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BEDTools: a flexible suite of utilities for comparing genomic features

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838	Annotation of the goat genome using next generation sequencing of microRNA expressed by the lactating mammary gland: comparison of three approaches. <b>2015</b> , 16, 285	24

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836	Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds. <b>2015</b> , 176, 282-91	22
835	Myc and SAGA rewire an alternative splicing network during early somatic cell reprogramming. <b>2015</b> , 29, 803-16	55
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725	Genome-wide analysis of aberrant position and sequence of plasma DNA fragment ends in patients with cancer. <b>2023</b> , 15,	1
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704	New insights into genome annotation in Podospora anserina through re-exploiting multiple RNA-seq data. <b>2022</b> , 23,	O
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647	Rapid, nonparallel genomic evolution of Brassica rapa (field mustard) under experimental drought.	0
646	A macroevolutionary role for chromosomal fusion and fission inErebiabutterflies.	О
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633	Duck pan-genome reveals two transposon-derived structural variations caused bodyweight enlarging and white plumage phenotype formation during evolution.	0
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618	Origin, Genetic Variation and Molecular Epidemiology of SARS-CoV-2 Strains Circulating in Sardinia (Italy) during the First and Second COVID-19 Epidemic Waves. <b>2023</b> , 15, 277	o
617	Inversions maintain differences between migratory phenotypes of a songbird. 2023, 14,	0
616	Gene Regulatory Interactions at Lamina-Associated Domains. <b>2023</b> , 14, 334	O
615	In Vivo Dissection of Chamber-Selective Enhancers Reveals Estrogen-Related Receptor as a Regulator of Ventricular Cardiomyocyte Identity.	1
614	A Comprehensive Investigation of Genomic Variants in Prostate Cancer Reveals 30 Putative Regulatory Variants. <b>2023</b> , 24, 2472	O
613	Genomic Sequence of Canadian Chenopodium berlandieri: A North American Wild Relative of Quinoa. <b>2023</b> , 12, 467	О
612	Histone acetylation insulator SET orchestrates PP2A inhibition and super-enhancer activation.	O
611	scm6A-seq reveals single-cell landscapes of the dynamic m6A during oocyte maturation and early embryonic development. <b>2023</b> , 14,	0
610	Mis-spliced transcripts generatede novoproteins in TDP-43-related ALS/FTD.	O
609	T helper cells exhibit a dynamic and reversible 3DTR landscape.	0
608	Common genetic variants contribute to heritability of age at onset of schizophrenia.	O
607	Aqueous microRNA profiling in age-related macular degeneration and polypoidal choroidal vasculopathy by next-generation sequencing. <b>2023</b> , 13,	0
606	Comparative analyses of copy number variations between swamp buffaloes and river buffaloes.	O
605	PerturbSci-Kinetics: Dissecting key regulators of transcriptome kinetics through scalable single-cell RNA profiling of pooled CRISPR screens.	О
604	Promoter-pervasive transcription causes RNA polymerase II pausing to boost DOG1 expression in response to salt.	0

603	Super-enhancer driven expression of BAHCC1 promotes melanoma cell proliferation and genome stability.	0
602	Macrophages Promote Ovarian Cancer-Mesothelial Cell Adhesion by Upregulation of ITGA2 and VEGFC in Mesothelial Cells. <b>2023</b> , 12, 384	O
601	Expanded MutaT7 toolkit efficiently and simultaneously accesses all possible transition mutations in bacteria.	0
600	RNA mis-splicing drives viral mimicry response after DNMTi therapy in SETD2-mutant kidney cancer. <b>2023</b> , 42, 112016	0
599	Dynamic Evolution of NLR Genes in Dalbergioids. <b>2023</b> , 14, 377	1
598	Prevalent introgression underlies convergent evolution in the diversification of Pungitius sticklebacks.	0
597	GRHL2 and AP2a coordinate early surface ectoderm lineage commitment during development. <b>2023</b> , 106125	0
596	Alternative polyadenylation transcriptome-wide association study identifies APA-linked susceptibility genes in brain disorders. <b>2023</b> , 14,	Ο
595	Detection of DNA Modification Using Nanopore Sequencers. <b>2023</b> , 79-90	0
594	Benchmarking of Nanopore R10.4 and R9.4.1 flow cells in single-cell whole-genome amplification and whole-genome shotgun sequencing. <b>2023</b> , 21, 2352-2364	0
593	Global hypomethylation in childhood asthma identified by genome-wide DNA-methylation sequencing preferentially affects enhancer regions.	0
592	A dual-activity topoisomerase complex promotes both transcriptional activation and repression in response to starvation. <b>2023</b> , 51, 2415-2433	0
591	MeCP2 regulates Gdf11, a dosage-sensitive gene critical for neurological function. 12,	0
590	Characterization of De Novo Promoter Variants in Autism Spectrum Disorder with Massively Parallel Reporter Assays. <b>2023</b> , 24, 3509	O
589	Transposon-encoded nucleases use guide RNAs to selfishly bias their inheritance.	0
588	Effect of tissue-grouped regulatory variants associated to type 2 diabetes in related secondary outcomes. <b>2023</b> , 13,	Ο
587	TFIIIC as a Potential Epigenetic Modulator of Histone Acetylation in Human Stem Cells. 2023, 24, 3624	0
586	Retro-miRs: Novel and functional miRNAs originated from mRNA retrotransposition.	Ο

585	An ASO therapy for Angelman syndrome that targets an evolutionarily conserved region at the start of the UBE3A-AS transcript. <b>2023</b> , 15,	O
584	Extensive de novo activity stabilizes epigenetic inheritance of CG methylation in Arabidopsis transposons. <b>2023</b> , 42, 112132	O
583	A sheep pangenome reveals the spectrum of structural variations and their effects on tail phenotypes. <b>2023</b> , 33, 463-477	О
582	A posttranscriptional pathway regulates cell wall mRNA expression in budding yeast. <b>2023</b> , 42, 112184	О
581	Widespread allele-specific topological domains in the human genome are not confined to imprinted gene clusters. <b>2023</b> , 24,	0
580	High-quality genome assembly and genetic mapping reveal a gene regulating flesh color in watermelon (Citrullus lanatus). 14,	О
579	An Integrated Pipeline for Trio-Rapid Genome Sequencing in Critically Ill Infants. 2023, 3,	О
578	Recent reactivation of a pathogenicity-associated transposable element triggers major chromosomal rearrangements in a fungal wheat pathogen.	O
577	Improving CRISPR-Cas9 mediated genome integration in interspecific hybrid yeasts. 2023,	О
576	Precise excision of HTLV-1 provirus with a designer-recombinase. 2023,	О
575	Whole genome sequencing of simmental cattle for SNP and CNV discovery. 2023, 24,	0
574	Selection and adaptive introgression guided the complex evolutionary history of the European common bean. <b>2023</b> , 14,	O
573	No Transcriptional Compensation for Extreme Gene Dosage Imbalance in Fragmented Bacterial Endosymbionts of Cicadas.	О
572	Mapping structural variations in Haemaphysalis longicornis and Rhipicephalus microplus reveals vector-pathogen adaptation. <b>2023</b> , 26, 106398	O
571	Premature termination of transcription is shaped by Rho and translated uORFS in Mycobacterium tuberculosis. <b>2023</b> , 26, 106465	О
570	An efficient CRISPR©as12a promoter editing system for crop improvement.	O
569	EccBase: a high-quality database for exploration and characterization of extrachromosomal circular DNAs in cancer. <b>2023</b> ,	О
568	CRISPR-Cas9-mediated genome engineering exaggerates genomic deletion at 10q23.31 including thePTENgene locus mimicking cancer profiles.	O

567	Rewiring of the 3D genome during acquisition of carboplatin resistance in a triple-negative breast cancer patient-derived xenograft. <b>2023</b> , 13,	0
566	Effects of heat and hyposalinity on the gene expression in Acropora pruinosa larvae. 10,	О
565	An allele-specific PCR assay for detection of mutations that confer benzimidazole resistance and zoxamide sensitivity in Phyllosticta citricarpa. 1-8	O
564	Genomes of the human filarial parasites Mansonella perstans and Mansonella ozzardi. 4,	o
563	FIPRESCI: droplet microfluidics based combinatorial indexing for massive-scale 5?-end single-cell RNA sequencing. <b>2023</b> , 24,	0
562	Comparative single cell epigenomic analysis of gene regulatory programs in the rodent and primate neocortex.	0
561	OBERON3 and SUPPRESSOR OF MAX2 1-LIKE proteins form a regulatory module driving phloem development. <b>2023</b> , 14,	О
560	Legume-wide comparative analysis of pod shatter locus PDH1 reveals phaseoloid specificity, high cowpea expression, and stress responsive genomic context.	О
559	Hunter-gatherer admixture facilitated natural selection in Neolithic European farmers. <b>2023</b> , 33, 1365-13	71.e3 <sub>0</sub>
558	3D genome organization drives gene expression in trypanosomes.	О
557	Comparative genomics analyses reveal sequence determinants underlying interspecies variations in	
	injury-responsive enhancers. <b>2023</b> , 24,	О
556	injury-responsive enhancers. <b>2023</b> , 24,  Strong purifying selection in haploid tissue-specific genes of Scots pine supports the masking theory.	0
556 555	Strong purifying selection in haploid tissue-specific genes of Scots pine supports the masking	
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555	Strong purifying selection in haploid tissue-specific genes of Scots pine supports the masking theory.  Dynamic antagonism between key repressive pathways maintains the placental epigenome. 2023, 25, 579-591	0
555 554	Strong purifying selection in haploid tissue-specific genes of Scots pine supports the masking theory.  Dynamic antagonism between key repressive pathways maintains the placental epigenome. 2023, 25, 579-591  Characterization of genome-wide STR variation in 6487 human genomes. 2023, 14,	0 0
555 554 553	Strong purifying selection in haploid tissue-specific genes of Scots pine supports the masking theory.  Dynamic antagonism between key repressive pathways maintains the placental epigenome. 2023, 25, 579-591  Characterization of genome-wide STR variation in 6487 human genomes. 2023, 14,  The little skate genome and the evolutionary emergence of wing-like fins.  SATB1 regulates 3D genome architecture in Titells by constraining chromatin interactions	o o o

