

# CITATION REPORT

List of articles citing

Fast and accurate short read alignment with  
Burrows-Wheeler transform

DOI: 10.1093/bioinformatics/btp324  
Bioinformatics, 2009, 25, 1754-60.

**Source:** <https://exaly.com/paper-pdf/46851375/citation-report.pdf>

**Version:** 2024-04-25

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
2189	.		
2188	Covalent Click Chemistry-Based Attachment of DNA onto Solid Phase Enables Iterative Molecular Analysis.		
2187	Chronic Exposure to an Environmentally Relevant Triclosan Concentration Induces Persistent Triclosan Resistance but Reversible Antibiotic Tolerance in Escherichia coli.		1
2186	Cloning and Transplantation of the Mesoplasma florum Genome.		
2185	Probing the Chemical Transformation of Seawater-Soluble Crude Oil Components during Microbial Oxidation.		
2184	2Mercapto-Quinazolinones as Inhibitors of Type II NADH Dehydrogenase and Mycobacterium tuberculosis: StructureActivity Relationships, Mechanism of Action and Absorption, Distribution, Metabolism, and Excretion Characterization.		
2183	.		
2182	.		
2181	Abstract.		0
2180	Visual repair of congenital aortic stenosis during hypothermia. <b>1958</b> , 35, 139-153		23
2179	Mitotic spindle regulation by Nde1 controls cerebral cortical size. <b>2004</b> , 44, 279-93		293
2178	Kenya: Language Situation. <b>2006</b> , 180-182		
2177	BFAST: an alignment tool for large scale genome resequencing. <b>2009</b> , 4, e7767		394
2176	Analyzing gene expression data from microarray and next-generation dna sequencing transcriptome profiling assays using GeneSifter analysis edition. <b>2009</b> , Chapter 7, Unit 7.14 7.14.1-35		4
2175	High Throughput Short Read Alignment via Bi-directional BWT. <b>2009</b> ,		45
2174	PerM: efficient mapping of short sequencing reads with periodic full sensitive spaced seeds. <i>Bioinformatics</i> , <b>2009</b> , 25, 2514-21	7.2	81
2173	Fast mapping of short sequences with mismatches, insertions and deletions using index structures. <b>2009</b> , 5, e1000502		384

2172	Effect of read-mapping biases on detecting allele-specific expression from RNA-sequencing data. <i>Bioinformatics</i> , <b>2009</b> , 25, 3207-12	7.2	390
2171	Sense from sequence reads: methods for alignment and assembly. <b>2009</b> , 6, S6-S12		261
2170	Genetic diagnosis by whole exome capture and massively parallel DNA sequencing. <b>2009</b> , 106, 19096-101		971
2169	Simultaneous alignment of short reads against multiple genomes. <b>2009</b> , 10, R98		178
2168	PROMOT: modular modeling for systems biology. <i>Bioinformatics</i> , <b>2009</b> , 25, 687-9	7.2	70
2167	SNP Discovery through De Novo Deep Sequencing Using the next Generation of DNA Sequencers. <b>2010</b> , 69-90		1
2166	Algorithmic Issues in the Analysis of Chip-Seq Data. <b>2010</b> , 425-448		
2165	Rare deletions at 16p13.11 predispose to a diverse spectrum of sporadic epilepsy syndromes. <b>2010</b> , 86, 707-18		206
2164	Exome sequencing in Brown-Vialetto-van Laere syndrome. <b>2010</b> , 87, 567-9; author reply 569-70		48
2163	Detecting heteroplasmy from high-throughput sequencing of complete human mitochondrial DNA genomes. <b>2010</b> , 87, 237-49		239
2162	Response to Johnson et al.. <b>2010</b> , 87, 569-570		7
2161	Mutations in SCARF2 are responsible for Van Den Ende-Gupta syndrome. <b>2010</b> , 87, 553-9		39
2160	Mutations in FLVCR1 cause posterior column ataxia and retinitis pigmentosa. <b>2010</b> , 87, 643-54		66
2159	RNA-seq: from technology to biology. <b>2010</b> , 67, 569-79		356
2158	Utilization of next-generation sequencing platforms in plant genomics and genetic variant discovery. <b>2010</b> , 25, 553-570		105
2157	Analysing 454 amplicon resequencing experiments using the modular and database oriented Variant Identification Pipeline. <b>2010</b> , 11, 269		14
2156	Geoseq: a tool for dissecting deep-sequencing datasets. <b>2010</b> , 11, 506		3
2155	Pash 3.0: A versatile software package for read mapping and integrative analysis of genomic and epigenomic variation using massively parallel DNA sequencing. <b>2010</b> , 11, 572		44

2154	Initial steps towards a production platform for DNA sequence analysis on the grid. <b>2010</b> , 11, 598	6
2153	MrsRF: an efficient MapReduce algorithm for analyzing large collections of evolutionary trees. <b>2010</b> , 11 Suppl 1, S15	30
2152	Galaxy CloudMan: delivering cloud compute clusters. <b>2010</b> , 11 Suppl 12, S4	111
2151	DNA copy number, including telomeres and mitochondria, assayed using next-generation sequencing. <b>2010</b> , 11, 244	42
2150	Mobile element scanning (ME-Scan) by targeted high-throughput sequencing. <b>2010</b> , 11, 410	75
2149	Combining target enrichment with barcode multiplexing for high throughput SNP discovery. <b>2010</b> , 11, 641	23
2148	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. <b>2010</b> , 11, 663	168
2147	De novo assembled expressed gene catalog of a fast-growing Eucalyptus tree produced by Illumina mRNA-Seq. <b>2010</b> , 11, 681	137
2146	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice ( <i>Oryza sativa</i> L.). <b>2010</b> , 11, 683	64
2145	Unexpected allelic heterogeneity and spectrum of mutations in Fowler syndrome revealed by next-generation exome sequencing. <b>2010</b> , 31, 918-23	100
2144	Genomic-scale capture and sequencing of endogenous DNA from feces. <b>2010</b> , 19, 5332-44	109
2143	New insights into the blood-stage transcriptome of <i>Plasmodium falciparum</i> using RNA-Seq. <b>2010</b> , 76, 12-24	283
2142	A comprehensive catalogue of somatic mutations from a human cancer genome. <b>2010</b> , 463, 191-6	1303
2141	Whole-exome sequencing identifies recessive WDR62 mutations in severe brain malformations. <b>2010</b> , 467, 207-10	395
2140	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <b>2010</b> , 468, 1053-60	1169
2139	Mutations in WDR62, encoding a centrosome-associated protein, cause microcephaly with simplified gyri and abnormal cortical architecture. <b>2010</b> , 42, 1015-20	236
2138	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. <b>2010</b> , 42, 931-6	98
2137	Target-enrichment strategies for next-generation sequencing. <b>2010</b> , 7, 111-8	863

2136	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <b>2010</b> , 7, 528-34		123
2135	De novo assembly and analysis of RNA-seq data. <b>2010</b> , 7, 909-12		701
2134	mrsFAST: a cache-oblivious algorithm for short-read mapping. <b>2010</b> , 7, 576-7		216
2133	Annotating non-coding regions of the genome. <b>2010</b> , 11, 559-71		303
2132	Advances in understanding cancer genomes through second-generation sequencing. <b>2010</b> , 11, 685-96		890
2131	Designing Efficient Spaced Seeds for SOLiD Read Mapping. <b>2010</b> ,		5
2130	Commercially available outbred mice for genome-wide association studies. <b>2010</b> , 6, e1001085		102
2129	The characterization of twenty sequenced human genomes. <b>2010</b> , 6, e1001111		133
2128	HMMSplicer: a tool for efficient and sensitive discovery of known and novel splice junctions in RNA-Seq data. <b>2010</b> , 5, e13875		44
2127	De novo transcriptome sequencing in <i>Anopheles funestus</i> using Illumina RNA-seq technology. <b>2010</b> , 5, e14202		117
2126	Statistical Analyses of Next Generation Sequence Data: A Partial Overview. <b>2010</b> , 3, 183-190		29
2125	Novel multi-nucleotide polymorphisms in the human genome characterized by whole genome and exome sequencing. <b>2010</b> , 38, 6102-11		32
2124	Classification of DNA sequences using Bloom filters. <i>Bioinformatics</i> , <b>2010</b> , 26, 1595-600	7.2	45
2123	ChimerDB 2.0--a knowledgebase for fusion genes updated. <b>2010</b> , 38, D81-5		70
2122	VARIID: a variation detection framework for color-space and letter-space platforms. <i>Bioinformatics</i> , <b>2010</b> , 26, i343-9	7.2	9
2121	Whole-genome profiling of mutagenesis in <i>Caenorhabditis elegans</i> . <b>2010</b> , 185, 431-41		104
2120	Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. <b>2010</b> , 20, 623-35		217
2119	Genetics of neurodegenerative diseases: insights from high-throughput resequencing. <b>2010</b> , 19, R65-70		57

2118	ZOOM Lite: next-generation sequencing data mapping and visualization software. <b>2010</b> , 38, W743-8		15
2117	Complete genome sequence of probiotic <i>Bifidobacterium animalis</i> subsp. <i>lactis</i> strain V9. <b>2010</b> , 192, 4080-1		32
2116	Challenges of sequencing human genomes. <b>2010</b> , 11, 484-98		114
2115	Defining the transcriptome and proteome in three functionally different human cell lines. <b>2010</b> , 6, 450		269
2114	Accurate detection and genotyping of SNPs utilizing population sequencing data. <b>2010</b> , 20, 537-45		84
2113	Whole-exome sequencing-based discovery of STIM1 deficiency in a child with fatal classic Kaposi sarcoma. <b>2010</b> , 207, 2307-12		236
2112	High quality SNP calling using Illumina data at shallow coverage. <i>Bioinformatics</i> , <b>2010</b> , 26, 1029-35	7.2	44
2111	Efficient construction of an assembly string graph using the FM-index. <i>Bioinformatics</i> , <b>2010</b> , 26, i367-73	7.2	164
2110	WebPrInSeS: automated full-length clone sequence identification and verification using high-throughput sequencing data. <b>2010</b> , 38, W378-84		5
2109	A statistical method for the detection of variants from next-generation resequencing of DNA pools. <i>Bioinformatics</i> , <b>2010</b> , 26, i318-24	7.2	141
2108	PSI-RA: A parallel sparse index for read alignment on genomes. <b>2010</b> ,		1
2107	The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. <b>2010</b> , 38, 1767-71		915
2106	MapSplice: accurate mapping of RNA-seq reads for splice junction discovery. <b>2010</b> , 38, e178		762
2105	Small insertions and deletions (INDELs) in human genomes. <b>2010</b> , 19, R131-6		221
2104	miRNAkey: a software for microRNA deep sequencing analysis. <i>Bioinformatics</i> , <b>2010</b> , 26, 2615-6	7.2	70
2103	Genome variation discovery with high-throughput sequencing data. <b>2010</b> , 11, 3-14		50
2102	Noisy splicing drives mRNA isoform diversity in human cells. <b>2010</b> , 6, e1001236		203
2101	Systematic inference of copy-number genotypes from personal genome sequencing data reveals extensive olfactory receptor gene content diversity. <b>2010</b> , 6, e1000988		54

2100	GC-biased evolution near human accelerated regions. <b>2010</b> , 6, e1000960		31
2099	Expression of linear and novel circular forms of an INK4/ARF-associated non-coding RNA correlates with atherosclerosis risk. <b>2010</b> , 6, e1001233		653
2098	Structural variation analysis with strobe reads. <i>Bioinformatics</i> , <b>2010</b> , 26, 1291-8	7.2	30
2097	H2A.Z demarcates intergenic regions of the plasmodium falciparum epigenome that are dynamically marked by H3K9ac and H3K4me3. <b>2010</b> , 6, e1001223		158
2096	inGAP: an integrated next-generation genome analysis pipeline. <i>Bioinformatics</i> , <b>2010</b> , 26, 127-9	7.2	52
2095	CNAseq--a novel framework for identification of copy number changes in cancer from second-generation sequencing data. <i>Bioinformatics</i> , <b>2010</b> , 26, 3051-8	7.2	86
2094	Exploring molecular signaling in plant-fungal symbioses using high throughput RNA sequencing. <b>2010</b> , 5, 1353-8		8
2093	GASSST: global alignment short sequence search tool. <i>Bioinformatics</i> , <b>2010</b> , 26, 2534-40	7.2	72
2092	REAL. <b>2010</b> ,		17
2091	Complete genome sequence of Mycoplasma hyorhinis strain HUB-1. <b>2010</b> , 192, 5844-5		24
2090	Integrating genome assemblies with MAIA. <i>Bioinformatics</i> , <b>2010</b> , 26, i433-9	7.2	31
2089	Genome-wide identification of TAL1's functional targets: insights into its mechanisms of action in primary erythroid cells. <b>2010</b> , 20, 1064-83		137
2088	SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors. <i>Bioinformatics</i> , <b>2010</b> , 26, 730-6	7.2	174
2087	Preparation and analysis of microRNA libraries using the Illumina massively parallel sequencing technology. <b>2010</b> , 650, 173-99		13
2086	Statistical Issues in the Analysis of CHIP-Seq and RNA-Seq Data. <b>2010</b> , 1, 317-34		11
2085	Next-generation sequencing techniques for eukaryotic microorganisms: sequencing-based solutions to biological problems. <b>2010</b> , 9, 1300-10		106
2084	Targeted exon sequencing by in-solution hybrid selection. <b>2010</b> , Chapter 18, Unit 18.4		37
2083	Next Generation Sequencing of miRNAs - Strategies, Resources and Methods. <b>2010</b> , 1, 70-84		92

