits. 2012 , 150, 1287-99	150
2114	Africa: continent of genome contrasts with implications for biomedical research and health. 2012 , 586, 2813-9	24
2113	Expanding data and resources for forensic use of SNPs in individual identification. 2012 , 6, 646-52	32

2112	Recent Findings on the Genetics of Obesity: Is there Public Health Relevance?. 2012 , 1, 239-248	3
2111	Identifying disease mutations in genomic medicine settings: current challenges and how to accelerate progress. 2012 , 4, 58	56
2110	A tale of two haplotypes: the EDA2R/AR Intergenic region is the most divergent genomic segment between Africans and East Asians in the human genome. 2012 , 84, 641-94	3
2109	PCAdmix: principal components-based assignment of ancestry along each chromosome in individuals with admixed ancestry from two or more populations. 2012 , 84, 343-64	121
2108	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. 2012 , 44, 981-90	1482
2107	Human genetic variation of CYP450 superfamily: analysis of functional diversity in worldwide populations. 2012 , 13, 1951-60	43
2106	Genomic variation in seven Khoe-San groups reveals adaptation and complex African history. 2012 , 338, 374-9	286
2105	Chromosome 9 ALS and FTD locus is probably derived from a single founder. 2012 , 33, 209.e3-8	103
2104	Systematic localization of common disease-associated variation in regulatory DNA. 2012 , 337, 1190-5	2262
2103	Ancient admixture in human history. 2012 , 192, 1065-93	1212
2102	Genome-wide association study in a Swedish population yields support for greater CNV and MHC involvement in schizophrenia compared with bipolar disorder. 2012 , 17, 880-6	196
2101	Genome-wide association study identifies multiple loci influencing human serum metabolite levels. 2012 , 44, 269-76	441
2100	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. 2012 , 21, 1444-55	74
2099	Extensive genetic variation in somatic human tissues. 2012 , 109, 18018-23	116
2098	Vitamin D receptor gene haplotypes and polymorphisms and risk of breast cancer: a nested case-control study. 2012 , 21, 1856-67	33
2097	Estimating kinship in admixed populations. 2012 , 91, 122-38	145
2096	Disease associated cytokine SNPs database: an annotation and dissemination model. 2012 , 57, 107-12	9
2095	Evolutionary meta-analysis of association studies reveals ancient constraints affecting disease marker discovery. 2012 , 29, 2087-94	17

2094	Fine-mapping classical HLA variation associated with durable host control of HIV-1 infection in African Americans. 2012 , 21, 4334-47	51
2093	SparSNP: fast and memory-efficient analysis of all SNPs for phenotype prediction. 2012 , 13, 88	25
2092	Estimating demographic parameters from large-scale population genomic data using Approximate Bayesian Computation. 2012 , 13, 22	32
2091	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. 2012 , 13, 34	50
2090	Accurate variant detection across non-amplified and whole genome amplified DNA using targeted next generation sequencing. 2012 , 13, 500	21
2089	Genetic variants associated with breast size also influence breast cancer risk. 2012 , 13, 53	50
2088	Shared ancestral susceptibility to colorectal cancer and other nutrition related diseases. 2012 , 13, 94	4
2087	Linkage disequilibrium analysis reveals an albuminuria risk haplotype containing three missense mutations in the cubilin gene with striking differences among European and African ancestry populations. 2012 , 13, 142	4
2086	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. 2012 , 5, 6	13
2085	Clinical review: Genome-wide association studies of skeletal phenotypes: what we have learned and where we are headed. 2012 , 97, E1958-77	80
2084	The UCSC Genome Browser. 2012 , Chapter 1, Unit1.4	69
2083	Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. 2012 , 44, 955-9	1292
2082	Population-based case-control association studies. 2012 , Chapter 1, Unit1.17	9
2081	Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. 2012 , 44, 1341-8	681
2080	Interpreting genetic effects through models of cardiac electromechanics. 2012 , 303, H1294-303	8
2079	Applying in silico integrative genomics to genetic studies of human disease. 2012 , 103, 133-56	1
2078	Identity by descent between distant relatives: detection and applications. 2012 , 46, 617-33	97
2077	Human genome sequencing in health and disease. 2012 , 63, 35-61	343

2076	Next-generation sequencing: impact of exome sequencing in characterizing Mendelian disorders. 2012 , 57, 621-32	155
2075	Personalized Medicine in the Genomics Era: highlights from an international symposium on childhood heart disease. 2012 , 8, 157-60	5
2074	A multiplex SNP assay for the dissection of human Y-chromosome haplogroup O representing the major paternal lineage in East and Southeast Asia. 2012 , 57, 65-9	20
2073	Parameters in dynamic models of complex traits are containers of missing heritability. 2012 , 8, e1002459	19
2072	Adaptive genetic variation and population differences. 2012 , 108, 461-89	8
2071	Clinical integration of next-generation sequencing technology. 2012 , 32, 585-99	49
2070	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE collaboration): a meta-analysis of genome-wide association studies. 2012 , 11, 951-62	359
2069	Phasing of many thousands of genotyped samples. 2012 , 91, 238-51	87
2068	Genomic patterns of homozygosity in worldwide human populations. 2012 , 91, 275-92	281
2067	Population genetic inference from personal genome data: impact of ancestry and admixture on human genomic variation. 2012 , 91, 660-71	77
2066	Exploring population admixture dynamics via empirical and simulated genome-wide distribution of ancestral chromosomal segments. 2012 , 91, 849-62	25
2065	Confirmation that the AKT1 (rs2494732) genotype influences the risk of psychosis in cannabis users. 2012 , 72, 811-6	184
2064	Functional analysis of HapMap SNPs. 2012 , 511, 358-63	5
2063	Is 'forward' the same as 'plus'? And other adventures in SNP allele nomenclature. 2012 , 28, 361-3	13
2062	Role of Genomic Medicine in Middle and Inner Ear Diseases. 2012 , 63, 470-479	
2061	[Role of genomic medicine in middle and inner ear diseases]. 2012 , 63, 470-9	1
2060	[Population genetics and human immunity: the interferon paradigm]. 2012 , 28, 1095-101	0
2059	Allele identification in assembled genomic sequence datasets. 2012 , 888, 197-211	1

2058 Genetic Tools in Gastrointestinal Diseases. **2012**, 65-73

2057 Genotyping of single nucleotide polymorphisms by 5' nuclease allelic discrimination. **2012**, 882, 173-82 22

2056 Identification of Nucleotide Variation in Genomes Using Next-Generation Sequencing. **2012**, 257-276

2055 A genetic variant near olfactory receptor genes influences cilantro preference. **2012**, 1, 50

2054 Common folate gene variant, MTHFR C677T, is associated with brain structure in two independent cohorts of people with mild cognitive impairment. **2012**, 1, 179-87 25

2053 Absolute quantification of somatic DNA alterations in human cancer. **2012**, 30, 413-21 1229

2052 Molecular Genetics and Personalized Medicine. **2012**, 1

2051 BRCA1 And BRCA2 analysis of Argentinean breast/ovarian cancer patients selected for age and family history highlights a role for novel mutations of putative south-American origin. **2012**, 1, 20 34

2050 Copy number variation of individual cattle genomes using next-generation sequencing. **2012**, 22, 778-90 204

2049 Functional genetic screen of human diversity reveals that a methionine salvage enzyme regulates inflammatory cell death. **2012**, 109, E2343-52 47

2048 Imputation of rare variants in next-generation association studies. **2012**, 74, 196-204 10

2047 Insights into the regulation of human CNV-miRNAs from the view of their target genes. **2012**, 13, 707 15

2046 Fine mapping of copy number variations on two cattle genome assemblies using high density SNP array. **2012**, 13, 376 71

2045 Annotate-it: a Swiss-knife approach to annotation, analysis and interpretation of single nucleotide variation in human disease. **2012**, 4, 73 27

2044 Multiple sclerosis risk variant HLA-DRB1*1501 associates with high expression of DRB1 gene in different human populations. **2012**, 7, e29819 67

2043 Genome-wide association scan identifies a risk locus for preeclampsia on 2q14, near the inhibin, beta B gene. **2012**, 7, e33666 70

2042 The Brisbane Systems Genetics Study: genetical genomics meets complex trait genetics. **2012**, 7, e35430 73

2041 Evaluation of the metabochip genotyping array in African Americans and implications for fine mapping of GWAS-identified loci: the PAGE study. **2012**, 7, e35651 59

2040	Cis-acting polymorphisms affect complex traits through modifications of microRNA regulation pathways. 2012 , 7, e36694	31
2039	Prenatal famine and genetic variation are independently and additively associated with DNA methylation at regulatory loci within IGF2/H19. 2012 , 7, e37933	118
2038	GLADX: an automated approach to analyze the lineage-specific loss and pseudogenization of genes. 2012 , 7, e38792	7
2037	Lactase persistence and lipid pathway selection in the Maasai. 2012 , 7, e44751	40
2036	Linkage disequilibrium decay and past population history in the human genome. 2012 , 7, e46603	14
2035	Predicting the functional effect of amino acid substitutions and indels. 2012 , 7, e46688	1840
2034	Selective constraint on the upstream open reading frames that overlap with coding sequences in animals. 2012 , 7, e48413	9
2033	HGDP and HapMap analysis by Ancestry Mapper reveals local and global population relationships. 2012 , 7, e49438	12
2032	Unexpected relationships and inbreeding in HapMap phase III populations. 2012 , 7, e49575	10
2031	Empirical distributions of F(ST) from large-scale human polymorphism data. 2012 , 7, e49837	32
2030	Assessment of genotype imputation performance using 1000 Genomes in African American studies. 2012 , 7, e50610	35
2029	Population Analysis of Pharmacogenetic Polymorphisms Related to Acute Lymphoblastic Leukemia Drug Treatment. 2012 , 32, 247-253	4
2028	Genotype Imputation for Latinos Using the HapMap and 1000 Genomes Project Reference Panels. 2012 , 3, 117	15
2027	Leveraging ethnic group incidence variation to investigate genetic susceptibility to glioma: a novel candidate SNP approach. 2012 , 3, 203	11
2026	Will personalized medicine challenge or reify categories of race and ethnicity?. 2012 , 14, 657-63	5
2025	Genetics and Genomics in Cardiovascular Gene Discovery. 2012 , 231-259	2
2024	Computational methods to work as first-pass filter in deleterious SNP analysis of alkaptonuria. 2012 , 2012, 738423	7
2023	A U-Statistic-based random Forest approach for genetic association study. 2012 , 4, 2607-2617	2

2022	Recent explosive human population growth has resulted in an excess of rare genetic variants. 2012 , 336, 740-3	387
2021	Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. 2012 , 336, 466-9	410
2020	The origin, global distribution, and functional impact of the human 8p23 inversion polymorphism. 2012 , 22, 1144-53	48
2019	Melanesian blond hair is caused by an amino acid change in TYRP1. 2012 , 336, 554	85
2018	Amino acid position 11 of HLA-DR β is a major determinant of chromosome 6p association with ulcerative colitis. 2012 , 13, 245-52	30
2017	MHC-resident variation affects risks after unrelated donor hematopoietic cell transplantation. 2012 , 4, 144ra101	44
2016	Structural haplotypes and recent evolution of the human 17q21.31 region. 2012 , 44, 881-5	86
2015	Single nucleotide polymorphism of Wilms' tumor 1 gene rs16754 in Korean patients with cytogenetically normal acute myeloid leukemia. 2012 , 91, 671-677	15
2014	The influence of race and ethnicity on the biology of cancer. 2012 , 12, 648-53	37
2013	Smoking and genetic risk variation across populations of European, Asian, and African American ancestry--a meta-analysis of chromosome 15q25. 2012 , 36, 340-51	63
2012	DIVERGENOME: a bioinformatics platform to assist population genetics and genetic epidemiology studies. 2012 , 36, 360-7	6
2011	A two-platform design for next generation genome-wide association studies. 2012 , 36, 400-8	12
2010	Using maximal segmental score in genome-wide association studies. 2012 , 36, 594-601	4
2009	Variants in ABCB1, TGFB1, and XRCC1 genes and susceptibility to viral hepatitis A infection in Mexican Americans. 2012 , 55, 1008-18	11
2008	Chromosomal variation in lymphoblastoid cell lines. 2012 , 33, 1075-86	29
2007	Human genomic disease variants: a neutral evolutionary explanation. 2012 , 22, 1383-94	32
2006	Impact of microRNA regulation on variation in human gene expression. 2012 , 22, 1243-54	182
2005	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. 2012 , 44, 631-5	184

2004	HapMap European American genotypes are compatible with the hypothesis of MHC-dependent mate choice (response to DOI 10.1002/bies.201200023, Derti and Roth). 2012 , 34, 871-2	3
2003	Identification of novel germline polymorphisms governing capecitabine sensitivity. 2012 , 118, 4063-73	23
2002	Genome-wide association analysis identifies susceptibility loci for migraine without aura. 2012 , 44, 777-82	243
2001	Non-random mate choice in humans: insights from a genome scan. 2012 , 21, 587-96	16
2000	Combined analysis of genome-wide association studies for Crohn disease and psoriasis identifies seven shared susceptibility loci. 2012 , 90, 636-47	224
1999	Genome-wide meta-analysis of psoriatic arthritis identifies susceptibility locus at REL. 2012 , 132, 1133-40	89
1998	Ethiopian genetic diversity reveals linguistic stratification and complex influences on the Ethiopian gene pool. 2012 , 91, 83-96	133
1997	Polymorphisms in the glial glutamate transporter SLC1A2 are associated with essential tremor. 2012 , 79, 243-8	94
1996	Genetic variants in IGF-I, IGF-II, IGFBP-3, and adiponectin genes and colon cancer risk in African Americans and Whites. 2012 , 23, 1127-38	35
1995	Genetic variants associated with the white blood cell count in 13,923 subjects in the eMERGE Network. 2012 , 131, 639-52	92
1994	Adaptive evolution of loci covarying with the human African Pygmy phenotype. 2012 , 131, 1305-17	24
1993	Rare deletions at the neurexin 3 locus in autism spectrum disorder. 2012 , 90, 133-41	155
1992	A general framework for two-stage analysis of genome-wide association studies and its application to case-control studies. 2012 , 90, 760-73	21
1991	Genetic adaptation of fatty-acid metabolism: a human-specific haplotype increasing the biosynthesis of long-chain omega-3 and omega-6 fatty acids. 2012 , 90, 809-20	148
1990	SHANK1 Deletions in Males with Autism Spectrum Disorder. 2012 , 90, 879-87	233
1989	Meta-analysis indicates that common variants at the DISC1 locus are not associated with schizophrenia. 2012 , 17, 634-41	61
1988	The genomics of autoimmune disease in the era of genome-wide association studies and beyond. 2012 , 11, 267-75	47
1987	Genome-wide association studies and prediction of normal tissue toxicity. 2012 , 22, 91-9	22

1986	Next-generation sequencing approaches for genetic mapping of complex diseases. 2012 , 248, 10-22	15
1985	Towards an understanding of the role of p53 in adrenocortical carcinogenesis. 2012 , 351, 101-10	49
1984	Direct mutation analysis by high-throughput sequencing: from germline to low-abundant, somatic variants. 2012 , 729, 1-15	67
1983	Human evolutionary genomics: ethical and interpretive issues. 2012 , 28, 137-45	18
1982	Current understanding of human genetics and genetic analysis of psoriasis. 2012 , 39, 231-41	44
1981	Copy number variation in the genomes of domestic animals. 2012 , 43, 503-17	97
1980	What can genetics tell us about the cause of fixed airflow obstruction?. 2012 , 42, 1176-82	6
1979	Search for regulatory SNPs associated with colon cancer in the APC and MLH1 genes. 2012 , 2, 222-228	3
1978	Genovar: a detection and visualization tool for genomic variants. 2012 , 13 Suppl 7, S12	1
1977	Evolutionary forces shaping genomic islands of population differentiation in humans. 2012 , 13, 107	40
1976	Predicting cancer-associated germline variations in proteins. 2012 , 13 Suppl 4, S8	2
1975	Epigenetic functions enriched in transcription factors binding to mouse recombination hotspots. 2012 , 10 Suppl 1, S11	6
1974	Next generation analytic tools for large scale genetic epidemiology studies of complex diseases. 2012 , 36, 22-35	47
1973	Genotype imputation of MetaboChip SNPs using a study-specific reference panel of ~4,000 haplotypes in African Americans from the Women's Health Initiative. 2012 , 36, 107-17	49
1972	Transmission distortion in Crohn's disease risk gene ATG16L1 leads to sex difference in disease association. 2012 , 18, 312-22	12
1971	The impact of Converso Jews on the genomes of modern Latin Americans. 2012 , 131, 251-63	29
1970	Fine mapping of 14q24.1 breast cancer susceptibility locus. 2012 , 131, 479-90	5
1969	Estimating population size via line graph reconstruction. 2013 , 8, 17	1

1968	Distribution, functional impact, and origin mechanisms of copy number variation in the barley genome. 2013 , 14, R58	81
1967	Multiplex target capture with double-stranded DNA probes. 2013 , 5, 50	15
1966	Inference of human continental origin and admixture proportions using a highly discriminative ancestry informative 41-SNP panel. 2013 , 4, 13	69
1965	Complete haplotype sequence of the human immunoglobulin heavy-chain variable, diversity, and joining genes and characterization of allelic and copy-number variation. 2013 , 92, 530-46	150
1964	Population Genetics. 2013 , 1-12	5
1963	Single-cell gene expression analysis reveals genetic associations masked in whole-tissue experiments. 2013 , 31, 748-52	173
1962	Genetic programs in human and mouse early embryos revealed by single-cell RNA sequencing. <i>Nature</i> , 2013 , 500, 593-7	50.4 622
1961	Pharmacogenetics and the development of personalized approaches for combination therapy in asthma. 2013 , 13, 443-52	9
1960	Small effective population size and genetic homogeneity in the Val Borbera isolate. 2013 , 21, 89-94	20
1959	Genotype imputation in genome-wide association studies. 2013 , Chapter 1, Unit 1.25	29
1958	Genetic evidence for recent population mixture in India. 2013 , 93, 422-38	177
1957	7th International Conference on Practical Applications of Computational Biology & Bioinformatics. 2013 ,	1
1956	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. 2013 , 5, 3-25	14
1955	Quantifying single nucleotide variant detection sensitivity in exome sequencing. 2013 , 14, 195	63
1954	DHCR7 mutations linked to higher vitamin D status allowed early human migration to northern latitudes. 2013 , 13, 144	43
1953	Detecting negative selection on recurrent mutations using gene genealogy. 2013 , 14, 37	3
1952	First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip. 2013 , 127, 559-72	38
1951	Genome-wide pathway analysis in major depressive disorder. 2013 , 51, 428-36	16

1950	Imputation across genotyping arrays for genome-wide association studies: assessment of bias and a correction strategy. 2013 , 132, 509-22	35
1949	Multifactorial Inheritance and Complex Diseases. 2013 , 1-15	1
1948	Rare-disease genetics in the era of next-generation sequencing: discovery to translation. 2013 , 14, 681-91	500
1947	Variation at diabetes- and obesity-associated Loci may mirror neutral patterns of human population diversity and diabetes prevalence in India. 2013 , 77, 392-408	3
1946	Immune Homeostasis. 2013 ,	0
1945	Pharmacogenomic Discovery Delineating the Genetic Basis of Drug Response. 2013 , 1, 143-149	8
1944	Genetics of Population Differences in Drug Response. 2013 , 1, 162-170	21
1943	A synonymous polymorphic variation in ACADM exon 11 affects splicing efficiency and may affect fatty acid oxidation. 2013 , 110, 122-8	18
1942	Detecting and characterizing genomic signatures of positive selection in global populations. 2013 , 92, 866-81	56
1941	Pharmacogenetics of olanzapine metabolism. 2013 , 14, 1319-36	28
1940	Genetic variants within the MHC region are associated with immune responsiveness to childhood vaccinations. 2013 , 31, 5381-91	32
1939	Detection of single nucleotide polymorphisms by PCR conformation-difference gel electrophoresis. 2013 , 35, 515-22	4
1938	Race, genetic ancestry and response to antidepressant treatment for major depression. 2013 , 38, 2598-606	27
1937	Using identity by descent estimation with dense genotype data to detect positive selection. 2013 , 21, 205-11	33
1936	IL1RN coding variant is associated with lower risk of acute respiratory distress syndrome and increased plasma IL-1 receptor antagonist. 2013 , 187, 950-9	59
1935	Pathway analysis of a genome-wide association study in schizophrenia. 2013 , 525, 107-15	41
1934	Design of targeted, capture-based, next generation sequencing tests for precision cancer therapy. 2013 , 206, 420-31	47
1933	MicroRNA associated with dyslipidemia and coronary disease in humans. 2013 , 45, 1199-205	5

1932	Exonic transcription factor binding directs codon choice and affects protein evolution. 2013 , 342, 1367-72	201
1931	Next Generation Sequencing. 2013 ,	10
1930	A comprehensive SNP and indel imputability database. 2013 , 29, 528-31	14
1929	Exploring the association between genetic variation in the SUMO isopeptidase gene USPL1 and breast cancer through integration of data from the population-based GENICA study and external genetic databases. 2013 , 133, 362-72	12
1928	Identifying rare variants associated with complex traits via sequencing. 2013 , Chapter 1, Unit 1.26	26
1927	Review of processing and analysis methods for DNA methylation array data. 2013 , 109, 1394-402	120
1926	A general linear model-based approach for inferring selection to climate. 2013 , 14, 87	15
1925	A SNP profiling panel for sample tracking in whole-exome sequencing studies. 2013 , 5, 89	45
1924	GLiMMPS: robust statistical model for regulatory variation of alternative splicing using RNA-seq data. 2013 , 14, R74	60
1923	Multiplex SNP genotyping by MALDI-TOF mass spectrometry: Frequencies of 56 immune response gene SNPs in human populations. 2013 , 47, 852-862	12
1922	YHap: a population model for probabilistic assignment of Y haplogroups from re-sequencing data. 2013 , 14, 331	3
1921	Insights from genome-wide association studies of drug response. 2013 , 53, 299-310	29
1920	High-resolution SNP microarray investigation of copy number variations on chromosome 18 in a control cohort. 2013 , 141, 16-25	
1919	Stroke in sickle cell anemia patients: a need for multidisciplinary approaches. 2013 , 229, 496-503	12
1918	Reliable identification of genomic variants from RNA-seq data. 2013 , 93, 641-51	247
1917	GeneOnEarth: fitting genetic PC plots on the globe. 2013 , 10, 1009-16	2
1916	A genome-wide association study of recipient genotype and medium-term kidney allograft function. 2013 , 27, 379-87	29
1915	The fibroblast growth factor receptor 2 p.Ala172Phe mutation in Pfeiffer syndrome--history repeating itself. 2013 , 161A, 1158-63	9

1914	Diagnostics for personalized medicine: what will change in the era of large-scale genomics studies?. 2013 , 10, 835-848	2
1913	Systems-based understanding of pharmacological responses with combinations of multidisciplinary methodologies. 2013 , 34, 489-507	7
1912	The Human Genome Project: big science transforms biology and medicine. 2013 , 5, 79	103
1911	Research in Computational Molecular Biology. 2013 ,	9
1910	The humankind genome: from genetic diversity to the origin of human diseases. 2013 , 56, 705-16	17
1909	The genetic basis for interindividual immune response variation to measles vaccine: new understanding and new vaccine approaches. 2013 , 12, 57-70	66
1908	Genetic determinants of dabigatran plasma levels and their relation to bleeding. 2013 , 127, 1404-12	174
1907	The role of BDNF, NTRK2 gene and their interaction in development of treatment-resistant depression: data from multicenter, prospective, longitudinal clinic practice. 2013 , 47, 8-14	47
1906	Genotype imputation via matrix completion. 2013 , 23, 509-18	42
1905	Cancer pharmacogenomics: strategies and challenges. 2013 , 14, 23-34	154
1904	Deep whole-genome sequencing of 100 southeast Asian Malays. 2013 , 92, 52-66	122
1903	Genome-wide data substantiate Holocene gene flow from India to Australia. 2013 , 110, 1803-8	78
1902	Omics and drug response. 2013 , 53, 475-502	112
1901	Single nucleotide polymorphisms in Mycobacterium tuberculosis and the need for a curated database. 2013 , 93, 30-9	39
1900	The Human Genome: A Window on Human Genetics, Biology, and Medicine. 2013 , 4-27	1
1899	Rare variant discovery and calling by sequencing pooled samples with overlaps. 2013 , 29, 29-38	5
1898	Diagnostic applications of high-throughput DNA sequencing. 2013 , 8, 381-410	45
1897	Deconstructing Mus gemischus: advances in understanding ancestry, structure, and variation in the genome of the laboratory mouse. 2013 , 24, 1-20	41

1896	MaCH-admix: genotype imputation for admixed populations. 2013 , 37, 25-37	100
1895	Multiway admixture deconvolution using phased or unphased ancestral panels. 2013 , 37, 1-12	44
1894	Performance and robustness of penalized and unpenalized methods for genetic prediction of complex human disease. 2013 , 37, 184-95	78
1893	Non-random mating, parent-of-origin, and maternal-fetal incompatibility effects in schizophrenia. 2013 , 143, 11-7	1
1892	Decoding asthma: translating genetic variation in IL33 and IL1RL1 into disease pathophysiology. 2013 , 131, 856-65	128
1891	Current relaxation of selection on the human genome: tolerance of deleterious mutations on olfactory receptors. 2013 , 66, 558-64	20
1890	Genome-wide sequencing to identify the cause of hereditary cancer syndromes: with examples from familial pancreatic cancer. 2013 , 340, 227-33	16
1889	Structural and phylogenetic comparison of napsin genes: the duplication, loss of function and human-specific pseudogenization of napsin B. 2013 , 517, 147-57	3
1888	CPAP: Cancer Panel Analysis Pipeline. 2013 , 34, 1340-6	3
1887	From FastQ data to high confidence variant calls: the Genome Analysis Toolkit best practices pipeline. 2013 , 43, 11.10.1-11.10.33	2907
1886	Free the data: one laboratory's approach to knowledge-based genomic variant classification and preparation for EMR integration of genomic data. 2013 , 34, 1183-8	40
1885	Clinical neurogenetics: stroke. 2013 , 31, 915-28	2
1884	Gene-based copy number variation study reveals a microdeletion at 12q24 that influences height in the Korean population. 2013 , 101, 134-8	16
1883	Candidate gene analysis: severe intraventricular hemorrhage in inborn preterm neonates. 2013 , 163, 1503-6.e1	13
1882	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. 2013 , 93, 463-70	55
1881	BDgene: a genetic database for bipolar disorder and its overlap with schizophrenia and major depressive disorder. 2013 , 74, 727-33	41
1880	Analysis of genomic abnormalities in tumors: a review of available methods for Illumina two-color SNP genotyping and evaluation of performance. 2013 , 206, 103-15	8
1879	Chemogenomic Profiling: Understanding the Cellular Response to Drug. 2013 , 153-176	2

1878	Distinguishing somatic and germline copy number events in cancer patient DNA hybridized to whole-genome SNP genotyping arrays. 2013 , 973, 355-72	5
1877	A mega-analysis of genome-wide association studies for major depressive disorder. 2013 , 18, 497-511	853
1876	Platelet Genomics. 2013 , 67-89	2
1875	Sequential sentinel SNP Regional Association Plots (SSS-RAP): an approach for testing independence of SNP association signals using meta-analysis data. 2013 , 77, 67-79	5
1874	Population genetic tools for dissecting innate immunity in humans. 2013 , 13, 280-93	87
1873	Designs for massively parallel sequencing approaches to identify causal mutations in human immune disorders. 2013 , 979, 175-87	
1872	The easy road to genome-wide medium density SNP screening in a non-model species: development and application of a 10 ⁴ K SNP-chip for the house sparrow (<i>Passer domesticus</i>). 2013 , 13, 429-39	35
1871	GWAS. 2013 , 23, R265-6	11
1870	Pharmacogenetics and Pharmacogenomics. 2013 , 362-371	
1869	Seven new loci associated with age-related macular degeneration. 2013 , 45, 433-9, 439e1-2	577
1868	Characterizing polymorphisms and allelic diversity of von Willebrand factor gene in the 1000 Genomes. 2013 , 11, 261-9	42
1867	The 1000 Genomes Project: paving the way for personalized genomic medicine. 2013 , 10, 321-324	4
1866	Genomics. 2013 , 43-66	
1865	Relation between variants in the neurotrophin receptor gene, NTRK3, and white matter integrity in healthy young adults. 2013 , 82, 146-53	28
1864	A genome-wide association study of a sustained pattern of antidepressant response. 2013 , 47, 1157-65	45
1863	Personalized cardiovascular medicine: concepts and methodological considerations. 2013 , 10, 308-16	23
1862	Meta-analysis identifies four new loci associated with testicular germ cell tumor. 2013 , 45, 680-5	132
1861	Discovery of novel non-synonymous SNP variants in 988 candidate genes from 6 centenarians by target capture and next-generation sequencing. 2013 , 134, 478-85	17

1860	DNA marker applications to molecular genetics and genomics in tomato. 2013 , 63, 21-30	29
1859	Marker-Assisted Selection in Cereals: Platforms, Strategies and Examples. 2013 , 375-411	10
1858	The power of meta-analysis in genome-wide association studies. 2013 , 14, 441-65	81
1857	Selective nucleic acid capture with shielded covalent probes. 2013 , 135, 9691-9	27
1856	Sequence Alignment, Analysis, and Bioinformatic Pipelines. 2013 , 59-77	
1855	Guidelines and Approaches to Compliance with Regulatory and Clinical Standards: Quality Control Procedures and Quality Assurance. 2013 , 255-273	3
1854	Detecting range expansions from genetic data. 2013 , 67, 3274-89	83
1853	Prioritization of genetic variants in the microRNA regulome as functional candidates in genome-wide association studies. 2013 , 34, 1049-56	33
1852	Variation and genetic control of protein abundance in humans. <i>Nature</i> , 2013 , 499, 79-82	50.4 272
1851	Genetic variability of glutathione S-transferase enzymes in human populations: functional inter-ethnic differences in detoxification systems. 2013 , 512, 102-7	34
1850	De novo transcriptome assembly and novel microsatellite marker information in <i>Capsicum annuum</i> varieties Saengryeg 211 and Saengryeg 213. 2013 , 54, 58	11
1849	Specialized Dynamical Properties of Promiscuous Residues Revealed by Simulated Conformational Ensembles. 2013 , 9, 5127-5147	30
1848	No evidence from genome-wide data of a Khazar origin for the Ashkenazi Jews. 2013 , 85, 859-900	49
1847	The role of memory-related gene <i>WWC1</i> (<i>KIBRA</i>) in lifetime posttraumatic stress disorder: evidence from two independent samples from African conflict regions. 2013 , 74, 664-71	20
1846	Implications of population history of European Romani on genetic susceptibility to disease. 2013 , 76, 194-200	7
1845	Mobile element scanning (ME-Scan) identifies thousands of novel Alu insertions in diverse human populations. 2013 , 23, 1170-81	47
1844	Exonic deletions in <i>AUTS2</i> cause a syndromic form of intellectual disability and suggest a critical role for the C terminus. 2013 , 92, 210-20	108
1843	A genome-wide association study in Han Chinese identifies a susceptibility locus for primary Sjögren's syndrome at 7q11.23. 2013 , 45, 1361-5	142

