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The variant call format and VCFtools

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#	Paper	IF	Citations
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402	Inversions maintain differences between migratory phenotypes of a songbird. **2023**, 14,	0
401	On the accuracy of threshold genomic prediction models for leaf miner and leaf rust resistance in arabica coffee. **2023**, 19,	0
400	Comparative phylogeography of a restricted and a widespread heather: genetic evidence of multiple independent introductions of Erica mackayana into Ireland from northern Spain.	0
399	Highly differentiated loci resolve phylogenetic relationships in the Bean Goose complex. **2023**, 23,	0
398	Flame resistant cotton lines generated by synergistic epistasis in a MAGIC population. **2023**, 18, e0278696	0
397	Complete chloroplast genomes of three sand-fixing Salix shrubs from Northwest China: comparative and phylogenetic analysis and interspecific identification.	0
396	Initiation of genomics-assisted breeding in Virginia-type peanuts through the generation of a de novo reference genome and informative markers. 13,	0
395	Genetic diversity and population structure ofEpichloefungal pathogens of plants in natural ecosystems.	0
394	Inter-chromosomal linkage disequilibrium and linked fitness cost loci associated with selection for herbicide resistance.	0
393	A 21-bp InDel in the promoter of STP1 selected during tomato improvement accounts for soluble solid content in fruits.	0
392	White Lupin Drought Tolerance: Genetic Variation, Trait Genetic Architecture, and Genome-Enabled Prediction. **2023**, 24, 2351	1
391	Prevalence of the GA risk haplotype of the rs1554483 and rs4864548 polymorphisms of the CLOCK gene associated with obesity and overweight in 26 populations. **2023**,	0

390	Prevalent introgression underlies convergent evolution in the diversification of Pungitius sticklebacks.	0
389	Comparative genomics of novel Bacteroides acidifaciens isolates reveals candidates for adaptation to host subspecies in house mice.	0
388	Design and implementation of a hybrid cloud system for large-scale human genomic research. **2023** , 10,	0
387	The revised reference genome of the leopard gecko (Eublepharis macularius) provides insight into the considerations of genome phasing and assembly.	0
386	Whole-exome sequencing of selected bread wheat recombinant inbred lines as a useful resource for allele mining and bulked segregant analysis. 13,	0
385	Genetic Structure and Diversity Study of Cassava (&lt;i&gt;Manihot esculenta&lt;/i&gt;) Germplasm for African Cassava Mosaic Disease and Fresh Storage Root Yield. **2023**, 13, 23-47	0
384	Discovery and Genetic Characterization of Single Cohort Adult Colonies With Male Aggregations, and Preliminary Evidence for Lekking in a Malagasy Kite Spider (Isoxya, Gasteracanthinae). **2023**, 7,	0
383	Copy Number Variation and Allele Ratio Analysis in Candida albicans Using Whole Genome Sequencing Data. **2023**, 105-125	0
382	Transcriptomic Approach for Global Distribution of SNP/Indel and Plant Genotyping. **2023**, 147-164	0
381	Polygenic adaptation from standing genetic variation allows rapid ecotype formation. 12,	2
380	Population-size history inferences from the coho salmon (Oncorhynchus kisutch) genome. **2023**, 13,	0
379	Genome-wide-association study and transcriptome analysis reveal the genetic basis controlling the formation of leaf wax inBrassica napus.	0
378	Genomic Insights into the Origin of a Thermotolerant Tomato Line and Identification of Candidate Genes for Heat Stress. **2023**, 14, 535	0
377	CATE: A fast and scalable CUDA implementation to conduct highly parallelized evolutionary tests on large scale genomic data.	0
376	Pathogen genetics identifies avirulence/virulence loci associated with barley chromosome 6H resistance in thePyrenophora teresf.teres□barley interaction.	0
375	Evidence of prezygotic isolation, but not assortative mating, between locally adapted populations of Fundulus heteroclitus across a salinity gradient. **2023**, 36, 687-697	0
374	An analysis of sugary endosperm in sorghum: Characterization of mutant phenotypes depending on alleles of the corresponding starch debranching enzyme. 14,	0
373	Single nucleotide polymorphism (SNP) in the doublesex (dsx) gene splice sites and relevance for its alternative splicing in the malaria vector Anopheles gambiae. 7, 31	0

372	Extensive crop–wild hybridization during Brassica evolution and selection during the domestication and diversification of Brassica crops. **2023**, 223,	0
371	Integrating Whole-Genome Resequencing and RNA Sequencing Data Reveals Selective Sweeps and Differentially Expressed Genes Related to Nervous System Changes in Luxi Gamecocks. **2023**, 14, 584	0
370	Advanced spawning in Pacific bluefin tuna, Thunnus orientalis, by a shift in consecutive photothermal regimes in a land-based tank. **2023**, 567, 739290	0
369	Genome-wide association study of 17 serum biochemical indicators in a chicken F2 resource population. **2023**, 24,	0
368	White Lupin Adaptation to Moderately Calcareous Soils: Phenotypic Variation and Genome-Enabled Prediction. **2023**, 12, 1139	0
367	A sheep pangenome reveals the spectrum of structural variations and their effects on tail phenotypes. **2023**, 33, 463-477	0
366	Genome-wide association studies reveal novel loci controlling tuber flesh color and oxidative browning inDioscorea alata.	0
365	Genomic divergence between two sister Medicago species triggered by the quaternary climatic oscillations on the Qinghai–Tibet plateau and northern China.	0
364	Ancestry dependent balancing selection of placental dysferlin at high-altitude. 11,	0
363	High-quality genome assembly and genetic mapping reveal a gene regulating flesh color in watermelon (Citrullus lanatus). 14,	0
362	The genomics and evolution of inter-sexual mimicry and female-limited polymorphisms in damselflies.	0
361	Genetic and ecophysiological evidence that hybridization facilitated lineage diversification in yellow Camellia (Theaceae) species: a case study of natural hybridization between C. micrantha and C. flavida. **2023**, 23,	0
360	Gossypium purpurascens genome provides insight into the origin and domestication of upland cotton. **2023**,	0
359	Current management practices do not adequately safeguard endangered plant species in conservation collections. **2023**, 280, 109955	0
358	Genomic insights into the genetic basis of cotton breeding in China. **2023**, 16, 662-677	0
357	History cooling events contributed to the endangered status of Pseudotsuga brevifolia endemic to limestone habitats. **2023**, 42, e02414	0
356	Whole genome sequencing of simmental cattle for SNP and CNV discovery. **2023**, 24,	0
355	Selection and adaptive introgression guided the complex evolutionary history of the European common bean. **2023**, 14,	0

