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Second-generation PLINK: rising to the challenge of larger and richer datasets

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2241	Genomic prediction of celiac disease targeting HLA-positive individuals. <b>2015</b> , 7, 72		20
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2239	Genome-wide association study and biological pathway analysis of the Eimeria maxima response in broilers. <b>2015</b> , 47, 91		12
2238	Barley landraces are characterized by geographically heterogeneous genomic origins. <b>2015</b> , 16, 173		84
2237	Genome-wide association study of schizophrenia in Ashkenazi Jews. <b>2015</b> , 168, 649-59		128
2236	Transcriptome Analysis of CD4+ T Cells in Coeliac Disease Reveals Imprint of BACH2 and IFN Regulation. <b>2015</b> , 10, e0140049		26
2235	The Genetic Structure of Marijuana and Hemp. <b>2015</b> , 10, e0133292		159
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2233	Proteasome system dysregulation and treatment resistance mechanisms in major depressive disorder. <b>2015</b> , 5, e687		17
2232	Discovery, genotyping and characterization of structural variation and novel sequence at single nucleotide resolution from de novo genome assemblies on a population scale. <i>GigaScience</i> , <b>2015</b> , 4, 64	7.6	16
2231	PRSice: Polygenic Risk Score software. <b>2015</b> , 31, 1466-8		724
2230	Second-generation PLINK: rising to the challenge of larger and richer datasets. <i>GigaScience</i> , <b>2015</b> , 4, 7	7.6	4156
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2228	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <b>2015</b> , 47, 1385-92		299
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2186	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <b>2016</b> , 135, 741-56	18
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2181	Identifying significant gene-environment interactions using a combination of screening testing and hierarchical false discovery rate control. <b>2016</b> , 40, 544-557	15
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2171	Impact of polygenic schizophrenia-related risk and hippocampal volumes on the onset of psychosis. <b>2016</b> , 6, e868	25
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2145	Changing Polygenic Penetrance on Phenotypes in the 20(th) Century Among Adults in the US Population. <b>2016</b> , 6, 30348	25
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2064	Potassium channel gene associations with joint processing speed and white matter impairments in schizophrenia. <b>2017</b> , 16, 515-521	10
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2050	Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. <b>2017</b> , 49, 666-673	81
2049	Shared genetic influences between dimensional ASD and ADHD symptoms during child and adolescent development. <b>2017</b> , 8, 18	48
2048	Phenome-wide association study for CYP2A6 alleles: rs113288603 is associated with hearing loss symptoms in elderly smokers. <b>2017</b> , 7, 1034	5
2047	Genome-Wide Identification of the Mutation Underlying Fleece Variation and Discriminating Ancestral Hairy Species from Modern Woolly Sheep. <b>2017</b> , 34, 1722-1729	24

2046	Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. <b>2017</b> , 206, 1113-1126	17
2045	A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. <b>2017</b> , 7, 2171-2184	6
2044	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. <b>2017</b> , 49, 978-985	254
2043	Polygenic scores via penalized regression on summary statistics. <b>2017</b> , 41, 469-480	117
2042	Genome-Wide Association Shows that Pigmentation Genes Play a Role in Skin Aging. <b>2017</b> , 137, 1887-1894	30
2041	The effects of Pleistocene climate change on biotic differentiation in a montane songbird clade from Wallacea. <b>2017</b> , 114, 353-366	14
2040	Association between a common immunoglobulin heavy chain allele and rheumatic heart disease risk in Oceania. <b>2017</b> , 8, 14946	74
2039	A pathway-centric approach to rare variant association analysis. <b>2016</b> , 25, 123-129	11
2038	Congruent population structure across paralogous and nonparalogous loci in Salish Sea chum salmon (Oncorhynchus keta). <b>2017</b> , 26, 4131-4144	9
2037	Whole genome sequencing predicts novel human disease models in rhesus macaques. <b>2017</b> , 109, 214-220	21
2036	Genetic influences on ADHD symptom dimensions: Examination of a priori candidates, gene-based tests, genome-wide variation, and SNP heritability. <b>2017</b> , 174, 458-466	14
2035	NeuroChip, an updated version of the NeuroX genotyping platform to rapidly screen for variants associated with neurological diseases. <b>2017</b> , 57, 247.e9-247.e13	54
2034	The last sea nomads of the Indonesian archipelago: genomic origins and dispersal. 2017, 25, 1004-1010	13
2033	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. <b>2017</b> , 27, 1450-1459	14
2032	Rare Copy Number Variants in NRXN1 and CNTN6 Increase Risk for Tourette Syndrome. 2017, 94, 1101-1111.6	<b>27</b> 103
2031	Polygenic risk for depression and the neural correlates of working memory in healthy subjects. <b>2017</b> , 79, 67-76	33
2030	The contribution of pathogenic variants in breast cancer susceptibility genes to familial breast cancer risk. <b>2017</b> , 3, 22	78
2029	The evolving genetic risk for sporadic ALS. <b>2017</b> , 89, 226-233	28

2028	Association Between Substance Use Disorder and Polygenic Liability to Schizophrenia. 2017, 82, 709-715	49
2027	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <b>2017</b> , 100, 885-894	48
2026	Massive introgression drives species radiation at the range limit of Anopheles gambiae. <b>2017</b> , 7, 46451	17
2025	Canine Brachycephaly Is Associated with a Retrotransposon-Mediated Missplicing of SMOC2. <b>2017</b> , 27, 1573-1584.e6	54
2024	The buffering capacity of stems: genetic architecture of nonstructural carbohydrates in cultivated Asian rice, Oryza sativa. <b>2017</b> , 215, 658-671	16
2023	Genetic-Variation-Driven Gene-Expression Changes Highlight Genes with Important Functions for Kidney Disease. <b>2017</b> , 100, 940-953	52
2022	Genome-wide Analysis of STAT3-Mediated Transcription during Early Human Th17 Cell Differentiation. <b>2017</b> , 19, 1888-1901	51
2021	Missense Mutation Associated With Fatty Acid Metabolism and Reduced Height in Greenlanders. <b>2017</b> , 10,	19
2020	Genome-wide association study of facial emotion recognition in children and association with polygenic risk for mental health disorders. <b>2017</b> , 174, 701-711	21
2019	Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. <b>2017</b> , 20, 533-546.e7	105
2018	The immunogenetics of narcolepsy associated with A(H1N1)pdm09 vaccination (Pandemrix) supports a potent gene-environment interaction. <b>2017</b> , 18, 75-81	19
2017	SeqArray-a storage-efficient high-performance data format for WGS variant calls. <b>2017</b> , 33, 2251-2257	65
2016	Stepwise Distributed Open Innovation Contests for Software Development: Acceleration of Genome-Wide Association Analysis. <i>GigaScience</i> , <b>2017</b> , 6, 1-10	12
2015	Genome-Wide Association Study of Post-Traumatic Stress Disorder in Two High-Risk Populations. <b>2017</b> , 20, 197-207	12
2014	The Relationship Between Mental Health, Disease Severity, and Genetic Risk for Depression in Early Rheumatoid Arthritis. <b>2017</b> , 79, 638-645	21
2013	Prefrontal gray matter volume mediates genetic risks for obesity. <b>2017</b> , 22, 703-710	42
2012	The druggable genome and support for target identification and validation in drug development. <b>2017</b> , 9,	212
2011	Genome-wide meta-analysis identifies novel loci of plaque burden in carotid artery. <b>2017</b> , 259, 32-40	22

2010	Genome-wide association study of cell-mediated immune response in chicken. <b>2017</b> , 134, 405-411	8
2009	Functional interactors of three genome-wide association study genes are differentially expressed in severe chronic obstructive pulmonary disease lung tissue. <b>2017</b> , 7, 44232	57
2008	Differential Aging Analysis in Human Cerebral Cortex Identifies Variants in TMEM106B and GRN that Regulate Aging Phenotypes. <b>2017</b> , 4, 404-415.e5	65
2007	TMEM230 in Parkinson's disease. <b>2017</b> , 56, 212.e1-212.e3	8
2006	Population genomics reveals structure at the individual, host-tree scale and persistence of genotypic variants of the undomesticated yeast Saccharomyces paradoxus in a natural woodland. <b>2017</b> , 26, 995-1007	9
2005	Resetting the bar: Statistical significance in whole-genome sequencing-based association studies of global populations. <b>2017</b> , 41, 145-151	36
2004	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. <b>2017</b> , 114, E327-E336	30
2003	Using Systems Genetics to Understanding the Etiology of Complex Disease. <b>2017</b> , 1488, 597-606	3
2002	The Genetic Architecture of Gene Expression in Peripheral Blood. <b>2017</b> , 100, 228-237	98
2001	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. <b>2017</b> , 4, 31-45.e6	31
2000	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. <b>2017</b> , 49, 274-281	182
1999	17q21.31 duplication causes prominent tau-related dementia with increased MAPT expression. <b>2017</b> , 22, 1119-1125	39
1998	Genetic association study identified a 20 kb regulatory element in WLS associated with osteoporosis and bone mineral density in Han Chinese. <b>2017</b> , 7, 13668	8
1997	A Chromosome-Scale Assembly of the Genome Provides Insight to the Genetic Basis of. <b>2017</b> , 7, 1927-1940	19
1996	Genomic Analyses of Pre-European Conquest Human Remains from the Canary Islands Reveal Close Affinity to Modern North Africans. <b>2017</b> , 27, 3396-3402.e5	32
1995	Male fertility restored by transplanting primordial germ cells into testes: a new way towards efficient transgenesis in chicken. <b>2017</b> , 7, 14246	19
1994	Genome-wide association analysis of residual feed intake in Junmu No. 1 White pigs. <b>2017</b> , 48, 686-690	6
1993	Whole genome sequencing-based association study to unravel genetic architecture of cooked grain width and length traits in rice. <b>2017</b> , 7, 12478	26

1992	Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <b>2017</b> , 101, 725-736	29
1991	Calibrating Population Stratification in Association Analysis. <b>2017</b> , 1666, 441-453	1
1990	Estimating Allele Frequencies. 2017, 1666, 61-81	2
1989	Estimating Disequilibrium Coefficients. <b>2017</b> , 1666, 117-132	2
1988	Genetic Mapping and Biochemical Basis of Yellow Feather Pigmentation in Budgerigars. <b>2017</b> , 171, 427-439.6	<b>2</b> \$0
1987	Regional variation in health is predominantly driven by lifestyle rather than genetics. <b>2017</b> , 8, 801	11
1986	Variation in SWI/SNF Chromatin Remodeling Complex Proteins is Associated with Alcohol Dependence and Antisocial Behavior in Human Populations. <b>2017</b> , 41, 2033-2040	7
1985	Influence of population structure on the compilation of the Bonsmara genomic reference population. <b>2017</b> , 8, s45-s47	O
1984	An eQTL variant of ZXDC is associated with IFN-[production following Mycobacterium tuberculosis antigen-specific stimulation. <b>2017</b> , 7, 12800	3
1983	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <b>2017</b> , 358, 652-655	223
1982	Prospects of Fine-Mapping Trait-Associated Genomic Regions by Using Summary Statistics from Genome-wide Association Studies. <b>2017</b> , 101, 539-551	111
1981	Loci associated with skin pigmentation identified in African populations. <b>2017</b> , 358,	179
1980	Disease-specific biases in alternative splicing and tissue-specific dysregulation revealed by multitissue profiling of lymphocyte gene expression in type 1 diabetes. <b>2017</b> , 27, 1807-1815	15
1979	Genotype imputation in a tropical crossbred dairy cattle population. 2017, 100, 9623-9634	6
1978	Analysis of Gene-Gene Interactions. <b>2017</b> , 95, 1.14.1-1.14.10	10
1977	An Evolutionary Genomic Perspective on the Breeding of Dwarf Chickens. <b>2017</b> , 34, 3081-3088	15
1976	The Genetic Legacy of Zoroastrianism in Iran and India: Insights into Population Structure, Gene Flow, and Selection. <b>2017</b> , 101, 353-368	10
1975	Do regional brain volumes and major depressive disorder share genetic architecture? A study of Generation Scotland (n=19 762), UK Biobank (n=24 048) and the English Longitudinal Study of Ageing (n=5766). <b>2017</b> , 7, e1205	37

1974	Haplotype of the Interleukin 17A gene is associated with osteitis after Bacillus Calmette-Guerin vaccination. <b>2017</b> , 7, 11691	10
1973	Educational Attainment and Personality Are Genetically Intertwined. 2017, 28, 1631-1639	35
1972	Iterative hard thresholding for model selection in genome-wide association studies. <b>2017</b> , 41, 756-768	2
1971	Linkage disequilibrium-dependent architecture of human complex traits shows action of negative selection. <b>2017</b> , 49, 1421-1427	204
1970	A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci. <b>2017</b> , 49, 1511-1516	629
1969	A Comparative Analysis of Genetic Ancestry and Admixture in the Colombian Populations of Choc and Medell <b>2017</b> , 7, 3435-3447	22
1968	Will Big Data Close the Missing Heritability Gap?. <b>2017</b> , 207, 1135-1145	34
1967	Genomewide association studies of suicide attempts in US soldiers. <b>2017</b> , 174, 786-797	34
1966	Ancestry Informative Marker Panel to Estimate Population Stratification Using Genome-wide Human Array. <b>2017</b> , 81, 225-233	11
1965	A Neolithic expansion, but strong genetic structure, in the independent history of New Guinea. <b>2017</b> , 357, 1160-1163	29
1964	Comparative and population genomic landscape of Phellinus noxius: A hypervariable fungus causing root rot in trees. <b>2017</b> , 26, 6301-6316	14
1963	HLA haplotypes in primary sclerosing cholangitis patients of admixed and non-European ancestry. <b>2017</b> , 90, 228-233	3
1962	Non-additive and epistatic effects of HLA polymorphisms contributing to risk of adult glioma. <b>2017</b> , 135, 237-244	7
1961	Complex Patterns of Admixture across the Indonesian Archipelago. <b>2017</b> , 34, 2439-2452	42
1960	Findings of a 1303 Korean whole-exome sequencing study. <b>2017</b> , 49, e356	23
1959	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. <b>2017</b> , 27, 2185-2193.ed	<b>5</b> 80
1958	Integrative studies implicate matrix metalloproteinase-12 as a culprit gene for large-artery atherosclerotic stroke. <b>2017</b> , 282, 429-444	20
1957	. 2017,	1

1956	Identification of positive selection signatures in pigs by comparing linkage disequilibrium variances. <b>2017</b> , 48, 600-605	5
1955	Genomic-polygenic and polygenic predictions for nine ultrasound and carcass traits in Angus-Brahman multibreed cattle using three sets of genotypes. <b>2017</b> , 202, 58-66	12
1954	The promise of discovering population-specific disease-associated genes in South Asia. <b>2017</b> , 49, 1403-1407	79
1953	Genomic landscape of human diversity across Madagascar. <b>2017</b> , 114, E6498-E6506	40
1952	Contribution to Alzheimer's disease risk of rare variants in TREM2, SORL1, and ABCA7 in 1779 cases and 1273 controls. <b>2017</b> , 59, 220.e1-220.e9	83
1951	A new approach to disentangle genetic and epigenetic components on disease comorbidities: studying correlation between genotypic and phenotypic disease networks. <b>2017</b> , 110, 453-458	2
1950	Evaluating mechanisms of diversification in a Guineo-Congolian tropical forest frog using demographic model selection. <b>2017</b> , 26, 5245-5263	91
1949	Impact of Sixteen Established Pancreatic Cancer Susceptibility Loci in American Jews. <b>2017</b> , 26, 1540-1548	5
1948	Genetic origins of the Minoans and Mycenaeans. <b>2017</b> , 548, 214-218	108
1947	Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network. <b>2017</b> , 7, 2919	9
1946	Using variable importance measures to identify a small set of SNPs to predict heading date in perennial ryegrass. <b>2017</b> , 7, 3566	11
1945	Common shared genetic variation behind decreased risk of breast cancer in celiac disease. <b>2017</b> , 7, 5942	2
1944	Associations between subjective well-being and subcortical brain volumes. <b>2017</b> , 7, 6957	10
1943	The utility of empirically assigning ancestry groups in cross-population genetic studies of addiction. <b>2017</b> , 26, 494-501	26
1942	A computational integrative approach based on alternative splicing analysis to compare immortalized and primary cancer cells. <b>2017</b> , 91, 116-123	3
1941	The genetic admixture in Tibetan-Yi Corridor. <b>2017</b> , 164, 522-532	24
1940	Genomewide DNA methylation analysis in combat veterans reveals a novel locus for PTSD. <b>2017</b> , 136, 493-505	41
1939	Variation in Recombination Rate and Its Genetic Determinism in Sheep Populations. <b>2017</b> , 207, 767-784	25

1938	Conservation genomics identifies impact of trade in a threatened songbird. <b>2017</b> , 214, 101-108	11
1937	Genotype-environment interaction on human cognitive function conditioned on the status of breastfeeding and maternal smoking around birth. <b>2017</b> , 7, 6087	8
1936	Genetic variation in GABRII and the risk for developing alcohol dependence. 2017, 27, 110-115	5
1935	The Irish DNA Atlas: Revealing Fine-Scale Population Structure and History within Ireland. <b>2017</b> , 7, 17199	15
1934	A large multi-ethnic genome-wide association study identifies novel genetic loci for intraocular pressure. <b>2017</b> , 8, 2108	58
1933	Mountain hare transcriptome and diagnostic markers as resources to monitor hybridization with European hares. <b>2017</b> , 4, 170178	3
1932	Machine learning shows association between genetic variability in and cerebral connectivity in preterm infants. <b>2017</b> , 114, 13744-13749	21
1931	An exome sequencing based approach for genome-wide association studies in the dog. <b>2017</b> , 7, 15680	9
1930	Genetic Influences on Evening Preference Overlap with Those for Bipolar Disorder in a Sample of Mexican Americans and American Indians. <b>2017</b> , 20, 499-510	7
1929	Penetrance of Polygenic Obesity Susceptibility Loci across the Body Mass Index Distribution. <b>2017</b> , 101, 925-938	73
1928	Transcriptome-wide association study revealed two novel genes associated with nonobstructive azoospermia in a Chinese population. <b>2017</b> , 108, 1056-1062.e4	11
1927	A PLAG1 mutation contributed to stature recovery in modern cattle. <b>2017</b> , 7, 17140	32
1926	Benchmarking Relatedness Inference Methods with Genome-Wide Data from Thousands of Relatives. <b>2017</b> , 207, 75-82	39
1925	High-resolution mapping of -regulatory variation in budding yeast. <b>2017</b> , 114, E10736-E10744	24
1924	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. 2017, 171, 1340-1353.e14	85
1923	Genome-wide mapping of genetic determinants influencing DNA methylation and gene expression in human hippocampus. <b>2017</b> , 8, 1511	37
1922	Genome-wide Association Study of Idiopathic Osteonecrosis of the Femoral Head. <b>2017</b> , 7, 15035	17
1921	A variant in PPP4R3A protects against alzheimer-related metabolic decline. <b>2017</b> , 82, 900-911	7

1920	Genetic diversity, population structure, and linkage disequilibrium of elite and local apple accessions from Belgium using the IRSC array. <b>2017</b> , 13, 1	17
1919	Current Scope and Challenges in Phenome-Wide Association Studies. <b>2017</b> , 4, 321-329	14
1918	The effect of artificial selection on phenotypic plasticity in maize. <b>2017</b> , 8, 1348	58
1917	The Genetic Legacy of the Indian Ocean Slave Trade: Recent Admixture and Post-admixture Selection in the Makranis of Pakistan. <b>2017</b> , 101, 977-984	19
1916	Potential damaging mutation in LRP5 from genome sequencing of the first reported chimpanzee with the Chiari malformation. <b>2017</b> , 7, 15224	4
1915	Imputation-Based Whole-Genome Sequence Association Study Rediscovered the Missing QTL for Lumbar Number in Sutai Pigs. <b>2017</b> , 7, 615	28
1914	Selective breeding and selection mapping using a novel wild-derived heterogeneous stock of mice revealed two closely-linked loci for tameness. <b>2017</b> , 7, 4607	8
1913	Genetic modifiers of Mendelian disease: Huntington's disease and the trinucleotide repeat disorders. <b>2017</b> , 26, R83-R90	37
1912	Prioritizing tests of epistasis through hierarchical representation of genomic redundancies. <b>2017</b> , 45, e131	9
1911	Burden of rare variants in ALS genes influences survival in familial and sporadic ALS. <b>2017</b> , 58, 238.e9-238.e15	27
1910	Evaluation of the accuracy of imputed sequence variant genotypes and their utility for causal variant detection in cattle. <b>2017</b> , 49, 24	53
1909	Detection of QTL for traits related to adaptation to sub-optimal climatic conditions in chickens. <b>2017</b> , 49, 39	10
1908	Pan-cancer analysis reveals technical artifacts in TCGA germline variant calls. <b>2017</b> , 18, 458	21
1907	Diversity analysis of cotton (Gossypium hirsutum L.) germplasm using the CottonSNP63K Array. <b>2017</b> , 17, 37	32
1906	"Like sugar in milk": reconstructing the genetic history of the Parsi population. 2017, 18, 110	18
1905	Meta-analysis of GWAS of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia. <b>2017</b> , 8, 21	320
1904	Linking rhizosphere microbiome composition of wild and domesticated Phaseolus vulgaris to	161
	genotypic and root phenotypic traits. <b>2017</b> , 11, 2244-2257	

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1902	blood pressure variation. <b>2017</b> , 49, 54-64	157
1901	Sex-Based Genetic Association Study Identifies CELSR1 as a Possible Chronic Obstructive Pulmonary Disease Risk Locus among Women. <b>2017</b> , 56, 332-341	22
1900	An Examination of Polygenic Score Risk Prediction in Individuals With First-Episode Psychosis. <b>2017</b> , 81, 470-477	126
1899	A genome wide association study suggests the association of muskelin with early onset bipolar disorder: Implications for a GABAergic epileptogenic neurogenesis model. <b>2017</b> , 208, 120-129	10
1898	Systems Genetics Identifies a Novel Regulatory Domain of Amylose Synthesis. 2017, 173, 887-906	49
1897	AKT: ancestry and kinship toolkit. <b>2017</b> , 33, 142-144	22
1896	Genetic and phenotypic characterization of the novel mouse substrain C57BL/6N Korl with increased body weight. <b>2017</b> , 7, 14217	6
1895	Insights into DDT Resistance from the Genetic Reference Panel. <b>2017</b> , 207, 1181-1193	35
1894	Genetic Stratification to Identify Risk Groups for Alzheimer's Disease. <b>2017</b> , 57, 275-283	21
1893	Childhood behaviour problems show the greatest gap between DNA-based and twin heritability. <b>2017</b> , 7, 1284	31
1892	Heritability of Atrial Fibrillation. <b>2017</b> , 10,	39
1891	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. <b>2017</b> , 8, 2062	53
1890	Genetic polymorphism related to monocyte-macrophage function is associated with graft-versus-host disease. <b>2017</b> , 7, 15666	14
1889	Deploying FPGAs to future-proof genome-wide analyses based on linkage disequilibrium. 2017,	O
1888	Population structure and genomic inbreeding in nine Swiss dairy cattle populations. 2017, 49, 83	32
1887	Exome-wide association study reveals novel psoriasis susceptibility locus at TNFSF15 and rare protective alleles in genes contributing to type I IFN signalling. <b>2017</b> , 26, 4301-4313	25
1886	Long-Term Impact of Optimum Contribution Selection Strategies on Local Livestock Breeds with Historical Introgression Using the Example of German Angler Cattle. <b>2017</b> , 7, 4009-4018	13
1885	Polygenic loading for major depression is associated with specific medical comorbidity. <b>2017</b> , 7, e1238	16

1884	Direct evidence for a polygenic etiology in familial multiple myeloma. <b>2017</b> , 1, 619-623	13
1883	Comparative Genomics Integrated with Association Analysis Identifies Candidate Effector Genes Corresponding to in Phenotype-Paired Isolates from Australia. <b>2017</b> , 8, 148	26
1882	Climate Clever Clovers: New Paradigm to Reduce the Environmental Footprint of Ruminants by Breeding Low Methanogenic Forages Utilizing Haplotype Variation. <b>2017</b> , 8, 1463	7
1881	Domestication Genomics of the Open-Pollinated Scarlet Runner Bean ( L.). <b>2017</b> , 8, 1891	25
1880	A Larger Chocolate Chip-Development of a 15K L. SNP Array to Create High-Density Linkage Maps. <b>2017</b> , 8, 2008	11
1879	Genetic Contribution to Alcohol Dependence: Investigation of a Heterogeneous German Sample of Individuals with Alcohol Dependence, Chronic Alcoholic Pancreatitis, and Alcohol-Related Cirrhosis. <b>2017</b> , 8,	8
1878	Molecular Genetic Influences on Normative and Problematic Alcohol Use in a Population-Based Sample of College Students. <b>2017</b> , 8, 30	18
1877	An Exploration of Gene-Gene Interactions and Their Effects on Hypertension. <b>2017</b> , 2017, 7208318	12
1876	A Genome-Wide Association Study of Vertical Cup-Disc Ratio in a Latino Population. 2017, 58, 87-95	15
1875	DNA and RNA-sequence based GWAS highlights membrane-transport genes as key modulators of milk lactose content. <b>2017</b> , 18, 968	32
1874	Genome-wide association study identifies a major gene for beech bark disease resistance in American beech (Fagus grandifolia Ehrh.). <b>2017</b> , 18, 547	11
1873	Highly accurate sequence imputation enables precise QTL mapping in Brown Swiss cattle. <b>2017</b> , 18, 999	10
1872	A novel TCF7L2 type 2 diabetes SNP identified from fine mapping in African American women. <b>2017</b> , 12, e0172577	7
1871	Whole genome structural analysis of Caribbean hair sheep reveals quantitative link to West African ancestry. <b>2017</b> , 12, e0179021	13
1870	Genome-wide analysis of the diversity and ancestry of Korean dogs. <b>2017</b> , 12, e0188676	6
1869	Genome-wide association study identifies a locus associated with rotator cuff injury. <b>2017</b> , 12, e0189317	14
1868	Genome-wide association analysis in dogs implicates 99 loci as risk variants for anterior cruciate ligament rupture. <b>2017</b> , 12, e0173810	25
1867	Genetic prediction of male pattern baldness. <b>2017</b> , 13, e1006594	59

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1866	Northeast African genomic variation shaped by the continuity of indigenous groups and Eurasian migrations. <b>2017</b> , 13, e1006976	32
1865	Identifying genetic variants that affect viability in large cohorts. <b>2017</b> , 15, e2002458	49
1864	Composite likelihood method for inferring local pedigrees. <b>2017</b> , 13, e1006963	15
1863	Genomic study and Medical Subject Headings enrichment analysis of early pregnancy rate and antral follicle numbers in Nelore heifers. <b>2017</b> , 95, 4796-4812	20
1862	Parkinson disease polygenic risk score is associated with Parkinson disease status and age at onset but not with alpha-synuclein cerebrospinal fluid levels. <b>2017</b> , 17, 198	35
1861	Risk and predictors of psoriasis in patients with breast cancer: a Swedish population-based cohort study. <b>2017</b> , 15, 154	8
1860	Clinical utility of the low-density Infinium QC genotyping Array in a genomics-based diagnostics laboratory. <b>2017</b> , 10, 57	1
1859	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. <b>2017</b> , 18, 146	27
1858	A putative causal relationship between genetically determined female body shape and posttraumatic stress disorder. <b>2017</b> , 9, 99	23
1857	Performance of gout definitions for genetic epidemiological studies: analysis of UK Biobank. <b>2017</b> , 19, 181	28
1856	The impact of methylation quantitative trait loci (mQTLs) on active smoking-related DNA methylation changes. <b>2017</b> , 9, 87	23
1855	Genome-wide meta-analysis in Japanese populations identifies novel variants at the TMC6-TMC8 and SIX3-SIX2 loci associated with HbA. <b>2017</b> , 7, 16147	25
1854	Unravelling the Genetic Diversity among Cassava Bemisia tabaci Whiteflies Using NextRAD Sequencing. <b>2017</b> , 9, 2958-2973	32
1853	Genetic Variants of RAMP2 and CLR are Associated with Stroke. <b>2017</b> , 24, 1267-1281	7
1852	Meta-analysis of sequence-based association studies across three cattle breeds reveals 25 QTL for fat and protein percentages in milk at nucleotide resolution. <b>2017</b> , 18, 853	34
1851	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. <b>2017</b> , 18, 910	26
1850	Genetic identification of a common collagen disease in puerto ricans via identity-by-descent mapping in a health system. <b>2017</b> , 6,	44
1849	Efficient genome-wide association in biobanks using topic modeling identifies multiple novel disease loci. <b>2017</b> , 23, 285-294	10