549	Phenotypic characterization of the wheat temperature-sensitive leaf color mutant and physical mapping of mutant gene by reduced-representation sequencing. <b>2023</b> , 330, 111657	О
548	Host-pathogen interaction involving cytoskeleton changes as well as non-coding regulation as primary mechanisms for SRS resistance in Atlantic salmon. <b>2023</b> , 136, 108711	O
547	A plastome phylogeny of Rumex (Polygonaceae) illuminates the divergent evolutionary histories of docks and sorrels. <b>2023</b> , 182, 107755	О
546	Improved protein production in yeast using cell engineering with genes related to a key factor in the unfolded protein response. <b>2023</b> , 77, 152-161	О
545	Identification of circular RNAs in tea plant during Helopeltis theivora infestation. 2023, 8, 100150	0
544	Prolonged activity of the transposase helper may raise safety concerns during DNA transposon-based gene therapy. <b>2023</b> , 29, 145-159	O
543	Molecular and phenotypic effects of early exposure to an environmentally relevant pesticide mixture in the Pacific oyster, Crassostrea gigas <b>2023</b> , 326, 121472	О
542	Phylogenomics and taxon-rich phylogenies of new and historical specimens shed light on the systematics of Hypnea (Cystocloniaceae, Rhodophyta). <b>2023</b> , 183, 107752	O
541	Generating minimum set of gRNA to cover multiple targets in multiple genomes with MINORg.	О
540	Comprehensive characterization of the embryonic factor LEUTX. 2023, 26, 106172	O
539	Hot spring distribution and survival mechanisms of thermophilic comammox Nitrospira.	О
538	Masculinizer is not post-transcriptionally regulated by female-specific piRNAs during sex determination in the Asian corn borer, Ostrinia furnacalis. <b>2023</b> , 103946	O
537	A multi-omics integrative analysis based on CRISPR screens re-defines the pluripotency regulatory network in ESCs. <b>2023</b> , 6,	О
536	Lepidoptera genomics based on 88 chromosomal reference sequences informs population genetic parameters for conservation.	O
535	Potential reservoirs of antimicrobial resistance in livestock waste and treated wastewater that can be disseminated to agricultural land. <b>2023</b> , 872, 162194	0
534	Chromosome-level genome assembly and population genomic resource to accelerate orphan crop lablab breeding. <b>2023</b> , 14,	O
533	Improved interpretability of bacterial genome-wide associations using gene cluster centric k-mers.	О
532	Protocol for Bulk-ATAC sequencing in head and neck squamous cell carcinoma. <b>2023</b> , 4, 102233	O

531	DNA methylation is associated with codon degeneracy in a species of bumblebee. 2023, 130, 188-195	О
530	Computational approach to evaluate scRNA-seq data quality and gene body coverage with SkewC. <b>2023</b> , 4, 102038	O
529	Ataxin-1 controls the expression of specific noncoding RNAs in B cells upon autoimmune demyelination. <b>2023</b> , 101, 358-367	0
528	A reference genome for Bluegill (Centrarchidae:Lepomis macrochirus). <b>2023</b> , 13,	O
527	Cdc73 protects Notch-induced T-cell leukemia cells from DNA damage and mitochondrial stress.	1
526	Enhanced recombination among Omicron subvariants of SARS-CoV-2 contributes to viral immune escape. <b>2023</b> , 95,	O
525	Natural methylation epialleles correlate with gene expression in maize.	0
524	Annelid functional genomics reveal the origins of bilaterian life cycles. 2023, 615, 105-110	1
523	Massively parallel knock-in engineering of human T cells.	1
522	Genomic health is dependent on long-term population demographic history. <b>2023</b> , 32, 1943-1954	O
521	Chromosomal-level genome assembly of Melastoma candidum provides insights into trichome evolution. 14,	0
520	EGRE: Calculating Enrichment Between Genomic Regions. <b>2022</b> , 67-79	O
519	RNA exosome ribonuclease DIS3 degrades Pou6f1 to promote mouse pre-implantation cell differentiation. <b>2023</b> , 42, 112047	0
518	A comparison of algorithms for identifying copy number variants in family-based whole-exome sequencing data and its implications in inheritance pattern analysis. <b>2023</b> , 861, 147237	O
517	An atrial fibrillation-associated regulatory region modulates cardiac Tbx5 levels and arrhythmia susceptibility. 12,	O
516	PorinPredict: In Silico Identification of OprD Loss from WGS Data for Improved Genotype-Phenotype Predictions of P. aeruginosa Carbapenem Resistance. <b>2023</b> , 11,	O
515	TXNIP in liver sinusoidal endothelial cells ameliorates alcohol-associated liver disease.	0
514	mRNA ageing shapes the Cap2 methylome in mammalian mRNA. <b>2023</b> , 614, 358-366	O

513	A Systematic Comparison of Human Mitochondrial Genome Assembly Tools.	0
512	Tracking the Emergence and Dissemination of a bla NDM-23 Gene in a Multidrug Resistance Plasmid of Klebsiella pneumoniae. <b>2023</b> , 11,	O
511	Identification of two □cell subtypes by 7 independent criteria.	0
510	Skeletal Muscles of Sedentary and Physically Active Aged People Have Distinctive Genic Extrachromosomal Circular DNA Profiles. <b>2023</b> , 24, 2736	1
509	Glucose deprivation promotes pseudo-hypoxia and de-differentiation in lung adenocarcinoma.	0
508	The Legacy of Infectious Disease Exposure on the Genomic Diversity of Indigenous Southern Mexicans. <b>2023</b> , 15,	O
507	NuRD-independent Mi-2 activity represses ectopic gene expression during neuronal maturation. <b>2023</b> , 24,	0
506	Integrase-associated niche differentiation of endogenous large DNA viruses in crustaceans.	O
505	EstroGene database reveals diverse temporal, context-dependent and directional estrogen receptor regulomes in breast cancer.	0
504	METTL3 regulates breast cancer-associated alternative splicing switches. <b>2023</b> , 42, 911-925	1
503	Low-affinity CTCF binding drives transcriptional regulation whereas high-affinity binding encompasses architectural functions. <b>2023</b> , 26, 106106	0
502	Epigenetic signals that direct cell typeEpecific interferon beta response in mouse cells. <b>2023</b> , 6, e202201823	O
501	Pangenome obtained by long-read sequencing of 11 genomes reveal hidden functional structural variants in pigs. <b>2023</b> , 26, 106119	О
500	Analysis of nucleotide variations in human g-quadruplex forming regions associated with disease states.	O
499	Whole-genome sequence of synthetically derived Brassica napus inbred cultivar Da-Ae. 2023, 13,	0
498	Unsupervised construction of gene regulatory network based on single-cell multi-omics data of colorectal cancer. <b>2023</b> , 24,	O
497	The F-box protein UFO controls flower development by redirecting the master transcription factor LEAFY to new cis-elements. <b>2023</b> , 9, 315-329	0
496	Genome-wide exploration reveals distinctive northern and southern variants of Clonorchis sinensis in the Far East. <b>2023</b> , 23, 833-843	Ο

495	Topological screen identifies hundreds of Cp190- and CTCF-dependent Drosophila chromatin insulator elements. <b>2023</b> , 9,	0
494	Centromere repositioning and shifts in wheat evolution. <b>2023</b> , 100556	1
493	Genomic and transcriptomic analyses enable the identification of important genes associated with subcutaneous fat deposition in Holstein cows. <b>2023</b> ,	0
492	Antigenic diversity in malaria parasites is maintained on extrachromosomal DNA.	Ο
491	RTCpredictor: Identification of Read-Through Chimeric RNAs from RNA Sequencing Data.	0
490	Self-supervised learning on millions of pre-mRNA sequences improves sequence-based RNA splicing prediction.	O
489	Host-specific subtelomere: structural variation and horizontal transfer in asexual filamentous fungal pathogens.	0
488	Missense mutations in CRX homeodomain cause dominant retinopathies through two distinct mechanisms.	Ο
487	A statistical approach to identify regulatory DNA variations.	Ο
486	FUS Alters circRNA Metabolism in Human Motor Neurons Carrying the ALS-Linked P525L Mutation. <b>2023</b> , 24, 3181	1
485	Assessment of copy number variants in three Brazilian locally adapted cattle breeds using whole-genome re-sequencing data.	O
484	Range-wide whole-genome resequencing of the brown bear reveals drivers of intraspecies divergence. <b>2023</b> , 6,	Ο
483	G4Beacon: An In Vivo G4 Prediction Method Using Chromatin and Sequence Information. 2023, 13, 292	Ο
482	Regulation of immunological tolerance by the p53-inhibitor iASPP. <b>2023</b> , 14,	Ο
481	Widespread contribution of transposable elements to the rewiring of mammalian 3D genomes. <b>2023</b> , 14,	0
480	Tracking population structure and phenology through time using ancient genomes from waterlogged white oak wood.	O
479	Cell-specific and shared enhancers control a high-density multi-gene locus active in mammary and salivary glands.	0
478	A Rapid, Shallow Whole Genome Sequencing Workflow Applicable to Limiting Amounts of Cell-Free DNA.	O