1842	Utilizing graph theory to select the largest set of unrelated individuals for genetic analysis. 2013 , 37, 136-41	33
1841	A calibrated human Y-chromosomal phylogeny based on resequencing. 2013 , 23, 388-95	108
1840	Stronger signal of recent selection for lactase persistence in Maasai than in Europeans. 2013 , 21, 550-3	27
1839	Informatics and clinical genome sequencing: opening the black box. 2013 , 15, 165-71	30
1838	Optimal methods for using posterior probabilities in association testing. 2013 , 75, 2-11	8
1837	Inferring admixture histories of human populations using linkage disequilibrium. 2013 , 193, 1233-54	293
1836	Influence of 23 coronary artery disease variants on recurrent myocardial infarction or cardiac death: the GRACE Genetics Study. 2013 , 34, 993-1001	31
1835	Comment on "Evidence of abundant purifying selection in humans for recently acquired regulatory functions". 2013 , 340, 682	15
1834	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. 2013 , 4, 2872	70
1833	Genes that escape X-inactivation in humans have high intraspecific variability in expression, are associated with mental impairment but are not slow evolving. 2013 , 30, 2588-601	81
1832	Anisotropic isolation by distance: the main orientations of human genetic differentiation. 2013 , 30, 513-25	27
1831	Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation. 2013 , 29, 1407-15	29
1830	Utilizing extended pedigree information for discovery and confirmation of copy number variable regions among Mexican Americans. 2013 , 21, 404-9	6
1829	Evolutionary balancing is critical for correctly forecasting disease-associated amino acid variants. 2013 , 30, 1252-7	17
1828	Human expression QTLs are enriched in signals of environmental adaptation. 2013 , 5, 1689-701	7
1827	Efficient haplotype block partitioning and tag SNP selection algorithms under various constraints. 2013 , 2013, 984014	5
1826	Comparative Analysis of CNV Calling Algorithms: Literature Survey and a Case Study Using Bovine High-Density SNP Data. 2013 , 2, 171-85	32
1825	Ubiquitous polygenicity of human complex traits: genome-wide analysis of 49 traits in Koreans. 2013 , 9, e1003355	50

1824	Genetic signatures reveal high-altitude adaptation in a set of ethiopian populations. 2013 , 30, 1877-88	137
1823	Genotype calling and phasing using next-generation sequencing reads and a haplotype scaffold. 2013 , 29, 84-91	39
1822	Genetic heterogeneity and risk of acute respiratory distress syndrome. 2013 , 34, 459-74	40
1821	The chromosome 3q25 genomic region is associated with measures of adiposity in newborns in a multi-ethnic genome-wide association study. 2013 , 22, 3583-96	32
1820	DeepSAGE reveals genetic variants associated with alternative polyadenylation and expression of coding and non-coding transcripts. 2013 , 9, e1003594	32
1819	Balancing selection on a regulatory region exhibiting ancient variation that predates human-neandertal divergence. 2013 , 9, e1003404	21
1818	Genome-wide assessment of the association of rare and common copy number variations to testicular germ cell cancer. 2013 , 4, 2	13
1817	Imputation-based meta-analysis of severe malaria in three African populations. 2013 , 9, e1003509	74
1816	Gene-based testing of interactions in association studies of quantitative traits. 2013 , 9, e1003321	67
1815	Analysis of the genetic basis of disease in the context of worldwide human relationships and migration. 2013 , 9, e1003447	58
1814	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. 2013 , 13, 35-43	45
1813	A genome-wide association study of central corneal thickness in Latinos. 2013 , 54, 2435-43	45
1812	Effects of gene regulatory reprogramming on gene expression in human and mouse developing hearts. 2013 , 368, 20120366	6
1811	Estimating individual admixture proportions from next generation sequencing data. 2013 , 195, 693-702	270
1810	A genome-wide perspective of human diversity and its implications in infectious disease. 2013 , 3, a012450	21
1809	Principles of Genetics and Genomics. 2013 , 131-141	1
1808	Deletions in 16q24.2 are associated with autism spectrum disorder, intellectual disability and congenital renal malformation. 2013 , 50, 163-73	30
1807	Overview of high throughput sequencing technologies to elucidate molecular pathways in cardiovascular diseases. 2013 , 112, 1613-23	77

1806	Genome Maps, a new generation genome browser. 2013 , 41, W41-6	22
1805	In search of low-frequency and rare variants affecting complex traits. 2013 , 22, R16-21	65
1804	DEXUS: identifying differential expression in RNA-Seq studies with unknown conditions. 2013 , 41, e198	20
1803	Improved ancestry inference using weights from external reference panels. 2013 , 29, 1399-406	85
1802	Molecular phylogeography of a human autosomal skin color locus under natural selection. 2013 , 3, 2059-67	15
1801	The essential detail: the genetics and genomics of the primate immune response. 2013 , 54, 181-95	16
1800	Random fluctuation of selection coefficients and the extent of nucleotide variation in human populations. 2013 , 110, 10676-81	6
1799	Estimating and interpreting FST: the impact of rare variants. 2013 , 23, 1514-21	276
1798	Rare variant detection using family-based sequencing analysis. 2013 , 110, 3985-90	42
1797	Distinct loci in the CHRNA5/CHRNA3/CHRNA4 gene cluster are associated with onset of regular smoking. 2013 , 37, 846-59	26
1796	RNAseq: efficient detection of local RNA secondary structure changes induced by SNPs. 2013 , 34, 546-56	90
1795	On association analysis of rare variants under population substructure: an approach for the detection of subjects that can cause bias in the analysis--T opt: an outlier detection method. 2013 , 37, 431-9	
1794	The Andaman Islanders in a regional genetic context: reexamining the evidence for an early peopling of the archipelago from South Asia. 2013 , 85, 153-72	27
1793	Ancestry inference in complex admixtures via variable-length Markov chain linkage models. 2013 , 20, 199-211	12
1792	A DPYD variant (Y186C) in individuals of african ancestry is associated with reduced DPD enzyme activity. 2013 , 94, 158-66	50
1791	Phenotype versus genotype methods for copy number variant analysis of glutathione S-transferases M1. 2013 , 77, 409-15	5
1790	Functional diversity of the glutathione peroxidase gene family among human populations: implications for genetic predisposition to disease and drug response. 2013 , 14, 1037-45	7
1789	The GenoChip: a new tool for genetic anthropology. 2013 , 5, 1021-31	44

1788	GWAS3D: Detecting human regulatory variants by integrative analysis of genome-wide associations, chromosome interactions and histone modifications. 2013 , 41, W150-8	86
1787	Polymorphisms affecting miRNA regulation: a new level of genetic variation affecting disorders and diseases of the human CNS. 2013 , 8, 411-431	3
1786	Genomic Tools and Resources: Development and Applications of an Equine SNP Genotyping Array. 2013 , 113-124	2
1785	Cumulative genetic risk predicts platinum/taxane-induced neurotoxicity. 2013 , 19, 5769-76	23
1784	Genomics. 2013 , 9-48	
1783	Mapping MHC haplotype effects in unrelated donor hematopoietic cell transplantation. 2013 , 121, 1896-905	48
1782	The Origin, Extent and Persistence of Variation: Is the Origin of Variation the Origin of Species? 2013 , 137, 68-79	
1781	Géotoxicité et exposition professionnelle ou environnementale. 2013 , 8, 1-15	
1780	The genetic contribution to disease risk and variability in response to diet: where is the hidden heritability?. 2013 , 72, 40-7	15
1779	Association of variants in NEDD4L with blood pressure response and adverse cardiovascular outcomes in hypertensive patients treated with thiazide diuretics. 2013 , 31, 698-704	50
1778	The impact of computer science in molecular medicine: enabling high-throughput research. 2013 , 13, 526-75	8
1777	Selection of Phototransduction Genes in Homo sapiens. 2013 , 54, 5489-96	
1776	Single Nucleotide Polymorphisms. 2013 , 442-444	1
1775	STUDY ON FOLLICLE STIMULATING HORMONE RECEPTOR GENE POLYMORPHISMS IN SOUTH INDIAN WOMEN WITH POLYCYSTIC OVARIAN SYNDROME. 2013 , 4, 160-167	3
1774	Variants in the 15q24/25 locus associate with lung function decline in active smokers. 2013 , 8, e53219	4
1773	Identity-by-descent mapping to detect rare variants conferring susceptibility to multiple sclerosis. 2013 , 8, e56379	16
1772	Visualization of SNPs with t-SNE. 2013 , 8, e56883	49
1771	Single nucleotide polymorphisms in the Wilms' tumour gene 1 in clear cell renal cell carcinoma. 2013 , 8, e58396	4

1770	Comparative studies of copy number variation detection methods for next-generation sequencing technologies. 2013 , 8, e59128	112
1769	Breakdown of methods for phasing and imputation in the presence of double genotype sharing. 2013 , 8, e60354	3
1768	Enhancing the power of genetic association studies through the use of silver standard cases derived from electronic medical records. 2013 , 8, e63481	15
1767	Case-control association testing of common variants from sequencing of DNA pools. 2013 , 8, e65410	
1766	Genome-wide meta-analysis of systolic blood pressure in children with sickle cell disease. 2013 , 8, e74193	15
1765	X-linked MTMR8 diversity and evolutionary history of sub-Saharan populations. 2013 , 8, e80710	1
1764	A silent exonic SNP in kdm3a affects nucleic acids structure but does not regulate experimental autoimmune encephalomyelitis. 2013 , 8, e81912	1
1763	Prioritization of Copy Number Variation Loci Associated with Autism from AutDB-An Integrative Multi-Study Genetic Database. 2013 , 8, e66707	12
1762	A Method for Inferring an Individual's Genetic Ancestry and Degree of Admixture Associated with Six Major Continental Populations. 2012 , 3, 322	28
1761	Maternal SNPs in the p53 Pathway: Risk Factors for Trisomy 21?. 2013 , 34, 41-49	6
1760	Genetic and molecular alterations in pancreatic cancer: implications for personalized medicine. 2013 , 19, 916-26	33
1759	Governmental and Academic Efforts to Advance the Field of Pharmacogenomics. 2013 , 63-88	2
1758	Linkage and associations. 1-12	
1757	Whole-genome sequencing of the world's oldest people. 2014 , 9, e112430	46
1756	An effective filter for IBD detection in large data sets. 2014 , 9, e92713	5
1755	Whole genome sequence of a Turkish individual. 2014 , 9, e85233	14
1754	ArchiLD: hierarchical visualization of linkage disequilibrium in human populations. 2014 , 9, e86761	2
1753	Fast principal component analysis of large-scale genome-wide data. 2014 , 9, e93766	160

1752	Variants of a <i>Thermus aquaticus</i> DNA polymerase with increased selectivity for applications in allele- and methylation-specific amplification. 2014 , 9, e96640	13
1751	Association of single nucleotide polymorphisms in the lens epithelium-derived growth factor (LEDGF/p75) with HIV-1 infection outcomes in Brazilian HIV-1+ individuals. 2014 , 9, e101780	1
1750	Assessing accuracy of genotype imputation in American Indians. 2014 , 9, e102544	2
1749	Copy number variation in Thai population. 2014 , 9, e104355	22
1748	Evaluating the coverage and potential of imputing the exome microarray with next-generation imputation using the 1000 Genomes Project. 2014 , 9, e106681	1
1747	Investigation of 15q11-q13, 16p11.2 and 22q13 CNVs in autism spectrum disorder Brazilian individuals with and without epilepsy. 2014 , 9, e107705	14
1746	Can evidence from genome-wide association studies and positive natural selection surveys be used to evaluate the thrifty gene hypothesis in East Asians?. 2014 , 9, e110974	5
1745	Exploring the distribution of genetic markers of pharmacogenomics relevance in Brazilian and Mexican populations. 2014 , 9, e112640	45
1744	Genome-wide analysis of the role of copy-number variation in pancreatic cancer risk. 2014 , 5, 29	10
1743	From genes to health - challenges and opportunities. 2014 , 2, 12	2
1742	Jumping on the Train of Personalized Medicine: A Primer for Non-Geneticist Clinicians: Part 1. Fundamental Concepts in Molecular Genetics. 2014 , 10, 91-100	5
1741	Association studies of sporadic Parkinson's disease in the genomic era. 2014 , 15, 2-10	20
1740	Jumping on the Train of Personalized Medicine: A Primer for Non- Geneticist Clinicians: Part 3. Clinical Applications in the Personalized Medicine Area. 2014 , 10, 118-132	10
1739	Etiology and early pathogenesis of malignant testicular germ cell tumors: towards possibilities for preinvasive diagnosis. 2015 , 17, 381-93	19
1738	Neanderthal introgression at chromosome 3p21.31 was under positive natural selection in East Asians. 2014 , 31, 683-95	46
1737	LIG1 polymorphisms: the Indian scenario. 2014 , 93, 459-69	
1736	A novel polymorphism of the GP78 gene is associated with coronary artery disease in Han population in China. 2014 , 13, 147	3
1735	Enhancer variants: evaluating functions in common disease. 2014 , 6, 85	133

1734	LD Score Regression Distinguishes Confounding from Polygenicity in Genome-Wide Association Studies. 2014,	7
1733	GWATCH: a web platform for automated gene association discovery analysis. 2014, 3, 18	2
1732	Extensive copy number variations in admixed Indian population of African ancestry: potential involvement in adaptation. 2014, 6, 3171-81	9
1731	Replicative association analysis of genetic markers of cognitive traits with Alzheimer's disease in the Russian population. 2014, 48, 835-844	12
1730	A dominant mutation in hexokinase 1 (HK1) causes retinitis pigmentosa. 2014, 55, 7147-58	36
1729	Analysis of schizophrenia-related genes and electrophysiological measures reveals ZNF804A association with amplitude of P300b elicited by novel sounds. 2014, 4, e346	24
1728	Large copy number variations in combination with point mutations in the TYMP and SCO2 genes found in two patients with mitochondrial disorders. 2014, 22, 431-4	8
1727	The impact of the metabotropic glutamate receptor and other gene family interaction networks on autism. 2014, 5, 4074	45
1726	A functional synonymous coding variant in the IL1RN gene is associated with survival in septic shock. 2014, 190, 656-64	28
1725	In silico detection of phylogenetic informative Y-chromosomal single nucleotide polymorphisms from whole genome sequencing data. 2014, 35, 3102-10	5
1724	Methodologies in the Era of Cardiovascular Omics 2014, 15-55	
1723	Moving into a new era of periodontal genetic studies: relevance of large case-control samples using severe phenotypes for genome-wide association studies. 2014, 49, 683-95	37
1722	Germline mutations in MAP3K6 are associated with familial gastric cancer. 2014, 10, e1004669	46
1721	Patterns of admixture and population structure in native populations of Northwest North America. 2014, 10, e1004530	49
1720	Imputation and quality control steps for combining multiple genome-wide datasets. 2014, 5, 370	90
1719	Immunogenetic factors affecting susceptibility of humans and rodents to hantaviruses and the clinical course of hantaviral disease in humans. 2014, 6, 2214-41	32
1718	Determining effects of non-synonymous SNPs on protein-protein interactions using supervised and semi-supervised learning. 2014, 10, e1003592	55
1717	Sequence divergence and diversity suggests ongoing functional diversification of vertebrate NAD metabolism. 2014, 23, 39-48	11

1716	Genetic variability of GCKR alters lipid profiles in children with monogenic and autoimmune diabetes. 2014 , 122, 503-9	4
1715	dbPSHP: a database of recent positive selection across human populations. 2014 , 42, D910-6	32
1714	Validation and genotyping of multiple human polymorphic inversions mediated by inverted repeats reveals a high degree of recurrence. 2014 , 10, e1004208	23
1713	Learning gene networks under SNP perturbations using eQTL datasets. 2014 , 10, e1003420	33
1712	Genome-wide meta-analysis of homocysteine and methionine metabolism identifies five one carbon metabolism loci and a novel association of ALDH1L1 with ischemic stroke. 2014 , 10, e1004214	57
1711	Population genomic analysis of ancient and modern genomes yields new insights into the genetic ancestry of the Tyrolean Iceman and the genetic structure of Europe. 2014 , 10, e1004353	73
1710	Ancient origins of vertebrate-specific innate antiviral immunity. 2014 , 31, 140-53	39
1709	A Web-based database of genetic association studies in cutaneous melanoma enhanced with network-driven data exploration tools. 2014 , 2014,	6
1708	Genotyping the gene by joint analysis of two linked single nucleotide polymorphisms using liver tissues for clinical and geographical comparisons. 2014 , 8, 2215-2220	12
1707	Early back-to-Africa migration into the Horn of Africa. 2014 , 10, e1004393	66
1706	Detecting local haplotype sharing and haplotype association. 2014 , 197, 823-38	18
1705	A novel and fast approach for population structure inference using kernel-PCA and optimization. 2014 , 198, 1421-31	19
1704	A homogenizing process of selection has maintained an "ultra-slow" acetylation NAT2 variant in humans. 2014 , 86, 185-214	12
1703	Mining massive SNP data for identifying associated SNPs and uncovering gene relationships. 2014 ,	
1702	The road from next-generation sequencing to personalized medicine. 2014 , 11, 523-544	29
1701	Reconstructing Austronesian population history in Island Southeast Asia. 2014 , 5, 4689	116
1700	seqCNA: an R package for DNA copy number analysis in cancer using high-throughput sequencing. 2014 , 15, 178	11
1699	Genome-wide SNP analysis reveals population structure and demographic history of the ryukyu islanders in the southern part of the Japanese archipelago. 2014 , 31, 2929-40	37

1698	Current sequencing technology makes microhaplotypes a powerful new type of genetic marker for forensics. 2014 , 12, 215-24	114
1697	Detection of structural variants involving repetitive regions in the reference genome. 2014 , 21, 219-33	13
1696	Positive perception of pharmacogenetic testing for psychotropic medications. 2014 , 29, 287-91	13
1695	De novo KCNB1 mutations in epileptic encephalopathy. 2014 , 76, 529-540	90
1694	The influence of admixture and consanguinity on population genetic diversity in Middle East. 2014 , 59, 615-22	11
1693	Benefits of Accurate Imputations in GWAS. 2014 , 877-889	
1692	Vascular endothelial growth factor-A is associated with chronic mountain sickness in the Andean population. 2014 , 15, 146-54	11
1691	A recessive genetic model and runs of homozygosity in major depressive disorder. 2014 , 165B, 157-66	19
1690	Genome-wide screening for DNA variants associated with reading and language traits. 2014 , 13, 686-701	78
1689	Detecting maternal-fetal genotype interactions associated with conotruncal heart defects: a haplotype-based analysis with penalized logistic regression. 2014 , 38, 198-208	10
1688	Dynamic Epstein-Barr virus gene expression on the path to B-cell transformation. 2014 , 88, 279-313	54
1687	Variants in the 1q21 risk region are associated with a visual endophenotype of autism and schizophrenia. 2014 , 13, 144-51	29
1686	Exome sequencing identifies potential risk variants for Mendelian disorders at high prevalence in Qatar. 2014 , 35, 105-16	37
1685	Local and global ancestry inference and applications to genetic association analysis for admixed populations. 2014 , 38 Suppl 1, S5-S12	29
1684	Accounting for population stratification in DNA methylation studies. 2014 , 38, 231-41	146
1683	A genome-wide association study identifies a LEPR gene as a novel predisposing factor for childhood fasting plasma glucose. 2014 , 104, 594-8	2
1682	A general efficient and flexible approach for genome-wide association analyses of imputed genotypes in family-based designs. 2014 , 38, 560-71	22
1681	iReport: a generalised Galaxy solution for integrated experimental reporting. 2014 , 3, 19	4

1680	Approaches to identify genetic variants that influence the risk for onset of fragile X-associated primary ovarian insufficiency (FXPOI): a preliminary study. 2014 , 5, 260	14
1679	Identifying genetic relatives without compromising privacy. 2014 , 24, 664-72	23
1678	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. 2014 , 51, 614-22	17
1677	Fine mapping of type 2 diabetes susceptibility loci. 2014 , 14, 549	21
1676	Private haplotypes can reveal local adaptation. 2014 , 15, 61	20
1675	Characterizing the genetic differences between two distinct migrant groups from Indo-European and Dravidian speaking populations in India. 2014 , 15, 86	22
1674	Systems genomics evaluation of the SH-SY5Y neuroblastoma cell line as a model for Parkinson's disease. 2014 , 15, 1154	87
1673	Genome-wide patterns of copy number variation in the diversified chicken genomes using next-generation sequencing. 2014 , 15, 962	49
1672	Genetic analysis of an allergic rhinitis cohort reveals an intercellular epistasis between FAM134B and CD39. 2014 , 15, 73	23
1671	Benchmarking mutation effect prediction algorithms using functionally validated cancer-related missense mutations. 2014 , 15, 484	95
1670	Expression profiles of long non-coding RNAs located in autoimmune disease-associated regions reveal immune cell-type specificity. 2014 , 6, 88	79
1669	A droplet digital PCR detection method for rare L1 insertions in tumors. 2014 , 5, 30	15
1668	Genetic variants in the major histocompatibility complex class I and class II genes are associated with diisocyanate-induced Asthma. 2014 , 56, 382-7	14
1667	The familial dementia gene revisited: a missense mutation revealed by whole-exome sequencing identifies ITM2B as a candidate gene underlying a novel autosomal dominant retinal dystrophy in a large family. 2014 , 23, 491-501	22
1666	Pharmacogenetics at 50: genomic personalization comes of age. 2014 , 6, 220ps1	18
1665	A cellular genome-wide association study reveals human variation in microtubule stability and a role in inflammatory cell death. 2014 , 25, 76-86	22
1664	Effects of genetic variations on microRNA: target interactions. 2014 , 42, 9543-52	35
1663	Neutral genomic regions refine models of recent rapid human population growth. 2014 , 111, 757-62	86

1662	A novel missense mutation in <i>CCDC88C</i> activates the JNK pathway and causes a dominant form of spinocerebellar ataxia. 2014 , 51, 590-5	54
1661	An integrated framework for discovery and genotyping of genomic variants from high-throughput sequencing experiments. 2014 , 42, e44	73
1660	Translational Bioinformatics. 2014 , 721-754	1
1659	Basic Genetics: The Cell, Mitosis and Meiosis, and Mendelian Laws. 2014 , 29-40	
1658	GTP cyclohydrolase I gene polymorphisms are associated with endothelial dysfunction and oxidative stress in patients with type 2 diabetes mellitus. 2014 , 9, e108587	10
1657	Genetic risk signatures of opioid-induced respiratory depression following pediatric tonsillectomy. 2014 , 15, 1749-1762	20
1656	Common variants of <i>GIP</i> are associated with visceral fat accumulation in Japanese adults. 2014 , 307, G1108-14	13
1655	Role of Environmental Confounding in the Association between <i>FKBP5</i> and First-Episode Psychosis. 2014 , 5, 84	16
1654	Dating rare mutations from small samples with dense marker data. 2014 , 197, 1315-27	35
1653	Integrating dilution-based sequencing and population genotypes for single individual haplotyping. 2014 , 15, 733	
1652	Breast cancer risk assessment using genetic variants and risk factors in a Singapore Chinese population. 2014 , 16, R64	22
1651	Evolution of the primate trypanolytic factor <i>APOL1</i> . 2014 , 111, E2130-9	145
1650	Evidence of heterogeneity by race/ethnicity in genetic determinants of QT interval. 2014 , 25, 790-8	15
1649	Variants at <i>IRX4</i> as prostate cancer expression quantitative trait loci. 2014 , 22, 558-63	27
1648	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. 2014 , 59, 20-27	29
1647	Chip-based direct genotyping of coding variants in genome wide association studies: utility, issues and prospects. 2014 , 540, 104-9	10
1646	The many facets of <i>WT1</i> in acute myeloid leukemia: clarity remains elusive. 2014 , 55, 235-7	4
1645	Familial breast cancer genetic testing in the West of Ireland. 2014 , 183, 199-206	2

1644	Genetics of disc-related disorders: current findings and lessons from other complex diseases. 2014 , 23 Suppl 3, S354-63	19
1643	Generation of SNP datasets for orangutan population genomics using improved reduced-representation sequencing and direct comparisons of SNP calling algorithms. 2014 , 15, 16	64
1642	Quantitative prediction of the effect of genetic variation using hidden Markov models. 2014 , 15, 5	12
1641	Replication of a GWAS signal in a Caucasian population implicates ADD3 in susceptibility to biliary atresia. 2014 , 133, 235-43	45
1640	Exome sequencing revealed novel germline mutations in Chinese Peutz-Jeghers syndrome patients. 2014 , 59, 64-71	11
1639	Dissecting the relationship between high-sensitivity serum C-reactive protein and increased fracture risk: the Rotterdam Study. 2014 , 25, 1247-54	29
1638	Exploring the occurrence of classic selective sweeps in humans using whole-genome sequencing data sets. 2014 , 31, 1850-68	57
1637	MutationTaster2: mutation prediction for the deep-sequencing age. 2014 , 11, 361-2	2455
1636	Transcriptional enhancers: from properties to genome-wide predictions. 2014 , 15, 272-86	820
1635	exomeSuite: Whole exome sequence variant filtering tool for rapid identification of putative disease causing SNVs/indels. 2014 , 103, 169-76	19
1634	Ancestry estimation and control of population stratification for sequence-based association studies. 2014 , 46, 409-15	82
1633	Single nucleotide polymorphisms in microRNA binding sites of oncogenes: implications in cancer and pharmacogenomics. 2014 , 18, 142-54	34
1632	A Crohn's disease variant in Atg16l1 enhances its degradation by caspase 3. <i>Nature</i> , 2014 , 506, 456-62	50.4 265
1631	Genome-wide pathway analysis in neuroblastoma. 2014 , 35, 3471-85	12
1630	Exome sequencing greatly expedites the progressive research of Mendelian diseases. 2014 , 8, 42-57	35
1629	Human testis-specific genes are under relaxed negative selection. 2014 , 289, 37-45	5
1628	Genetic contributors to otitis media: agnostic discovery approaches. 2014 , 14, 411	9
1627	Changing interpretation of chromosomal microarray over time in a community cohort with intellectual disability. 2014 , 164A, 377-85	34

1626	Laying a solid foundation for Manhattan--'setting the functional basis for the post-GWAS era'. 2014 , 30, 140-9	68
1625	Heritability and genomics of gene expression in peripheral blood. 2014 , 46, 430-7	258
1624	On detecting incomplete soft or hard selective sweeps using haplotype structure. 2014 , 31, 1275-91	214
1623	Genetic variation associated with euphorogenic effects of d-amphetamine is associated with diminished risk for schizophrenia and attention deficit hyperactivity disorder. 2014 , 111, 5968-73	15
1622	Finding the genetic determinants of adverse reactions to radiotherapy. 2014 , 26, 301-8	34
1621	Natural selection and infectious disease in human populations. 2014 , 15, 379-93	255
1620	A common 16p11.2 inversion underlies the joint susceptibility to asthma and obesity. 2014 , 94, 361-72	46
1619	Outfoxed by RBFOX1-a caution about ascertainment bias. 2014 , 164A, 1411-8	8
1618	Conotruncal heart defects and common variants in maternal and fetal genes in folate, homocysteine, and transsulfuration pathways. 2014 , 100, 116-26	23
1617	Determining causality and consequence of expression quantitative trait loci. 2014 , 133, 727-35	34
1616	Molecular analysis of common polymorphisms within the human Tyrosinase locus and genetic association with pigmentation traits. 2014 , 27, 552-64	26
1615	Genome-scale neurogenetics: methodology and meaning. 2014 , 17, 756-63	74
1614	Genotype-guided dosing of vitamin K antagonists. 2014 , 370, 1763-4	23
1613	rSNPBase: a database for curated regulatory SNPs. 2014 , 42, D1033-9	89
1612	Colorectal cancer risk and patients' survival: influence of polymorphisms in genes somatically mutated in colorectal tumors. 2014 , 25, 759-69	13
1611	Gene hunting in the genomic era: approaches to diagnostic dilemmas in patients with primary immunodeficiencies. 2014 , 134, 262-8	27
1610	Allele-specific regulation of DISC1 expression by miR-135b-5p. 2014 , 22, 840-3	14
1609	Combinatorial effects of multiple enhancer variants in linkage disequilibrium dictate levels of gene expression to confer susceptibility to common traits. 2014 , 24, 1-13	258