354	Species-Level Recognition and Redescription of the Kentucky Arrow Darter, Etheostoma spilotum Gilbert (Percidae: litocara). **2023**, 64,	0
353	The third symbiotic partner of the volcano lichenCladonia vulcaniSavicz drove adaptation to an extreme environment.	0
352	Phylogenomics reveal extensive phylogenetic discordance due to incomplete lineage sorting following the rapid radiation of alpine butterflies (Papilionidae: Parnassius).	0
351	Structural variation (SV)-based pan-genome and GWAS reveal the impacts of SVs on the speciation and diversification of allotetraploid cottons. **2023**, 16, 678-693	0
350	The genome of the pygmy right whale illuminates the evolution of rorquals. **2023**, 21,	0
349	Phylogeography of the blacklegged tick (Ixodes scapularis) throughout the USA identifies candidate loci for differences in vectorial capacity.	0
348	Impact of pathogen genetics on clinical phenotypes in a population ofTalaromyces marneffeifrom Vietnam.	0
347	The genome sequence and demographic history of Przewalskia tangutica (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau.	0
346	Strong purifying selection in haploid tissue-specific genes of Scots pine supports the masking theory.	0
345	Characterization of genome-wide STR variation in 6487 human genomes. **2023**, 14,	0
344	Domestication affects sex-biased gene expression evolution in the duck. **2023**, 10,	0
343	Long-read sequencing of diagnosis and post-therapy medulloblastoma reveals complex rearrangement patterns and epigenetic signatures. **2023**, 3, 100281	0
342	Evaluation of Large-scale Highly Polymorphic Microhaplotypes in Complex DNA Mixtures Analysis Using RMNE Method. **2023**, 102874	0
341	Whole-Genome Resequencing Reveals the Genetic Diversity and Selection Signatures of the Brassica juncea from the Yunnan□Guizhou Plateau. **2023**, 13, 1053	0
340	Molecular phylogeny and inflorescence evolution of Prunus (Rosaceae) based on RAD-seq and genome skimming analyses. **2023**,	0
339	Metabolome-Based Genome-Wide Association Study of Duck Meat Leads to Novel Genetic and Biochemical Insights.	0
338	Systematically exploring the performance of a self-developed Multi-InDel system in forensic identification, ancestry inference and genetic structure analysis of Chinese Manchu and Mongolian groups. **2023**, 346, 111637	0
337	The hybridization origin of the Chinese endemic herb genus Notopterygium (Apiaceae): Evidence from population genomics and ecological niche analysis. **2023**, 182, 107736	0

336 Population genomics indicate three different modes of divergence and speciation with gene flow in the green-winged teal duck complex. **2023**, 182, 107733 o

335 Diversification and introgression in four chromosomal taxa of the Pearson's horseshoe bat (Rhinolophus pearsoni) group. **2023**, 183, 107784 o

334 Comparative evaluation of the MAPlex, Precision ID Ancestry Panel, and VISAGE Basic Tool for biogeographical ancestry inference. **2023**, 64, 102850 o

333 Deep genome-wide divergences among species in White Cloud Mountain minnow Tanichthys albonubes (Cypriniformes: Tanichthyidae) complex: Conservation and species management implications. **2023**, 182, 107734 o

332 Lead exposure is correlated with reduced nesting success of an urban songbird. **2023**, 227, 115711 o

331 A genome-wide scan to identify signatures of selection in Lueyang black -bone chicken. **2023**, 102721 o

330 Genetic fine-mapping reveals single nucleotide polymorphism mutations in the MC1R regulatory region associated with duck melanism. o

329 Preliminary Investigation of Essentially Derived Variety of Tea Tree and Development of SNP Markers. **2023**, 12, 1643 o

328 Genomic prediction of survival against Vibrio harveyi in leopard coral grouper (Plectropomus leopardus) using GBLUP, weighted GBLUP, and BayesC **2023**, 572, 739536 o

327 Genome-wide association study and candidate gene analysis of cadmium accumulation in Fujian oysters (Crasosstrea angulata). **2023**, 572, 739546 o

326 Geography and past climate changes have shaped the evolution of a widespread lizard in arid Central Asia. **2023**, 184, 107781 o

325 Population genomics of Corsican wildcats: Paving the way toward a new subspecies within the Felis silvestris spp. complex?. **2023**, 32, 1908-1924 o

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323 Fine scale genetics reveals the subtle negative effects of roads on an endangered bat. **2023**, 869, 161705 o

322 Genomic diversity and differentiation between island and mainland populations of white-tailed eagles (Haliaeetus albicilla). **2023**, 32, 1925-1942 o

321 Genomic evidence for adaptation to tuberculosis in the Andes before European contact. **2023**, 26, 106034 o

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319 A pangenome analysis pipeline provides insights into functional gene identification in rice. **2023**, 24, o

318	Extensive hybridisation between multiple differently adapted species may aid persistence in a changing climate.	0
317	Genomic health is dependent on long-term population demographic history. **2023**, 32, 1943-1954	0
316	Runs of homozygosity reveal past bottlenecks and contemporary inbreeding across diverging populations of an island-colonizing bird. **2023**, 32, 1972-1989	0
315	Genetic responses in sexual diploid and unisexual triploid goldfish (Carassius auratus) introduced into a high-altitude environment. **2023**, 32, 1955-1971	0
314	Whole genome sequencing revealed genetic diversity, population structure, and selective signature of Panou Tibetan sheep. **2023**, 24,	0
313	The tragedy of the common? A comparative population genomic study of two bumblebee species.	0
312	The Legacy of Infectious Disease Exposure on the Genomic Diversity of Indigenous Southern Mexicans. **2023**, 15,	0
311	Winter connectivity and leapfrog migration in a migratory passerine. **2023**, 13,	0
310	When sex scarce: A rapid approach to sexing individuals by RAD-seq using a reference genome.	0
309	Pangenome obtained by long-read sequencing of 11 genomes reveal hidden functional structural variants in pigs. **2023**, 26, 106119	0
308	Genomic analysis of Bornean geckos (Gekkonidae: Cyrtodactylus) reveals need for updated taxonomy. **2023**, 52, 249-263	0
307	Genomic Underpinnings of Population Persistence in Isle Royale Moose. **2023**, 40,	0
306	De Novo Mutations Contributes Approximately 7% of Pathogenicity in Inherited Eye Diseases. **2023** , 64, 5	0
305	Genome-wide exploration reveals distinctive northern and southern variants of Clonorchis sinensis in the Far East. **2023**, 23, 833-843	0
304	Modern Japanese ancestry-derived variants reveal the formation process of the current Japanese regional gradations. **2023**, 26, 106130	0
303	Whole-genome resequencing reveals selection signatures for caviar yield in Russian sturgeon (Acipenser gueldenstaedtii). **2023**, 568, 739312	0
302	Life on a beach leads to phenotypic divergence despite gene flow for an island lizard. **2023**, 6,	0
301	Hidden impacts of conservation management on fertility of the critically endangered kkp11, e14675	0