1848	Transformation of Summary Statistics from Linear Mixed Model Association on All-or-None Traits to Odds Ratio. <b>2018</b> , 208, 1397-1408	62
1847	Origins and genetic legacies of the Caribbean Taino. <b>2018</b> , 115, 2341-2346	45
1846	Alzheimer risk loci and associated neuropathology in a population-based study (Vantaa 85+). <b>2018</b> , 4, e211	13
1845	Effects of breed proportion and components of heterosis for semen traits in a composite cattle breed. <b>2018</b> , 135, 45-53	3
1844	A Genomic Reference Panel for. <b>2018</b> , 8, 1335-1346	11
1843	Identification of an Amino Acid Motif in HLA-DRI That Distinguishes Uveitis in Patients With Juvenile Idiopathic Arthritis. <b>2018</b> , 70, 1155-1165	28
1842	Genome-wide analysis of insomnia disorder. <b>2018</b> , 23, 2238-2250	39
1841	Genome-wide Association Study Identifies a Regulatory Variant of RGMA Associated With Opioid Dependence in European Americans. <b>2018</b> , 84, 762-770	41
1840	Natural variation in the parameters of innate immune cells is preferentially driven by genetic factors. <b>2018</b> , 19, 302-314	112
1839	Dysregulated invertebrate tropomyosin-dectin-1 interaction confers susceptibility to allergic diseases. <b>2018</b> , 3,	36
1838	Expression Quantitative Trait Locus Study of Bone Mineral Density GWAS Variants in Human Osteoclasts. <b>2018</b> , 33, 1044-1051	22
1837	Genome-Wide Association and Genomic Selection for Resistance to Amoebic Gill Disease in Atlantic Salmon. <b>2018</b> , 8, 1195-1203	67
1836	Genetics and Crime: Integrating New Genomic Discoveries Into Psychological Research About Antisocial Behavior. <b>2018</b> , 29, 791-803	37
1835	A transcriptome-wide association study identifies PALMD as a susceptibility gene for calcific aortic valve stenosis. <b>2018</b> , 9, 988	53
1834	The genetic assimilation in language borrowing inferred from Jing People. <b>2018</b> , 166, 638-648	6
1833	Assessment of the Genetic Architecture of Alzheimer's Disease Risk in Rate of Memory Decline. <b>2018</b> , 62, 745-756	29
1832	Incorporating Functional Genomic Information to Enhance Polygenic Signal and Identify Variants Involved in Gene-by-Environment Interaction for Young Adult Alcohol Problems. <b>2018</b> , 42, 413-423	8
1831	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <b>2018</b> , 9, 859	61

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1830	Molecular Genetic Analysis Subdivided by Adversity Exposure Suggests Etiologic Heterogeneity in Major Depression. <b>2018</b> , 175, 545-554	43
1829	Genetic risk factors for osteochondrosis in various horse breeds. <b>2018</b> , 50, 556-563	16
1828	Genome-wide Association Study of Dimensional Psychopathology Using Electronic Health Records. <b>2018</b> , 83, 1005-1011	16
1827	Genomic profiling in advanced stage non-small-cell lung cancer patients with platinum-based chemotherapy identifies germline variants with prognostic value in SMYD2. <b>2018</b> , 15, 21-31	8
1826	Genomics of habitat choice and adaptive evolution in a deep-sea fish. <b>2018</b> , 2, 680-687	16
1825	A large electronic-health-record-based genome-wide study of serum lipids. <b>2018</b> , 50, 401-413	127
1824	Common Variants in ALPL Gene Contribute to the Risk of Kidney Stones in the Han Chinese Population. <b>2018</b> , 22, 187-192	8
1823	Genetic validation of bipolar disorder identified by automated phenotyping using electronic health records. <b>2018</b> , 8, 86	14
1822	Polygenic risk score for schizophrenia is not strongly associated with the expression of specific genes or gene sets. <b>2018</b> , 28, 59-65	4
1821	A data-driven investigation of relationships between bipolar psychotic symptoms and schizophrenia genome-wide significant genetic loci. <b>2018</b> , 177, 468-475	8
1820	The Evolution of Polymorphic Hybrid Incompatibilities in House Mice. <b>2018</b> , 209, 845-859	27
1819	The effects of recent changes in breeding preferences on maintaining traditional Dutch chicken genomic diversity. <b>2018</b> , 121, 564-578	17
1818	Genomic variation in 3,010 diverse accessions of Asian cultivated rice. <b>2018</b> , 557, 43-49	582
1817	Biological Insights Into Muscular Strength: Genetic Findings in the UK Biobank. <b>2018</b> , 8, 6451	42
1816	Genomic signatures of fine-scale local selection in Atlantic salmon suggest involvement of sexual maturation, energy homeostasis and immune defence-related genes. <b>2018</b> , 27, 2560-2575	29
1815	Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. <b>2018</b> , 9, 1612	61
1814	Developing reduced SNP assays from whole-genome sequence data to estimate introgression in an organism with complex genetic patterns, the Iberian honeybee (). <b>2018</b> , 11, 1270-1282	20
1813	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <b>2018</b> , 9, 1470	226

1812	Signatures of negative selection in the genetic architecture of human complex traits. 2018, 50, 746-753	178
1811	Contrasting results from GWAS and QTL mapping on wing length in great reed warblers. <b>2018</b> , 18, 867-876	13
1810	Physiological and Genetic Adaptations to Diving in Sea Nomads. <b>2018</b> , 173, 569-580.e15	82
1809	Genome-wide association analyses identify new loci influencing intraocular pressure. <b>2018</b> , 27, 2205-2213	41
1808	Item-level analyses reveal genetic heterogeneity in neuroticism. <b>2018</b> , 9, 905	94
1807	Evolution of Sex Determination Loci in Atlantic Salmon. <b>2018</b> , 8, 5664	26
1806	Narrow-sense heritability estimation of complex traits using identity-by-descent information. <b>2018</b> , 121, 616-630	14
1805	Genome-wide analysis of adolescent psychotic-like experiences shows genetic overlap with psychiatric disorders. <b>2018</b> , 177, 416-425	46
1804	Whole-genome resequencing reveals signatures of selection and timing of duck domestication.  GigaScience, 2018, 7,	45
1803	Exome Sequencing in Children With Pulmonary Arterial Hypertension Demonstrates Differences Compared With Adults. <b>2018</b> , 11, e001887	65
1802	Genome evolution across 1,011 Saccharomyces cerevisiae isolates. <b>2018</b> , 556, 339-344	428
1801	A high-density SNP chip for genotyping great tit (Parus major) populations and its application to studying the genetic architecture of exploration behaviour. <b>2018</b> , 18, 877-891	25
1800	Comprehensive pathway analyses of schizophrenia risk loci point to dysfunctional postsynaptic signaling. <b>2018</b> , 199, 195-202	18
1799	Polygenic risk for schizophrenia and measured domains of cognition in individuals with psychosis and controls. <b>2018</b> , 8, 78	30
1798	A High-risk Haplotype for Premature Menopause in Childhood Cancer Survivors Exposed to Gonadotoxic Therapy. <b>2018</b> , 110, 895-904	13
1797	Analysis combining correlated glaucoma traits identifies five new risk loci for open-angle glaucoma. <b>2018</b> , 8, 3124	25
1796	PINK1 Phosphorylates MIC60/Mitofilin to Control Structural Plasticity of Mitochondrial Crista Junctions. <b>2018</b> , 69, 744-756.e6	58
1795	Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. <b>2018</b> , 50, 390-400	325

1794	Association Analysis Identifies New Risk Loci for Coal Workers' Pneumoconiosis in Han Chinese Men. <b>2018</b> , 163, 206-213	9
1793	Clinical, Social, and Genetic Factors Associated with Obesity at 12 Months of Age. <b>2018</b> , 196, 175-181.e7	4
1792	Genetic Risk Score Is Associated with Vertical Cup-to-Disc Ratio and Improves Prediction of Primary Open-Angle Glaucoma in Latinos. <b>2018</b> , 125, 815-821	12
1791	Genotype- and provenance-related variation in the leaf surface secondary metabolites of silver birch. <b>2018</b> , 48, 494-505	12
1790	The pharmacoepigenomics informatics pipeline defines a pathway of novel and known warfarin pharmacogenomics variants. <b>2018</b> , 19, 413-434	2
1789	A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth. <b>2018</b> , 8, 226	21
1788	Genomic variation in Pekin duck populations developed in three different countries as revealed by whole-genome data. <b>2018</b> , 49, 132-136	7
1787	Genomic associations with bill length and disease reveal drift and selection across island bird populations. <b>2018</b> , 2, 22-36	14
1786	A genome-wide association study in the Japanese population identifies the 12q24 locus for habitual coffee consumption: The J-MICC Study. <b>2018</b> , 8, 1493	22
1785	Genome-wide association study of Hirschsprung disease detects a novel low-frequency variant at the RET locus. <b>2018</b> , 26, 561-569	11
1784	Genome-wide associations identify novel candidate loci associated with genetic susceptibility to tuberculosis in wild boar. <b>2018</b> , 8, 1980	11
1783	A rapid epistatic mixed-model association analysis by linear retransformations of genomic estimated values. <b>2018</b> , 34, 1817-1825	9
1782	Causal associations between risk factors and common diseases inferred from GWAS summary data. <b>2018</b> , 9, 224	346
1781	A Large Panel of Drosophila simulans Reveals an Abundance of Common Variants. <b>2018</b> , 10, 189-206	23
1780	Integration of Multi-omics Data from Mouse Diversity Panel Highlights Mitochondrial Dysfunction in Non-alcoholic Fatty Liver Disease. <b>2018</b> , 6, 103-115.e7	69
1779	Polygenic Risk Score Prediction of Alcohol Dependence Symptoms Across Population-Based and Clinically Ascertained Samples. <b>2018</b> , 42, 520-530	14
1778	QTL mapping and GWAS reveal candidate genes controlling capsaicinoid content in Capsicum. <b>2018</b> , 16, 1546	70
1777	Methylation-based enrichment facilitates low-cost, noninvasive genomic scale sequencing of populations from feces. <b>2018</b> , 8, 1975	39

1776	Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap. <b>2018</b> , 359, 693-697	547
1775	Epigenome-wide association study of DNA methylation in narcolepsy: an integrated genetic and epigenetic approach. <b>2018</b> , 41,	12
1774	The genomic ancestry, landscape genetics and invasion history of introduced mice in New Zealand. <b>2018</b> , 5, 170879	12
1773	Genome-wide association study of self-reported food reactions in Japanese identifies shrimp and peach specific loci in the HLA-DR/DQ gene region. <b>2018</b> , 8, 1069	18
1772	Uncovering Genomic Regions Associated with Infections in Wild Populations of the Tsetse Fly. <b>2018</b> , 8, 887-897	5
1771	Reconstructing the demographic history of the Himalayan and adjoining populations. <b>2018</b> , 137, 129-139	11
1770	Prediction of inherited genomic susceptibility to 20 common cancer types by a supervised machine-learning method. <b>2018</b> , 115, 1322-1327	18
1769	A genome-wide association study of wheat yield and quality-related traits in southwest China. <b>2018</b> , 38, 1	30
1768	Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate. <b>2018</b> , 61, 241-247	10
1767	Association analysis in over 329,000 individuals identifies 116 independent variants influencing neuroticism. <b>2018</b> , 50, 6-11	202
1766	Population Genomics Reveals Genetic Divergence and Adaptive Differentiation of Chinese Sea Bass (Lateolabrax maculatus). <b>2018</b> , 20, 45-59	16
1765	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. <b>2018</b> , 8, 9	48
1764	Multi-allelic exact tests for Hardy-Weinberg equilibrium that account for gender. <b>2018</b> , 18, 461-473	12
1763	The Comoros Show the Earliest Austronesian Gene Flow into the Swahili Corridor. <b>2018</b> , 102, 58-68	17
1762	Genetics of the human face: Identification of large-effect single gene variants. 2018, 115, E676-E685	33
1761	Pharmacogenomic survey of Qatari populations using whole-genome and exome sequences. <b>2018</b> , 18, 590-600	11
1760	High Levels of Copy Number Variation of Ampliconic Genes across Major Human Y Haplogroups. <b>2018</b> , 10, 1333-1350	10
1759	A survey of functional genomic variation in domesticated chickens. <b>2018</b> , 50, 17	21

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1758	behavioral traits. <b>2018</b> , 10, 24	2
1757	Characterization of the enhancer and promoter landscape of inflammatory bowel disease from human colon biopsies. <b>2018</b> , 9, 1661	41
1756	FarmCPUpp: Efficient large-scale genomewide association studies. <b>2018</b> , 2, e00053	13
1755	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. <b>2018</b> , 102, 874-889	38
1754	Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. <b>2018</b> , 50, 737-745	131
1753	Whole-Exome Sequencing Reveals Uncaptured Variation and Distinct Ancestry in the Southern African Population of Botswana. <b>2018</b> , 102, 731-743	25
1752	Haplotype Sharing Provides Insights into Fine-Scale Population History and Disease in Finland. <b>2018</b> , 102, 760-775	34
1751	Taking advantage from phenotype variability in a local animal genetic resource: identification of genomic regions associated with the hairless phenotype in Casertana pigs. <b>2018</b> , 49, 321-325	14
1750	Genomic investigation of porcine periweaning failure to thrive syndrome (PFTS). 2018, 183, 95	3
1749	Genetic Risk Score Is Associated With Prevalence of Advanced Neoplasms in a Colorectal Cancer Screening Population. <b>2018</b> , 155, 88-98.e10	35
1748	Efficient analysis of large-scale genome-wide data with two R packages: bigstatsr and bigsnpr. <b>2018</b> , 34, 2781-2787	83
1747	Genome-wide association analysis identifies new candidate risk loci for familial intracranial aneurysm in the French-Canadian population. <b>2018</b> , 8, 4356	10
1746	Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. <b>2018</b> , 360, 548-552	83
1745	Height and overall cancer risk and mortality: evidence from a Mendelian randomisation study on 310,000 UK Biobank participants. <b>2018</b> , 118, 1262-1267	27
1744	Polygenic Risk Scores in Clinical Psychology: Bridging Genomic Risk to Individual Differences. <b>2018</b> , 14, 119-157	64
1743	Rare variants in 2 German families with Alzheimer disease. <b>2018</b> , 4, e224	9
1742	Genetic predisposition in anti-LGI1 and anti-NMDA receptor encephalitis. 2018, 83, 863-869	82
1741	Polygenic signal for symptom dimensions and cognitive performance in patients with chronic schizophrenia. <b>2018</b> , 12, 11-19	16

1740	Genome-wide Analyses Identify KIF5A as a Novel ALS Gene. 2018, 97, 1268-1283.e6	296
1739	Strong selection during the last millennium for African ancestry in the admixed population of Madagascar. <b>2018</b> , 9, 932	33
1738	pedigreejs: a web-based graphical pedigree editor. <b>2018</b> , 34, 1069-1071	5
1737	Genome-wide scan of depressive symptomatology in two representative cohorts in the United States and the United Kingdom. <b>2018</b> , 100, 63-70	3
1736	Evaluating the genetic susceptibility to peer reported bullying behaviors. <b>2018</b> , 263, 193-198	2
1735	POLARIS: Polygenic LD-adjusted risk score approach for set-based analysis of GWAS data. <b>2018</b> , 42, 366-377	16
1734	A genome-wide association study of growth and fatness traits in two pig populations with different genetic backgrounds. <b>2018</b> , 96, 806-816	22
1733	Kernel machine SNP set analysis provides new insight into the association between obesity and polymorphisms located on the chromosomal 16q.12.2 region: Tehran Lipid and Glucose Study. <b>2018</b> , 658, 146-151	5
1732	Comprehensive genetic study of fatty acids helps explain the role of noncoding inflammatory bowel disease associated SNPs and fatty acid metabolism in disease pathogenesis. <b>2018</b> , 130, 1-10	5
1731	Genome-wide association identifies a novel locus for delirium risk. <b>2018</b> , 68, 160.e9-160.e14	9
1730	Targeted resequencing reveals genomic signatures of barley domestication. 2018, 218, 1247-1259	48
1729	Largest GWAS of PTSD (N=20 070) yields genetic overlap with schizophrenia and sex differences in heritability. <b>2018</b> , 23, 666-673	248
1728	Critical Issues in the Inclusion of Genetic and Epigenetic Information in Prevention and Intervention Trials. <b>2018</b> , 19, 58-67	9
1727	Genetic risk for schizophrenia and psychosis in Alzheimer disease. <b>2018</b> , 23, 963-972	35
1726	A genome-wide gene-by-trauma interaction study of alcohol misuse in two independent cohorts identifies PRKG1 as a risk locus. <b>2018</b> , 23, 154-160	32
1725	HDL Cholesterol, LDL Cholesterol, and Triglycerides as Risk Factors for CKD: A Mendelian Randomization Study. <b>2018</b> , 71, 166-172	59
1724	Genome-wide association study identifies inversion in the locus to modify risk for alcoholic and non-alcoholic chronic pancreatitis. <b>2018</b> , 67, 1855-1863	54
1723	A low-frequency haplotype spanning SLX4/FANCP constitutes a new risk locus for early-onset breast cancer (. <b>2018</b> , 142, 757-768	4

1722	Genetic correlates of insight in schizophrenia. <b>2018</b> , 195, 290-297	10
1721	Susceptibility Loci-Associated Cutaneous Squamous Cell Carcinoma Invasiveness. <b>2018</b> , 138, 557-561	9
1720	Robust symptom networks in recurrent major depression across different levels of genetic and environmental risk. <b>2018</b> , 227, 313-322	24
1719	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. <b>2018</b> , 142, 540-546	21
1718	Applying landscape genomic tools to forest management and restoration of Hawaiian koa () in a changing environment. <b>2018</b> , 11, 231-242	30
1717	Genetic risk scores and family history as predictors of schizophrenia in Nordic registers. <b>2018</b> , 48, 1201-1208	18
1716	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <b>2018</b> , 84, 138-147	48
1715	Single-nucleotide polymorphism data describe contemporary population structure and diversity in allochronic lineages of pink salmon (Oncorhynchus gorbuscha). <b>2018</b> , 75, 987-997	7
1714	Phylogenetic Relationships, Breeding Implications, and Cultivation History of Hawaiian Taro (Colocasia Esculenta) Through Genome-Wide SNP Genotyping. <b>2018</b> , 109, 272-282	10
1713	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. <b>2018</b> , 48, 1055-1067	48
1712	Associations between alcohol dehydrogenase genes and alcohol use across early and middle adolescence: Moderation Preventive intervention. <b>2018</b> , 30, 297-313	9
1711	Theory, practice, and conservation in the age of genomics: The Galþagos giant tortoise as a case study. <b>2018</b> , 11, 1084-1093	21
1710	Association Between Schizophrenia-Related Polygenic Liability and the Occurrence and Level of Mood-Incongruent Psychotic Symptoms in Bipolar Disorder. <b>2018</b> , 75, 28-35	66
1709	Genome-wide gene-environment interaction in depression: A systematic evaluation of candidate genes: The childhood trauma working-group of PGC-MDD. <b>2018</b> , 177, 40-49	43
1708	A common variant in ARHGEF10 alters delta-6 desaturase activity and influence susceptibility to hypertriglyceridemia. <b>2018</b> , 12, 311-320.e3	8
1707	Urban landscape genomics identifies fine-scale gene flow patterns in an avian invasive. <b>2018</b> , 120, 138-153	13
1706	Metabolome-wide association studies for agronomic traits of rice. <b>2018</b> , 120, 342-355	19
1705	Investigating the genetic architecture of dementia with Lewy bodies: a two-stage genome-wide association study. <b>2018</b> , 17, 64-74	121

1704	Effect of minor allele frequency on the number of single nucleotide polymorphisms needed for accurate parentage assignment: A methodology illustrated using Atlantic salmon. <b>2018</b> , 49, 1368-1372	10
1703	daTALbase: A Database for Genomic and Transcriptomic Data Related to TAL Effectors. <b>2018</b> , 31, 471-480	9
1702	Analysis of Copy Number Variants on Chromosome 21 in Down Syndrome-Associated Congenital Heart Defects. <b>2018</b> , 8, 105-111	10
1701	Genome-wide association study for white coat effect in Japanese middle-aged to elderly people: The HOMED-BP study. <b>2018</b> , 40, 363-369	2
1700	Genetic analysis of impulsive personality traits: Examination of a priori candidates and genome-wide variation. <b>2018</b> , 259, 398-404	23
1699	Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. <b>2018</b> , 137, 1027-1038	133
1698	Sulfasalazine-Induced Agranulocytosis Is Associated With the Human Leukocyte Antigen Locus. <b>2018</b> , 103, 843-853	12
1697	Evolutionary significance of selected EDAR variants in Tibetan high-altitude adaptations. <b>2018</b> , 61, 68-78	1
1696	Targeted sequencing identifies a missense variant in the BEST3 gene associated with antihypertensive response to hydrochlorothiazide. <b>2018</b> , 28, 251-255	5
1695	The new era of whole-exome sequencing in congenital heart disease: brand-new insights into rare pathogenic variants. <b>2018</b> , 10, S1923-S1929	6
1694	GRIPT: a novel case-control analysis method for Mendelian disease gene discovery. <b>2018</b> , 19, 203	2
1693	Expression reflects population structure. <b>2018</b> , 14, e1007841	9
1692	Polygenic risk score for schizophrenia is more strongly associated with ancestry than with schizophrenia. <b>2018</b> , 28, 85-89	68
1691	Misconceptions Regarding the Role of Introgression in the Origin of subsp <b>2018</b> , 9, 1750	5
1690	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. <b>2018</b> , 210, 1125-1138	24
1689	Genetic and genomic stability across lymphoblastoid cell line expansions. <b>2018</b> , 11, 558	6
1688	Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. <b>2018</b> , 8, 3255-3267	17
1687	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. <b>2018</b> , 9, 4674	19

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1686	Genomes reveal marked differences in the adaptive evolution between orangutan species. <b>2018</b> , 19, 193	5
1685	Frailty Index associates with GRIN2B in two representative samples from the United States and the United Kingdom. <b>2018</b> , 13, e0207824	4
1684	Hotspots of recent hybridization between pigs and wild boars in Europe. <b>2018</b> , 8, 17372	25
1683	Influence of Fetal and Maternal Genetic Susceptibility to Obesity on Birthweight in African Ancestry Populations. <b>2018</b> , 9, 511	5
1682	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <b>2018</b> , 50, 58	41
1681	Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. <b>2018</b> , 8, 252	34
1680	Exploring the genetic basis of gene transcript abundance and metabolite levels in loblolly pine (Pinus taeda L.) using association mapping and network construction. <b>2018</b> , 19, 100	8
1679	Signatures of selection and environmental adaptation across the goat genome post-domestication. <b>2018</b> , 50, 57	69
1678	Functional SNP panel for parentage assessment and assignment in worldwide goat breeds. <b>2018</b> , 50, 55	10
1677	Genome-wide patterns of homozygosity provide clues about the population history and adaptation of goats. <b>2018</b> , 50, 59	36
1676	Population genomics of grey wolves and wolf-like canids in North America. 2018, 14, e1007745	26
1675	The Genomic Formation of South and Central Asia. 2018,	15
1674	Understanding the role of bitter taste perception in coffee, tea and alcohol consumption through Mendelian randomization. <b>2018</b> , 8, 16414	22
1673	Development and Validation of 58K SNP-Array and High-Density Linkage Map in Nile Tilapia (). <b>2018</b> , 9, 472	33
1672	Computational Tools for Population Genomics. <b>2018</b> , 127-160	2
1671	Association of Copy Number Variation at Intron 3 of With Navel Length in. <b>2018</b> , 9, 627	9
1670	Interleukin-1 Receptor Antagonist Is Associated With Pediatric Acute Respiratory Distress Syndrome and Worse Outcomes in Children With Acute Respiratory Failure. <b>2018</b> , 19, 930-938	15
1669	Identification of deleterious and regulatory genomic variations in known asthma loci. <b>2018</b> , 19, 248	4

1668	Genetic effects of BDKRB2 and KNG1 on deep venous thrombosis after orthopedic surgery and the potential mediator. <b>2018</b> , 8, 17332	1
1667	GWAS identifies 14 loci for device-measured physical activity and sleep duration. <b>2018</b> , 9, 5257	123
1666	Origin and age of the causative mutations in KLC2, IMPA1, MED25 and WNT7A unravelled through Brazilian admixed populations. <b>2018</b> , 8, 16552	3
1665	Genetic ancestry, admixture and health determinants in Latin America. <b>2018</b> , 19, 861	45
1664	Meta-analysis of Immunochip data of four autoimmune diseases reveals novel single-disease and cross-phenotype associations. <b>2018</b> , 10, 97	46
1663	Latin Americans show wide-spread Converso ancestry and imprint of local Native ancestry on physical appearance. <b>2018</b> , 9, 5388	65
1662	Genetic Determinants of Telomere Length in African American Youth. <b>2018</b> , 8, 13265	15
1661	A novel deletion in KRT75L4 mediates the frizzle trait in a Chinese indigenous chicken. <b>2018</b> , 50, 68	4
1660	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. <b>2018</b> , 9, 5407	37
1659	AdaptMap: exploring goat diversity and adaptation. <b>2018</b> , 50, 61	26
1659 1658	AdaptMap: exploring goat diversity and adaptation. <b>2018</b> , 50, 61  Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. <b>2018</b> , 362, 1309-1313	<ul><li>26</li><li>97</li></ul>
1658	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. 2018,	
1658	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. <b>2018</b> , 362, 1309-1313	97
1658 1657	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. 2018, 362, 1309-1313  The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. 2018, 103, 918-929	97
1658 1657 1656	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. 2018, 362, 1309-1313  The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. 2018, 103, 918-929  The association between neonatal vitamin D status and risk of schizophrenia. 2018, 8, 17692  Genotyping-by-sequencing identifies date palm clone preference in agronomics of the State of	97 22 49
1658 1657 1656	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. 2018, 362, 1309-1313  The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. 2018, 103, 918-929  The association between neonatal vitamin D status and risk of schizophrenia. 2018, 8, 17692  Genotyping-by-sequencing identifies date palm clone preference in agronomics of the State of Qatar. 2018, 13, e0207299  Genomic characterization of the Braque FranBis type PyrBBs dog and relationship with other	97 22 49
1658 1657 1656 1655	Multiproxy evidence highlights a complex evolutionary legacy of maize in South America. 2018, 362, 1309-1313  The Genetic Ancestry of Modern Indus Valley Populations from Northwest India. 2018, 103, 918-929  The association between neonatal vitamin D status and risk of schizophrenia. 2018, 8, 17692  Genotyping-by-sequencing identifies date palm clone preference in agronomics of the State of Qatar. 2018, 13, e0207299  Genomic characterization of the Braque FranBis type PyrBBs dog and relationship with other breeds. 2018, 13, e0208548	97 22 49 5