1608	Genomics meets proteomics: identifying the culprits in disease. 2014 , 133, 689-700	16
1607	Pharmacogenetics: implications of race and ethnicity on defining genetic profiles for personalized medicine. 2014 , 133, 16-26	127
1606	Genome-wide evidence of Austronesian-Bantu admixture and cultural reversion in a hunter-gatherer group of Madagascar. 2014 , 111, 936-41	61
1605	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. 2014 , 30, 1112-1119	49
1604	Revisiting the thrifty gene hypothesis via 65 loci associated with susceptibility to type 2 diabetes. 2014 , 94, 176-85	59
1603	Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014 , 505, 87-91	581
1602	Ancient west Eurasian ancestry in southern and eastern Africa. 2014 , 111, 2632-7	176
1601	Human genetics of tuberculosis: a long and winding road. 2014 , 369, 20130428	114
1600	Human pharmacogenomic variation of antihypertensive drugs: from population genetics to personalized medicine. 2014 , 15, 157-67	9
1599	PRIMUS: rapid reconstruction of pedigrees from genome-wide estimates of identity by descent. 2014 , 95, 553-64	88
1598	Human leukocyte antigen haplotype phasing by allele-specific enrichment with peptide nucleic acid probes. 2014 , 2, 245-53	1
1597	Autoimmune predisposition in Down syndrome may result from a partial central tolerance failure due to insufficient intrathymic expression of AIRE and peripheral antigens. 2014 , 193, 3872-9	68
1596	Guidelines for genetic studies in single patients: lessons from primary immunodeficiencies. 2014 , 211, 2137-49	158
1595	Single-nucleotide polymorphisms interact to affect ADH7 transcription. 2014 , 38, 921-9	7
1594	BAT2 and BAT3 polymorphisms as novel genetic risk factors for rejection after HLA-related SCT. 2014 , 49, 1400-1404	5
1593	AGXT2: a promiscuous aminotransferase. 2014 , 35, 575-82	46
1592	Association of leptin/receptor and TNF- α gene variants with adolescent obesity in Malaysia. 2014 , 56, 689-97	10
1591	Comprehensive variation discovery in single human genomes. 2014 , 46, 1350-5	154

1590	Evidence for the role of EPHX2 gene variants in anorexia nervosa. 2014 , 19, 724-32	57
1589	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. 2014 , 29, 3-11	11
1588	Host genetics and immune control of HIV-1 infection: fine mapping for the extended human MHC region in an African cohort. 2014 , 15, 275-81	9
1587	Rare and low-frequency variants in human common diseases and other complex traits. 2014 , 51, 705-14	21
1586	G-quadruplex formation of FXVD1 pre-mRNA indicates the possibility of regulating expression of its protein product. 2014 , 560, 52-8	6
1585	Genome-wide association study of ancestry-specific TB risk in the South African Coloured population. 2014 , 23, 796-809	117
1584	Exome sequencing identifies a novel frameshift mutation of MYO6 as the cause of autosomal dominant nonsyndromic hearing loss in a Chinese family. 2014 , 78, 410-23	7
1583	A meta-analysis of gene expression quantitative trait loci in brain. 2014 , 4, e459	56
1582	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. 2014 , 5, 4871	46
1581	Pathway analysis of genome-wide association study on serum prostate-specific antigen levels. 2014 , 551, 86-91	14
1580	Screening of the GPX3 gene identifies the "T" allele of the SNP -861A/T as a risk for ischemic stroke in young Asian Indians. 2014 , 23, 2060-2068	7
1579	The Path to Personalized Cardiovascular Medicine. 2014 , 837-871	
1578	Screening of the NOS3 gene identifies the variants 894G/T, 1998C/G and 2479G/A to be associated with acute onset ischemic stroke in young Asian Indians. 2014 , 344, 69-75	3
1577	Genetics, genomics, and their relevance to pathology and therapy. 2014 , 28, 175-89	14
1576	Genetic variants underlying risk of endometriosis: insights from meta-analysis of eight genome-wide association and replication datasets. 2014 , 20, 702-16	131
1575	An enhancer-blocking element regulates the cell-specific expression of alcohol dehydrogenase 7. 2014 , 547, 239-44	3
1574	Toward a new history and geography of human genes informed by ancient DNA. 2014 , 30, 377-89	163
1573	Adaptations to local environments in modern human populations. 2014 , 29, 1-8	53

1572	Characterizing genetic variants for clinical action. 2014 , 166C, 93-104	41
1571	Using population isolates in genetic association studies. 2014 , 13, 371-7	55
1570	Molecular convergence of neurodevelopmental disorders. 2014 , 95, 490-508	51
1569	Genetic liability for schizophrenia predicts risk of immune disorders. 2014 , 159, 347-52	34
1568	WinHAP2: an extremely fast haplotype phasing program for long genotype sequences. 2014 , 15, 164	5
1567	Variant detection sensitivity and biases in whole genome and exome sequencing. 2014 , 15, 247	144
1566	A non-parametric approach for detecting gene-gene interactions associated with age-at-onset outcomes. 2014 , 15, 79	2
1565	Discovery of common sequences absent in the human reference genome using pooled samples from next generation sequencing. 2014 , 15, 685	16
1564	Estimating and adjusting for ancestry admixture in statistical methods for relatedness inference, heritability estimation, and association testing. 2014 , 8, S5	14
1563	Use of admixture and association for detection of quantitative trait loci in the Type 2 Diabetes Genetic Exploration by Next-Generation Sequencing in Ethnic Samples (T2D-GENES) study. 2014 , 8, S6	7
1562	The Red Queen's long race: human adaptation to pathogen pressure. 2014 , 29, 31-8	34
1561	Sequencing pools of individuals - mining genome-wide polymorphism data without big funding. 2014 , 15, 749-63	443
1560	SMAsh: a benchmarking toolkit for human genome variant calling. 2014 , 30, 2787-95	32
1559	Inbreeding coefficient estimation with dense SNP data: comparison of strategies and application to HapMap III. 2014 , 77, 49-62	33
1558	Defining the role of common variation in the genomic and biological architecture of adult human height. 2014 , 46, 1173-86	1339
1557	The WWOX gene modulates high-density lipoprotein and lipid metabolism. 2014 , 7, 491-504	26
1556	HLA class I, KIR, and genome-wide SNP diversity in the RV144 Thai phase 3 HIV vaccine clinical trial. 2014 , 66, 299-310	12
1555	Investigation of SCGB3A1 (UGRP2) gene arrays in patients with nasal polyposis. 2014 , 271, 3209-14	4

1554	A genetic association study detects haplotypes associated with obstructive heart defects. 2014 , 133, 1127-38	8
1553	BRCA1 point mutations in premenopausal breast cancer patients from Central Sudan. 2014 , 13, 437-44	12
1552	Genome-wide association analysis of eosinophilic esophagitis provides insight into the tissue specificity of this allergic disease. 2014 , 46, 895-900	185
1551	CHD2 haploinsufficiency is associated with developmental delay, intellectual disability, epilepsy and neurobehavioural problems. 2014 , 6, 9	59
1550	A genome-wide association study of anorexia nervosa. 2014 , 19, 1085-94	224
1549	Association of HMGB1 and HMGB2 genetic polymorphisms with lung cancer chemotherapy response. 2014 , 41, 408-15	24
1548	Development of a SNP set for human identification: A set with high powers of discrimination which yields high genetic information from naturally degraded DNA samples in the Thai population. 2014 , 11, 166-73	21
1547	Intercellular adhesion molecule-1 polymorphisms in patients with Behçet disease: a meta-analysis. 2014 , 24, 481-6	5
1546	Frontotemporal dementia and its subtypes: a genome-wide association study. 2014 , 13, 686-99	207
1545	8th International Conference on Practical Applications of Computational Biology & Bioinformatics (PACBB 2014). 2014 ,	1
1544	Hot spots in protein-protein interfaces: towards drug discovery. 2014 , 116, 165-73	101
1543	Introduction to deep sequencing and its application to drug addiction research with a focus on rare variants. 2014 , 49, 601-14	9
1542	Genome-wide pathway analysis of breast cancer. 2014 , 35, 7699-705	13
1541	Genetic determinants of renal transplant outcome: where do we stand?. 2014 , 27, 247-56	11
1540	Comparison of genotype clustering tools with rare variants. 2014 , 15, 52	6
1539	Information compression exploits patterns of genome composition to discriminate populations and highlight regions of evolutionary interest. 2014 , 15, 66	12
1538	Deleted copy number variation of Hanwoo and Holstein using next generation sequencing at the population level. 2014 , 15, 240	32
1537	Exome capture from saliva produces high quality genomic and metagenomic data. 2014 , 15, 262	26

1536	Applying genome-wide gene-based expression quantitative trait locus mapping to study population ancestry and pharmacogenetics. 2014 , 15, 319	6
1535	Evaluating the possibility of detecting evidence of positive selection across Asia with sparse genotype data from the HUGO Pan-Asian SNP Consortium. 2014 , 15, 332	7
1534	Quality control and conduct of genome-wide association meta-analyses. 2014 , 9, 1192-212	278
1533	Whole-genome sequence variation, population structure and demographic history of the Dutch population. 2014 , 46, 818-25	514
1532	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. 2014 , 46, 234-44	784
1531	Native American ancestry is associated with severe diabetic retinopathy in Latinos. 2014 , 55, 6041-5	19
1530	An excess of risk-increasing low-frequency variants can be a signal of polygenic inheritance in complex diseases. 2014 , 94, 437-52	37
1529	The genome revolution and its role in understanding complex diseases. 2014 , 1842, 1889-1895	39
1528	Mining the 3'UTR of autism-implicated genes for SNPs perturbing microRNA regulation. 2014 , 12, 92-104	23
1527	Associations of MYH3 gene copy number variations with transcriptional expression and growth traits in Chinese cattle. 2014 , 535, 106-11	35
1526	Many inflammatory bowel disease risk loci include regions that regulate gene expression in immune cells and the intestinal epithelium. 2014 , 146, 1040-7	82
1525	MicroRNA miR-513a-3p acts as a co-regulator of luteinizing hormone/chorionic gonadotropin receptor gene expression in human granulosa cells. 2014 , 390, 65-72	22
1524	Validation of copy number variants associated with prostate cancer risk and prognosis. 2014 , 32, 44.e15-44.e20	
1523	Genetic studies of Crohn's disease: past, present and future. 2014 , 28, 373-86	73
1522	Inferring human population size and separation history from multiple genome sequences. 2014 , 46, 919-25	569
1521	Detecting structure of haplotypes and local ancestry. 2014 , 196, 625-42	101
1520	Neanderthal origin of the haplotypes carrying the functional variant Val92Met in the MC1R in modern humans. 2014 , 31, 1994-2003	23
1519	Human genetics. The genetics of Mexico recapitulates Native American substructure and affects biomedical traits. 2014 , 344, 1280-5	331

1518	Interactions between RNA polymerase and the "core recognition element" counteract pausing. 2014 , 344, 1285-9	121
1517	Maritime route of colonization of Europe. 2014 , 111, 9211-6	51
1516	Whole-exome sequencing identifies KIZ as a ciliary gene associated with autosomal-recessive rod-cone dystrophy. 2014 , 94, 625-33	42
1515	Admixture facilitates genetic adaptations to high altitude in Tibet. 2014 , 5, 3281	133
1514	Human genome variability, natural selection and infectious diseases. 2014 , 30, 9-16	49
1513	Next-generation sequencing for research and diagnostics in kidney disease. 2014 , 10, 433-44	73
1512	A definitive haplotype map of structural variations determined by microarray analysis of duplicated haploid genomes. 2014 , 2, 55-9	1
1511	Protein-protein interactions and genetic diseases: The interactome. 2014 , 1842, 1971-1980	75
1510	A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. 2014 , 22, 248-53	31
1509	Analysis of WT1 mutations, expression levels and single nucleotide polymorphism rs16754 in de novo non-M3 acute myeloid leukemia. 2014 , 55, 349-57	14
1508	A Single-Array-Based Method for Detecting Copy Number Variants Using Affymetrix High Density SNP Arrays and its Application to Breast Cancer. 2014 , 13, 95-103	
1507	Fine Mapping Type 2 Diabetes Susceptibility Loci. 2014 , 14-28	1
1506	The NIH Toolbox Cognition Battery: results from a large normative developmental sample (PING). 2014 , 28, 1-10	120
1505	Genetic variant in folate homeostasis is associated with lower warfarin dose in African Americans. 2014 , 124, 2298-305	49
1504	Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1. 2014 , 124, 2767-74	75
1503	Whole genome sequencing of 35 individuals provides insights into the genetic architecture of Korean population. 2014 , 15 Suppl 11, S6	26
1502	Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. 2014 , 15, R88	51
1501	Progress and promise in understanding the genetic basis of common diseases. 2015 , 282, 20151684	98

1500 Genetic background of urinary incontinence [State-of-the-art and perspectives. **2015**, 11,

1499 Genetic differences among ethnic groups. **2015**, 16, 1093 78

1498 Contemporary Trends in Onset and Completion of Puberty, Gain in Height and Adiposity. **2016**, 29, 122-33 27

1497 β 1 tubulin R307H SNP alters microtubule dynamics and affects severity of a hereditary thrombocytopenia. **2015**, 13, 651-9 13

1496 Inbreeding and homozygosity in breast cancer survival. **2015**, 5, 16467 4

1495 Identification and Characterization of Protein Posttranslational Modifications by Differential Fluorescent Labeling. **2015**, 243-262

1494 The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape. **2015**, 5, 9996 21

1493 Quantitative assessment of common genetic variations in HLA-DP with hepatitis B virus infection, clearance and hepatocellular carcinoma development. **2015**, 5, 14933 17

1492 Evaluating information content of SNPs for sample-tagging in re-sequencing projects. **2015**, 5, 10247 16

1491 Mapping the genetic diversity of HLA haplotypes in the Japanese populations. **2015**, 5, 17855 6

1490 The role of common genetic variation in educational attainment and income: evidence from the National Child Development Study. **2015**, 5, 16509 10

1489 GIW and InCoB, two premier bioinformatics conferences in Asia with a combined 40 years of history. **2015**, 16 Suppl 12, 11

1488 Estimating copy numbers of alleles from population-scale high-throughput sequencing data. **2015**, 16 Suppl 1, S4

1487 iJGVD: an integrative Japanese genome variation database based on whole-genome sequencing. **2015**, 2, 15050 86

1486 NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. **2015**, 31, 4009-11 39

1485 Functional and Structural Consequence of Rare Exonic Single Nucleotide Polymorphisms: One Story, Two Tales. **2015**, 7, 2929-40 9

1484 Leveraging local ancestry to detect gene-gene interactions in genome-wide data. **2015**, 16, 124 8

1483 Characterization of the biological processes shaping the genetic structure of the Italian population. **2015**, 16, 132 7

1482	Whole genome sequences are required to fully resolve the linkage disequilibrium structure of human populations. 2015 , 16, 666	12
1481	CPAG: software for leveraging pleiotropy in GWAS to reveal similarity between human traits links plasma fatty acids and intestinal inflammation. 2015 , 16, 190	11
1480	Cpipe: a shared variant detection pipeline designed for diagnostic settings. 2015 , 7, 68	62
1479	Fine-scale population structure of Malays in Peninsular Malaysia and Singapore and implications for association studies. 2015 , 9, 16	7
1478	Genome-wide association study of lymphoblast cell viability after clozapine exposure. 2015 , 168B, 116-22	6
1477	Robust inference of population structure for ancestry prediction and correction of stratification in the presence of relatedness. 2015 , 39, 276-93	170
1476	GeneYenta: a phenotype-based rare disease case matching tool based on online dating algorithms for the acceleration of exome interpretation. 2015 , 36, 432-8	15
1475	Prioritization of cancer-related genomic variants by SNP association network. 2015 , 14, 57-70	4
1474	Differences in body mass index according to fat mass- and obesity-associated (FTO) genotype in Mexican patients with bipolar disorder. 2015 , 17, 662-9	8
1473	Metastatic pheochromocytoma in a 23-year-old woman with an unclassified variant in the von Hippel Lindau disease gene: how can the pathogenicity of this variant be determined?. 2015 , 83, 15-9	3
1472	Exome sequencing in seven families and gene-based association studies indicate genetic heterogeneity and suggest possible candidates for fibromuscular dysplasia. 2015 , 33, 1802-10; discussion 1810	24
1471	Associations of common variants in the BST2 region with HIV-1 acquisition in African American and European American people who inject drugs. 2015 , 29, 767-77	12
1470	LinkImpute: Fast and Accurate Genotype Imputation for Nonmodel Organisms. 2015 , 5, 2383-90	221
1469	A Genetic Basis for Motivated Exercise. 2015 , 43, 231-7	19
1468	Persistent phylogeny. 2015 ,	10
1467	Genome-wide pathway analysis in glioma. 2015 , 62, 230-8	10
1466	Genome-wide pathway analysis in amyotrophic lateral sclerosis. 2015 , 14, 6429-38	1
1465	Neon: An R Package to Estimate Human Effective Population Size and Divergence Time from Patterns of Linkage Disequilibrium between SNPs. 2015 , 8,	21

1464	Research Methodologies of Evolutionary Psychiatry. 2015 , 54, 49	1
1463	Targeted next generation sequencing identifies novel mutations in RP1 as a relatively common cause of autosomal recessive rod-cone dystrophy. 2015 , 2015, 485624	21
1462	Risk-Reducing Genetic Variant of Wilms Tumor 1 Gene rs16754 in Korean Patients With BCR-ABL1-Negative Myeloproliferative Neoplasm. 2015 , 35, 348-51	0
1461	Screening of three ERBB4 gene polymorphisms in a group of Turkish schizophrenia patients and controls / ERBB4 genindeki polimorfizmin bir Türk şizofreni hasta grubunda ve kontrollerde taraması 2015 , 40,	
1460	Discovery of Protein-lncRNA Interactions by Integrating Large-Scale CLIP-Seq and RNA-Seq Datasets. 2014 , 2, 88	56
1459	Ancestry of the Timorese: age-related macular degeneration associated genotype and allele sharing among human populations from throughout the world. 2015 , 6, 238	4
1458	dcVar: a method for identifying common variants that modulate differential correlation structures in gene expression data. 2015 , 6, 312	5
1457	Affected kindred analysis of human X chromosome exomes to identify novel X-linked intellectual disability genes. 2015 , 10, e0116454	38
1456	No Additional Prognostic Value of Genetic Information in the Prediction of Vascular Events after Cerebral Ischemia of Arterial Origin: The PROMISE Study. 2015 , 10, e0119203	5
1455	One Size Doesn't Fit All - RefEditor: Building Personalized Diploid Reference Genome to Improve Read Mapping and Genotype Calling in Next Generation Sequencing Studies. 2015 , 11, e1004448	6
1454	A Dual Model for Prioritizing Cancer Mutations in the Non-coding Genome Based on Germline and Somatic Events. 2015 , 11, e1004583	14
1453	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. 2015 , 11, e1005230	59
1452	Leveraging Identity-by-Descent for Accurate Genotype Inference in Family Sequencing Data. 2015 , 11, e1005271	2
1451	Evidence for a Common Origin of Blacksmiths and Cultivators in the Ethiopian Ari within the Last 4500 Years: Lessons for Clustering-Based Inference. 2015 , 11, e1005397	104
1450	Functional Impact and Evolution of a Novel Human Polymorphic Inversion That Disrupts a Gene and Creates a Fusion Transcript. 2015 , 11, e1005495	18
1449	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. 2015 , 11, e1005527	13
1448	Family-Based Benchmarking of Copy Number Variation Detection Software. 2015 , 10, e0133465	7
1447	Genome-Wide Study of Structural Variants in Bovine Holstein, Montbllarde and Normande Dairy Breeds. 2015 , 10, e0135931	40

1446	Investigating the Molecular Basis of Retinal Degeneration in a Familial Cohort of Pakistani Decent by Exome Sequencing. 2015 , 10, e0136561	25
1445	Distinct Transcript Isoforms of the Atypical Chemokine Receptor 1 (ACKR1)/Duffy Antigen Receptor for Chemokines (DARC) Gene Are Expressed in Lymphoblasts and Altered Isoform Levels Are Associated with Genetic Ancestry and the Duffy-Null Allele. 2015 , 10, e0140098	12
1444	Expression Quantitative Trait Loci Information Improves Predictive Modeling of Disease Relevance of Non-Coding Genetic Variation. 2015 , 10, e0140758	16
1443	Genomic Ancestry, Self-Rated Health and Its Association with Mortality in an Admixed Population: 10 Year Follow-Up of the Bambui-Epigen (Brazil) Cohort Study of Ageing. 2015 , 10, e0144456	10
1442	Genetic Admixture. 2015 , 887-897	
1441	How to Use SNP_TATA_Comparator to Find a Significant Change in Gene Expression Caused by the Regulatory SNP of This Gene's Promoter via a Change in Affinity of the TATA-Binding Protein for This Promoter. 2015 , 2015, 359835	19
1440	A Survival Association Study of 102 Polymorphisms Previously Associated with Survival Outcomes in Colorectal Cancer. 2015 , 2015, 968743	4
1439	NUDT21-spanning CNVs lead to neuropsychiatric disease and altered MeCP2 abundance via alternative polyadenylation. 2015 , 4,	49
1438	An analytical framework for optimizing variant discovery from personal genomes. 2015 , 6, 6275	73
1437	Large-scale recent expansion of European patrilineages shown by population resequencing. 2015 , 6, 7152	56
1436	A functional SNP in MIR124-1, a brain expressed miRNA gene, is associated with aggressiveness in a Colombian sample. 2015 , 30, 499-503	15
1435	De novo assembly of a haplotype-resolved human genome. 2015 , 33, 617-22	57
1434	Differences in Histone Modifications Between Individuals. 2015 , 55-82	
1433	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. 2015 , 20, 735-43	39
1432	Pathway Analysis and Its Applications. 2015 , 215-239	
1431	Drug and Gene Electrotransfer in Cancer Therapy. 2015 , 3-15	1
1430	Accurate and fast multiple-testing correction in eQTL studies. 2015 , 96, 857-68	18
1429	The Human Genome Project: Where Are We Now and Where Are We Going?. 2015 , 7-31	

1428	GSTM1, GSTP1, and GSTT1 genetic variability in Turkish and worldwide populations. 2015 , 27, 310-6	21
1427	Human Mate Choice. 2015 , 335-339	
1426	Canadian Open Genetics Repository (COGR): a unified clinical genomics database as a community resource for standardising and sharing genetic interpretations. 2015 , 52, 438-45	23
1425	Effect modification by vitamin D receptor genetic polymorphisms in the association between cumulative lead exposure and pulse pressure: a longitudinal study. 2015 , 14, 5	12
1424	Detecting individual ancestry in the human genome. 2015 , 6, 7	15
1423	Genome-wide inbreeding estimation within Lebanese communities using SNP arrays. 2015 , 23, 1364-9	10
1422	A mutation in FRIZZLED2 impairs Wnt signaling and causes autosomal dominant omdysplasia. 2015 , 24, 3399-409	22
1421	Whole genome prediction for preimplantation genetic diagnosis. 2015 , 7, 35	23
1420	Exome Sequencing for The Identification of Mendelian Disease Genes. 2015 , 36, 139-143	
1419	Progress of cancer genomics. 2015 , 6, 557-60	
1418	Fine-mapping additive and dominant SNP effects using group-LASSO and fractional resample model averaging. 2015 , 39, 77-88	13
1417	Targeted Next-Generation Sequencing Analysis of 1,000 Individuals with Intellectual Disability. 2015 , 36, 1197-204	122
1416	Genomic copy number variation in <i>Mus musculus</i> . 2015 , 16, 497	28
1415	Increased burden of de novo predicted deleterious variants in complex congenital diaphragmatic hernia. 2015 , 24, 4764-73	44
1414	Evolutionary patterns of DNA base composition and correlation to polymorphisms in DNA repair systems. 2015 , 43, 3614-25	8
1413	Parente2: a fast and accurate method for detecting identity by descent. 2015 , 25, 280-9	14
1412	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. 2015 , 112, 14658-63	108
1411	A Comparison of Optimality Measures for Estimating Untyped SNP Using the Allele Frequencies of Neighboring SNPs. 2015 ,	

1410	Identification of low abundance microbiome in clinical samples using whole genome sequencing. 2015 , 16, 265	67
1409	Linkage and whole genome sequencing identify a locus on 6q25-26 for formal thought disorder and implicate MEF2A regulation. 2015 , 169, 441-446	8
1408	Variable conceptions of population in community resource genetic projects: a challenge for governance. 2015 , 34, 294-318	4
1407	Association of Wilms' tumor 1 gene single-nucleotide polymorphism rs16754 with colorectal cancer. 2015 , 3, 1401-1405	3
1406	Genetic Predisposition to Dyslipidemia and Risk of Preeclampsia. 2015 , 28, 915-23	12
1405	Genetic contributions to urgency urinary incontinence in women. 2015 , 193, 2020-7	18
1404	Common variation in COL4A1/COL4A2 is associated with sporadic cerebral small vessel disease. 2015 , 84, 918-26	84
1403	Common single nucleotide variants underlying drug addiction: more than a decade of research. 2015 , 20, 845-71	70
1402	Confirmation of a founder effect in a Northern European population of a new Hb globin variant: HBB:c.23_26dup (codons 8/9 (+AGAA)). 2015 , 23, 1158-64	1
1401	The RIG-I-like helicase receptor MDA5 (IFIH1) is involved in the host defense against Candida infections. 2015 , 34, 963-974	46
1400	Dominance genetic variation contributes little to the missing heritability for human complex traits. 2015 , 96, 377-85	138
1399	Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. 2015 , 96, 283-94	161
1398	Congenital stationary night blindness: an analysis and update of genotype-phenotype correlations and pathogenic mechanisms. 2015 , 45, 58-110	198
1397	GenoExp: a web tool for predicting gene expression levels from single nucleotide polymorphisms. 2015 , 31, 1848-50	8
1396	LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. 2015 , 47, 291-5	2096
1395	Differential positive selection of malaria resistance genes in three indigenous populations of Peninsular Malaysia. 2015 , 134, 375-92	17
1394	CODEX: a normalization and copy number variation detection method for whole exome sequencing. 2015 , 43, e39	91
1393	Effects of copy number variable regions on local gene expression in white blood cells of Mexican Americans. 2015 , 23, 1229-35	6

1392	A copy number variation map of the human genome. 2015 , 16, 172-83	487
1391	A coding single-nucleotide polymorphism in lysine demethylase KDM4A associates with increased sensitivity to mTOR inhibitors. 2015 , 5, 245-54	20
1390	A high-resolution copy-number variation resource for clinical and population genetics. 2015 , 17, 747-52	54
1389	Single Nucleotide Variant Detection Using Next Generation Sequencing. 2015 , 109-127	6
1388	Reference Databases for Disease Associations. 2015 , 191-216	
1387	Protein Biomarkers for Detecting Cancer: Molecular Screening. 2015 , 331-346.e5	
1386	Mutation in mitochondrial ribosomal protein S7 (MRPS7) causes congenital sensorineural deafness, progressive hepatic and renal failure and lactic acidemia. 2015 , 24, 2297-307	48
1385	Biological interpretation of genome-wide association studies using predicted gene functions. 2015 , 6, 5890	489
1384	Personalized Treatment Options in Dermatology. 2015 ,	4
1383	The National Longitudinal Study of Adolescent to Adult Health (Add Health) sibling pairs genome-wide data. 2015 , 45, 12-23	29
1382	Genome-wide haplotype association study identifies BLM as a risk gene for prostate cancer in Chinese population. 2015 , 36, 2703-7	9
1381	Fast individual ancestry inference from DNA sequence data leveraging allele frequencies for multiple populations. 2015 , 16, 4	28
1380	Genetic diversity of disease-associated loci in Turkish population. 2015 , 60, 193-8	4
1379	Development of a forensic identity SNP panel for Indonesia. 2015 , 129, 681-91	3
1378	Increased rate of deleterious variants in long runs of homozygosity of an inbred population from Qatar. 2015 , 79, 14-9	22
1377	[Genetic predisposition and Pediatric Acute Respiratory Distress Syndrome: New tools for genetic study]. 2015 , 86, 73-9	
1376	Lupus risk variants in the PTK locus alter B-cell receptor internalization. 2014 , 5, 450	22
1375	Genographic Project. 2015 , 22-31	

1374	Chimeric EWSR1-FLI1 regulates the Ewing sarcoma susceptibility gene EGR2 via a GGAA microsatellite. 2015 , 47, 1073-8	103
1373	Population-specific genotype imputations using minimac or IMPUTE2. 2015 , 10, 1285-96	59
1372	Genotype screening of APLN rs3115757 variant in Egyptian women population reveals an association with obesity and insulin resistance. 2015 , 109, 40-7	11
1371	A New Era of Low-Dose Radiation Epidemiology. 2015 , 2, 236-49	17
1370	Evidence for negative selection of gene variants that increase dependence on dietary choline in a Gambian cohort. 2015 , 29, 3426-35	14
1369	Genetics of autoimmune diseases: insights from population genetics. 2015 , 60, 657-64	86
1368	Haplotype differences for copy number variants in the 22q11.23 region among human populations: a pigmentation-based model for selective pressure. 2015 , 23, 116-23	7
1367	MAGMA: generalized gene-set analysis of GWAS data. 2015 , 11, e1004219	1128
1366	Genomic ancestry and ethnoracial self-classification based on 5,871 community-dwelling Brazilians (The Epigen Initiative). 2015 , 5, 9812	94
1365	Modeling the 3D geometry of the cortical surface with genetic ancestry. 2015 , 25, 1988-92	23
1364	Genome-wide genotype and sequence-based reconstruction of the 140,000 year history of modern human ancestry. 2014 , 4, 6055	42
1363	Fine Mapping Causal Variants with an Approximate Bayesian Method Using Marginal Test Statistics. 2015 , 200, 719-36	132
1362	Leveraging Functional-Annotation Data in Trans-ethnic Fine-Mapping Studies. 2015 , 97, 260-71	119
1361	Large-scale genomics unveil polygenic architecture of human cortical surface area. 2015 , 6, 7549	25
1360	Conservation of the coding regions of the glycine N-acyltransferase gene further suggests that glycine conjugation is an essential detoxification pathway. 2015 , 571, 126-34	16
1359	POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans. 2015 , 349, aab3884	317
1358	Meta-Analysis of Genome-Wide Association Studies Identifies Genetic Risk Factors for Stroke in African Americans. 2015 , 46, 2063-8	44
1357	Significant lethality following liver resection in A20 heterozygous knockout mice uncovers a key role for A20 in liver regeneration. 2015 , 22, 2068-77	12