2082	From RNA-seq reads to differential expression results. <b>2010</b> , 11, 220	471
2081	Whole genome sequencing of enriched chloroplast DNA using the Illumina GAII platform. <b>2010</b> , 6, 22	54
2080	Integrative analysis of the melanoma transcriptome. <b>2010</b> , 20, 413-27	216
2079	A distributed system for fast alignment of next-generation sequencing data. <b>2010</b> , 2010, 579-584	
2078	Algorithms in Bioinformatics. <b>2010</b> ,	
2077	Functional and structural characterization of the $\alpha 2/\alpha 2$ hemoglobin from <i>Synechococcus</i> sp. PCC 7002. <b>2010</b> , 49, 7000-11	41
2076	Exploring plant transcriptomes using ultra high-throughput sequencing. <b>2010</b> , 9, 118-28	91
2075	BWtr: A tool for searching for tandem repeats in DNA sequences based on the Burrows-Wheeler transform. <b>2010</b> , 96, 316-21	20
2074	Genomic SELEX: a discovery tool for genomic aptamers. <b>2010</b> , 52, 125-32	47
2073	Roles of xanthophyll carotenoids in protection against photoinhibition and oxidative stress in the cyanobacterium <i>Synechococcus</i> sp. strain PCC 7002. <b>2010</b> , 504, 86-99	85
2072	The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. <b>2010</b> , 20, 1297-303	14079
2071	Uncovering the roles of rare variants in common disease through whole-genome sequencing. <b>2010</b> , 11, 415-25	1082
2070	An algorithm for mapping short reads to a dynamically changing genomic sequence. <b>2010</b> ,	1
2069	A survey of sequence alignment algorithms for next-generation sequencing. <b>2010</b> , 11, 473-83	632
2068	RADSeq: next-generation population genetics. <b>2010</b> , 9, 416-23	449
2067	Fast and SNP-tolerant detection of complex variants and splicing in short reads. <i>Bioinformatics</i> , <b>2010</b> , 26, 873-81	7.2 1457
2066	The genetics of eating disorders. <b>2011</b> , 6, 157-75	31
2065	Bioinformatics approaches for genomics and post genomics applications of next-generation sequencing. <b>2010</b> , 11, 181-97	120

2064	Identification of novel SNPs by next-generation sequencing of the genomic region containing the APC gene in colorectal cancer patients in China. <b>2010</b> , 14, 315-25	7
2063	Rapid, low-input, low-bias construction of shotgun fragment libraries by high-density in vitro transposition. <b>2010</b> , 11, R119	377
2062	Homoeolog-specific retention and use in allotetraploid <i>Arabidopsis suecica</i> depends on parent of origin and network partners. <b>2010</b> , 11, R125	65
2061	Enhanced structural variant and breakpoint detection using SVMerge by integration of multiple detection methods and local assembly. <b>2010</b> , 11, R128	99
2060	A first genome assembly of the barley fungal pathogen <i>Pyrenophora teres</i> f. <i>teres</i> . <b>2010</b> , 11, R109	73
2059	Improved variant discovery through local re-alignment of short-read next-generation sequencing data using SRMA. <b>2010</b> , 11, R99	57
2058	Sequencing and analysis of an Irish human genome. <b>2010</b> , 11, R91	35
2057	Whole exome capture in solution with 3 Gbp of data. <b>2010</b> , 11, R62	136
2056	Estimating enrichment of repetitive elements from high-throughput sequence data. <b>2010</b> , 11, R69	81
2055	Screening the human exome: a comparison of whole genome and whole transcriptome sequencing. <b>2010</b> , 11, R57	106
2054	Fast in-memory XPath search using compressed indexes. <b>2010</b> ,	16
2053	The missing graphical user interface for genomics. <b>2010</b> , 11, 128	10
2052	A re-sequencing tool for high mismatch-tolerant short read alignment based on Burrows-Wheeler Transform. <b>2010</b> ,	
2051	Mapping short reads to a genomic sequence with circular structure. <b>2010</b> ,	
2050	Exploring parallelism in short sequence mapping using Burrows-Wheeler Transform. <b>2010</b> ,	5
2049	Fast and accurate long-read alignment with Burrows-Wheeler transform. <i>Bioinformatics</i> , <b>2010</b> , 26, 589-95.2	6791
2048	Storage and retrieval of highly repetitive sequence collections. <b>2010</b> , 17, 281-308	121
2047	SeqHive: A Reconfigurable Computer Cluster for Genome Re-sequencing. <b>2010</b> ,	

2046	A fast CUDA implementation of agrep algorithm for approximate nucleotide sequence matching. <b>2011</b> ,		8
2045	Parallel Mapping Approaches for GNUMAP. <b>2011</b> , 2011, 435-443		6
2044	RATT: Rapid Annotation Transfer Tool. <b>2011</b> , 39, e57		224
2043	Comparative analysis of RNA-Seq alignment algorithms and the RNA-Seq unified mapper (RUM). <i>Bioinformatics</i> , <b>2011</b> , 27, 2518-28	7.2	261
2042	PTPan--overcoming memory limitations in oligonucleotide string matching for primer/probe design. <i>Bioinformatics</i> , <b>2011</b> , 27, 2797-805	7.2	2
2041	Comparative analysis of algorithms for next-generation sequencing read alignment. <i>Bioinformatics</i> , <b>2011</b> , 27, 2790-6	7.2	167
2040	mrNA: The MPI Randomized Numerical Aligner. <b>2011</b> ,		0
2039	Evaluation of Normalization Methods for RNA-Seq Gene Expression Estimation. <b>2011</b> , 2011, 50-57		3
2038	SNP annotation from next generation sequencing data. <b>2011</b> ,		0
2037	Multiplexed shotgun genotyping for rapid and efficient genetic mapping. <b>2011</b> , 21, 610-7		304
2036	Multiple emergences of genetically diverse amphibian-infecting chytrids include a globalized hypervirulent recombinant lineage. <b>2011</b> , 108, 18732-6		318
2035	A novel bioinformatics pipeline for identification and characterization of fusion transcripts in breast cancer and normal cell lines. <b>2011</b> , 39, e100		82
2034	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <b>2011</b> , 475, 101-5		1206
2033	Exploring the feasibility of next-generation sequencing and microarray data meta-analysis. <b>2011</b> , 2011, 7618-21		1
2032	Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. <b>2011</b> , 21, 1601-15		166
2031	Dindel: accurate indel calls from short-read data. <b>2011</b> , 21, 961-73		341
2030	Pol III binding in six mammals shows conservation among amino acid isotypes despite divergence among tRNA genes. <b>2011</b> , 43, 948-55		67
2029	Transcriptome profiling using single-molecule direct RNA sequencing. <b>2011</b> , 733, 51-61		27

2028	Chromothripsis is a common mechanism driving genomic rearrangements in primary and metastatic colorectal cancer. <b>2011</b> , 12, R103	140
2027	Spontaneous epigenetic variation in the Arabidopsis thaliana methylome. <b>2011</b> , 480, 245-9	533
2026	Sequencing transcriptomes in toto. <b>2011</b> , 3, 522-8	16
2025	Frequent mutations of chromatin remodeling genes in transitional cell carcinoma of the bladder. <b>2011</b> , 43, 875-8	554
2024	Chloroplast genome variation in upland and lowland switchgrass. <b>2011</b> , 6, e23980	62
2023	Structural variation in two human genomes mapped at single-nucleotide resolution by whole genome de novo assembly. <b>2011</b> , 29, 723-30	99
2022	Transcription Profiling of the Model Cyanobacterium Synechococcus sp. Strain PCC 7002 by Next-Gen (SOLiD) Sequencing of cDNA. <b>2011</b> , 2, 41	109
2021	Whole-genome sequencing of multiple Arabidopsis thaliana populations. <b>2011</b> , 43, 956-63	737
2020	Mutations in BRIP1 confer high risk of ovarian cancer. <b>2011</b> , 43, 1104-7	285
2019	Exome sequencing supports a de novo mutational paradigm for schizophrenia. <b>2011</b> , 43, 864-8	372
2018	Increased exonic de novo mutation rate in individuals with schizophrenia. <b>2011</b> , 43, 860-3	333
2017	Evaluation of next-generation sequencing software in mapping and assembly. <b>2011</b> , 56, 406-14	104
2016	Computational analysis of high throughput sequencing data. <b>2011</b> , 719, 199-217	5
2015	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. <b>2011</b> , 10, 322-33	30
2014	Identification of recurring tumor-specific somatic mutations in acute myeloid leukemia by transcriptome sequencing. <b>2011</b> , 25, 821-7	49
2013	Efficient alignment of pyrosequencing reads for re-sequencing applications. <b>2011</b> , 12, 163	6
2012	SeqGene: a comprehensive software solution for mining exome- and transcriptome- sequencing data. <b>2011</b> , 12, 267	36
2011	Molecular characterization of a long range haplotype affecting protein yield and mastitis susceptibility in Norwegian Red cattle. <b>2011</b> , 12, 70	17

2010	ERA: a parallel sparse index for genomic read alignment. <b>2011</b> , 12 Suppl 2, S7	3
2009	Evaluation of short read metagenomic assembly. <b>2011</b> , 12 Suppl 2, S8	40
2008	Next generation sequencing has lower sequence coverage and poorer SNP-detection capability in the regulatory regions. <b>2011</b> , 1, 55	61
2007	Benchmarking Short Sequence Mapping Tools. <b>2011</b> ,	5
2006	Algorithms in Bioinformatics. <b>2011</b> ,	
2005	Exome sequencing identifies a spectrum of mutation frequencies in advanced and lethal prostate cancers. <b>2011</b> , 108, 17087-92	211
2004	Behavioral Neurobiology of Eating Disorders. <b>2011</b> ,	9
2003	A public genome-scale lentiviral expression library of human ORFs. <b>2011</b> , 8, 659-61	373
2002	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. <b>2011</b> , 43, 1098-103	203
2001	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <b>2011</b> , 476, 298-303	1180
2000	Sequence Finishing on New Platforms. <b>2011</b> ,	
1999	High-Throughput Sequencing. <b>2011</b> , 461-478	2
1998	WITHDRAWN: Evaluation of next-generation sequencing software in mapping and assembly. <b>2011</b> ,	0
1997	Precise manipulation of chromosomes in vivo enables genome-wide codon replacement. <b>2011</b> , 333, 348-53	424
1996	CREST maps somatic structural variation in cancer genomes with base-pair resolution. <b>2011</b> , 8, 652-4	396
1995	Efficient targeted resequencing of human germline and cancer genomes by oligonucleotide-selective sequencing. <b>2011</b> , 29, 1024-7	40
1994	Identification of low-frequency variants associated with gout and serum uric acid levels. <b>2011</b> , 43, 1127-30	117
1993	String Matching in Hardware Using the FM-Index. <b>2011</b> ,	25

1992	Discovery and characterization of heme enzymes from unsequenced bacteria: application to microbial lignin degradation. <b>2011</b> , 133, 18006-9	84
1991	Detection of low prevalence somatic mutations in solid tumors with ultra-deep targeted sequencing. <b>2011</b> , 12, R124	73
1990	High-throughput RNA interference screening using pooled shRNA libraries and next generation sequencing. <b>2011</b> , 12, R104	89
1989	Hybrid selection for sequencing pathogen genomes from clinical samples. <b>2011</b> , 12, R73	80
1988	EMIRGE: reconstruction of full-length ribosomal genes from microbial community short read sequencing data. <b>2011</b> , 12, R44	256
1987	A vertebrate case study of the quality of assemblies derived from next-generation sequences. <b>2011</b> , 12, R31	27
1986	Analyzing and minimizing PCR amplification bias in Illumina sequencing libraries. <b>2011</b> , 12, R18	740
1985	Dicer recognizes the 5' end of RNA for efficient and accurate processing. <b>2011</b> , 475, 201-5	348
1984	Identification of improved IL28B SNPs and haplotypes for prediction of drug response in treatment of hepatitis C using massively parallel sequencing in a cross-sectional European cohort. <b>2011</b> , 3, 57	57
1983	Recognition of a mononucleosomal histone modification pattern by BPTF via multivalent interactions. <b>2011</b> , 145, 692-706	261
1982	Adaptation to P element transposon invasion in <i>Drosophila melanogaster</i> . <b>2011</b> , 147, 1551-63	176
1981	Bioinformatics challenges for personalized medicine. <i>Bioinformatics</i> , <b>2011</b> , 27, 1741-8	7.2 173
1980	Metagenomic analysis of a permafrost microbial community reveals a rapid response to thaw. <b>2011</b> , 480, 368-71	499
1979	Bayesian inference of ancient human demography from individual genome sequences. <b>2011</b> , 43, 1031-4	387
1978	Small RNA discovery and characterisation in eukaryotes using high-throughput approaches. <b>2011</b> , 722, 239-54	6
1977	Epigenetics in Male Reproduction: A Practical Introduction to the Informatics of Next Generation Sequencing. <b>2011</b> , 231-258	
1976	Exome capture and massively parallel sequencing identifies a novel HPSE2 mutation in a Saudi Arabian child with Ochoa (urofacial) syndrome. <b>2011</b> , 7, 569-73	22
1975	Evaluation of microsatellite variation in the 1000 Genomes Project pilot studies is indicative of the quality and utility of the raw data and alignments. <b>2011</b> , 97, 193-9	31