1650	Genome-wide association study reveals novel genetic locus associated with intra-individual variability in response time. <b>2018</b> , 8, 207	8
1649	Genomic Analyses of Human European Diversity at the Southwestern Edge: Isolation, African Influence and Disease Associations in the Canary Islands. <b>2018</b> , 35, 3010-3026	11
1648	Evaluation of Common Variants in Matrix Metalloproteinase-9 Gene with Lumbar Disc Herniation in Han Chinese Population. <b>2018</b> , 22, 622-629	3
1647	Clinical and Genetic Determinants of Varicose Veins. <b>2018</b> , 138, 2869-2880	54
1646	Burden Testing of Rare Variants Identified through Exome Sequencing via Publicly Available Control Data. <b>2018</b> , 103, 522-534	67
1645	Genome-wide association study using haplotype alleles for the evaluation of reproductive traits in Nelore cattle. <b>2018</b> , 13, e0201876	6
1644	The interplay between externalizing disorders polygenic risk scores and contextual factors on the development of marijuana use disorders. <b>2018</b> , 191, 365-373	8
1643	2D association and integrative omics analysis in rice provides systems biology view in trait analysis. <b>2018</b> , 1, 153	3
1642	Population structure, genetic diversity and selection signatures within seven indigenous Pakistani goat populations. <b>2018</b> , 49, 592-604	13
1641	Genome-Wide Association Study Reveals Genetic Link between Diarrhea-Associated Entamoeba histolytica Infection and Inflammatory Bowel Disease. <b>2018</b> , 9,	16
1640	Multiple genomic regions influence root morphology and seedling growth in cultivated sunflower (Helianthus annuus L.) under well-watered and water-limited conditions. <b>2018</b> , 13, e0204279	11
1639	Conditional and interaction gene-set analysis reveals novel functional pathways for blood pressure. <b>2018</b> , 9, 3768	23
1638	Genome-wide burden and association analyses implicate copy number variations in asthma risk among children and young adults from Latin America. <b>2018</b> , 8, 14475	3
1637	Renal compartment-specific genetic variation analyses identify new pathways in chronic kidney disease. <b>2018</b> , 24, 1721-1731	94
1636	Relationships between estimated autozygosity and complex traits in the UK Biobank. <b>2018</b> , 14, e1007556	14
1635	Meta-Analysis of Genetic Influences on Initial Alcohol Sensitivity. <b>2018</b> , 42, 2349-2359	12
1634	TIMP3 and TIMP1 are risk genes for bicuspid aortic valve and aortopathy in Turner syndrome. <b>2018</b> , 14, e1007692	32
1633	Direct-to-consumer DNA testing of 6,000 dogs reveals 98.6-kb duplication associated with blue eyes and heterochromia in Siberian Huskies. <b>2018</b> , 14, e1007648	11

1632	The accuracy of LD Score regression as an estimator of confounding and genetic correlations in genome-wide association studies. <b>2018</b> , 42, 783-795	19
1631	Genome-wide analysis of polymorphism & odium interaction effect on blood pressure identifies a novel 3'-BCL11B gene desert locus. <b>2018</b> , 8, 14162	8
1630	Genetic variation in the locus is associated with erectile dysfunction. <b>2018</b> , 115, 11018-11023	14
1629	Genetic signature to provide robust risk assessment of psoriatic arthritis development in psoriasis patients. <b>2018</b> , 9, 4178	61
1628	Genotype effects contribute to variation in longitudinal methylome patterns in older people. <b>2018</b> , 10, 75	21
1627	Identification of a two-SNP PLA2R1 Haplotype and HLA-DRB1 Alleles as Primary Risk Associations in Idiopathic Membranous Nephropathy. <b>2018</b> , 8, 15576	7
1626	Exome sequencing in large, multiplex bipolar disorder families from Cuba. <b>2018</b> , 13, e0205895	11
1625	Imputation-Based Whole-Genome Sequence Association Study Reveals Constant and Novel Loci for Hematological Traits in a Large-Scale Swine F Resource Population. <b>2018</b> , 9, 401	16
1624	A striking new species of leaf warbler from the Lesser Sundas as uncovered through morphology and genomics. <b>2018</b> , 8, 15646	5
1623	Tissue-specific pathways and networks underlying sexual dimorphism in non-alcoholic fatty liver disease. <b>2018</b> , 9, 46	40
1622	Genetic diversities and population structures of four popular Myanmar local cattle breeds. <b>2018</b> , 89, 1648-1655	3
1621	Genetic determinants of childhood and adult height associated with osteosarcoma risk. <b>2018</b> , 124, 3742-3752	11
1620	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. <b>2018</b> , 137, 847-862	25
1619	Genome-wide association studies for corneal and refractive astigmatism in UK Biobank demonstrate a shared role for myopia susceptibility loci. <b>2018</b> , 137, 881-896	25
1618	Analysis of genetic and nongenetic factors influencing triglycerides-lowering drug effects based on paired observations. <b>2018</b> , 12, 46	3
1617	Assessment of shared alleles in drought-associated candidate genes among southern California white oak species (Quercus sect. Quercus). <b>2018</b> , 19, 88	9
1616	GBS-derived SNP catalogue unveiled wide genetic variability and geographical relationships of Italian olive cultivars. <b>2018</b> , 8, 15877	35
1615	Evaluation of whole exome sequencing as an alternative to BeadChip and whole genome sequencing in human population genetic analysis. <b>2018</b> , 19, 778	7

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1614	Applying polygenic risk scoring for psychiatric disorders to a large family with bipolar disorder and major depressive disorder. <b>2018</b> , 1, 163	11
1613	Incomplete lineage sorting rather than hybridization explains the inconsistent phylogeny of the wisent. <b>2018</b> , 1, 169	40
1612	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <b>2018</b> , 19, 168	19
1611	An atlas of genetic associations in UK Biobank. <b>2018</b> , 50, 1593-1599	282
1610	A histone acetylome-wide association study of Alzheimer's disease identifies disease-associated H3K27ac differences in the entorhinal cortex. <b>2018</b> , 21, 1618-1627	7 <sup>2</sup>
1609	Exome-wide analysis of bi-allelic alterations identifies a Lynch phenotype in The Cancer Genome Atlas. <b>2018</b> , 10, 69	4
1608	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. <b>2018</b> , 21, 1482-1492	48
1607	Accurate Genomic Prediction of Human Height. <b>2018</b> , 210, 477-497	67
1606	Rare genetic variation in mitochondrial pathways influences the risk for Parkinson's disease. <b>2018</b> , 33, 1591-1600	30
1605	A genetic risk score and number of myopic parents independently predict myopia. <b>2018</b> , 38, 492-502	25
1604	Genomic evidence for asymmetric introgression by sexual selection in the common wall lizard. <b>2018</b> , 27, 4213-4224	15
1603	Novel genome and genome-wide SNPs reveal early fragmentation effects in an edge-tolerant songbird population across an urbanized tropical metropolis. <b>2018</b> , 8, 12804	8
1602	NT5C2 germline variants alter thiopurine metabolism and are associated with acquired NT5C2 relapse mutations in childhood acute lymphoblastic leukaemia. <b>2018</b> , 32, 2527-2535	8
1601	The genetic architecture of socially-affected traits: a GWAS for direct and indirect genetic effects on survival time in laying hens showing cannibalism. <b>2018</b> , 50, 38	10
1600	OBSOLETE: Bioinformatics Principles for Deciphering Cardiovascular Diseases. 2018,	1
1599	Association of schizophrenia polygenic risk score with manic and depressive psychosis in bipolar disorder. <b>2018</b> , 8, 188	28
1598	CisPi: a transcriptomic score for disclosing cis-acting disease-associated lincRNAs. <b>2018</b> , 34, i664-i670	O
1597	Genome-wide meta-analysis and replication studies in multiple ethnicities identify novel adolescent idiopathic scoliosis susceptibility loci. <b>2018</b> , 27, 3986-3998	13

1596	Analysis of evolution and genetic diversity of sweetpotato and its related different polyploidy wild species I. trifida using RAD-seq. <b>2018</b> , 18, 181	13
1595	Prediction model for pancreatic cancer risk in the general Japanese population. 2018, 13, e0203386	15
1594	Rigor and reproducibility in genetic research on eating disorders. <b>2018</b> , 51, 593-607	11
1593	Detecting past and ongoing natural selection among ethnically Tibetan women at high altitude in Nepal. <b>2018</b> , 14, e1007650	24
1592	Genome-Wide Characterization of Selection Signatures and Runs of Homozygosity in Ugandan Goat Breeds. <b>2018</b> , 9, 318	46
1591	The Influence of Genetic Variation on Social Disposition, Romantic Relationships and Social Networks: a Replication Study. <b>2018</b> , 4, 400-422	14
1590	Inbreeding and runs of homozygosity before and after genomic selection in North American Holstein cattle. <b>2018</b> , 19, 98	61
1589	Can Deep Learning Improve Genomic Prediction of Complex Human Traits?. <b>2018</b> , 210, 809-819	79
1588	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. <b>2018</b> , 50, 1483-1493	34
1587	Genome-wide association analyses identify 39 new susceptibility loci for diverticular disease. <b>2018</b> , 50, 1359-1365	49
1586	Rare gene deletions in genetic generalized and Rolandic epilepsies. <b>2018</b> , 13, e0202022	3
1585	A Nonsynonymous Change in Adhesion G Protein Coupled Receptor L3 Associated With Risk for Equine Degenerative Myeloencephalopathy in the Caspian Horse. <b>2018</b> , 70, 96-100	4
1584	Genetic polymorphisms of GZMB and vitiligo: A genetic association study based on Chinese Han population. <b>2018</b> , 8, 13001	12
1583	Genome-wide association study reveals the locus responsible for microtia in Valle del Belice sheep breed. <b>2018</b> , 49, 636-640	6
1582	Multitrait genome association analysis identifies new susceptibility genes for human anthropometric variation in the GCAT cohort. <b>2018</b> , 55, 765-778	12
1581	PRS-on-Spark (PRSoS): a novel, efficient and flexible approach for generating polygenic risk scores. <b>2018</b> , 19, 295	10
1580	Population genetic analysis of aquaculture salmonid populations in China using a 57K rainbow trout SNP array. <b>2018</b> , 13, e0202582	4
1579	Evaluating recovery potential of the northern white rhinoceros from cryopreserved somatic cells. <b>2018</b> , 28, 780-788	23

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1578	Human activities and landscape features interact to closely define the distribution and dispersal of an urban commensal. <b>2018</b> , 11, 1598-1608	12
1577	Mitochondrial peptidase loss-of-function in childhood cerebellar atrophy. <b>2018</b> , 55, 599-606	22
1576	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <b>2018</b> , 50, 834-848	135
1575	Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. <b>2018</b> , 10, 220-238	8
1574	Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. <b>2018</b> , 102, 1048-1061	83
1573	Thirty loci identified for heart rate response to exercise and recovery implicate autonomic nervous system. <b>2018</b> , 9, 1947	29
1572	Brain APOE expression quantitative trait loci-based association study identified one susceptibility locus for Alzheimer's disease by interacting with APOE 4. <b>2018</b> , 8, 8068	10
1571	Cleaner fish escape salmon farms and hybridize with local wrasse populations. <b>2018</b> , 5, 171752	29
1570	Common genetic variation in the autoimmune regulator (AIRE) locus is associated with autoimmune Addison's disease in Sweden. <b>2018</b> , 8, 8395	14
1569	Using Genomic Data to Find Disease-Modifying Loci in Huntington's Disease (HD). <b>2018</b> , 1780, 443-461	1
1568	Genetic susceptibility of postmenopausal osteoporosis on sulfide quinone reductase-like gene. <b>2018</b> , 29, 2041-2047	8
1567	Japanese GWAS identifies variants for bust-size, dysmenorrhea, and menstrual fever that are eQTLs for relevant protein-coding or long non-coding RNAs. <b>2018</b> , 8, 8502	9
1566	Genome wide analysis of rare copy number variations in alcohol abuse or dependence. <b>2018</b> , 103, 212-218	5
1565	Genetic variants in the HLA class II region associated with risk of cutaneous squamous cell carcinoma. <b>2018</b> , 67, 1123-1133	8
1564	Exploring the role of low-frequency and rare exonic variants in alcohol and tobacco use. <b>2018</b> , 188, 94-101	7
1563	Gene-Centric Analysis of Preeclampsia Identifies Maternal Association at. <b>2018</b> , 72, 408-416	20
1562	Bioinformatics Principles for Deciphering Cardiovascular Diseases. <b>2018</b> , 273-292	2
1561	Genomic signatures of different adaptations to environmental stimuli between wild and cultivated L. <b>2018</b> , 5, 34	20

1560	Age at first birth in women is genetically associated with increased risk of schizophrenia. <b>2018</b> , 8, 10168	11
1559	An association between differential expression and genetic divergence in the Patagonian olive mouse (Abrothrix olivacea). <b>2018</b> , 27, 3274	17
1558	Two MC1R loss-of-function alleles in cream-coloured Australian Cattle Dogs and white Huskies. <b>2018</b> , 49, 284-290	12
1557	Evolutionary genomic dynamics of Peruvians before, during, and after the Inca Empire. 2018, 115, E6526-E653	<b>35</b> 68
1556	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <b>2018</b> , 50, 956-967	239
1555	Genetic association and functional analysis of rs7903456 in FAM35A gene and hyperuricemia: a population based study. <b>2018</b> , 8, 9579	3
1554	Pharmacogenetic evaluation of a DISP1 gene variant in antidepressant treatment of obsessive-compulsive disorder. <b>2018</b> , 33, e2659	6
1553	NUDT15 codon 139 is the best pharmacogenetic marker for predicting thiopurine-induced severe adverse events in Japanese patients with inflammatory bowel disease: a multicenter study. <b>2018</b> , 53, 1065-1078	58
1552	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. <b>2018</b> , 50, 920-927	312
1551	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <b>2018</b> , 50, 912-919	475
1550	Computing Empirical P-Values for Estimating Gene-Gene Interactions in Genome-Wide Association Studies: A Parallel Computing Approach. <b>2018</b> ,	
1549	Genetic contributions to lupus nephritis in a multi-ethnic cohort of systemic lupus erythematous patients. <b>2018</b> , 13, e0199003	23
1548	Project MinE: study design and pilot analyses of a large-scale whole-genome sequencing study in amyotrophic lateral sclerosis. <b>2018</b> , 26, 1537-1546	75
1547	Inferring Identical-by-Descent Sharing of Sample Ancestors Promotes High-Resolution Relative Detection. <b>2018</b> , 103, 30-44	19
1546	Consortium-based genome-wide meta-analysis for childhood dental caries traits. 2018, 27, 3113-3127	20
1545	Field synopsis and systematic meta-analyses of genetic association studies in isolated dystonia. <b>2018</b> , 57, 50-57	6
1544	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. <b>2018</b> , 8, 11424	28
1543	Exploring Cuba's population structure and demographic history using genome-wide data. <b>2018</b> , 8, 11422	18

1542	Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <b>2018</b> , 361, 511-516	36
1541	Collective interaction effects associated with mammalian behavioral traits reveal genetic factors connecting fear and hemostasis. <b>2018</b> , 18, 175	
1540	Mediation analysis to understand genetic relationships between habitual coffee intake and gout. <b>2018</b> , 20, 135	7
1539	Genome-wide association study in Guillain-Barr syndrome. <b>2018</b> , 323, 109-114	9
1538	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <b>2018</b> , 9, 3121	74
1537	Signatures of human-commensalism in the house sparrow genome. <b>2018</b> , 285,	32
1536	Comparative Genome-Wide-Association Mapping Identifies Common Loci Controlling Root System Architecture and Resistance to in Pea. <b>2017</b> , 8, 2195	27
1535	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <b>2018</b> , 50, 1112-1121	950
1534	Design and evaluation of a sequence capture system for genome-wide SNP genotyping in highly heterozygous plant genomes: a case study with a keystone Neotropical hardwood tree genome. <b>2018</b> , 25, 535-545	7
1533	Two HLA Class II Gene Variants Are Independently Associated with Pediatric Osteosarcoma Risk. <b>2018</b> , 27, 1151-1158	3
1532	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <b>2018</b> , 9, 2941	262
1531	Human genetic variants and age are the strongest predictors of humoral immune responses to common pathogens and vaccines. <b>2018</b> , 10, 59	64
1530	The genomic impact of historical hybridization with massive mitochondrial DNA introgression. <b>2018</b> , 19, 91	39
1529	Capturing variation in (Fabaceae): Development and utility of an exome capture array for lentil. <b>2018</b> , 6, e01165	27
1528	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. <b>2018</b> , 9, 2905	36
1527	Analysis of shared heritability in common disorders of the brain. <b>2018</b> , 360,	666
1526	Regional genetic differences among Japanese populations and performance of genotype imputation using whole-genome reference panel of the Tohoku Medical Megabank Project. <b>2018</b> , 19, 551	9
1525	A multi-ethnic meta-analysis confirms the association of rs6570507 with adolescent idiopathic scoliosis. <b>2018</b> , 8, 11575	21

1524	SNPrune: an efficient algorithm to prune large SNP array and sequence datasets based on high linkage disequilibrium. <b>2018</b> , 50, 34	15
1523	The molecular genetic basis of herbivory between butterflies and their host plants. <b>2018</b> , 2, 1418-1427	36
1522	Modifier locus mapping of a transgenic F2 mouse population identifies CCDC115 as a novel aggressive prostate cancer modifier gene in humans. <b>2018</b> , 19, 450	6
1521	Population Structure and Genomic Breed Composition in an Angus-Brahman Crossbred Cattle Population. <b>2018</b> , 9, 90	11
1520	Joint Genomic Prediction of Canine Hip Dysplasia in UK and US Labrador Retrievers. 2018, 9, 101	6
1519	Genome-Wide Association Studies Identify Candidate Genes for Coat Color and Mohair Traits in the Iranian Markhoz Goat. <b>2018</b> , 9, 105	29
1518	Jointly Modelling Single Nucleotide Polymorphisms With Longitudinal and Time-to-Event Trait: An Application to Type 2 Diabetes and Fasting Plasma Glucose. <b>2018</b> , 9, 210	1
1517	viGEN: An Open Source Pipeline for the Detection and Quantification of Viral RNA in Human Tumors. <b>2018</b> , 9, 1172	9
1516	Pleiotropic Effects of Variants in Dementia Genes in Parkinson Disease. <b>2018</b> , 12, 230	11
1515	Genome-wide association study of coronary artery disease among individuals with diabetes: the UK Biobank. <b>2018</b> , 61, 2174-2179	12
1514	TLR10 and NFKBIA contributed to the risk of hip osteoarthritis: systematic evaluation based on Han Chinese population. <b>2018</b> , 8, 10243	3
1513	NKG2D gene variation and susceptibility to viral bronchiolitis in childhood. <b>2018</b> , 84, 451-457	3
1512	Fast score test with global null estimation regardless of missing genotypes. <b>2018</b> , 13, e0199692	2
1511	Facilitating Anti-Cancer Combinatorial Drug Discovery by Targeting Epistatic Disease Genes. <b>2018</b> , 23,	5
1510	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <b>2018</b> , 50, 1072-1080	52
1509	Common variation near IRF6 is associated with IFN-Induced liver injury in multiple sclerosis. <b>2018</b> , 50, 1081-1085	28
1508	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <b>2018</b> , 19, 87	25
1507	Genome-Wide Assessment of Diversity and Divergence Among Extant Galapagos Giant Tortoise Species. <b>2018</b> , 109, 611-619	12

1506	Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. <b>2018</b> , 559, 350-355	144
1505	Education, Smoking, and Cohort Change: Forwarding a Multidimensional Theory of the Environmental Moderation of Genetic Effects. <b>2018</b> , 83, 802-832	34
1504	Efficiency of different strategies to mitigate ascertainment bias when using SNP panels in diversity studies. <b>2018</b> , 19, 22	49
1503	Genotyping by sequencing reveals contrasting patterns of population structure, ecologically mediated divergence, and long-distance dispersal in North American palms. <b>2018</b> , 8, 5873-5890	12
1502	Variation in coagulation and fibrinolysis genes evaluated for their contribution to cerebrovascular complications in adults with bacterial meningitis in the Netherlands. <b>2018</b> , 77, 54-59	1
1501	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <b>2018</b> , 9, 1825	367
1500	Host genetic variation and its microbiome interactions within the Human Microbiome Project. <b>2018</b> , 10, 6	86
1499	Ensemble genomic analysis in human lung tissue identifies novel genes for chronic obstructive pulmonary disease. <b>2018</b> , 12, 1	20
1498	WISARD: workbench for integrated superfast association studies for related datasets. <b>2018</b> , 11, 39	7
1497	Common genetic variation and novel loci associated with volumetric mammographic density. <b>2018</b> , 20, 30	10
1496	Identity-by-descent refines mapping of candidate regions for preaxial polydactyly II /III in a large Chinese pedigree. <b>2018</b> , 155, 2	
1495	Association of BET1L and TNRC6B with uterine leiomyoma risk and its relevant clinical features in Han Chinese population. <b>2018</b> , 8, 7401	3
1494	Linked genetic variation and not genome structure causes widespread differential expression associated with chromosomal inversions. <b>2018</b> , 115, 5492-5497	22
1493	PhenotypeSimulator: A comprehensive framework for simulating multi-trait, multi-locus genotype to phenotype relationships. <b>2018</b> , 34, 2951-2956	9
1492	Genomic Analysis Suggests KITLG is Responsible for a Roan Pattern in two Pakistani Goat Breeds. <b>2018</b> , 109, 315-319	11
1491	Comparison of Genotypic and Phenotypic Correlations: Cheverud's Conjecture in Humans. <b>2018</b> , 209, 941-948	48
1490	Exploiting phenotype diversity in a local animal genetic resource: Identification of a single nucleotide polymorphism associated with the tail shape phenotype in the autochthonous Casertana pig breed. <b>2018</b> , 216, 148-152	5
1489	High burden of birthweight-lowering genetic variants in Africans and Asians. <b>2018</b> , 16, 70	9

1488	Fractional anisotropy of the uncinate fasciculus and cingulum in bipolar disorder type I, type II, unaffected siblings and healthy controls. <b>2018</b> , 213, 548-554	17
1487	Revealing the selection history of adaptive loci using genome-wide scans for selection: an example from domestic sheep. <b>2018</b> , 19, 71	40
1486	Joint genome-wide association study of progressive supranuclear palsy identifies novel susceptibility loci and genetic correlation to neurodegenerative diseases. <b>2018</b> , 13, 41	41
1485	Glucose and Insulin-Related Traits, Type 2 Diabetes and Risk of Schizophrenia: A Mendelian Randomization Study. <b>2018</b> , 34, 182-188	17
1484	Invited review: Bioinformatic methods to discover the likely causal variant of a new autosomal recessive genetic condition using genome-wide data. <b>2018</b> , 12, 2221-2234	2
1483	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. <b>2018</b> , 50, 1219-1224	1073
1482	Sequence analysis of European maize inbred line F2 provides new insights into molecular and chromosomal characteristics of presence/absence variants. <b>2018</b> , 19, 119	17
1481	Targeted Sequencing of Alzheimer Disease Genes in African Americans Implicates Novel Risk Variants. <b>2018</b> , 12, 592	16
1480	Melatonin receptor type 1A gene linked to Alzheimer's disease in old age. <b>2018</b> , 41,	18
1479	Reduced-representation sequencing identifies small effective population sizes of Anopheles gambiae in the north-western Lake Victoria basin, Uganda. <b>2018</b> , 17, 285	3
1478	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal influence of schizophrenia. <b>2018</b> , 21, 1161-1170	270
1477	To ERV Is Human: A Phenotype-Wide Scan Linking Polymorphic Human Endogenous Retrovirus-K Insertions to Complex Phenotypes. <b>2018</b> , 9, 298	20
1476	A comprehensive analysis of SNCA-related genetic risk in sporadic parkinson disease. <b>2018</b> , 84, 117-129	33
1475	Vitamin D and overall cancer risk and cancer mortality: a Mendelian randomization study. <b>2018</b> , 27, 4315-4322	32
1474	Long-term exposure to insulin and volumetric mammographic density: observational and genetic associations in the Karma study. <b>2018</b> , 20, 93	2
1473	A study of Kibbutzim in Israel reveals risk factors for cardiometabolic traits and subtle population structure. <b>2018</b> , 26, 1848-1858	7
1472	A Large Multiethnic Genome-Wide Association Study of Adult Body Mass Index Identifies Novel Loci. <b>2018</b> , 210, 499-515	64
1471	Genome-Wide Association Study in Vestibular Neuritis: Involvement of the Host Factor for HSV-1 Replication. <b>2018</b> , 9, 591	17

1470 An Atlas of Genetic Variation Linking Pathogen-Induced Cellular Traits to Human Disease. **2018**, 24, 308-323.e625

1469	Genome-wide association study results for educational attainment aid in identifying genetic heterogeneity of schizophrenia. <b>2018</b> , 9, 3078	39
1468	Genetic variation in CHRNA7 and CHRFAM7A is associated with nicotine dependence and response to varenicline treatment. <b>2018</b> , 26, 1824-1831	7
1467	Multivariate genome-wide association analysis identifies novel and relevant variants associated with anterior cruciate ligament rupture risk in the dog model. <b>2018</b> , 19, 39	11
1466	Population genomics of Culiseta melanura, the principal vector of Eastern equine encephalitis virus in the United States. <b>2018</b> , 12, e0006698	4
1465	Retrospective Evaluation of Marker-Assisted Selection for Resistance to Bacterial Cold Water Disease in Three Generations of a Commercial Rainbow Trout Breeding Population. <b>2018</b> , 9, 286	14
1464	Food Consumption as a Modifier of the Association between Gene Variants and Excess Body Weight in Children and Adolescents: A Study of the SCAALA Cohort. <b>2018</b> , 10,	4
1463	Genetic study of multimodal imaging Alzheimer's disease progression score implicates novel loci. <b>2018</b> , 141, 2167-2180	34
1462	Human-Mediated Introgression of Haplotypes in a Modern Dairy Cattle Breed. <b>2018</b> , 209, 1305-1317	14
1461	Genomic atlas of the human plasma proteome. <b>2018</b> , 558, 73-79	529
1460	Quality Control of Common and Rare Variants. <b>2018</b> , 1793, 25-36	7
1459	A model selection approach for multiple sequence segmentation and dimensionality reduction. <b>2018</b> , 167, 319-330	2
1458	1,000x Faster Than PLINK: Genome-Wide Epistasis Detection with Logistic Regression Using Combined FPGA and GPU Accelerators. <b>2018</b> , 368-381	1
1457	No evidence for association between APOL1 kidney disease risk alleles and Human African Trypanosomiasis in two Ugandan populations. <b>2018</b> , 12, e0006300	9
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1453	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. <b>2018</b> , 23, 2254-2265	13

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1450	Signatures of balancing selection in toll-like receptor (TLRs) genes - novel insights from a free-living rodent. <b>2018</b> , 8, 8361	24
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1445	Parallel altitudinal clines reveal trends in adaptive evolution of genome size in Zea mays. <b>2018</b> , 14, e1007162	56
1444	A greedy feature selection algorithm for Big Data of high dimensionality. <b>2019</b> , 108, 149-202	23
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1264	Genome-wide germline correlates of the epigenetic landscape of prostate cancer. <b>2019</b> , 25, 1615-1626	25
1263	The impact of genomic selection on genetic diversity and genetic gain in three French dairy cattle breeds. <b>2019</b> , 51, 52	30
1262	Functional genomic characterization of the locus in African Americans. <b>2019</b> , 51, 517-528	2
1261	Selection and gene flow shape niche-associated variation in pheromone response. <b>2019</b> , 3, 1455-1463	17
1260	Native American admixture recapitulates population-specific migration and settlement of the continental United States. <b>2019</b> , 15, e1008225	18
1259	A GWAS in Latin Americans highlights the convergent evolution of lighter skin pigmentation in Eurasia. <b>2019</b> , 10, 358	72
1258	Apparent latent structure within the UK Biobank sample has implications for epidemiological analysis. <b>2019</b> , 10, 333	131
1257	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. <b>2019</b> , 68, 854-865	39
1256	Genome-wide analysis identifies potentially causative genes explaining the phenotypic variability in Pinzirita sheep. <b>2019</b> , 50, 189-190	2
1255	Integrating predicted transcriptome from multiple tissues improves association detection. <b>2019</b> , 15, e1007889	100