477	Signal-induced enhancer activation requires Ku70 to read topoisomerase1 <b>D</b> NA covalent complexes. <b>2023</b> , 30, 148-158	О
476	Design and off-target prediction for antisense oligomers targeting bacterial mRNAs with the MASON web server. <b>2023</b> , 29, 570-583	Ο
475	Cell-specific and shared enhancers control a high-density multi-gene locus active in mammary and salivary glands.	0
474	The SET domain protein PsKMT3 regulates histone H3K36 trimethylation and modulates effector gene expression in the soybean pathogen Phytophthora sojae. <b>2023</b> , 24, 346-358	Ο
473	A high-quality reference genome for the fission yeast Schizosaccharomyces osmophilus. <b>2023</b> , 13,	Ο
472	CriSNPr, a single interface for the curated and de novo design of gRNAs for CRISPR diagnostics using diverse Cas systems. 12,	Ο
47 <sup>1</sup>	An assessment of bioinformatics tools for the detection of human endogenous retroviral insertions in short-read genome sequencing data. 2,	0
470	Aberrant phase separation and nucleolar dysfunction in rare genetic diseases.	Ο
469	RL-MD: A Novel Reinforcement Learning Approach for DNA Motif Discovery. 2022,	Ο
468	Loss of Heterozygosity and Its Importance in Evolution.	Ο
467	Temporal-iCLIP captures co-transcriptional RNA-protein interactions. <b>2023</b> , 14,	
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466	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. <b>2023</b> , 14,	0
466 465	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. <b>2023</b> ,	
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465	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. 2023, 14,  The human inactive X chromosome modulates expression of the active X chromosome. 2023, 3, 100259  Targeted pseudouridylation: An approach for suppressing nonsense mutations in disease genes.	0
465 464	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. 2023, 14,  The human inactive X chromosome modulates expression of the active X chromosome. 2023, 3, 100259  Targeted pseudouridylation: An approach for suppressing nonsense mutations in disease genes. 2023, 83, 637-651.e9  Using Multiplex Amplicon PCR Technology to Efficiently and Timely Generate Rift Valley Fever	0 0
465 464 463	Macroevolutionary diversity of traits and genomes in the model yeast genus Saccharomyces. 2023, 14,  The human inactive X chromosome modulates expression of the active X chromosome. 2023, 3, 100259  Targeted pseudouridylation: An approach for suppressing nonsense mutations in disease genes. 2023, 83, 637-651.e9  Using Multiplex Amplicon PCR Technology to Efficiently and Timely Generate Rift Valley Fever Virus Sequence Data for Genomic Surveillance. 2023, 15, 477  Genome-wide identification of lncRNAs associated with viral infection in Spodoptera frugiperda.	o o o

459	Transcription factor SOX15 regulates stem cell pluripotency and promotes neural fate during differentiation by activating the neurogenic gene Hes5. <b>2023</b> , 299, 102996	0
458	Deep learning for detecting and elucidating human T-cell leukemia virus type 1 integration in the human genome. <b>2023</b> , 4, 100674	O
457	Mousepost 2.0, a major expansion of the resource. <b>2023</b> , 51, 1652-1661	О
456	Stepwise recombination suppression around the mating-type locus in an ascomycete fungus with self-fertile spores. <b>2023</b> , 19, e1010347	O
455	Captive rearing effects on the methylome of Atlantic salmon after oceanic migration: Sex-specificity and intergenerational stability.	O
454	ZBTB12 is a molecular barrier to dedifferentiation in human pluripotent stem cells. <b>2023</b> , 14,	O
453	Epigenomic variability is associated with age-specific na $\mathbb{I}$ e CD4 T cell response to activation in infants and adolescents.	0
452	Spatial genomic diversity associated with APOBEC mutagenesis in squamous cell carcinoma arising from ovarian teratoma.	O
451	Pan-cancer pseudogene RNA analysis reveals a regulatory network promoting cancer cell proliferation. <b>2023</b> , 4, 85-97	0
450	Identification of androgen response-related lncRNAs in prostate cancer. <b>2023</b> , 83, 590-601	O
449	Structural and functional classification of G-quadruplex families within the human genome.	O
448	Functional control and metabolic integration of stolen organelles in a photosynthetic ciliate. <b>2023</b> , 33, 973-980.e5	O
447	The Dynamic Linkage between Provirus Integration Sites and the Host Functional Genome Property Alongside HIV-1 Infections Associated with Antiretroviral Therapy. <b>2023</b> , 11, 402	0
446	The yeast RNA methylation complex consists of conserved yet reconfigured components with m6A-dependent and independent roles.	o
445	Co-inhibition of topoisomerase 1 and BRD4-mediated pause release selectively kills pancreatic cancerviareadthrough transcription.	O
444	H3.3 contributes to chromatin accessibility and transcription factor binding at promoter-proximal regulatory elements in embryonic stem cells. <b>2023</b> , 24,	O
443	Selection on many loci drove the origin and spread of a key innovation.	0
442	Histone remodeling reflects conserved mechanisms of bovine and human preimplantation development. <b>2023</b> , 24,	o

441	Computational Protocol for DNA Methylation Profiling in Plants Using Restriction Enzyme-Based Genome Reduction. <b>2023</b> , 23-36	О
440	Amniotes co-opt intrinsic genetic instability to protect germ-line genome integrity. <b>2023</b> , 14,	О
439	The Hypersaline Archaeal Histones HpyA and HstA Are DNA Binding Proteins That Defy Categorization According to Commonly Used Functional Criteria.	0
438	Toxoplasma gondii AP2XII-2 Contributes to Transcriptional Repression for Sexual Commitment. <b>2023</b> , 8,	o
437	Completede novoassembly of Tricholoma bakamat sutake chromosomes revealed the structural divergence and differentiation of Tricholomage nomes.	О
436	RNA Methylome Reveals the m6A-mediated Regulation of Flavor Metabolites in Tea Leaves under Solar-withering. <b>2023</b> ,	O
435	Cis-regulatory landscapes of the fat-tailed dunnart and mouse provide insights into the drivers of craniofacial heterochrony.	0
434	PipeIT2: A tumor-only somatic variant calling workflow for molecular diagnostic Ion Torrent sequencing data. <b>2023</b> , 115, 110587	О
433	High turnover ofde novotranscripts inDrosophila melanogaster.	0
432	Integrative multi-ancestry genetic analysis of gene regulation in coronary arteries prioritizes disease risk loci.	o
431	A chromosome-level genome assembly of Ostrea denselamellosa provides initial insights into its evolution. <b>2023</b> , 115, 110582	0
430	Brown Seaweed Extract (BSE) Application Influences Auxin- and ABA-Related Gene Expression, Root Development, and Sugar Yield in Beta vulgaris L <b>2023</b> , 12, 843	o
429	Reproducible evaluation of transposable element detectors with McClintock 2 guides accurate inference of Ty insertion patterns in yeast.	O
428	Recent transposable element bursts are associated with the proximity to genes in a fungal plant pathogen. <b>2023</b> , 19, e1011130	o
427	Mitochondrial single-cell ATAC-seq for high-throughput multi-omic detection of mitochondrial genotypes and chromatin accessibility.	O
426	Viral proteogenomic and expression profiling during fully productive replication of a skin-tropic herpesvirus in the natural host.	o
425	Genomic profiling of HIV-1 integration in microglia cells links viral integration to the topologically associated domains. <b>2023</b> , 42, 112110	0
424	The composition of piRNA clusters inDrosophila melanogasterdeviates from expectations under the trap model.	O

423	Blood transcriptome responses to PFOA and GenX treatment in the marsupial biomedical model Monodelphis domestica. 14,	0
422	AMLs harboring DNMT3A-destabilizing variants show increased intratumor DNA methylation heterogeneity at bivalent chromatin domains.	O
421	Optimization of Molecular Methods for Detecting Duckweed-Associated Bacteria. <b>2023</b> , 12, 872	Ο
420	Human gene regulatory evolution is driven by the divergence of regulatory element function in bothcisandtrans.	O
419	Aging and obesity prime the methylome and transcriptome of adipose stem cells for disease and dysfunction. <b>2023</b> , 37,	Ο
418	Taxonomically Restricted Genes inBacillusmay Form Clusters of Homologs and Can be Traced to a Large Reservoir of Noncoding Sequences. <b>2023</b> , 15,	O
417	Telomere-to-telomere assembly of diploid chromosomes with Verkko.	0
416	Massively parallel characterization of psychiatric disorder-associated and cell-type-specific regulatory elements in the developing human cortex.	O
415	Characterization of Histone Modifications in Late-Stage Rotator Cuff Tendinopathy. 2023, 14, 496	0
414	S-Locus Genotyping in Japanese Plum by High Throughput Sequencing Using a Synthetic S-Loci Reference Sequence. <b>2023</b> , 24, 3932	Ο
413	Dual specificity and target gene selection by the MADS-domain protein FRUITFULL. 2023, 9, 473-485	0
412	Gene expression differences consistent with water loss reduction underlie desiccation tolerance of natural Drosophila populations. <b>2023</b> , 21,	O
411	Comprehensive single-cell genome analysis at nucleotide resolution using the PTA Analysis Toolbox.	0
410	Evaluating the mouse neural precursor line, SN4741, as a suitable proxy for midbrain dopaminergic neurons.	O
409	Nsun2 coupling with RoREshapes the fate of Th17 cells and promotes colitis. 2023, 14,	Ο
408	Semi-conservative transmission of DNA N6-adenine methylation in a unicellular eukaryote.	Ο
407	The super-enhancer repertoire in porcine liver. <b>2023</b> , 101,	0
406	Widespread perturbation of ETS factor binding sites in cancer. <b>2023</b> , 14,	O

405	Tracking the evolution of esophageal squamous cell carcinoma under dynamic immune selection by multi-omics sequencing. <b>2023</b> , 14,	0
404	Regulation of endogenous retrovirus derived regulatory elements by GATA2/3 and MSX2 in human trophoblast stem cells. <b>2023</b> , 33, 197-207	Ο
403	Copy number variation-associated lncRNAs may contribute to the etiologies of congenital heart disease. <b>2023</b> , 6,	Ο
402	NSD1 deposits histone H3 lysine 36 dimethylation to pattern non-CG DNA methylation in neurons.	Ο
401	Distinct genomic contexts predict gene presence-absence variation in different pathotypes of a fungal plant pathogen.	0
400	Pangolin genomes offer key insights and resources for the world most trafficked wild mammals.	Ο
399	CRISPR/Cas9-mediated A4GALT suppression rescues Fabry disease phenotypes in a kidney organoid model. <b>2023</b> ,	O
398	Chromatin accessibility associated with aquaculture relevant traits in tilapia.	Ο
397	Assessment of attenuation of varicella-zoster virus vaccines based on genomic comparison. <b>2023</b> , 95,	0
396	Population genomics-guided engineering of phenazine biosynthesis inPseudomonas chlororaphis.	Ο
395	Sweepstakes reproductive success via pervasive and recurrent selective sweeps. 12,	Ο
394	Genome Size Changes by Duplication, Divergence, and Insertion inCaenorhabditisWorms. <b>2023</b> , 40,	O
393	A shared Nulnerability codelunderpins varying sources of DNA damage throughout paternal germline transmission in mouse. <b>2023</b> , 51, 2319-2332	Ο
392	Deciphering transcription factors and their corresponding regulatory elements during inhibitory interneuron differentiation using deep neural networks. 11,	Ο
391	Detailed molecular and epigenetic characterization of the pig IPEC-J2 and chicken SL-29 cell lines. <b>2023</b> , 26, 106252	0
390	Chromosome-level genome assembly of tree sparrow reveals a burst of new genes driven by segmental duplications.	O
389	Off-target piRNA gene silencing in Drosophila melanogaster rescued by a transposable element insertion. <b>2023</b> , 19, e1010598	0
388	Kinetic networks identify TWIST2 as a key regulatory node in adipogenesis. <b>2023</b> , 33, 314-331	O