300	3D-GBS: a universal genotyping-by-sequencing approach for genomic selection and other high-throughput low-cost applications in species with small to medium-sized genomes. **2023**, 19,	0
299	A highly multiplexed assay to monitor pathogenicity, fungicide resistance and gene flow in the fungal wheat pathogen Zymoseptoria tritici. **2023**, 18, e0281181	0
298	Range-wide whole-genome resequencing of the brown bear reveals drivers of intraspecies divergence. **2023**, 6,	0
297	RADseq-based population genomic analysis and environmental adaptation of rare and endangered recretohalophyte Reaumuria trigyna.	0
296	Forest health in the Anthropocene: the emergence of a novel tree disease is associated with poplar cultivation. **2023**, 378,	1
295	Population Survey Combined with Genomic-Wide Genetic Variation Unravels the Endangered Status of Quercus gilva. **2023**, 15, 230	0
294	Genome-wide association study identifies novel candidate malaria resistance genes in Cameroon.	0
293	Divergent Outcomes of Direct Conspecific Pathogen Strain Interaction and Plant Co-Infection Suggest Consequences for Disease Dynamics. **2023**, 11,	0
292	Robust SNP-based prediction of rheumatoid arthritis through machine-learning-optimized polygenic risk score. **2023**, 21,	0
291	The SlDOG1 Affect Biosynthesis of Steroidal Glycoalkaloids by Regulating GAME Expression in Tomato. **2023**, 24, 3360	0
290	Genetic architectures of postmating isolation and morphology of two highly diverged rockfishes (genusSebastes).	0
289	Whole-body adipose tissue multi-omic analyses in sheep reveal molecular mechanisms underlying local adaptation to extreme environments. **2023**, 6,	0
288	The broad use of the Pm8 resistance gene in wheat resulted in hypermutation of the AvrPm8 gene in the powdery mildew pathogen. **2023**, 21,	0
287	Cooperative role of AtRsmD and AtRimM proteins in modification and maturation of 16S rRNA in plastids. **2023**, 114, 310-324	0
286	Contributions of rare and common variation to early-onset and atypical dementia risk.	0
285	Mitonuclear Interactions and the Origin of Macaque Societies. **2023**, 15,	0
284	The population genetics of speciation by cascade reinforcement. **2023**, 13,	0
283	A complex genomic architecture underlies reproductive isolation in a North American oriole hybrid zone. **2023**, 6,	0

282	754. Implementation of single-step GBLUP for complex behaviour traits in Labrador Retrievers used as service dogs. **2022**,	0
281	189. Exploring genetic diversity and selection signatures in indigenous African cattle breeds. **2022**,	0
280	A chromosome-level reference genome of the wax gourd (Benincasa hispida). **2023**, 10,	0
279	Development and characterization of a sorghum multi-parent advanced generation intercross (MAGIC) population for capturing diversity among seed parent gene pool. **2023**, 13,	0
278	517. Olfaction: a critical force driving adaptive evolution in yaks. **2022**,	0
277	Retrospective analysis of Plasmodium vivax genomes from a pre-elimination China inland population in the 2010s. 14,	0
276	265. Unravelling the effect of structural variants from whole-genome sequence for depigmentation in Nellore cattle. **2022**,	0
275	796. Whole-genome screening for resilience against PRRSV outbreaks in breeding sows. **2022**,	0
274	Genome and haplotype provide insights into the population differentiation and breeding improvement of Gossypium barbadense. **2023**,	0
273	Insights into the differentiation and adaptation within Circaeasteraceae from Circaeaster agrestis genome sequencing and resequencing. **2023**, 26, 106159	0
272	Evidence that genetic drift not adaptation drivesfast-Zandlarge-Zeffects inFicedulaflycatchers.	0
271	Captive rearing effects on the methylome of Atlantic salmon after oceanic migration: Sex-specificity and intergenerational stability.	0
270	Genome-wide SNP discovery in native American and Hungarian Robinia pseudoacacia genotypes using next-generation double-digest restriction-site-associated DNA sequencing (ddRAD-Seq). **2023**, 19,	0
269	Genomic architecture of migration timing in a long-distance migratory songbird. **2023**, 13,	0
268	Genomic decoding of breeding history to guide breeding-by-design in rice. **2023**, 10,	0
267	HaploBlocks: Efficient Detection of Positive Selection in Large Population Genomic Datasets. **2023**, 40,	0
266	The blowfly Chrysomya latifrons inhabits fragmented rainforests, but shows no population structure. **2023**, 201, 703-719	0
265	Extensive set of African ancestry-informative markers (AIMs) to study ancestry and population health. 14,	0