1254	Medaka Population Genome Structure and Demographic History Described via Genotyping-by-Sequencing. <b>2019</b> , 9, 217-228	6
1253	Prioritizing Crohn's disease genes by integrating association signals with gene expression implicates monocyte subsets. <b>2019</b> , 20, 577-588	4
1252	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. <b>2019</b> , 22, 353-361	93
1251	Variants in ABCG8 and TRAF3 genes confer risk for gallstone disease in admixed Latinos with Mapuche Native American ancestry. <b>2019</b> , 9, 772	16
1250	Reducing inbreeding rates with a breeding circle: Theory and practice in Veluws Heideschaap. <b>2019</b> , 136, 51-62	4
1249	Evaluating the Accuracy of Imputation Methods in a Five-Way Admixed Population. <b>2019</b> , 10, 34	27
1248	Association Mapping of Fertility Restorer Gene for CMS PET1 in Sunflower. <b>2019</b> , 9, 49	11
1247	The genetic architecture of adaptation: convergence and pleiotropy in Heliconius wing pattern evolution. <b>2019</b> , 123, 138-152	21
1246	Genome-wide analysis of expression quantitative trait loci identified potential lung cancer susceptibility variants among Asian populations. <b>2019</b> , 40, 263-268	3
1245	Identification of 12 genetic loci associated with human healthspan. <b>2019</b> , 2, 41	49
1244	Genome-wide signatures of local adaptation among seven stoneflies species along a nationwide latitudinal gradient in Japan. <b>2019</b> , 20, 84	8
1243	Modeling Gene-Environment Interaction for the Risk of Non-hodgkin Lymphoma. <b>2018</b> , 8, 657	1
1242	Population structure of human gut bacteria in a diverse cohort from rural Tanzania and Botswana. <b>2019</b> , 20, 16	51
1241	Using phenome-wide association to investigate the function of a schizophrenia risk locus at SLC39A8. <b>2019</b> , 9, 45	7
<b>124</b> 0	Polymorphisms in Attention-Deficit/Hyperactivity Disorder (ADHD): Further Evidence Linking Sleep and Circadian Disturbances and ADHD. <b>2019</b> , 10,	10
1239	Transethnic meta-analysis of rare coding variants in PLCG2, ABI3, and TREM2 supports their general contribution to Alzheimer's disease. <b>2019</b> , 9, 55	19
1238	Prioritizing putative influential genes in cardiovascular disease susceptibility by applying tissue-specific Mendelian randomization. <b>2019</b> , 11, 6	19
1237	Genetic regulatory mechanisms in human osteoclasts suggest a role for the STMP1 and DCSTAMP genes in Paget's disease of bone. <b>2019</b> , 9, 1052	10

1236	Genome-wide identification of circulating-miRNA expression quantitative trait loci reveals the role of several miRNAs in the regulation of cardiometabolic phenotypes. <b>2019</b> , 115, 1629-1645	34
1235	A Genome-Wide Association Study for Susceptibility to Visual Experience-Induced Myopia. <b>2019</b> , 60, 559-569	7
1234	Genetic associations with suicide attempt severity and genetic overlap with major depression. <b>2019</b> , 9, 22	48
1233	Genome-Wide Association Study of H/L Traits in Chicken. <b>2019</b> , 9,	3
1232	Quantile regression analysis reveals widespread evidence for gene-environment or gene-gene interactions in myopia development. <b>2019</b> , 2, 167	18
1231	Genomewide Association Study Confirming the Association of with Susceptibility to Antituberculosis Drug-Induced Liver Injury in Thai Patients. <b>2019</b> , 63,	13
1230	TB DEPOT (Data Exploration Portal): A multi-domain tuberculosis data analysis resource. <b>2019</b> , 14, e0217410	4
1229	Assortative Mating on Ancestry-Variant Traits in Admixed Latin American Populations. <b>2019</b> , 10, 359	8
1228	Genetic analyses of human fetal retinal pigment epithelium gene expression suggest ocular disease mechanisms. <b>2019</b> , 2, 186	10
1227	Whole Genome Sequencing of Giant Schnauzer Dogs with Progressive Retinal Atrophy Establishes as a Novel Candidate Gene for Retinal Degeneration. <b>2019</b> , 10,	6
1226	A Comparison of Mainstream Genotyping Platforms for the Evaluation and Use of Barley Genetic Resources. <b>2019</b> , 10, 544	23
1225	Genetic analysis of a worldwide barley collection for resistance to net form of net blotch disease (Pyrenophora teres f. teres). <b>2019</b> , 132, 2633-2650	13
1224	Genes for Good: Engaging the Public in Genetics Research via Social Media. <b>2019</b> , 105, 65-77	8
1223	Genome-wide association study implicates CHRNA2 in cannabis use disorder. <b>2019</b> , 22, 1066-1074	60
1222	Genomic structure and diversity of Plasmodium falciparum in Southeast Asia reveal recent parasite migration patterns. <b>2019</b> , 10, 2665	20
1221	Genetic analyses of diverse populations improves discovery for complex traits. <b>2019</b> , 570, 514-518	291
1220	Effect of selection and selective genotyping for creation of reference on bias and accuracy of genomic prediction. <b>2019</b> , 136, 390-407	8
1219	Consequences of PCA graphs, SNP codings, and PCA variants for elucidating population structure. <b>2019</b> , 14, e0218306	12

1218	Genetic studies of abdominal MRI data identify genes regulating hepcidin as major determinants of liver iron concentration. <b>2019</b> , 71, 594-602	10
1217	Insights into Impact of DNA Copy Number Alteration and Methylation on the Proteogenomic Landscape of Human Ovarian Cancer via a Multi-omics Integrative Analysis. <b>2019</b> , 18, S52-S65	15
1216	The origins and adaptation of European potatoes reconstructed from historical genomes. <b>2019</b> , 3, 1093-1101	41
1215	Association Between Genetic Risk and Development of Type 2 Diabetes in a General Japanese Population: The Hisayama Study. <b>2019</b> , 104, 3213-3222	9
1214	Genome-wide association study identifies loci for arterial stiffness index in 127,121 UK Biobank participants. <b>2019</b> , 9, 9143	11
1213	Combined analysis of keratinocyte cancers identifies novel genome-wide loci. <b>2019</b> , 28, 3148-3160	20
1212	Resolving a 150-year-old paternity case in Mormon history using DTC autosomal DNA testing of distant relatives. <b>2019</b> , 42, 1-7	3
1211	A Fast and Flexible Framework for Network-Assisted Genomic Association. <b>2019</b> , 16, 155-161	8
<b>121</b> 0	Comprehensive analysis of coding variants highlights genetic complexity in developmental and epileptic encephalopathy. <b>2019</b> , 10, 2506	22
1209	A Novel Gene Underlies Bleomycin-Response Variation in. <b>2019</b> , 212, 1453-1468	15
1208	Human genes influence the interaction between Streptococcus mutans and host caries susceptibility: a genome-wide association study in children with primary dentition. <b>2019</b> , 11, 19	7
1207	Palaeogenomic insights into the origins of French grapevine diversity. <b>2019</b> , 5, 595-603	54
1206	A genome-wide association meta-analysis of prognostic outcomes following cognitive behavioural therapy in individuals with anxiety and depressive disorders. <b>2019</b> , 9, 150	24
1205	Alzheimer's disease polygenic risk score as a predictor of conversion from mild-cognitive impairment. <b>2019</b> , 9, 154	31
1204	Rapid identification and interpretation of gene-environment associations using the new R.SamBada landscape genomics pipeline. <b>2019</b> , 19, 1355-1365	8
1203	Joint Estimation of Pedigrees and Effective Population Size Using Markov Chain Monte Carlo. <b>2019</b> , 212, 855-868	3
1202	A Social Determinant of Health May Modify Genetic Associations for Blood Pressure: Evidence From a SNP by Education Interaction in an African American Population. <b>2019</b> , 10, 428	3
1201	Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. <b>2019</b> , 104, 1169-1181	50

1200	Genomic signatures of extensive inbreeding in Isle Royale wolves, a population on the threshold of extinction. <b>2019</b> , 5, eaau0757	82
1199	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <b>2019</b> , 51, 957-972	217
1198	Rare variant phasing using paired tumor:normal sequence data. <b>2019</b> , 20, 265	1
1197	HLA-C*01:02 and HLA-A*02:07 Confer Risk Specific for Psoriatic Patients in Southern China. <b>2019</b> , 139, 2045-2048.e4	4
1196	Genome-wide analyses of psychological resilience in U.S. Army soldiers. <b>2019</b> , 180, 310-319	22
1195	ukbtools: An R package to manage and query UK Biobank data. <b>2019</b> , 14, e0214311	15
1194	GWAS of Suicide Attempt in Psychiatric Disorders and Association With Major Depression Polygenic Risk Scores. <b>2019</b> , 176, 651-660	103
1193	BarkBase: Epigenomic Annotation of Canine Genomes. <b>2019</b> , 10,	12
1192	East Anglian early Neolithic monument burial linked to contemporary Megaliths. 2019, 46, 145-149	17
1191	Genome-wide analysis identifies rare copy number variations associated with inflammatory bowel disease. <b>2019</b> , 14, e0217846	9
1190	Genome-wide estimates of genetic diversity, inbreeding and effective size of experimental and commercial rainbow trout lines undergoing selective breeding. <b>2019</b> , 51, 26	31
1189	Apolipoprotein E Homozygous A Allele Status: A Deteriorating Effect on Visuospatial Working Memory and Global Brain Structure. <b>2019</b> , 10, 552	5
1188	Population divergence and gene flow in two East Asian shorebirds on the verge of speciation. <b>2019</b> , 9, 8546	5
1187	Risk of spontaneous preterm birth and fetal growth associates with fetal SLIT2. <b>2019</b> , 15, e1008107	13
1186	Genome-Wide Association Study Reveals Candidate Genes for Growth Relevant Traits in Pigs. <b>2019</b> , 10, 302	19
1185	Benefits and limitations of genome-wide association studies. <b>2019</b> , 20, 467-484	516
1184	A longitudinal big data approach for precision health. <b>2019</b> , 25, 792-804	183
1183	High marker density GWAS provides novel insights into the genomic architecture of terpene oil yield in Eucalyptus. <b>2019</b> , 223, 1489-1504	17

1182	The causal influence of brain size on human intelligence: Evidence from within-family phenotypic associations and GWAS modeling. <b>2019</b> , 75, 48-58	14
1181	Associations of schizophrenia risk genes ZNF804A and CACNA1C with schizotypy and modulation of attention in healthy subjects. <b>2019</b> , 208, 67-75	10
1180	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. <b>2019</b> , 212, 577-586	1
1179	Integrated analysis of genomics, longitudinal metabolomics, and Alzheimer's risk factors among 1,111 cohort participants. <b>2019</b> , 43, 657-674	12
1178	The role of polygenic risk score gene-set analysis in the context of the omnigenic model of schizophrenia. <b>2019</b> , 44, 1562-1569	22
1177	The role of genetic variation in DGKK on moderate and severe hypospadias. <b>2019</b> , 111, 932-937	4
1176	Quality and quantity of genetic relatedness data affect the analysis of social structure. <b>2019</b> , 19, 1181-1194	5
1175	Genome-wide association study and linkage analysis on resistance to rice black-streaked dwarf virus disease. <b>2019</b> , 39, 1	5
1174	Classical HLA alleles are associated with prevalent and persistent cervical high-risk HPV infection in African women. <b>2019</b> , 80, 723-730	4
1173	A combined genome-wide approach identifies a new potential candidate marker associated with the coat color sidedness in cattle. <b>2019</b> , 225, 91-95	3
1172	A commonly occurring genetic variant within the NPLOC4-TSPAN10-PDE6G gene cluster is associated with the risk of strabismus. <b>2019</b> , 138, 723-737	16
1171	Genome of the African cassava whitefly Bemisia tabaci and distribution and genetic diversity of cassava-colonizing whiteflies in Africa. <b>2019</b> , 110, 112-120	21
1170	Relationship Between Genetic Polymorphisms of the Gene and Hallux Valgus Susceptibility. <b>2019</b> , 23, 380-386	3
1169	Sequence imputation from low density single nucleotide polymorphism panel in a black poplar breeding population. <b>2019</b> , 20, 302	3
1168	A Single-Cell Model for Synaptic Transmission and Plasticity in Human iPSC-Derived Neurons. <b>2019</b> , 27, 2199-2211.e6	40
1167	The lysosomal disease caused by mutant VPS33A. <b>2019</b> , 28, 2514-2530	14
1166	IRAK2 and TLR10 confer risk of Hashimoto's disease: a genetic association study based on the Han Chinese population. <b>2019</b> , 64, 617-623	3
1165	Glycated Serum Protein Genetics and Pleiotropy with Cardiometabolic Risk Factors. <b>2019</b> , 2019, 2310235	3

1164	Overlap in the Genetic Architecture of Stroke Risk, Early Neurological Changes, and Cardiovascular Risk Factors. <b>2019</b> , 50, 1339-1345	10
1163	Chromosomal imbalance in pigs showing a syndromic form of cleft palate. <b>2019</b> , 20, 349	10
1162	An ADAMTS3 missense variant is associated with Norwich Terrier upper airway syndrome. <b>2019</b> , 15, e1008102	2 11
1161	A Missense Variant in in Alpine Dachsbracke Dogs Affected by Spinocerebellar Ataxia. <b>2019</b> , 10,	3
1160	Interferon inducible X-linked gene CXorf21 may contribute to sexual dimorphism in Systemic Lupus Erythematosus. <b>2019</b> , 10, 2164	35
1159	Reliable heritability estimation using sparse regularization in ultrahigh dimensional genome-wide association studies. <b>2019</b> , 20, 219	2
1158	Genome-Wide Signatures of Selection Detection in Three South China Indigenous Pigs. <b>2019</b> , 10,	9
1157	Genome-wide association study of medication-use and associated disease in the UK Biobank. <b>2019</b> , 10, 1891	48
1156	Analysis of Heritability and Genetic Architecture of Pancreatic Cancer: A PanC4 Study. <b>2019</b> , 28, 1238-1245	27
1155	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <b>2019</b> , 8,	166
1154	Genetic risk, body mass index, and weight control behaviors: Unlocking the triad. <b>2019</b> , 52, 825-833	12
1153	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. <b>2019</b> , 177, 587-596.e9	265
1152	Genome sequencing analysis of blood cells identifies germline haplotypes strongly associated with drug resistance in osteosarcoma patients. <b>2019</b> , 19, 357	11
1151	Association of the variant rs5743557 with susceptibility to tuberculosis. <b>2019</b> , 11, 583-594	3
1150	Polygenic prediction via Bayesian regression and continuous shrinkage priors. <b>2019</b> , 10, 1776	191
1149	A Genome-Wide Association Study of Bisphosphonate-Associated Atypical Femoral Fracture. <b>2019</b> , 105, 51-67	10
1148	Association between taste perception and adiposity in overweight or obese older subjects with metabolic syndrome and identification of novel taste-related genes. <b>2019</b> , 109, 1709-1723	21
1147	Random PCR-based genotyping by sequencing technology GRAS-Di (genotyping by random amplicon sequencing, direct) reveals genetic structure of mangrove fishes. <b>2019</b> , 19, 1153-1163	21

1146	Duplication of a domestication locus neutralized a cryptic variant that caused a breeding barrier in tomato. <b>2019</b> , 5, 471-479	35
1145	TAGOOS: genome-wide supervised learning of non-coding loci associated to complex phenotypes. <b>2019</b> , 47, e79	3
1144	Differential methylation of enhancer at IGF2 is associated with abnormal dopamine synthesis in major psychosis. <b>2019</b> , 10, 2046	33
1143	Longitudinal plasma metabolomics of aging and sex. <b>2019</b> , 11, 1262-1282	64
1142	Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. <b>2019</b> , 10, 1992	16
1141	The genetic history of admixture across inner Eurasia. <b>2019</b> , 3, 966-976	69
1140	A biologically-informed polygenic score identifies endophenotypes and clinical conditions associated with the insulin receptor function on specific brain regions. <b>2019</b> , 42, 188-202	27
1139	A Genome-Wide Functional Genomics Approach Identifies Susceptibility Pathways to Fungal Bloodstream Infection in Humans. <b>2019</b> , 220, 862-872	13
1138	Genes, Roommates, and Residence Halls: A Multidimensional Study of the Role of Peer Drinking on College Students' Alcohol Use. <b>2019</b> , 43, 1254-1262	6
1137	Genome-wide association study identified genes in the response to Salmonella pullorum infection in chickens. <b>2019</b> , 50, 403-406	1
1136	Genome-wide association study identifies 30 loci associated with bipolar disorder. <b>2019</b> , 51, 793-803	662
1135	Dissecting human North African gene-flow into its western coastal surroundings. <b>2019</b> , 286, 20190471	6
1134	Comparing signals of natural selection between three Indigenous North American populations. <b>2019</b> , 116, 9312-9317	16
1133	Natural Selection Footprints Among African Chicken Breeds and Village Ecotypes. <b>2019</b> , 10, 376	15
1132	IPCAPS: an R package for iterative pruning to capture population structure. <b>2019</b> , 14, 2	4
1131	Association of expression quantitative trait loci for long noncoding RNAs with lung cancer risk in Asians. <b>2019</b> , 58, 1303-1313	5
1130	Genetic components of human pain sensitivity: a protocol for a genome-wide association study of experimental pain in healthy volunteers. <b>2019</b> , 9, e025530	9
1129	Polygenic Risk Score Is Associated With Intraocular Pressure and Improves Glaucoma Prediction in the UK Biobank Cohort. <b>2019</b> , 8, 10	16

1128	Clinical, genetic, and pathologic characterization of Mexican founder mutation c.1387A>G. <b>2019</b> , 5, e315	7
1127	Using Whole Genome Sequencing in an African Subphenotype of Myasthenia Gravis to Generate a Pathogenetic Hypothesis. <b>2019</b> , 10, 136	9
1126	Brown rat demography reveals pre-commensal structure in eastern Asia before expansion into Southeast Asia. <b>2019</b> , 29, 762-770	16
1125	Association between polygenic risk for tobacco or alcohol consumption and liability to licit and illicit substance use in young Australian adults. <b>2019</b> , 197, 271-279	17
1124	Rainbow trout resistance to bacterial cold water disease: two new quantitative trait loci identified after a natural disease outbreak on a French farm. <b>2019</b> , 50, 293-297	8
1123	Analyses of Neanderthal introgression suggest that Levantine and southern Arabian populations have a shared population history. <b>2019</b> , 169, 227-239	4
1122	Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia. <b>2019</b> , 10, 1218	40
1121	Genetic Ancestry Analysis Reveals Misclassification of Commonly Used Cancer Cell Lines. <b>2019</b> , 28, 1003-1009	14
1120	Genome wide analysis for mouth ulcers identifies associations at immune regulatory loci. <b>2019</b> , 10, 1052	22
1119	A novel nonsense variant in SUPT20H gene associated with Rheumatoid Arthritis identified by Whole Exome Sequencing of multiplex families. <b>2019</b> , 14, e0213387	4
1118	Genome-wide association meta-analysis and Mendelian randomization analysis confirm the influence of ALDH2 on sleep durationin the Japanese population. <b>2019</b> , 42,	8
1117	Interrogating the Genetic Determinants of Tourette's Syndrome and Other Tic Disorders Through Genome-Wide Association Studies. <b>2019</b> , 176, 217-227	95
1116	Increased Risk of Multiple Outpatient Surgeries in African-American Carriers of Val122Ile Mutation Is Modulated by Non-Coding Variants. <b>2019</b> , 8,	9
1115	Genomic Variations in Susceptibility to Intracranial Aneurysm in the Korean Population. 2019, 8,	15
1114	Copy Number Variants in miR-138 as a Potential Risk Factor for Early-Onset Alzheimer's Disease. <b>2019</b> , 68, 1243-1255	9
1113	Unravelling the invasion history of the Asian tiger mosquito in Europe. <b>2019</b> , 28, 2360-2377	35
1112	Widespread introgression in Chinese indigenous chicken breeds from commercial broiler. <b>2019</b> , 12, 610-621	11
1111	Multi-Ancestry Genome-Wide Association Study of Spontaneous Clearance of Hepatitis C Virus. <b>2019</b> , 156, 1496-1507.e7	20

1110	The impact of donor and recipient common clinical and genetic variation on estimated glomerular filtration rate in a European renal transplant population. <b>2019</b> , 19, 2262-2273	4
1109	Identification of genetic heterogeneity of Alzheimer's disease across age. <b>2019</b> , 84, 243.e1-243.e9	18
1108	Alcohol-responsive genes identified in human iPSC-derived neural cultures. <b>2019</b> , 9, 96	9
1107	Relationship of common variants in Interleukin 33 gene with susceptibility and prognosis of osteosarcoma in Han Chinese population. <b>2019</b> , 10, 1138-1144	3
1106	Differential BDNF methylation in combat exposed veterans and the association with exercise. <b>2019</b> , 698, 107-112	11
1105	The genetic legacy of continental scale admixture in Indian Austroasiatic speakers. <b>2019</b> , 9, 3818	12
1104	Variations in circadian genes and individual nocturnal symptoms of insomnia. The HUNT study. <b>2019</b> , 36, 681-688	4
1103	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <b>2019</b> , 28, 2062-2077	28
1102	An association study using imputed whole-genome sequence data identifies novel significant loci for growth-related traits in a Duroc Erhualian F population. <b>2019</b> , 136, 217-228	6
1101	Probabilistic ancestry maps: a method to assess and visualize population substructures in genetics. <b>2019</b> , 20, 116	4
1100	Population Substructure Has Implications in Validating Next-Generation Cancer Genomics Studies with TCGA. <b>2019</b> , 20,	4
1099	Genomic and Transcriptomic Analysis of Amoebic Gill Disease Resistance in Atlantic Salmon ( L.). <b>2019</b> , 10, 68	20
1098	Genomewide Study of Epigenetic Biomarkers of Opioid Dependence in European- American Women. <b>2019</b> , 9, 4660	14
1097	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <b>2019</b> , 11, 49	13
1096	Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. <b>2019</b> , 15, e1007530	20
1095	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. <b>2019</b> , 25, 4104-4116	15
1094	Adjustment for index event bias in genome-wide association studies of subsequent events. <b>2019</b> , 10, 1561	38
1093	Genetics and the geography of health, behaviour and attainment. <b>2019</b> , 3, 576-586	26

1092	Genomic and epigenomic mapping of leptin-responsive neuronal populations involved in body weight regulation. <b>2019</b> , 1, 475-484	9
1091	Genome-wide association study in Turkish and Iranian populations identify rare familial Mediterranean fever gene (MEFV) polymorphisms associated with ankylosing spondylitis. <b>2019</b> , 15, e1008038	22
1090	Towards population genomics in non-model species with large genomes: a case study of the marine zooplankton. <b>2019</b> , 6, 180608	20
1089	Exome array analysis of rare and low frequency variants in amyotrophic lateral sclerosis. <b>2019</b> , 9, 5931	6
1088	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans: Genomic Prediction. <b>2019</b> , 211, 1131-1141	47
1087	Genome-wide association study of suicide attempt in a Mexican population: a study protocol. <b>2019</b> , 9, e025335	2
1086	A splice donor variant in CCDC189 is associated with asthenospermia in Nordic Red dairy cattle. <b>2019</b> , 20, 286	11
1085	Multiple Deeply Divergent Denisovan Ancestries in Papuans. <b>2019</b> , 177, 1010-1021.e32	105
1084	Analysis of 100 high-coverage genomes from a pedigreed captive baboon colony. <b>2019</b> , 29, 848-856	12
1083	Pharmacogenomic Variants and Drug Interactions Identified Through the Genetic Analysis of Clozapine Metabolism. <b>2019</b> , 176, 477-486	21
1082	Genetic Architectures of Childhood- and Adult-Onset Asthma Are Partly Distinct. 2019, 104, 665-684	83
1081	Genomic, Transcriptomic, and Epigenomic Features Differentiate Genes That Are Relevant for Muscular Polyunsaturated Fatty Acids in the Common Carp. <b>2019</b> , 10, 217	7
1080	Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. <b>2019</b> , 10, 1499	164
1079	Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. <b>2019</b> , 11, 1417-1430	20
1078	metapop2: Re-implementation of software for the analysis and management of subdivided populations using gene and allelic diversity. <b>2019</b> , 19, 1095-1100	14
1077	Integrative Approach to Reveal Cell Type Specificity and Gene Candidates for Psoriatic Arthritis Outside the MHC. <b>2019</b> , 10, 304	5
1076	Chromosome-scale assemblies reveal the structural evolution of African cichlid genomes. <i>GigaScience</i> , <b>2019</b> , 8,	46
1075	BGData - A Suite of R Packages for Genomic Analysis with Big Data. <b>2019</b> , 9, 1377-1383	6

1074	Interaction between lifestyle and genetic susceptibility in myopia: the Generation R study. <b>2019</b> , 34, 777-784	19
1073	Positive selection in Europeans and East-Asians at the ABCA12 gene. <b>2019</b> , 9, 4843	
1072	Survey of allele specific expression in bovine muscle. <b>2019</b> , 9, 4297	8
1071	A genome-wide association study of bitter and sweet beverage consumption. <b>2019</b> , 28, 2449-2457	45
1070	Genome sequencing for rightward hemispheric language dominance. <b>2019</b> , 18, e12572	10
1069	Ancestry-Specific Analyses Reveal Differential Demographic Histories and Opposite Selective Pressures in Modern South Asian Populations. <b>2019</b> , 36, 1628-1642	13
1068	Associations between an educational attainment polygenic score with educational attainment in an African American sample. <b>2019</b> , 18, e12558	12
1067	Potential functional variants in SMC2 and TP53 in the AURORA pathway genes and risk of pancreatic cancer. <b>2019</b> , 40, 521-528	13
1066	Origin of the Aromatic Group of Cultivated Rice (Oryza sativa L.) Traced to the Indian Subcontinent. <b>2019</b> , 11, 832-843	21
1065	Relative effects of LDL-C on ischemic stroke and coronary disease: A Mendelian randomization study. <b>2019</b> , 92, e1176-e1187	16
1064	Genome-wide association studies for yield-related traits in soft red winter wheat grown in Virginia. <b>2019</b> , 14, e0208217	32
1063	Genome-wide association meta-analysis of functional outcome after ischemic stroke. <b>2019</b> , 92, e1271-e1283	40
1062	Assessment of APOE in atypical parkinsonism syndromes. <b>2019</b> , 127, 142-146	10
1061	Genome-Wide Characterization of Arabian Peninsula Populations: Shedding Light on the History of a Fundamental Bridge between Continents. <b>2019</b> , 36, 575-586	18
1060	Effect of increased body mass index on risk of diagnosis or death from cancer. <b>2019</b> , 120, 565-570	13
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1057	Pandemrix-induced narcolepsy is associated with genes related to immunity and neuronal survival. <b>2019</b> , 40, 595-604	22