1974	ILLUMINATOR, a desktop program for mutation detection using short-read clonal sequencing. <b>2011</b> , 98, 302-9	4
1973	A whole-genome analysis of premature termination codons. <b>2011</b> , 98, 337-42	10
1972	Genome sequencing of mouse induced pluripotent stem cells reveals retroelement stability and infrequent DNA rearrangement during reprogramming. <b>2011</b> , 9, 366-73	91
1971	A hexanucleotide repeat expansion in C9ORF72 is the cause of chromosome 9p21-linked ALS-FTD. <b>2011</b> , 72, 257-68	3018
1970	Imaging of Plasmodium liver stages to drive next-generation antimalarial drug discovery. <b>2011</b> , 334, 1372-7	243
1969	Inference of human population history from individual whole-genome sequences. <b>2011</b> , 475, 493-6	1299
1968	SNP discovery in black cottonwood ( <i>Populus trichocarpa</i> ) by population transcriptome resequencing. <b>2011</b> , 11 Suppl 1, 81-92	96
1967	PRGmatic: an efficient pipeline for collating genome-enriched second-generation sequencing data using a 'provisional-reference genome'. <b>2011</b> , 11, 743-8	25
1966	Exome sequencing in sporadic autism spectrum disorders identifies severe de novo mutations. <b>2011</b> , 43, 585-9	899
1965	Dynamics of mitochondrial heteroplasmy in three families investigated via a repeatable re-sequencing study. <b>2011</b> , 12, R59	83
1964	Targeted enrichment beyond the consensus coding DNA sequence exome reveals exons with higher variant densities. <b>2011</b> , 12, R68	157
1963	Next-generation human genetics. <b>2011</b> , 12, 408	35
1962	Targeted analysis of nucleotide and copy number variation by exon capture in allotetraploid wheat genome. <b>2011</b> , 12, R88	113
1961	Targeted genomic capture and massively parallel sequencing to identify genes for hereditary hearing loss in Middle Eastern families. <b>2011</b> , 12, R89	163
1960	Exome sequencing identifies a missense mutation in <i>Isl1</i> associated with low penetrance otitis media in dearisch mice. <b>2011</b> , 12, R90	20
1959	First somatic mutation of E2F1 in a critical DNA binding residue discovered in well-differentiated papillary mesothelioma of the peritoneum. <b>2011</b> , 12, R96	16
1958	A comparative analysis of exome capture. <b>2011</b> , 12, R97	99
1957	Modularly assembled designer TAL effector nucleases for targeted gene knockout and gene replacement in eukaryotes. <b>2011</b> , 39, 6315-25	324

1956	. <b>2011</b> ,	16
1955	Gene Expression Analysis Using RNA-Seq from Organisms Lacking Substantial Genomic Resources. <b>2011</b> ,	
1954	Application of RNA-seq to reveal the transcript profile in bacteria. <b>2011</b> , 10, 1707-18	52
1953	NovelSNPer: A Fast Tool for the Identification and Characterization of Novel SNPs and InDels. <b>2011</b> , 2011, 657341	5
1952	Early Diagnosis of Werner's Syndrome Using Exome-Wide Sequencing in a Single, Atypical Patient. <b>2011</b> , 2, 8	8
1951	Estimating allele frequency from next-generation sequencing of pooled mitochondrial DNA samples. <b>2011</b> , 2, 51	7
1950	Characterizing ncRNAs in Human Pathogenic Protists Using High-Throughput Sequencing Technology. <b>2011</b> , 2, 96	8
1949	Draft Genome Sequences of <i>Xanthomonas sacchari</i> and Two Banana-Associated <i>Xanthomonas</i> Reveal Insights into the <i>Xanthomonas</i> Group 1 Clade. <b>2011</b> , 2, 1050-65	38
1948	PoolHap: inferring haplotype frequencies from pooled samples by next generation sequencing. <b>2011</b> , 6, e15292	28
1947	PoPoolation: a toolbox for population genetic analysis of next generation sequencing data from pooled individuals. <b>2011</b> , 6, e15925	372
1946	ReadDepth: a parallel R package for detecting copy number alterations from short sequencing reads. <b>2011</b> , 6, e16327	158
1945	Performance of microarray and liquid based capture methods for target enrichment for massively parallel sequencing and SNP discovery. <b>2011</b> , 6, e16486	20
1944	Fast identification and removal of sequence contamination from genomic and metagenomic datasets. <b>2011</b> , 6, e17288	471
1943	Annotation of two large contiguous regions from the <i>Haemonchus contortus</i> genome using RNA-seq and comparative analysis with <i>Caenorhabditis elegans</i> . <b>2011</b> , 6, e23216	21
1942	LOCAS--a low coverage assembly tool for resequencing projects. <b>2011</b> , 6, e23455	18
1941	GENE-counter: a computational pipeline for the analysis of RNA-Seq data for gene expression differences. <b>2011</b> , 6, e25279	50
1940	Metagenomic profile of the bacterial communities associated with <i>Ixodes ricinus</i> ticks. <b>2011</b> , 6, e25604	182
1939	AGO6 functions in RNA-mediated transcriptional gene silencing in shoot and root meristems in <i>Arabidopsis thaliana</i> . <b>2011</b> , 6, e25730	48

1938	Very few RNA and DNA sequence differences in the human transcriptome. <b>2011</b> , 6, e25842	64
1937	S-MART, a software toolbox to aid RNA-Seq data analysis. <b>2011</b> , 6, e25988	29
1936	Rates of mutation and host transmission for an Escherichia coli clone over 3 years. <b>2011</b> , 6, e26907	82
1935	Dual function of histone H3 lysine 36 methyltransferase ASH1 in regulation of Hox gene expression. <b>2011</b> , 6, e28171	31
1934	Identification of sequence variants in genetic disease-causing genes using targeted next-generation sequencing. <b>2011</b> , 6, e29500	113
1933	CASSys: an integrated software-system for the interactive analysis of ChIP-seq data. <b>2011</b> , 8, 1-13	4
1932	A Fast Divide-and-Conquer Algorithm for Indexing Human Genome Sequences. <b>2011</b> , E94-D, 1369-1377	
1931	Effects of inversions on within- and between-species recombination and divergence. <b>2011</b> , 3, 830-41	88
1930	A massively parallel sequencing approach uncovers ancient origins and high genetic variability of endangered Przewalski's horses. <b>2011</b> , 3, 1096-106	44
1929	The extent of linkage disequilibrium and computational challenges of single nucleotide polymorphisms in genome-wide association studies. <b>2011</b> , 12, 498-506	4
1928	Exome sequencing identifies GATA-2 mutation as the cause of dendritic cell, monocyte, B and NK lymphoid deficiency. <b>2011</b> , 118, 2656-8	316
1927	Mutation analysis of the tyrosine phosphatase PTPN2 in Hodgkin's lymphoma and T-cell non-Hodgkin's lymphoma. <b>2011</b> , 96, 1723-7	48
1926	[Next-generation analysis on hereditary neurodegenerative disorders using next-generation sequencers]. <b>2011</b> , 51, 970-2	
1925	A Storage-Efficient Suffix Tree Construction Algorithm for Human Genome Sequences. <b>2011</b> , E94-D, 2557-2560	2
1924	The next generation: using new sequencing technologies to analyse gene regulation. <b>2011</b> , 16, 210-22	37
1923	Next-generation mapping of Arabidopsis genes. <b>2011</b> , 67, 715-25	228
1922	Application of high-throughput genome sequencing to intrapathovar variation in Pseudomonas syringae. <b>2011</b> , 12, 829-38	17
1921	The effect of next-generation sequencing technology on complex trait research. <b>2011</b> , 41, 561-7	36

1920	Regulatory mechanisms underlying C4 photosynthesis. <b>2011</b> , 190, 9-20	35
1919	PICS: probabilistic inference for ChIP-seq. <b>2011</b> , 67, 151-63	53
1918	Exploring the Transcriptome Landscape of Pomegranate Fruit Peel for Natural Product Biosynthetic Gene and SSR Marker Discovery(F). <b>2011</b> , 53, 800-13	49
1917	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. <b>2011</b> , 43, 316-20	228
1916	Exome sequencing identifies somatic mutations of DNA methyltransferase gene DNMT3A in acute monocytic leukemia. <b>2011</b> , 43, 309-15	618
1915	High-resolution characterization of a hepatocellular carcinoma genome. <b>2011</b> , 43, 464-9	241
1914	A framework for variation discovery and genotyping using next-generation DNA sequencing data. <b>2011</b> , 43, 491-8	7264
1913	Recessive LAMC3 mutations cause malformations of occipital cortical development. <b>2011</b> , 43, 590-4	85
1912	Computational methods for transcriptome annotation and quantification using RNA-seq. <b>2011</b> , 8, 469-77	711
1911	Genotype and SNP calling from next-generation sequencing data. <b>2011</b> , 12, 443-51	959
1910	Genome-wide genetic marker discovery and genotyping using next-generation sequencing. <b>2011</b> , 12, 499-510	1723
1909	Targeted resequencing of a genomic region influencing tameness and aggression reveals multiple signals of positive selection. <b>2011</b> , 107, 205-14	25
1908	Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. <b>2011</b> , 29, 68-72	816
1907	Haplotype-resolved genome sequencing of a Gujarati Indian individual. <b>2011</b> , 29, 59-63	194
1906	De novo genome sequencing and comparative genomics of date palm ( <i>Phoenix dactylifera</i> ). <b>2011</b> , 29, 521-7	300
1905	A simple method for the parallel deep sequencing of full influenza A genomes. <b>2011</b> , 178, 243-8	33
1904	Genetic diagnosis in consanguineous families with kidney disease by homozygosity mapping coupled with whole-exome sequencing. <b>2011</b> , 58, 186-95	14
1903	Hes6 is required for actin cytoskeletal organization in differentiating C2C12 myoblasts. <b>2011</b> , 317, 1590-602	10

1902	De novo sequence assembly and characterization of the floral transcriptome in cross- and self-fertilizing plants. <b>2011</b> , 12, 298	71
1901	Annotation-based genome-wide SNP discovery in the large and complex <i>Aegilops tauschii</i> genome using next-generation sequencing without a reference genome sequence. <b>2011</b> , 12, 59	121
1900	CloudAligner: A fast and full-featured MapReduce based tool for sequence mapping. <b>2011</b> , 4, 171	70
1899	Next-generation sequencing technologies and applications for human genetic history and forensics. <b>2011</b> , 2, 23	81
1898	Regenerant <i>Arabidopsis</i> lineages display a distinct genome-wide spectrum of mutations conferring variant phenotypes. <b>2011</b> , 21, 1385-90	65
1897	Preservation of the Y transcriptome in a 10-million-year-old plant sex chromosome system. <b>2011</b> , 21, 1470-4	101
1896	Population genetics of <i>Vibrio cholerae</i> from Nepal in 2010: evidence on the origin of the Haitian outbreak. <b>2011</b> , 2, e00157-11	224
1895	Bacterial transcriptomics: what is beyond the RNA hori-z-ome?. <b>2011</b> , 9, 658-69	107
1894	Analysis of high-throughput sequencing data. <b>2011</b> , 678, 1-11	5
1893	Chromatin immunoprecipitation and high-throughput sequencing from paraffin-embedded pathology tissue. <b>2011</b> , 6, 1905-19	47
1892	Review of massively parallel DNA sequencing technologies. <b>2011</b> , 5, 1-12	54
1891	SEAL: a distributed short read mapping and duplicate removal tool. <i>Bioinformatics</i> , <b>2011</b> , 27, 2159-60	7.2 87
1890	In vivo and transcriptome-wide identification of RNA binding protein target sites. <b>2011</b> , 44, 828-40	124
1889	Genome-wide studies of copy number variation and exome sequencing identify rare variants in BAG3 as a cause of dilated cardiomyopathy. <b>2011</b> , 88, 273-82	264
1888	A genome-wide comparison of the functional properties of rare and common genetic variants in humans. <b>2011</b> , 88, 458-68	72
1887	Next-generation sequencing strategies enable routine detection of balanced chromosome rearrangements for clinical diagnostics and genetic research. <b>2011</b> , 88, 469-81	132
1886	The essential role of centrosomal NDE1 in human cerebral cortex neurogenesis. <b>2011</b> , 88, 523-35	118
1885	Exome sequencing identifies mitochondrial alanyl-tRNA synthetase mutations in infantile mitochondrial cardiomyopathy. <b>2011</b> , 88, 635-42	195