1356	Common variation at 2p13.3, 3q29, 7p13 and 17q25.1 associated with susceptibility to pancreatic cancer. 2015 , 47, 911-6	171
1355	Posterior predictive checks to quantify lack-of-fit in admixture models of latent population structure. 2015 , 112, E3441-50	7
1354	Characterization of TCF21 Downstream Target Regions Identifies a Transcriptional Network Linking Multiple Independent Coronary Artery Disease Loci. 2015 , 11, e1005202	36
1353	Immunogenetic influences on acquisition of HIV-1 infection: consensus findings from two African cohorts point to an enhancer element in IL19 (1q32.2). 2015 , 16, 213-20	2
1352	DISSCO: direct imputation of summary statistics allowing covariates. 2015 , 31, 2434-42	16
1351	Single nucleotide polymorphisms in type 2 diabetes among Hispanic adults. 2015 , 108, e25-7	2
1350	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. 2015 , 36, 1605.e7-12	70
1349	Comparing the evolutionary conservation between human essential genes, human orthologs of mouse essential genes and human housekeeping genes. 2015 , 16, 922-31	7
1348	Susceptibility variants in the CD58 gene locus point to a role of microRNA-548ac in the pathogenesis of multiple sclerosis. 2015 , 763, 161-7	13
1347	Genetic architectures of seropositive and seronegative rheumatic diseases. 2015 , 11, 401-14	30
1346	ARID1A and TERT promoter mutations in dedifferentiated meningioma. 2015 , 208, 345-50	57
1345	Lupus Risk Variant Increases pSTAT1 Binding and Decreases ETS1 Expression. 2015 , 96, 731-9	31
1344	The association of previously reported polymorphisms for microvascular complications in a meta-analysis of diabetic retinopathy. 2015 , 134, 247-57	48
1343	Replicative study of susceptibility to childhood-onset schizophrenia in Kazakhs. 2015 , 51, 185-192	4
1342	Combinatorial Conflicting Homozygosity (CCH) analysis enables the rapid identification of shared genomic regions in the presence of multiple phenocopies. 2015 , 16, 163	4
1341	PacBio-LITS: a large-insert targeted sequencing method for characterization of human disease-associated chromosomal structural variations. 2015 , 16, 214	48
1340	Rare variant association studies: considerations, challenges and opportunities. 2015 , 7, 16	134
1339	Self-reported race/ethnicity in the age of genomic research: its potential impact on understanding health disparities. 2015 , 9, 1	190

1338	CHRNA5 risk variant predicts delayed smoking cessation and earlier lung cancer diagnosis--a meta-analysis. 2015 , 107,	55
1337	A candidate gene study reveals association between a variant of the Peroxisome Proliferator-Activated Receptor Gamma (PPAR- γ) gene and systemic sclerosis. 2015 , 17, 128	21
1336	Heritability, SNP- and Gene-Based Analyses of Cannabis Use Initiation and Age at Onset. 2015 , 45, 503-13	19
1335	Impact of QTL properties on the accuracy of multi-breed genomic prediction. 2015 , 47, 42	35
1334	Genetic evidence for PLASMINOGEN as a shared genetic risk factor of coronary artery disease and periodontitis. 2015 , 8, 159-67	61
1333	Unravelling the hidden ancestry of American admixed populations. 2015 , 6, 6596	78
1332	The Current Status and Challenges in Computational Analysis of Genomic Big Data. 2015 , 2, 12-18	25
1331	Sensitive detection of chromatin-altering polymorphisms reveals autoimmune disease mechanisms. 2015 , 12, 458-64	41
1330	Evidence for archaic adaptive introgression in humans. 2015 , 16, 359-71	328
1329	The Kalash genetic isolate: ancient divergence, drift, and selection. 2015 , 96, 775-83	37
1328	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. 2015 , 348, 648-60	3242
1327	Genetic Basis of Common Human Disease: Insight into the Role of Missense SNPs from Genome-Wide Association Studies. 2015 , 427, 2271-89	32
1326	Leveraging Multi-ethnic Evidence for Mapping Complex Traits in Minority Populations: An Empirical Bayes Approach. 2015 , 96, 740-52	11
1325	The MUC5B promoter polymorphism is associated with idiopathic pulmonary fibrosis in a Mexican cohort but is rare among Asian ancestries. 2015 , 147, 460-464	68
1324	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. 2015 , 24, 1504-12	7
1323	Analysis of WNT4 polymorphism in Chinese Han women with endometriosis. 2015 , 30, 415-20	9
1322	Common variants spanning PLK4 are associated with mitotic-origin aneuploidy in human embryos. 2015 , 348, 235-8	80
1321	Human gephyrin is encompassed within giant functional noncoding yin-yang sequences. 2015 , 6, 6534	10

1320	Wilms Tumor 1 rs16754 predicts favorable clinical outcomes for acute myeloid leukemia patients in South Chinese population. 2015 , 39, 568-74	11
1319	Polygenic risk, stressful life events and depressive symptoms in older adults: a polygenic score analysis. 2015 , 45, 1709-20	71
1318	RNA Sequencing and Analysis. 2015 , 2015, 951-69	293
1317	Genetic Diversity and Societally Important Disparities. 2015 , 201, 1-12	17
1316	Partitioning heritability by functional annotation using genome-wide association summary statistics. 2015 , 47, 1228-35	1143
1315	An atlas of genetic correlations across human diseases and traits. 2015 , 47, 1236-41	1841
1314	Effect of genetic ancestry on leukocyte global DNA methylation in cancer patients. 2015 , 15, 434	25
1313	Strategies for Imputing and Analyzing Rare Variants in Association Studies. 2015 , 31, 556-563	22
1312	Mixed Ancestry and Disease Risk Transferability. 2015 , 3, 151-157	1
1311	Genomics, Personalized Medicine and Oral Disease. 2015 ,	1
1310	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. 2015 , 24, 7445-9	49
1309	Admixture Dynamics, Natural Selection and Diseases in Admixed Populations. 2015 ,	1
1308	Analysis of the genetic architecture of susceptibility to cervical cancer indicates that common SNPs explain a large proportion of the heritability. 2015 , 36, 992-8	17
1307	Integrative analysis of RNA, translation, and protein levels reveals distinct regulatory variation across humans. 2015 , 25, 1610-21	115
1306	The role of climate and out-of-Africa migration in the frequencies of risk alleles for 21 human diseases. 2015 , 16, 81	6
1305	Genome-wide pathway analysis for diabetic nephropathy in type 1 diabetes. 2016 , 41, 21-7	5
1304	Quantitating and dating recent gene flow between European and East Asian populations. 2015 , 5, 9500	20
1303	Expression quantitative trait locus analysis for translational medicine. 2015 , 7, 60	49

1302	BOOGIE: Predicting Blood Groups from High Throughput Sequencing Data. 2015 , 10, e0124579	20
1301	WhatsHap: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. 2015 , 22, 498-509	172
1300	Impact of genetic similarity on imputation accuracy. 2015 , 16, 90	16
1299	Natural selection on HFE in Asian populations contributes to enhanced non-heme iron absorption. 2015 , 16, 61	19
1298	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. 2015 , 6, 7213	54
1297	Bayesian integration of genetics and epigenetics detects causal regulatory SNPs underlying expression variability. 2015 , 6, 8555	20
1296	Japanica array: improved genotype imputation by designing a population-specific SNP array with 1070 Japanese individuals. 2015 , 60, 581-7	79
1295	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. 2015 , 6, 8018	270
1294	The Crohn's disease-associated polymorphism in ATG16L1 (rs2241880) reduces SHIP gene expression and activity in human subjects. 2015 , 16, 452-61	10
1293	Assessing Rare Variation in Complex Traits. 2015 ,	1
1292	Sex-Specific Parental Effects on Offspring Lipid Levels. 2015 , 4,	5
1291	Common polygenic variation contributes to risk of migraine in the Norfolk Island population. 2015 , 134, 1079-87	9
1290	Greenlandic Inuit show genetic signatures of diet and climate adaptation. 2015 , 349, 1343-7	298
1289	Two Novel Mutations in the SLC25A4 Gene in a Patient with Mitochondrial Myopathy. 2015 , 22, 39-45	21
1288	New insights into the history of the C-14010 lactase persistence variant in Eastern and Southern Africa. 2015 , 156, 661-4	17
1287	The IRF5-TNPO3 association with systemic lupus erythematosus has two components that other autoimmune disorders variably share. 2015 , 24, 582-96	57
1286	Clinical and pharmacogenomic implications of genetic variation in a Southern Ethiopian population. 2015 , 15, 101-108	13
1285	Association of rs1466535 LRP1 but not rs3019885 SLC30A8 and rs6674171 TDRD10 gene polymorphisms with abdominal aortic aneurysm in Italian patients. 2015 , 61, 787-92	18

1284	Convergence of advances in genomics, team science, and repositories as drivers of progress in psychiatric genomics. 2015 , 77, 6-14	14
1283	HLA-DQA1 and PLCG2 Are Candidate Risk Loci for Childhood-Onset Steroid-Sensitive Nephrotic Syndrome. 2015 , 26, 1701-10	92
1282	Novel genomic signals of recent selection in an Ethiopian population. 2015 , 23, 1085-92	23
1281	Pathway analysis for a genome-wide association study of pneumoconiosis. 2015 , 232, 284-92	6
1280	Overview of Technical Aspects and Chemistries of Next-Generation Sequencing. 2015 , 3-19	7
1279	Software Engineering, Artificial Intelligence, Networking and Parallel/Distributed Computing. 2015 ,	
1278	Exploring the function of genetic variants in the non-coding genomic regions: approaches for identifying human regulatory variants affecting gene expression. 2015 , 16, 393-412	38
1277	Genomic profiling of thousands of candidate polymorphisms predicts risk of relapse in 778 Danish and German childhood acute lymphoblastic leukemia patients. 2015 , 29, 297-303	20
1276	The promise of psychiatric pharmacogenomics. 2015 , 77, 29-35	40
1275	Current trend of annotating single nucleotide variation in humans--A case study on SNVrap. 2015 , 79-80, 32-40	9
1274	Haplotypes of CpG-related SNPs and associations with DNA methylation patterns. 193-207	1
1273	Investigating Splicing Variants Uncovered by Next-Generation Sequencing the Alzheimer's Disease Candidate Genes, CLU, PICALM, CR1, ABCA7, BIN1, the MS4A Locus, CD2AP, EPHA1 and CD33. 2016 , 06,	
1272	Effects of Single Nucleotide Polymorphism Marker Density on Haplotype Block Partition. 2016 , 14, 196-204	7
1271	The Association between Gene-Environment Interactions and Diseases Involving the Human GST Superfamily with SNP Variants. 2016 , 13, 379	47
1270	Functional relevance of naturally occurring mutations in adhesion G protein-coupled receptor ADGRD1 (GPR133). 2016 , 17, 609	11
1269	Associations of potentially functional variants in IL-6, JAKs and STAT3 with gastric cancer risk in an eastern Chinese population. 2016 , 7, 28112-23	15
1268	Detecting Gene-Gene Interactions Associated with Multiple Complex Traits with U-Statistics. 2016 , 17, 403-415	2
1267	Admixture into and within sub-Saharan Africa. 2016 , 5,	77

1266	The Impact of Evolutionary Driving Forces on Human Complex Diseases: A Population Genetics Approach. 2016 , 2016, 2079704	7
1265	Structural characterization of single nucleotide variants at ligand binding sites and enzyme active sites of human proteins. 2016 , 13, 157-163	6
1264	Population Screening for Biological and Environmental Properties of the Human Metabolic Phenotype. 2016 , 167-211	18
1263	Population Stratification in the Context of Diverse Epidemiologic Surveys Sans Genome-Wide Data. 2016 , 7, 76	8
1262	Candidate SNP Markers of Gender-Biased Autoimmune Complications of Monogenic Diseases Are Predicted by a Significant Change in the Affinity of TATA-Binding Protein for Human Gene Promoters. 2016 , 7, 130	13
1261	The Genetics of Osteoarthritis: A Review. 2016 , 1, 140-153	26
1260	Efficient analysis of large datasets and sex bias with ADMIXTURE. 2016 , 17, 218	20
1259	Genome-wide imputation study identifies novel HLA locus for pulmonary fibrosis and potential role for auto-immunity in fibrotic idiopathic interstitial pneumonia. 2016 , 17, 74	54
1258	Construction of an integrative regulatory element and variation map of the murine Tst locus. 2016 , 17, 77	1
1257	Multiethnic genome-wide association study identifies ethnic-specific associations with body mass index in Hispanics and African Americans. 2016 , 17, 78	29
1256	Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. 2016 , 25, 4339-4349	7
1255	Prevalent Accumulation of Non-Optimal Codons through Somatic Mutations in Human Cancers. 2016 , 11, e0160463	4
1254	Inference of Ancestral Recombination Graphs through Topological Data Analysis. 2016 , 12, e1005071	24
1253	Strong Selection at MHC in Mexicans since Admixture. 2016 , 12, e1005847	38
1252	Computational Characterization of Osteoporosis Associated SNPs and Genes Identified by Genome-Wide Association Studies. 2016 , 11, e0150070	24
1251	System-Wide Associations between DNA-Methylation, Gene Expression, and Humoral Immune Response to Influenza Vaccination. 2016 , 11, e0152034	33
1250	The Genetics of Bene Israel from India Reveals Both Substantial Jewish and Indian Ancestry. 2016 , 11, e0152056	12
1249	A Protein Domain and Family Based Approach to Rare Variant Association Analysis. 2016 , 11, e0153803	5

1248	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. 2016 , 11, e0160316	11
1247	Fire Usage and Ancient Hominin Detoxification Genes: Protective Ancestral Variants Dominate While Additional Derived Risk Variants Appear in Modern Humans. 2016 , 11, e0161102	6
1246	Evidence of Recent Intricate Adaptation in Human Populations. 2016 , 11, e0165870	5
1245	Genetics of Allergic Asthma and Current Perspectives on Therapeutic Management. 2016 ,	2
1244	Next-Generation Sequencing [An Overview of the History, Tools, and [omic] Applications. 2016 ,	57
1243	Ulcerative Colitis Is Under Dual (Mitochondrial and Nuclear) Genetic Control. 2016 , 22, 774-81	6
1242	TNFRSF1B Is Associated with ANCA in IBD. 2016 , 22, 1346-52	4
1241	A novel random effect model for GWAS meta-analysis and its application to trans-ethnic meta-analysis. 2016 , 72, 945-54	8
1240	Analysis of Post-Translational Modifications and Proteolysis in Neuroscience. 2016 ,	0
1239	Association of MHC region SNPs with irritant susceptibility in healthcare workers. 2016 , 13, 738-44	11
1238	Testing Allele Transmission of an SNP Set Using a Family-Based Generalized Genetic Random Field Method. 2016 , 40, 341-51	4
1237	Genetics of systemic lupus erythematosus and Sjögren's syndrome: an update. 2016 , 28, 506-14	29
1236	Whole-genome sequencing in French Canadians from Quebec. 2016 , 135, 1213-1221	13
1235	Identity by descent fine mapping of familial adult myoclonus epilepsy (FAME) to 2p11.2-2q11.2. 2016 , 135, 1117-25	16
1234	PADRE: Pedigree-Aware Distant-Relationship Estimation. 2016 , 99, 154-62	22
1233	Evaluation of a Two-Stage Approach in Trans-Ethnic Meta-Analysis in Genome-Wide Association Studies. 2016 , 40, 284-92	8
1232	Genetics in Keratoconus: where are we?. 2016 , 3, 16	61
1231	Genetic structure of human populations based on 5 gene loci: A preliminary report from Northern India. 2016 , 4, 244-248	1

1230	Genome-Wide Association Study in an Amerindian Ancestry Population Reveals Novel Systemic Lupus Erythematosus Risk Loci and the Role of European Admixture. 2016 , 68, 932-43	93
1229	Meta-analysis and association of two common polymorphisms of the human oxytocin receptor gene in autism spectrum disorder. 2016 , 9, 1036-1045	30
1228	Rare copy number variants implicated in posterior urethral valves. 2016 , 170, 622-33	16
1227	Cancer Bioinformatics. 2016 , 1-14	
1226	The Role of Host Genetics (and Genomics) in Tuberculosis. 2016 , 4,	17
1225	Comparing performance of modern genotype imputation methods in different ethnicities. 2016 , 6, 34386	22
1224	A microRNA-328 binding site in PAX6 is associated with centrotemporal spikes of rolandic epilepsy. 2016 , 3, 512-22	23
1223	Flanking monomer repeats determine decreased context complexity of single nucleotide polymorphism sites in the human genome. 2016 , 6, 809-815	
1222	Genetic Component of Type 2 Diabetes in a Mexican Population. 2016 , 47, 496-505	12
1221	Serum calcium and risk of migraine: a Mendelian randomization study. 2017 , 26, 820-828	11
1220	DNA Methylation Identifies Loci Distinguishing Hereditary Nonpolyposis Colorectal Cancer Without Germ-Line MLH1/MSH2 Mutation from Sporadic Colorectal Cancer. 2016 , 7, e208	4
1219	Detailed analysis of inversions predicted between two human genomes: errors, real polymorphisms, and their origin and population distribution. 2017 , 26, 567-581	8
1218	Genome-wide association study of response to cognitive-behavioural therapy in children with anxiety disorders. 2016 , 209, 236-43	27
1217	Length Distribution of Ancestral Tracks under a General Admixture Model and Its Applications in Population History Inference. 2016 , 6, 20048	15
1216	From integrative genomics to systems genetics in the rat to link genotypes to phenotypes. 2016 , 9, 1097-1110	20
1215	Applications of the 1000 Genomes Project resources. 2017 , 16, 163-170	18
1214	Genome-wide association analysis in schizophrenia. 106-122	
1213	A variant at 9p21.3 functionally implicates CDKN2B in paediatric B-cell precursor acute lymphoblastic leukaemia aetiology. 2016 , 7, 10635	37

1212	large rare copy-number variations contribute to conotruncal heart disease in Chinese patients. 2016 , 1, 16033	6
1211	Comparative analyses across cattle genders and breeds reveal the pitfalls caused by false positive and lineage-differential copy number variations. 2016 , 6, 29219	16
1210	Genetics of Bronchopulmonary Dysplasia. 2016 , 109-127	1
1209	Progress and challenges in bioinformatics approaches for enhancer identification. 2016 , 17, 967-979	54
1208	Next generation sequencing: implications in personalized medicine and pharmacogenomics. 2016 , 12, 1818-30	63
1207	Multi-ethnic genome-wide association study identifies novel locus for type 2 diabetes susceptibility. 2016 , 24, 1175-80	54
1206	Systematic identification of genetic influences on methylation across the human life course. 2016 , 17, 61	331
1205	A computational method for prediction of rSNPs in human genome. 2016 , 62, 96-103	1
1204	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. 2016 , 18, 814-22	25
1203	Allele-Skewed DNA Modification in the Brain: Relevance to a Schizophrenia GWAS. 2016 , 98, 956-962	17
1202	A Syndromic Intellectual Disability Disorder Caused by Variants in TELO2, a Gene Encoding a Component of the TTT Complex. 2016 , 98, 909-918	19
1201	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. 2016 , 117, 51-61	54
1200	Estimating IBD tracts from low coverage NGS data. 2016 , 32, 2096-102	23
1199	Sequencing Approaches to Type 2 Diabetes. 2016 , 111-126	
1198	Opportunities and challenges of big data for the social sciences: The case of genomic data. 2016 , 59, 13-22	11
1197	Loss of Nicastrin from Oligodendrocytes Results in Hypomyelination and Schizophrenia with Compulsive Behavior. 2016 , 291, 11647-56	12
1196	GENeSTATION 1.0: a synthetic resource of diverse evolutionary and functional genomic data for studying the evolution of pregnancy-associated tissues and phenotypes. 2016 , 44, D908-16	6
1195	Genetic Mapping of Human Immune System Function. 2016 , 151-164	

1194	A high-throughput sequencing test for diagnosing inherited bleeding, thrombotic, and platelet disorders. 2016 , 127, 2791-803	135
1193	DNA methylation signature of human fetal alcohol spectrum disorder. 2016 , 9, 25	93
1192	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. 2016 , 204, 303-14	59
1191	Genetic Risk Can Be Decreased: Quitting Smoking Decreases and Delays Lung Cancer for Smokers With High and Low CHRNA5 Risk Genotypes - A Meta-Analysis. 2016 , 11, 219-226	27
1190	Rare intronic variants of TCF7L2 arising by selective sweeps in an indigenous population from Mexico. 2016 , 17, 68	3
1189	Computationally Characterizing Genomic Pipelines Using High-confident Call Sets. 2016 , 80, 1023-1032	
1188	A comprehensive and scalable database search system for metaproteomics. 2016 , 17, 642	34
1187	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016 , 538, 248-254	266
1186	The Pro12Ala polymorphism in the PPAR- α gene is not associated to obesity and type 2 diabetes mellitus in a Cameroonian population. 2016 , 3, 26	10
1185	Pediatric Biomedical Informatics. 2016 ,	1
1184	SLCO1B1 Gene Variations Among Tanzanians, Ethiopians, and Europeans: Relevance for African and Worldwide Precision Medicine. 2016 , 20, 538-45	19
1183	Native American Genomics and Population Histories. 2016 , 45, 319-340	21
1182	Biology of the Human Graft-versus-Tumor Response and How to Exploit It. 2016 , 166-181	1
1181	Meta-Analysis of Rare Variant Association Tests in Multiethnic Populations. 2016 , 40, 57-65	6
1180	Baseline genetic associations in the Parkinson's Progression Markers Initiative (PPMI). 2016 , 31, 79-85	47
1179	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. 2016 , 115, 752-60	10
1178	Determinants of Power in Gene-Based Burden Testing for Monogenic Disorders. 2016 , 99, 527-539	17
1177	Associations between Nine Polymorphisms in EXO1 and Cancer Susceptibility: A Systematic Review and Meta-Analysis of 39 Case-control Studies. 2016 , 6, 29270	9

1176	IRF7 inhibition prevents destructive innate immunity-A target for nonantibiotic therapy of bacterial infections. 2016 , 8, 336ra59	20
1175	An ethnically relevant consensus Korean reference genome is a step towards personal reference genomes. 2016 , 7, 13637	38
1174	Systems genetics identifies Hp1bp3 as a novel modulator of cognitive aging. 2016 , 46, 58-67	24
1173	Microduplications at the pseudoautosomal SHOX locus in autism spectrum disorders and related neurodevelopmental conditions. 2016 , 53, 536-47	19
1172	Translational plasticity facilitates the accumulation of nonsense genetic variants in the human population. 2016 , 26, 1639-1650	24
1171	Direct chromosome-length haplotyping by single-cell sequencing. 2016 , 26, 1565-1574	34
1170	Whole-exome sequencing to identify genetic risk variants underlying inhibitor development in severe hemophilia A patients. 2016 , 127, 2924-33	20
1169	Proceedings of the 15th Annual UT-KBRIN Bioinformatics Summit 2016 : Cadiz, KY, USA. 8-10 April 2016. 2016 , 17, 297	
1168	KIDNEY DISEASE GENETICS AND THE IMPORTANCE OF DIVERSITY IN PRECISION MEDICINE. 2016 ,	1
1167	Detecting Heterogeneity in Population Structure Across the Genome in Admixed Populations. 2016 , 204, 43-56	5
1166	Association Strategies. 2016 , 133-139	
1165	Identification of copy number variations in three Chinese horse breeds using 70K single nucleotide polymorphism BeadChip array. 2016 , 47, 560-9	11
1164	Testing neutrality at copy-number-variable loci under the finite-allele and finite-site models. 2016 , 112, 1-13	3
1163	Consensus Genome-Wide Expression Quantitative Trait Loci and Their Relationship with Human Complex Trait Disease. 2016 , 20, 400-14	34
1162	Robust Inference of Identity by Descent from Exome-Sequencing Data. 2016 , 99, 1106-1116	6
1161	Enhanced copy number variants detection from whole-exome sequencing data using EXCAVATOR2. 2016 , 44, e154	51
1160	The genetic history of Cochin Jews from India. 2016 , 135, 1127-43	8
1159	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. 2016 , 167, 1415-1429.e19	637

1158	Colocalization of GWAS and eQTL Signals Detects Target Genes. 2016 , 99, 1245-1260	311
1157	Compositional Data Analysis. 2016 ,	3
1156	Germline and somatic BAP1 mutations in high-grade rhabdoid meningiomas. 2017 , 19, 535-545	60
1155	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. 2016 , 7, 12989	70
1154	ImmunoChip analysis identifies novel susceptibility loci in the human leukocyte antigen region for acquired thrombotic thrombocytopenic purpura. 2016 , 14, 2356-2367	8
1153	Genetics of Parkinson's disease. 2016 , 30, 386-396	198
1152	Replication of genome-wide association study (GWAS) susceptibility loci in a Latino bipolar disorder cohort. 2016 , 18, 520-527	16
1151	Genomic study of the Ket: a Paleo-Eskimo-related ethnic group with significant ancient North Eurasian ancestry. 2016 , 6, 20768	37
1150	Exome Array Analysis of Susceptibility to Pneumococcal Meningitis. 2016 , 6, 29351	6
1149	The framework for population epigenetic study. 2018 , 19, 89-100	6
1148	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. 2016 , 167, 643-656.e17	224
1147	Omics studies: their use in diagnosis and reclassification of SLE and other systemic autoimmune diseases. 2017 , 56, i78-i87	17
1146	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. 2016 , 1,	11
1145	Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. 2016 , 17, 400	6
1144	Genetic affinities of the Jewish populations of India. 2016 , 6, 19166	13
1143	Genetic diversity and natural selection footprints of the glycine amidinotransferase gene in various human populations. 2016 , 6, 18755	6
1142	Hypothetical SNP markers that significantly affect the affinity of the TATA-binding protein to VEGFA, ERBB2, IGF1R, FLT1, KDR, and MET oncogene promoters as chemotherapy targets. 2016 , 50, 141-152	7
1141	PWHATSHAP: efficient haplotyping for future generation sequencing. 2016 , 17, 342	9

1140	Analysis of optimal alignments unfolds aligners' bias in existing variant profiles. 2016 , 17, 349	4
1139	Prediction and verification of the influence of the rs367781716 SNP on the interaction of the Binding protein with the promoter of the human B-gene. 2016 , 6, 785-791	0
1138	The Global Genome Biodiversity Network (GGBN) Data Standard specification. 2016 , 2016,	30
1137	Lactase non-persistence and general patterns of dairy intake in indigenous and mestizo chilean populations. 2016 , 28, 213-9	5
1136	Different evolutionary patterns of SNPs between domains and unassigned regions in human protein-coding sequences. 2016 , 291, 1127-36	1
1135	Linking short tandem repeat polymorphisms with cytosine modifications in human lymphoblastoid cell lines. 2016 , 135, 223-32	2
1134	Current Concepts of Pharmacogenetics, Pharmacogenomics, and the Druggable Genome. 2016 , 161-183	
1133	The rise of genomics. 2016 , 339, 231-9	13
1132	GHap: an R package for genome-wide haplotyping. 2016 , 32, 2861-2	20
1131	Systems proteomics of liver mitochondria function. 2016 , 352, aad0189	193
1130	Evolutionary triangulation: informing genetic association studies with evolutionary evidence. 2016 , 9, 12	4
1129	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. 2016 , 48, 856-66	355
1128	Nutrigenomics. 2016 ,	2
1127	A model for the clustered distribution of SNPs in the human genome. 2016 , 64, 94-98	4
1126	A comparison of DMET Plus microarray and genome-wide technologies by assessing population substructure. 2016 , 26, 147-153	9
1125	Massively parallel sequencing of short tandem repeats-Population data and mixture analysis results for the PowerSeq system. 2016 , 24, 86-96	95
1124	Whole-exome sequencing to analyze population structure, parental inbreeding, and familial linkage. 2016 , 113, 6713-8	37
1123	Molecular evolution of WDR62, a gene that regulates neocortico genesis. 2016 , 9, 1-9	13

1122	The implications of genetic variation for the pharmacokinetics and pharmacodynamics of aromatase inhibitors. 2016 , 12, 851-63	2
1121	Eigenanalysis of SNP data with an identity by descent interpretation. 2016 , 107, 65-76	21
1120	Genetic structure of the Newfoundland and Labrador population: founder effects modulate variability. 2016 , 24, 1063-70	14
1119	Detection of Allelic Frequency Differences between the Sexes in Humans: A Signature of Sexually Antagonistic Selection. 2016 , 8, 1489-500	41
1118	Aquaporin 11 variant associates with kidney disease in type 2 diabetic patients. 2016 , 310, F416-25	13
1117	An integrated analysis tool for analyzing hybridization intensities and genotypes using new-generation population-optimized human arrays. 2016 , 17, 266	2
1116	Novel genetic risk factors for asthma in African American children: Precision Medicine and the SAGE II Study. 2016 , 68, 391-400	46
1115	Genome-Wide Association Studies Suggest Limited Immune Gene Enrichment in Schizophrenia Compared to 5 Autoimmune Diseases. 2016 , 42, 1176-84	42
1114	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. 2016 , 55, 1-31	39
1113	Improved imputation accuracy in Hispanic/Latino populations with larger and more diverse reference panels: applications in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). 2016 , 25, 3245-3254	12
1112	Mutation screening of SCN2A in schizophrenia and identification of a novel loss-of-function mutation. 2016 , 26, 60-5	33
1111	MultiGeMS: detection of SNVs from multiple samples using model selection on high-throughput sequencing data. 2016 , 32, 1486-92	2
1110	Impact of host genetic polymorphisms on vaccine induced antibody response. 2016 , 12, 907-15	34
1109	Genomic variations in non-coding RNAs: Structure, function and regulation. 2016 , 107, 59-68	49
1108	Imputing Genotypes in Biallelic Populations from Low-Coverage Sequence Data. 2016 , 202, 487-95	34
1107	Genetics of Human Aging. 2016 , 327-358	
1106	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. 2016 , 15, 174-184	159
1105	A systematic review and meta-analysis of the impact of WT1 polymorphism rs16754 in the effectiveness of standard chemotherapy in patients with acute myeloid leukemia. 2016 , 16, 30-40	7