1056	The first chromosome-level genome for a marine mammal as a resource to study ecology and evolution. <b>2019</b> , 19, 944-956	15
1055	An African-specific haplotype in MRGPRX4 is associated with menthol cigarette smoking. <b>2019</b> , 15, e1007916	12
1054	Analysis of Genetic Diversity and Population Structure in Three Forest Musk Deer Captive Populations with Different Origins. <b>2019</b> , 9, 1037-1044	6
1053	Detection of Selection Signatures Among Brazilian, Sri Lankan, and Egyptian Chicken Populations Under Different Environmental Conditions. <b>2018</b> , 9, 737	27
1052	Genomewide Association Study of Fracture Nonunion Using Electronic Health Records. <b>2019</b> , 3, 23-28	6
1051	Genome-wide association scan identifies new variants associated with a cognitive predictor of dyslexia. <b>2019</b> , 9, 77	42
1050	Polygenic impact of common genetic risk loci for Alzheimer's disease on cerebral blood flow in young individuals. <b>2019</b> , 9, 467	12
1049	Epigenomic analysis reveals DNA motifs regulating histone modifications in human and mouse. <b>2019</b> , 116, 3668-3677	15
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1047	Identification of common genetic risk variants for autism spectrum disorder. <b>2019</b> , 51, 431-444	746
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964	Allele frequency-free inference of close familial relationships from genotypes or low-depth sequencing data. <b>2019</b> , 28, 35-48	28
963	Combining population genomics and forward simulations to investigate stocking impacts: A case study of Muskellunge () from the St. Lawrence River basin. <b>2019</b> , 12, 902-922	10
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946	Complex Structural Variant Associated with Non-syndromic Canine Retinal Degeneration. <b>2019</b> , 9, 425-437	10
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940	Assessing the Genetic Correlations Between Blood Plasma Proteins and Osteoporosis: A Polygenic Risk Score Analysis. <b>2019</b> , 104, 171-181	3
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928	Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research. <b>2019</b> , 105, 1256-1262	43
927	Meta-analysis of genome-wide association studies for body fat distribution in 694´649 individuals of European ancestry. <b>2019</b> , 28, 166-174	258
926	Childhood maltreatment moderates the influence of genetic load for obesity on reward related brain structure and function in major depression. <b>2019</b> , 100, 18-26	6
925	A weighted burden test using logistic regression for integrated analysis of sequence variants, copy number variants and polygenic risk score. <b>2019</b> , 27, 114-124	11
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874	Genetic and epidemiological characterization of restless legs syndrome in QuBec. 2020, 43,	4
873	Individual and joint performance of DNA methylation profiles, genetic risk score and environmental risk scores for predicting breast cancer risk. <b>2020</b> , 14, 42-53	7
872	Population genomic structure of the gelatinous zooplankton species in its nonindigenous range in the North Sea. <b>2020</b> , 10, 11-25	1
871	Novel IQCE variations confirm its role in postaxial polydactyly and cause ciliary defect phenotype in zebrafish. <b>2020</b> , 41, 240-254	2
870	Using DNA From Mothers and Children to Study Parental Investment in Children's Educational Attainment. <b>2020</b> , 91, 1745-1761	21
869	Natural variation in HsfA2 pre-mRNA splicing is associated with changes in thermotolerance during tomato domestication. <b>2020</b> , 225, 1297-1310	24
868	Genetic risk and atrial fibrillation in patients with heart failure. 2020, 22, 519-527	3
867	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <b>2020</b> , 11, 163	140
866	Genetic Variants Associated with Chronic Kidney Disease in a Spanish Population. 2020, 10, 144	16
865	Polygenic risk scores outperform machine learning methods in predicting coronary artery disease status. <b>2020</b> , 44, 125-138	14
864	Comparative evaluation of genomic inbreeding parameters in seven commercial and autochthonous pig breeds. <b>2020</b> , 14, 910-920	15
863	The association between genome-wide polymorphisms and chronic postoperative pain: a prospective observational study. <b>2020</b> , 75 Suppl 1, e111-e120	3
862	Polygenic risk for Alzheimer's disease shapes hippocampal scene-selectivity. <b>2020</b> , 45, 1171-1178	3
861	A lost world in Wallacea: Description of a montane archipelagic avifauna. <b>2020</b> , 367, 167-170	23
860	Do different rates of gene flow underlie variation in phenotypic and phenological clines in a montane grasshopper community?. <b>2020</b> , 10, 980-997	4
859	Genetic Risk Underlying Psychiatric and Cognitive Symptoms in Huntington's Disease. <b>2020</b> , 87, 857-865	13

858	Genome-wide association study of cognitive performance in U.S. veterans with schizophrenia or bipolar disorder. <b>2020</b> , 183, 181-194	9
857	Genome-wide association study of shared liability to anxiety disorders in Army STARRS. <b>2020</b> , 183, 197-207	5
856	Longitudinal RNA-Seq Analysis of the Repeatability of Gene Expression and Splicing in Human Platelets Identifies a Platelet Splice QTL. <b>2020</b> , 126, 501-516	15
855	SNP genotypes reveal breed substructure, selection signatures and highly inbred regions in Pi <b>E</b> rain pigs. <b>2020</b> , 51, 32-42	15
854	Genome-wide association studies in a barley (Hordeum vulgare) diversity set reveal a limited number of loci for resistance to spot blotch (Bipolaris sorokiniana). <b>2020</b> , 139, 521-535	4
853	Association of Genetic Variation With Keratoconus. <b>2020</b> , 138, 174-181	24
852	Does polygenic risk influence associations between sun exposure and melanoma? A prospective cohort analysis. <b>2020</b> , 183, 303-310	4
851	A flexible and nearly optimal sequential testing approach to randomized testing: QUICK-STOP. <b>2020</b> , 44, 139-147	2
850	A major role for common genetic variation in anxiety disorders. <b>2020</b> , 25, 3292-3303	114
849	Alzheimer Disease Pathology-Associated Polymorphism in a Complex Variable Number of Tandem Repeat Region Within the MUC6 Gene, Near the AP2A2 Gene. <b>2020</b> , 79, 3-21	13
848	Wnt receptor gene was associated with schizophrenia in genome-wide SNP analysis of the Australian Schizophrenia Research Bank cohort. <b>2020</b> , 54, 902-908	4
847	Comparison of Genetic Liability for Sleep Traits Among Individuals With Bipolar Disorder I or II and Control Participants. <b>2020</b> , 77, 303-310	19
846	Statistical genetic concepts in psychiatric genomics. <b>2020</b> , 103-116	
845	Post-GWAS analysis of six substance use traits improves the identification and functional interpretation of genetic risk loci. <b>2020</b> , 206, 107703	8
844	Searching for parent-of-origin effects on cardiometabolic traits in imprinted genomic regions. <b>2020</b> , 28, 646-655	1
843	A Genetic Risk Score for the Estimation of Weight Loss After Bariatric Surgery. <b>2020</b> , 30, 1482-1490	5
842	Genome-wide association study for growth and fatness traits in Chinese Sujiang pigs. <b>2020</b> , 51, 314-318	5
841	Identification of Restless Legs Syndrome Genes by Mutational Load Analysis. <b>2020</b> , 87, 184-193	9

840	Cannabis use, depression and self-harm: phenotypic and genetic relationships. <b>2020</b> , 115, 482-492	16
839	Genome-Wide Association Study Identifies Single Nucleotide Polymorphism Markers Associated with Mycelial Growth (at 15, 20, and 25°C), Mefenoxam Resistance, and Mating Type in. <b>2020</b> , 110, 822-833	4
838	Genome-wide analyses reveal the regions involved in the phenotypic diversity in Sicilian pigs. <b>2020</b> , 51, 101-105	5
837	OPRM1, OPRK1, and COMT genetic polymorphisms associated with opioid effects on experimental pain: a randomized, double-blind, placebo-controlled study. <b>2020</b> , 20, 471-481	6
836	Clinical and Genetic Contributors to New-Onset Atrial Fibrillation in Critically Ill Adults. <b>2020</b> , 48, 22-30	2
835	Whole genome sequencing of orofacial cleft trios from the Gabriella Miller Kids First Pediatric Research Consortium identifies a new locus on chromosome 21. <b>2020</b> , 139, 215-226	8
834	Genetic diversity, population structure and runs of homozygosity in Ethiopian short fat-tailed and Awassi sheep breeds using genome-wide 50k SNP markers. <b>2020</b> , 232, 103899	2
833	Genome-wide association studies of beef cow terrain-use traits using Bayesian multiple-SNP regression. <b>2020</b> , 232, 103900	7
832	Comparative analysis of genomic variability for drug-resistant strains of Mycobacterium tuberculosis: The special case of Belarus. <b>2020</b> , 78, 104137	3
831	Genomic prediction of depression risk and resilience under stress. <b>2020</b> , 4, 111-118	15
8 <sub>3</sub> 0	Genomic prediction of depression risk and resilience under stress. 2020, 4, 111-118  Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. 2020, 51, 78-86	0
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830	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. <b>2020</b> , 51, 78-86	0
830 829	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. <b>2020</b> , 51, 78-86  X-chromosome association studies of congenital heart defects. <b>2020</b> , 182, 250-254	0
830 829 828	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. <b>2020</b> , 51, 78-86  X-chromosome association studies of congenital heart defects. <b>2020</b> , 182, 250-254  Human Genomic Diversity Where the Mediterranean Joins the Atlantic. <b>2020</b> , 37, 1041-1055	o o 7
830 829 828 827	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. 2020, 51, 78-86  X-chromosome association studies of congenital heart defects. 2020, 182, 250-254  Human Genomic Diversity Where the Mediterranean Joins the Atlantic. 2020, 37, 1041-1055  Genetic liability to ADHD and substance use disorders in individuals with ADHD. 2020, 115, 1368-1377  Pathways Between a Polygenic Score for Educational Attainment and Higher Educational	o o 7
8 <sub>2</sub> 9 8 <sub>2</sub> 8 8 <sub>2</sub> 7 8 <sub>2</sub> 6	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. 2020, 51, 78-86  X-chromosome association studies of congenital heart defects. 2020, 182, 250-254  Human Genomic Diversity Where the Mediterranean Joins the Atlantic. 2020, 37, 1041-1055  Genetic liability to ADHD and substance use disorders in individuals with ADHD. 2020, 115, 1368-1377  Pathways Between a Polygenic Score for Educational Attainment and Higher Educational Attainment in an African American Sample. 2020, 50, 14-25  Genome-wide genetic diversity detection and population structure analysis in sweetpotato	O O 7 18 2

822	Genome-wide association study applied to type traits related to milk yield in water buffaloes (Bubalus bubalis). <b>2020</b> , 103, 1642-1650	4
821	Familial Influences on Neuroticism and Education in the UK Biobank. <b>2020</b> , 50, 84-93	3
820	No genetic evidence for involvement of alcohol dehydrogenase genes in risk for Parkinson's disease. <b>2020</b> , 87, 140.e19-140.e22	4
819	Association between CUBN gene variants, type 2 diabetes and vitamin D concentrations in an elderly Greek population. <b>2020</b> , 198, 105549	3
818	Unraveling the genetic diversity of Belgian Milk Sheep using medium-density SNP genotypes. <b>2020</b> , 51, 258-265	12
817	Influence of Genetic Variation in on Endothelial Function and Stroke. <b>2020</b> , 75, 365-371	1
816	Effect of Divergent Selection for Intramuscular Fat Content on Muscle Lipid Metabolism in Chickens. <b>2019</b> , 10,	10
815	GBS Data Identify Pigmentation-Specific Genes of Potential Role in Skin-Photosensitization in Two Tunisian Sheep Breeds. <b>2019</b> , 10,	3
814	Genetic Screening of Plasticity Regulating Nogo-Type Signaling Genes in Migraine. 2019, 10,	
813	Genome-wide association study to identify genetic loci associated with gastrointestinal nematode resistance in Katahdin sheep. <b>2020</b> , 51, 330-335	10
812	Genome-wide association study for feed efficiency in collective cage-raised rabbits under full and restricted feeding. <b>2020</b> , 51, 799-810	2
811	Genetically-regulated transcriptomics & copy number variation of proctitis points to altered mitochondrial and DNA repair mechanisms in individuals of European ancestry. <b>2020</b> , 20, 954	2
810	Genome-wide association analysis of idiopathic epilepsy in the Belgian shepherd. <b>2020</b> , 7,	3
809	A whole-genome sequenced control population in northern Sweden reveals subregional genetic differences. <b>2020</b> , 15, e0237721	О
808	Short or Long Sleep Duration and CKD: A Mendelian Randomization Study. <b>2020</b> , 31, 2937-2947	21
807	Genome-Wide Association Study of Smoking Behavior Traits in a Chinese Han Population. <b>2020</b> , 11, 564239	3
806	Genetics of Arthrogryposis and Macroglossia in Piemontese Cattle Breed. <b>2020</b> , 10,	1
805	lncRNAKB, a knowledgebase of tissue-specific functional annotation and trait association of long noncoding RNA. <b>2020</b> , 7, 326	16

804	The role of TPH2 variant rs4570625 in shaping infant attention to social signals. <b>2020</b> , 60, 101471	1
803	Genome-wide association study reveals new insights into the heritability and genetic correlates of developmental dyslexia. <b>2021</b> , 26, 3004-3017	22
802	A genome-wide association analysis for body, udder, and leg conformation traits recorded in Murciano-Granadina goats. <b>2020</b> , 103, 11605-11617	1
801	A Survey of Rare Epigenetic Variation in 23,116 Human Genomes Identifies Disease-Relevant Epivariations and CGG Expansions. <b>2020</b> , 107, 654-669	12
800	Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years. <b>2020</b> , 30, 4307-4315.e13	27
799	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <b>2020</b> , 11, 4796	16
798	PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. <b>2020</b> , 27, 1675-1687	12
797	Deletion of porcine BOLL is associated with defective acrosomes and subfertility in Yorkshire boars. <b>2020</b> , 51, 945-949	3
796	Genetic factors for susceptibility to and manifestations of neuromyelitis optica. <b>2020</b> , 7, 2082-2093	7
795	Angiotensin-converting enzyme 2 (ACE2) levels in relation to risk factors for COVID-19 in two large cohorts of patients with atrial fibrillation. <b>2020</b> , 41, 4037-4046	52
794	Sex-specific association between infant caudate volumes and a polygenic risk score for major depressive disorder. <b>2020</b> , 98, 2529-2540	1
793	The shaping of immunological responses through natural selection after the Roma Diaspora. <b>2020</b> , 10, 16134	1
79²	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. <b>2020</b> , 177, 917-927	24
791	Use of gene expression and whole-genome sequence information to improve the accuracy of genomic prediction for carcass traits in Hanwoo cattle. <b>2020</b> , 52, 54	4
790	Validation and association of candidate markers for adult migration timing and fitness in Chinook Salmon. <b>2020</b> , 13, 2316-2332	8
789	Automated feature extraction from population wearable device data identified novel loci associated with sleep and circadian rhythms. <b>2020</b> , 16, e1009089	1
788	Detecting Selection from Linked Sites Using an -Model. <b>2020</b> , 216, 1205-1215	3
787	The gene is a key regulator of progranulin expression and modifies the risk of multiple neurodegenerative diseases. <b>2020</b> , 6,	5

786	Deleterious Missense Variant Associated with Type 1 Primary Hyperoxaluria (PH1) in Zwartbles Sheep. <b>2020</b> , 11,	1
785	Effect of DPYD, MTHFR, ABCB1, XRCC1, ERCC1 and GSTP1 on chemotherapy related toxicity in colorectal carcinoma. <b>2020</b> , 35, 388-398	3
784	Genetic Status of the Swedish Central collection of heirloom apple cultivars. <b>2020</b> , 272, 109599	6
783	Origin and adaptation to high altitude of Tibetan semi-wild wheat. <b>2020</b> , 11, 5085	27
782	Two genetic variants explain the association of European ancestry with multiple sclerosis risk in African-Americans. <b>2020</b> , 10, 16902	3
781	Explaining the Genetic Causality for Complex Phenotype via Deep Association Kernel Learning. <b>2020</b> , 1, 100057	3
780	Inferring Gene-by-Environment Interactions with a Bayesian Whole-Genome Regression Model. <b>2020</b> , 107, 698-713	9
779	Genome-wide association study of bone quality and feed efficiency-related traits in Pekin ducks. <b>2020</b> , 112, 5021-5028	3
778	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. 2020, 586, 769-775	32
777	Meta-analysis of whole-exome sequencing data from two independent cohorts finds no evidence for rare variant enrichment in Parkinson disease associated loci. <b>2020</b> , 15, e0239824	3
776	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <b>2020</b> , 7, 340	26
775	Genetic substructure and admixture of Mongolians and Kazakhs inferred from genome-wide array genotyping. <b>2020</b> , 47, 620-628	4
774	Limited genetic parallelism underlies recent, repeated incipient speciation in geographically proximate populations of an Arctic fish (Salvelinus alpinus). <b>2020</b> , 29, 4280-4294	9
773	Phenotypic variability and population structure analysis of Tanzanian free-range local chickens. <b>2020</b> , 16, 360	3
772	Runs of homozygosity islands in Italian cosmopolitan and autochthonous pig breeds identify selection signatures in the porcine genome. <b>2020</b> , 240, 104219	12
771	Mendelian randomization while jointly modeling cis genetics identifies causal relationships between gene expression and lipids. <b>2020</b> , 11, 4930	8
770	A genome resource for green millet Setaria viridis enables discovery of agronomically valuable loci. <b>2020</b> , 38, 1203-1210	43
769	Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. <b>2020</b> , 52, 1169-1177	51

768	Neural correlates of polygenic risk score for autism spectrum disorders in general population. <b>2020</b> , 2, fcaa092	5
767	Variants in and are associated with higher tau deposition. <b>2020</b> , 2, fcaa159	3
766	Investigating the genetic characteristics of the Csangos, a traditionally Hungarian speaking ethnic group residing in Romania. <b>2020</b> , 65, 1093-1103	1
765	MR-LDP: a two-sample Mendelian randomization for GWAS summary statistics accounting for linkage disequilibrium and horizontal pleiotropy. <b>2020</b> , 2, lqaa028	10
764	European genetic ancestry associated with risk of childhood ependymoma. <b>2020</b> , 22, 1637-1646	5
763	Somalier: rapid relatedness estimation for cancer and germline studies using efficient genome sketches. <b>2020</b> , 12, 62	10
762	PWAS: proteome-wide association study-linking genes and phenotypes by functional variation in proteins. <b>2020</b> , 21, 173	9
761	Fine-scale genomic analyses of admixed individuals reveal unrecognized genetic ancestry components in Argentina. <b>2020</b> , 15, e0233808	7
760	Genome-wide association study of milk components in Chinese Holstein cows using single nucleotide polymorphism. <b>2020</b> , 233, 103951	4
759	QTL mapping and candidate gene analysis of cadmium accumulation in polished rice by genome-wide association study. <b>2020</b> , 10, 11791	7
758	Intronic variation of the SOHLH2 gene confers risk to male reproductive impairment. <b>2020</b> , 114, 398-406	3
757	Partial Support for an Interaction Between a Polygenic Risk Score for Major Depressive Disorder and Prenatal Maternal Depressive Symptoms on Infant Right Amygdalar Volumes. <b>2020</b> , 30, 6121-6134	7
756	Genetic determinants of the humoral immune response in MS. <b>2020</b> , 7,	3
755	Genetic Diversity in Invasive Populations of Argentine Stem Weevil Associated with Adaptation to Biocontrol. <b>2020</b> , 11,	4
754	Gene-environment interaction with smoking for increased non-muscle-invasive bladder cancer tumor size. <b>2020</b> , 9, 1329-1337	2
753	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. <b>2021</b> , 106, 2233-2241	1
752	The Genetic Population Structure of Robinson Crusoe Island, Chile. <b>2020</b> , 11, 669	
751	Identification of genetic variants controlling RNA editing and their effect on RNA structure stabilization. <b>2020</b> , 28, 1753-1762	3

750	Admixture and natural selection shaped genomes of an Austronesian-speaking population in the Solomon Islands. <b>2020</b> , 10, 6872	4
749	The direction of genital asymmetry is expressed stochastically in internally fertilizing anablepid fishes. <b>2020</b> , 287, 20200969	1
748	Cooperation between and Its Symbiotic Fungal Community To Improve Local Adaptation of the Host. <b>2020</b> , 86,	1
747	Functional investigation of the coronary artery disease gene SVEP1. <b>2020</b> , 115, 67	5
746	Multiple waves of freshwater colonization of the three-spined stickleback in the Japanese Archipelago. <b>2020</b> , 20, 143	1
745	Candidate Gene Analysis Reveals Strong Association of Variants With High Density Lipoprotein Cholesterol and Variants With Low Density Lipoprotein Cholesterol in Ghanaian Adults: An AWI-Gen Sub-Study. <b>2020</b> , 11, 456661	2
744	Exome Sequencing of Native Populations From the Amazon Reveals Patterns on the Peopling of South America. <b>2020</b> , 11, 548507	2
743	Common germline risk variants impact somatic alterations and clinical features across cancers.	O
742	Leveraging global multi-ancestry meta-analysis in the study of idiopathic pulmonary fibrosis genetics. <b>2022</b> , 2, 100181	O
741	Common variability in oestrogen-related genes and pancreatic ductal adenocarcinoma risk in women. <b>2022</b> , 12,	1
740	Parasite Genotype Is a Major Predictor of Mortality from Visceral Leishmaniasis.	0
739	The causal associations of circulating amino acids with blood pressure: a Mendelian randomization study. <b>2022</b> , 20,	O
738	Identity-by-descent analysis of a large Tourettell syndrome pedigree from Costa Rica implicates genes involved in neuronal development and signal transduction.	0
737	Frontotemporal degeneration genetic risk loci and transcription regulation as a possible mechanistic link to disease risk. <b>2022</b> , 101, e31078	O
736	Assessing the causal relationships between gout and hypertension: a bidirectional Mendelian randomisation study with coarsened exposures. <b>2022</b> , 24,	O
735	Oligogenic prediction of eye and hair colour in the Danish population.	O
734	Genomic Tools for the Characterization of Local Animal Genetic Resources: Application in Mascaruna Goat. <b>2022</b> , 12, 2840	O
733	Genome-wide association study identifies multiple HLA loci for sarcoidosis susceptibility.	O

732	Declining autozygosity over time: an exploration in over 1 million individuals from three diverse cohorts.	0
731	An insight into the runs of homozygosity distribution and breed differentiation in Mangalitsa pigs. 13,	О
730	Human impact on the recent population history of the elusive European wildcat inferred from whole genome data. <b>2022</b> , 23,	O
729	Repeat polymorphisms in non-coding DNA underlie top genetic risk loci for glaucoma and colorectal cancer.	О
728	Tracking footprints of artificial and natural selection signatures in breeding and non-breeding cats. <b>2022</b> , 12,	1
727	Genetics reveals shifts in reproductive behaviour of the invasive bird parasite Philornis downsi collected from Darwin finch nests.	О
726	Genetic variants for prediction of gestational diabetes mellitus and modulation of susceptibility by a nutritional intervention based on a Mediterranean diet. 13,	O
725	Characterisation of ethnic differences in DNA methylation between UK-resident South Asians and Europeans. <b>2022</b> , 14,	1
724	Kernel-based geneënvironment interaction tests for rare variants with multiple quantitative phenotypes. <b>2022</b> , 17, e0275929	0
723	Mapping of Candidate Genes in Response to Low Nitrogen in Rice Seedlings. <b>2022</b> , 15,	2
722	A Pilot Study of Associations Between the Occurrence of Palpitations and Cytokine Gene Variations in Women Prior to Breast Cancer Surgery. 109980042211346	O
721	Weak genetic differentiation but strong climate-induced selective pressure toward the rear edge of mountain pine in north-eastern Spain. <b>2022</b> , 159778	1
720	Shared Genetic Regulatory Networks Contribute to Neuropathic and Inflammatory Pain: Multi-Omics Systems Analysis. <b>2022</b> , 12, 1454	O
719	Predictive Network Analysis IdentifiesJMJD6and Other Novel Key Drivers in Alzheimer Disease.	O
718	Genetic admixture history and forensic characteristics of Tibeto-Burman-speaking Qiang people explored via the newly developed Y-STR panel and genome-wide SNP data. 10,	O
717	Systematic Mendelian randomization using the human plasma proteome to discover potential therapeutic targets for stroke. <b>2022</b> , 13,	О
716	The contribution of functional HNF1A variants and polygenic susceptibility to risk of type 2 diabetes in ancestrally diverse populations.	O
715	The genome-wide allele and haplotype-sharing patterns suggested one unique Hmong- Mein-related lineage in Southwest China.	O

714	Leveraging functional genomic annotations and genome coverage to improve polygenic prediction of complex traits within and between ancestries.	O
713	Genome Wide Association Study with Imputed Whole Genome Sequence Data Identifies a 431 kb Risk Haplotype on CFA18 for Congenital Laryngeal Paralysis in Alaskan Sled Dogs. <b>2022</b> , 13, 1808	O
712	Validation of Polygenic Risk Scores for Coronary Heart Disease in a Middle Eastern Cohort Using Whole Genome Sequencing.	0
711	Polygenic heterogeneity in antidepressant treatment and placebo response. <b>2022</b> , 12,	O
710	Dissecting the genetic architecture of sunflower head diameter using genome-wide association study.	O
709	Age-dependent topic modelling of comorbidities in UK Biobank identifies disease subtypes with differential genetic risk.	O
708	A genetic risk score improves risk stratification for anticoagulation-related intracerebral hemorrhage.	О
707	Structural models of genome-wide covariance identify multiple common dimensions in autism.	O
706	The power of geohistorical boundaries for modeling the genetic background of human populations: the case of the rural Catalan Pyrenees.	О
705	Association between genetic variants and the risk of nivolumab-induced immune-related adverse events.	O
704	Genetic map of regional sulcal morphology in the human brain from UK biobank data. 2022, 13,	O
703	Multi-Omic analyses characterize the ceramide/sphingomyelin pathway as a therapeutic target in Alzheimer disease. <b>2022</b> , 5,	1
702	Investigation of clinical characteristics and genome associations in the $\mbox{U}$ K Lipoedemaltohort. 2022 , 17, e0274867	1
701	Genome sequencing reveals evidence of adaptive variation in the genus Zea.	1
700	The HUNT study: A population-based cohort for genetic research. 2022, 2, 100193	O
699	Gene-vegetarianism interactions detected in genome-wide analyses across 30 serum biomarkers.	O
698	Phylogeographic structure of Heteroplexis (Asteraceae), an endangered endemic genus in the limestone karst regions of southern China. 13,	О
697	Analysis of Y chromosome haplogroups in Parkinson⊠ disease.	O

696	Improving fine-mapping by modeling infinitesimal effects.	O
695	Resequencing of 558 Chinese mungbean landraces identifies genetic loci associated with key agronomic traits. 13,	O
694	The first high-density genetic map of common cockle (Cerastoderma edule) reveals a major QTL controlling shell color variation. <b>2022</b> , 12,	О
693	Gene Sequencing Identifies Perturbation in Nitric Oxide Signaling as a Nonlipid Molecular Subtype of Coronary Artery Disease.	O
692	Sex differences in multilayer functional network topology over the course of aging in 37543 UK Biobank participants. 1-40	O
691	A genome-wide association study identified new variants associated with mathematical abilities in Chinese children.	O
690	Evolutionary Responses of a Reef-building Coral to Climate Change at the End of the Last Glacial Maximum. <b>2022</b> , 39,	О
689	PGG.SV: a whole-genome-sequencing-based structural variant resource and data analysis platform.	O
688	Mechanism and modeling of human disease-associated near-exon intronic variants that perturb RNA splicing.	O
687	Genomic Signatures of Freshwater Adaptation in Pacific Herring (Clupea pallasii). <b>2022</b> , 13, 1856	O
686	Metabolome-wide association study on ABCA7 indicates a role of ceramide metabolism in Alzheimer disease. <b>2022</b> , 119,	1
685	Accurate detection of shared genetic architecture from GWAS summary statistics in the small-sample context.	O
684	Genomic detection of a secondary family burial in a single jar coffin in early Medieval Korea.	O
683	Assessing Genetic Diversity and Searching for Selection Signatures by Comparison between the Indigenous Livni and Duroc Breeds in Local Livestock of the Central Region of Russia. <b>2022</b> , 14, 859	O
682	Assessment of the genetic and clinical determinants of hip fracture risk: Genome-wide association and Mendelian randomization study. <b>2022</b> , 3, 100776	O
681	Century-long timelines of herbarium genomes predict plant stomatal response to climate change.	O
680	Influences of rare copy-number variation on human complex traits. <b>2022</b> , 185, 4233-4248.e27	О
679	PheWAS and cross-disorder analyses reveal genetic architecture, pleiotropic loci and phenotypic correlations across 11 autoimmune disorders.	O