1884	Nonsense mutations in SMPX, encoding a protein responsive to physical force, result in X-chromosomal hearing loss. <b>2011</b> , 88, 621-7	60
1883	Exome sequencing and functional analysis identifies BANF1 mutation as the cause of a hereditary progeroid syndrome. <b>2011</b> , 88, 650-6	148
1882	A mutation in the Golgi Qb-SNARE gene GOSR2 causes progressive myoclonus epilepsy with early ataxia. <b>2011</b> , 88, 657-63	85
1881	Adaptor protein complex 4 deficiency causes severe autosomal-recessive intellectual disability, progressive spastic paraplegia, shy character, and short stature. <b>2011</b> , 88, 788-795	160
1880	Using VAAST to Identify an X-linked Disorder Resulting in Lethality in Male Infants Due to N-Terminal Acetyltransferase Deficiency. <b>2011</b> , 89, 345	4
1879	Denisova admixture and the first modern human dispersals into Southeast Asia and Oceania. <b>2011</b> , 89, 516-28	390
1878	XX ovarian dysgenesis is caused by a PSMC3IP/HOP2 mutation that abolishes coactivation of estrogen-driven transcription. <b>2011</b> , 89, 572-9	80
1877	Assessment of 2q23.1 microdeletion syndrome implicates MBD5 as a single causal locus of intellectual disability, epilepsy, and autism spectrum disorder. <b>2011</b> , 89, 551-63	166
1876	Mutation altering the miR-184 seed region causes familial keratoconus with cataract. <b>2011</b> , 89, 628-33	202
1875	Ciliopathies with skeletal anomalies and renal insufficiency due to mutations in the IFT-A gene WDR19. <b>2011</b> , 89, 634-43	180
1874	Muscarinic Acetylcholine Receptor M3 Mutation Causes Urinary Bladder Disease and a Prune-Belly-like Syndrome. <b>2011</b> , 89, 668-74	74
1873	Whole-exome sequencing identifies mutations of KIF22 in spondyloepimetaphyseal dysplasia with joint laxity, leptodactylic type. <b>2011</b> , 89, 760-6	34
1872	Recurrent dominant mutations affecting two adjacent residues in the motor domain of the monomeric kinesin KIF22 result in skeletal dysplasia and joint laxity. <b>2011</b> , 89, 767-72	23
1871	Posterior column ataxia with retinitis pigmentosa in a Japanese family with a novel mutation in FLVCR1. <b>2011</b> , 12, 117-21	31
1870	RNA-Seq of the xylose-fermenting yeast <i>Scheffersomyces stipitis</i> cultivated in glucose or xylose. <b>2011</b> , 92, 1237-49	25
1869	Genomic DNA pooling strategy for next-generation sequencing-based rare variant discovery in abdominal aortic aneurysm regions of interest-challenges and limitations. <b>2011</b> , 4, 271-80	19
1868	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. <b>2011</b> , 4, 50-65	36
1867	High-performance single-chip exon capture allows accurate whole exome sequencing using the Illumina Genome Analyzer. <b>2011</b> , 54, 945-52	6

1866	Overview of available methods for diverse RNA-Seq data analyses. <b>2011</b> , 54, 1121-8	49
1865	Deep sequencing of gastric carcinoma reveals somatic mutations relevant to personalized medicine. <b>2011</b> , 9, 119	71
1864	ChIP-seq Analysis in R (CSAR): An R package for the statistical detection of protein-bound genomic regions. <b>2011</b> , 7, 11	49
1863	SNP discovery in apple cultivars using next generation sequencing. <b>2011</b> , 5,	4
1862	Identification of gene fusion transcripts by transcriptome sequencing in BRCA1-mutated breast cancers and cell lines. <b>2011</b> , 4, 75	33
1861	Agile parallel bioinformatics workflow management using Pwrake. <b>2011</b> , 4, 331	17
1860	H3K9me3-binding proteins are dispensable for SETDB1/H3K9me3-dependent retroviral silencing. <b>2011</b> , 4, 12	33
1859	Evaluation of genomic high-throughput sequencing data generated on Illumina HiSeq and genome analyzer systems. <b>2011</b> , 12, R112	395
1858	A novel and well-defined benchmarking method for second generation read mapping. <b>2011</b> , 12, 210	51
1857	Querying large read collections in main memory: a versatile data structure. <b>2011</b> , 12, 242	10
1856	UMARS: Un-MAppable Reads Solution. <b>2011</b> , 12 Suppl 1, S9	7
1855	ClipCrop: a tool for detecting structural variations with single-base resolution using soft-clipping information. <b>2011</b> , 12 Suppl 14, S7	35
1854	Detection of splicing events and multiread locations from RNA-seq data based on a geometric-tail (GT) distribution of intron length. <b>2011</b> , 12 Suppl 5, S2	
1853	Assembly of non-unique insertion content using next-generation sequencing. <b>2011</b> , 12 Suppl 6, S3	9
1852	STELLAR: fast and exact local alignments. <b>2011</b> , 12 Suppl 9, S15	19
1851	Whole mitochondrial genome sequencing of domestic horses reveals incorporation of extensive wild horse diversity during domestication. <b>2011</b> , 11, 328	75
1850	PoPoolation DB: a user-friendly web-based database for the retrieval of natural polymorphisms in Drosophila. <b>2011</b> , 12, 27	10
1849	Transcriptome characterization and high throughput SSRs and SNPs discovery in Cucurbita pepo (Cucurbitaceae). <b>2011</b> , 12, 104	153

1848	Cross species comparison of C/EBP $\beta$ and PPAR $\alpha$ profiles in mouse and human adipocytes reveals interdependent retention of binding sites. <b>2011</b> , 12, 152	74
1847	Accurate and exact CNV identification from targeted high-throughput sequence data. <b>2011</b> , 12, 184	156
1846	Sequencing and characterization of the guppy ( <i>Poecilia reticulata</i> ) transcriptome. <b>2011</b> , 12, 202	76
1845	Building a model: developing genomic resources for common milkweed ( <i>Asclepias syriaca</i> ) with low coverage genome sequencing. <b>2011</b> , 12, 211	89
1844	ngs_backbone: a pipeline for read cleaning, mapping and SNP calling using next generation sequence. <b>2011</b> , 12, 285	47
1843	Evolutionary conserved microRNAs are ubiquitously expressed compared to tick-specific miRNAs in the cattle tick <i>Rhipicephalus (Boophilus) microplus</i> . <b>2011</b> , 12, 328	31
1842	Addressing challenges in the production and analysis of illumina sequencing data. <b>2011</b> , 12, 382	99
1841	BLAST Ring Image Generator (BRIG): simple prokaryote genome comparisons. <b>2011</b> , 12, 402	1617
1840	SAMQA: error classification and validation of high-throughput sequenced read data. <b>2011</b> , 12, 419	11
1839	Deep sequencing-based transcriptome analysis of <i>Plutella xylostella</i> larvae parasitized by <i>Diadegma semiclausum</i> . <b>2011</b> , 12, 446	73
1838	Global assessment of genomic variation in cattle by genome resequencing and high-throughput genotyping. <b>2011</b> , 12, 557	57
1837	AluScan: a method for genome-wide scanning of sequence and structure variations in the human genome. <b>2011</b> , 12, 564	13
1836	Whole genome sequencing of peach ( <i>Prunus persica</i> L.) for SNP identification and selection. <b>2011</b> , 12, 569	57
1835	De novo assembly of <i>Euphorbia fischeriana</i> root transcriptome identifies prostratin pathway related genes. <b>2011</b> , 12, 600	57
1834	The genome sequence of <i>E. coli</i> W (ATCC 9637): comparative genome analysis and an improved genome-scale reconstruction of <i>E. coli</i> . <b>2011</b> , 12, 9	121
1833	Perfect Hamming code with a hash table for faster genome mapping. <b>2011</b> , 12 Suppl 3, S8	4
1832	UASIS: Universal Automatic SNP Identification System. <b>2011</b> , 12 Suppl 3, S9	3
1831	Rare variants in the CYP27B1 gene are associated with multiple sclerosis. <b>2011</b> , 70, 881-6	171

1830	Confounded by sequencing depth in association studies of rare alleles. <b>2011</b> , 35, 261-8		21
1829	Biocompute 2.0: an improved collaborative workspace for data intensive bio-science. <b>2011</b> , 23, 2305-2314		5
1828	Mutations in NOTCH2 in families with Hajdu-Cheney syndrome. <b>2011</b> , 32, 1114-7		79
1827	First implication of STRA6 mutations in isolated anophthalmia, microphthalmia, and coloboma: a new dimension to the STRA6 phenotype. <b>2011</b> , 32, 1417-26		62
1826	Exome resequencing combined with linkage analysis identifies novel PTH1R variants in primary failure of tooth eruption in Japanese. <b>2011</b> , 26, 1655-61		44
1825	Comprehensive identification and quantification of microbial transcriptomes by genome-wide unbiased methods. <b>2011</b> , 22, 32-41		54
1824	Epigenome sequencing comes of age in development, differentiation and disease mechanism research. <b>2011</b> , 3, 207-20		5
1823	MapReducing a genomic sequencing workflow. <b>2011</b> ,		11
1822	DynMap. <b>2011</b> ,		3
1821	Probabilistic alignments with quality scores: an application to short-read mapping toward accurate SNP/indel detection. <i>Bioinformatics</i> , <b>2011</b> , 27, 3085-92	7.2	15
1820	SVA: software for annotating and visualizing sequenced human genomes. <i>Bioinformatics</i> , <b>2011</b> , 27, 1998-2000		57
1819	Genome sequence of <i>Gluconacetobacter</i> sp. strain SXCC-1, isolated from Chinese vinegar fermentation starter. <b>2011</b> , 193, 3395-6		12
1818	Faster Short DNA Sequence Alignment with Parallel BWA. <b>2011</b> ,		5
1817	Comparative copy number variation from whole genome sequencing. <b>2011</b> ,		1
1816	ComB: SNP calling and mapping analysis for color and nucleotide space platforms. <b>2011</b> , 18, 795-807		9
1815	An Exact Matching Approach for High Throughput Sequencing Based on BWT and GPUs. <b>2011</b> ,		6
1814	Interval Trees for Detection of Overlapping Genetic Entities. <b>2011</b> ,		1
1813	Accurate estimation of expression levels of homologous genes in RNA-seq experiments. <b>2011</b> , 18, 459-68		28

1812	Data Decomposition in Biomedical e-Science Applications. <b>2011</b> ,		2
1811	Exome sequencing and disease-network analysis of a single family implicate a mutation in KIF1A in hereditary spastic paraparesis. <b>2011</b> , 21, 658-64		153
1810	A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. <i>Bioinformatics</i> , <b>2011</b> , 27, 2987-93	7.2	3095
1809	inGAP-sv: a novel scheme to identify and visualize structural variation from paired end mapping data. <b>2011</b> , 39, W567-75		63
1808	Complete genome sequence of <i>Mycoplasma hyopneumoniae</i> strain 168. <b>2011</b> , 193, 1016-7		39
1807	Inference of population mutation rate and detection of segregating sites from next-generation sequence data. <b>2011</b> , 189, 595-605		7
1806	Replication stress induces 53BP1-containing OPT domains in G1 cells. <b>2011</b> , 193, 97-108		234
1805	Complete genome sequence of <i>Streptococcus thermophilus</i> strain ND03. <b>2011</b> , 193, 793-4		57
1804	Complete genome sequence of <i>Staphylococcus aureus</i> T0131, an ST239-MRSA-SCCmec type III clone isolated in China. <b>2011</b> , 193, 3411-2		27
1803	An integrated proteomics/transcriptomics approach points to oxygen as the main electron sink for methanol metabolism in <i>Methylobacterium mobilis</i> . <b>2011</b> , 193, 4758-65		18
1802	vipR: variant identification in pooled DNA using R. <i>Bioinformatics</i> , <b>2011</b> , 27, i77-84	7.2	33
1801	Complete genome sequence of the probiotic <i>Lactobacillus plantarum</i> ST-III. <b>2011</b> , 193, 313-4		72
1800	Efficient storage of high throughput DNA sequencing data using reference-based compression. <b>2011</b> , 21, 734-40		233
1799	BiQ Analyzer HT: locus-specific analysis of DNA methylation by high-throughput bisulfite sequencing. <b>2011</b> , 39, W551-6		99
1798	DNA rearrangement has occurred in the carbazole-degradative plasmid pCAR1 and the chromosome of its unsuitable host, <i>Pseudomonas fluorescens</i> Pf0-1. <b>2011</b> , 157, 3405-3416		7
1797	GAMES identifies and annotates mutations in next-generation sequencing projects. <i>Bioinformatics</i> , <b>2011</b> , 27, 9-13	7.2	25
1796	Exact and complete short-read alignment to microbial genomes using Graphics Processing Unit programming. <i>Bioinformatics</i> , <b>2011</b> , 27, 1351-8	7.2	71
1795	SEED: efficient clustering of next-generation sequences. <i>Bioinformatics</i> , <b>2011</b> , 27, 2502-9	7.2	46