1104	RBP-Var: a database of functional variants involved in regulation mediated by RNA-binding proteins. 2016 , 44, D154-63	31
1103	Multiple thrombophilic single nucleotide polymorphisms lack a significant effect on outcomes in fresh IVF cycles: an analysis of 1717 patients. 2016 , 33, 67-73	15
1102	Clinical Pharmacology: Current Topics and Case Studies. 2016 ,	0
1101	The association of single nucleotide polymorphisms of the maternal cystathionine- β -synthase gene with early-onset preeclampsia. 2016 , 6, 60-5	11
1100	Bronchopulmonary Dysplasia. 2016 ,	3
1099	RhesusBase PopGateway: Genome-Wide Population Genetics Atlas in Rhesus Macaque. 2016 , 33, 1370-5	14
1098	Multiallelic Positions in the Human Genome: Challenges for Genetic Analyses. 2016 , 37, 231-234	14
1097	Mutation pattern is an influential factor on functional mutation rates in cancer. 2015 , 16, 2	2
1096	Targeted resequencing identifies PTCH1 as a major contributor to ocular developmental anomalies and extends the SOX2 regulatory network. 2016 , 26, 474-85	27
1095	A Burden of Rare Variants Associated with Extremes of Gene Expression in Human Peripheral Blood. 2016 , 98, 299-309	61
1094	Assessing the genetic overlap between BMI and cognitive function. 2016 , 21, 1477-82	29
1093	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. 2016 , 98, 229-42	54
1092	Advancing Pharmacogenomics Education in the Core PharmD Curriculum through Student Personal Genomic Testing. 2016 , 80, 3	52
1091	Rapid detection of germline mutations for hereditary gastrointestinal polyposis/cancers using HaloPlex target enrichment and high-throughput sequencing technologies. 2016 , 15, 553-62	16
1090	Pseudo-De Novo Assembly and Analysis of Unmapped Genome Sequence Reads in Wild Zebrafish Reveal Novel Gene Content. 2016 , 13, 95-102	11
1089	GEMINI: a computationally-efficient search engine for large gene expression datasets. 2016 , 17, 102	9
1088	Higher-Resolution Structure of the Human Insulin Receptor Ectodomain: Multi-Modal Inclusion of the Insert Domain. 2016 , 24, 469-76	95
1087	Introgression of Neandertal- and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. 2016 , 98, 22-33	156

1086	Model-free Estimation of Recent Genetic Relatedness. 2016 , 98, 127-48	164
1085	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. 2016 , 98, 165-84	181
1084	Machine Learning in Genomic Medicine: A Review of Computational Problems and Data Sets. 2016 , 104, 176-197	132
1083	Next Generation Sequencing in Dysmorphology. 2016 , 137-151	1
1082	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. 2016 , 33, 1177-87	28
1081	Allele Frequencies Net Database: Improvements for storage of individual genotypes and analysis of existing data. 2016 , 77, 238-248	89
1080	Genetic Risk Score for Essential Hypertension and Risk of Preeclampsia. 2016 , 29, 17-24	11
1079	Nascent RNA folding mitigates transcription-associated mutagenesis. 2016 , 26, 50-9	14
1078	Reveal: large-scale population genotyping using low-coverage sequencing data. 2016 , 32, 1686-96	5
1077	RMBase: a resource for decoding the landscape of RNA modifications from high-throughput sequencing data. 2016 , 44, D259-65	121
1076	Genesis of two most prevalent PROP1 gene variants causing combined pituitary hormone deficiency in 21 populations. 2016 , 24, 415-20	22
1075	Genetic variants in TNF β TGFB1, PTGS1 and PTGS2 genes are associated with diisocyanate-induced asthma. 2016 , 13, 119-26	22
1074	Systematic re-evaluation of genes from candidate gene association studies in migraine using a large genome-wide association data set. 2016 , 36, 604-14	29
1073	The Pediatric Imaging, Neurocognition, and Genetics (PING) Data Repository. 2016 , 124, 1149-1154	177
1072	Computational analyses of type 2 diabetes-associated loci identified by genome-wide association studies. 2017 , 9, 362-377	14
1071	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. 2017 , 81, 325-335	129
1070	Characterising private and shared signatures of positive selection in 37 Asian populations. 2017 , 25, 499-508	15
1069	Association of Genome-Wide Association Study (GWAS) Identified SNPs and Risk of Breast Cancer in an Indian Population. 2017 , 7, 40963	11

1068	Reconstructing the population history of the largest tribe of India: the Dravidian speaking Gond. 2017 , 25, 493-498	7
1067	Securing the use of existing sample collections for future human genetic research. 2017 , 25, 522-529	
1066	Multiregion ultra-deep sequencing reveals early intermixing and variable levels of intratumoral heterogeneity in colorectal cancer. 2017 , 11, 124-139	31
1065	Comprehensive Screening for Disease Risk Variants in Early-Onset Alzheimer's Disease Genes in African Americans Identifies Novel PSEN Variants. 2017 , 56, 1215-1222	2
1064	Association between IL-27 gene polymorphisms and risk of papillary thyroid carcinoma. 2017 , 11, 141-149	9
1063	Personality traits as an endophenotype in genetic studies on suicidality in bipolar disorder. 2017 , 29, 115-121	5
1062	Genome-wide screening for highly discriminative SNPs for personal identification and their assessment in world populations. 2017 , 28, 118-127	15
1061	Galactosylation of IgA1 Is Associated with Common Variation in. 2017 , 28, 2158-2166	65
1060	Role of HLA-DP and HLA-DQ on the clearance of hepatitis B virus and the risk of chronic infection in a multiethnic population. 2017 , 37, 1476-1487	11
1059	Detection of Turner syndrome using X-chromosome inactivation specific differentially methylated CpG sites: A pilot study. 2017 , 468, 174-179	4
1058	Admixture Mapping Identifies an Amerindian Ancestry Locus Associated with Albuminuria in Hispanics in the United States. 2017 , 28, 2211-2220	17
1057	Sex-specific genetic diversity is shaped by cultural factors in Inner Asian human populations. 2017 , 162, 627-640	16
1056	Strong Amerindian Mitonuclear Discordance in Puerto Rican Genomes Suggests Amerindian Mitochondrial Benefit. 2017 , 81, 59-77	1
1055	Whole-genome single nucleotide variant distribution on genomic regions and its relationship to major depression. 2017 , 252, 75-79	12
1054	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. 2017 , 7, 410-423	77
1053	Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with polynomial functions. 2017 , 118, 503-510	9
1052	Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. 2017 , 7, 45652	26
1051	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. 2017 , 25, 877-885	43

1050	Improved imputation accuracy of rare and low-frequency variants using population-specific high-coverage WGS-based imputation reference panel. 2017 , 25, 869-876	82
1049	It's about time: Insights into temporal genetic patterns in oceanic zooplankton from biodiversity indices. 2017 , 62, 1836-1852	5
1048	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. 2017 , 206, 1113-1126	17
1047	Association study and expression analysis of CYP4A11 gene copy number variation in Chinese cattle. 2017 , 7, 46599	21
1046	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. 2017 , 49, 978-985	254
1045	Enhancing genetic gain in the era of molecular breeding. 2017 , 68, 2641-2666	111
1044	A pathway-centric approach to rare variant association analysis. 2016 , 25, 123-129	11
1043	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. 2017 , 135, 2336-2353	36
1042	Recent advances in sequence assembly: principles and applications. 2017 , 16, 361-378	9
1041	Inferring Human Demographic Histories of Non-African Populations from Patterns of Allele Sharing. 2017 , 100, 766-772	17
1040	Widespread Allelic Heterogeneity in Complex Traits. 2017 , 100, 789-802	49
1039	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. 2017 , 7, 45040	70
1038	Analysis of Genome-Wide Association Data. 2017 , 1526, 161-173	6
1037	Genome Annotation. 2017 , 1525, 107-121	2
1036	Copy number variants in a population-based investigation of Klippel-Trenaunay syndrome. 2017 , 173, 352-359	7
1035	CanProVar 2.0: An Updated Database of Human Cancer Proteome Variation. 2017 , 16, 421-432	26
1034	Human ancestry correlates with language and reveals that race is not an objective genomic classifier. 2017 , 7, 1572	30
1033	A latent genetic subtype of major depression identified by whole-exome genotyping data in a Mexican-American cohort. 2017 , 7, e1134	16

1032	Evolutionary Triangulation to Refine Genetic Association Studies of Spontaneous Preterm Birth. 2017 , 34, 1041-1047	
1031	Extremely low-coverage whole genome sequencing in South Asians captures population genomics information. 2017 , 18, 396	18
1030	Genomic landscape of high-grade meningiomas. 2017 , 2,	78
1029	How mice are indispensable for understanding obesity and diabetes genetics. 2017 , 24, 83-91	21
1028	Pharmacogenetics and Pharmacogenomics. 2017 , 89-107	3
1027	Meiotic Recombination in the Human Germ Line. 2017 , 59-85	
1026	The impact of rare and low-frequency genetic variants in common disease. 2017 , 18, 77	174
1025	Introduction. 2017 , 1-9	
1024	Gene and Genome Sequencing: Interpreting Genetic Variation at the Nucleotide Level. 2017 , 419-454	4
1023	Immunology and genetics of tumour necrosis factor in allergic contact dermatitis. 2017 , 76, 257-271	9
1022	Reporting Correct p Values in VEGAS Analyses. 2017 , 20, 257-259	3
1021	Convergent Balancing Selection on the Mu-Opioid Receptor in Primates. 2017 , 34, 1629-1643	10
1020	A novel strategy for clustering major depression individuals using whole-genome sequencing variant data. 2017 , 7, 44389	13
1019	Genotype Calling from Population-Genomic Sequencing Data. 2017 , 7, 1393-1404	44
1018	High mutation rates explain low population genetic divergence at copy-number-variable loci in Homo sapiens. 2017 , 7, 43178	1
1017	Rare copy number variants in a population-based investigation of hypoplastic right heart syndrome. 2017 , 109, 8-15	6
1016	Resetting the bar: Statistical significance in whole-genome sequencing-based association studies of global populations. 2017 , 41, 145-151	36
1015	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. 2017 , 114, E327-E336	30

1014	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. 2017 , 49, 274-281	182
1013	Reconstructing genetic history of Siberian and Northeastern European populations. 2017 , 27, 1-14	62
1012	rehh 2.0: a reimplementaion of the R package rehh to detect positive selection from haplotype structure. 2017 , 17, 78-90	116
1011	SNP-Based Heritability Estimates of Common and Specific Variance in Self- and Informant-Reported Neuroticism Scales. 2017 , 85, 906-919	5
1010	APOL1 Nephropathy: A Population Genetics and Evolutionary Medicine Detective Story. 2017 , 37, 490-507	28
1009	Reconstructing human population history from dental phenotypes. 2017 , 7, 12495	25
1008	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. 2017 , 358, 659-662	160
1007	Evolutionarily derived networks to inform disease pathways. 2017 , 41, 866-875	1
1006	Emerging Opportunities for Target Discovery in Rare Cancers. 2017 , 24, 1075-1091	24
1005	Association of vitamin D receptor gene polymorphisms and periodontitis in a Taiwanese Han population. 2017 , 12, 360-367	8
1004	Founder Effect of the RET Mutation in Multiple Endocrine Neoplasia 2A in Denmark: A Nationwide Study. 2017 , 27, 1505-1510	14
1003	A Dementia-Associated Risk Variant near TMEM106B Alters Chromatin Architecture and Gene Expression. 2017 , 101, 643-663	46
1002	A Comparison of Heritability Estimates by Classical Twin Modeling and Based on Genome-Wide Genetic Relatedness for Cardiac Conduction Traits. 2017 , 20, 489-498	10
1001	Human genetic variation in regulates invasion and typhoid fever through modulation of cholesterol. 2017 , 114, E7746-E7755	31
1000	Hidden heritability due to heterogeneity across seven populations. 2017 , 1, 757-765	94
999	Population resequencing of European mitochondrial genomes highlights sex-bias in Bronze Age demographic expansions. 2017 , 7, 12086	12
998	Models, methods and tools for ancestry inference and admixture analysis. 2017 , 5, 236-250	6
997	FOXO3 longevity interactome on chromosome 6. 2017 , 16, 1016-1025	32

996	Computational Prediction of Position Effects of Apparently Balanced Human Chromosomal Rearrangements. 2017 , 101, 206-217	38
995	Pitfalls of exome sequencing: a case study of the attribution of HAP2 rs7080536 in familial non-medullary thyroid cancer. 2017 , 2,	7
994	Evidence of selection on splicing-associated loci in human populations and relevance to disease loci mapping. 2017 , 7, 5980	7
993	Inclusion of Population-specific Reference Panel from India to the 1000 Genomes Phase 3 Panel Improves Imputation Accuracy. 2017 , 7, 6733	10
992	Whole Y-chromosome sequences reveal an extremely recent origin of the most common North African paternal lineage E-M183 (M81). 2017 , 7, 15941	15
991	Benchmarking Relatedness Inference Methods with Genome-Wide Data from Thousands of Relatives. 2017 , 207, 75-82	39
990	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. 2017 , 171, 1340-1353.e14	85
989	Deep RNA Sequencing Uncovers a Repertoire of Human Macrophage Long Intergenic Noncoding RNAs Modulated by Macrophage Activation and Associated With Cardiometabolic Diseases. 2017 , 6,	27
988	Genome-wide Association Study of Idiopathic Osteonecrosis of the Femoral Head. 2017 , 7, 15035	17
987	A functional strategy to characterize expression Quantitative Trait Loci. 2017 , 136, 1477-1487	3
986	The Genetic Legacy of the Indian Ocean Slave Trade: Recent Admixture and Post-admixture Selection in the Makranis of Pakistan. 2017 , 101, 977-984	19
985	An Integrative Approach for Identifying Network Biomarkers of Breast Cancer Subtypes Using Genomic, Interactomic, and Transcriptomic Data. 2017 , 24, 756-766	3
984	The Relation Between Inflation in Type-I and Type-II Error Rate and Population Divergence in Genome-Wide Association Analysis of Multi-Ethnic Populations. 2017 , 47, 360-368	5
983	A common deletion in the haptoglobin gene associated with blood cholesterol levels among Chinese women. 2017 , 62, 911-914	9
982	. 2017 ,	
981	Sexual dimorphism in the genetic influence on human childlessness. 2017 , 25, 1067-1074	5
980	The association of insertions/deletions (INDELs) and variable number tandem repeats (VNTRs) with obesity and its related traits and complications. 2017 , 36, 25	12
979	The genomic landscape of African populations in health and disease. 2017 , 26, R225-R236	43

978	SurvivalGWAS_SV: software for the analysis of genome-wide association studies of imputed genotypes with "time-to-event" outcomes. 2017 , 18, 265	10
977	Intricacies in arrangement of SNP haplotypes suggest "Great Admixture" that created modern humans. 2017 , 18, 433	2
976	Genetic risk score and risk of stage 3 chronic kidney disease. 2017 , 18, 32	15
975	SNPPhenA: a corpus for extracting ranked associations of single-nucleotide polymorphisms and phenotypes from literature. 2017 , 8, 14	10
974	Genome-wide copy number variation in the bovine genome detected using low coverage sequence of popular beef breeds. 2017 , 48, 141-150	22
973	PSE-HMM: genome-wide CNV detection from NGS data using an HMM with Position-Specific Emission probabilities. 2016 , 18, 30	0
972	Cross-Phenotype Polygenic Risk Score Analysis of Persistent Post-Concussive Symptoms in U.S. Army Soldiers with Deployment-Acquired Traumatic Brain Injury. 2017 , 34, 781-789	20
971	Complex Ancient Genetic Structure and Cultural Transitions in Southern African Populations. 2017 , 205, 303-316	31
970	The PHF21B gene is associated with major depression and modulates the stress response. 2017 , 22, 1015-1025	42
969	Acute Lung Injury and Repair. 2017 ,	
968	DNA methylation-based variation between human populations. 2017 , 292, 5-35	56
967	Reactive Oxygen Species in Melanoma Etiology. 2017 , 283-300	
966	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. 2017 , 33, 79-86	4
965	Novel HLA-DP region susceptibility loci associated with severe acute GvHD. 2017 , 52, 95-100	6
964	Chronic Periodontitis Genome-wide Association Study in the Hispanic Community Health Study / Study of Latinos. 2017 , 96, 64-72	45
963	A copy number variation in PKD1L2 is associated with colorectal cancer predisposition in Korean population. 2017 , 140, 86-94	4
962	Genetic predisposition to elevated levels of C-reactive protein is associated with a decreased risk for preeclampsia. 2017 , 36, 30-35	3
961	Genetic analysis of hyperemesis gravidarum reveals association with intracellular calcium release channel (RYR2). 2017 , 439, 308-316	14

960	Landscape of Genomic Alterations in Pituitary Adenomas. 2017 , 23, 1841-1851	64
959	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. 2017 , 33, 272-279	541
958	Genome-Wide Association Study of Loneliness Demonstrates a Role for Common Variation. 2017 , 42, 811-821	53
957	An overview of human genetic privacy. 2017 , 1387, 61-72	36
956	Evolution of the Human Genome I. 2017 ,	0
955	CNVs and Microsatellite DNA Polymorphism. 2017 , 143-155	1
954	Childhood behaviour problems show the greatest gap between DNA-based and twin heritability. 2017 , 7, 1284	31
953	Dissolving the Missing Heritability Problem. 2017 , 84, 1055-1067	20
952	Genetic approaches to neurodegenerative disease. 57-76	
951	Admixture and Ancestry Inference from Ancient and Modern Samples through Measures of Population Genetic Drift. 2017 , 89, 21-46	13
950	Novel methods for genotype imputation to whole-genome sequence and a simple linear model to predict imputation accuracy. 2017 , 18, 120	4
949	The Role of Host Genetics (and Genomics) in Tuberculosis. 2017 , 411-452	
948	XCAVATOR: accurate detection and genotyping of copy number variants from second and third generation whole-genome sequencing experiments. 2017 , 18, 747	17
947	The Neurogenetics of Parkinson's Disease and Putative Links to Other Neurodegenerative Disorders. 2017 , 1-40	1
946	SNP_TATA_Comparator: genomewide landmarks for preventive personalized medicine. 2017 , 9, 276-306	8
945	The Empirical Distribution of Singletons for Geographic Samples of DNA Sequences. 2017 , 8, 139	11
944	Mitochondrial DNA Activates the NLRP3 Inflammasome and Predisposes to Type 1 Diabetes in Murine Model. 2017 , 8, 164	49
943	SNP Variants in Major Histocompatibility Complex Are Associated with Sarcoidosis Susceptibility-A Joint Analysis in Four European Populations. 2017 , 8, 422	20

942	Microbial Disease Spectrum Linked to a Novel IL-12R α N-Terminal Signal Peptide Stop-Gain Homozygous Mutation with Paradoxical Receptor Cell-Surface Expression. 2017 , 8, 616	12
941	Exome sequencing reveals novel IRXI mutation in congenital heart disease. 2017 , 15, 3193-3197	10
940	Single Nucleotide Polymorphisms (SNPs) ?. 2017 ,	
939	Identifying the Risky SNP of Osteoporosis with ID3-PEP Decision Tree Algorithm. 2017 , 2017, 1-8	1
938	biMM: efficient estimation of genetic variances and covariances for cohorts with high-dimensional phenotype measurements. 2017 , 33, 2405-2407	6
937	Natural Selection Associated With Infectious Diseases. 2017 , 177-191	2
936	The fine-scale genetic structure and evolution of the Japanese population. 2017 , 12, e0185487	21
935	Epidemiologic and Population Genetic Studies. 2017 , 313-326	2
934	Identification of shared risk loci and pathways for bipolar disorder and schizophrenia. 2017 , 12, e0171595	53
933	Functional annotation of Alzheimer's disease associated loci revealed by GWASs. 2017 , 12, e0179677	20
932	Genetic variants alter T-bet binding and gene expression in mucosal inflammatory disease. 2017 , 13, e1006587	24
931	Pathway-based discovery of genetic interactions in breast cancer. 2017 , 13, e1006973	47
930	Between Lake Baikal and the Baltic Sea: genomic history of the gateway to Europe. 2017 , 18, 110	25
929	Evidence of reduced recombination rate in human regulatory domains. 2017 , 18, 193	23
928	Discovery of rare, diagnostic Yb8/9 elements in diverse human populations. 2017 , 8, 9	8
927	Using variant databases for variant prioritization and to detect erroneous genotype-phenotype associations. 2017 , 18, 535	5
926	Frequency of common polymorphisms in () gene in adults with high serum triglycerides from Colombian Caribbean Coast. 2017 , 48, 167-173	5
925	Weighted likelihood inference of genomic autozygosity patterns in dense genotype data. 2017 , 18, 928	7

924	Hepatitis C virus pharmacogenomics in Latin American populations: implications in the era of direct-acting antivirals. 2017 , 10, 79-91	2
923	Immunogenetics and Vaccination. 2017 , 113-133	1
922	A Mild PUM1 Mutation Is Associated with Adult-Onset Ataxia, whereas Haploinsufficiency Causes Developmental Delay and Seizures. 2018 , 172, 924-936.e11	65
921	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. 2018 , 50, 381-389	787
920	Genetic relatedness of indigenous ethnic groups in northern Borneo to neighboring populations from Southeast Asia, as inferred from genome-wide SNP data. 2018 , 82, 216-226	6
919	Genetic Contributions and Personalized Medicine. 2018 , 3-16	0
918	Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records. 2018 , 8, 86	14
917	Natural selection interacts with recombination to shape the evolution of hybrid genomes. 2018 , 360, 656-660	176
916	A plausibly causal functional lupus-associated risk variant in the STAT1-STAT4 locus. 2018 , 27, 2392-2404	22
915	Ensembl 2018. 2018 , 46, D754-D761	1822
914	Signatures of negative selection in the genetic architecture of human complex traits. 2018 , 50, 746-753	178
913	Expanding the global prevalence of spinocerebellar ataxia type 42. 2018 , 4, e232	10
912	Genotype imputation performance of three reference panels using African ancestry individuals. 2018 , 137, 281-292	23
911	Polygenic risk for schizophrenia and measured domains of cognition in individuals with psychosis and controls. 2018 , 8, 78	30
910	Human individual radiation sensitivity and prospects for prediction. 2018 , 47, 126-141	28
909	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. 2018 , 50, 390-400	325
908	Association between fetal exposure to phthalate endocrine disruptor and genome-wide DNA methylation at birth. 2018 , 162, 261-270	29
907	Association of IGFN1 variant with polypoidal choroidal vasculopathy. 2018 , 20, e3007	5

906	Genome-Wide Association Study in African Americans with Acute Respiratory Distress Syndrome Identifies the Selectin P Ligand Gene as a Risk Factor. 2018 , 197, 1421-1432	29
905	Genetics and Genomics of Coronary Artery Disease. 2018 , 661-678	1
904	Inference of multiple-wave admixtures by length distribution of ancestral tracks. 2018 , 121, 52-63	11
903	Data integration and predictive modeling methods for multi-omics datasets. 2018 , 14, 8-25	46
902	Associations of GBP2 gene copy number variations with growth traits and transcriptional expression in Chinese cattle. 2018 , 647, 101-106	18
901	Cost-effective and accurate method of measuring fetal fraction using SNP imputation. 2018 , 34, 1086-1091	6
900	The Expanding Landscape of Alternative Splicing Variation in Human Populations. 2018 , 102, 11-26	162
899	Nonparametric Finite Mixture of Gaussian Graphical Models. 2018 , 60, 511-521	6
898	The Post-GWAS Era: From Association to Function. 2018 , 102, 717-730	294
897	TIA: algorithms for development of identity-linked SNP islands for analysis by massively parallel DNA sequencing. 2018 , 19, 126	1
896	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. 2018 , 102, 874-889	38
895	A new perspective on lipid research in age-related macular degeneration. 2018 , 67, 56-86	94
894	Smoking Interacts With CHRNA5, a Nicotinic Acetylcholine Receptor Subunit Gene, to Influence the Risk of IBD-Related Surgery. 2018 , 24, 1057-1064	1
893	Whole-Exome Sequencing Reveals Uncaptured Variation and Distinct Ancestry in the Southern African Population of Botswana. 2018 , 102, 731-743	25
892	Effective discovery of rare variants by pooled target capture sequencing: A comparative analysis with individually indexed target capture sequencing. 2018 , 809, 24-31	6
891	West African Ancestry and Nocturnal Blood Pressure in African Americans: The Jackson Heart Study. 2018 , 31, 706-714	2
890	Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. 2018 , 18, 127-135	9
889	ASD and schizophrenia show distinct developmental profiles in common genetic overlap with population-based social communication difficulties. 2018 , 23, 263-270	69

888	Rett-like Severe Encephalopathy Caused by a De Novo GRIN2B Mutation Is Attenuated by D-serine Dietary Supplement. 2018 , 83, 160-172	6
887	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. 2018 , 27, 395-404	25
886	Pharmacogenomics study of thiazide diuretics and QT interval in multi-ethnic populations: the cohorts for heart and aging research in genomic epidemiology. 2018 , 18, 215-226	2
885	A low-frequency haplotype spanning SLX4/FANCP constitutes a new risk locus for early-onset breast cancer (. 2018 , 142, 757-768	4
884	RMBase v2.0: deciphering the map of RNA modifications from epitranscriptome sequencing data. 2018 , 46, D327-D334	184
883	A new haplotype block detection method for dense genome sequencing data based on interval graph modeling of clusters of highly correlated SNPs. 2018 , 34, 388-397	16
882	Integrating genome-wide association study and expression quantitative trait locus study identifies multiple genes and gene sets associated with schizophrenia. 2018 , 81, 50-54	16
881	Mechanisms underlying human genetic diversity: consequence for antigrift antibody responses. 2018 , 31, 239-250	10
880	Clinical and genetic analysis of a rare syndrome associated with neoteny. 2018 , 20, 495-502	2
879	Differences in Neurocognitive Impairment Among HIV-Infected Latinos in the United States. 2018 , 24, 163-175	22
878	New genetic tools in the diagnosis of growth defects. 2018 , 38, 24-28	3
877	Shared genetic etiology of hypertension and stroke: evidence from bioinformatics analysis of genome-wide association studies. 2017 , 32, 34-39	3
876	Rare copy number variants identified in prune belly syndrome. 2018 , 61, 145-151	16
875	Statistical challenges in high-dimensional molecular and genetic epidemiology. 2018 , 46, 24-40	
874	Genome-wide association study of delay discounting in 23,217 adult research participants of European ancestry. 2018 , 21, 16-18	56
873	The cAMP responsive element-binding (CREB)-1 gene increases risk of major psychiatric disorders. 2018 , 23, 1957-1967	25
872	Genetic clustering of depressed patients and normal controls based on single-nucleotide variant proportion. 2018 , 227, 450-454	4
871	Modeling coverage gaps in haplotype frequencies via Bayesian inference to improve stem cell donor selection. 2018 , 70, 279-292	3

870	On the Null Distribution of Bayes Factors in Linear Regression. 2018 , 113, 1362-1371	10
869	Polygenic risk score for schizophrenia is more strongly associated with ancestry than with schizophrenia. 2018 , 28, 85-89	68
868	The Control of Meiotic Recombination in the Human Genome. 2018 , 28, 187-204	3
867	Early human dispersals within the Americas. 2018 , 362,	118
866	CODEX2: full-spectrum copy number variation detection by high-throughput DNA sequencing. 2018 , 19, 202	34
865	Imprint of assortative mating on the human genome. 2018 , 2, 948-954	45
864	Population structure in genetic studies: Confounding factors and mixed models. 2018 , 14, e1007309	62
863	FORGe: prioritizing variants for graph genomes. 2018 , 19, 220	38
862	Pharmacogenomic Profiling of ADME Gene Variants: Current Challenges and Validation Perspectives. 2018 , 7,	15
861	Genetic Determinants of Telomere Length in African American Youth. 2018 , 8, 13265	15
860	Transcriptome-wide isoform-level dysregulation in ASD, schizophrenia, and bipolar disorder. 2018 , 362,	434
859	The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. 2018 , 103, 918-929	22
858	Copy number variants in hypoplastic right heart syndrome. 2018 , 176, 2760-2767	5
857	Burden Testing of Rare Variants Identified through Exome Sequencing via Publicly Available Control Data. 2018 , 103, 522-534	67
856	The interplay between externalizing disorders polygenic risk scores and contextual factors on the development of marijuana use disorders. 2018 , 191, 365-373	8
855	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. 2018 , 9, 4079	65
854	Pharmacogenetics of Antiretroviral Drug Response and Pharmacokinetic Variations in Indigenous South African Populations. 2018 , 22, 589-597	1
853	Personalised Medicine: The Odyssey from Hope to Practice. 2018 , 8,	7

852	The signalling conformation of the insulin receptor ectodomain. 2018 , 9, 4420	59
851	A survey of inter-individual variation in DNA methylation identifies environmentally responsive co-regulated networks of epigenetic variation in the human genome. 2018 , 14, e1007707	24
850	Phenome-wide association studies across large population cohorts support drug target validation. 2018 , 9, 4285	76
849	Variations on a Chip: Technologies of Difference in Human Genetics Research. 2018 , 51, 841-873	8
848	Large-scale genome-wide enrichment analyses identify new trait-associated genes and pathways across 31 human phenotypes. 2018 , 9, 4361	48
847	Ancestry-specific recent effective population size in the Americas. 2018 , 14, e1007385	51
846	Genomic history of the Sardinian population. 2018 , 50, 1426-1434	42
845	Genome-wide association meta-analysis and Mendelian randomization analysis confirm the influence of ALDH2 on sleep duration in the Japanese population. 2019 , 42,	8
844	Exome array analysis of rare and low frequency variants in amyotrophic lateral sclerosis. 2019 , 9, 5931	6
843	Identification of trans-eQTLs using mediation analysis with multiple mediators. 2019 , 20, 126	15
842	Intraocular and Intracranial Pressure Gradient in Glaucoma. 2019 ,	2
841	Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. 2019 , 10, 1499	164
840	A generalized model for combining dependent SNP-level summary statistics and its extensions to statistics of other levels. 2019 , 9, 5461	3
839	Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations. 2019 , 36, 1628-1642	13
838	Genome-wide Analysis of Common Copy Number Variation and Epithelial Ovarian Cancer Risk. 2019 , 28, 1117-1126	8
837	Germline TP53 mutation spectrum in Sudanese premenopausal breast cancer patients: correlations with reproductive factors. 2019 , 175, 479-485	3
836	A genetic variant associated with multiple sclerosis inversely affects the expression of CD58 and microRNA-548ac from the same gene. 2019 , 15, e1007961	12
835	Identification of common genetic risk variants for autism spectrum disorder. 2019 , 51, 431-444	746