387	A molecular atlas reveals the tri-sectional spinning mechanism of spider dragline silk. 2023, 14,	O
386	Genome assembly ofMusa beccariishows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. <b>2022</b> , 12,	O
385	Evaluation of five commercial DNA extraction kits using Salmonella as a model for implementation of rapid Nanopore sequencing in routine diagnostic laboratories. <b>2023</b> , 5,	О
384	A methyl-seq tool to capture genomic imprinted loci.	Ο
383	Structure of the human DICERBre-miRNA complex in a dicing state. <b>2023</b> , 615, 331-338	0
382	Draft Genome Sequences of Spacecraft-Associated Microbes Isolated from Six NASA Missions. <b>2023</b> , 12,	Ο
381	TET1 Catalytic Activity is Required for Reprogramming of Imprinting Control Regions and Patterning of Sperm-Specific Hypomethylated Regions.	0
380	Patterns of transposable element accumulation at resistance loci: a comparative genomic analysis in aphids.	Ο
379	Epigenetic association study uncovered H3K27 acetylation enhancers and dysregulated genes in high-fat-diet-induced nonalcoholic fatty liver disease in rats. <b>2022</b> , 14, 1523-1540	0
378	Global Molecular Response of Paracoccidioides brasiliensis to Zinc Deprivation: Analyses at Transcript, Protein and MicroRNA Levels. <b>2023</b> , 9, 281	Ο
377	Rapid introgression of non-native alleles following hybridization between a native Anolis lizard species and altryptic invader across an urban landscape.	0
376	Fragmented habitat compensates for the adverse effects of genetic bottleneck. <b>2023</b> , 33, 1009-1018.e7	Ο
375	Concerning the eXclusion in human genomics: The choice of sex chromosome representation in the human genome drastically affects number of identified variants.	0
374	Sequence determinant of small RNA production by DICER. 2023, 615, 323-330	Ο
373	Predicting Response to Radical Chemoradiotherapy with Circulating HPV DNA (cHPV-DNA) in Locally Advanced Uterine Cervix Cancer. <b>2023</b> , 15, 1387	0
372	MacroH2A histone variants modulate enhancer activity to repress oncogenic programs and cellular reprogramming. <b>2023</b> , 6,	0
371	Spatial transcriptomics reveals niche-specific enrichment and vulnerabilities of radial glial stem-like cells in malignant gliomas. <b>2023</b> , 14,	О
370	TEFM variants impair mitochondrial transcription causing childhood-onset neurological disease. <b>2023</b> , 14,	O

369	Contrasting Patterns of Single Nucleotide Polymorphisms and Structural Variation Across Multiple Invasions. <b>2023</b> , 40,	O
368	Seasonal activities of the phyllosphere microbiome of perennial crops. 2023, 14,	О
367	Retrospective analysis of enhancer activity and transcriptome history.	О
366	Complete chloroplast genomes of six Neotropical palm tree species: genome structure comparison, identification of repeats sequences and evolutionary dynamic patterns.	O
365	METTL16 promotes translation and lung tumorigenesis by sequestering cytoplasmic eIF4E2. <b>2023</b> , 42, 112150	О
364	Vitamin B6, B12 and folate modulate deregulated pathways and protein aggregation in yeast model of Huntington disease. <b>2023</b> , 13,	О
363	Detection and characterization of constitutive replication origins defined by DNA polymerase epsilon. <b>2023</b> , 21,	0
362	scCircle-seq unveils the diversity and complexity of circular DNAs in single cells.	О
361	A thousand-genome panel retraces the global spread and adaptation of a major fungal crop pathogen. <b>2023</b> , 14,	О
<b>3</b> 60	Genomic differences and species delimitation: a case for two species in the zoonotic cestodeDipylidium caninum.	О
359	Identifying Eukaryotes and Factors Influencing Their Biogeography in Drinking Water Metagenomes. <b>2023</b> , 57, 3645-3660	О
358	Identification and characterization of extrachromosomal circular DNA in the silk gland of Bombyx mori.	О
357	Interpersonal variability of the human gut virome confounds disease signal detection in IBD. <b>2023</b> , 6,	0
356	Linker histone H1 modulates defense priming and immunity in plants.	О
355	Cooperativity between H3.3K27M and PDGFRA poses multiple therapeutic vulnerabilities in human iPSC-derived diffuse midline glioma avatars.	0
354	Spatial transcriptomic atlas of shoot organogenesis in tomato callus.	О
353	A Cre-LoxP-based approach for combinatorial chromosome rearrangements in human HAP1 cells. <b>2023</b> , 31,	0
352	Phylogenomic analysis of the Lake Kronotskoe species flock of Dolly Varden charr reveals genetic signatures of sympatric radiation.	О

351	Disruption of polyhomeotic polymerization decreases nucleosome occupancy and alters genome accessibility. <b>2023</b> , 6, e202201768	О
350	MeCP2 Represses the Activity of Topoisomerase II□in Long Neuronal Genes.	O
349	Translational landscape in human early neural fate determination. 2023, 150,	О
348	Whole-genome re-sequencing provides key genomic insights in farmed Arctic charr (Salvelinus alpinus) populations of anadromous and landlocked origin from Scandinavia.	O
347	Prediction of mammalian tissue-specific CLOCK-BMAL1 binding to E-box motifs.	O
346	Ribosomes in RNA Granules Are Stalled on mRNA Sequences That Are Consensus Sites for FMRP Association. <b>2023</b> , 43, 2440-2459	O
345	cfSNV: a software tool for the sensitive detection of somatic mutations from cell-free DNA.	О
344	The Effect of Human and Bovine Milk Osteopontin on Intestinal Caco-2 Cells: A Transcriptome Comparison. <b>2023</b> , 15, 1166	1
343	Transcription elongation defects link oncogenic splicing factor mutations to targetable alterations in chromatin landscape.	О
342	Heat stress response and transposon control in plant shoot stem cells.	Ο
341	Nanopore-Based Direct RNA Sequencing of the Trypanosoma brucei Transcriptome Identifies Novel lncRNAs. <b>2023</b> , 14, 610	0
340	Large haplotypes highlight a complex age structure within the maize pan-genome. 2023, 33, 359-370	O
339	ATAC-seq Data Processing. 2023, 305-323	О
338	Lower viral evolutionary pressure under stable versus fluctuating conditions in subzero Arctic brines.	O
337	Regulatory de novo mutations underlying intellectual disability. <b>2023</b> , 6, e202201843	О
336	Requirements for establishment and epigenetic stability of mammalian heterochromatin.	O
335	Comparative analysis of SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (SPL) gene family between bryophytes and seed plants.	О
334	SMCHD1 loss triggers DUX4 expression by disrupting splicing in FSHD2.	O

333	First in family Rhabdiasidae: the reference-guided genome assembly of an invasive parasite, the cane toad lungworm (Rhabdias pseudosphaerocephala).	Ο
332	Distinct roles for canonical and variant histone H3 lysine-36 in Polycomb silencing. <b>2023</b> , 9,	O
331	EBS-seq: enrichment-based method for accurate analysis of 5-hydroxymethylcytosine at single-base resolution. <b>2023</b> , 15,	0
330	Genome-wide identification of the auxin transporter gene families in sweet potato (Ipomoea batatas) and their expression during tuberization.	Ο
329	Distinct chromatin signatures in the Arabidopsis male gametophyte. <b>2023</b> , 55, 706-720	O
328	Analysis of structural variation among inbred mouse strains. <b>2023</b> , 24,	O
327	Gene silencing dynamics are modulated by transiently active regulatory elements. 2023, 83, 715-730.e6	О
326	Functional annotation of the animal genomes: An integrated annotation resource for the horse. <b>2023</b> , 19, e1010468	O
325	PGNneo: A Proteogenomics-Based Neoantigen Prediction Pipeline in Noncoding Regions. 2023, 12, 782	О
324	Transcription of MERVL retrotransposons is required for preimplantation embryo development. <b>2023</b> , 55, 484-495	O
323	Fluctuations in chromatin state at regulatory loci occur spontaneously under relaxed selection and are associated with epigenetically inherited variation in C. elegans gene expression. <b>2023</b> , 19, e1010647	O
322	A CUT&RUN protocol to determine patterns of epigenetic marks in imaginal discs of Drosophila. <b>2023</b> , 4, 101878	Ο
321	The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. <b>2023</b> , 186, 1279-1294.e19	0
320	Shotgun metagenomics reveals interkingdom association between intestinal bacteria and fungi involving competition for nutrients.	Ο
319	Linking chromatin acylation mark-defined proteome and genome in living cells. 2023, 186, 1066-1085.e36	2
318	ARF suppression by MYC but not MYCN confers increased malignancy of aggressive pediatric brain tumors. <b>2023</b> , 14,	Ο
317	Endogenous retrovirus-derived enhancers confer the transcriptional regulation of human trophoblast syncytialization.	0
316	Microhomology-Mediated Circular DNA Formation from Oligonucleosomal Fragments During Spermatogenesis.	Ο