678	Cohort profile: the Food Chain Plus (FoCus) cohort. <b>2022</b> , 37, 1087-1105	О
677	Taiwan Biobank: A rich biomedical research database of the Taiwanese population. <b>2022</b> , 100197	O
676	Historical dispersal and host-switching formed the evolutionary history of a globally distributed multi-host parasite - theLigula intestinalisspecies complex.	0
675	Hereditary variants of unknown significance in African American women with breast cancer. <b>2022</b> , 17, e0273835	O
674	Natural Variation inBrachypodium distachyonResponses to Combined Abiotic Stresses.	O
673	Nidogen-1 could play a role in diabetic kidney disease development in type 2 diabetes: a genome-wide association meta-analysis. <b>2022</b> , 16,	O
672	Association of Kallikrein Related Peptidase 3 (KLK3) Gene with Dermatophytosis in the UK Biobank cohort.	0
671	Constructing an atlas of associations between polygenic scores from across the human phenome and circulating metabolic biomarkers. 11,	O
670	Rare coding variants inCHRNB2reduce the likelihood of smoking.	O
669	Gene set analysis of transcriptomics data identifies new biological processes associated with early markers of atherosclerosis but not with those of osteoporosis: Atherosclerosis-osteoporosis co/multimorbidity study in the Young Finns Study. <b>2022</b> , 361, 1-9	o
668	Meta-analysis of gestational duration and spontaneous preterm birth identifies new maternal risk loci.	0
667	A database of 5305 healthy Korean individuals reveals genetic and clinical implications for an East Asian population.	1
666	Common and rare variants of EGF increase the genetic risk of Alzheimer's disease as revealed by targeted sequencing of growth factors in Han Chinese. <b>2022</b> ,	O
665	Genome-Wide Association Study of Adhesive Capsulitis Suggests Significant Genetic Risk Factors. <b>2022</b> , 104, 1869-1876	0
664	Meta-analysis of epigenome-wide association studies of major depressive disorder. 2022, 12,	0
663	The difficulty of predicting evolutionary change in response to novel ecological interactions: a field experiment with Anolis lizards.	O
662	ParseCNV2: efficient sequencing tool for copy number variation genome-wide association studies.	0
661	Genetics of randomly bred cats support the cradle of cat domestication being in the Near East.	1

660	A secreted protease-like protein inZymoseptoria triticiis responsible for avirulence onStb9resistance gene in wheat.	O
659	Population genomic evidence of adaptive response during the invasion history ofPlasmodium falciparumin the Americas.	O
658	Shared genetic risk factors and causal association between psoriasis and coronary artery disease. <b>2022</b> , 13,	O
657	Using Genomic Structural Equation Modeling to Partition the Genetic Covariance Between Birthweight and Cardiometabolic Risk Factors into Maternal and Offspring Components in the Norwegian HUNT Study.	O
656	Immune and Genomic Analysis of Boxer Dog Breed and Its Relationship with Leishmania infantum Infection. <b>2022</b> , 9, 608	O
655	Mendelian randomization analysis of factors related to ovulation and reproductive function and endometrial cancer risk. <b>2022</b> , 20,	O
654	The Molecular Human 🖪 Roadmap of Molecular Interactions Linking Multiomics Networks with Disease Endpoints	O
653	Characterization of Arabian Peninsula whole exomes: Contributing to the catalogue of human diversity. <b>2022</b> , 25, 105336	O
652	Analysis of the caudate nucleus transcriptome in individuals with schizophrenia highlights effects of antipsychotics and new risk genes. <b>2022</b> , 25, 1559-1568	2
651	Identification of quantitative trait loci for related traits of stalk lodging resistance using genome-wide association studies in maize (Zea mays L.). <b>2022</b> , 23,	O
650	A stop-gain variant in BTNL9 is associated with atherogenic lipid profiles. <b>2023</b> , 4, 100155	O
649	Identification of key adipogenic transcription factors for the pork belly parameters via the association weight matrix. <b>2023</b> , 195, 109015	1
648	Associations between abdominal adipose tissue, reproductive span, and brain characteristics in post-menopausal women. <b>2022</b> , 36, 103239	О
647	Genetic susceptibility, homocysteine levels, and risk of all-cause and cause-specific mortality: A prospective cohort study. <b>2023</b> , 538, 1-8	1
646	Effects of DNA degradation and genotype imputation on high-density SNP microarray in pairwise kinship analysis. <b>2023</b> , 60, 102158	O
645	Ancestry,ACKR1and leucopenia in patients with systemic lupus erythematosus. <b>2022</b> , 9, e000790	O
644	Association of demographic and clinical factors with risk of acute pancreatitis: An exposure-wide Mendelian randomization study.	O
643	Understanding Mendelian errors in SNP arrays data using a Gochu Asturcelta pig pedigree: genomic alterations, family size and calling errors. <b>2022</b> , 12,	O

642	The contribution of common and rare genetic variants to variation in metabolic traits in 288,137 East Asians. <b>2022</b> , 13,	O
641	Immune and spermatogenesis-related loci are involved in the development of extreme patterns of male infertility. <b>2022</b> , 5,	O
640	A genome wide association study of chronic spontaneous urticaria risk and heterogeneity. 2022,	O
639	Identification of genomic regions associated with total and progressive sperm motility in Italian Holstein bulls. <b>2022</b> ,	1
638	Genome-wide admixture and association analysis identifies African ancestry specific risk loci of eosinophilic esophagitis in African American. <b>2022</b> ,	1
637	Polygenic risk scores for schizophrenia and major depression are associated with socio-economic indicators of adversity in two British community samples. <b>2022</b> , 12,	O
636	A genome-wide association study of mammographic texture variation. 2022, 24,	O
635	Dissecting the loci underlying maturation timing in Atlantic salmon using haplotype and multi-SNP based association methods.	O
634	Shared genetic influences between blood analyte levels and risk of severe COVID-19. <b>2022</b> , 111708	0
633	Genetic association models are robust to common population kinship estimation biases.	O
632	Denisovan and Neanderthal archaic introgression differentially impacted the genetics of complex traits in modern populations. <b>2022</b> , 20,	1
631	Genome-wide contribution of common short-tandem repeats to Parkinson disease genetic risk.	O
630	Retrotransposon insertions associated with risk of neurologic and psychiatric diseases.	O
629	Kinship and genetic variation in aquarium-spawned Acropora hyacinthus corals. 9,	O
628	Meta-analysis fine-mapping is often miscalibrated at single-variant resolution. 2022, 100210	O
627	Genome-wide SNPs in the spiny lobster Panulirus homarus reveal a hybrid origin for its subspecies. <b>2022</b> , 23,	O
626	Pilot genome-wide association study of antibody response to inactivated SARS-CoV-2 vaccines. 13,	0
625	Post-GWAS multiomic functional investigation of the TNIP 1 locus in Alzheimer II disease implicates mediation through GPX3.	O

624	Higher Waist Hip Ratio Genetic Risk Score Is Associated with Reduced Weight Loss in Patients with Severe Obesity Completing a Meal Replacement Programme. <b>2022</b> , 12, 1881	0
623	Genome-wide association study of host resistance to the ectoparasite 1chthyophthirius multifiliis in the Amazon fish Colossoma macropomum.	0
622	Population-based discovery and Mendelian randomization analysis identify telmisartan as a candidate medicine for Alzheimer's disease in African Americans.	1
621	A comparison of classical and machine learning-based phenotype prediction methods on simulated data and three plant species. 13,	0
620	Multi-ancestry meta-analysis of asthma identifies novel associations and highlights the value of increased power and diversity. <b>2022</b> , 100212	1
619	HCLC-FC: A novel statistical method for phenome-wide association studies. <b>2022</b> , 17, e0276646	0
618	Repeated out-of-Africa expansions of Helicobacter pylori driven by replacement of deleterious mutations. <b>2022</b> , 13,	0
617	Genome-wide association study and genomic prediction of tolerance to acute hypoxia in rainbow trout. <b>2022</b> , 739068	1
616	Human genetics uncovers MAP3K15 as an obesity-independent therapeutic target for diabetes. <b>2022</b> , 8,	O
615	Identifying causal serum protein-cardiometabolic trait relationships using whole genome sequencing.	O
614	Genome- and transcriptome-wide association studies of 386,000 Asian and European-ancestry women provide new insights into breast cancer genetics. <b>2022</b> ,	1
613	Identification of PCSK9-like human gene knockouts using metabolomics, proteomics, and whole-genome sequencing in a consanguineous population. <b>2022</b> , 100218	O
612	Simultaneous detection of novel genes and SNPs by adaptive p-value combination. 13,	0
611	Single-cell genome-wide association reveals that a nonsynonymous variant in ERAP1 confers increased susceptibility to influenza virus. <b>2022</b> , 2, 100207	O
610	Ecological speciation promoted by divergent regulation of functional genes within African cichlid fishes.	0
609	Association studies between chromosomal regions 1q21.3, 5q21.3, 14q21.2 and 17q21.31 and numbers of children in Poland. <b>2022</b> , 12,	O
608	Genomics reveals introgression and purging of deleterious mutations in the Arabian leopard (Panthera pardus nimr).	О
607	Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. <b>2022</b> , 5,	1

606	Genetic Susceptibility of Dipeptidyl Peptidase-4 Inhibitor Associated Bullous Pemphigoid in Chinese Patients with Type 2 Diabetes.	O
605	Comparative serum proteomic analysis of a selected protein panel in individuals with schizophrenia and bipolar disorder and the impact of genetic risk burden on serum proteomic profiles. <b>2022</b> , 12,	O
604	Consequences of exposure to pollutants on respiratory health: From genetic correlations to causal relationships. <b>2022</b> , 17, e0277235	O
603	Cross-trait assortative mating is widespread and inflates genetic correlation estimates. <b>2022</b> , 378, 754-761	1
602	Genetic adaptations to potato starch digestion in the Peruvian Andes.	0
601	Association analyses of the autosomal genome and mitochondrial DNA with accelerometry-derived sleep parameters in depressed UK biobank subjects. <b>2022</b> ,	O
600	H3AGWAS: a portable workflow for genome wide association studies. <b>2022</b> , 23,	O
599	Cost-effectively dissecting the genetic architecture of complex wool traits in rabbits by low-coverage sequencing. <b>2022</b> , 54,	O
598	Family-based analysis of the contribution of rare and common genetic variants to school performance in schizophrenia.	O
597	Ancestrally polymorphic chromosomal inversions as potential drivers of speciation.	O
596	Education interacts with genetic variants near GJD2, RBFOX1, LAMA2, KCNQ5 and LRRC4C to confer susceptibility to myopia. <b>2022</b> , 18, e1010478	0
595	Genomic signals of local adaptation and hybridization in Asian white birch.	O
594	Histone H2A monoubiquitination in the thalamus regulates cocaine effects and addiction risk.	О
593	HLA-associated outcomes in peanut oral immunotherapy trials identify mechanistic and clinical determinants of therapeutic success. 13,	O
592	DPYSL2/CRMP2 isoform B knockout in human iPSC-derived glutamatergic neurons confirms its role in mTOR signaling and neurodevelopmental disorders.	O
591	Mapping brain endophenotypes associated with idiopathic pulmonary fibrosis genetic risk. <b>2022</b> , 86, 104356	O
590	Classification of cattle breeds based on the random forest approach. <b>2023</b> , 267, 105143	О
589	Genetic influences on human blood metabolites in the Japanese population. <b>2023</b> , 26, 105738	O

588	Inherited rare variants in homologous recombination and neurodevelopmental genes are associated with increased risk of neuroblastoma. <b>2023</b> , 87, 104395	0
587	Contribution bias of parental genomes to the hybrid lineages of black Amur bream and topmouth culter revealed by low-coverage whole-genome sequencing. <b>2023</b> , 852, 147058	O
586	Genetic diversity of two native sheep breeds by genome-wide analysis of single nucleotide polymorphisms. <b>2023</b> , 17, 100690	О
585	Segregation patterns and inheritance rate of copy number variations regions assessed in a Gochu Asturcelta pig pedigree. <b>2023</b> , 854, 147111	O
584	Deciphering the genetic basis and prediction genomic estimated breeding values of heat tolerance in Zhikong scallop Chlamys farreri. <b>2023</b> , 565, 739090	О
583	Protocol to analyze population structure and migration history based on human genome variation data. <b>2023</b> , 4, 101928	O
582	Associations of renal sinus fat with blood pressure and ectopic fat in a diverse cohort of adults. <b>2023</b> , 16, 200165	0
581	Genome-wide association study of osteonecrosis of the jaw in Danish patients receiving antiresorptive therapy for osteoporosis: A case-control study. <b>2023</b> , 18, 101648	O
580	A combined clinical and genetic model for predicting risk of ovarian cancer. <b>2023</b> , 32, 57-64	0
579	Polygenic risk scores adaptation for Height in a Vietnamese population. <b>2022</b> ,	O
578	Risk Factors Associated With First and Second Primary Melanomas in a High-Incidence Population.	O
577	Vitamin D and the preclinical Alzheimer cognitive composite cognition (PACC) score: a two-sample mendelian randomization study.	O
576	The impact of assortative mating, participation bias, and socioeconomic status on the polygenic risk of behavioral and psychiatric traits.	0
575	Heritability estimates of distichiasis in Staffordshire bull terriers using pedigrees and genome-wide SNP data. <b>2022</b> , 64,	O
574	Quantifying the causal impact of biological risk factors on healthcare costs.	0
573	Natural genetic variation in the pheromone production ofC. elegans.	1
572	The impact of genetic risk for Alzheimer disease on the structural brain networks of young adults. 16,	O
571	A genome-wide association study identifies a novel association between SDC3 and apparent treatment-resistant hypertension. <b>2022</b> , 20,	O

570	Targeted screening of genetic associations with COVID-19 susceptibility and severity. 13,	O
569	The genetic risk of gestational diabetes in South Asian women. 11,	O
568	Meta-analysis of genome-wide association studies uncovers shared candidate genes across breeds for pig fatness trait. <b>2022</b> , 23,	1
567	Genetically personalised organ-specific metabolic models in health and disease. <b>2022</b> , 13,	O
566	Polygenic coronary artery disease association with brain atrophy in the cognitively impaired. <b>2022</b> , 4,	O
565	Hepatic WDR23 proteostasis mediates insulin clearance by regulating insulin-degrading enzyme activity.	O
564	Phenotyping with Positive Unlabelled Learning for Genome-Wide Association Studies. 2023, 117-135	O
563	Genetic influences on the interplay between obsessive-compulsive behavior symptoms and cannabis use during adolescence.	O
562	Epigenome-wide association study of serum folate in maternal peripheral blood leukocytes.	0
561	Genome-wide association study for wattles trait in the dairy goat breed. 1-7	O
561 560	Genome-wide association study for wattles trait in the dairy goat breed. 1-7  Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular Filtration Rate Decline in Korea Based on Genome Metabolomic Integrative Analysis. 2022, 12, 1139	0
	Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular	
560	Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular Filtration Rate Decline in Korea Based on Genome Metabolomic Integrative Analysis. <b>2022</b> , 12, 1139	0
560 559	Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular Filtration Rate Decline in Korea Based on Genome Metabolomic Integrative Analysis. 2022, 12, 1139  A frequent ancestral NFKB1 variant predicts risk of infection or allergy.  k2v: A Containerized Workflow for Creating VCF Files from Kintelligence Targeted Sequencing	0
560 559 558	Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular Filtration Rate Decline in Korea Based on Genome Metabolomic Integrative Analysis. 2022, 12, 1139  A frequent ancestral NFKB1 variant predicts risk of infection or allergy.  k2v: A Containerized Workflow for Creating VCF Files from Kintelligence Targeted Sequencing Data.  Associations between attention-deficit hyperactivity disorder genetic liability and ICD-10 medical	0 0
560 559 558 557	Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular Filtration Rate Decline in Korea Based on Genome Metabolomic Integrative Analysis. 2022, 12, 1139  A frequent ancestral NFKB1 variant predicts risk of infection or allergy.  k2v: A Containerized Workflow for Creating VCF Files from Kintelligence Targeted Sequencing Data.  Associations between attention-deficit hyperactivity disorder genetic liability and ICD-10 medical conditions in adults: Utilizing electronic health records in a Phenome-Wide Association Study.  A Shigella sonnei clone with extensive drug resistance associated with waterborne outbreaks in	0 0
560 559 558 557 556	Identifying Genetic Variants and Metabolites Associated with Rapid Estimated Glomerular Filtration Rate Decline in Korea Based on GenomeMetabolomic Integrative Analysis. 2022, 12, 1139  A frequent ancestral NFKB1 variant predicts risk of infection or allergy.  k2v: A Containerized Workflow for Creating VCF Files from Kintelligence Targeted Sequencing Data.  Associations between attention-deficit hyperactivity disorder genetic liability and ICD-10 medical conditions in adults: Utilizing electronic health records in a Phenome-Wide Association Study.  A Shigella sonnei clone with extensive drug resistance associated with waterborne outbreaks in China. 2022, 13,	<ul><li>O</li><li>O</li><li>O</li><li>O</li></ul>

552	PYPE: A Python pipeline for phenome-wide association (PheWAS) and mendelian randomization in investigator-driven phenotypes and genotypes of biobank data.	O
551	SDPRX: A statistical method for cross-population prediction of complex traits. <b>2022</b> ,	О
550	Reconstruction of the Major Maternal and Paternal Lineages in the Feral New Zealand Kaimanawa Horses. <b>2022</b> , 12, 3508	O
549	Rare variants in SLC34A3 explain missing heritability of urinary stone disease.	O
548	Pharmacogenetics of CYP2A6, CYP2B6, and UGT2B7 in the Context of HIV Treatments in African Populations. <b>2022</b> , 12, 2013	0
547	Kalpra: A kernel approach for longitudinal pathway regression analysis integrating network information with an application to the longitudinal PsyCourse Study. 13,	О
546	Rapid and predictable genome evolution across three hybrid ant populations. 2022, 20, e3001914	О
545	Whole-genome sequencing reveals diverse mechanisms underlying quantitative pathogenicity and host adaptation in a fungal plant pathogen.	О
544	Predicting the prevalence of complex genetic diseases from individual genotype profiles using capsule networks.	0
543	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.	o
542	Analytic pipelines to assess the relationship between immune response and germline genetics in human tumors. <b>2022</b> , 3, 101809	0
541	Development and validation of genome-wide polygenic risk scores for predicting breast cancer incidence in Japanese females: a population-based case-cohort study.	О
540	Genetic variants in Telomerase Reverse Transcriptase contribute to solar lentigines. 2022,	О
539	Genome-wide association study identifies novel loci associated with skin autofluorescence in individuals without diabetes. <b>2022</b> , 23,	О
538	Disentangling the causal relationship between rabbit growth and cecal microbiota through structural equation models. <b>2022</b> , 54,	0
537	The missing link between genetic association and regulatory function. 11,	o
536	Genome-wide association and mendelian randomisation study of metabolites and pregnancy dysglycemia in a UK multi-ethnic birth cohort.	0
535	Cultural and demic co-diffusion of Tubo Empire on Tibetan Plateau. <b>2022</b> , 25, 105636	0

534	Genetic Diversity and Population Differentiation of Dongxiang Wild Rice (Oryza rufipogon Griff.) Based on SNP Markers. <b>2022</b> , 12, 3056	О
533	LRRK2 Kinase Activity Regulates Parkinson Disease-Relevant Lipids at the Lysosome.	Ο
532	Uncovering the genomic basis of infection through co-genomic sequencing of hosts and parasites.	O
531	Challenges in selecting admixture models and marker sets to infer genetic ancestry in a Brazilian admixed population. <b>2022</b> , 12,	O
530	Evaluation of the causal associations between brain imaging-derived phenotypes and type 2 diabetes: a bidirectional Mendelian randomization study.	0
529	Genome-wide association study of REM sleep behavior disorder identifies polygenic risk and brain expression effects. <b>2022</b> , 13,	1
528	Contribution of TEX15 genetic variants to the risk of developing severe non-obstructive oligozoospermia. 10,	О
527	Genomic differentiation with isolation by distance along a latitudinal gradient in the spotted-leg treefrog Polypedates megacephalus.	0
526	Phenome-wide association study of loci harboring de novo tandem repeat mutations in UK Biobank exomes. <b>2022</b> , 13,	0
525	Genome-wide detection of positive and balancing selection signatures shared by four domesticated rainbow trout populations (Oncorhynchus mykiss).	0
524	Genome-wide association study of multiple neuropathology endophenotypes identifies novel risk loci and provides insights into known Alzheimer risk loci.	O
523	Dynamic Interactomics by Cross-Linking Mass Spectrometry: Mapping the Daily Cell Life in Postgenomic Era. <b>2022</b> , 26, 633-649	0
522	Lacustrine speciation associated with chromosomal inversion in a lineage of riverine fishes.	0
521	Genome-wide association study reveals ethnicity-specific SNPs associated with ankylosing spondylitis in the Taiwanese population. <b>2022</b> , 20,	O
520	Association between Dietary Behaviors and BMI Stratified by Sex and the ALDH2 rs671 Polymorphism in Japanese Adults. <b>2022</b> , 14, 5116	О
519	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants. <b>2022</b> , 54, 1803-1815	3
518	Domestic dog lineages reveal genetic drivers of behavioral diversification. <b>2022</b> , 185, 4737-4755.e18	1
517	Comparison of two multi-trait association testing methods and sequence-based fine mapping of six QTL in Swiss Large White pigs.	0

516	Germline Genetic and Treatment-Related Risk Factors for Diabetes Mellitus in Survivors of Childhood Cancer: A Report From the Childhood Cancer Survivor Study and St Jude Lifetime Cohorts. <b>2022</b> ,	O
515	Historic DNA uncovers genetic effects of climate change and landscape alteration in two wild bee species.	О
514	Taxonomic assessment of two wild house mouse subspecies using whole-genome sequencing. <b>2022</b> , 12,	О
513	The role of Neanderthal introgression in liver cancer. <b>2022</b> , 15,	О
512	Divergent selection predating the Last Glacial Maximum mainly acted on macro-phenotypes in Norway spruce.	О
511	Variation and genetic control of individual recombination rates in Norwegian Red dairy cattle. <b>2022</b> ,	О
510	Genome-wide association study of obstructive sleep apnea in the Million Veteran Program uncovers genetic heterogeneity by sex.	O
509	Analysis of merged transcriptomic and genomic datasets to identify genes and pathways underlying residual feed intake in growing pigs. <b>2022</b> , 12,	О
508	Genome-wide association study for vascular aging highlights pathways shared with cardiovascular traits in Koreans. 9,	О
507	Polygenic effect on tau pathology progression in Alzheimer's disease.	О
506	Genetic correlations between gut microbiome genera, Alzheimer disease diagnosis, and APOE genotypes: a polygenic risk score study.	0
505	Development and Validation of 105 SNP Markers in Chionodraco rastrospinosus.	1
504	Polygenic risk scores for nicotine use and family history of smoking are associated with smoking behaviour.	0
503	Polygenic score for sleep duration in relation to risk of Alzheimer disease: results from the UK Biobank.	О
502	Genome-Wide Association Study Identifies CDKN1A as a Novel Locus Associated with Muscle Fiber Composition. <b>2022</b> , 11, 3910	3
501	Spatiotemporal fluctuations of population structure in the Americas revealed by a meta-analysis of the first decade of archaeogenomes.	О
500	Identification of the riceRcgene as a main regulator of seed survival under dry storage conditions.	O
499	Demographic model and biological adaptation inferred from the genome-wide single nucleotide polymorphism data reveal tripartite origins of southernmost C hinese H uis.	О

498	Stress, Genetics and Mood: Impact of COVID-19 on a College Freshman Sample.	O
497	Genetic risk for attention-deficit/hyperactivity disorder predicts cognitive decline and development of Alzheimer disease pathophysiology in cognitively unimpaired older adults.	o
496	Does selection occur at the intermediate zone of two insufficiently isolated populations? A whole-genome analysis along an altitudinal gradient.	0
495	Population genetic analyses unveiled genetic stratification and differential natural selection signatures across the G-gene of viral hemorrhagic septicemia virus. 13,	o
494	TTLL11 gene is associated with sustained attention performance and brain networks: A genome-wide association study of a healthy Chinese sample.	0
493	Plant GWAS. <b>2022</b> , 181-189	О
492	Genetic architecture of heart failure with preserved versus reduced ejection fraction. 2022, 13,	0
491	Applying multi-omics data to study the genetic background of bovine respiratory disease infection in feedlot crossbred cattle. 13,	1
490	Identification of Novel, Replicable Genetic Risk Loci for Suicidal Thoughts and Behaviors Among US Military Veterans.	1
489	Implementation and Evaluation of Personal Genetic Testing As Part of Genomics Analysis Courses in German Universities.	O
488	Identification of breed-specific genomic variants in Colombian Creole pig breeds by whole-genome sequencing.	O
487	Association of genetic ancestry with HER2, GRB7 AND estrogen receptor expression among Colombian women with breast cancer. 12,	O
486	Whole genome sequencing identifies rare variants inANK1, LRRN1, HAS1, and other genes and gene regulatory regions for stroke in type 1 diabetes.	0
485	Genome-wide association study of thyroid-stimulating hormone highlights new genes, pathways and associations with thyroid disease susceptibility and age-of-onset.	o
484	Association between NOTCH3 gene and Parkinson⊠ disease based on whole-exome sequencing. 14,	0
483	Comprehensive characterization of putative genetic influences on plasma metabolome in a pediatric cohort. <b>2022</b> , 16,	o
482	Identification of key variants correlated with susceptibility of primary osteoporosis in the Chinese Han group.	0
481	Spatial and temporal heterogeneity in human mobility patterns in Holocene Southwest Asia and the East Mediterranean. <b>2022</b> ,	О

480	Historical dispersal and host-switching formed the evolutionary history of a globally distributed multi-host parasite - the Ligula intestinalis species complex. <b>2022</b> , 107677	0
479	Relationship among genetic variants, obesity traits and asthma in the Taiwan Biobank. <b>2022</b> , 9, e001355	O
478	Genetic architecture and evolution of color variation in American black bears. 2022,	О
477	Altered and allele-specific open chromatin landscape reveals epigenetic and genetic regulators of innate immunity in COVID-19. <b>2022</b> , 100232	1
476	Testing hypotheses of hybrid taxon formation in the shrubby beardtongues ( Penstemon subgenus Dasanthera ).	Ο
475	Genetic Variants at the Nebulette Locus Are Associated with Myxomatous Mitral Valve Disease Severity in Cavalier King Charles Spaniels. <b>2022</b> , 13, 2292	O
474	Genome-wide association study (GWAS) of circulating vitamin D outcomes among individuals of African-ancestry. <b>2022</b> ,	1
473	Korea4K: whole genome sequences of 4,157 Koreans with 107 phenotypes derived from extensive health check-ups.	O
472	Resistance to chicken amyloid arthropathy is associated with a dysfunctional mutation in serum amyloid A. <b>2023</b> , 37,	O
471	Meta-analysis of atopic dermatitis in 1,094,060 individuals identifies new risk loci, and sub-analysis characterizes the loci with disease severity and onset.	O
470	Multiple founding paternal lineages inferred from the newly-developed SNPSeqTyper 639 Y-SNP panel suggested the complex admixture and migration history of Chinese people.	O
469	Tracing the geographic origin of endangered plant species using transcriptome-derived SNPs : An example of Cathaya argyrophylla.	O
468	Genome-wide association studies of viral infections short guide to a successful experimental and statistical analysis. 2,	O
467	Genomes of endangered great hammerhead and shortfin mako sharks reveal historic population declines and high levels of inbreeding in great hammerhead. <b>2022</b> , 105815	O
466	The evolutionary history of Drosophila simulans Y chromosomes reveals molecular signatures of resistance to sex ratio meiotic drive.	O
465	Comparative Silk Transcriptomics Illuminates Distinctive Impact of Artificial Selection in Silkworm Modern Breeding. <b>2022</b> , 13, 1163	O
464	A multi-phenotype analysis reveals 19 susceptibility loci for basal cell carcinoma and 15 for squamous cell carcinoma. <b>2022</b> , 13,	0
463	Common protein-coding variants influence the racing phenotype in galloping racehorse breeds. <b>2022</b> , 5,	O