834	Genetic association and transcriptome integration identify contributing genes and tissues at cystic fibrosis modifier loci. 2019 , 15, e1008007	33
833	Whole Genome Sequence, Variant Discovery and Annotation in Mapuche-Huilliche Native South Americans. 2019 , 9, 2132	6
832	Genomic evidence for shared common ancestry of East African hunting-gathering populations and insights into local adaptation. 2019 , 116, 4166-4175	23
831	Genome-wide Significance Thresholds for Admixture Mapping Studies. 2019 , 104, 454-465	11
830	Mixture deconvolution by massively parallel sequencing of microhaplotypes. 2019 , 133, 719-729	27
829	The effect of genetic vulnerability and military deployment on the development of post-traumatic stress disorder and depressive symptoms. 2019 , 29, 405-415	5
828	A Population Genetic Perspective on Korean Prehistory. 2019 ,	
827	Genetic variants of calcium and vitamin D metabolism in kidney stone disease. 2019 , 10, 5175	27
826	Genetic evidence for assortative mating on alcohol consumption in the UK Biobank. 2019 , 10, 5039	21
825	Screening Human Embryos for Polygenic Traits Has Limited Utility. 2019 , 179, 1424-1435.e8	34
824	Targeted ultra-deep sequencing of a South African Bantu-speaking cohort to comprehensively map and characterize common and novel variants in 65 pharmacologically-related genes. 2019 , 29, 167-178	5
823	An update on the genetics of systemic lupus erythematosus. 2019 , 31, 659-668	15
822	Genetic variability of five ADRB2 polymorphisms among Mexican Amerindian ethnicities and the Mestizo population. 2019 , 14, e0225030	3
821	MultiWaver 2.0: modeling discrete and continuous gene flow to reconstruct complex population admixtures. 2019 , 27, 133-139	13
820	The Alkaline Phosphatase (ALPL) Locus Is Associated with B6 Vitamer Levels in CSF and Plasma. 2018 , 10,	8
819	Genome-Wide Association Study Confirming a Strong Effect of HLA and Identifying Variants in on Chromosome 12q13.13 Associated With Susceptibility to Fulminant Type 1 Diabetes. 2019 , 68, 665-675	17
818	Clinical whole exome sequencing in severe hypertriglyceridemia. 2019 , 488, 31-39	4
817	Shades of complexity: New perspectives on the evolution and genetic architecture of human skin. 2019 , 168 Suppl 67, 4-26	28

816	Population Genetics. 2019 , 359-373	4
815	Comparison of genotype imputation strategies using a combined reference panel for chicken population. 2019 , 13, 1119-1126	7
814	AIM-SNPtag: A computationally efficient approach for developing ancestry-informative SNP panels. 2019 , 38, 245-253	8
813	CAV1 polymorphisms rs1049334, rs1049337, rs7804372 might be the potential risk in tumorigenicity of urinary cancer: A systematic review and meta-analysis. 2019 , 215, 151-158	12
812	Integration of Genetic Testing and Pathology for the Diagnosis of Adults with FSGS. 2019 , 14, 213-223	56
811	Inverse PCR to perform long-distance haplotyping: main applications to improve preimplantation genetic diagnosis in hemophilia. 2019 , 27, 603-611	2
810	An accurate and powerful method for copy number variation detection. 2019 , 35, 2891-2898	3
809	PopHumanScan: the online catalog of human genome adaptation. 2019 , 47, D1080-D1089	9
808	Identification of complement-related host genetic risk factors associated with influenza A(H1N1)pdm09 outcome: challenges ahead. 2019 , 208, 631-640	11
807	Multifactorial Inheritance and Complex Diseases. 2019 , 323-358	0
806	Common-variant associations with fragile X syndrome. 2019 , 24, 338-344	4
805	Population-scale genomics-Enabling precision public health. 2019 , 103, 119-161	7
804	SumHer better estimates the SNP heritability of complex traits from summary statistics. 2019 , 51, 277-284	91
803	Understanding the role of genetic variability in LRRK2 in Indian population. 2019 , 34, 496-505	6
802	Microhaplotypes in forensic genetics. 2019 , 38, 54-69	69
801	Elucidating the editome: bioinformatics approaches for RNA editing detection. 2019 , 20, 436-447	43
800	Genome-wide association study of alcohol use disorder identification test (AUDIT) scores in 20 328 research participants of European ancestry. 2019 , 24, 121-131	49
799	Detecting Population-Differentiation Copy Number Variants in Human Population Tree by Sparse Group Selection. 2019 , 16, 538-549	2

798	Discovery and Characterization of Cancer Genetic Susceptibility Alleles. 2020 , 323-336.e3	1
797	Risk factors and an early prediction model for persistent methamphetamine-related psychiatric symptoms. 2020 , 25, e12709	4
796	F and the triangle inequality for biallelic markers. 2020 , 133, 117-129	0
795	Cattle genomics: genome projects, current status, and future applications. 2020 , 3-28	0
794	Animal-ImputeDB: a comprehensive database with multiple animal reference panels for genotype imputation. 2020 , 48, D659-D667	5
793	Identifying causal variants and genes using functional genomics in specialized cell types and contexts. 2020 , 139, 95-102	9
792	Polygenic and environmental influences on the course of African Americans' alcohol use from early adolescence through young adulthood. 2020 , 32, 703-718	
791	A likelihood method for estimating present-day human contamination in ancient male samples using low-depth X-chromosome data. 2020 , 36, 828-841	7
790	Genotype imputation and reference panel: a systematic evaluation on haplotype size and diversity. 2019 ,	12
789	Novel insights into non-HLA alloimmunity in kidney transplantation. 2020 , 33, 5-17	15
788	Bioinformatics and Computational Tools for Next-Generation Sequencing Analysis in Clinical Genetics. 2020 , 9,	54
787	High-resolution inference of genetic relationships among Jewish populations. 2020 , 28, 804-814	1
786	Role of gene polymorphisms related to progesterone elevation in women undergoing long GnRH agonist protocols. 2020 , 40, 381-392	1
785	Integrating Biology With Rat Genomic Tools. 2020 , 811-825	
784	What is the impact of BIRC5 gene polymorphisms on urinary cancer susceptibility? Evidence from 9348 subjects. 2020 , 733, 144268	3
783	The pathogenesis of systemic lupus erythematosus: Harnessing big data to understand the molecular basis of lupus. 2020 , 110, 102359	50
782	Investigating Causality Between Blood Metabolites and Emotional and Behavioral Responses to Traumatic Stress: a Mendelian Randomization Study. 2020 , 57, 1542-1552	3
781	Epistasis between phenylethanolamine N-methyltransferase and α -adrenergic receptor influences extracellular epinephrine level and associates with the susceptibility to allergic asthma. 2020 , 50, 352-363	5

780	A whole-genome sequenced control population in northern Sweden reveals subregional genetic differences. 2020 , 15, e0237721	0
779	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. 2021 , 26, 3004-3017	22
778	Role of a genetic variation in the microRNA-4421 binding site of ERP29 regarding risk of oropharynx cancer and prognosis. 2020 , 10, 17039	3
777	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. 2020 , 44, 854	9
776	Links Between Inflammatory Bowel Disease and Chronic Obstructive Pulmonary Disease. 2020 , 11, 2144	16
775	Assessing Genetic Overlap Between Platelet Parameters and Neurodegenerative Disorders. 2020 , 11, 02127	4
774	Determinants of placental leptin receptor gene expression and association with measures at birth. 2020 , 100, 89-95	5
773	The genetic architecture of the association between eating behaviors and obesity: combining genetic twin modeling and polygenic risk scores. 2020 , 112, 956-966	4
772	Investigating the genetic characteristics of the Csangos, a traditionally Hungarian speaking ethnic group residing in Romania. 2020 , 65, 1093-1103	1
771	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. 2021 , 106, 2233-2241	1
770	Genetic influence on the metabolome. 2020 , 105-121	
769	Do AKT1, COMT and FAAH influence reports of acute cannabis intoxication experiences in patients with first episode psychosis, controls and young adult cannabis users?. 2020 , 10, 143	5
768	Currently Applied Molecular Assays for Identifying Mutations in Patients with Advanced Breast Cancer. 2020 , 21,	2
767	Evaluation of consensus strategies for haplotype phasing. 2021 , 22,	0
766	Accurate assembly of the olive baboon (<i>Papio anubis</i>) genome using long-read and Hi-C data. 2020 , 9,	8
765	imputeqc: an R package for assessing imputation quality of genotypes and optimizing imputation parameters. 2020 , 21, 304	3
764	Human essential hypertension: no significant association of polygenic risk scores with antihypertensive drug responses. 2020 , 10, 11940	3
763	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations. 2020 , 11, 3865	42

762	The fractal dimension as a measure for characterizing genetic variation of the human genome. 2020 , 87, 107278	2
761	Unsupervised detection of ancestry tracks with the GHap r package. 2020 , 11, 1448-1454	2
760	Analysis of Comprehensive Pharmacogenomic Profiling of VIP Variants Among the Genetically Isolated Chechen Subpopulation from Jordan. 2020 , 13, 199-215	0
759	The Brazilian Initiative on Precision Medicine (BIPMed): fostering genomic data-sharing of underrepresented populations. 2020 , 5, 42	13
758	Dystonia genes functionally converge in specific neurons and share neurobiology with psychiatric disorders. 2020 , 143, 2771-2787	20
757	Effect of Education on Myopia: Evidence from the United Kingdom ROSLA 1972 Reform. 2020 , 61, 7	10
756	AuthentiCT: a model of ancient DNA damage to estimate the proportion of present-day DNA contamination. 2020 , 21, 246	9
755	Association of CNVs with methylation variation. 2020 , 5, 41	4
754	The GTEx Consortium atlas of genetic regulatory effects across human tissues. 2020 , 369, 1318-1330	589
753	Machine Learning based histology phenotyping to investigate the epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits. 2020 , 16, e1008044	5
752	Inferring the ancestry of parents and grandparents from genetic data. 2020 , 16, e1008065	2
751	On the cross-population generalizability of gene expression prediction models. 2020 , 16, e1008927	14
750	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease. 2020 , 11, 6258	2
749	Evaluating brain structure traits as endophenotypes using polygenicity and discoverability. 2020 ,	9
748	Clinical Interpretation and Management of Genetic Variants. 2020 , 5, 1029-1042	9
747	Genome-wide association study of MRI markers of cerebral small vessel disease in 42,310 participants. 2020 , 11, 2175	21
746	Quantifying genetic effects on disease mediated by assayed gene expression levels. 2020 , 52, 626-633	69
745	The Opioid receptor gene A118G polymorphism is associated with insecure attachment in children with disruptive mood regulation disorder and their mothers. 2020 , 10, e01659	8

744	Detecting Genotype-Population Interaction Effects by Ancestry Principal Components. 2020 , 11, 379	2
743	Efficient toolkit implementing best practices for principal component analysis of population genetic data. 2020 , 36, 4449-4457	20
742	Progress, Challenges, and Surprises in Annotating the Human Genome. 2020 , 21, 55-79	6
741	Differentiation of Hispanic biogeographic ancestry with 80 ancestry informative markers. 2020 , 10, 7745	2
740	Quantifying the Predictive Accuracy of a Polygenic Risk Score for Predicting Incident Cancer Cases : Application to the CARTaGENE Cohort. 2020 , 11, 408	
739	The Evolution of Constitutional Sequence Variant Interpretation. 2020 , 40, 135-148	1
738	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. 2020 , 52, 680-691	140
737	Editorial: Overcoming current limitations of genetic testing in cardiovascular medicine. 2020 , 35, 187-190	
736	Population-Specific Genetic and Expression Differentiation in Europeans. 2020 , 12, 358-369	2
735	Genetic Architecture of Parkinson's Disease in the Indian Population: Harnessing Genetic Diversity to Address Critical Gaps in Parkinson's Disease Research. 2020 , 11, 524	7
734	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. 2020 , 52, 669-679	85
733	A Population Genetic Perspective on Korean Prehistory. 2020 , 44, 27-53	
732	KRGDB: the large-scale variant database of 1722 Koreans based on whole genome sequencing. 2020 , 2020,	15
731	Evaluating and improving heritability models using summary statistics. 2020 , 52, 458-462	34
730	Precise and Cost-Effective Nanopore Sequencing for Post-GWAS Fine-Mapping and Causal Variant Identification. 2020 , 23, 100971	4
729	The Fabry disease-causing mutation, GLA IVS4+919G>A, originated in Mainland China more than 800 years ago. 2020 , 65, 619-625	5
728	Genome-wide association study of word reading: Overlap with risk genes for neurodevelopmental disorders. 2020 , 19, e12648	12
727	A Genome-wide Association Study of Circulating Levels of Atorvastatin and Its Major Metabolites. 2020 , 108, 287-297	12

726 Overview of the human genome. **2020**, 9-26

725 An Activity-Mediated Transition in Transcription in Early Postnatal Neurons. **2020**, 107, 874-890.e8 15

724 Polygenic Risk Scores and Physical Activity. **2020**, 52, 1518-1524 5

723 Sequencing and imputation in GWAS: Cost-effective strategies to increase power and genomic coverage across diverse populations. **2020**, 44, 537-549 10

722 Ethnic differences in normal retinal capillary density and foveal avascular zone measurements. **2020**, 40, 3043-3048 3

721 Racial/ethnic differences in circulating natriuretic peptide levels: The Diabetes Prevention Program. **2020**, 15, e0229280 4

720 Association of West African ancestry and blood pressure control among African Americans taking antihypertensive medication in the Jackson Heart Study. **2020**, 22, 157-166 3

719 Methylation of the LEP gene promoter in blood at 12 months and BMI at 4 years of age—a population-based cohort study. **2020**, 44, 842-847 2

718 A backward procedure for change-point detection with applications to copy number variation detection. **2020**, 48, 366-385 0

717 Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. **2020**, 25, 1673-1687 30

716 Genetic variability of T cell responses in hypersensitivity pneumonitis identified using the BXD genetic reference panel. **2020**, 318, L631-L643 3

715 WITHDRAWN: Genetics of Parkinson's disease. **2020**, 101471

714 LD scores are associated with differences in allele frequencies between populations but LD score regression can still distinguish confounding from polygenicity. **2020**, 84, 412-416 0

713 Whole-Genome Resequencing of Twenty Individuals Provides a Brand-New Variant Dataset for. **2020**, 2020, 3697342 2

712 Identification of a novel uterine leiomyoma GWAS locus in a Japanese population. **2020**, 10, 1197 6

711 Analytic and Translational Genetics. **2020**, 3, 217-241 0

710 Gene expression profiling identifies pathways involved in seed maturation of *Jatropha curcas*. **2020**, 21, 290 1

709 Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. **2020**, 11, 1647 58

708	Copy Number Variation of the Gene in Sheep and Its Association Analysis with Growth Traits. 2020 , 10,	6
707	EpiGEN: an epistasis simulation pipeline. 2020 , 36, 4957-4959	2
706	Polygenic Risk of Psychiatric Disorders Exhibits Cross-trait Associations in Electronic Health Record Data From European Ancestry Individuals. 2021 , 89, 236-245	8
705	Integrating genomic correlation structure improves copy number variations detection. 2021 , 37, 312-317	0
704	Integrative genomic analysis in African American children with asthma finds three novel loci associated with lung function. 2021 , 45, 190-208	1
703	These Are the Genes You're Looking For: Finding Host Resistance Genes. 2021 , 29, 346-362	1
702	Assessment and visualization of phenome-wide causal relationships using genetic data: an application to dental caries and periodontitis. 2021 , 29, 300-308	10
701	Finding the root graph through minimum edge deletion. 2021 , 289, 59-74	0
700	The Population-Specific Impact of Neandertal Introgression on Human Disease. 2021 , 13,	4
699	Characterizing the effect of background selection on the polygenicity of brain-related traits. 2021 , 113, 111-119	5
698	Pathogenic Huntingtin Repeat Expansions in Patients with Frontotemporal Dementia and Amyotrophic Lateral Sclerosis. 2021 , 109, 448-460.e4	20
697	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health. 2021 , 57,	17
696	Practical guide for managing large-scale human genome data in research. 2021 , 66, 39-52	7
695	Causal links between major depressive disorder and insomnia: A Mendelian randomisation study. 2021 , 768, 145271	3
694	Rare Functional Variants Associated with Antidepressant Remission in Mexican-Americans: Short title: Antidepressant remission and pharmacogenetics in Mexican-Americans. 2021 , 279, 491-500	1
693	FASTQuick: rapid and comprehensive quality assessment of raw sequence reads. 2021 , 10,	
692	Challenges and opportunities in rare diseases research. 2021 , 263-284	
691	Exploring Networks in the STRING and Reactome Database. 2021 , 507-520	4

690	Leveraging fine-mapping and non-European training data to improve cross-population polygenic risk scores.	14
689	America. 2021 , 211-229	
688	Machine Learning and Deep Learning in Genetics and Genomics. 2021 , 163-181	
687	What Have We Learned from GWAS?. 2021 , 159-183	
686	Genetic Variation and Unintended Risk in the Context of Old and New Breeding Techniques. 2021 , 40, 68-108	5
685	Prevalence of the Factor V Leiden Mutation Arg534Gln in Western Region of Saudi Arabia: Functional Alteration and Association Study With Different Populations. 2021 , 27, 1076029620978532	1
684	The genetic architecture of human complex phenotypes is modulated by linkage disequilibrium and heterozygosity. 2021 , 217,	2
683	Deleterious variants in genes regulating mammalian reproduction in Neanderthals, Denisovans and extant humans. 2021 , 36, 734-755	2
682	Prediction of Single-Nucleotide Polymorphisms within microRNAs Binding Sites of Neuronal Genes Related to Multiple Sclerosis: A Preliminary Study. 2021 , 10, 8	1
681	Revisiting the genome-wide significance threshold for common variant GWAS. 2021 , 11,	9
680	Inferring Human Demographic History from Genetic Data. 2021 , 187-204	
679	Natural Selection, Genetic Variation, and Human Diversity. 2021 , 205-234	
678	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. 2021 , 12, 20211	16
677	Biomaterials in Tissue Engineering and Regenerative Medicine: In Vitro Disease Models and Advances in Gene-Based Therapies. 2021 , 485-504	
676	Linkage Disequilibrium. 2021 , 31-45	
675	The indigenous populations as the model by nature to understand human genomic-phenomics interactions. 2021 ,	
674	Dissecting dynamics and differences of selective pressures in the evolution of human pigmentation. 2021 , 10,	3
673	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL Study.	

672	Population-specific causal disease effect sizes in functionally important regions impacted by selection. 2021 , 12, 1098	16
671	From one human genome to a complex tapestry of ancestry. <i>Nature</i> , 2021 , 590, 220-221	50.4 6
670	Brain transcriptional regulatory architecture and schizophrenia etiology converge between East Asian and European ancestral populations.	
669	Second-hand smoke and NFE2L2 genotype interaction increases paediatric asthma risk and severity. 2021 , 51, 801-810	3
668	Widespread signatures of natural selection across human complex traits and functional genomic categories. 2021 , 12, 1164	12
667	The need for precision nutrition, genetic variation and resolution in Covid-19 patients. 2021 , 77, 100943	13
666	Individual variations in Brain age relate to early life factors more than to longitudinal brain change.	2
665	The putative causal effect of type 2 diabetes in risk of cataract: a Mendelian randomization study in East Asian.	0
664	High coverage whole genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios.	31
663	Mendelian Randomization Analysis Using Multiple Biomarkers of an Underlying Common Exposure.	
662	Genetic ancestry plays a central role in population pharmacogenomics. 2021 , 4, 171	3
661	Topologically associating domain boundaries that are stable across diverse cell types are evolutionarily constrained and enriched for heritability. 2021 , 108, 269-283	23
660	Filtering the Junk: Assigning Function to the Mosquito Non-Coding Genome. 2021 , 12,	5
659	Genome sequencing analysis identifies new loci associated with Lewy body dementia and provides insights into its genetic architecture. 2021 , 53, 294-303	31
658	Functional Characterisation of Three Glycine -Acyltransferase Variants and the Effect on Glycine Conjugation to Benzoyl-CoA. 2021 , 22,	1
657	Correction for sample overlap, winner's curse and weak instrument bias in two-sample Mendelian Randomization.	5
656	: Genetic Variation, Heritable Methylation and Disease Association. 2021 , 22,	3
655	CNAHap: a germline haplotyping method using tumor allele-specific copy number alteration.	

654	Genetic control of the human brain proteome. 2021 , 108, 400-410	4
653	The Genetic Variation of Lactase Persistence Alleles in Sudan and South Sudan. 2021 , 13,	1
652	Robust, flexible, and scalable tests for Hardy-Weinberg equilibrium across diverse ancestries. 2021 , 218,	0
651	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. 2021 ,	5
650	Calculating the divergence time by direct comparison between individuals and the out-group.	
649	Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy Body diseases.	
648	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. 2021 ,	7
647	Shared heritability of human face and brain shape. 2021 , 53, 830-839	7
646	Harnessing pluripotent stem cells as models to decipher human evolution. 2021 ,	2
645	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. 2021 , 108, 564-582	7
644	Archaeogenomic distinctiveness of the Isthmo-Colombian area. 2021 , 184, 1706-1723.e24	5
643	Distortion Discovery: A Framework to Model, Spot and Explain Tumor Heterogeneity and Mitigate its Negative Impact on Cancer Risk Assessment.	
642	MutationTaster2021. 2021 , 49, W446-W451	14
641	Clinical pharmacogenomics in action: design, assessment and implementation of a novel pharmacogenetic panel supporting drug selection for diseases of the central nervous system (CNS). 2021 , 19, 151	2
640	Endocannabinoid Gene \times Gene Interaction Association to Alcohol Use Disorder in Two Adolescent Cohorts. 2021 , 12, 645746	1
639	De novo mutations in domestic cat are consistent with an effect of reproductive longevity on both the rate and spectrum of mutations.	4
638	Disentangling Ancestry From Social Determinants of Health in Hypertension Disparities-An Important Step Forward. 2020 ,	2
637	Determinants of Response and Intrinsic Resistance to PD-1 Blockade in Microsatellite Instability-High Gastric Cancer. 2021 , 11, 2168-2185	27

636	Genetic Variants Increase Susceptibility to Diabetic Kidney Disease in Chinese Patients with Type 2 Diabetes: A Cross-Sectional Case Control Study. 2021 , 2021, 5521050	0
635	Genetic interactions effects for cancer disease identification using computational models: a review. 2021 , 59, 733-758	1
634	Why most Principal Component Analyses (PCA) in population genetic studies are wrong.	3
633	Resource Profile and User Guide of the Polygenic Index Repository.	0
632	Population genetic considerations for using biobanks as international resources in the pandemic era and beyond. 2021 , 22, 351	3
631	Mechanistic aspects of carotenoid health benefits - where are we now?. 2021 , 34, 276-302	14
630	Integrated Analysis of Whole Genome and Epigenome Data Using Machine Learning Technology: Toward the Establishment of Precision Oncology. 2021 , 11, 666937	8
629	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. 2021 , 90, 611-620	17
628	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. 2021 , 108, 786-798	19
627	Modeling regulatory network topology improves genome-wide analyses of complex human traits. 2021 , 12, 2851	4
626	Evaluation of polygenic prediction methodology within a reference-standardized framework. 2021 , 17, e1009021	22
625	Genetic variation affects morphological retinal phenotypes extracted from UK Biobank optical coherence tomography images. 2021 , 17, e1009497	5
624	Super.FELT: supervised feature extraction learning using triplet loss for drug response prediction with multi-omics data. 2021 , 22, 269	0
623	The genomic history of the Aegean palatial civilizations. 2021 , 184, 2565-2586.e21	7
622	Accelerating Medicines Partnership: Parkinson's Disease. Genetic Resource. 2021 , 36, 1795-1804	5
621	Genetics and genomics of arrhythmic risk: current and future strategies to prevent sudden cardiac death. 2021 , 18, 774-784	1
620	Genome Evolutionary Dynamics Meets Functional Genomics: A Case Story on the Identification of SLC25A44. 2021 , 22,	0
619	Liver and Kidney Function Biomarkers, Blood Cell Traits and Risk of Severe COVID-19: A Mendelian Randomization Study. 2021 , 12, 647303	3

618	Multivariate Modeling of Direct and Proxy GWAS Indicates Substantial Common Variant Heritability of Alzheimer's Disease.	1
617	Dissection of multiple sclerosis genetics identifies B and CD4+ T cells as driver cell subsets.	1
616	A prospective trial of abiraterone acetate plus prednisone in Black and White men with metastatic castrate-resistant prostate cancer. 2021 , 127, 2954-2965	7
615	Genetic landscape of Gullah African Americans. 2021 , 175, 905-919	2
614	BrainXcan identifies brain features associated with behavioral and psychiatric traits using large scale genetic and imaging data.	0
613	Shall genomic correlation structure be considered in copy number variants detection?. 2021 , 22,	
612	Genetic architecture of 11 organ traits derived from abdominal MRI using deep learning. 2021 , 10,	9
611	PIP-SNP: a pipeline for processing SNP data featured as linkage disequilibrium bin mapping, genotype imputing and marker synthesizing. 2021 , 3, lqab060	
610	BMI-CNV: A Bayesian framework for multiple genotyping platforms detection of copy number variation.	1
609	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. 2021 , 30, 2190-2204	0
608	Common genetic variation influencing human white matter microstructure. 2021 , 372,	18
607	Investigating the effect of sexual behaviour on oropharyngeal cancer risk: a methodological assessment of Mendelian randomization.	1
606	Resource profile and user guide of the Polygenic Index Repository. 2021 ,	5
605	Benchmarking germline CNV calling tools from exome sequencing data. 2021 , 11, 14416	3
604	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits. 2021 , 12, 4481	6
603	Geographical and linguistic structure in the people of Kenya demonstrated using 21 autosomal STRs. 2021 , 53, 102535	
602	Cross-platform transcriptional profiling identifies common and distinct molecular pathologies in Lewy body diseases. 2021 , 142, 449-474	0
601	The Thousand Polish Genomes Project: a national database of Polish variant allele frequencies.	0

600	Admixture mapping reveals the association between Native American ancestry at 3q13.11 and reduced risk of Alzheimer's disease in Caribbean Hispanics. 2021 , 13, 122	0
599	Human brain anatomy reflects separable genetic and environmental components of socioeconomic status.	1
598	Genetic influences on the intrinsic and extrinsic functional organizations of the cerebral cortex.	0
597	Interactions between exposure to polycyclic aromatic hydrocarbons and xenobiotic metabolism genes, and risk of breast cancer. 2021 , 1	1
596	An imputed whole-genome sequence-based GWAS approach pinpoints causal mutations for complex traits in a specific swine population. 2021 , 1	0
595	Susceptibility loci and polygenic architecture highlight population specific and common genetic features in inguinal hernias: genetics in inguinal hernias. 2021 , 70, 103532	1
594	Analysis of Selected Variants of and Genes in Combat Athletes. 2021 , 12,	
593	Socially stratified epigenetic profiles are associated with cognitive functioning in children and adolescents.	0
592	SpecHap: a diploid phasing algorithm based on spectral graph theory. 2021 , 49, e114	1
591	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. 2021 , 24, 1367-1376	10
590	Identifying SNP associations and predicting disease risk from Genome-wide association studies using LassoNet.	
589	Genomic partitioning of inbreeding depression in humans. 2021 , 108, 1488-1501	3
588	Sex differences in the risk of cataract associated with type 2 diabetes: a Mendelian randomization study.	
587	A second hit somatic (p.R905W) and a novel germline intron-mutation of TSC2 gene is found in intestinal lymphangioliomyomatosis: a case report with literature review. 2021 , 16, 83	0
586	An efficient method to identify, date and describe admixture events using haplotype information.	0
585	Joint Analysis of Genome-Wide Association Data Reveals No Genetic Correlations Between Low Back Pain and Neurodegenerative Diseases. 2021 , 12, 744299	0
584	False discovery rate control in genome-wide association studies with population structure. 2021 , 118,	4
583	The relationships between women's reproductive factors: a Mendelian randomization analysis.	