315	Release of Histone H3K4-reading transcription factors from chromosomes in mitosis is independent of adjacent H3 phosphorylation.	О
314	A gene regulatory network for neural induction. 12,	Ο
313	DNA methylation landscape reveals LIN7A as a decitabine-responsive marker in patients with t(8;21) acute myeloid leukemia. <b>2023</b> , 15,	O
312	Processing genome-wide association studies within a repository of heterogeneous genomic datasets. <b>2023</b> , 24,	O
311	Tapping Culture Collections for Fungal Endophytes: First Genome Assemblies for Three Genera and Five Species in theAscomycota. <b>2023</b> , 15,	0
310	Systematic Identification of Post-Transcriptional Regulatory Modules.	O
309	Genome biology and evolution of mating type loci in four cereal rust fungi.	0
308	The landscape of human p53-regulated long non-coding RNAs reveals critical host gene co-regulation.	Ο
307	Structural and Functional Classification of G-Quadruplex Families within the Human Genome. <b>2023</b> , 14, 645	О
306	The long noncoding RNA Charme supervises cardiomyocyte maturation by controlling cell differentiation programs in the developing heart. 12,	O
305	Single-cell chromatin accessibility and transcriptome atlas of mouse embryos. <b>2023</b> , 42, 112210	0
304	The gut microbiome and resistome of conventionally- vs. pasture-raised pigs.	Ο
303	Genomes of two Extinct-in-the-Wild reptiles from Christmas Island reveal distinct evolutionary histories and conservation insights.	О
302	The Transcription Factor NRF2 Has Epigenetic Regulatory Functions Modulating HDACs, DNMTs, and miRNA Biogenesis. <b>2023</b> , 12, 641	O
301	Evolution of synchronous female bilateral breast cancers and response to treatment. <b>2023</b> , 29, 646-655	О
300	Combined analysis of transposable elements and structural variation in maize genomes reveals genome contraction outpaces expansion.	O
299	Release from sexual selection leads to rapid genome-wide evolution in Aedes aegypti. <b>2023</b> , 33, 1351-1357.6	25 o
298	Developing and reusing bioinformatics data analysis pipelines using scientific workflow systems. <b>2023</b> , 21, 2075-2085	0

297	Arabidopsis thalianaBBX14 is a target of GLK1 and involved in high-light acclimation, photomorphogenesis and GUN-type retrograde signaling.	0
296	Improved hepatitis delta virus genome characterization by single molecule full-length genome sequencing combined with VIRiONT pipeline. <b>2023</b> , 95,	O
295	Massive Somatic and Germline Chromosomal Integrations of Polydnaviruses in Lepidopterans. <b>2023</b> , 40,	0
294	Enhancing HIV-1 latency reversal through regulating the elongating RNA Pol II pause-release by a small-molecule disruptor of PAF1C. <b>2023</b> , 9,	O
293	Morphine Re-arranges Chromatin Spatial Architecture of Primate Cortical Neurons.	0
292	Tigerfish designs oligonucleotide-basedin situhybridization probes targeting intervals of highly repetitive DNA at the scale of genomes.	Ο
291	Discovery of long non-coding RNAs in the liver fluke,Fasciola hepatica.	O
290	ORC1 binds tocis-transcribed RNAs for efficient activation of replication origins.	O
289	The giant diploid faba genome unlocks variation in a global protein crop. 2023, 615, 652-659	O
288	Mapping the Complex Genetic Landscape of Human Neurons.	Ο
288	Mapping the Complex Genetic Landscape of Human Neurons.  Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. 2023, 15, 699	0
	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern	
287	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. <b>2023</b> , 15, 699  TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary	О
287 286	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. 2023, 15, 699  TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary properties and function.	0
287 286 285	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. 2023, 15, 699  TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary properties and function.  Core genome multilocus sequence typing scheme for Bacillus cereus group bacteria. 2023, 104050  Pioneer factor Foxa2 mediates chromatin conformation changes in ligand-dependent activation of	0 0
287 286 285	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. 2023, 15, 699  TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary properties and function.  Core genome multilocus sequence typing scheme for Bacillus cereus group bacteria. 2023, 104050  Pioneer factor Foxa2 mediates chromatin conformation changes in ligand-dependent activation of nuclear receptor FXR.  Campus Sewage Water Surveillance based dynamics and infection trends of SARS-CoV-2 variants	0 0
287 286 285 284	Discovery of Avian Paramyxoviruses APMV-1 and APMV-6 in Shorebirds and Waterfowl in Southern Ukraine. 2023, 15, 699  TAD Evolutionary and functional characterization reveals diversity in mammalian TAD boundary properties and function.  Core genome multilocus sequence typing scheme for Bacillus cereus group bacteria. 2023, 104050  Pioneer factor Foxa2 mediates chromatin conformation changes in ligand-dependent activation of nuclear receptor FXR.  Campus Sewage Water Surveillance based dynamics and infection trends of SARS-CoV-2 variants during third wave of COVID-19 in Pune, India.	0 0 0

279	Immunomodulatory Microparticles Epigenetically Modulate T Cells and Systemically Ameliorate Autoimmune Arthritis. <b>2023</b> , 10,	0
278	Coverage-preserving sparsification of overlap graphs for long-read assembly. <b>2023</b> , 39,	O
277	Adaptation to spindle assembly checkpoint inhibition through the selection of specific aneuploidies. <b>2023</b> , 37, 171-190	Ο
276	Pharmacological disruption of mSWI/SNF complex activity restricts SARS-CoV-2 infection. <b>2023</b> , 55, 471-483	O
275	Genus-Wide Genomic Characterization of Macrococcus: Insights into Evolution, Population Structure, and Functional Potential.	0
274	Target-enriched enzymatic methyl sequencing: Flexible, scalable and inexpensive hybridization capture for quantifying DNA methylation. <b>2023</b> , 18, e0282672	Ο
273	L1 retrotransposons drive human neuronal transcriptome complexity and functional diversification.	О
272	Seagrass genomes reveal a hexaploid ancestry facilitating adaptation to the marine environment.	Ο
271	Extensive sequence duplication in Arabidopsis revealed by pseudo-heterozygosity. 2023, 24,	0
270	Transcription Factor Dynamics in Cross-Regulation of Plant Hormone Signaling Pathways.	O
269	Global loss of cellular m6A RNA methylation following infection with different SARS-CoV-2 variants. <b>2023</b> , 33, 299-313	0
268	G4mismatch: Deep neural networks to predict G-quadruplex propensity based on G4-seq data. <b>2023</b> , 19, e1010948	O
267	An XBP1sBIM-2 positive feedback loop controls IL-15thediated survival of natural killer cells. <b>2023</b> , 8,	O
266	KRAB zinc finger proteins ZNF587/ZNF417 protect lymphoma cells from replicative stress-induced inflammation.	O
265	Metabolic and Transcriptomic Changes in the Mouse Brain in Response to Short-Term High-Fat Metabolic Stress. <b>2023</b> , 13, 407	0
264	Phenylalanine Ammonia-Lyase: A Key Gene for Color Discrimination of Edible Mushroom Flammulina velutipes. <b>2023</b> , 9, 339	O
263	Loss of MC1R signaling implicates TBX3 in pheomelanogenesis and melanoma predisposition.	0
262	VirRep: accurate identification of viral genomes from human gut metagenomic data via a hybrid language representation learning framework.	O

261	A multi-omics integrative analysis based on CRISPR screens re-defines the pluripotency regulatory network in ESCs.	0
260	Multiplex single-cell chemical genomics reveals the kinase dependence of the response to targeted therapy.	O
259	Leukemic stem cells hijack lineage inappropriate signalling pathways to promote their growth.	0
258	Heterochromatin rewiring and domain disruption-mediated chromatin compaction during erythropoiesis. <b>2023</b> , 30, 463-474	O
257	Fragment length profiles of cancer mutations enhance detection of circulating tumor DNA in patients with early-stage hepatocellular carcinoma. <b>2023</b> , 23,	0
256	Association between Variants in the OCA2-HERC2 Region and Blue Eye Colour in HERC2 rs12913832 AA and AG Individuals. <b>2023</b> , 14, 698	O
255	Cell-specific clock-controlled gene expression program regulates rhythmic fiber cell growth in cotton. <b>2023</b> , 24,	O
254	Site-specific analysis reveals candidate cross-kingdom small RNAs, tRNA and rRNA fragments, and signs of fungal RNA phasing in the barleypowdery mildew interaction.	O
253	Hybrid inferiority and genetic incompatibilities drive divergence of fungal pathogens infecting the same host.	0
252	Impaired ATF3 Signaling Involves SNAP25 in SOD1 Mutant ALS Patients.	O
251	Attenuation of IFN signaling due to m6A modification of the host epitranscriptome promotes EBV lytic reactivation. <b>2023</b> , 30,	0
250	Conservation and divergence of canonical and non-canonical imprinting in murids. 2023, 24,	O
249	Mycobacterial RNase E cleaves with a distinct sequence preference and controls the degradation rates of mostMycolicibacterium smegmatismRNAs.	0
248	Therapeutic immune cell engineering with an mRNA : AAV-Sleeping Beautycomposite system.	O
247	The plant response to high CO 2 levels is heritable and orchestrated by DNA methylation.	0
246	Whole exome sequencing study identifies candidate loss of function variants and locus heterogeneity in familial cholesteatoma. <b>2023</b> , 18, e0272174	O
245	Whole-genome doubling drives oncogenic loss of chromatin segregation. 2023, 615, 925-933	0
244	GenoPipe: identifying the genotype of origin within (epi)genomic datasets.	O