1794	Combined malonic and methylmalonic aciduria: exome sequencing reveals mutations in the ACSF3 gene in patients with a non-classic phenotype. <b>2011</b> , 48, 602-5	39
1793	Complete genome sequence of the probiotic bacterium <i>Lactobacillus casei</i> LC2W. <b>2011</b> , 193, 3419-20	40
1792	A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. <b>2011</b> , 6, e19379	3791
1791	Revealing the genetic structure of a trait by sequencing a population under selection. <b>2011</b> , 21, 1131-8	185
1790	Phased whole-genome genetic risk in a family quartet using a major allele reference sequence. <b>2011</b> , 7, e1002280	112
1789	Reciprocal sign epistasis between frequently experimentally evolved adaptive mutations causes a rugged fitness landscape. <b>2011</b> , 7, e1002056	189
1788	Cocaine dynamically regulates heterochromatin and repetitive element unsilencing in nucleus accumbens. <b>2011</b> , 108, 3035-40	146
1787	Complete genome sequence of <i>Lactobacillus helveticus</i> H10. <b>2011</b> , 193, 2666-7	33
1786	Complete genome sequence of the probiotic strain <i>Lactobacillus casei</i> BD-II. <b>2011</b> , 193, 3160-1	31
1785	Retrogenes in rice ( <i>Oryza sativa</i> L. ssp. <i>japonica</i> ) exhibit correlated expression with their source genes. <b>2011</b> , 3, 1357-68	43
1784	wapRNA: a web-based application for the processing of RNA sequences. <i>Bioinformatics</i> , <b>2011</b> , 27, 3076-77.2	51
1783	A novel 5-bp deletion in <i>Clarin 1</i> in a family with Usher syndrome. <b>2011</b> , 32, 245-9	7
1782	A survey for novel imprinted genes in the mouse placenta by mRNA-seq. <b>2011</b> , 189, 109-22	75
1781	Novel inborn error of folate metabolism: identification by exome capture and sequencing of mutations in the <i>MTHFD1</i> gene in a single proband. <b>2011</b> , 48, 590-2	52
1780	Gain-of-function human <i>STAT1</i> mutations impair IL-17 immunity and underlie chronic mucocutaneous candidiasis. <b>2011</b> , 208, 1635-48	599
1779	TotalReCaller: improved accuracy and performance via integrated alignment and base-calling. <i>Bioinformatics</i> , <b>2011</b> , 27, 2330-7	7.2 9
1778	RseqFlow: workflows for RNA-Seq data analysis. <i>Bioinformatics</i> , <b>2011</b> , 27, 2598-600	7.2 22
1777	True single-molecule DNA sequencing of a pleistocene horse bone. <b>2011</b> , 21, 1705-19	99

1776	Characterization of complex chromosomal rearrangements by targeted capture and next-generation sequencing. <b>2011</b> , 21, 1720-7			35
1775	Human single-nucleotide polymorphisms alter p53 sequence-specific binding at gene regulatory elements. <b>2011</b> , 39, 178-89			24
1774	ParameciumDB in 2011: new tools and new data for functional and comparative genomics of the model ciliate <i>Paramecium tetraurelia</i> . <b>2011</b> , 39, D632-6			87
1773	Discovery of genome-wide DNA polymorphisms in a landrace cultivar of Japonica rice by whole-genome sequencing. <b>2011</b> , 52, 274-82			100
1772	Regenerative phenotype in mice with a point mutation in transforming growth factor beta type I receptor (TGFBR1). <b>2011</b> , 108, 14560-5			32
1771	A pipeline for RNA-seq data processing and quality assessment. <i>Bioinformatics</i> , <b>2011</b> , 27, 867-9	7.2		48
1770	SAMStat: monitoring biases in next generation sequencing data. <i>Bioinformatics</i> , <b>2011</b> , 27, 130-1	7.2		130
1769	A probabilistic method for the detection and genotyping of small indels from population-scale sequence data. <i>Bioinformatics</i> , <b>2011</b> , 27, 2047-53	7.2		16
1768	Systematic comparison of three methods for fragmentation of long-range PCR products for next generation sequencing. <b>2011</b> , 6, e28240			87
1767	mapDamage: testing for damage patterns in ancient DNA sequences. <i>Bioinformatics</i> , <b>2011</b> , 27, 2153-5	7.2		209
1766	SHRiMP2: sensitive yet practical SHort Read Mapping. <i>Bioinformatics</i> , <b>2011</b> , 27, 1011-2	7.2		270
1765	SVseq: an approach for detecting exact breakpoints of deletions with low-coverage sequence data. <i>Bioinformatics</i> , <b>2011</b> , 27, 3228-34	7.2		27
1764	Computational challenges of sequence classification in microbiomic data. <b>2011</b> , 12, 614-25			11
1763	Next-generation mapping of complex traits with phenotype-based selection and introgression. <b>2011</b> , 189, 1203-9			19
1762	ABMapper: a suffix array-based tool for multi-location searching and splice-junction mapping. <i>Bioinformatics</i> , <b>2011</b> , 27, 421-2	7.2		14
1761	Human piRNAs are under selection in Africans and repress transposable elements. <b>2011</b> , 28, 3061-7			27
1760	SNP detection and genotyping from low-coverage sequencing data on multiple diploid samples. <b>2011</b> , 21, 952-60			117
1759	TMPRSS2-ERG-mediated feed-forward regulation of wild-type ERG in human prostate cancers. <b>2011</b> , 71, 5387-92			40

1758	Revised genome sequence of <i>Brucella suis</i> 1330. <b>2011</b> , 193, 6410		12
1757	Complete genome sequence of <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> strain ND02. <b>2011</b> , 193, 3426-7		32
1756	Application and comparison of large-scale solution-based DNA capture-enrichment methods on ancient DNA. <b>2011</b> , 1, 74		87
1755	PoPoolation2: identifying differentiation between populations using sequencing of pooled DNA samples (Pool-Seq). <i>Bioinformatics</i> , <b>2011</b> , 27, 3435-6	7.2	474
1754	RNA sequencing reveals the role of splicing polymorphisms in regulating human gene expression. <b>2011</b> , 21, 545-54		93
1753	Exome sequencing and analysis of induced pluripotent stem cells identify the cilia-related gene male germ cell-associated kinase (MAK) as a cause of retinitis pigmentosa. <b>2011</b> , 108, E569-76		163
1752	Outcrossing, mitotic recombination, and life-history trade-offs shape genome evolution in <i>Saccharomyces cerevisiae</i> . <b>2011</b> , 108, 1987-92		120
1751	Evidence for compensatory upregulation of expressed X-linked genes in mammals, <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> . <b>2011</b> , 43, 1179-85		206
1750	Stampy: a statistical algorithm for sensitive and fast mapping of Illumina sequence reads. <b>2011</b> , 21, 936-9		832
1749	A rare penetrant mutation in CFH confers high risk of age-related macular degeneration. <b>2011</b> , 43, 1232-6		251
1748	Discovery of rare mutations in populations: TILLING by sequencing. <b>2011</b> , 156, 1257-68		190
1747	. <b>2011</b> ,		4
1746	FR-HIT, a very fast program to recruit metagenomic reads to homologous reference genomes. <i>Bioinformatics</i> , <b>2011</b> , 27, 1704-5	7.2	62
1745	Chromothripsis as a mechanism driving complex de novo structural rearrangements in the germline. <b>2011</b> , 20, 1916-24		223
1744	Trans genomic capture and sequencing of primate exomes reveals new targets of positive selection. <b>2011</b> , 21, 1686-94		74
1743	Accurate and comprehensive sequencing of personal genomes. <b>2011</b> , 21, 1498-505		153
1742	Metatranscriptomic analyses of chlorophototrophs of a hot-spring microbial mat. <b>2011</b> , 5, 1279-90		70
1741	A functional variant at a prostate cancer predisposition locus at 8q24 is associated with PVT1 expression. <b>2011</b> , 7, e1002165		125

1740	The statistics of bulk segregant analysis using next generation sequencing. <b>2011</b> , 7, e1002255		144
1739	Characterization and improvement of RNA-Seq precision in quantitative transcript expression profiling. <i>Bioinformatics</i> , <b>2011</b> , 27, i383-91	7.2	108
1738	SlideSort: all pairs similarity search for short reads. <i>Bioinformatics</i> , <b>2011</b> , 27, 464-70	7.2	18
1737	CLIPZ: a database and analysis environment for experimentally determined binding sites of RNA-binding proteins. <b>2011</b> , 39, D245-52		111
1736	Bambino: a variant detector and alignment viewer for next-generation sequencing data in the SAM/BAM format. <i>Bioinformatics</i> , <b>2011</b> , 27, 865-6	7.2	82
1735	Hunger artists: yeast adapted to carbon limitation show trade-offs under carbon sufficiency. <b>2011</b> , 7, e1002202		92
1734	Homozygosity mapping and exome sequencing reveal GATAD1 mutation in autosomal recessive dilated cardiomyopathy. <b>2011</b> , 4, 585-94		55
1733	Molecular investigations of a locally acquired case of melioidosis in Southern AZ, USA. <b>2011</b> , 5, e1347		18
1732	HiTEC: accurate error correction in high-throughput sequencing data. <i>Bioinformatics</i> , <b>2011</b> , 27, 295-302	7.2	93
1731	Sensitive and fast mapping of di-base encoded reads. <i>Bioinformatics</i> , <b>2011</b> , 27, 1915-21	7.2	16
1730	Metabolic reconstruction for metagenomic data and its application to the human microbiome. <b>2012</b> , 8, e1002358		730
1729	The quest for rare variants: pooled multiplexed next generation sequencing in plants. <b>2012</b> , 3, 133		13
1728	The expression of embryonic liver development genes in hepatitis C induced cirrhosis and hepatocellular carcinoma. <b>2012</b> , 4, 945-68		13
1727	Faster-X evolution of gene expression in <i>Drosophila</i> . <b>2012</b> , 8, e1003013		63
1726	A new isolation with migration model along complete genomes infers very different divergence processes among closely related great ape species. <b>2012</b> , 8, e1003125		83
1725	Multiple mutations in heterogeneous miltefosine-resistant <i>Leishmania</i> major population as determined by whole genome sequencing. <b>2012</b> , 6, e1512		71
1724	Deep sequencing of <i>Porphyromonas gingivalis</i> and comparative transcriptome analysis of a LuxS mutant. <b>2012</b> , 2, 79		21
1723	Bpipe: a tool for running and managing bioinformatics pipelines. <i>Bioinformatics</i> , <b>2012</b> , 28, 1525-6	7.2	111

1722	BRCA1 and BRCA2 mutations correlate with TP53 abnormalities and presence of immune cell infiltrates in ovarian high-grade serous carcinoma. <b>2012</b> , 25, 740-50		113
1721	Correcting for cancer genome size and tumour cell content enables better estimation of copy number alterations from next-generation sequence data. <i>Bioinformatics</i> , <b>2012</b> , 28, 40-7	7.2	143
1720	Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. <i>Bioinformatics</i> , <b>2012</b> , 28, 3232-9	7.2	108
1719	Application of serial analysis of gene expression to the study of the gene expression profile of <i>Leishmania infantum</i> chagasi promastigote. <b>2012</b> , 2012, 673458		1
1718	Context-dependent dual role of SKI8 homologs in mRNA synthesis and turnover. <b>2012</b> , 8, e1002652		24
1717	Accurate estimation of short read mapping quality for next-generation genome sequencing. <i>Bioinformatics</i> , <b>2012</b> , 28, i349-i355	7.2	22
1716	H4K20me1 contributes to downregulation of X-linked genes for <i>C. elegans</i> dosage compensation. <b>2012</b> , 8, e1002933		60
1715	A low-pathogenic avian influenza H6N1 outbreak in a turkey flock in France: a comprehensive case report. <b>2012</b> , 41, 569-77		13
1714	Generation of <i>Leishmania</i> hybrids by whole genomic DNA transformation. <b>2012</b> , 6, e1817		8
1713	Role of Fig1, a component of the low-affinity calcium uptake system, in growth and sexual development of filamentous fungi. <b>2012</b> , 11, 978-88		33
1712	Detecting genomic indel variants with exact breakpoints in single- and paired-end sequencing data using SplazerS. <i>Bioinformatics</i> , <b>2012</b> , 28, 619-27	7.2	84
1711	Rapid de novo evolution of X chromosome dosage compensation in <i>Silene latifolia</i> , a plant with young sex chromosomes. <b>2012</b> , 10, e1001308		117
1710	Confidence-based somatic mutation evaluation and prioritization. <b>2012</b> , 8, e1002714		26
1709	Chapter 6: Structural variation and medical genomics. <b>2012</b> , 8, e1002821		24
1708	Parallel mapping and simultaneous sequencing reveals deletions in BCAN and FAM83H associated with discrete inherited disorders in a domestic dog breed. <b>2012</b> , 8, e1002462		58
1707	Accurate prediction of inducible transcription factor binding intensities in vivo. <b>2012</b> , 8, e1002610		43
1706	A comparison of brain gene expression levels in domesticated and wild animals. <b>2012</b> , 8, e1002962		91
1705	Insights from genomics into bacterial pathogen populations. <b>2012</b> , 8, e1002874		66