264	Genomic Resources for Asian (Elephas maximus) and African Savannah Elephant (Loxodonta africana) Conservation and Health Research.	0
263	Limited role of generation time changes in driving the evolution of the mutation spectrum in humans. 12,	0
262	Selection on many loci drove the origin and spread of a key innovation.	0
261	Comparative analysis of histopathological parameters, genome-wide copy number alterations, and variants in genes involved in cell cycle regulation in chordomas of the skull base and sacrum. **2023**, 82, 312-323	0
260	Origins, timing and introgression of domestic geese revealed by whole genome data. **2023**, 14,	0
259	Genome-wide identification, expression pattern and genetic variation analysis of SWEET gene family in barley reveal the artificial selection of HvSWEET1a during domestication and improvement. 14,	0
258	XY sex determination in a cnidarian. **2023**, 21,	0
257	A Pellino-2 variant is associated with constitutive NLRP3 inflammasome activation in a family with ocular pterygium▯digital keloid dysplasia.	0
256	Genome assembly, resequencing and genome-wide association analyses provide novel insights into the origin, evolution and flower colour variations of flowering cherry.	0
255	Genetic diversity variation during the natural regeneration of Vatica guangxiensis, an endangered tree species with extremely small populations. **2023**, 42, e02400	0
254	PipeIT2: A tumor-only somatic variant calling workflow for molecular diagnostic Ion Torrent sequencing data. **2023**, 115, 110587	0
253	Identification of candidate genes for LepR1 resistance against Leptosphaeria maculans in Brassica napus. 14,	0
252	Integrative multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci.	0
251	Reproducible evaluation of transposable element detectors with McClintock 2 guides accurate inference of Ty insertion patterns in yeast.	0
250	Genomic analysis reveals a KIT -related chromosomal translocation associated with the white coat phenotype in yak. **2023**, 140, 330-342	0
249	The genetic basis and potential molecular mechanism of yellow-albino northern snakehead (Channa argus). **2023**, 13,	1
248	Tree-Level Growth Patterns and Genetic Associations Depict Drought Legacies in the Relict Forests of Abies marocana. **2023**, 12, 873	0
247	Analysis of the correlation between genetic and species diversity in a temperate forest: Variation in cohorts and effect of disturbance. **2023**, 300, 152243	0

246	An improved reference genome for Trifolium subterraneum L. provides insight into molecular diversity and intra-specific phylogeny. 14,	0
245	Population Structure, Demographic History, and Adaptation of Giant Honeybees in China Revealed by Population Genomic Data. **2023**, 15,	0
244	De Novo SNP Discovery and Genotyping of Masson Pine (Pinus massoniana Lamb.) via Genotyping-by-Sequencing. **2023**, 14, 387	0
243	Phylogenomic analyses reveal incongruences between divergence times and fossil records of freshwater snails in East Asia. **2023**, 182, 107728	0
242	The Incompetence of Mosquitoes Can Zika Virus Be Adapted To Infect Culex tarsalis Cells?. **2023**, 8,	0
241	Amazonian birds in more dynamic habitats have less population genetic structure and higher gene flow.	0
240	Accumulation of gene copy number variations during the early phase of free-spawning abalone speciation. **2023**, 13,	0
239	Hypothesis-free phenotype prediction within a genetics-first framework. **2023**, 14,	0
238	Insights into the Genetic Determination of the Autotetraploid Potato Plant Height. **2023**, 14, 507	0
237	Parallel evolution and cryptic diversification in a common and widespread Amazonian tree, Protium subserratum.	0
236	The idiosyncratic genome of Korean long-tailed chicken as a valuable genetic resource. **2023**, 26, 106236	0
235	Role of long non-coding RNA in regulatory network response to Candidatus Liberibacter asiaticus in citrus. 14,	0
234	Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. 14,	0
233	Genome Polymorphism Analysis and Selected Sweep Regions Detection via the Genome Resequencing of 91 Cabbage (Brassica oleracea) Accessions. **2023**, 9, 283	0
232	The genetic architecture of soybean photothermal adaptation to high latitudes.	0
231	Genome-Wide Genetic Structure of Henan Indigenous Chicken Breeds. **2023**, 13, 753	0
230	Species boundaries and conservation implications of Cinnamomum japonicum , an endangered plant in China.	0
229	Cloning of an Albino Mutation of Arabidopsis thaliana Using Mapping-by-Sequencing. **2023**, 24, 4196	0

228	Chromosome-level genome assembly and population genomics of Mongolian racerunner (Eremias argus) provide insights into high-altitude adaptation in lizards. **2023**, 21,	0
227	Genomics of Secondarily Temperate Adaptation in the Only Non-Antarctic Icefish. **2023**, 40,	0
226	Utilizing Variants Identified with Multiple Genome-Wide Association Study Methods Optimizes Genomic Selection for Growth Traits in Pigs. **2023**, 13, 722	0
225	Effective population size in a partially clonal plant is not predicted by the number of genetic individuals. **2023**, 16, 750-766	0
224	Gene expression plasticity followed by genetic change during colonization a high-elevation environment.	0
223	Escape from X-inactivation in twins exhibits intra- and inter-individual variability across tissues and is heritable. **2023**, 19, e1010556	0
222	Frequency and types of alternative breeding strategies employed by nesting American black ducks in North Carolina. **2023**, 18, e0278905	0
221	Identifying Targets of Selection in Laboratory Evolution Experiments.	0
220	Large-scale population structure and genetic architecture of agronomic traits of garlic.	0
219	Thermal heterogeneity is an important factor for maintaining the genetic differentiation pattern of the pelagic barnacle Lepas anatifera in the northwest Pacific. **2023**, 13,	0
218	Synthesising environmental, epidemiological, and genetic data to assist decision making for onchocerciasis elimination.	0
217	De novo variants in MAST4 related to neurodevelopmental disorders with developmental delay and infantile spasms: Genotype-phenotype association. 16,	0
216	Genomic selection in algae with biphasic lifecycles: A Saccharina latissima (sugar kelp) case study. 10,	0
215	Fragmented habitat compensates for the adverse effects of genetic bottleneck. **2023**, 33, 1009-1018.e7	0
214	The allotetraploidNicotiana tabacumgenome and GenBank genomics highlight the genomic features, genetic diversity and regulation of morphological, metabolic and disease-resistance traits.	0
213	Genomic prediction for complex traits across multiples harvests in alfalfa (Medicago sativa L.) is enhanced by enviromics.	0
212	Genomics reveals the role of admixture in the evolution of structure among sperm whale populations within the Mediterranean Sea.	0
211	Conservation genomics reveals low connectivity among populations of threatened roseate terns (Sterna dougallii) in the Atlantic Basin.	0