- 582 Socially stratified DNA-methylation profiles are associated with disparities in child and adolescent mental health.
- 581 SVAT: Secure Outsourcing of Variant Annotation and Genotype Aggregation.
- 580 Donor Chimerism Study by Single Nucleotide Polymorphism using SYBR green based Real Time PCR.. **2021**, 37, 1795-1799
- 579 Mendelian randomization study reveals a population-specific putative causal effect of type 2 diabetes in risk of cataract. **2021**, 0
- 578 Evaluation of Vicinity-based Hidden Markov Models for Genotype Imputation.
- 577 HIF-1 β Pulmonary Phenotype Wide Association Study Unveils a Link to Inflammatory Airway Conditions. **2021**, 12, 756645 3
- 576 Polygenic Risk Scores for Kidney Function and Their Associations with Circulating Proteome, and Incident Kidney Diseases. **2021**, 0
- 575 Genotypes of informative loci from 1000 Genomes data allude evolution and mixing of human populations. **2021**, 11, 17741
- 574 Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. **2021**, 131, 15
- 573 Role of Genetic Interactions in Lung Diseases Detection using Computational Approaches: A Review. **2021**, 01,
- 572 Advances and challenges in quantitative delineation of the genetic architecture of complex traits.. **2021**, 9, 168-184
- 571 Systematic analysis of binding of transcription factors to noncoding variants. *Nature*, **2021**, 591, 147-15150.4 23
- 570 PopHumanVar: an interactive application for the functional characterization and prioritization of adaptive genomic variants in humans. **2021**, 1
- 569 Tumor Mutational Burden Is Polygenic and Genetically Associated with Complex Traits and Diseases. **2021**, 81, 1230-1239 3
- 568 Genetic variants in human () are associated with ulcerative forms of Buruli ulcer. **2021**, 10, 223-225 2
- 567 Genomic sequencing of rare diseases. **2021**, 61-95 0
- 566 Construction and integration of three de novo Japanese human genome assemblies toward a population-specific reference. **2021**, 12, 226 14
- 565 Biomedical Informatics: The Science and the Pragmatics. **2014**, 3-37 3

564	High-throughput translational medicine: challenges and solutions. 2014 , 799, 39-67	7
563	Biological knowledge-driven analysis of epistasis in human GWAS with application to lipid traits. 2015 , 1253, 35-45	9
562	Impact of Nonsynonymous Single-Nucleotide Variations on Post-Translational Modification Sites in Human Proteins. 2017 , 1558, 159-190	2
561	WhatsHap: Haplotype Assembly for Future-Generation Sequencing Reads. 2014 , 237-249	17
560	An Application of the Isometric Log-Ratio Transformation in Relatedness Research. 2016 , 75-84	2
559	Biobanks in Low Resource Contexts. 2017 , 169-198	2
558	Ancestry Inference in Complex Admixtures via Variable-Length Markov Chain Linkage Models. 2012 , 12-28	4
557	An Accurate Method for Inferring Relatedness in Large Datasets of Unphased Genotypes via an Embedded Likelihood-Ratio Test. 2013 , 212-229	3
556	Targeted Therapies and Biomarkers for Personalized Treatment of Psoriasis. 2015 , 77-100	1
555	Genetic Basis of Intervertebral Disc Degeneration. 2014 , 157-176	1
554	Mining Genetic Resources via Ecotilling. 2014 , 349-365	7
553	High resolution HLA haplotyping by imputation for a British population bioresource. 2017 , 78, 242-251	16
552	Investigation of copy number variation in subjects with major depression based on whole-genome sequencing data. 2017 , 220, 38-42	8
551	Three-dimensional genome restructuring across timescales of activity-induced neuronal gene expression. 2020 , 23, 707-717	33
550	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. 2020 , 23, 809-818	69
549	Lighting up single-nucleotide variation in situ in single cells and tissues. 2020 , 49, 1932-1954	15
548	Ancient DNA from Guam and the peopling of the Pacific. 2021 , 118,	6
547	A comprehensive analysis of methods for assessing polygenic burden on Alzheimer's disease pathology and risk beyond. 2020 , 2, fcz047	18

546	SCN11A variants may influence postoperative pain sensitivity after gynecological surgery in Chinese Han female patients. 2017 , 96, e8149	9
545	Genome-wide association studies suggest limited immune gene enrichment in schizophrenia compared to five autoimmune diseases.	2
544	A high-quality reference panel reveals the complexity and distribution of structural genome changes in a human population.	3
543	Mega-analysis of 31,396 individuals from 6 countries uncovers strong gene-environment interaction for human fertility.	7
542	Colocalization of GWAS and eQTL Signals Detects Target Genes.	5
541	Familial migration of the Neolithic contrasts massive male migration during Bronze Age in Europe inferred from ancient X chromosomes.	3
540	Empirical Bayes estimation of semi-parametric hierarchical mixture models for unbiased characterization of polygenic disease architectures.	1
539	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders.	2
538	Population history of the Sardinian people inferred from whole-genome sequencing.	6
537	A performance assessment of relatedness inference methods using genome-wide data from thousands of relatives.	0
536	Genome-wide association study results for educational attainment aid in identifying genetic heterogeneity of schizophrenia.	1
535	A standardized framework for representation of ancestry data in genomics studies, with application to the NHGRI-EBI GWAS Catalog.	2
534	Widespread signatures of negative selection in the genetic architecture of human complex traits.	7
533	Genome-wide association study of Alcohol Use Disorder Identification Test (AUDIT) scores in 20,328 research participants of European ancestry.	4
532	A large-scale genome-wide enrichment analysis identifies new trait-associated genes, pathways and tissues across 31 human phenotypes*.	5
531	BITE: an R package for biodiversity analyses.	25
530	The Human Leukocyte Antigen Locus and Susceptibility to Rheumatic Heart Disease in South Asians and Europeans.	2
529	Scaling accurate genetic variant discovery to tens of thousands of samples.	392

528	Topologically associating domain (TAD) boundaries stable across diverse cell types are evolutionarily constrained and enriched for heritability.	6
527	Recent fluctuations in Mexican American genomes have altered the genetic architecture of biomedical traits.	1
526	Theoretical and empirical quantification of the accuracy of polygenic scores in ancestry divergent populations.	4
525	Mapping heritability of obesity by brain cell types.	2
524	Synchronized genetic activities in Alzheimer's brains revealed by heterogeneity-capturing network analysis.	1
523	Transcriptomic analysis of dystonia-associated genes reveals functional convergence within specific cell types and shared neurobiology with psychiatric disorders.	1
522	Natural selection influenced the genetic architecture of brain structure, behavioral and neuropsychiatric traits.	1
521	The genetic variation of lactase persistence alleles in northeast Africa.	1
520	Dynamics of Brain Structure and its Genetic Architecture over the Lifespan. 2020,	7
519	The Genetic Architecture of DNA Replication Timing in Human Pluripotent Stem Cells.	2
518	Common genetic variation influencing human white matter microstructure.	5
517	Quantifying the contribution of Neanderthal introgression to the heritability of complex traits.	3
516	Genetic influences on hub connectivity of the human connectome.	8
515	Genetic architecture of 11 abdominal organ traits derived from abdominal MRI using deep learning.	3
514	Evaluating brain structure traits as endophenotypes using polygenicity and discoverability.	1
513	Evaluation of Polygenic Prediction Methodology within a Reference-Standardized Framework.	1
512	Common variants contribute to intrinsic human brain functional networks.	2
511	FDR control in GWAS with population structure.	2

510	The MRC IEU OpenGWAS data infrastructure.	61
509	Negative short-range genomic autocorrelation of causal effects on human complex traits.	2
508	Multivariate genomic analysis of 1.5 million people identifies genes related to addiction, antisocial behavior, and health.	6
507	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals.	3
506	Accelerating Medicines Partnership: Parkinson's Disease. Genetic Resource.	2
505	Genetic analysis of de novo variants reveals sex differences in complex and isolated congenital diaphragmatic hernia and indicates MYRFas a candidate gene.	3
504	Equivalence of LD-Score Regression and Individual-Level-Data Methods. 2019,	8
503	Phenome-wide association studies (PheWAS) across large real-world data population cohorts support drug target validation.	5
502	The Evolutionary Genomic Dynamics of Peruvians Before, During, and After the Inca Empire.	1
501	Common risk variants identified in autism spectrum disorder.	32
500	Bivariate causal mixture model quantifies polygenic overlap between complex traits beyond genetic correlation.	2
499	Generalizing Genetic Risk Scores from Europeans to Hispanics/Latinos.	2
498	Patterns of genetic differentiation and the footprints of historical migrations in the Iberian Peninsula.	4
497	Whole genome sequence of Mapuche-Huilliche Native Americans.	1
496	Better estimation of SNP heritability from summary statistics provides a new understanding of the genetic architecture of complex traits.	6
495	Polygenic risk score for schizophrenia is more strongly associated with ancestry than with schizophrenia.	7
494	HIV Peptidome-Wide Association Study Reveals Patient-Specific Epitope Repertoires Associated with HIV Control.	1
493	Genetic analyses in UK Biobank identifies 78 novel loci associated with urinary biomarkers providing new insights into the biology of kidney function and chronic disease.	1

492	An Atlas of Human and Murine Genetic Influences on Osteoporosis.	3
491	Reduced signal for polygenic adaptation of height in UK Biobank.	24
490	LDpred-funct: incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets.	29
489	Alcohol consumption and mate choice in UK Biobank: comparing observational and Mendelian randomization estimates.	2
488	Genetic and Epigenetic Fine Mapping of Complex Trait Associated Loci in the Human Liver.	2
487	Moving beyond neurons: the role of cell type-specific gene regulation in Parkinson's disease heritability.	2
486	Functional disease architectures reveal unique biological role of transposable elements.	3
485	Economic status mediates the relationship between educational attainment and posttraumatic stress disorder: a multivariable Mendelian randomization study.	1
484	Using the structure of genome data in the design of deep neural networks for predicting amyotrophic lateral sclerosis from genotype.	1
483	Sequencing and Imputation in GWAS: Cost-Effective Strategies to Increase Power and Genomic Coverage Across Diverse Populations.	2
482	On the cross-population generalizability of gene expression prediction models.	6
481	Genomic analysis reveals a functional role for myocardial trabeculae in adults.	1
480	The great tit HapMap project: a continental-scale analysis of genomic variation in a songbird.	6
479	Recovery of trait heritability from whole genome sequence data.	83
478	A likelihood method for estimating present-day human contamination in ancient DNA samples using low-depth haploid chromosome data.	1
477	Multivariate GWAS of psychiatric disorders and their cardinal symptoms reveal two dimensions of cross-cutting genetic liabilities.	15
476	Accurate assembly of the olive baboon (<i>Papio anubis</i>) genome using long-read and Hi-C data.	1
475	Detecting genotype-population interaction effects by ancestry principal components.	1

474	Quantifying genetic effects on disease mediated by assayed gene expression levels.	6
473	Integrating Comprehensive Functional Annotations to Boost Power and Accuracy in Gene-Based Association Analysis.	2
472	Meta-analysis of problematic alcohol use in 435,563 individuals identifies 29 risk variants and yields insights into biology, pleiotropy and causality.	6
471	Reconstruction of nine thousand years of agriculture-based diet and impact on human genetic diversity in Asia.	1
470	Bayesian analysis of GWAS summary data reveals differential signatures of natural selection across human complex traits and functional genomic categories.	8
469	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium.	2
468	Population-specific causal disease effect sizes in functionally important regions impacted by selection.	4
467	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration.	2
466	Construction and Integration of Three De Novo Japanese Human Genome Assemblies toward a Population-Specific Reference.	1
465	Genetic Underpinnings of Risky Behaviour Relate to Altered Neuroanatomy.	1
464	The impact of natural selection on health and disease: uses of the population genetics approach in humans. 2013 , 6, 596-607	24
463	Mind the dbGAP: the application of data mining to identify biological mechanisms. 2011 , 11, 95-102	5
462	Urinary Albumin, Sodium, and Potassium and Cardiovascular Outcomes in the UK Biobank: Observational and Mendelian Randomization Analyses. 2020 , 75, 714-722	12
461	DNA damage and growth hormone hypersecretion in pituitary somatotroph adenomas. 2020 , 130, 5738-5755	17
460	Effects of germline DHFR and FPGS variants on methotrexate metabolism and relapse of leukemia. 2020 , 136, 1161-1168	4
459	Automated quality control for genome wide association studies. 2016 , 5, 1889	7
458	Fast and Rigorous Computation of Gene and Pathway Scores from SNP-Based Summary Statistics. 2016 , 12, e1004714	201
457	Pleiotropic Effects of Immune Responses Explain Variation in the Prevalence of Fibroproliferative Diseases. 2015 , 11, e1005568	10

456	Sex-Specific Selection and Sex-Biased Gene Expression in Humans and Flies. 2016 , 12, e1006170	66
455	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. 2017 , 13, e1006719	60
454	Down-Regulation of TLR and JAK/STAT Pathway Genes Is Associated with Diffuse Cutaneous Leishmaniasis: A Gene Expression Analysis in NK Cells from Patients Infected with <i>Leishmania mexicana</i> . 2016 , 10, e0004570	19
453	Efficient and cost effective population resequencing by pooling and in-solution hybridization. 2011 , 6, e18353	41
452	4-aminobutyrate aminotransferase (ABAT): genetic and pharmacological evidence for an involvement in gastro esophageal reflux disease. 2011 , 6, e19095	8
451	Copy number variants in candidate genes are genetic modifiers of Hirschsprung disease. 2011 , 6, e21219	53
450	Sequence imputation of HPV16 genomes for genetic association studies. 2011 , 6, e21375	59
449	Genome-wide local ancestry approach identifies genes and variants associated with chemotherapeutic susceptibility in African Americans. 2011 , 6, e21920	21
448	Genome-wide mapping of copy number variation in humans: comparative analysis of high resolution array platforms. 2011 , 6, e27859	51
447	Analysis of microsatellite variation in <i>Drosophila melanogaster</i> with population-scale genome sequencing. 2012 , 7, e33036	28
446	Genotype-based test in mapping cis-regulatory variants from allele-specific expression data. 2012 , 7, e38667	6
445	Genome-wide analysis in Brazilian Xavante Indians reveals low degree of admixture. 2012 , 7, e42702	10
444	North African populations carry the signature of admixture with Neandertals. 2012 , 7, e47765	52
443	The rs1024611 regulatory region polymorphism is associated with CCL2 allelic expression imbalance. 2012 , 7, e49498	29
442	Contribution of genome-wide association studies to scientific research: a bibliometric survey of the citation impacts of GWAS and candidate gene studies published during the same period and in the same journals. 2012 , 7, e51408	12
441	SNPflow: a lightweight application for the processing, storing and automatic quality checking of genotyping assays. 2013 , 8, e59508	5
440	Comprehensive investigation of the caveolin 2 gene: resequencing and association for kidney transplant outcomes. 2013 , 8, e63358	5
439	Comprehensive functional annotation of seventy-one breast cancer risk Loci. 2013 , 8, e63925	38

438	HGGPD: the human gene population genetic difference database. 2013 , 8, e64150	3
437	Imputation of variants from the 1000 Genomes Project modestly improves known associations and can identify low-frequency variant-phenotype associations undetected by HapMap based imputation. 2013 , 8, e64343	42
436	Role of HLA-DP polymorphisms on chronicity and disease activity of hepatitis B infection in Southern Chinese. 2013 , 8, e66920	31
435	Genome-wide copy number variation in sporadic amyotrophic lateral sclerosis in the Turkish population: deletion of EPHA3 is a possible protective factor. 2013 , 8, e72381	17
434	Genetic structure of Tibeto-Burman populations of Bangladesh: evaluating the gene flow along the sides of Bay-of-Bengal. 2013 , 8, e75064	12
433	Afghan Hindu Kush: where Eurasian sub-continent gene flows converge. 2013 , 8, e76748	73
432	Comprehensive analysis of single nucleotide polymorphisms in human microRNAs. 2013 , 8, e78028	29
431	From days to hours: reporting clinically actionable variants from whole genome sequencing. 2014 , 9, e86803	3
430	Ultra high-resolution gene centric genomic structural analysis of a non-syndromic congenital heart defect, Tetralogy of Fallot. 2014 , 9, e87472	9
429	Human transporter database: comprehensive knowledge and discovery tools in the human transporter genes. 2014 , 9, e88883	17
428	Relationship between Interleukin-6 gene polymorphism and hippocampal volume in antipsychotic-naïve schizophrenia: evidence for differential susceptibility?. 2014 , 9, e96021	52
427	Genome at juncture of early human migration: a systematic analysis of two whole genomes and thirteen exomes from Kuwaiti population subgroup of inferred Saudi Arabian tribe ancestry. 2014 , 9, e99069	24
426	Whole genome and exome sequencing of monozygotic twins with trisomy 21, discordant for a congenital heart defect and epilepsy. 2014 , 9, e100191	17
425	The rs225017 polymorphism in the 3'UTR of the human DIO2 gene is associated with increased insulin resistance. 2014 , 9, e103960	9
424	The interplay between natural selection and susceptibility to melanoma on allele 374F of SLC45A2 gene in a South European population. 2014 , 9, e104367	13
423	Association studies with imputed variants using expectation-maximization likelihood-ratio tests. 2014 , 9, e110679	1
422	Examining the polymorphisms in the hypoxia pathway genes in relation to outcome in colorectal cancer. 2014 , 9, e113513	7
421	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. 2015 , 10, e0121644	12

420	Association of MMP-9 Haplotypes and TIMP-1 Polymorphism with Spontaneous Deep Intracerebral Hemorrhage in the Taiwan Population. 2015 , 10, e0125397	17
419	Genetic Affinity of the Bhil, Kol and Gond Mentioned in Epic Ramayana. 2015 , 10, e0127655	13
418	Genomic Scans of Zygotic Disequilibrium and Epistatic SNPs in HapMap Phase III Populations. 2015 , 10, e0131039	4
417	Comparison of Genetic Variants in Cancer-Related Genes between Chinese Hui and Han Populations. 2015 , 10, e0145170	4
416	Single Nucleotide Variant rs2232710 in the Protein Z-Dependent Protease Inhibitor (ZPI, SERPINA10) Gene Is Not Associated with Deep Vein Thrombosis. 2016 , 11, e0151347	6
415	Incorporating Non-Coding Annotations into Rare Variant Analysis. 2016 , 11, e0154181	7
414	Comprehensive Analysis of Genome Rearrangements in Eight Human Malignant Tumor Tissues. 2016 , 11, e0158995	6
413	Demonstration of Protein-Based Human Identification Using the Hair Shaft Proteome. 2016 , 11, e0160653	78
412	Evidence of Polygenic Adaptation in the Systems Genetics of Anthropometric Traits. 2016 , 11, e0160654	8
411	Genetic Variants in Isolated Ebstein Anomaly Implicated in Myocardial Development Pathways. 2016 , 11, e0165174	10
410	Extensive Association of Common Disease Variants with Regulatory Sequence. 2016 , 11, e0165893	7
409	HacDivSel: Two new methods (haplotype-based and outlier-based) for the detection of divergent selection in pairs of populations. 2017 , 12, e0175944	6
408	An ancestral haplotype of the human PERIOD2 gene associates with reduced sensitivity to light-induced melatonin suppression. 2017 , 12, e0178373	12
407	Genome wide association study of incomplete hippocampal inversion in adolescents. 2020 , 15, e0227355	6
406	Multi-ethnic transcriptome-wide association study of prostate cancer. 2020 , 15, e0236209	4
405	ABCC2-24C > T polymorphism is associated with the response to platinum/5-Fu-based neoadjuvant chemotherapy and better clinical outcomes in advanced gastric cancer patients. 2016 , 7, 55449-55457	16
404	Associations of genotypes and haplotypes of IL-17 with risk of gastric cancer in an eastern Chinese population. 2016 , 7, 82384-82395	7
403	Genome-wide haplotype association study identify the FGFR2 gene as a risk gene for acute myeloid leukemia. 2017 , 8, 7891-7899	17

402	Genes with stable DNA methylation levels show higher evolutionary conservation than genes with fluctuant DNA methylation levels. 2015 , 6, 40235-46	2
401	NTRK1 fusions for the therapeutic intervention of Korean patients with colon cancer. 2016 , 7, 8399-412	16
400	MAPK activation and HRAS mutation identified in pituitary spindle cell oncocytoma. 2016 , 7, 37054-37063	24
399	Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression.	2
398	Human complex trait genetics: lifting the lid of the genomics toolbox - from pathways to prediction. 2012 , 13, 213-24	8
397	Targeting the individual cancer patient. 2011 , 8-28	1
396	Genetic variations in the Dravidian population of South West coast of India: Implications in designing case-control studies. 2017 , 145, 753-757	1
395	A Database of Gene-Environment Interactions Pertaining to Blood Lipid Traits, Cardiovascular Disease and Type 2 Diabetes. 2011 , 2,	47
394	Practical Consideration of Genotype Imputation: Sample Size, Window Size, Reference Choice, and Untyped Rate. 2011 , 4, 339-352	19
393	An extended Tajima's D neutrality test incorporating SNP calling and imputation uncertainties. 2015 , 8, 447-456	2
392	Developing genetic resources for pre-breeding in Brassica oleracea L.: an overview of the UK perspective. 2012 , 39, 62-68	9
391	InterPregGen: genetic studies of pre-eclampsia in three continents. 2014 , 24, 141-146	8
390	Prediction and Analysis of Breast Cancer Related Deleterious Non-Synonymous Single Nucleotide Polymorphisms in the PTEN Gene. 2016 , 17, 2199-203	4
389	Passive and active DNA methylation and the interplay with genetic variation in gene regulation. 2013 , 2, e00523	295
388	Reduced signal for polygenic adaptation of height in UK Biobank. 2019 , 8,	181
387	Genetic mapping of etiologic brain cell types for obesity. 2020 , 9,	21
386	Recent shifts in the genomic ancestry of Mexican Americans may alter the genetic architecture of biomedical traits. 2020 , 9,	3
385	Hi-MC: a novel method for high-throughput mitochondrial haplogroup classification. 2018 , 6, e5149	6

384	Ancestry-informative markers for African Americans based on the Affymetrix Pan-African genotyping array. 2014 , 2, e660	2
383	Gene Expression Analysis in Three Posttraumatic Stress Disorder Cohorts Implicates Inflammation and Innate Immunity Pathways and Uncovers Shared Genetic Risk With Major Depressive Disorder. 2021 , 15, 678548	2
382	Influence of Sociodemographic Characteristics and Inflammation-Related Gene Variants on the Comfort Level of Caregivers of Patients With Head and Neck Cancer. 2021 , 8980101211046738	0
381	Genome-wide association study of colorectal polyps identified highly overlapping polygenic architecture with colorectal cancer. 2021 ,	0
380	Genetic overlap and causality between blood metabolites and migraine. 2021 , 108, 2086-2098	2
379	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. 2021 , 12, 5929	4
378	Phase II study of ceralasertib (AZD6738) in combination with durvalumab in patients with advanced/metastatic melanoma who have failed prior anti-PD-1 therapy. 2021 ,	8
377	Estimation of cell-free fetal DNA fraction from maternal plasma based on linkage disequilibrium information. 2021 , 6, 85	0
376	Incorporating functional priors improves polygenic prediction accuracy in UK Biobank and 23andMe data sets. 2021 , 12, 6052	7
375	Allelic Association. 2004 ,	
374	Marker. 2004 ,	
373	Genome-wide association studies: Where we are heading?. 2011 , 1, 23	0
372	Broader Considerations of Medical and Dental Data Integration. 2012 , 167-298	
371	Identifying highly conserved and highly differentiated gene ontology categories in human populations. 2011 , 6, e27871	
370	Genome-Wide Association Studies in Disease Risk Calculation: The Role of Bioinformatics in Patient Care. 2012 , 103-129	
369	Novel Methods in the Study of the Breast Cancer Genome: Towards a Better Understanding of the Disease of Breast Cancer. 2012 , 03, 797-809	
368	Microarray Technology and Other Methods in Pharmacogenomics Testing. 185-200	
367	Personalized Genome, Current Status, and the Future of Pharmacogenomics. 2013 , 19-37	

- 366 Analysing Quality Measures of Phasing Algorithms in Genome-Wide Haplotyping. **2013**, 37-44
- 365 Do the Estimated Admixture Times Confirm the Proposed Holocene Gene Flow from India to Australia? **2013**, 10, 27-32
- 364 Primer Design for Large-Scale Multiplex PCR and Arrayed Primer Extension. **2013**, 199-208
- 363 Bioinformatics Approaches for the Identification and Annotation of RNA Editing Sites. **2013**, 10, 27-32
- 362 Integrative analysis of mRNA expression and half-life data reveals trans-acting genetic variants associated with increased expression of stable transcripts. **2013**, 8, e79627 1
- 361 Effective population size of korean populations. **2014**, 12, 208-15 0
- 360 Mutation Analysis in PARK2 Gene Uncovers Patterns of Associated Genetic Variants. **2014**, 145-152
- 359 Human Genome Project: Reassessment and Philosophical Analysis. **2015**, 123, 67-73
- 358 Formalgenetik. **2015**, 459-523
- 357 Use of Appropriate Controls in Rare-Variant Studies. **2015**, 239-252
- 356 Understanding the Human Genetics and Evolution: High School Biology. **2015**, 123, 67-73
- 355 Bisphosphonate Related Osteonecrosis of the Jaw. **2015**, 311-331
- 354 Non-synonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies. **2015**, 1-27
- 353 An Evaluation of the MiDCoP Method for Imputing Allele Frequency in Genome Wide Association Studies. **2015**, 57-67
- 352 The Revolution in Genetic Sequencing and Analysis. **2015**, 1-43
- 351 Exploring function of conserved non-coding DNA in its chromosomal context. **2015**, 2, 773-793 1
- 350 Association Studies to Map Genes for Disease-Related Traits in Humans. **2015**, 53-66
- 349 Materials and Methods. **2015**, 93-109

- 348 Copy Number Variations and Chronic Diseases. **2015**, 85-101
- 347 Analysis of pharmacogenomic variants associated with population differentiation. **2015**, 10, e0119994 ○
- 346 A method to associate all possible combinations of genetic and environmental factors using GxE landscape plot. **2015**, 11, 161-4
- 345 The genetics of Bene Israel from India reveals both substantial Jewish and Indian ancestry.
- 344 HacDivSel: Two new methods (haplotype-based and outlier-based) for the detection of divergent selection in pairs of populations.
- 343 Accurate interrogation of FCGR3A rs396991 in European and Asian populations using a widely available TaqMan genotyping method. **2015**, 25, 569-72 1
- 342 On the Recombination Rate Estimation in the Presence of Population Substructure. **2015**, 10, e0145152
- 341 Genomic Medicine and Ethnic Differences in Cardiovascular Disease Risk. **2016**, 209-235
- 340 Application of Genomics to the Study of Human Growth Disorders. **2016**, 363-384
- 339 Nonsynonymous Single-Nucleotide Variations as Cardiovascular System Disease Biomarkers and Their Roles in Bridging Genomic and Proteomic Technologies. **2016**, 821-847
- 338 Human Genomic Variation. **2016**, 25-44
- 337 The Revolution in Genetic Sequencing and Analysis. **2016**, 2793-2835
- 336 Novel Genetic Risk factors for Asthma in African American Children: Precision Medicine and The SAGE II Study.
- 335 Complex ancient genetic structure and cultural transitions in southern African populations.
- 334 FlashPCA: fast sparse canonical correlation analysis of genomic data.
- 333 Evidence of a recombination rate valley in human regulatory domains. 1
- 332 The multiple testing burden in sequencing-based disease studies of global populations. 1
- 331 A comprehensive and scalable database search system for metaproteomics.

- 330 Using imputed genotype data in the joint score tests for genetic association and gene-environment interactions in case-control studies.
- 329 Cross-disorder analysis of schizophrenia and 19 immune diseases reveals genetic correlation.
- 328 rehh 2.0: a reimplementation of the R package rehh to detect positive selection from haplotype structure.
- 327 Ethnically relevant consensus Korean reference genome towards personal reference genomes.
- 326 Widespread allelic heterogeneity in complex traits. 3
- 325 Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with polynomial functions.
- 324 Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. 1
- 323 Genetic and Genomic Approaches to Acute Lung Injury. **2017**, 133-159
- 322 Familial heterogeneity in breast cancer predisposition: a study of 22 Utah families.
- 321 Inference of Multiple-wave Admixtures by Length Distribution of Ancestral Tracks.
- 320 Review: Population Structure in Genetic Studies: Confounding Factors and Mixed Models. 2
- 319 A computational method for detection of structural variants using Deviant Reads and read pair Orientation: DevRO.
- 318 Genetics and Genomic Basis of Sleep Disorders in Humans. **2017**, 322-339.e7 0
- 317 Fine-scale human population structure in southern Africa reflects ecogeographic boundaries.
- 316 Reporting correct p-values in VEGAS analyses.
- 315 Common Variant Associations with Fragile X Syndrome.
- 314 Genetic architecture of early childhood growth phenotypes gives insights into their link with later obesity. 0
- 313 A dementia-associated risk variant near TMEM106B alters chromatin architecture and gene expression.

- 312 Weighted likelihood inference of genomic autozygosity patterns in dense genotype data.
- 311 Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records.
- 310 A survey of DNA methylation polymorphism identifies environmentally responsive co-regulated networks of epigenetic variation in the human genome. 1
- 309 Cytokine Polymorphisms, Immunosenescence, and Neurodegeneration. **2018**, 1-34
- 308 Une perspective génétique sur notre histoire : migrations humaines et adaptation à l'environnement. **2017**, 33-60
- 307 CoDEX2: full-spectrum copy number variation detection by high-throughput DNA sequencing. 0
- 306 Leveraging molecular QTL to understand the genetic architecture of diseases and complex traits. 5
- 305 An atlas of genetic variation for linking pathogen-induced cellular traits to human disease.
- 304 Loter: A software package to infer local ancestry for a wide range of species. 0
- 303 Imputation of posterior linkage probability relations reveals a significant influence of structural 3D constraints on linkage disequilibrium. 1
- 302 Genome-wide association analysis of lifetime cannabis use (N=184,765) identifies new risk loci, genetic overlap with mental health, and a causal influence of schizophrenia on cannabis use. 1
- 301 Genotype Imputation Performance of Three Reference Panels Using African Ancestry Individuals.
- 300 Dissecting dynamics and differences of selective pressures in the evolution of human pigmentation. 1
- 299 Mathematical Modeling the Biology of Single Nucleotide Polymorphisms (SNPs) in Whole Genome Adaptation. **2018**, 09, 520-533
- 298 Pathway-based analysis of genome-wide association study of circadian phenotypes. **2018**, 32, 361-370
- 297 Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. 3
- 296 Evidence for a potential role of miR-1908-5p and miR-3614-5p in autoimmune disease risk using genome-wide analyses. 0
- 295 Genetic Determinants of Telomere Length in African American Youth.

- 294 Differential DNA modification of an enhancer at the IGF2 locus affects dopamine synthesis in patients with major psychosis. 0
- 293 Inferring the ancestry of parents and grandparents from genetic data. 0
- 292 Phenotype-specific enrichment of Mendelian disorder genes near GWAS regions across 62 complex traits.
- 291 A one penny imputed genome from next generation reference panels. 1
- 290 Large-scale transcriptome-wide association study identifies new prostate cancer risk regions.
- 289 No evidence that mate choice in humans is dependent on the MHC.
- 288 Genome-wide association studies of impulsive personality traits (BIS-11 and UPPSP) and drug Experimentation in up to 22,861 adult research participants.
- 287 AIM-SNPtag: a computationally efficient approach for developing ancestry-informative SNP panels.
- 286 Genome-Wide Association Studies of malaria susceptibility and resistance: progress, pitfalls and prospects.
- 285 A machine-learning approach for accurate detection of copy-number variants from exome sequencing.
- 284 Functional and evolutionary impact of polymorphic inversions in the human genome. 0
- 283 GWAS identifies nine nephrolithiasis susceptibility loci related with metabolic metabolic and crystallization pathways. 1
- 282 Selective sweeps. **2019**, 99-113
- 281 Cytokine Polymorphisms, Immunosenesence, and Neurodegeneration. **2019**, 1057-1090
- 280 Genetic variants of calcium and vitamin D metabolism in kidney stone disease.
- 279 Genome-wide Association Study of Alcohol Consumption and Use Disorder in Multiple Populations (N = 274,424).
- 278 CHAPTER 7: Toxicogenomics and Toxicoinformatics: Supporting Systems Biology in the Big Data Era. **2019**, 214-241
- 277 Metabolome-Wide Mendelian Randomization Analysis of Emotional and Behavioral Responses to Traumatic Stress.