1704	Primary and secondary siRNAs in geminivirus-induced gene silencing. <b>2012</b> , 8, e1002941		113
1703	The <i>Paramecium</i> germline genome provides a niche for intragenic parasitic DNA: evolutionary dynamics of internal eliminated sequences. <b>2012</b> , 8, e1002984		113
1702	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. <b>2012</b> , 8, e1002704		43
1701	Exome sequencing identifies rare deleterious mutations in DNA repair genes FANCC and BLM as potential breast cancer susceptibility alleles. <b>2012</b> , 8, e1002894		144
1700	The many landscapes of recombination in <i>Drosophila melanogaster</i> . <b>2012</b> , 8, e1002905		315
1699	A likelihood-based framework for variant calling and de novo mutation detection in families. <b>2012</b> , 8, e1002944		60
1698	Whole genome sequencing of field isolates provides robust characterization of genetic diversity in <i>Plasmodium vivax</i> . <b>2012</b> , 6, e1811		52
1697	Molecular changes in <i>Opisthorchis viverrini</i> (Southeast Asian liver fluke) during the transition from the juvenile to the adult stage. <b>2012</b> , 6, e1916		18
1696	Population genomics of the <i>Wolbachia</i> endosymbiont in <i>Drosophila melanogaster</i> . <b>2012</b> , 8, e1003129		135
1695	Evidence for widespread positive and purifying selection across the European rabbit ( <i>Oryctolagus cuniculus</i> ) genome. <b>2012</b> , 29, 1837-49		57
1694	Widespread site-dependent buffering of human regulatory polymorphism. <b>2012</b> , 8, e1002599		53
1693	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. <i>Bioinformatics</i> , <b>2012</b> , 28, 479-86	7.2	20
1692	NARWHAL, a primary analysis pipeline for NGS data. <i>Bioinformatics</i> , <b>2012</b> , 28, 284-5	7.2	37
1691	Bioinformatics for the Human Microbiome Project. <b>2012</b> , 8, e1002779		54
1690	The contribution of RNA decay quantitative trait loci to inter-individual variation in steady-state gene expression levels. <b>2012</b> , 8, e1003000		80
1689	Recessive mutations in SPTBN2 implicate $\beta$ III spectrin in both cognitive and motor development. <b>2012</b> , 8, e1003074		74
1688	SNP Discovery through Next-Generation Sequencing and Its Applications. <b>2012</b> , 2012, 831460		170
1687	Controls of nucleosome positioning in the human genome. <b>2012</b> , 8, e1003036		196

1686	Snakemake--a scalable bioinformatics workflow engine. <i>Bioinformatics</i> , <b>2012</b> , 28, 2520-2	7.2	1115
1685	Genome-wide analysis reveals distinct patterns of epigenetic features in long non-coding RNA loci. <b>2012</b> , 40, 10018-31		110
1684	Genomic variation and its impact on gene expression in <i>Drosophila melanogaster</i> . <b>2012</b> , 8, e1003055		85
1683	Tools for mapping high-throughput sequencing data. <i>Bioinformatics</i> , <b>2012</b> , 28, 3169-77	7.2	211
1682	A dominantly acting murine allele of <i>Mcm4</i> causes chromosomal abnormalities and promotes tumorigenesis. <b>2012</b> , 8, e1003034		28
1681	Whole genome sequences of three <i>Treponema pallidum</i> ssp. <i>pertenue</i> strains: yaws and syphilis treponemes differ in less than 0.2% of the genome sequence. <b>2012</b> , 6, e1471		86
1680	Identification of novel imidazo[1,2-a]pyridine inhibitors targeting <i>M. tuberculosis</i> QcrB. <b>2012</b> , 7, e52951		135
1679	Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection. <b>2012</b> , 8, e1002789		85
1678	Discovery of variants unmasked by hemizygous deletions. <b>2012</b> , 20, 748-53		17
1677	Efficient SNP-sensitive alignment and database-assisted SNP calling for low coverage samples. <b>2012</b> ,		
1676	A generic framework for efficient and effective subsequence retrieval. <b>2012</b> , 5, 1579-1590		6
1675	Massive genomic data processing and deep analysis. <b>2012</b> , 5, 1906-1909		5
1674	FusionAnalyser: a new graphical, event-driven tool for fusion rearrangements discovery. <b>2012</b> , 40, e123		28
1673	Exome sequencing identified a missense mutation of <i>EPS8L3</i> in Marie Unna hereditary hypotrichosis. <b>2012</b> , 49, 727-30		15
1672	The cytonuclear dimension of allopolyploid evolution: an example from cotton using <i>rubisco</i> . <b>2012</b> , 29, 3023-36		25
1671	Purifying selection, sequence composition, and context-specific indel mutations shape intraspecific variation in a bacterial endosymbiont. <b>2012</b> , 4, 44-51		11
1670	Whole exome sequencing to identify a novel gene ( <i>caveolin-1</i> ) associated with human pulmonary arterial hypertension. <b>2012</b> , 5, 336-43		268
1669	Analysis of human accelerated DNA regions using archaic hominin genomes. <b>2012</b> , 7, e32877		32

1668	Novel microcephalic primordial dwarfism disorder associated with variants in the centrosomal protein ninein. <b>2012</b> , 97, E2140-51	49
1667	Rate and molecular spectrum of spontaneous mutations in the bacterium <i>Escherichia coli</i> as determined by whole-genome sequencing. <b>2012</b> , 109, E2774-83	418
1666	Thymidine kinase 2 mutations in autosomal recessive progressive external ophthalmoplegia with multiple mitochondrial DNA deletions. <b>2012</b> , 21, 66-75	81
1665	Coxsackievirus B3 mutator strains are attenuated in vivo. <b>2012</b> , 109, E2294-303	105
1664	Reduced infectivity of adenovirus type 5 particles and degradation of entering viral genomes associated with incomplete processing of the preterminal protein. <b>2012</b> , 86, 13554-65	8
1663	Interaction of nucleolin with ribosomal RNA genes and its role in RNA polymerase I transcription. <b>2012</b> , 40, 9441-54	90
1662	Evidence for population-specific positive selection on immune genes of <i>Anopheles gambiae</i> . <b>2012</b> , 2, 1505-19	16
1661	Using a priori knowledge to align sequencing reads to their exact genomic position. <b>2012</b> , 40, e125	4
1660	Joint genotyping on the fly: identifying variation among a sequenced panel of inbred lines. <b>2012</b> , 22, 966-74	18
1659	Genomic impacts of chromosomal inversions in parapatric <i>Drosophila</i> species. <b>2012</b> , 367, 422-9	92
1658	Heterozygous TBK1 mutations impair TLR3 immunity and underlie herpes simplex encephalitis of childhood. <b>2012</b> , 209, 1567-82	196
1657	Detection of microRNAs in color space. <i>Bioinformatics</i> , <b>2012</b> , 28, 318-23	7.2 57
1656	Alignment-free population genomics: an efficient estimator of sequence diversity. <b>2012</b> , 2, 883-9	4
1655	Structure, diversity, and mobility of the <i>Salmonella</i> pathogenicity island 7 family of integrative and conjugative elements within Enterobacteriaceae. <b>2012</b> , 194, 1494-504	41
1654	Exploiting the mutanome for tumor vaccination. <b>2012</b> , 72, 1081-91	556
1653	Whole-Genome Sequencing of <i>Sordaria macrospora</i> Mutants Identifies Developmental Genes. <b>2012</b> , 2, 261-70	70
1652	Navigating the tip of the genomic iceberg: Next-generation sequencing for plant systematics. <b>2012</b> , 99, 349-64	386
1651	Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species. <b>2012</b> , 7, e37135	1857

1650	SCALCE: boosting sequence compression algorithms using locally consistent encoding. <i>Bioinformatics</i> , <b>2012</b> , 28, 3051-7	7.2	89
1649	Research resource: whole transcriptome RNA sequencing detects multiple 1 $\alpha$ ,25-dihydroxyvitamin D(3)-sensitive metabolic pathways in developing zebrafish. <b>2012</b> , 26, 1630-42		33
1648	TREAT: a bioinformatics tool for variant annotations and visualizations in targeted and exome sequencing data. <i>Bioinformatics</i> , <b>2012</b> , 28, 277-8	7.2	50
1647	Genotypic and phenotypic evaluation of the evolution of high-level daptomycin nonsusceptibility in vancomycin-resistant <i>Enterococcus faecium</i> . <b>2012</b> , 56, 6051-3		49
1646	Hobbes: optimized gram-based methods for efficient read alignment. <b>2012</b> , 40, e41		40
1645	CONTRA: copy number analysis for targeted resequencing. <i>Bioinformatics</i> , <b>2012</b> , 28, 1307-13	7.2	236
1644	Complete genome sequence of <i>Brucella suis</i> VBI22, isolated from bovine milk. <b>2012</b> , 194, 910		9
1643	Hybridization-based reconstruction of small non-coding RNA transcripts from deep sequencing data. <b>2012</b> , 40, 7633-43		8
1642	YOABS: yet other aligner of biological sequences--an efficient linearly scaling nucleotide aligner. <i>Bioinformatics</i> , <b>2012</b> , 28, 1070-7	7.2	10
1641	Accurate identification of A-to-I RNA editing in human by transcriptome sequencing. <b>2012</b> , 22, 142-50		246
1640	Histone H3K4 demethylation is negatively regulated by histone H3 acetylation in <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 109, 18505-10		41
1639	Fidelity of capture-enrichment for mtDNA genome sequencing: influence of NUMTs. <b>2012</b> , 40, e137		80
1638	Molecular spectrum of somaclonal variation in regenerated rice revealed by whole-genome sequencing. <b>2012</b> , 53, 256-64		77
1637	High efficiency recombineering in lactic acid bacteria. <b>2012</b> , 40, e76		147
1636	Bioinformatic approaches for functional annotation and pathway inference in metagenomics data. <b>2012</b> , 13, 696-710		60
1635	Pooled DNA resequencing of 68 myocardial infarction candidate genes in French Canadians. <b>2012</b> , 5, 547-54		9
1634	Hereditary myopathy with early respiratory failure associated with a mutation in A-band titin. <b>2012</b> , 135, 1682-94		80
1633	After the bottleneck: Genome-wide diversification of the <i>Mycobacterium tuberculosis</i> complex by mutation, recombination, and natural selection. <b>2012</b> , 22, 721-34		115

1632	Disruption of RAB40AL function leads to Martin--Probst syndrome, a rare X-linked multisystem neurodevelopmental human disorder. <b>2012</b> , 49, 332-40	13
1631	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. <b>2012</b> , 22, 1995-2007	181
1630	Rsx is a metatherian RNA with Xist-like properties in X-chromosome inactivation. <b>2012</b> , 487, 254-8	111
1629	HuR's post-transcriptional regulation of Death Receptor 5 in pancreatic cancer cells. <b>2012</b> , 13, 946-55	35
1628	Calling amplified haplotypes in next generation tumor sequence data. <b>2012</b> , 22, 362-74	8
1627	Whole genome sequencing of matched primary and metastatic acral melanomas. <b>2012</b> , 22, 196-207	126
1626	Bactobolin resistance is conferred by mutations in the L2 ribosomal protein. <b>2012</b> , 3,	32
1625	Experimental and Computational Challenges from Array-Based to Sequence-Based ChIP Techniques. <b>2012</b> , 7, 447-453	2
1624	Double indexing overcomes inaccuracies in multiplex sequencing on the Illumina platform. <b>2012</b> , 40, e3	681
1623	Challenges and approaches for distributed workflow-driven analysis of large-scale biological data. <b>2012</b> ,	17
1622	Long read alignment based on maximal exact match seeds. <i>Bioinformatics</i> , <b>2012</b> , 28, i318-i324	7.2 62
1621	Newly identified genetic variations in common Escherichia coli MG1655 stock cultures. <b>2012</b> , 194, 303-6	47
1620	Human-specific CpG "beacons" identify loci associated with human-specific traits and disease. <b>2012</b> , 7, 1188-99	30
1619	Global transcriptome response to ionic liquid by a tropical rain forest soil bacterium, <i>Enterobacter lignolyticus</i> . <b>2012</b> , 109, E2173-82	81
1618	A de Bruijn graph approach to the quantification of closely-related genomes in a microbial community. <b>2012</b> , 19, 814-25	11
1617	A genome sequence resource for the aye-aye ( <i>Daubentonia madagascariensis</i> ), a nocturnal lemur from Madagascar. <b>2012</b> , 4, 126-35	48
1616	Genome sequence and assembly of <i>Bos indicus</i> . <b>2012</b> , 103, 342-8	72
1615	FANSe: an accurate algorithm for quantitative mapping of large scale sequencing reads. <b>2012</b> , 40, e83	33