210	Phytophthora cambivora. **2023**, 14,	0
209	Long divergent haplotypes introgressed from wild sheep are associated with distinct morphological and adaptive characteristics in domestic sheep. **2023**, 19, e1010615	0
208	Genomic responses to parallel temperature gradients in the eelgrass Zostera marina in adjacent bays.	0
207	The Genotypic Variability among Short-Season Soybean Cultivars for Nitrogen Fixation under Drought Stress. **2023**, 12, 1004	0
206	Quantifying genetic differentiation and population assignment between two contingents of Atlantic mackerel (Scomber scombrus) in the Northwest Atlantic.	0
205	Contrasting Patterns of Single Nucleotide Polymorphisms and Structural Variation Across Multiple Invasions. **2023**, 40,	0
204	Whole-genome resequencing data support a single introduction of the invasive white pine sawfly, Diprion similis.	0
203	Signatures of co-evolution and co-regulation in the CYP3A and CYP4F genes in humans.	0
202	CAS Array: design and assessment of a genotyping array for Chinese biobanking. **2023**, 6,	0
201	A thousand-genome panel retraces the global spread and adaptation of a major fungal crop pathogen. **2023**, 14,	0
200	Whole genome sequencing of a wild swan goose population. 14,	0
199	Combining multiple lines of evidence to elucidate the origin and introduction pathway of bitou bush (Chrysanthemoides monilifera subsp. rotundata) in Australia.	0
198	Rapid genotyping of porcine reproductive and respiratory syndrome virus (PRRSV) using MinION nanopore sequencing.	0
197	Weak range-wide population structure in the blackfin tuna (Thunnus atlanticus) revealed by analysis of genome-wide SNPs.	0
196	A minimal genome design to maximally guarantee fertile inter-subspecific hybrid rice. **2023**, 16, 726-738	1
195	Environmental drivers behind the genetic differentiation in mountain chickadees (Poecile gambeli).	0
194	Genomic diversity and signals of selection processes in wild and farm-reared red-legged partridges (Alectoris rufa). **2023**, 115, 110591	0
193	Whole-Genome Sequencing Data Reveal New Loci Affecting Milk Production in German Black Pied Cattle (DSN). **2023**, 14, 581	0

192	Conservation implications of elucidating the Korean wolf taxonomic ambiguity through whole-genome sequencing.	0
191	Genome-wide association study revealed suggestive QTLs for production and reproduction traits in Indian Murrah buffalo. **2023**, 13,	0
190	Genetic relationships among laboratory lines of the egg parasitoid Trissolcus japonicus from native and adventive populations. 82, 145-161	0
189	Whole-genome re-sequencing provides key genomic insights in farmed Arctic charr (Salvelinus alpinus) populations of anadromous and landlocked origin from Scandinavia.	0
188	Studies on the Origin of Asian Cultivated Rice Based on 15 Domestication Region.	0
187	Evolutionary origin and establishment of a dioecious diploid-tetraploid complex.	0
186	Screening of candidate genes related to differences in growth and development between Chinese indigenous and Western pig breeds. **2023**, 55, 147-153	0
185	Broad-scale signatures of linked selection under divergent recombination landscapes and mating systems in natural populations of rye and barley.	0
184	Gene conversion drives allelic dimorphism in two paralogous surface antigens of the malaria parasiteP. falciparum.	0
183	Genome-Wide Association Analysis of Fruit Shape-Related Traits in Areca catechu. **2023**, 24, 4686	0
182	Human Genome Polymorphisms and Computational Intelligence Approach Revealed a Complex Genomic Signature for COVID-19 Severity in Brazilian Patients. **2023**, 15, 645	0
181	An oligogenic architecture underlying ecological and reproductive divergence in sympatric populations. 12,	0
180	First in family Rhabdiasidae: the reference-guided genome assembly of an invasive parasite, the cane toad lungworm (Rhabdias pseudosphaerocephala).	0
179	Using visual scores and categorical data for genomic prediction of complex traits in breeding programs.	0
178	Convergence or redundancy: alternative views about the evolutionary genomics of character displacement.	0
177	Introgressive hybridization in the west Pacific pen shells (genus Atrina): Restricted interspecies gene flow within the genome.	0
176	Non-Synonymous Variants in Fat QTL Genes among High- and Low-Milk-Yielding Indigenous Breeds. **2023**, 13, 884	0
175	Limited genetic variations of the Rh5-CyRPA-Ripr invasion complex in Plasmodium falciparum parasite population in selected malaria-endemic regions, Kenya. 4,	0

174	Whole-genome sequencing reveals a complex African population demographic history and signatures of local adaptation. **2023**, 186, 923-939.e14	1
173	Dual domestications and origin of traits in grapevine evolution. **2023**, 379, 892-901	1
172	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. **2023**, 186, 1279-1294.e19	0
171	Chromosome-level reference genome of Tetrastigma hemsleyanum (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids.	0
170	Recombination Variation Shapes Phylogeny and Introgression in Wild Diploid Strawberries. **2023**, 40,	0
169	Developing Methods for Maintaining Genetic Diversity in Novel Aquaculture Species: The Case of Seriola lalandi. **2023**, 13, 913	0
168	Large-scale genomic and transcriptomic analyses elucidate the genetic basis of high meat yield in chickens. **2023**,	0
167	Identification of Selection Signatures and Loci Associated with Important Economic Traits in Yunan Black and Huainan Pigs. **2023**, 14, 655	0
166	Genomic analysis of Leishmania turanica strains from different regions of Central Asia. **2023**, 17, e0011145	0
165	Song features correlate with male reproductive success and avian malaria infection in a promiscuous songbird with female-only parental care.	0
164	Three sequential sex chromosome □autosome fusions inHeliconiusbutterflies.	0
163	Whole genome analyses reveal weak signatures of population structure and environmentally associated local adaptation in an important North American pollinator, the bumble beeBombus vosnesenskii.	0
162	High performance imputation of structural and single nucleotide variants in Atlantic salmon using low-coverage whole genome sequencing.	0
161	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. **2023**, 14, 665	0
160	Genomic selection for agronomic traits in a winter wheat breeding program. **2023**, 136,	0
159	Resolution of the Eremophila tietkensii (Scrophulariaceae) species complex based on congruence between morphological and molecular pattern analyses. **2022**, 35, 1-18	0
158	Identification of structural variations related to drought tolerance in wheat (Triticum aestivum L.). **2023**, 136,	0
157	Population whole-genome resequencing reveals the phylogenetic relationships and population structure of four Hunan typical tea landraces. **2023**, 3, 0-0	0