243	RNA Pol II preferentially regulates ribosomal protein expression by trapping disassociated subunits. <b>2023</b> , 83, 1280-1297.e11	О
242	Lineage-specific differences and regulatory networks governing human chondrocyte development. 12,	O
241	Synthetic maize centromeres transmit chromosomes across generations. <b>2023</b> , 9, 433-441	О
240	Exploration of genotype-by-environment interactions affecting gene expression responses in porcine immune cells. 14,	Ο
239	Motif elucidation in ChIP-seq datasets with a knockout control. <b>2023</b> , 3,	0
238	Chromatin profiling identifies transcriptional readthrough as a conserved mechanism for piRNA biogenesis in mosquitoes. <b>2023</b> , 42, 112257	O
237	A genetic linkage map and improved genome assembly of the termite symbiont Termitomyces cryptogamus. <b>2023</b> , 24,	0
236	A central chaperone-like role for 14-3-3 proteins in human cells. <b>2023</b> , 83, 974-993.e15	Ο
235	Hematopoietic/erythroid enhancers activate nearby target genes by extending histone H3K27ac and transcribing intergenic RNA. <b>2023</b> , 37,	О
234	Analysis of the external signals driving the transcriptional regulation of the main genes involved in denitrification in Haloferax mediterranei. 14,	O
233	A stimulus-contingent positive feedback loop enables IFN-\(\Pi\) dose-dependent activation of pro-inflammatory genes.	0
232	Transcriptomes reveal microRNAs and mRNAs in different photoperiods influencing cashmere growth in goat. <b>2023</b> , 18, e0282772	O
231	TXNIP loss expands Myc-dependent transcriptional programs by increasing Myc genomic binding. <b>2023</b> , 21, e3001778	0
230	Loss of Kmt2c in vivo leads to EMT, mitochondrial dysfunction and improved response to lapatinib in breast cancer. <b>2023</b> , 80,	O
229	Phylogenetic Analysis of Allotetraploid Species Using Polarized Genomic Sequences.	0
228	Targeted DNA integration in human cells without double-strand breaks using CRISPR RNA-guided transposases.	O
227	Cancer mutations rewire the RNA methylation specificity of METTL3-METTL14.	0
226	6mA-Sniper: Quantifying 6mA Sites in Eukaryotes at Single-Nucleotide Resolution.	O

225	Pioneer factor ASCL1 cooperates with the mSWI/SNF complex at distal regulatory elements to regulate human neural differentiation. <b>2023</b> , 37, 218-242	O
224	Reference mouse strain assemblies for BALB/c Nude and NOD/SCID mouse models.	O
223	Noradrenergic Tone is Not Required for Neuronal Activity-Induced Rebound Sleep in Zebrafish.	O
222	Comprehensive transcriptomic analysis to identify biological and clinical differences in cholangiocarcinoma.	O
221	Stepwise activities of mSWI/SNF family chromatin remodeling complexes direct T cell activation and exhaustion. <b>2023</b> , 83, 1216-1236.e12	O
220	Selective whole-genome amplification reveals population genetics of Leishmania braziliensis directly from patient skin biopsies. <b>2023</b> , 19, e1011230	O
219	Bamboozle: A bioinformatic tool for identification and quantification of intraspecific barcodes.	0
218	Lymphocyte mitochondrial genome integrity is not altered by cladribine.	O
217	Functional and Taxonomic Diversity of Anaerobes in Supraglacial Microbial Communities. 2023, 11,	O
216	Nanopore Cas9-targeted sequencing enables accurate and simultaneous identification of transgene integration sites, their structure and epigenetic status in recombinant Chinese hamster ovary cells.	O
215	Characterization of meiotic chromosome behavior in the autopolyploid Saccharum spontaneum reveals preferential chromosome pairing without distinct DNA sequence variation. <b>2023</b> ,	О
214	Genomic insights into greater yam tuber quality traits.	O
213	Metabolic and Transcriptomic Signatures of the Acute Psychological Stress Response in the Mouse Brain. <b>2023</b> , 13, 453	0
212	Analysis of Small Non-coding RNAs as Signaling Intermediates of Environmentally Integrated Responses to Abiotic Stress. <b>2023</b> , 403-427	O
211	Epigenetic dosage identifies two major and functionally distinct 🛭 cell subtypes. 2023,	О
210	Identification of antigenic epitopes recognized by tumor infiltrating lymphocytes in high grade serous ovarian cancer by multi-omics profiling of the auto-antigen repertoire.	O
209	Retro-miRs: Novel and functional miRNAs originating from mRNA retrotransposition.	О
208	Characteristics of the rumen virome in Japanese cattle.	O

207	A transcription factor of the NAC family regulates nitrate-induced legume nodule senescence.	O
206	Identification and characterization of extrachromosomal circular DNA in patients with high myopia and cataract. <b>2023</b> , 18,	O
205	Adaptive protein evolution through length variation of short tandem repeats in Arabidopsis. <b>2023</b> , 9,	0
204	Adaptation of the Porcine Pituitary Transcriptome, Spliceosome and Editome during Early Pregnancy. <b>2023</b> , 24, 5946	O
203	ZmHOX32 is related to photosynthesis and likely functions in plant architecture of maize. 14,	O
202	Phylogroup-specific variation shapes the clustering of antimicrobial resistance genes and defence systems across regions of genome plasticity in Pseudomonas aeruginosa. <b>2023</b> , 90, 104532	O
201	A view of the pan-genome of domesticated Cowpea (Vigna unguiculata [L.] Walp.).	0
200	Recovery of metagenomic data from the Aedes aegypti microbiome using a reproducible snakemake pipeline: MINUUR. 8, 131	Ο
199	Strain-Level Dynamics Reveal Regulatory Roles in Atopic Eczema by Gut Bacterial Phages. <b>2023</b> , 11,	0
198	Chromosome-level analysis of the Colletotrichum graminicola genome reveals the unique characteristics of core and minichromosomes. 14,	O
197	The evolution of white-tailed jackrabbit camouflage in response to past and future seasonal climates. <b>2023</b> , 379, 1238-1242	0
196	Nutrigenomic regulation of sensory plasticity. 12,	O
195	Impact of the Dimethyl Sulfoxide Reductase Superfamily on the Evolution of Biogeochemical Cycles. <b>2023</b> , 11,	O
194	Detection of Selection Signatures on the X Chromosome in Iranian Dromedary Camels using Whole Genome Sequencing Data. <b>2022</b> , 13, 155-161	O
193	Chiropterans are a hotspot for horizontal transfer of DNA transposons in Mammalia.	0
192	OverexpressedMalat1Drives Metastasis through Inflammatory Reprogramming of Lung Adenocarcinoma Microenvironment.	Ο
191	A comprehensive map of hotspots of de novo telomere addition inSaccharomyces cerevisiae.	0
190	The m6A reader PRRC2A is essential for meiosis I completion during spermatogenesis. <b>2023</b> , 14,	O

189	Proteomic Profiling of Colorectal Adenomas Identifies a Predictive Risk Signature for Development of Metachronous Advanced Colorectal Neoplasia. <b>2023</b> ,	O
188	U1 snRNP increases RNA Pol II elongation rate to enable synthesis of long genes. <b>2023</b> , 83, 1264-1279.e10	O
187	Integrating long-read RNA sequencing improves locus-specific quantification of transposable element expression.	O
186	A haplotype resolved chromosome-scale assembly of North American wild appleMalus fuscaand comparative genomics of the fire blightMfu10locus. Genome of the Pacific CrabappleMalus fusca.	O
185	Gene-metabolite annotation with shortest reactional distance enhances metabolite genome-wide association studies results.	О
184	An explainable deep learning classifier of bovine mastitis based on whole genome sequence data -circumventing the p>>n problem.	O
183	Global effects of identity and aging on the human sperm methylome.	О
182	Cbp1-Cren7 chromatinization of CRISPR arrays favours transcription from leader-over cryptic promoters.	O
181	Extensive search of genetic sex markers in Siberian (Acipenser baerii) and Atlantic (A. oxyrinchus) sturgeons. <b>2023</b> , 739517	O
180	An improved reference of the grapevine genome reasserts the origin of the PN40024 highly homozygous genotype.	O
179	CRELD1 variants are associated with bicuspid aortic valve in Turner syndrome. <b>2023</b> , 142, 523-530	0
178	Massive genome reduction occurred prior to the origin of coral algal symbionts.	O
177	Inbreeding depression explains killer whale population dynamics.	O
176	QTL mapping and transcriptome analysis identify novel QTLs and candidate genes in Brassica villosa for quantitative resistance against Sclerotinia sclerotiorum. <b>2023</b> , 136,	O
175	Dynamics of histone acetylation during human early embryogenesis. <b>2023</b> , 9,	0
174	Genome-wide identification of tandem repeats associated with splicing variation across 49 tissues in humans. <b>2023</b> , 33, 435-447	O
173	A small number of human lineage mutations regulated RNA-protein binding of conserved genes and promoted human evolution.	О
172	Pan-cancer analysis identifies tumor-specific antigens derived from transposable elements. <b>2023</b> , 55, 631-639	O

171	The characteristics of extrachromosomal circular DNA in patients with end-stage renal disease. <b>2023</b> , 28,	0
170	Benchmarking datasets for assembly-based variant calling using high-fidelity long reads. 2023, 24,	O
169	Histone deacetylase 1 maintains lineage integrity through histone acetylome refinement during early embryogenesis. 12,	О
168	Integrative epigenome profiling of 47XXY provides insights into whole genomic DNA hypermethylation and active chromatin accessibility. 10,	О
167	A self-propagating, barcoded transposon system for the dynamic rewiring of genomic networks.	0
166	Nascent evolution of recombination rate differences as a consequence of chromosomal rearrangements.	O
165	Sensing the rainbow: genetic and physiological responses to light quality in Ostreococcus, an ecologically important photosynthetic picoeukaryote.	0
164	Sterile faecal filtrate transplantation alters phage-microbe dynamics in individuals with metabolic syndrome: a double blind, randomised, placebo-controlled clinical trial assessing efficacy and safety.	O
163	Arabidopsis TRB proteins function in H3K4me3 demethylation by recruiting JMJ14. 2023, 14,	O
162	Differential bumble bee gene expression associated with pathogen infection and pollen diet. <b>2023</b> , 24,	O
161	Loss of Ezh2 function remodels the DNA replication initiation landscape. <b>2023</b> , 42, 112280	О
160	BIND&MODIFY: a long-range method for single-molecule mapping of chromatin modifications in eukaryotes. <b>2023</b> , 24,	O
159	A-MYB and BRDT-dependent RNA Polymerase II pause release orchestrates transcriptional regulation in mammalian meiosis. <b>2023</b> , 14,	О
158	Single-cell analysis of bidirectional reprogramming between early embryonic states reveals mechanisms of differential lineage plasticities.	О
157	Intraspecies genomic divergence of coral algal symbionts shaped by gene duplication.	О
156	BRWD3 promotes KDM5 degradation to maintain H3K4 methylation levels.	О
155	Ribonuclease E strongly impacts bacterial adaptation to different growth conditions. <b>2023</b> , 20, 120-135	O
154	Structural elements promote architectural stripe formation and facilitate ultra-long-range gene regulation at a human disease locus. <b>2023</b> ,	O