1614	Evaluation of GPU-based Seed Generation for Computational Genomics Using Burrows-Wheeler Transform. <b>2012,</b>	6
1613	RNA-seq analysis of the <i>C. briggsae</i> transcriptome. <b>2012, 22, 1567-80</b>	20
1612	Incorporating RNA-seq data into the zebrafish Ensembl genebuild. <b>2012, 22, 2067-78</b>	72
1611	Integrative analyses for omics data: a Bayesian mixture model to assess the concordance of ChIP-chip and ChIP-seq measurements. <b>2012, 75, 461-70</b>	12
1610	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. <b>2012, 22, 602-10</b>	97
1609	A new strategy to reduce allelic bias in RNA-Seq readmapping. <b>2012, 40, e127</b>	74
1608	Analysis of context-dependent errors for illumina sequencing. <b>2012, 10, 1241005</b>	13
1607	MeQA: a pipeline for MeDIP-seq data quality assessment and analysis. <i>Bioinformatics</i> , <b>2012, 28, 587-8</b>	7.2 24
1606	Summarizing and correcting the GC content bias in high-throughput sequencing. <b>2012, 40, e72</b>	524
1605	Mutations in the colony stimulating factor 1 receptor (CSF1R) gene cause hereditary diffuse leukoencephalopathy with spheroids. <b>2011, 44, 200-5</b>	344
1604	A functional haplotype of UBE2L3 confers risk for systemic lupus erythematosus. <b>2012, 13, 380-7</b>	45
1603	miRDeep2 accurately identifies known and hundreds of novel microRNA genes in seven animal clades. <b>2012, 40, 37-52</b>	1631
1602	Analysis of the <i>Saccharomyces cerevisiae</i> pan-genome reveals a pool of copy number variants distributed in diverse yeast strains from differing industrial environments. <b>2012, 22, 908-24</b>	160
1601	Computational analysis of protein-DNA interactions from ChIP-seq data. <b>2012, 786, 263-73</b>	9
1600	De novo gain-of-function KCNT1 channel mutations cause malignant migrating partial seizures of infancy. <b>2012, 44, 1255-9</b>	344
1599	<i>Plasmodium cynomolgi</i> genome sequences provide insight into <i>Plasmodium vivax</i> and the monkey malaria clade. <b>2012, 44, 1051-5</b>	133
1598	Mutations at a single codon in Mad homology 2 domain of SMAD4 cause Myhre syndrome. <b>2011, 44, 85-8</b>	107
1597	Chimeric piggyBac transposases for genomic targeting in human cells. <b>2012, 40, 6978-91</b>	42

1596	Integration of Hi-C and ChIP-seq data reveals distinct types of chromatin linkages. <b>2012</b> , 40, 7690-704		76
1595	A bit-parallel dynamic programming algorithm suitable for DNA sequence alignment. <b>2012</b> , 10, 1250002		4
1594	Two novel <i>CCDC88C</i> mutations confirm the role of DAPLE in autosomal recessive congenital hydrocephalus. <b>2012</b> , 49, 708-12		44
1593	Mutational dynamics of aroid chloroplast genomes. <b>2012</b> , 4, 1316-23		75
1592	Activity-dependent A-to-I RNA editing in rat cortical neurons. <b>2012</b> , 192, 281-7		30
1591	Detecting selective sweeps from pooled next-generation sequencing samples. <b>2012</b> , 29, 2177-86		64
1590	PRISM: pair-read informed split-read mapping for base-pair level detection of insertion, deletion and structural variants. <i>Bioinformatics</i> , <b>2012</b> , 28, 2576-83	7.2	90
1589	Beijing sublineages of <i>Mycobacterium tuberculosis</i> differ in pathogenicity in the guinea pig. <b>2012</b> , 19, 1227-37		76
1588	Serial translocation by means of circular intermediates underlies colour sidedness in cattle. <b>2012</b> , 482, 81-4		98
1587	Genome sequence of <i>Vibrio</i> sp. strain EJY3, an agarolytic marine bacterium metabolizing 3,6-anhydro-L-galactose as a sole carbon source. <b>2012</b> , 194, 2773-4		20
1586	Exome sequencing identifies <i>MXRA5</i> as a novel cancer gene frequently mutated in non-small cell lung carcinoma from Chinese patients. <b>2012</b> , 33, 1797-805		44
1585	A forward genetic screen identifies eukaryotic translation initiation factor 3, subunit H (eIF3h), as an enhancer of variegation in the mouse. <b>2012</b> , 2, 1393-6		17
1584	PARALLEL ALGORITHMS FOR MAPPING SHORT DEGENERATE AND WEIGHTED DNA SEQUENCES TO A REFERENCE GENOME. <b>2012</b> , 23, 249-259		1
1583	Deep sequencing identifies viral and wasp genes with potential roles in replication of <i>Microplitis demolitor</i> Bracovirus. <b>2012</b> , 86, 3293-306		64
1582	E2F7 represses a network of oscillating cell cycle genes to control S-phase progression. <b>2012</b> , 40, 3511-23		73
1581	Whole-exome sequencing of human pancreatic cancers and characterization of genomic instability caused by <i>MLH1</i> haploinsufficiency and complete deficiency. <b>2012</b> , 22, 208-19		95
1580	Exome sequencing and complex disease: practical aspects of rare variant association studies. <b>2012</b> , 21, R1-9		104
1579	Libgapmis: An ultrafast library for short-read single-gap alignment. <b>2012</b> ,		2

1578	A collection of INDEL markers for map-based cloning in seven Arabidopsis accessions. <b>2012</b> , 63, 2491-501	57
1577	Read-mapping using personalized diploid reference genome for RNA sequencing data reduced bias for detecting allele-specific expression. <b>2012</b> , 2012, 718-724	11
1576	Complete genome sequence of Streptococcus thermophilus strain MN-ZLW-002. <b>2012</b> , 194, 4428-9	31
1575	Exome analysis of a family with pleiotropic congenital heart disease. <b>2012</b> , 5, 175-82	56
1574	A novel GUCY2D mutation, V933A, causes central areolar choroidal dystrophy. <b>2012</b> , 53, 4748-53	16
1573	Efficient de novo assembly of large genomes using compressed data structures. <b>2012</b> , 22, 549-56	501
1572	Translating exome sequencing from research to clinical diagnostics. <b>2011</b> , 50, 1161-8	10
1571	Exome sequencing and digital PCR analyses reveal novel mutated genes related to the metastasis of pancreatic ductal adenocarcinoma. <b>2012</b> , 13, 871-9	32
1570	Diagnosis of fanconi anemia: mutation analysis by next-generation sequencing. <b>2012</b> , 2012, 132856	33
1569	Whole-Genome Profiling of a Novel Mutagenesis Technique Using Proofreading-Deficient DNA Polymerase $\beta$ <b>2012</b> , 2012, 860797	22
1568	Genome-wide analysis of p63 binding sites identifies AP-2 factors as co-regulators of epidermal differentiation. <b>2012</b> , 40, 7190-206	72
1567	WHAM. <b>2012</b> , 37, 1-39	11
1566	Conserved molecular interactions within the HBO1 acetyltransferase complexes regulate cell proliferation. <b>2012</b> , 32, 689-703	59
1565	Temporal patterns of nucleotide misincorporations and DNA fragmentation in ancient DNA. <b>2012</b> , 7, e34131	325
1564	Genome analysis of the domestic dog (Korean Jindo) by massively parallel sequencing. <b>2012</b> , 19, 275-87	9
1563	Indel-tolerant read mapping with trinucleotide frequencies using cache-oblivious kd-trees. <i>Bioinformatics</i> , <b>2012</b> , 28, i325-i332	7.2 3
1562	De novo detection of copy number variation by co-assembly. <i>Bioinformatics</i> , <b>2012</b> , 28, 3195-202	7.2 57
1561	Genome sequence of Shigella flexneri serotype 5a strain M90T Sm. <b>2012</b> , 194, 3022	33

1560	Complete genome sequence of the thermophilic bacterium <i>Geobacillus thermoleovorans</i> CCB_US3_UF5. <b>2012</b> , 194, 1239		26
1559	High-performance data management for genome sequencing centers using Globus Online: A case study. <b>2012</b> ,		1
1558	Novel insight into the non-coding repertoire through deep sequencing analysis. <b>2012</b> , 40, e86		16
1557	Identification of high-confidence somatic mutations in whole genome sequence of formalin-fixed breast cancer specimens. <b>2012</b> , 40, e107		69
1556	Prospects and limitations of full-text index structures in genome analysis. <b>2012</b> , 40, 6993-7015		23
1555	A family-based probabilistic method for capturing de novo mutations from high-throughput short-read sequencing data. <b>2012</b> , 11,		12
1554	Variant repeats are interspersed throughout the telomeres and recruit nuclear receptors in ALT cells. <b>2012</b> , 199, 893-906		94
1553	Acclimation of the Global Transcriptome of the Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002 to Nutrient Limitations and Different Nitrogen Sources. <b>2012</b> , 3, 145		101
1552	Genome analyses of an aggressive and invasive lineage of the Irish potato famine pathogen. <b>2012</b> , 8, e1002940		260
1551	CLEVER: clique-enumerating variant finder. <i>Bioinformatics</i> , <b>2012</b> , 28, 2875-82	7.2	79
1550	Gene discovery using mutagen-induced polymorphisms and deep sequencing: application to plant disease resistance. <b>2012</b> , 192, 139-46		35
1549	Ontogeny of the maize shoot apical meristem. <b>2012</b> , 24, 3219-34		60
1548	Laboratory evolution of new lactate transporter genes in a <i>jen1</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. <b>2012</b> , 12, 359-374		33
1547	Allelic ratios and the mutational landscape reveal biologically significant heterozygous SNVs. <b>2012</b> , 190, 1225-33		10
1546	High-resolution genome-wide analysis of irradiated (UV and $\gamma$ rays) diploid yeast cells reveals a high frequency of genomic loss of heterozygosity (LOH) events. <b>2012</b> , 190, 1267-84		56
1545	APJ1 and GRE3 homologs work in concert to allow growth in xylose in a natural <i>Saccharomyces sensu stricto</i> hybrid yeast. <b>2012</b> , 191, 621-32		20
1544	DETECTING HIGHLY DIFFERENTIATED COPY-NUMBER VARIANTS FROM POOLED POPULATION SEQUENCING. <b>2012</b> ,		1
1543	Transcriptome and comparative gene expression analysis of <i>Sogatella furcifera</i> (Horv�th) in response to southern rice black-streaked dwarf virus. <b>2012</b> , 7, e36238		71

1542	Whole genome sequences of a male and female supercentenarian, ages greater than 114 years. <b>2011</b> , 2, 90	40
1541	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. <b>2012</b> , 5, 27-33	
1540	Efficient indexing algorithms for approximate pattern matching in text. <b>2012</b> ,	3
1539	Lyndon fountains and the Burrows-Wheeler transform. <b>2012</b> ,	
1538	Whole transcriptome sequencing reveals recurrent NOTCH1 mutations in mantle cell lymphoma. <b>2012</b> , 119, 1963-71	264
1537	GATA2 zinc finger 1 mutations associated with biallelic CEBPA mutations define a unique genetic entity of acute myeloid leukemia. <b>2012</b> , 120, 395-403	120
1536	ChIP-Seq Analytics: Methods and Systems to Improve ChIP-Seq Peak Identification. <b>2012</b> , 87-112	1
1535	Predicting MicroRNAs. <b>2012</b> , 189-207	1
1534	Dynamic population changes in Mycobacterium tuberculosis during acquisition and fixation of drug resistance in patients. <b>2012</b> , 206, 1724-33	137
1533	Oral spirochetes implicated in dental diseases are widespread in normal human subjects and carry extremely diverse integron gene cassettes. <b>2012</b> , 78, 5288-96	16
1532	Euolsan: a cloud computing-based framework facilitating high throughput sequencing analyses. <i>Bioinformatics</i> , <b>2012</b> , 28, 1542-3	7.2 104
1531	Differential relationship of DNA replication timing to different forms of human mutation and variation. <b>2012</b> , 91, 1033-40	172
1530	Exome sequencing followed by large-scale genotyping suggests a limited role for moderately rare risk factors of strong effect in schizophrenia. <b>2012</b> , 91, 303-12	73
1529	Histone H2A.Z inheritance during the cell cycle and its impact on promoter organization and dynamics. <b>2012</b> , 19, 1076-83	82
1528	Novel mutation in VCP gene causes atypical amyotrophic lateral sclerosis. <b>2012</b> , 79, 2201-8	43
1527	Coverage-based consensus calling (CbCC) of short sequence reads and comparison of CbCC results to identify SNPs in chickpea ( <i>Cicer arietinum</i> ; Fabaceae), a crop species without a reference genome. <b>2012</b> , 99, 186-92	29
1526	NMNAT1 mutations cause Leber congenital amaurosis. <b>2012</b> , 44, 1040-5	143
1525	Mutations in NMNAT1 cause Leber congenital amaurosis and identify a new disease pathway for retinal degeneration. <b>2012</b> , 44, 1035-9	147