156	Weak reproductive isolation and extensive gene flow betweenMimulus glaucescensandM. guttatusin northern California.	o
155	Genomic clines across the species boundary between a hybrid pine and its progenitor in the eastern Tibetan Plateau. **2023**, 100574	o
154	Homozygous haplotype deficiency in Manech Tt̋e Rousse dairy sheep revealed a nonsense variant inMMUTgene affecting newborn lamb viability.	o
153	Loss of daylength sensitivity by splice site mutation in Cannabis.	o
152	Geographic-genomic and geographic-phenotypic differentiation of the Aquilegia viridiflora complex.	o
151	There and Back Again: The Unexpected Journeys of Metridium de Blainville, 1824 between the Old Oceans and throughout the Modern World. 000-000	o
150	Characterization of the USDA Cucurbita pepo, C. moschata, and C. maxima germplasm collections. 14,	o
149	Population Structure, Genetic Diversity and Candidate Genes for the Adaptation to Environmental Stress in Picea koraiensis. **2023**, 12, 1266	o
148	Change in the Gut Microbiome and Immunity by Lacticaseibacillusrhamnosus Probio-M9. **2023**, 11,	o
147	Aspergillus fumigatus Can Display Persistence to the Fungicidal Drug Voriconazole. **2023**, 11,	o
146	Archaic humans have contributed to large-scale variation in modern human T´cell receptor genes. **2023**, 56, 635-652.e6	o
145	A single base pair duplication inSLC33A1gene causes fetal losses and neonatal lethality in Manech Tt̋e Rousse dairy sheep.	o
144	SafeMut: UMI-aware variant simulator incorporating allele-fraction overdispersion in read editing.	o
143	Molecular signature of domestication in the arboviral vectorAedes aegypti.	o
142	Population genetics and geographic origins of mallards harvested in northwestern Ohio. **2023**, 18, e0282874	o
141	Population Structure and Genetic Diversity Analysis of Yufen 1□H Line Chickens Using Whole-Genome Resequencing. **2023**, 13, 793	o
140	Population structure and adaptive differentiation in the sea cucumber Apostichopus californicus and implications for spatial resource management. **2023**, 18, e0280500	o
139	An evolutionary perspective on genetic load in small, isolated populations as informed by whole genome resequencing and forward-time simulations. **2023**, 77, 690-704	o

138	Geographic variability of hybridization between red-breasted and red-naped sapsuckers. **2023**, 77, 580-592	0
137	Asexual male production by ZW recombination inArtemia parthenogenetica. **2023**, 77, 1-12	0
136	Assessment of the Genetic Diversity and Population Structure of the Peruvian Andean Legume, Tarwi (Lupinus mutabilis), with High Quality SNPs. **2023**, 15, 437	0
135	Exploring the sorghum race level diversity utilizing 272 sorghum accessions genomic resources. 14,	0
134	The genomic characteristics affect phenotypic diversity from the perspective of genetic improvement of economic traits. **2023**, 26, 106426	0
133	Local adaptation in shell shape traits of a brooding chiton with strong population genomic differentiation. **2023**, 77, 210-220	0
132	Long-term biogeographical processes dominate patterns of genetic diversity in a wingless grasshopper despite substantial recent habitat fragmentation.	0
131	Ornithine aminotransferase OsOAT is critical for male fertility and cold tolerance during rice plant development.	0
130	Determinants of genetic diversity in sticklebacks.	0
129	Diverse and Abundant Viruses Exploit Conjugative Plasmids.	0
128	De novomutation rates in sticklebacks.	0
127	Analysis of Genetic Diversity in Coilia nasus Based on 2b-RAD Simplified Genome Sequencing. **2023**, 15, 1173	0
126	Selective whole-genome amplification reveals population genetics of Leishmania braziliensis directly from patient skin biopsies. **2023**, 19, e1011230	0
125	Genome-wide survey identified superior and rare haplotypes for plant height in the north-eastern soybean germplasm of China. **2023**, 43,	0
124	Genome-wide phylogeography reveals cryptic speciation in the circumglobal planktonic calcifier Limacina bulimoides.	0
123	Relatedness within colonies of three North American species of carpenter ants (Subgenus: Camponotus) and a comparison with relatedness estimates across Formicinae.	0
122	Systematics of the avian family Alaudidae using multilocus and genomic data. **2023**, 100095	0
121	Different waves of postglacial recolonisation and genomic structure of bank vole populations in NE Poland.	0

120	Intraspecific Comparative Analysis Reveals Genomic Variation of Didymella arachidicola and Pathogenicity Factors Potentially Related to Lesion Phenotype. **2023**, 12, 476	0
119	Performance and limitations of linkage-disequilibrium-based methods for inferring the genomic landscape of recombination and detecting hotspots: a simulation study. 3,	0
118	Evidence for a single, ancient origin of a genus-wide alternative life history strategy. **2023**, 9,	0
117	Fire frequency, as well as stress response and developmental gene control serotiny level variation in a widespread pioneer Mediterranean conifer, Pinus halepensis. **2023**, 13,	0
116	ZmHOX32 is related to photosynthesis and likely functions in plant architecture of maize. 14,	0
115	Current allele distribution of the human longevity gene APOE in Europe can mainly be explained by ancient admixture.	0
114	Artificial selection footprints in domestic chicken genomes.	0
113	GWAS of grain color and tannin content in Chinese sorghum based on whole-genome sequencing. **2023**, 136,	0
112	Depression: an adaptive disease?.	0
111	A role for heritable transcriptomic variation in maize adaptation to temperate environments. **2023**, 24,	0
110	A diverse panel of 755 bread wheat accessions harbors untapped genetic diversity in landraces and reveals novel genetic regions conferring powdery mildew resistance.	1
109	Transcriptomic Prediction of Breeding Values in Loblolly Pine.	0
108	An explainable deep learning classifier of bovine mastitis based on whole genome sequence data - circumventing the p>>>n problem.	0
107	Understanding Complex Trait Susceptibilities and Ethnical Diversity in a Sample of 4,145 Russians Through Analysis of Clinical and Genetic Data.	0
106	MutationExplorer - a webserver for mutation of proteins and 3D visualization of energetic impacts.	0
105	Comprehensive genomic analyses of Vigna unguiculata provide insights into population differentiation and the genetic basis of key agricultural traits.	0
104	Genetic diversity and signatures of selection in BoHuai goat revealed by whole-genome sequencing. **2023**, 24,	0
103	A 37´K SNP array for the management and conservation of Golden Eagles (Aquila chrysaetos).	0