153	HERV-K (HML-2) insertion polymorphisms in the 8q24.13 region and their potential etiological associations with acute myeloid leukemia. <b>2023</b> , 168,	О
152	High level of novelty under the hood of convergent evolution. <b>2023</b> , 379, 1043-1049	O
151	Ornithine aminotransferase supports polyamine synthesis in pancreatic cancer. <b>2023</b> , 616, 339-347	О
150	Targeted DNA integration in human cells without double-strand breaks using CRISPR-associated transposases.	O
149	Transcription Factor Co-Expression Mediates Lineage Priming for Embryonic and Extra-Embryonic Differentiation.	O
148	In silico prioritisation of microRNA-associated common variants in multiple sclerosis. 2023, 17,	Ο
147	Transfer learning identifies sequence determinants of cell-type specific regulatory element accessibility. <b>2023</b> , 5,	O
146	The EN-TEx resource of multi-tissue personal epigenomes& variant-impact models. <b>2023</b> , 186, 1493-	1511. <b>e</b> 40
145	Urinary phthalate metabolites and small non-coding RNAs from seminal plasma extracellular vesicles among men undergoing infertility treatment <b>2023</b> , 121529	0
144	RNA Polymerase II transcription independent of TBP. 12,	O
143	Hidden Compositional Heterogeneity of Fish Chromosomes in the Era of Polished Genome Assemblies. <b>2023</b> , 8, 185	0
142	Genome structures resolve the early diversification of teleost fishes. <b>2023</b> , 379, 572-575	O
141	Genome-wide analysis emancipates genomic diversity and signature of selection in Altay white-headed cattle of Xinjiang, China. 14,	0
140	Chemical modulation of Schistosoma mansoni lysine specific demethylase 1 (SmLSD1) induces wide-scale biological and epigenomic changes. 8, 146	O
139	Novel enhancers conferring compensatory transcriptional regulation of Nkx2-5 in heart development. <b>2023</b> , 26, 106509	0
138	Analysis of genetic dominance in the UK Biobank. <b>2023</b> , 379, 1341-1348	O
137	Bacterial defences interact synergistically by disrupting phage cooperation.	0
136	Leptospiratranscriptome sequencing using long-read technology reveals unannotated transcripts and potential polyadenylation of mRNA molecules.	O

135	Systemic Lupus Erythematosus Patients with DNASE1L3IDeficiency Have a Distinctive and Specific Genic Circular DNA Profile in Plasma. <b>2023</b> , 12, 1061	O
134	Highly connected 3D chromatin networks established by an oncogenic fusion protein shape tumor cell identity. <b>2023</b> , 9,	O
133	GAGA-associated factor fosters loop formation in the Drosophila genome. 2023,	0
132	MYC reshapes CTCF-mediated chromatin architecture in prostate cancer. 2023, 14,	O
131	Target-capture probes for phylogenomics of the Caenogastropoda.	О
130	No evidence for a common blood microbiome based on a population study of 9,770 healthy humans.	О
129	Functional genomic effects of indels using Bayesian genome-phenome wide association studies in sorghum. 14,	О
128	Colocalization of blood cell traits GWAS associations and variation in PU.1 genomic occupancy prioritizes causal noncoding regulatory variants.	O
127	Role of the RNA-binding protein ZC3H41 in the regulation of ribosomal protein messenger RNAs in trypanosomes. <b>2023</b> , 16,	О
126	Whole Genome Sequencing Provides Information on the Genomic Architecture and Diversity of Cultivated Gilthead Seabream (Sparus aurata) Broodstock Nuclei. <b>2023</b> , 14, 839	O
125	PAK1-dependant mechanotransduction enables myofibroblast nuclear adaptation and chromatin organisation during fibrosis.	О
124	RIF1 regulates replication origin activity and early replication timing in B cells.	O
123	Confounding factors in profiling of locus-specific human endogenous retrovirus (HERV) transcript signatures in primary T cells using multi-study-derived datasets. <b>2023</b> , 16,	0
122	ERCC6L2 mitigates replication stress and promotes centromere stability. <b>2023</b> , 42, 112329	O
121	PEACOCK: a machine learning approach to assess the validity of cell type-specific enhancer-gene regulatory relationships. <b>2023</b> , 9,	O
120	Genome-Wide Association Study on Reproductive Traits Using Imputation-Based Whole-Genome Sequence Data in Yorkshire Pigs. <b>2023</b> , 14, 861	O
119	Homoeologous evolution of the allotetraploid genome of Poa annua L	О
118	Genome-wide SNPs show hybridization of Varroa mites from different Apis hosts in Vietnam and Taiwan. <b>2023</b> , 54,	O

117	Plasmodium falciparum gametocytes display global chromatin remodelling during sexual differentiation. <b>2023</b> , 21,	O
116	Major proliferation of transposable elements shaped the genome of the soybean rust pathogen Phakopsora pachyrhizi. <b>2023</b> , 14,	O
115	Transposable Elements are differentially activated in cell lineages during the developing murine submandibular gland.	O
114	CORE CONSERVED TRANSCRIPTIONAL REGULATORY NETWORKS DEFINE THE INVASIVE TROPHOBLAST CELL LINEAGE.	O
113	Functionally distinct promoter classes initiate transcription via different mechanisms reflected in focused versus dispersed initiation patterns.	0
112	Investigating miR-9 as a mediator in laryngeal cancer health disparities. 13,	O
111	Cross-species regulatory landscapes and elements revealed by novel joint systematic integration of human and mouse blood cell epigenomes.	O
110	NSD2 E1099K drives relapse in pediatric acute lymphoblastic leukemia by disrupting 3D chromatin organization. <b>2023</b> , 24,	O
109	An epigenetic switch controls an alternative NR2F2 isoform that unleashes a metastatic program in melanoma. <b>2023</b> , 14,	0
108	Overexpression of Ultrabithorax Changes the Development of Silk Gland and the Expression of Fibroin Genes in Bombyx mori. <b>2023</b> , 24, 6670	O
107	Activated Natural Killer Cell Inoculation Alleviates Fibrotic Liver Pathology in a Carbon Tetrachloride-Induced Liver Cirrhosis Mouse Model. <b>2023</b> , 11, 1090	O
106	Spurious intragenic transcription is a feature of mammalian cellular senescence and tissue aging. <b>2023</b> , 3, 402-417	O
105	Multi-omics analysis reveals a crucial role for Retinoic Acid in promoting epigenetic and transcriptional competence of anin vitromodel of human Pharyngeal Endoderm.	O
104	Investigation of NLR Genes Reveals Divergent Evolution on NLRome in Diploid and Polyploid Species in Genus Trifolium. <b>2023</b> , 14, 867	O
103	The interplay of 3D genome organization with UV-induced DNA damage and repair. 2023, 104679	0
102	The m6A reader YTHDC1 and the RNA helicase DDX5 control the production of rhabdomyosarcoma-enriched circRNAs. <b>2023</b> , 14,	O
101	Condensed but liquid-like domain organization of active chromatin regions in living human cells. <b>2023</b> , 9,	0
100	Differential contributions of nuclear lamina association and genome compartmentalization to gene regulation. <b>2023</b> , 14,	O

99	PuCRZ1, an C2H2 transcription factor from Polyporus umbellatus, positively regulates mycelium response to osmotic stress. 14,	O
98	m6A epitranscriptomic regulation of tissue homeostasis during primate aging.	O
97	Acetylation of histone H2B marks active enhancers and predicts CBP/p300 target genes. <b>2023</b> , 55, 679-692	O
96	Obligate chimerism in male yellow crazy ants. <b>2023</b> , 380, 55-58	O
95	Graded BMP signaling within intestinal crypt architecture directs self-organization of the Wnt-secreting stem cell niche. <b>2023</b> , 30, 433-449.e8	О
94	Escape from oncogene-induced senescence is controlled by POU2F2 and memorized by chromatin scars. <b>2023</b> , 3, 100293	O
93	Analysis of the P.Ilividus sea urchin genome highlights contrasting trends of genomic and regulatory evolution in deuterostomes. <b>2023</b> , 3, 100295	О
92	The ENCODE Uniform Analysis Pipelines.	O
91	Resolution of structural variation in diverse mouse genomes reveals chromatin remodeling due to transposable elements. <b>2023</b> , 100291	О
90	Ancient origin of Jingchuvirales derived glycoproteins integrated in arthropod genomes. 2023, 46,	O
89	PRC2.1- and PRC2.2-specific accessory proteins drive recruitment of different forms of canonical PRC1. <b>2023</b> ,	0
88	Genome-wide identification and characterization of circRNAs in wheat tiller. 2023, 136,	O
87	Endothelial Brg1 fine-tunes Notch signaling during zebrafish heart regeneration. 2023, 8,	О
86	Transposable elements are associated with the variable response to influenza infection. <b>2023</b> , 100292	O
85	A Weighted Two-stage Sequence Alignment Framework to Identify DNA Motifs from ChIP-exo Data.	О
84	Systematic visualisation of molecular QTLs reveals variant mechanisms at GWAS loci.	O
83	Ancient DNA Contradicts the Presence of Social Voles (Genus Microtus, Subgenus Sumeriomys) in the Late Pleistocene of Western Europe. <b>2023</b> , 15, 538	O
82	Genetic Screening of Targeted Region on the Chromosome 22q11.2 in Patients with Microtia and Congenital Heart Defect. <b>2023</b> , 14, 879	O