- 276 LD scores are associated with differences in allele frequencies between populations but LD score regression can still distinguish confounding from polygenicity.
- 275 Genome-wide association study of Parkinson's disease progression biomarkers in 12 longitudinal patients' cohorts.
- 274 FST and the Triangle Inequality for Biallelic Markers.
- 273 ERASE: Extended Randomization for assessment of annotation enrichment in ASE datasets.
- 272 Genome-Wide Association Study Identifies a Genetic Prediction Model for Postoperative Survival in Patients with Hepatocellular Carcinoma. **2019**, 25, 2452-2478 1
- 271 Genotype Imputation and Reference Panel: A Systematic Evaluation. 1
- 270 Screening human embryos for polygenic traits has limited utility.
- 269 Machine Learning based histology phenotyping to investigate epidemiologic and genetic basis of adipocyte morphology and cardiometabolic traits.
- 268 Linkage Disequilibrium and Heterozygosity Modulate the Genetic Architecture of Human Complex Phenotypes.
- 267 Population-specific sequence and expression differentiation in Europeans.
- 266 Evaluating and improving heritability models using summary statistics. 0
- 265 HaploHide: A Data Hiding Framework for Privacy Enhanced Sharing of Personal Genetic Data.
- 264 Efficient toolkit implementing best practices for principal component analysis of population genetic data. 0
- 263 Polygenic risk of psychiatric disorders exhibits cross-trait associations in electronic health record data.
- 262 Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma.
- 261 Host genomics of the HIV-1 reservoir size and its decay rate during suppressive antiretroviral treatment.
- 260 Inference and visualization of phenome-wide causal relationships using genetic data: an application to dental caries and periodontitis. 1
- 259 SpecHap: a diploid phasing algorithm based on spectral graph theory.

258	Gene expression profiling identifies pathways involved in seed maturation of <i>Jatropha curcas</i> .	
257	Gene expression profiling identifies pathways involved in seed maturation of <i>Jatropha curcas</i> .	
256	Integrative genomic analysis in African American children with asthma finds 3 novel loci associated with lung function.	
255	FASTQuick: Rapid and comprehensive quality assessment of raw sequence reads.	
254	Robust, flexible, and scalable tests for Hardy-Weinberg Equilibrium across diverse ancestries.	
253	Genome-wide analyses of behavioural traits biased by misreports and longitudinal changes.	1
252	Multi-ethnic transcriptome-wide association study of prostate cancer.	0
251	Shared heritability of face and brain shape distinct from cognitive traits.	0
250	Genetic analysis of obstructive sleep apnoea discovers a strong association with cardiometabolic health.	3
249	Using the UK Biobank as a global reference of worldwide populations: application to measuring ancestry diversity from GWAS summary statistics.	1
248	Integrating comprehensive functional annotations to boost power and accuracy in gene-based association analysis. 2020 , 16, e1009060	3
247	Novel susceptibility loci for steroid-associated osteonecrosis of the femoral head in systemic lupus erythematosus. 2021 ,	0
246	Large scale genome-wide association study in a Japanese population identified 45 novel susceptibility loci for 22 diseases.	2
245	CluStrat: a structure informed clustering strategy for population stratification.	2
244	Precision Medicine in Critical Illness: Sepsis and Acute Respiratory Distress Syndrome. 2020 , 267-288	0
243	The impact of post-alignment processing procedures on whole-exome sequencing data. 2020 , 43, e20200047	
242	CHAPTER 6:Detection of Disease-associated Mutations and Biomarkers Using Next-generation Sequencing. 2020 , 117-136	
241	Improving the informativeness of Mendelian disease-derived pathogenicity scores for common disease.	2

240	Formalgenetik. 2020 , 569-642	
239	Genetik und Anthropologie. 2020 , 897-962	
238	A whole-genome sequenced control population in northern Sweden reveals subregional genetic differences.	
237	Modeling Regulatory Network Topology Improves Genome-Wide Analyses of Complex Human Traits.	1
236	Fine-mapping and QTL tissue-sharing information improve causal gene identification and transcriptome prediction performance.	2
235	Genetic risk scores of disease and mortality capture differences in longevity, economic behavior, and insurance outcomes.	1
234	Integrating Genomic Correlation Structure Improves Copy Number Variations Detection.	
233	Linkage analysis identifies an isolated strabismus locus at 14q12 overlapping with FOXP1 syndrome region.	
232	Polygenic risk score across distinct colorectal cancer screening outcomes: from premalignant polyps to colorectal cancer. 2021 , 19, 261	1
231	Heart-brain connections: phenotypic and genetic insights from 40,000 cardiac and brain magnetic resonance images.	0
230	A comparative analysis of current phasing and imputation software.	1
229	Genetic variation affects morphological retinal phenotypes extracted from UK Biobank Optical Coherence Tomography images.	0
228	Evaluation of consensus strategies for haplotype phasing.	0
227	Genetic Landscape of Gullah African Americans.	1
226	Ancient DNA from Guam and the Peopling of the Pacific.	0
225	Peptide vaccine candidate mimics the heterogeneity of natural SARS-CoV-2 immunity in convalescent humans and induces broad T cell responses in mice models.	
224	Plant-ImputeDB: an integrated multiple plant reference panel database for genotype imputation. 2021 , 49, D1480-D1488	1
223	Archaeogenomic Distinctiveness of the Isthmo-Colombian Area.	

222	Polygenic Risk Scores for Kidney Function to the Circulating Proteome, and Incident Kidney Diseases: the Atherosclerosis Risk in Communities Study.	0
221	Linkage analysis identifies an isolated strabismus locus at 14q12 overlapping with FOXG1 syndrome region. 2020 ,	0
220	The SNPs within 3'UTR of miRNA Target Genes Related to Multiple Sclerosis: A Computational Prediction. 2020 , 17, 133-147	
219	Mutational screening of VSX1, SPARC, SOD1, LOX, and TIMP3 in keratoconus. 2011 , 17, 2482-94	68
218	Using the R Package crlmm for Genotyping and Copy Number Estimation. 2011 , 40, 1-32	445
217	Characterization of the Metabochip in diverse populations from the International HapMap Project in the Epidemiologic Architecture for Genes Linked to Environment (EAGLE) project. 2013 , 188-99	7
216	Detecting highly differentiated copy-number variants from pooled population sequencing. 2013 , 344-55	6
215	Screening the visual system homeobox 1 gene in keratoconus and posterior polymorphous dystrophy cohorts identifies a novel variant. 2013 , 19, 852-60	16
214	Cumulative Effect of Common Genetic Variants Predicts Incident Type 2 Diabetes: A Study of 21,183 Subjects from Three Large Prospective Cohorts. 2011 , 1, 108	1
213	Genome-wide association study for radiographic vertebral fractures: a potential role for the 16q24 BMD locus. 2014 , 59, 20-7	16
212	Genotype-guided dosing of vitamin K antagonists. 2014 , 370, 1762-3	7
211	Association of matrix metalloproteinase-7 (-181A/G) promoter polymorphism in chronic pancreatitis. 2014 , 140, 609-15	3
210	Association between WT1 polymorphisms and susceptibility to breast cancer: results from a case-control study in a southwestern Chinese population. 2015 , 5, 1234-50	2
209	KIDNEY DISEASE GENETICS AND THE IMPORTANCE OF DIVERSITY IN PRECISION MEDICINE. 2016 , 21, 285-96	3
208	Association study between the DNMT3A -448A>G polymorphism and risk of Alzheimer's disease in Caucasians of Italian origin. 2016 , 5, 85-93	3
207	Novel splice-site mutation in TTLL5 causes cone dystrophy in a consanguineous family. 2017 , 23, 131-139	7
206	[Association of WT1 rs16754 polymorphism with clinical features and prognosis in patients with acute myeloid leukemia]. 2016 , 37, 898-902	0
205	Genotype frequency and use of single nucleotide polymorphisms for detection of informative allele by polymerase chain reaction. 2020 , 36, 1567-1571	2

204 Study Design for Genetic Studies. **2021**, 58-78

203 Individual variations in 'brain age' relate to early-life factors more than to longitudinal brain change. **2021**, 10, 11

202 The genetic architecture of DNA replication timing in human pluripotent stem cells. **2021**, 12, 6746 4

201 Genetic Risk for Smoking: Disentangling Interplay Between Genes and Socioeconomic Status. **2021**, 1 0

200 Genome-Wide association between EYA1 and Aspirin-induced peptic ulceration. **2021**, 74, 103728 0

199 Phenome risk classification enables phenotypic imputation and gene discovery in developmental stuttering. **2021**, 108, 2271-2283 3

198 Polygenic architecture and cardiovascular risk of familial combined hyperlipidemia.. **2022**, 340, 35-43 2

197 A Saturated Map of Common Genetic Variants Associated with Human Height from 5.4 Million Individuals of Diverse Ancestries. 0

196 Ancestry- and sex-specific effects underlying inguinal hernia susceptibility identified in a multiethnic genome-wide association study meta-analysis.. **2022**,

195 Genotype frequency and use of single nucleotide polymorphisms for detection of informative 'allele' by polymerase chain reaction. **2020**, 36, 1567-1571 2

194 Linkage Disequilibrium and Association Analysis. **2021**, 182-204

193 Association with HLA-DRB1 position 37 distinguishes juvenile Dermatomyositis from adult-onset myositis.. **2022**, 0

192 Detecting selection using extended haplotype homozygosity (EHH)-based statistics in unphased or unpolarized data.. **2022**, 17, e0262024 1

191 Regenerating zebrafish scales express a subset of evolutionary conserved genes involved in human skeletal disease.. **2022**, 20, 21 3

190 Indigenous peoples in eastern Brazil: insights from 19th century genomes and metagenomes.

189 Interaction Testing and Polygenic Risk Scoring to Estimate the Association of Common Genetic Variants With Treatment Resistance in Schizophrenia.. **2022**, 2

188 Investigating the effect of sexual behaviour on oropharyngeal cancer risk: a methodological assessment of Mendelian randomization.. **2022**, 20, 40 1

187 Empirical Bayes PCA in high dimensions.

186	Carl von Linné The Development of the Idea of Binomial Nomenclature. 096777202110653	
185	Limb development genes underlie variation in human fingerprint patterns.. 2022, 185, 95-112.e18	2
184	Comprehensive Statistical and Bioinformatics Analysis in the Deciphering of Putative Mechanisms by Which Lipid-Associated GWAS Loci Contribute to Coronary Artery Disease.. 2022, 10,	1
183	Chromosomal microarray analysis of 410 Han Chinese patients with autism spectrum disorder or unexplained intellectual disability and developmental delay.. 2022, 7, 1	1
182	Population-based genetic effects for developmental stuttering.. 2022, 3, 100073	1
181	Fine-Scale Genetic Structure in the United Arab Emirates Reflects Endogamous and Consanguineous Culture, Population History, and Geography.. 2022, 39,	
180	Genetic analysis in African American children supports ancestry specific neuroblastoma susceptibility.. 2022,	
179	The role of single-nucleotide polymorphisms of the 8q24 chromosome region in patients with concomitant bladder and prostate cancer.. 2022, 1-5	0
178	High Quality Phasing Using Linked-Read Whole Genome Sequencing of Patient Cohorts Informs Genetic Understanding of Complex Traits.	
177	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations.. 2022,	0
176	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data.. 2022,	6
175	Epigenome-Wide Analysis Reveals DNA Methylation Alteration in and Its Target in a Mexican Population Cohort with Autism.. 2022, 9,	0
174	Positive selection acts on regulatory genetic variants in populations of European ancestry that affect ALDH2 gene expression.. 2022, 12, 4563	0
173	Genetic mosaicism in the human brain: from lineage tracing to neuropsychiatric disorders.. 2022,	2
172	Investigating relative contributions to psychiatric disease architecture from sequence elements originating across multiple evolutionary time-scales.	0
171	Sub-cellular level resolution of common genetic variation in the photoreceptor layer identifies continuum between rare disease and common variation.	
170	Novel Methods for Multi-ancestry Polygenic Prediction and their Evaluations in 3.7 Million Individuals of Diverse Ancestry.	0
169	The relationships between women's reproductive factors: a Mendelian randomisation analysis.. 2022, 20, 103	0

168	Towards the detection of copy number variation from single sperm sequencing in cattle.. 2022 , 23, 215	
167	The Construction of Multi-ethnic Polygenic Risk Score using Transfer Learning.	0
166	A Local Genetic Correlation Analysis Provides Biological Insights Into the Shared Genetic Architecture of Psychiatric and Substance Use Phenotypes.. 2022 ,	0
165	Genetic variants associated with longitudinal changes in brain structure across the lifespan.. 2022 , 25, 421-432	1
164	Genome-wide identification of the shared genetic basis of cannabis and cigarette smoking and schizophrenia implicates NCAM1 and neuronal abnormality.. 2022 , 310, 114453	0
163	Common variants contribute to intrinsic human brain functional networks.. 2022 , 54, 508-517	1
162	Early Tumor-Immune Microenvironmental Remodeling and Response to Frontline Fluoropyrimidine and Platinum Chemotherapy in Advanced Gastric Cancer.. 2021 ,	4
161	Cross-ancestry meta-analysis of opioid use disorder uncovers novel loci with predominant effects on brain.	0
160	Genome-wide association study and multi-trait analysis of opioid use disorder identifies novel associations in 639,709 individuals of European and African ancestry.	0
159	Early Pregnancy Exposure to Ambient Air Pollution among Late-Onset Preeclamptic Cases Is Associated with Placental DNA Hypomethylation of Specific Genes and Slower Placental Maturation.. 2021 , 9,	1
158	A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids.	0
157	The CAG-triplet in the androgen receptor gene and single-nucleotide polymorphisms in androgen pathway genes in patients with concomitant bladder and prostate cancer.. 2022 ,	0
156	Predicting causal genes from psychiatric genome-wide association studies using high-level etiological knowledge.. 2022 ,	0
155	Computationally repurposing drugs for breast cancer subtypes using a network-based approach.. 2022 , 23, 143	1
154	The admixture histories of Cabo Verde.	1
153	Data_Sheet_1.pdf. 2019 ,	
152	Data_Sheet_1.XLSX. 2018 ,	
151	Presentation_1.pdf. 2018 ,	

150 Presentation_1.pdf. **2018,**

149 Table_1.xlsx. **2019,**

148 Table_1.DOCX. **2019,**

147 Table_2.DOCX. **2019,**

146 Table_3.DOCX. **2019,**

145 Table_4.DOCX. **2019,**

144 Data_Sheet_1.pdf. **2020,**

143 DataSheet_1.pdf. **2020,**

142 Image_1.pdf. **2020,**

141 Data_Sheet_1.pdf. **2019,**

140 The sexual brain, genes, and cognition: A machine-predicted brain sex score explains individual differences in cognitive intelligence and genetic influence in young children.. **2022,**

1

139 Investigation of Interferon Gamma Activity Using Bioinformatics Methods.. **2021,** 76, 1245-1253

138 A flexible modeling and inference framework for estimating variant effect sizes from GWAS summary statistics.

0

137 The contribution of Neanderthal introgression and natural selection to neurodegenerative diseases.

0

136 TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data.. **2022,**

0

135 Genetic analyses identify pleiotropy and causality for blood proteins and highlight Wnt/ β -catenin signalling in migraine.. **2022,** 13, 2593

1

134 Analysis of MRI-derived spleen iron in the UK Biobank identifies genetic variation linked to iron homeostasis and hemolysis.. **2022,**

0

133 An eigenvalue ratio approach to inferring population structure from whole genome sequencing data.. **2022,**

- 132 Revolution in Genetics. **2021**, 1-48
- 131 SVA retrotransposons and a low copy repeat in humans and great apes: a mobile connection.. **2022**, 0
- 130 Large-scale GWAS of food liking reveals genetic determinants and genetic correlations with distinct neurophysiological traits.. **2022**, 13, 2743 0
- 129 Human brain anatomy reflects separable genetic and environmental components of socioeconomic status.. **2022**, 8, eabm2923 0
- 128 Innovative in Silico Approaches for Characterization of Genes and Proteins. **2022**, 13, 1
- 127 Imaging and genetics in Parkinson's disease: assessment of the GBA1 mutation.
- 126 Fast and Accurate Bayesian Polygenic Risk Modeling with Variational Inference. 0
- 125 Genetic Architecture And Clinical Outcomes Of The Fredrickson-Levy-Lees Dyslipoproteinemias.
- 124 Using the UK Biobank as a global reference of worldwide populations: application to measuring ancestry diversity from GWAS summary statistics. 0
- 123 Assessment of Bidirectional Relationships between Leisure Sedentary Behaviors and Neuropsychiatric Disorders: A Two-Sample Mendelian Randomization Study. **2022**, 13, 962
- 122 Local genetic correlations exist among neurodegenerative and neuropsychiatric diseases.
- 121 Integrated analysis of direct and proxy genome wide association studies highlights polygenicity of Alzheimer's disease outside of the APOE region. **2022**, 18, e1010208 0
- 120 Using genetic variation to disentangle the complex relationship between food intake and health outcomes. **2022**, 18, e1010162 0
- 119 Working memory and reaction time variability mediate the relationship between polygenic risk and ADHD traits in a general population sample.
- 118 Dissection of multiple sclerosis genetics identifies B and CD4+ T cells as driver cell subsets. **2022**, 23, 0
- 117 Linkage Disequilibrium Score Statistic Regression for Identifying Novel Trait Associations.
- 116 The female protective effect against autism spectrum disorder. **2022**, 2, 100134 2
- 115 De novo Mutations in Domestic Cat are Consistent with an Effect of Reproductive Longevity on Both the Rate and Spectrum of Mutations. **2022**, 39, 1

- 114 Identifying Causes of Fracture Beyond Bone Mineral Density: Evidence From Human Genetics. ○
- 113 Multivariate GWAS of psychiatric disorders and their cardinal symptoms reveal two dimensions of cross-cutting genetic liabilities. **2022**, 2, 100140 1
- 112 Genome-wide Scan of Dental Fear and Anxiety Nominates Novel Genes. 002203452211052
- 111 A Polygenic Risk Score for Hand Grip Strength Predicts Muscle Strength and Proximal and Distal Functional Outcomes among Older Women. Publish Ahead of Print, ○
- 110 Identifying genes targeted by disease-associated non-coding SNPs with a protein knowledge graph. **2022**, 17, e0271395
- 109 Identification of Putative Causal Relationships Between Type 2 Diabetes and Blood-Based Biomarkers in East Asians by Mendelian Randomization. ○
- 108 Response to Mitr and Pollack.
- 107 LDK-GBAT: fast and powerful gene-based association testing using summary statistics.
- 106 Genome-wide association study in individuals of European and African ancestry and multi-trait analysis of opioid use disorder identifies 19 independent genome-wide significant risk loci. 2
- 105 Sequence Variations Within HLA-G and HLA-F Genomic Segments at the Human Leukocyte Antigen Telomeric End Associated With Acute Graft-Versus-Host Disease in Unrelated Bone Marrow Transplantation. 13,
- 104 An efficient method to identify, date, and describe admixture events using haplotype information. gr.275994.121
- 103 Frontiers of Bio-Decolonization: Indigenous Data Sovereignty as a Possible Model for Community-Based Participatory Genomic Health Research for Racialized Peoples in Postgenomic Canada. **2022**, 6, 68
- 102 The genetic echo of the Tarim mummies in modern Central Asians. 1
- 101 Cardiovascular Image-Derived Phenotypes from Abdominal MRI at a Population Scale.
- 100 A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids. **2022**, 109, 1366-1387 ○
- 99 Causal effects on complex traits are similar across segments of different continental ancestries within admixed individuals. ○
- 98 dbPepVar: A Novel Cancer Proteogenomics Database. **2022**, 10, 90982-90994 ○
- 97 Evaluation of vicinity-based hidden Markov models for genotype imputation. **2022**, 23, ○

96	Principal Component Analyses (PCA)-based findings in population genetic studies are highly biased and must be reevaluated. 2022 , 12,	3
95	Using a polygenic score in a family design to understand genetic influences on musicality. 2022 , 12,	1
94	Genetic evidence for a causal relationship between type 2 diabetes and peripheral artery disease in both Europeans and East Asians. 2022 , 20,	0
93	Cross-ancestry meta-analysis of opioid use disorder uncovers novel loci with predominant effects in brain regions associated with addiction. 2022 , 25, 1279-1287	0
92	Mapping sleep phenotypic and genetic links to the brain and heart: a systematic analysis of multimodal brain and cardiac images in the UK Biobank.	0
91	Direct inference and control of genetic population structure from RNA sequencing data.	0
90	Exploring the association of interleukin polymorphisms with aggression and internalizing behaviors in children and adolescents.	1
89	Working memory and reaction time variability mediate the relationship between polygenic risk and ADHD traits in a general population sample.	0
88	SALAI-Net: species-agnostic local ancestry inference network. 2022 , 38, ii27-ii33	0
87	BMI-CNV: A Bayesian framework for multiple genotyping platforms detection of copy number variants.	0
86	Activation of the human insulin receptor by non-insulin-related peptides. 2022 , 13,	0
85	High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios. 2022 , 185, 3426-3440.e19	9
84	Genome Reporting for Healthy Populations Pipeline for Genomic Screening from the GENCOV COVID-19 Study. 2022 , 2,	0
83	SVAT: Secure outsourcing of variant annotation and genotype aggregation. 2022 , 23,	0
82	Genetic Liabilities Differentiating Bipolar Disorder, Schizophrenia, and Major Depressive Disorder, and Phenotypic Heterogeneity in Bipolar Disorder. 2022 , 79, 1032	1
81	Revolution in Genetics. 2022 , 3153-3200	0
80	Animal-SNPAtlas: a comprehensive SNP database for multiple animals.	0
79	Leveraging functional genomic annotations and genome coverage to improve polygenic prediction of complex traits within and between ancestries.	0

78	Age-dependent topic modelling of comorbidities in UK Biobank identifies disease subtypes with differential genetic risk.	0
77	A saturated map of common genetic variants associated with human height. 2022 , 610, 704-712	2
76	Cancer Bioinformatics. 1-14	0
75	Rare coding variants inCHRNA2reduce the likelihood of smoking.	0
74	The construction of cross-population polygenic risk scores using transfer learning. 2022 , 109, 1998-2008	0
73	Genetics of Keratoconus. 2023 , 33-50	0
72	Histocompatibility in Live Donor Kidney Transplantation. 2022 , 69-86	0
71	High-quality read-based phasing of cystic fibrosis cohort informs genetic understanding of disease modification. 2023 , 4, 100156	0
70	Transfer Learning in Genome-Wide Association Studies with Knockoffs.	0
69	Acute and Long-term Neurological Complications of Acute Lymphoblastic Leukemia (ALL) Therapy in Latino Children. 2023 , 43-53	0
68	The effect of heteroscedasticity on the prediction efficiency of genome-wide polygenic score for body mass index. 13,	0
67	Shared genetic influences between blood analyte levels and risk of severe COVID-19. 2022 , 111708	0
66	Genome screening, reporting, and genetic counseling for healthy populations.	0
65	ChIPBase v3.0: the encyclopedia of transcriptional regulations of non-coding RNAs and protein-coding genes.	0
64	Genetic influences on human blood metabolites in the Japanese population. 2023 , 26, 105738	0
63	The Human Genome. 2022 ,	0
62	False Discovery Rate Control for Grouped Variable Selection in High-Dimensional Linear Models Using the T-Knock Filter. 2022 ,	0
61	Genome-Wide Association Study of Obsessive-Compulsive Symptoms including 33 943 individuals from the general population.	0

- 60 Examination of a novel expression-based gene-SNP annotation strategy to identify tissue-specific contributions to heritability in multiple traits. ○
- 59 High-resolution African HLA resource uncovers HLA-DRB1 expression effects underlying vaccine response. ○
- 58 LDAK-GBAT: Fast and powerful gene-based association testing using summary statistics. **2022**, ○
- 57 Kalpra: A kernel approach for longitudinal pathway regression analysis integrating network information with an application to the longitudinal PsyCourse Study. 13, ○
- 56 Association between genetic risk of alcohol consumption and alcohol-related morbidity and mortality under different alcohol policy conditions: evidence from the Finnish alcohol price reduction of 2004. ○
- 55 Joint Multi-Ancestry and Admixed GWAS Reveals the Complex Genetics behind Human Cranial Vault Shape. ○
- 54 Genetic diversity fuels gene discovery for tobacco and alcohol use. **2022**, 612, 720-724 3
- 53 Event-based high throughput computing: A series of case studies on a massively parallel softcore machine. ○
- 52 HAPNEST: efficient, large-scale generation and evaluation of synthetic datasets for genotypes and phenotypes. ○
- 51 Genetic underpinnings of brain structural connectome for young adults. 1-26 ○
- 50 Genetic Divergence Within Southern Africa During the Later Stone Age. **2022**, 19-28 ○
- 49 Recent Advances in Genetic Epidemiology of Colorectal Cancer in Chinese Population. **2022**, 187-214 ○
- 48 GWAS of depression in 4,520 individuals from the Russian population highlights the role of MAGI2 (S-SCAM) in the gut-brain axis. 13, ○
- 47 Incorporating discovery and replication GWAS into summary data Mendelian randomization studies: A review of current methods and a simple, general and powerful alternative. ○
- 46 Genome-wide screen of otosclerosis in population biobanks: 27 loci and shared associations with skeletal structure. **2023**, 14, ○
- 45 Genetic predictors of lifelong medication-use patterns in cardiometabolic diseases. ○
- 44 The genetic architecture of changes in adiposity during adulthood. ○
- 43 Transcriptional signatures of heroin intake and seeking throughout the brain reward circuit. ○

- 42 Are Alzheimer's and coronary artery diseases genetically related to longevity?. 13,
- 41 Polygenic prediction across populations is influenced by ancestry, genetic architecture, and methodology.
- 40 Visual masking deficits in schizophrenia: a view into the genetics of the disease through an endophenotype. **2022**, 12,
- 39 Generation of Induced Pluripotent Stem Cells from Lymphoblastoid Cell Lines by Electroporation of Episomal Vectors. **2022**,
- 38 Introduction to Genomic Diagnostics. **2019**, 38-75
- 37 The chromatin modulating NSL complex regulates genes and pathways genetically linked to Parkinson's disease.
- 36 Multi-ancestry study of the genetics of problematic alcohol use in >1 million individuals.
- 35 A comprehensive investigation into the genetic relationship between music engagement and mental health. **2023**, 13,
- 34 Population analyses of mosaic X chromosome loss identify genetic drivers and widespread signatures of cellular selection.
- 33 Proteomic analysis of 92 circulating proteins and their effects in cardiometabolic diseases.
- 32 Fast and accurate Bayesian polygenic risk modeling with variational inference. **2023**,
- 31 Sequential pembrolizumab cooperates with platinum/5FU to remodel the tumor microenvironment in advanced gastric cancer: a phase II chemoimmunotherapy trial.
- 30 ME-Bayes SL: Enhanced Bayesian Polygenic Risk Prediction Leveraging Information across Multiple Ancestry Groups.
- 29 The contribution of Neanderthal introgression and natural selection to neurodegenerative diseases. **2023**, 180, 106082
- 28 Large-scale Integrative Analysis of Juvenile Idiopathic Arthritis for New Insight into Its Pathogenesis.
- 27 Global diversity in individualized cortical network topography.
- 26 Genes and Genomes. **2021**, 45-86
- 25 Post Stroke Motor Recovery Genome Wide Association Study:A Domain-Specific Approach.

- 24 Cerebellar Morphological Differences in Bipolar Disorder Type I. ○
- 23 Cross-trait analyses identify shared genetics between migraine, headache, and glycemic traits, and a causal relationship with fasting proinsulin. ○
- 22 CAS Array: design and assessment of a genotyping array for Chinese biobanking. **2023**, 6, ○
- 21 Inference of Causal Relationships Between Genetic Risk Factors for Cardiometabolic Phenotypes and Female-Specific Health Conditions. **2023**, 12, 1
- 20 The genetic architecture of pain intensity in a sample of 598,339 U.S. veterans. ○
- 19 The genetic architecture of pain intensity in a sample of 598,339 U.S. veterans. ○
- 18 An Ensemble Penalized Regression Method for Multi-ancestry Polygenic Risk Prediction. ○
- 17 Multivariate genome-wide association meta-analysis of over 1 million subjects identifies loci underlying multiple substance use disorders. **2023**, 1, 210-223 ○
- 16 Schrödinger's Cat in Simulations in Genome-wide Association Studies. ○
- 15 Associations of polygenic inheritance of physical activity with aerobic fitness, cardiometabolic risk factors and diseases: the HUNT Study. ○
- 14 Causal effects on complex traits are similar for common variants across segments of different continental ancestries within admixed individuals. **2023**, 55, 549-558 ○
- 13 Shared genetic liability for alcohol consumption, alcohol problems, and suicide attempt: Evaluating the role of impulsivity. **2023**, 13, ○
- 12 A small number of human lineage mutations regulated RNA-protein binding of conserved genes and promoted human evolution. ○
- 11 Hidden Genetic Regulation of Human Complex Traits via Brain Isoforms. ○
- 10 Statistical examination of shared loci in neuropsychiatric diseases using genome-wide association study summary statistics. ○
- 9 Frequencies of variants in genes associated with dyslipidemias identified in Costa Rican genomes. 14, ○
- 8 Genome-wide polygenic risk score for muscle strength predicts lower risk for common diseases and longer life span among the Finnish population: a prospective population based cohort study of the 342 443 FinnGen participants. ○
- 7 Multi-ancestry meta-analysis of tobacco use disorders based on electronic health record data prioritizes novel candidate risk genes and reveals associations with numerous health outcomes. ○

- 6 Analysis of genetic dominance in the UK Biobank. **2023**, 379, 1341-1348
- 5 Association of polygenic risk score with response to deep brain stimulation in Parkinson's disease. **2023**, 23,
- 4 Bias correction for inverse variance weighting Mendelian randomization.
- 3 PGSbuilder: An end-to-end platform for human genome association analysis and polygenic risk score predictions.
- 2 Genotype-by-environment interactions in chronic back pain. **2023**,
- 1 A rarefaction approach for measuring population differences in rare and common variation.