102	Genetic mapping and molecular mechanism behind color variation in the Asian vine snake. **2023**, 24,	0
101	No association of a Vascular endothelial growth factor A (VEGFA) gene polymorphism with pre-eclampsia among pregnant women in Uganda. **2023**, 24,	0
100	Evidence for ancient selective sweeps followed by differentiation among three species ofSphyrapicussapsuckers.	0
99	srdA mutations suppress the rseA/cpsA deletion mutant conidiation defect in Aspergillus nidulans. **2023**, 13,	0
98	Genomic assessment reveals signal of adaptive selection in populations of the Spotted rose snapper Lutjanus guttatus from the Tropical Eastern Pacific. 11, e15029	0
97	Rare genetic variants inSEC24Dmodify orofacial cleft phenotypes.	0
96	Genome-wide identification and annotation of SNPs and their mapping in candidate genes related to milk production and fertility traits in Badri cattle. **2023**, 55,	0
95	Preselection of QTL markers enhances accuracy of genomic selection in Norway spruce. **2023**, 24,	0
94	Integration of Selection Signatures and Protein Interactions Reveals NR6A1, PAPPA2, and PIK3C2B as the Promising Candidate Genes Underlying the Characteristics of Licha Black Pig. **2023**, 12, 500	0
93	Large haploblocks underlie rapid adaptation in the invasive weed Ambrosia artemisiifolia. **2023**, 14,	0
92	Elucidating SNP-Based Population Structure and Genetic Diversity of Bruguiera gymnorhiza (L.) Savigny in Thailand. **2023**, 14, 693	0
91	GVC: efficient random access compression for gene sequence variations. **2023**, 24,	0
90	Phylogenomics and morphological evolution of the mega-diverse genus Artemisia (Asteraceae: Anthemideae): implications for its circumscription and infrageneric taxonomy.	0
89	Global multi-omics profiling reveals evolutionary drivers of phylogeographic diversity of fungal specialized metabolism.	0
88	In silico prioritisation of microRNA-associated common variants in multiple sclerosis. **2023**, 17,	0
87	Replicate contact zones suggest a limited role of plumage in reproductive isolation among subspecies of the variable seedeater (Sporophila corvina).	0
86	Genome-wide analysis emancipates genomic diversity and signature of selection in Altay white-headed cattle of Xinjiang, China. 14,	0
85	A Genomic Quantitative Study on the Contribution of the Ancestral-State Bases Relative to Derived Bases in the Divergence and Local Adaptation of Populus davidiana. **2023**, 14, 821	0

84	Population Structure and Selection Signatures of Domestication in Geese. **2023**, 12, 532	0
83	Apolipoprotein E (APOE) Haplotypes in Healthy Subjects from Worldwide Macroareas: A Population Genetics Perspective for Cardiovascular Disease, Neurodegeneration, and Dementia. **2023**, 45, 2817-2831	0
82	Genotyping of Haliotis discus hannai and machine learning models to predict the heat resistant phenotype based on genotype. 14,	0
81	Functional genomic effects of indels using Bayesian genome-phenome wide association studies in sorghum. 14,	0
80	Oral metagenomes from Native American Ancestors reveal distinct microbial lineages in the pre-contact era.	0
79	PanGraphViewer: A Versatile Tool to Visualize Pangenome Graphs.	0
78	Does social antagonism facilitate supergene expansion? A novel region of suppressed recombination in a 4-haplotype supergene system.	0
77	Isolation by resistance explains genetic diversity in the Arremon brushfinches of northern Mesoamerica.	0
76	Genomic characteristics and selection signals of Zhongshan ducks. **2023**, 100797	0
75	Phylogeographic and demographic patterns reveal congruent histories in seven Amazonian White-Sand ecosystems birds.	0
74	SSR and SNP Marker-Based Investigation of Indian Rice Landraces in Relation to Their Genetic Diversity, Population Structure, and Geographical Isolation. **2023**, 13, 823	0
73	A complete gap-free diploid genome in Saccharum complex and the genomic footprints of evolution in the highly polyploid Saccharum genus. **2023**, 9, 554-571	0
72	Genome-wide association study reveals that the IBSP locus affects ear size in cattle.	0
71	Using visual scores and categorical data for genomic prediction of complex traits in breeding programs.	0
70	The genomic architecture of a continuous color polymorphism in the European barn owl (Tyto alba).	0
69	Insight into the evolutionary and domesticated history of the most widely cultivated mushroom Agaricus bisporus via mitogenome sequences of 361 global strains. **2023**, 24,	0
68	Assessing the current genetic status of Lubei white goat based on the whole-genome data.	0
67	Genomic adaptation to extreme climate conditions in beef cattle as a consequence of cross-breeding program. **2023**, 24,	0

66	Chromosome-level genome assembly of the yellow boxfish (Ostracion cubicus) provides insights into the evolution of bone plates and ostracitoxin secretion. 10,	0
65	Genomic Relationships of Glycine remota, a Recently Discovered Perennial Relative of Soybean, within Glycine. **2023**, 48, 78-87	0
64	Genome-Wide Identification of Variants Associated with Antifungal Drug Resistance. **2023**, 81-103	0
63	Multiomics of human aortic endothelial cells reveals cell subtypes with heterogeneous responses to canonical endothelial-to-mesenchymal perturbations.	0
62	Echoes from the last Green Sahara: whole genome analysis of Fulani, a key population to unveil the genetic evolutionary history of Africa.	0
61	Population structure and genome-wide evolutionary signatures reveal putative climate-driven habitat change and local adaptation in the large yellow croaker.	0
60	Geographically consistent hybridization dynamics between the Black-crested and Tufted Titmouse with evidence of hybrid zone expansion.	0
59	Fine-scale spatial genetic structure in a locally abundant native bunchgrass (Achnatherum thurberianum) including distinct lineages revealed within seed transfer zones.	0
58	Genetic Screening of Targeted Region on the Chromosome 22q11.2 in Patients with Microtia and Congenital Heart Defect. **2023**, 14, 879	0
57	Whole Genome Resequencing Reveals Genetic Diversity and Selection Signatures of Ethiopian Indigenous Cattle Adapted to Local Environments. **2023**, 15, 540	0
56	AmelHap: Leveraging drone whole-genome sequence data to create a honey bee HapMap. **2023**, 10,	0
55	Genomic surveillance uncovers a pandemic clonal lineage of the wheat blast fungus. **2023**, 21, e3002052	0
54	Genomic resources for population analyses of an invasive insect pest Oryctes rhinoceros. **2023**, 10,	0
53	Identification of breed-specific genomic variants in Colombian Creole pig breeds by whole-genome sequencing. **2023**, 55,	0
52	Genomic analysis of two phlebotomine sand fly vectors of leishmania from the new and old World. **2023**, 17, e0010862	0
51	Genome-wide association screening and MassARRAY for detection of high-temperature resistance-related SNPs and genes in a hybrid abalone (Haliotis discus hannai ?H. fulgens ?) based on super genotyping-by-sequencing. **2023**, 573, 739576	0
50	Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. **2023**, 14,	0
49	Haplotyping interspecific hybrids by dual alignment to both parental genomes.	0