462	Novel Genetic Variants in TP37, PIK3R1, CALM1, and PLCG2 of the Neurotrophin Signaling Pathway Are Associated with the Progression from Mild Cognitive Impairment to Alzheimer Disease. <b>2022</b> , 1-11	О
461	Association of Supernumerary Sex Chromosome Aneuploidies With Venous Thromboembolism. <b>2023</b> , 329, 235	O
460	Identification of runs of homozygosity in Western honey bees (Apis mellifera) using whole-genome sequencing data. <b>2023</b> , 13,	О
459	Cryo-EM structure of the cytosolic AhR complex. <b>2023</b> ,	O
458	Fine-mapping across diverse ancestries drives the discovery of putative causal variants underlying human complex traits and diseases.	O
457	Distinct traces of mixed ancestry in western commercial pig genomes following gene flow from Chinese indigenous breeds. 13,	О
456	The power of geohistorical boundaries for modeling the genetic background of human populations: The case of the rural catalan Pyrenees. 13,	O
455	Population-specific positive selection on low CR1 expression in malaria-endemic regions. <b>2023</b> , 18, e0280282	О
454	Genetic architecture of brain age and its casual relations with brain and mental disorders.	О
453	Characterization of Danube Swabian population samples on a high-resolution genome-wide basis. <b>2023</b> , 24,	O
452	DNA extraction from clotted blood in genotyping quality.	О
451	Multi-omic association study identifies DNA methylation-mediated genotype and smoking exposure effects on lung function in children living in urban settings. <b>2023</b> , 19, e1010594	О
450	Genome-Wide Association Studies of Seven Root Traits in Soybean (Glycine max L.) Landraces. <b>2023</b> , 24, 873	О
449	GWAS of depression in 4,520 individuals from the Russian population highlights the role of MAGI2 (S-SCAM) in the gut-brain axis. 13,	О
448	Differentiated genomic footprints and connections inferred from 440 Hmong-Mien genomes suggest their isolation and long-distance migration.	О
447	Shared patterns of population genomic variation and phenotypic response across rapid range expansions in two invasive lady beetle species.	О
446	The genetic architecture of the human skeletal form.	О
445	Explainable machine learning aggregates polygenic risk scores and electronic health records for Alzheimer disease prediction. <b>2023</b> , 13,	О

444	Size and composition of haplotype reference panels impact the accuracy of imputation from low-pass sequencing in cattle.	О
443	Combining Clinical and Genetic Data to Predict Response to Fingolimod Treatment in Relapsing Remitting Multiple Sclerosis Patients: A Precision Medicine Approach. <b>2023</b> , 13, 122	O
442	Loci Associated with Negative Heterosis for Viability and Meat Productivity in Interspecific Sheep Hybrids. <b>2023</b> , 13, 184	0
441	Risk factors for, and genetic association with, intestinal atresia in dairy calves.	O
440	Genetics of varicose veins reveals polygenic architecture and genetic overlap with arterial and venous disease. <b>2023</b> , 2, 44-57	0
439	Genome-wide screen of otosclerosis in population biobanks: 27 loci and shared associations with skeletal structure. <b>2023</b> , 14,	O
438	Integrating Common Risk Factors with Polygenic Scores Improves the Prediction of Type 2 Diabetes. <b>2023</b> , 24, 984	O
437	Multiple founding paternal lineages inferred from the newly-developed 639-plex Y-SNP panel suggested the complex admixture and migration history of Chinese people.	O
436	Maize cytolines as models to study the impact of different cytoplasms on gene expression under heat stress conditions. <b>2023</b> , 23,	O
435	Synchronous effective population size changes and genetic stability of forest trees through glacial cycles.	o
434	The male-heterogametic sex determination system on chromosome 15 of Salix triandra and Salix arbutifolia reveals ancestral male heterogamety and subsequent turnover events in the genus Salix.	O
433	Genetic architecture of brain age and its casual relations with brain and mental disorders.	O
432	Genome-wide analyses of platinum-induced ototoxicity in childhood cancer patients: Results of GO-CAT and United Kingdom MAGIC consortia. 13,	O
431	Phenotypic and Genetic Factors Associated with Absence of Cardiomyopathy Symptoms in PLN:c.40_42delAGA Carriers.	O
430	Pleiotropy structures plant height and seed weight scaling in barley despite long history of domestication and breeding selection.	0
429	Organoids of patient-derived medullary thyroid carcinoma: The first milestone towards a new in vitro model in dogs.	O
428	Genetic diversity and structure in wild Robusta coffee (Coffea canephora A. Froehner) populations in Yangambi (DR Congo) and their relation to forest disturbance.	0
427	The genetic history of Scandinavia from the Roman Iron Age to the present. <b>2023</b> , 186, 32-46.e19	O

426	Sleep Duration, Midday Napping, and Serum Homocysteine Levels: A GeneEnvironment Interaction Study. <b>2023</b> , 15, 210	О
425	Global Biobank analyses provide lessons for developing polygenic risk scores across diverse cohorts. <b>2023</b> , 3, 100241	O
424	Automated quantitative trait locus analysis (AutoQTL).	О
423	Detecting and Adjusting for Hidden Biases due to Phenotype Misclassification in Genome-Wide Association Studies.	O
422	Genomic atlas of the plasma metabolome prioritizes metabolites implicated in human diseases. <b>2023</b> , 55, 44-53	О
421	Psychiatric traits and intracerebral hemorrhage: A Mendelian randomization study. 13,	O
420	Association between Genetic Variants and Peripheral Neuropathy in Patients with NSCLC Treated with First-Line Platinum-Based Therapy. <b>2023</b> , 14, 170	О
419	MRBEE: A novel bias-corrected multivariable Mendelian Randomization method.	O
418	MicroRNA-eQTLs in the developing human neocortex link miR-4707-3p expression to brain size. 12,	0
417	The UCLA ATLAS Community Health Initiative: Promoting precision health research in a diverse biobank. <b>2023</b> , 3, 100243	O
416	Pathogen exposure misclassification can bias association signals in GWAS of infectious diseases when using population-based common control subjects. <b>2023</b> ,	O
415	Genetic heritability as a tool to evaluate the precision of 24-hour recall dietary questionnaire variables in UK Biobank. 13,	O
414	Epidemiologic and Genetic Associations of Endometriosis With Depression, Anxiety, and Eating Disorders. <b>2023</b> , 6, e2251214	О
413	Genome-wide association study of school grades identifies genetic overlap between language ability, psychopathology and creativity. <b>2023</b> , 13,	Ο
412	Genome-wide association study of brain biochemical phenotypes reveals distinct genetic architecture of Alzheimer disease related proteins. <b>2023</b> , 18,	О
411	Genetic, individual, and familial risk correlates of brain network controllability in major depressive disorder.	1
410	Spatial genetic structure of European wild boar, with inferences on late-Pleistocene and Holocene demographic history.	Ο
409	Complex multiple introductions drive fall armyworm invasions into Asia and Australia. 2023, 13,	O

408	The genetic architecture of changes in adiposity during adulthood.	О
407	Evaluating the Genetic Effects of Gut Microbiota on the Development of Neuroticism and General Happiness: A Polygenic Score Analysis and Interaction Study Using UK Biobank Data. <b>2023</b> , 14, 156	O
406	No evidence for sex chromosomes in natural populations of the cichlid fish Astatotilapia burtoni.	0
405	Efficient genelinvironment interaction testing through bootstrap aggregating. 2023, 13,	Ο
404	Chromosome-level genome assembly of the Cape cliff lizard (Hemicordylus capensis).	0
403	A statistical boosting framework for polygenic risk scores based on large-scale genotype data. 13,	1
402	Genetic diversity in early maturity Chinese and European elite soybeans: A comparative analysis. <b>2023</b> , 219,	0
401	From Wisent to the Lab and Back Again Complex SNP Set for Population Management as an Effective Tool in European Bison Conservation. <b>2023</b> , 15, 116	2
400	Integrated health-related phenotype by Polygenic Risk Scores stratifies risk population for all-cause mortality: A cohort study based on UK Biobank.	0
399	Potential of imputation for cost-efficient genomic selection for resistance toFlavobacterium columnarein rainbow trout (Oncorhynchus mykiss).	0
398	Genetic contributions to transdiagnostic symptom dimensions in patients with major depressive disorder, bipolar disorder, and schizophrenia spectrum disorders. <b>2023</b> , 252, 161-171	0
397	Polygenic risk scores for schizophrenia and treatment resistance: New data, systematic review and meta-analysis. <b>2023</b> , 252, 189-197	0
396	A network-guided protocol to discover susceptibility genes in genome-wide association studies using stability selection. <b>2023</b> , 4, 101998	О
395	Polygenic prediction across populations is influenced by ancestry, genetic architecture, and methodology.	O
394	Deep learning-derived cardiovascular age shares a genetic basis with other cardiac phenotypes. <b>2022</b> , 12,	О
393	A critical role of brain network architecture in a continuum model of autism spectrum disorders spanning from healthy individuals with genetic liability to individuals with ASD.	O
392	xAtlas: scalable small variant calling across heterogeneous next-generation sequencing experiments. <b>2022</b> , 12,	1
391	Machine Learning to Understand Genetic and Clinical Factors Associated With the Pulse Waveform Dicrotic Notch.	0

390	GENOME-WIDE ASSOCIATION STUDIES FOR SOMATIC CELLS COUNT AND THEIR MORPHOLOGICAL DIFFERENTIATION IN COWS[MILK. <b>2022</b> , 12-17	О
389	Long-term Small Population Size, Deleterious Variation, and Altitude Adaptation in the Ethiopian Wolf, a Severely Endangered Canid. <b>2023</b> , 40,	O
388	A comparison of marker-based estimators of inbreeding and inbreeding depression. <b>2022</b> , 54,	O
387	Development and application of an efficient genomic mating method to maximize the production performances of three-way crossbred pigs. <b>2023</b> , 24,	О
386	Species boundaries to the limit: validating species delimitation methods is critical to avoid taxonomic inflation in the genomic era.	O
385	Preference Matrix Guided Sparse Canonical Correlation Analysis for Genetic Study of Quantitative Traits in Alzheimer Disease. <b>2022</b> ,	O
384	Golgi apparatus, endoplasmic reticulum and mitochondrial function implicated in Alzheimer disease through polygenic risk and RNA sequencing.	O
383	Portability of Polygenic Risk Scores for Sleep Duration, Insomnia and Chronotype in 33,493 Individuals. <b>2023</b> , 5, 10-20	O
382	SNEP-DB: An integrated database to associate genomic and pathological aspects of psychiatric disorders. <b>2022</b> ,	О
381	412. Genetic diversity of the Cameroon Blackbelly sheep, an indigenous sheep from West Africa. <b>2022</b> ,	O
380	419. Estimation of breed admixture levels in Sri Lanka cattle and its relation to performance traits. <b>2022</b> ,	O
379	257. Discovery of a genetic variant in serum amyloid A that might protect chickens from amyloid arthropathy. <b>2022</b> ,	О
378	210. Genomic diversity of Czech and Slovak native goat breeds. <b>2022</b> ,	0
377	706. Inbreeding and effective population size of United States Katahdin sheep. <b>2022</b> ,	O
376	725. Estimation of linkage disequilibrium in Pag and Istrian sheep breed: towards genomic optimum contribution selection. <b>2022</b> ,	О
375	374. Multibreed sequence level genome-wide association study of semen traits in tropical Australian cattle. <b>2022</b> ,	O
374	258. Genetic background of the porcine immune system using SNP chip data and whole genome sequencing data. <b>2022</b> ,	0
373	567. Implementation of genomic selection on production and quality traits and linkage disequilibrium in Crassostrea gigas. <b>2022</b> ,	O

372	229. The genomic inbreeding trend over the last 25 years in three Italian pig breeds. <b>2022</b> ,	0
371	213. Following the hidden footsteps of past human migrations via the goat genome. <b>2022</b> ,	О
370	742. Measures of diversity based on autosomal and sex chromosomes of Valachian sheep. <b>2022</b> ,	O
369	188. Patterns of inbreeding and selection using runs of homozygosity in North American dairy cattle. <b>2022</b> ,	O
368	Genome-wide meta-analysis identifies 93 risk loci and enables risk prediction equivalent to monogenic forms of venous thromboembolism.	0
367	Causal relevance of different blood pressure traits on risk of cardiovascular diseases: GWAS and Mendelian randomisation in 100,000 Chinese adults.	0
366	Variance component estimates, phenotypic characterization, and genetic evaluation of bovine congestive heart failure in commercial feeder cattle.	0
365	First GWAS on Alzheimer∄ Disease in Argentina and Chile populations.	o
364	Genetically Predicted Body Selenium Concentration and estimated GFR: A Mendelian Randomization Study. <b>2023</b> ,	0
363	Quality control and removal of technical variation of NMR metabolic biomarker data in ~120,000 UK Biobank participants. <b>2023</b> , 10,	О
362	Polygenic risk for mental disorders as predictors of posttraumatic stress disorder after mild traumatic brain injury. <b>2023</b> , 13,	0
361	TLR4 and MD2 variation among horses with differential TNFB aseline concentrations and response to intravenous lipopolysaccharide infusion. <b>2023</b> , 13,	О
360	Analysis of Arabidopsis non-reference accessions reveals high diversity of metabolic gene clusters and discovers new candidate cluster members. 14,	O
359	Emergence of Antifungal Resistant Subclades in the Global Predominant Phylogenetic Population of Candida albicans.	О
358	Genome-wide allele and haplotype-sharing patterns suggested one unique HmongMein-related lineage and biological adaptation history in Southwest China. <b>2023</b> , 17,	O
357	A genome-wide association study of germline variation and melanoma prognosis. 12,	О
356	Exploring Factors Underlying Poorly-Controlled Asthma in Adults by Integrating Phenotypes and Genotypes Associated with Obesity and Asthma: A Case-Control Study. Volume 16, 135-147	1
355	Genetic architecture of the HLA/MHC locus in cardiometabolic disease, severe mental illness, and related traits	О

354	Novel Genetic Variants Associated with Chronic Kidney Disease Progression. <b>2023</b> , Publish Ahead of Print,	0
353	Chromosome-level wild Hevea brasiliensis genome provides new tools for genomic-assisted breeding and valuable loci to elevate rubber yield.	1
352	Reintroducing genetic diversity in populations from cryopreserved material: The case of Abondance, a French local dairy cattle breed.	0
351	Genomic insight into the influence of selection, crossbreeding, and geography on population structure in poultry. <b>2023</b> , 55,	O
350	Modeling of African population history usingf-statistics can be highly biased and is not addressed by previously suggested SNP ascertainment schemes.	О
349	Comparison of the loci associated with HbA1c and blood glucose levels identified by a genome-wide association study in the Japanese population.	O
348	Linking genetic and environmental factors through marker effect networks to understand trait plasticity.	O
347	Causal linkage of tobacco smoking with ageing: Mendelian randomization analysis towards telomere attrition and sarcopenia.	O
346	Joint analysis of multiple phenotypes for extremely unbalanced case-control association studies.	O
345	Taxonomic study of Scytosiphon (Phaeophyceae) from temperate coasts of Argentina.	O
344	Bayesian mixed model analysis uncovered 21 risk loci for chronic kidney disease in boxer dogs. <b>2023</b> , 19, e1010599	O
343	Multi-ancestry study of the genetics of problematic alcohol use in >1 million individuals.	O
342	Duck pan-genome reveals two transposon-derived structural variations caused bodyweight enlarging and white plumage phenotype formation during evolution.	O
341	GSEL: a fast, flexible python package for detecting signatures of diverse evolutionary forces on genomic regions. <b>2023</b> , 39,	O
340	Characterization of a sex-determining locus and development of early molecular assays in Telfairia occidentalisHook. F., a dioecious cucurbit.	O
339	Population genetic analysis of the microsporidium Ordospora colligata reveals the role of natural selection and phylogeography on its extremely compact and reduced genome.	O
338	Integrated GWAS and transcriptomic analysis reveal the candidate salt-responding genes regulating Na+/K+ balance in barley (Hordeum vulgare L.). 13,	O
337	Genome-wide association study suggests a critical contribution of the adaptive immune system to chronic post-surgical pain.	O

336	Polygenic scores for psychiatric disorders in a diverse postmortem brain tissue cohort.	O
335	Exploring the genetic diversity of the Japanese Population: Insights from a Large-Scale Whole Genome Sequencing Analysis.	O
334	Gene burden analysis identifies genes associated with increased risk and severity of adult-onset hearing loss in a diverse hospital-based cohort. <b>2023</b> , 19, e1010584	0
333	Estimation and implications of the genetic architecture of fasting and non-fasting blood glucose. <b>2023</b> , 14,	O
332	Genome-wide association study reveals the candidate genes for reproduction traits in Yunong black pigs.	0
331	Polygenic Risk for Schizophrenia, Major Depression, and Post-traumatic Stress Disorder and Hippocampal Subregion Volumes in Middle Childhood.	O
330	Characterizing Alcohol Expectancies in the ABCD Study: Associations with Sociodemographic Factors, the Immediate Social Environment, and Genetic Propensities.	0
329	LDL lowering effect of PCSK9 inhibition is reduced in women.	1
328	DRAGON-Data: a platform and protocol for integrating genomic and phenotypic data across large psychiatric cohorts. <b>2023</b> , 9,	О
327	Evaluating DNA cross-contamination risk using different tissue sampling procedures on board fishing and research vessels.	O
326	Polygenic adaptation from standing genetic variation allows rapid ecotype formation. 12,	2
325	Effects of genellfestyle interactions on obesity based on a multi-locus risk score: A cross-sectional analysis. <b>2023</b> , 18, e0279169	o
324	Reciprocal causation mixture model for robust Mendelian randomization analysis using genome-scale summary data. <b>2023</b> , 14,	О
323	Integrating oculomics with genomics reveals imaging biomarkers for preventive and personalized prediction of arterial aneurysms. <b>2023</b> , 14, 73-86	o
322	Population-size history inferences from the coho salmon (Oncorhynchus kisutch) genome. <b>2023</b> , 13,	O
321	Polygenic scores for tobacco use provide insights into systemic health risks in a diverse EHR-linked biobank in Los Angeles.	O
320	Evidence of prezygotic isolation, but not assortative mating, between locally adapted populations of Fundulus heteroclitus across a salinity gradient. <b>2023</b> , 36, 687-697	0
319	Integrating Whole-Genome Resequencing and RNA Sequencing Data Reveals Selective Sweeps and Differentially Expressed Genes Related to Nervous System Changes in Luxi Gamecocks. <b>2023</b> , 14, 584	O

318	Haptools: a toolkit for admixture and haplotype analysis. <b>2023</b> , 39,	0
317	Multi-ancestry genome-wide study in >2.5 million individuals reveals heterogeneity in mechanistic pathways of type 2 diabetes and complications.	0
316	Genomics of Dwarfism in Italian Local Chicken Breeds. <b>2023</b> , 14, 633	0
315	Genetic Risk Score Improves Risk Stratification for Anticoagulation-Related Intracerebral Hemorrhage. <b>2023</b> , 54, 791-799	O
314	Admixture Mapping of Peripheral Artery Disease in a Dominican Population Reveals a Novel Risk Locus on 2q35.	0
313	Clinically relevant combined effect of polygenic background, rare pathogenic germline variants, and family history on colorectal cancer incidence. <b>2023</b> , 16,	0
312	RELEVANCE OF CODING VARIATION IN FILAGGRIN AND DOCK8 IN FINNISH PEDIATRIC PATIENTS WITH EARLY-ONSET MODERATE-TO-SEVERE ATOPIC DERMATITIS. <b>2023</b> , 100203	O
311	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. <b>2023</b> ,	0
310	Fast and accurate Bayesian polygenic risk modeling with variational inference. 2023,	Ο
309	Genomic insights into the genetic basis of cotton breeding in China. <b>2023</b> , 16, 662-677	O
308	PSReliP: an integrated pipeline for analysis and visualization of population structure and relatedness based on genome-wide genetic variant data. <b>2023</b> , 24,	0
307	Simplified Genomic Data Revealing the Decline of Aleuritopteris grevilleoides Population Accompanied by the Uplift of Dry-Hot Valley in Yunnan, China. <b>2023</b> , 12, 1579	Ο
306	Low and differential polygenic score generalizability among African populations due largely to genetic diversity. <b>2023</b> , 4, 100184	O
305	Mapping structural variations in Haemaphysalis longicornis and Rhipicephalus microplus reveals vector-pathogen adaptation. <b>2023</b> , 26, 106398	0
304	Hunter-gatherer admixture facilitated natural selection in Neolithic European farmers. <b>2023</b> , 33, 1365-1	371.e3o
303	Recombulator-X: a fast and user-friendly tool for estimating X chromosome recombination rates in forensic genetics.	0
302	ME-Bayes SL: Enhanced Bayesian Polygenic Risk Prediction Leveraging Information across Multiple Ancestry Groups.	O
301	Haplotype analysis of genomic prediction by incorporating genomic pathway information based on high-density SNP marker in Chinese yellow-feathered chicken. <b>2023</b> , 102, 102549	Ο

300	Genetic impact on the association of sleep patterns and chronic kidney disease: A prospective cohort study of 157,175 UK Biobank participants. <b>2023</b> , 169, 111323	Ο
299	Evidence of causal effects of blood pressure on back pain and back pain on type II diabetes provided by a bidirectional Mendelian randomization study. <b>2023</b> ,	O
298	Maternal depression and the polygenic p factor: A family perspective on direct and indirect effects. <b>2023</b> , 332, 159-167	O
297	Genomic prediction of survival against Vibrio harveyi in leopard coral grouper (Plectropomus leopardus) using GBLUP, weighted GBLUP, and BayesCII <b>2023</b> , 572, 739536	O
296	Geography and past climate changes have shaped the evolution of a widespread lizard in arid Central Asia. <b>2023</b> , 184, 107781	О
295	Population genomics of Corsican wildcats: Paving the way toward a new subspecies within the Felis silvestris spp. complex?. <b>2023</b> , 32, 1908-1924	O
294	Exploring the overlap between alopecia areata and major depressive disorder: Epidemiological and genetic perspectives.	О
293	Genome-Wide Analysis of Structural Variants in Parkinson Disease.	1
292	Genomic evidence for adaptation to tuberculosis in the Andes before European contact. <b>2023</b> , 26, 106034	О
291	Aggregation tests identify new gene associations with breast cancer in populations with diverse ancestry. <b>2023</b> , 15,	O
290	Multi-breed genomic predictions and functional variants for fertility of tropical bulls. <b>2023</b> , 18, e0279398	0
289	Genome-wide analyses of ADHD identify 27 risk loci, refine the genetic architecture and implicate several cognitive domains. <b>2023</b> , 55, 198-208	1
288	Accuracy of haplotype estimation and whole genome imputation affects complex trait analyses in complex biobanks. <b>2023</b> , 6,	О
287	Runs of homozygosity reveal past bottlenecks and contemporary inbreeding across diverging populations of an island-colonizing bird. <b>2023</b> , 32, 1972-1989	O
286	Genetic Diversity and Population Structure of a Wide Pisum spp. Core Collection. 2023, 24, 2470	1
285	Considering strategies for SNP selection in genetic and polygenic risk scores. 13,	O
284	Multiple Genetic Loci Associated with Pug Dog Thoracolumbar Myelopathy. <b>2023</b> , 14, 385	О
283	X chromosome associations with chronic obstructive pulmonary disease and related phenotypes: an X chromosome-wide association study. <b>2023</b> , 24,	O

282	The Legacy of Infectious Disease Exposure on the Genomic Diversity of Indigenous Southern Mexicans. <b>2023</b> , 15,	О
281	Estimating the genetic parameters of yield-related traits under different nitrogen conditions in maize. <b>2023</b> , 223,	O
280	Genome-wide Association Study Points to Novel Locus for Gilles de la Tourette Syndrome. 2023,	O
279	Combining genome-wide association study based on low-coverage whole genome sequencing and transcriptome analysis to reveal the key candidate genes affecting meat color in pigs.	O
278	Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal ancestry proportions. <b>2023</b> , 110, 359-367	1
277	Landscape of pathogenic mutations in premature ovarian insufficiency. <b>2023</b> , 29, 483-492	1
276	A review of pre-implantation genetic testing technologies and applications. 2023, 7, 20-31	O
275	Whole-genome resequencing reveals selection signatures for caviar yield in Russian sturgeon (Acipenser gueldenstaedtii). <b>2023</b> , 568, 739312	O
274	X-Chromosome Association Study in Latin American Cohorts Identifies New Loci in Parkinson Disease.	О
273	Comparison of two multi-trait association testing methods and sequence-based fine mapping of six QTL in Swiss Large White pigs.	O
272	eXclusionarY: Ten years later, where are the sex chromosomes in GWAS?.	O
271	Membranous Nephropathy in the UK Biobank.	O
270	Unraveling the causal genes and transcriptomic determinants of human telomere length.	O
269	Gene-x-environment analysis supports protective effects of eveningness chronotype on self-reported and actigraphy-derived sleep duration among those who always work night shifts in the UK Biobank.	O
268	Newly identified sex chromosomes in the Sphagnum (peat moss) genome alter carbon sequestration and ecosystem dynamics. <b>2023</b> , 9, 238-254	0
267	Genetic and self-perceived ancestries in Argentina: Beyond the three-hybrid model. 2023, 181, 85-95	O
266	Discovering novel clues of natural selection on four worldwide goat breeds. 2023, 13,	O
265	Genetic analysis of infectious bronchitis virus (IBV) in vaccinated poultry populations over a period of 10 years. 1-11	O

264	Parametric mapping of QTL for resistance to European canker in apple in Aromalli iscovery 2023, 19,	Ο
263	Genome-wide association study identifies novel candidate malaria resistance genes in Cameroon.	O
262	The association of gene polymorphisms with milk production and mastitis resistance phenotypic traits in dairy cattle. <b>2023</b> ,	0
261	Functional link between sarcoidosis-associated gene variants and quantitative levels of bronchoalveolar lavage fluid cell types. 10,	O
260	Rare variant aggregation in 148,508 exomes identifies genes associated with proxy dementia. <b>2023</b> , 13,	0
259	Selecting Covariates for Genome-Wide Association Studies.	0
258	Identification of novel genetic variants, including PIM1 and LINC01491, with ICD-10 based diagnosis of pulmonary arterial hypertension in the UK Biobank cohort. 3,	0
257	Phenotypic heterogeneity in 22q11.2 deletion syndrome: Copy Number Variants as genetic modifiers for congenital heart disease in a Brazilian cohort. <b>2023</b> , 191, 1273-1281	O
256	Genome-wide association study using whole-genome sequencing identifies risk loci for Parkinson disease in Chinese population. <b>2023</b> , 9,	0
255	105. Heritability of scurs in Wagyu and tropically adapted composite beef cattle. <b>2022</b> ,	0
254	358. MiXBLUP 3.0 Isoftware for large genomic evaluations in animal breeding programs. 2022,	0
253	461. Development of a low-density SNP panel for local Ghanaian and Tanzanian chicken ecotypes. <b>2022</b> ,	O
252	515. Selection signatures analyses revealed genes associated with adaptation in selected goat breeds in Kenya. <b>2022</b> ,	0
251	Rare and low-frequency coding genetic variants contribute to pediatric-onset multiple sclerosis. 1352458522	11507
250	189. Exploring genetic diversity and selection signatures in indigenous African cattle breeds. <b>2022</b> ,	0
249	753. Genome-wide signals of positive selection identified in Livestock Guardian Dogs. <b>2022</b> ,	0
248	751. Linkage disequilibrium variability in the Czechoslovakian wolfdog genome as a result of long-term artificial selection. <b>2022</b> ,	0
247	186. Common heterozygosity-rich regions across the genomes of commercial and local goat breeds. <b>2022</b> ,	0

246	798. Sequencing-based genome-wide association study for resilience indicators in growing pigs. <b>2022</b> ,	O
245	235. Signatures of selection and runs of homozygosity in the genome of several fancy and meat rabbit breeds. <b>2022</b> ,	O
244	205. Estimation of sex chromosome inbreeding depression on milk production in cattle. 2022,	О
243	232. Genomic diversity of two indigenous Croatian goat breeds. <b>2022</b> ,	O
242	757. Genomic diversity in selected Austrian dog populations. <b>2022</b> ,	О
241	560. Large-scale cis-eQTL analysis of gene expression in blood of young healthy pigs using PigGTEx. <b>2022</b> ,	O
240	231. Effect of genomic selection on genetic variability in chromosomal level in the Finnish Ayrshire. <b>2022</b> ,	О
239	251. Pangenomes of haplotype-resolved assemblies enable population-scale genotyping of cattle structural variation. <b>2022</b> ,	O
238	750. Genome-wide association study for ectopic ureter in three dog breeds. 2022,	О
237	260. Prioritisation of variants from whole-genome sequence data for validation of their association with traits of interest. <b>2022</b> ,	O
236	298. Including selected sequence variants in genomic predictions for age at first calving in Nellore cattle. <b>2022</b> ,	О
235	749. Diversity status and future breeding strategy for Tatra hound in Slovakia. <b>2022</b> ,	O
234	Evaluation of genetic alterations in hereditary cancer susceptibility genes in the Ashkenazi Jewish women community of Mexico. 14,	О
233	Youth Team Sports Participation Associates With Reduced Dimensional Psychopathology Through Interaction With Biological Risk Factors. <b>2023</b> ,	O
232	Interleukin 6 and interferon gamma haplotypes are related to cytokine serum levels in dogs in an endemic Leishmania infantum region. <b>2023</b> , 12,	О
231	Genetic polymorphism (rs6587666) in FLG protects from eczema in admixed Brazilian children population with high African ancestry. <b>2023</b> , 9, e13659	O
230	Application potential of chicken DNA chip in domestic pigeon species i Preliminary results. <b>2023</b> , 30, 103594	О
229	Increasing serum iron levels and their role in the risk of infectious diseases: a Mendelian randomization approach.	O