81	Identification of Long Intergenic Noncoding RNAs in Rhizoctonia cerealis following Inoculation of Wheat.	O
80	RIP-PEN-seq identifies a class of kink-turn RNAs as splicing regulators.	O
79	Identification of copy number variations in the genome of Dairy Gir cattle. 2023, 18, e0284085	O
78	Telomeric retrotransposons show propensity to form G-quadruplexes in various eukaryotic species. <b>2023</b> , 14,	O
77	Small vault RNA1-2 modulates expression of cell membrane proteins through nascent RNA silencing. <b>2023</b> , 6, e202302054	O
76	Rewiring of RNA methylation by the oncometabolite fumarate in renal cell carcinoma.	O
75	Ancestry-related differences in chromatin accessibility and gene expression of APOE 4 are associated with Alzheimer's disease risk.	O
74	The soil-borne white root rot pathogenRosellinia necatrixexpresses antimicrobial proteins during host colonization.	O
73	Genotypic and phenotypic diversity of the multidrug-resistant Mycobacterium tuberculosis strains from eastern India.	0
72	A multi-omics atlas of the human retina at single-cell resolution. <b>2023</b> , 100298	O
71	Whole transcriptome sequencing reveals HOXD11-AGAP3, a novel fusion transcript in the Indian acute leukemia cohort. 14,	O
70	The genomic and evolutionary landscapes of anaplastic thyroid carcinoma.	O
69	Establishment of an artificial particulate matter-induced lung disease model through analyzing pathological changes and transcriptomic profiles in mice. <b>2023</b> , 13,	O
68	Comparison of two molecular barcodes for the study of equine strongylid communities with amplicon sequencing. 11, e15124	O
67	The Genomic Variation and Differentially Expressed Genes on the 6P Chromosomes in WheatAgropyron cristatum Addition Lines 5113 and II-30-5 Confer Different Desirable Traits. <b>2023</b> , 24, 7056	O
66	The anti-cancer compound JTE-607 reveals hidden sequence specificity of the mRNA 3? processing machinery.	O
65	An improved genome assembly of the saguaro cactus (Carnegiea gigantea(Engelm.) Britton & Rose).	О
64	TAR Syndrome-associated Rbm8a deficiency causes hematopoietic defects and attenuates Wnt/PCP signaling.	O

63	Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF inactivating mutations in acute Ttell leukemia. <b>2023</b> , 42, 112373	0
62	Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. 2023, 14,	Ο
61	Fob1-dependent condensin recruitment and loop extrusion on yeast chromosome III. 2023, 19, e1010705	0
60	Never judge a bird by its feathers: genetics unveils the true target of trafficking in morphologically similarCopsychusspecies.	О
59	Using haplotype and QTL analysis to fix favorable alleles in diploid potato breeding.	0
58	Evaluating the Transition from Targeted to Exome Sequencing: A Guide for Clinical Laboratories. <b>2023</b> , 24, 7330	Ο
57	Dynamic changes in P300 enhancers and enhancer-promoter contacts control mouse cardiomyocyte maturation. <b>2023</b> ,	0
56	Interspecies blastocyst complementation generates functional rat cell-derived forebrain tissues in mice.	Ο
55	Dynamic evolution of retroviral envelope genes in egg-laying mammalian genomes.	0
54	The initiation and maintenance of CHH methylation and its effects on gene expression are unique in maize.	O
53	Genetic and karyotype divergence between parents affect clonality and sterility in hybrids.	O
52	Haplotype mapping of H3K27me3-associated chromatin interactions defines topological regulation of gene silencing in rice. <b>2023</b> , 42, 112350	O
51	R-loop landscape in mature human sperm: Regulatory and evolutionary implications. 14,	0
50	Chemogenomic Profiling of a Plasmodium falciparum Transposon Mutant Library Reveals Shared Effects of Dihydroartemisinin and Bortezomib on Lipid Metabolism and Exported Proteins.	Ο
49	Genomics reveals broad hybridization in deeply divergent Palearctic grass and water snakes (Natrix spp.). <b>2023</b> , 107787	0
48	Ancient diversity in host-parasite interaction genes in a model parasitic nematode.	Ο
47	A 1.5 Mb continuous endogenous viral element region in the arbuscular mycorrhizal fungusRhizophagus irregularis.	0
46	Using landscape genomics to assess local adaptation and genomic vulnerability of a perennial herb Tetrastigma hemsleyanum (Vitaceae) in subtropical China. 14,	Ο

45	Disease-related p63 DBD mutations impair DNA binding by distinct mechanisms and varying degree. <b>2023</b> , 14,	0
44	CamoTSS: analysis of alternative transcription start sites for cellular phenotypes and regulatory patterns from 5IscRNA-seq data.	O
43	Single worm long read sequencing reveals genome diversity in free-living nematodes.	О
42	Transgressive and parental dominant gene expression and cytosine methylation during seed development in Brassica napus hybrids. <b>2023</b> , 136,	O
41	Lamin B1 overexpression alters chromatin organization and gene expression. 2023, 14,	О
40	RNA degradome analysis reveals DNE1 endoribonuclease is required for the turnover of diverse mRNA substrates in Arabidopsis.	O
39	A VEL3 histone deacetylase complex establishes a maternal epigenetic state controlling progeny seed dormancy. <b>2023</b> , 14,	О
38	Reversal of the diabetic bone signature with anabolic therapies in mice. 2023, 11,	О
37	Genetic determinants of switchgrass-root-associated microbiota in field sites spanning its natural range. <b>2023</b> ,	О
36	Cell Type-Specific Regulation by a Heptad of Transcription Factors in Human Hematopoietic Stem and Progenitor Cells.	O
35	The histone H3K36 demethylase Fbxl11 plays pivotal roles in the development of retinal late-born cell types.	О
34	Subgenome-aware analyses suggest a reticulate allopolyploidization origin in three Papaver genomes. <b>2023</b> , 14,	O
33	Oncogenic CDK13 mutations impede nuclear RNA surveillance. <b>2023</b> , 380,	О
32	A small RNA system ensures accurate homologous pairing and unpaired silencing of meiotic chromosomes.	O
31	Gapless genome assembly of Fusarium verticillioides, a filamentous fungus threatening plant and human health. <b>2023</b> , 10,	О
30	The evolution of two transmissible cancers in Tasmanian devils. <b>2023</b> , 380, 283-293	O
29	Glucocorticoid activation of anti-inflammatory macrophages protects against insulin resistance. <b>2023</b> , 14,	О
28	The RNA m6A landscape of mouse oocytes and preimplantation embryos.	0

27	Epigenetic Gene-Regulatory Loci in Alu Elements Associated with Autism Susceptibility in the Prefrontal Cortex of ASD. <b>2023</b> , 24, 7518	О
26	exRNA-eCLIP intersection analysis reveals a map of extracellular RNA binding proteins and associated RNAs across major human biofluids and carriers. <b>2023</b> , 100303	O
25	Human immune and gut microbial parameters associated with inter-individual variations in COVID-19 mRNA vaccine-induced immunity. <b>2023</b> , 6,	0
24	Epidemiological and genomic investigation of chikungunya virus in Rio de Janeiro state, Brazil, between 2015 and 2018.	O
23	Genome-Wide Mapping of 5? Isoforms with 5?-Seq. <b>2023</b> , 3,	0
22	Epidemiological Surveillance Reveals the Rise and Establishment of the Omicron SARS-CoV-2 Variant in Brazil. <b>2023</b> , 15, 1017	O
21	Igh and Igk loci use different folding principles for V gene recombination due to distinct chromosomal architectures of pro-B and pre-B cells. <b>2023</b> , 14,	О
20	DNA methylation protocol for analyzing cell-free DNA in the spent culture medium of human preimplantation embryos. <b>2023</b> , 4, 102247	Ο
19	NF- <b>B</b> /p52 augments ETS1 binding genome-wide to promote glioma progression. <b>2023</b> , 6,	0
18	The mitochondrial genome of the diploid oat Avena longiglumis. <b>2023</b> , 23,	O
17	Electroconductive and mechano-competent PUCL@CNT nanohybrid scaffolds guiding neuronal specification of neural stem/progenitor cells. <b>2023</b> , 466, 143125	0
16	Novel Chromatin Insulating Activities Uncovered upon Eliminating Known Insulatorsin vivo.	Ο
15	Topologically associating domain underlies tissue specific expression of long intergenic non-coding RNAs. <b>2023</b> , 26, 106640	0
14	MORC proteins regulate transcription factor binding by mediating chromatin compaction in active chromatin regions. <b>2023</b> , 24,	O
13	PSGL-1 attenuates early TCR signaling to suppress CD8+ Tcell progenitor differentiation and elicit terminal CD8+ Tcell exhaustion. <b>2023</b> , 42, 112436	0
12	MYT1L is required for suppressing earlier neuronal development programs in the adult mouse brain. <b>2023</b> , 33, 541-556	O
11	Exploring Microbial Diversity and Functional Potential along the Bay of Bengal Coastline in Bangladesh: Insights from Amplicon Sequencing and Shotgun Metagenomics.	O
10	A second unveiling: Haplotig masking of the eastern oyster genome improves population-level inference.	O

9	Evolutionary constraint and innovation across hundreds of placental mammals. 2023, 380,	О
8	Genetic and physical localization of a major susceptibility gene to Pyrenophora teres f. maculata in barley. <b>2023</b> , 136,	O
7	Complementary strategies for directing in vivo transcription factor binding through DNA binding domains and intrinsically disordered regions. <b>2023</b> , 83, 1462-1473.e5	O
6	Identification of transcription factor co-binding patterns with non-negative matrix factorization.	O
5	Ancestral genome reconstruction enhances transposable element annotation by identifying degenerate integrants.	О
4	Mouse B2 SINE elements function as IFN-inducible enhancers. 12,	O
3	PIBF1 regulates multiple gene expression via impeding long-range chromatin interaction to drive the malignant transformation of HPV16 integration epithelial cells. <b>2023</b> ,	О
2	RNA polymerase drives ribonucleotide excision DNA repair in E.[coli. 2023,	O
1	Multifunctional dendrimer@nanoceria engineered GelMA hydrogel accelerates bone regeneration through orchestrated cellular responses. 2023, 20, 100664	0