48	An omics strategy increasingly improves the discovery of genetic loci and genes for seed-coat color formation in soybean.	o
47	GBC: a parallel toolkit based on highly addressable byte-encoding blocks for extremely large-scale genotypes of species. **2023**, 24,	o
46	Comparative population genomics provide new insight into the evolutionary history and adaptive potential of World Ocean krill.	o
45	Genetic Diversity and Population Structure of Coilia nasus Revealed by 2b-RAD Sequencing. **2023**, 12, 600	o
44	Uniparental Inheritance and Recombination as Strategies to Avoid Competition and Combat Muller’s Ratchet among Mitochondria in Natural Populations of the Fungus Amanita phalloides. **2023**, 9, 476	o
43	Y-linked copy number polymorphism of target of rapamycin (TOR) is associated with sexual size dimorphism in seed beetles.	o
42	Integration of non-additive genome-wide association study with a multi-tissue transcriptome analysis of growth and carcass traits in Duroc pigs. **2023**, 100817	o
41	White coat color of a Black Angus calf attributed to an occurrence of the delR217 variant of MITF.	o
40	Whole-genome selective scans detect genes associated with important phenotypic traits in goat (Capra hircus). 14,	o
39	Population genomics of fall armyworm by genotyping-by-sequencing: Implications for pest management. **2023**, 18, e0284587	o
38	Using landscape genomics to assess local adaptation and genomic vulnerability of a perennial herb Tetrastigma hemsleyanum (Vitaceae) in subtropical China. 14,	o
37	A multi-dimensional selective landscape drives adaptive divergence between and within closely relatedPhloxspecies.	o
36	mitoSplitter: A mitochondrial variants-based method for efficient demultiplexing of pooled single-cell RNA-seq.	o
35	Genetic consequence of widespread plantations of Cryptomeria japonica var. sinensis in Southern China: implications for afforestation strategies under climate change. **2023**, 19,	o
34	Presence of known feline ALMS1 and MYBPC3 variants in a diverse cohort of cats with hypertrophic cardiomyopathy in Japan. **2023**, 18, e0283433	o
33	Identification and characterisation of de novo germline structural variants in two commercial pig lines using trio-based whole genome sequencing. **2023**, 24,	o
32	Identifying climatic drivers of hybridization with a new ancestral niche reconstruction method.	o
31	Population Genetic Analysis of Six Chinese Indigenous Pig Meta-Populations Based on Geographically Isolated Regions. **2023**, 13, 1396	o

30	Genetic analysis of global faba bean diversity, agronomic traits and selection signatures. **2023**, 136,	0
29	Novel QTL for Lateral Root Density and Length improve Phosphorus Uptake in Rice (Oryza sativa L.).	0
28	Mapping genomic regulation of kidney disease and traits through high-resolution and interpretable eQTLs. **2023**, 14,	0
27	Integrating Genomics into the Genetic Management of the Endangered Mountain Yellow-Legged Frog.	0
26	Mitochondrial Heteroplasmy and PCR Amplification Bias Lead to Wrong Species Delimitation with High Confidence in the South American and Antarctic Marine Bivalve Aequiyoldia eightsii Species Complex. **2023**, 14, 935	0
25	Highly accurate species identification of Eastern Pacific rockfishes (Sebastes spp.) with high-throughput DNA sequencing.	0
24	Diverse evolutionary rates and gene duplication patterns among families of functional olfactory receptor genes in humans. **2023**, 18, e0282575	0
23	Purifying Selection and Persistent Polymorphism among Nuclei in the Multinucleate Arbuscular Mycorrhizal (AM) Fungi.	0
22	Human immune and gut microbial parameters associated with inter-individual variations in COVID-19 mRNA vaccine-induced immunity. **2023**, 6,	0
21	Genome diversity of Leishmania aethiopica. 13,	0
20	DivBrowse□interactive visualization and exploratory data analysis of variant call matrices. **2022**, 12,	0
19	The Regulatory Mendelian Mutation score for GRCh38. **2022**, 12,	0
18	A novel SNP panel developed for targeted genotyping-by-sequencing (GBS) reveals genetic diversity and population structure of Musa spp. germplasm collection.	0
17	Genome-wide association study for biomass accumulation traits in soybean. **2023**, 43,	0
16	Patterns of repeatability and heritability in the songs of wild Alston’s singing mice, Scotinomys teguina. **2023**, 200, 91-103	0
15	Genome-wide data reveal cryptic diversity and hybridization in a group of tree ferns. **2023**, 107801	0
14	The evolutionary patterns, expression profiles, and genetic diversity of expanded genes in barley. 14,	0
13	Hybrid Genome Assemblies of 245 Avian and Broiler Barn Environment-Associated Escherichia coli Strains Isolated from Saskatchewan Broiler Farms. **2023**, 12,	0

12	Genetic structure of an endangered species Ormosia henryi in southern China, and implications for conservation. **2023**, 23,	0
11	Genome structure and population genomics of the canine heartwormDirofilaria immitis.	0
10	Construction of high coverage whole-genome sequencing libraries from single colon crypts without DNA extraction or whole-genome amplification. **2023**, 16,	0
9	A second unveiling: Haplotig masking of the eastern oyster genome improves population-level inference.	0
8	A Long-Standing Hybrid Population Between Pacific and Atlantic Herring in a Subarctic Fjord of Norway. **2023**, 15,	0
7	Integrated testis transcriptome and whole genome analysis of sexual maturity in Large White and Tongcheng pigs.	0
6	Genomic analyses provide insights into the polyploidization-driven herbicide adaptation in Leptochloa weeds.	0
5	Integrated microbiome-metabolome-genome axis data of Laiwu and Lulai pigs. **2023**, 10,	0
4	The role of oceanic currents in the dispersal and connectivity of the mangrove Rhizophora mangle on the Southwest Atlantic region.	0
3	A first annotated genome sequence for Haliotis midae with genomic insights into abalone evolution and traits of economic importance. **2023**, 70, 101044	0
2	Identification of Runs of Homozygosity Islands and Functional Variants in Wenchang Chicken. **2023**, 13, 1645	0
1	Comparative Genome Analysis of Old World and New World TYLCV Reveals a Biasness toward Highly Variable Amino Acids in Coat Protein. **2023**, 12, 1995	0