228	Selection on many loci drove the origin and spread of a key innovation.	O
227	The approach to patient clustering based on the microchip data confined to distinct loci using the combinations of variants. <b>2023</b> ,	O
226	Pan-Genomic Regulation of Gene Expression in Normal and Pathological Human Placentas. <b>2023</b> , 12, 578	O
225	Genomic, genetic and phylogenetic evidence for a new falcon species using chromosome-level genome assembly of the gyrfalcon and population genomics.	O
224	Predicting the prevalence of complex genetic diseases from individual genotype profiles using capsule networks. <b>2023</b> , 5, 114-125	O
223	Genome-Wide Association Studies (GWAS). <b>2023</b> , 123-146	O
222	An Oxylipin-Related Nutrient Pattern and Risk of Type 1 Diabetes in the Diabetes Autoimmunity Study in the Young (DAISY). <b>2023</b> , 15, 945	1
221	Integrative multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci.	O
220	Role of genetics in capturing racial disparities in cardiovascular disease.	O
219	Exploiting the mediating role of the metabolome to unravel transcript-to-phenotype associations.	1
218	The genetic basis and potential molecular mechanism of yellow-albino northern snakehead (Channa argus). <b>2023</b> , 13,	1
217	Tree-Level Growth Patterns and Genetic Associations Depict Drought Legacies in the Relict Forests of Abies marocana. <b>2023</b> , 12, 873	O
216	Ancient hybridization leads to the repeated evolution of red flowers across a monkeyflower radiation.	O
215	Genome-wide polygenic risk score for major osteoporotic fractures in postmenopausal women using associated single nucleotide polymorphisms. <b>2023</b> , 21,	O
214	Identification of new risk loci shared across systemic vasculitides points towards potential target genes for drug repurposing. ard-2022-223697	O
213	Eye-brain connections revealed by multimodal retinal and brain imaging genetics in the UK Biobank.	O
212	Genome-wide Association Study of Traumatic Brain Injury in U.S. Military Veterans Enrolled in the VA Million Veteran Program.	0
211	Growth rates of human induced pluripotent stem cells and neural stem cells from attention-deficit hyperactivity disorder patients: a preliminary study. <b>2023</b> , 130, 243-252	O

210	A Genomic Risk Score Identifies Individuals at High Risk for Intracerebral Hemorrhage. <b>2023</b> , 54, 973-982	O
209	Deciphering local adaptation of native Indian cattle (Bos indicus) breeds using landscape genomics and in-silico prediction of deleterious SNP effects on protein structure and function. <b>2023</b> , 13,	O
208	Large effective population size masks population genetic structure in Hirondellea amphipods within the deepest marine ecosystem, the Mariana Trench.	O
207	MR-BOIL: Causal inference in one-sample Mendelian randomization for binary outcome with integrated likelihood method.	O
206	Genome Polymorphism Analysis and Selected Sweep Regions Detection via the Genome Resequencing of 91 Cabbage (Brassica oleracea) Accessions. <b>2023</b> , 9, 283	O
205	Utilizing Variants Identified with Multiple Genome-Wide Association Study Methods Optimizes Genomic Selection for Growth Traits in Pigs. <b>2023</b> , 13, 722	O
204	Genome-wide association study reveals markers and candidate genes associated with growth in the rice flower carp, an economic fish species of integrated rice-fish culture in China. 10,	O
203	Estimating inbreeding rate and effective population size in the Finnish Ayrshire population in the era of genomic selection. <b>2023</b> , 140, 343-353	O
202	Frequency and types of alternative breeding strategies employed by nesting American black ducks in North Carolina. <b>2023</b> , 18, e0278905	O
201	Polygenic risk score prediction of multiple sclerosis in individuals of South Asian ancestry. <b>2023</b> , 5,	O
200	Hypertension as a Novel Link for Shared Heritability in Age at Menarche and Cardiometabolic Traits.	O
199	Socio-cultural practices affect sexual dimorphism in stature in Early Neolithic Europe.	O
198	Genetic variation supports a causal role for valproate in prevention of ischemic stroke.	0
197	Fragmented habitat compensates for the adverse effects of genetic bottleneck. <b>2023</b> , 33, 1009-1018.e7	O
196	The coefficients of inbreeding revealed by ROH study among inbred individuals belonging to each type of the first cousin marriage: A preliminary report from North India.	0
195	Phylogeography and population structure of the global, wide host-range hybrid pathogen Phytophthora Lambivora. <b>2023</b> , 14,	O
194	Ethnic disparities in mortality and group-specific risk factors in the UK Biobank. 2023, 3, e0001560	O
193	Signatures of co-evolution and co-regulation in the CYP3A and CYP4F genes in humans.	O

192	The genetic and evolutionary basis of gene expression variation in East Africans. 2023, 24,	O
191	CAS Array: design and assessment of a genotyping array for Chinese biobanking. 2023, 6,	O
190	A novel method for multiple phenotype association studies based on genotype and phenotype network.	O
189	Genomic diversity and signals of selection processes in wild and farm-reared red-legged partridges (Alectoris rufa). <b>2023</b> , 115, 110591	O
188	Conservation implications of elucidating the Korean wolf taxonomic ambiguity through whole-genome sequencing.	O
187	Sub-cellular level resolution of common genetic variation in the photoreceptor layer identifies continuum between rare disease and common variation. <b>2023</b> , 19, e1010587	O
186	Whole-genome re-sequencing provides key genomic insights in farmed Arctic charr (Salvelinus alpinus) populations of anadromous and landlocked origin from Scandinavia.	O
185	Studies on the Origin of Asian Cultivated Rice Based on 15 Domestication Region.	O
184	Inference of Causal Relationships Between Genetic Risk Factors for Cardiometabolic Phenotypes and Female-Specific Health Conditions. <b>2023</b> , 12,	1
183	Whole-genome sequencing of ethnolinguistic diverse northwestern Chinese Hexi Corridor people from the 10K_CPGDP project suggested the differentiated East-West genetic admixture along the Silk Road and their biological adaptations.	O
182	Disentangling clustering configuration intricacies for divergently selected chicken breeds. 2023, 13,	O
181	Evolutionary origin and establishment of a dioecious diploid-tetraploid complex.	O
180	Genetic association models are robust to common population kinship estimation biases.	O
179	Genetic Determinants of Vitamin D Deficiency in the Middle Eastern Qatari Population by a Genome-Wide Association Study.	O
178	An oligogenic architecture underlying ecological and reproductive divergence in sympatric populations. 12,	O
177	Assessing the Genomics Structure of Dorper and White Dorper Variants, and Dorper Populations in South Africa and Hungary. <b>2023</b> , 12, 386	O
176	C9orf72 hexanucleotide repeat allele tagging SNPs: Associations with ALS risk and longevity. 14,	O
175	Investigating an Unknown Biodiversity: Evidence of Distinct Lineages of the Endemic Chola Guitarfish Pseudobatos percellens Walbaum, 1792 in the Western Atlantic Ocean. <b>2023</b> , 15, 344	O

<sup>1</sup> 74	Pathway-specific polygenic risk scores correlate with clinical status and Alzheimerß-related biomarkers.	О
173	Whole-genome sequencing reveals a complex African population demographic history and signatures of local adaptation. <b>2023</b> , 186, 923-939.e14	1
172	Genome-wide analysis identifies genetic effects on reproductive success and ongoing natural selection at the FADS locus.	О
171	A statistical genetic investigation of psychiatric resilience. <b>2023</b> , 14,	О
170	Fine mapping spatiotemporal mechanisms of genetic variants underlying cardiac traits and disease. <b>2023</b> , 14,	0
169	Maternal and genetic effects on embryonic survival from fertilization to swim up stage and reproductive success in a farmed rainbow trout line. <b>2023</b> , 29, 101523	O
168	Genome-wide association study for Streptococcus iniae in Nile tilapia (Oreochromis niloticus) identifies a significant QTL for disease resistance. 14,	О
167	Dual domestications and origin of traits in grapevine evolution. <b>2023</b> , 379, 892-901	1
166	A clustering linear combination method for multiple phenotype association studies based on GWAS summary statistics. <b>2023</b> , 13,	О
165	Loci Associated with Postpartum Depression: A Genome-Wide Association Study.	О
164	Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. <b>2023</b> , 40,	О
163	Genetic validation of psoriasis phenotyping in UK Biobank supports the utility of self-reported data and composite definitions for large genetic and epidemiological studies. <b>2023</b> ,	O
162	The impact of Short Tandem Repeats on grey matter brain imaging derived phenotypes in UK Biobank.	О
161	Genome-wide association study for the primary feather color trait in a native Chinese duck. 14,	O
160	The dogs of Chernobyl: Demographic insights into populations inhabiting the nuclear exclusion zone. <b>2023</b> , 9,	О
159	Polygenic analyses show important differences between MDD symptoms collected using PHQ9 and CIDI-SF.	О
158	Developing Methods for Maintaining Genetic Diversity in Novel Aquaculture Species: The Case of Seriola lalandi. <b>2023</b> , 13, 913	О
157	Detecting Cotton Leaf Curl Virus Resistance Quantitative Trait Loci in Gossypium hirsutum and iCottonQTL a New R/Shiny App to Streamline Genetic Mapping. <b>2023</b> , 12, 1153	О

156	Geography, environment, and colonization history interact with morph type to shape genomic variation in an Arctic fish.	О
155	Genomic Diversity and Runs of Homozygosity in Bernese Mountain Dogs. <b>2023</b> , 14, 650	О
154	Identification of Selection Signatures and Loci Associated with Important Economic Traits in Yunan Black and Huainan Pigs. <b>2023</b> , 14, 655	0
153	Associations of polygenic risk scores with posttraumatic stress symptom trajectories following combat deployment. 1-10	O
152	Effect of polygenic risk score, family load of schizophrenia and exposome risk score, and their interactions, on the long-term outcome of first-episode psychosis. 1-10	O
151	Human-specific evolutionary markers linked to foetal neurodevelopment modulate brain surface area in schizophrenia.	О
150	Exploring regional aspects of 3D facial variation within European individuals. 2023, 13,	О
149	Genome-wide significant risk loci for mood disorders in the Old Order Amish founder population.	O
148	Integrative analysis of multi-omics and imaging data with incorporation of biological information via structural Bayesian factor analysis. <b>2023</b> , 24,	O
147	RORB, an Alzheimer disease susceptibility gene, is associated with viral encephalitis, an Alzheimer disease risk factor.	O
146	Persistent DNA methylation changes associated with prenatal NO2exposure in a Canadian prospective birth study.	0
145	Polygenic risk of type 2 diabetes is associated with incident vascular dementia: a prospective cohort study. <b>2023</b> , 5,	О
144	Identification of de novo Mutations in the Chinese Autism Spectrum Disorder Cohort via Whole-Exome Sequencing Unveils Brain Regions Implicated in Autism.	О
143	Kazakh national dog breed Tazy: What do we know?. <b>2023</b> , 18, e0282041	О
142	Potentially causal associations between placental DNA methylation and schizophrenia and other neuropsychiatric disorders.	O
141	Population dynamics and genome-wide selection scan for dogs in Chernobyl. <b>2023</b> , 10,	О
140	Evidence of polygenic regulation of the physiological presence of neurofilament light chain in human serum. 14,	0
139	Correlates of suicidal behaviors and genetic risk among United States veterans with schizophrenia or bipolar I disorder.	О

138	Genome Analysis Using Whole-Exome Sequencing of Non-Syndromic Cleft Lip and/or Palate from Malagasy Trios Identifies Variants Associated with Cilium-Related Pathways and Asian Genetic Ancestry. <b>2023</b> , 14, 665	О
137	Genome wide association study based on clustering by obesity-related variables shed light on a genetic architecture of obesity in Japanese and UK population.	O
136	A bootstrap model comparison test for identifying genes with context-specific patterns of genetic regulation.	O
135	Current sika deer effective population size is near to reaching its historically highest level in the Japanese archipelago by release from hunting rather than climate change and top predator extinction. 095968362311570	0
134	Identification of the rice Rc gene as a main regulator of seed survival under dry storage conditions.	0
133	Imputation-powered whole-exome analysis identifies genes associated with kidney function and disease in the UK Biobank. <b>2023</b> , 14,	О
132	Deep learning based phenotyping of medical images improves power for gene discovery of complex disease.	О
131	Associations of atrial natriuretic peptide with measures of insulin and adipose depots. 2023, 11,	O
130	Genetic and neural bases of the Neuroticism general factor.	О
129	Genomic clines across the species boundary between a hybrid pine and its progenitor in the eastern Tibetan Plateau. <b>2023</b> , 100574	O
128	Genome-wide association study reveals new QTL and functional candidate genes for the number of ribs and carcass length in pigs.	О
127	The genetic architecture of pain intensity in a sample of 598,339 U.S. veterans.	О
126	Epigenetic then genetic variations underpin rapid adaptation of oyster populations (Crassostrea gigas) to Pacific Oyster Mortality Syndrome (POMS).	0
125	Testing for differences in polygenic scores in the presence of confounding.	О
124	The genetic architecture of pain intensity in a sample of 598,339 U.S. veterans.	Ο
123	MICA and MICB allele assortment in Finland.	O
122	An inverse causal association between genetically predicted vitamin D and chronic obstructive pulmonary disease risk. 10,	О
121	A Survey of Processing Systems for Phylogenetics and Population Genetics.	О

120	An evolutionary perspective on genetic load in small, isolated populations as informed by whole genome resequencing and forward-time simulations. <b>2023</b> , 77, 690-704	0
119	Statistical Methods for Disease Risk Prediction with Genotype Data. <b>2023</b> , 331-347	O
118	Germline-mediated immunoediting sculpts breast cancer subtypes and metastatic proclivity.	0
117	Polygenic scores for tobacco use provide insights into systemic health risks in a diverse EHR-linked biobank in Los Angeles.	Ο
116	Pharmacogenomic and Statistical Analysis. <b>2023</b> , 305-330	0
115	Standardizing and applying a mating-based whole-genome simulation approach reveals caution in using chromosome-level PCA and kinship estimates.	0
114	Boosting multivariate structured additive distributional regression models.	0
113	De novomutation rates in sticklebacks.	O
112	Genome-wide association study identifies four pan-ancestry loci for suicidal ideation in the Million Veteran Program. <b>2023</b> , 19, e1010623	0
111	Past Connectivity but Recent Inbreeding in Cross River Gorillas Determined Using Whole Genomes from Single Hairs. <b>2023</b> , 14, 743	0
110	A syntelog-based pan-genome provides insights into rice domestication and de-domestication.	0
109	Different waves of postglacial recolonisation and genomic structure of bank vole populations in NE Poland.	0
108	Evidence for a single, ancient origin of a genus-wide alternative life history strategy. 2023, 9,	0
107	Investigating Vitamin D Receptor Genetic Markers in a Cluster Headache Meta-Analysis. <b>2023</b> , 24, 5950	O
106	Genomic clustering by geography not species in taxonomically complex British and Irish eyebrights (Euphrasia).	0
105	Genetic associations with age at dementia onset in the PSEN1 E280A Colombian kindred.	O
104	GPR41/43 regulates blood pressure by improving gut epithelial barrier integrity to prevent TLR4 activation and renal inflammation.	О
103	Genome-wide mapping of signatures of selection using a high-density array identified candidate genes for growth traits and local adaptation in chickens. <b>2023</b> , 55,	O

102	Depression: an adaptive disease?.	O
101	Exploring the growth trait molecular markers in two sheep breeds based on Genome-wide association analysis. <b>2023</b> , 18, e0283383	O
100	A genome-wide association study of childhood adiposity and blood lipids. 6, 303	O
99	Germline genetic variants and pediatric rhabdomyosarcoma outcomes: a report from the Children Oncology Group.	O
98	A role for heritable transcriptomic variation in maize adaptation to temperate environments. <b>2023</b> , 24,	O
97	Multi-locus genome-wide association study of chickpea reference set identifies genetic determinants of Pratylenchus thornei resistance. 14,	O
96	Genome-wide analysis of a collective grave from Mentesh Tepe provides insight into the population structure of early neolithic population in the South Caucasus. <b>2023</b> , 6,	O
95	Understanding Complex Trait Susceptibilities and Ethnical Diversity in a Sample of 4,145 Russians Through Analysis of Clinical and Genetic Data.	O
94	A common variant rs2054564 in ADAMTS17 is associated with susceptibility to lumbar spondylosis. <b>2023</b> , 13,	0
93	An integrative framework for circular RNA quantitative trait locus discovery with application in human T cells.	Ο
92	Analysis of evolutionary dynamics and clonal architecture in prostate cancer.	O
91	Family-based analysis of the contribution of rare and common genetic variants to school performance in schizophrenia.	0
90	Causal effects on complex traits are similar for common variants across segments of different continental ancestries within admixed individuals. <b>2023</b> , 55, 549-558	O
89	Rank concordance of polygenic indices.	O
88	Genetic mapping and molecular mechanism behind color variation in the Asian vine snake. 2023, 24,	0
87	A genome-wide association study of frailty identifies significant genetic correlation with neuropsychiatric, cardiovascular, and inflammation pathways.	O
86	Associations of genome-wide and regional autozygosity with 96 complex traits in old order Amish. <b>2023</b> , 24,	0
85	Rare genetic variants inSEC24Dmodify orofacial cleft phenotypes.	Ο

84	Allele-dependent interaction of LRRK2 and NOD2 in leprosy. 2023, 19, e1011260	O
83	Genome-wide identification of tandem repeats associated with splicing variation across 49 tissues in humans. <b>2023</b> , 33, 435-447	O
82	Integration of Selection Signatures and Protein Interactions Reveals NR6A1, PAPPA2, and PIK3C2B as the Promising Candidate Genes Underlying the Characteristics of Licha Black Pig. <b>2023</b> , 12, 500	O
81	Large haploblocks underlie rapid adaptation in the invasive weed Ambrosia artemisiifolia. 2023, 14,	O
80	Genome-wide analysis of oxylipins and oxylipin profiles in a pediatric population. 10,	O
79	Alzheimer disease genetic risk and cognitive reserve in relationship to long-term cognitive trajectories among cognitively normal individuals. <b>2023</b> , 15,	O
78	Epigenome-wide association study of serum folate in maternal peripheral blood leukocytes. <b>2023</b> , 15, 39-52	О
77	Multiple founding paternal lineages inferred from the newly-developed 639-plex Y-SNP panel suggested the complex admixture and migration history of Chinese people. <b>2023</b> , 17,	O
76	Genome-wide association study of obstructive sleep apnoea in the Million Veteran Program uncovers genetic heterogeneity by sex. <b>2023</b> , 90, 104536	O
75	Genetic structure and genome-wide association study of the traditional Kazakh horses.	O
74	An atlas of genetic scores to predict multi-omic traits. <b>2023</b> , 616, 123-131	0
73	Association of polygenic scores with chronic kidney disease phenotypes in a longitudinal study of older adults. <b>2023</b> ,	O
72	Entwined African and Asian genetic roots of medieval peoples of the Swahili coast. 2023, 615, 866-873	O
71	In silico prioritisation of microRNA-associated common variants in multiple sclerosis. 2023, 17,	O
70	Cross-phenotype association analysis of gastric cancer: in-silico functional annotation based on the diseasegene network.	О
69	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.	O
68	A five-safes approach to a secure and scalable genomics data repository. <b>2023</b> , 26, 106546	О
67	Runs of homozygosity and signatures of selection for number of oocytes and embryos in the Gir Indicine cattle.	O

66	Genetic correlations between Alzheimer disease and gut microbiome genera. 2023, 13,	O
65	Refining patterns of MEF2C effects in white matter microstructure and psychiatric features. <b>2023</b> , 130, 697-706	O
64	Genomic characteristics and selection signals of Zhongshan ducks. 2023, 100797	0
63	Association of cumulative prenatal adversity with infant subcortical structure volumes and child problem behavior and its moderation by a coexpression polygenic risk score of the serotonin system. 1-16	O
62	Association of polygenic risk score with response to deep brain stimulation in Parkinson disease. <b>2023</b> , 23,	О
61	Runs of homozygosity and cross-generational inbreeding of Iranian fat-tailed sheep.	O
60	Genome-wide association study in 404,302 individuals identifies 7 significant loci for reaction time variability.	0
59	Implementation and evaluation of personal genetic testing as part of genomics analysis courses in German universities. <b>2023</b> , 16,	O
58	OTTERS: a powerful TWAS framework leveraging summary-level reference data. 2023, 14,	О
57	<del>原知明的</del> - <del>明, 8日初</del> -0- <b>明-2023</b> , 30-31	O
56	High-density SNP markers reveals the population structure of two local chicken genetic resources. <b>2023</b> , 102692	0
55	Genomic adaptation to extreme climate conditions in beef cattle as a consequence of cross-breeding program. <b>2023</b> , 24,	O
54	HLA-DQA1*05 and upstream variants of PPARGC1B are associated with infliximab persistence in Japanese Crohn∄ disease patients.	O
53	Exploring the genetic and genomic connection underlying neurodegeneration with brain iron accumulation and the risk for Parkinson disease. <b>2023</b> , 9,	O
52	Human variation impacting MCOLN2 restricts Salmonella Typhi replication by magnesium deprivation. <b>2023</b> , 100290	0
51	Association between birth by caesarian section and anxiety, self-harm: a gene-environment interaction study using UK Biobank data. <b>2023</b> , 23,	O
50	CARE: a novel wearable-derived feature linking circadian amplitude to human cognitive functions.	O
49	Effects of epigenetic age acceleration on kidney function: a Mendelian randomization study. <b>2023</b> , 15,	O

48	The Queensland Twin Adolescent Brain Project, a longitudinal study of adolescent brain development. <b>2023</b> , 10,	O
47	Identification of rare variants involved in high myopia unraveled by whole genome sequencing. <b>2023</b> , 100303	O
46	Independently evolved pollution resistance in four killifish populations is largely explained by few variants of large effect.	0
45	The origin of a mountain biota: hyper-aridity shaped reptile diversity in an Arabian biodiversity hotspot.	O
44	Analysis of the Combined Effect of rs699 and rs5051 on Angiotensinogen Expression and Hypertension.	0
43	Extensive variation of leaf specialized metabolite production in sessile oak (Quercus petraea) populations is to a large extent genetically determined but not locally adaptive.	O
42	Automated quantitative trait locus analysis (AutoQTL). 2023, 16,	O
41	Comparison of two multi-trait association testing methods and sequence-based fine mapping of six additive QTL in Swiss Large White pigs. <b>2023</b> , 24,	O
40	Dense sampling of ethnic groups within African countries reveals fine-scale genetic structure and extensive historical admixture. <b>2023</b> , 9,	O
39	AmelHap: Leveraging drone whole-genome sequence data to create a honey bee HapMap. <b>2023</b> , 10,	O
38	Identification of copy number variations in the genome of Dairy Gir cattle. 2023, 18, e0284085	0
37	Polygenic Risk Score in African populations: progress and challenges. 11, 175	O
36	Homozygosity mapping in the Kazakh national dog breed Tazy.	0
35	Estimating heritability explained by local ancestry and evaluating stratification bias in admixture mapping from summary statistics.	O
34	Genetic susceptibility for autoimmune diseases and white blood cell count. 2023, 13,	0
33	Identification of breed-specific genomic variants in Colombian Creole pig breeds by whole-genome sequencing. <b>2023</b> , 55,	O
32	Genomic analysis of two phlebotomine sand fly vectors of leishmania from the new and old World. <b>2023</b> , 17, e0010862	0
31	G2GSnake: A Snakemake workflow for host-pathogen genomic association studies.	O

30	Repurposing antidiabetic drugs for rheumatoid arthritis: results from a two-sample Mendelian randomization study.	O
29	Optimal HLA imputation of admixed population with dimension reduction.	O
28	PGSbuilder: An end-to-end platform for human genome association analysis and polygenic risk score predictions.	O
27	Genetic haplotypes associated with immune response to Leishmania infantum infection in dogs.	O
26	Dissecting the polygenic basis of atherosclerosis via disease-associated cell state signatures. 2023,	O
25	Fast and flexible joint fine-mapping of multiple traits via the Sum of Single Effects model.	O
24	Comparative population genomics provide new insight into the evolutionary history and adaptive potential of World Ocean krill.	O
23	Evidence for the role of selection for reproductively advantageous alleles in human aging.	O
22	Sex differences in the associations of genetic, sociodemographic and cardiovascular risk factors with depression in the Canadian Longitudinal Study on Aging (CLSA).	O
21	Redefining rock doves,Columba livia, using historical whole genome sequences.	O
20	Genetic variants associated with spontaneous preterm birth in women from India: a prospective cohort study. <b>2023</b> , 100190	0
19	An Integrated Genomic and Transcriptomic Analysis Reveals Distinct Molecular Features Associated with Mild-to-moderate Atopic Dermatitis.	O
18	Exogenous exposures shape genetic predisposition to lipids, AlzheimerB, and coronary heart disease in the MLXIPL gene locus.	0
17	Validation of a QTL for Flavobacterium psychrophilum resistance in rainbow trout Oncorhynchus mykiss. <b>2023</b> , 30, 101573	O
16	Genome-wide association analyses identified novel susceptibility loci for pulmonary embolism among Han Chinese population. <b>2023</b> , 21,	0
15	Interactions between the lipidome and genetic and environmental factors in autism. 2023, 29, 936-949	O
14	Reintroducing genetic diversity in populations from cryopreserved material: the case of Abondance, a French local dairy cattle breed. <b>2023</b> , 55,	0
13	Identifying high-impact variants and genes in exomes of Ashkenazi Jewish inflammatory bowel disease patients. <b>2023</b> , 14,	O

12	Genetics of myocardial interstitial fibrosis in the human heart and association with disease.	O
11	Associating broad and clinically defined polygenic scores for depression with depression-related phenotypes. <b>2023</b> , 13,	O
10	PRDM1 DNA-binding zinc finger domain is required for normal limb development and is disrupted in split hand/foot malformation. <b>2023</b> , 16,	0
9	SNP-Based Heritability of Osteochondrosis Dissecans in Hanoverian Warmblood Horses. <b>2023</b> , 13, 1462	O
8	The genetic determinants of recurrent somatic mutations in 43,693 blood genomes. 2023, 9,	0
7	Large multi-ethnic genetic analyses of amyloid imaging identify new genes for Alzheimer disease. <b>2023</b> , 11,	O
6	Genetic structure of an endangered species Ormosia henryi in southern China, and implications for conservation. <b>2023</b> , 23,	O
5	Construction of high coverage whole-genome sequencing libraries from single colon crypts without DNA extraction or whole-genome amplification. <b>2023</b> , 16,	O
4	A Long-Standing Hybrid Population Between Pacific and Atlantic Herring in a Subarctic Fjord of Norway. <b>2023</b> , 15,	0
3	Temperature and day length drive local adaptation in the Patagonian foundation tree speciesNothofagus pumilio.	O
2	Association of Genetic Variants of HLA-DQA1 with Bullous Pemphigoid Induced by Dipeptidyl Peptidase-4 Inhibitors. <b>2023</b> ,	0
1	Integrated microbiome-metabolome-genome axis data of Laiwu and Lulai pigs. <b>2023</b> , 10,	