1524	Missense mutations in the sodium-gated potassium channel gene KCNT1 cause severe autosomal dominant nocturnal frontal lobe epilepsy. <b>2012</b> , 44, 1188-90	253
1523	Next-generation sequencing-based transcriptomic and proteomic analysis of the common reed, <i>Phragmites australis</i> (Poaceae), reveals genes involved in invasiveness and rhizome specificity. <b>2012</b> , 99, 232-47	39
1522	A genome-wide association study of venous thromboembolism identifies risk variants in chromosomes 1q24.2 and 9q. <b>2012</b> , 10, 1521-31	116
1521	Immunodeficiency, autoinflammation and amylopectinosis in humans with inherited HOIL-1 and LUBAC deficiency. <b>2012</b> , 13, 1178-86	320
1520	High-throughput detection of actionable genomic alterations in clinical tumor samples by targeted, massively parallel sequencing. <b>2012</b> , 2, 82-93	425
1519	Transcriptome analysis using RNA-Seq. <b>2013</b> , 923, 221-39	32
1518	Conserved DNA methylation patterns in healthy blood cells and extensive changes in leukemia measured by a new quantitative technique. <b>2012</b> , 7, 1368-78	55
1517	The simple fool's guide to population genomics via RNA-Seq: an introduction to high-throughput sequencing data analysis. <b>2012</b> , 12, 1058-67	191
1516	High-throughput sequencing analysis of the chromosome 7q32 deletion reveals IRF5 as a potential tumour suppressor in splenic marginal-zone lymphoma. <b>2012</b> , 158, 712-26	34
1515	Multiple clonal MLL fusions in a patient receiving CHOP-based chemotherapy. <b>2012</b> , 159, 50-7	3
1514	Genome-wide patterns of latitudinal differentiation among populations of <i>Drosophila melanogaster</i> from North America. <b>2012</b> , 21, 4748-69	192
1513	Genomic dissection of small RNAs in wild rice ( <i>Oryza rufipogon</i> ): lessons for rice domestication. <b>2012</b> , 196, 914-925	29
1512	Field monitoring of avian influenza viruses: whole-genome sequencing and tracking of neuraminidase evolution using 454 pyrosequencing. <b>2012</b> , 50, 2881-7	18
1511	How deep is deep enough for RNA-Seq profiling of bacterial transcriptomes?. <b>2012</b> , 13, 734	162
1510	5' end-centered expression profiling using cap-analysis gene expression and next-generation sequencing. <b>2012</b> , 7, 542-61	182
1509	Sporadic autism exomes reveal a highly interconnected protein network of de novo mutations. <b>2012</b> , 485, 246-50	1587
1508	Comparing Bowtie and BWA to Align Short Reads from a RNA-Seq Experiment. <b>2012</b> , 197-207	1
1507	Mutations in DDHD2, encoding an intracellular phospholipase A(1), cause a recessive form of complex hereditary spastic paraplegia. <b>2012</b> , 91, 1073-81	128

1506	CUSHAW: a CUDA compatible short read aligner to large genomes based on the Burrows-Wheeler transform. <i>Bioinformatics</i> , <b>2012</b> , 28, 1830-7	7.2	111
1505	SortMeRNA: fast and accurate filtering of ribosomal RNAs in metatranscriptomic data. <i>Bioinformatics</i> , <b>2012</b> , 28, 3211-7	7.2	1172
1504	Molecular diagnosis of infantile mitochondrial disease with targeted next-generation sequencing. <b>2012</b> , 4, 118ra10		362
1503	CD45-deficient severe combined immunodeficiency caused by uniparental disomy. <b>2012</b> , 109, 10456-61		33
1502	Artemis: an integrated platform for visualization and analysis of high-throughput sequence-based experimental data. <i>Bioinformatics</i> , <b>2012</b> , 28, 464-9	7.2	665
1501	Estimate of the spontaneous mutation rate in <i>Chlamydomonas reinhardtii</i> . <b>2012</b> , 192, 1447-54		84
1500	Using Exome Sequencing to Reveal Mutations in TREM2 Presenting as a Frontotemporal Dementia-like Syndrome Without Bone Involvement. <b>2012</b> , 1		5
1499	Genome-wide detection of single-nucleotide and copy-number variations of a single human cell. <b>2012</b> , 338, 1622-6		756
1498	Whole-genome sequencing in autism identifies hot spots for de novo germline mutation. <b>2012</b> , 151, 1431-42		392
1497	Genome sequences of wild and domestic bactrian camels. <b>2012</b> , 3, 1202		105
1496	Direct, genome-wide assessment of DNA mutations in single cells. <b>2012</b> , 40, 2032-40		55
1495	A beginners guide to SNP calling from high-throughput DNA-sequencing data. <b>2012</b> , 131, 1541-54		76
1494	Bioinformatics tools and databases for analysis of next-generation sequence data. <b>2012</b> , 11, 12-24		59
1493	Analysis of RNA Transcripts by High-Throughput RNA Sequencing. <b>2012</b> , 544-554		1
1492	Identification of molecular pathway aberrations in uterine serous carcinoma by genome-wide analyses. <b>2012</b> , 104, 1503-13		191
1491	<i>Shigella sonnei</i> genome sequencing and phylogenetic analysis indicate recent global dissemination from Europe. <b>2012</b> , 44, 1056-9		203
1490	Improved gap size estimation for scaffolding algorithms. <i>Bioinformatics</i> , <b>2012</b> , 28, 2215-22	7.2	14
1489	Accurate identification of human Alu and non-Alu RNA editing sites. <b>2012</b> , 9, 579-81		266

1488	Guthrie card methylomics identifies temporally stable epialleles that are present at birth in humans. <b>2012</b> , 22, 2138-45	53
1487	Independent domestication of Asian rice followed by gene flow from japonica to indica. <b>2012</b> , 29, 1471-9	51
1486	Poxviruses deploy genomic accordions to adapt rapidly against host antiviral defenses. <b>2012</b> , 150, 831-41	180
1485	High-performance short sequence alignment with GPU acceleration. <b>2012</b> , 30, 385-399	10
1484	Dissecting the regulatory architecture of gene expression QTLs. <b>2012</b> , 13, R7	151
1483	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. <b>2012</b> , 13, R82	41
1482	Chromatin accessibility reveals insights into androgen receptor activation and transcriptional specificity. <b>2012</b> , 13, R88	53
1481	Cytosine methylation and hydroxymethylation mark DNA for elimination in <i>Oxytricha trifallax</i> . <b>2012</b> , 13, R99	38
1480	All Your Base: a fast and accurate probabilistic approach to base calling. <b>2012</b> , 13, R13	24
1479	An integrative probabilistic model for identification of structural variation in sequencing data. <b>2012</b> , 13, R22	101
1478	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. <b>2012</b> , 13, 26	122
1477	Genetic basis of transcriptome differences between the founder strains of the rat HXB/BXH recombinant inbred panel. <b>2012</b> , 13, r31	28
1476	A new approach for detecting low-level mutations in next-generation sequence data. <b>2012</b> , 13, R34	74
1475	Genomic diversity of the human intestinal parasite <i>Entamoeba histolytica</i> . <b>2012</b> , 13, R38	31
1474	The multiplicity of divergence mechanisms in a single evolving population. <b>2012</b> , 13, R41	45
1473	The genomic landscape shaped by selection on transposable elements across 18 mouse strains. <b>2012</b> , 13, R45	124
1472	Toward almost closed genomes with GapFiller. <b>2012</b> , 13, R56	740
1471	Genome-wide distribution of 5-formylcytosine in embryonic stem cells is associated with transcription and depends on thymine DNA glycosylase. <b>2012</b> , 13, R69	188

1470	Impaired intrinsic immunity to HSV-1 in human iPSC-derived TLR3-deficient CNS cells. <b>2012</b> , 491, 769-73	240
1469	Elucidation of bacterial genome complexity using next-generation sequencing. <b>2012</b> , 17, 887-899	2
1468	Analysis of the bread wheat genome using whole-genome shotgun sequencing. <b>2012</b> , 491, 705-10	821
1467	Analysing and interpreting DNA methylation data. <b>2012</b> , 13, 705-19	398
1466	Complex reorganization and predominant non-homologous repair following chromosomal breakage in karyotypically balanced germline rearrangements and transgenic integration. <b>2012</b> , 44, 390-7, S1	190
1465	CSF1R mutations identified in three families with autosomal dominantly inherited leukoencephalopathy. <b>2012</b> , 159B, 951-7	29
1464	Association of two independent functional risk haplotypes in TNIP1 with systemic lupus erythematosus. <b>2012</b> , 64, 3695-705	64
1463	Evaluation and optimisation of preparative semi-automated electrophoresis systems for Illumina library preparation. <b>2012</b> , 33, 3521-8	19
1462	High throughput sequencing approaches to mutation discovery in the mouse. <b>2012</b> , 23, 499-513	4
1461	Samaritan myopathy, an ultimately benign congenital myopathy, is caused by a RYR1 mutation. <b>2012</b> , 124, 575-81	16
1460	Molecular convergence of the parasitic plant species <i>Cuscuta reflexa</i> and <i>Phelipanche aegyptiaca</i> . <b>2012</b> , 236, 557-66	3
1459	Glucosylated hydroxymethyluracil, DNA base J, prevents transcriptional readthrough in <i>Leishmania</i> . <b>2012</b> , 150, 909-21	109
1458	The importance of being regular: <i>Caenorhabditis elegans</i> and <i>Pristionchus pacificus</i> defecation mutants are hypersusceptible to bacterial pathogens. <b>2012</b> , 42, 747-53	27
1457	Improved variation calling via an iterative backbone remapping and local assembly method for bacterial genomes. <b>2012</b> , 100, 271-6	5
1456	Bioinformatic analysis of barcoded cDNA libraries for small RNA profiling by next-generation sequencing. <b>2012</b> , 58, 171-87	49
1455	Genome-wide identification of miRNA targets by PAR-CLIP. <b>2012</b> , 58, 94-105	79
1454	Argonaute CLIP--a method to identify in vivo targets of miRNAs. <b>2012</b> , 58, 106-12	28
1453	Late onset of symptoms in an atypical patient with the <i>cbJ</i> inborn error of vitamin B12 metabolism: diagnosis and novel mutation revealed by exome sequencing. <b>2012</b> , 107, 664-8	31

1452	Single nucleotide analysis of cytosine methylation by whole-genome shotgun bisulfite sequencing. <b>2012</b> , Chapter 21, Unit21.23	22
1451	Recurrent R-spondin fusions in colon cancer. <b>2012</b> , 488, 660-4	711
1450	Adaptation to a new environment allows cooperators to purge cheaters stochastically. <b>2012</b> , 109, 19079-86	84
1449	SNVerGUI: a desktop tool for variant analysis of next-generation sequencing data. <b>2012</b> , 49, 753-5	11
1448	Next-generation sequencing for simultaneous determination of human papillomavirus load, subtype, and associated genomic copy number changes in tumors. <b>2012</b> , 14, 104-11	42
1447	Biclustering of linear patterns in gene expression data. <b>2012</b> , 19, 619-31	4
1446	Exploring single-sample SNP and INDEL calling with whole-genome de novo assembly. <i>Bioinformatics</i> , <b>2012</b> , 28, 1838-44	7.2 242
1445	Loss-of-function mutations in IGSF1 cause an X-linked syndrome of central hypothyroidism and testicular enlargement. <b>2012</b> , 44, 1375-81	147
1444	Recessive mutations in MCM4/PRKDC cause a novel syndrome involving a primary immunodeficiency and a disorder of DNA repair. <b>2012</b> , 49, 242-5	48
1443	Identification of novel NRF2-regulated genes by ChIP-Seq: influence on retinoid X receptor alpha. <b>2012</b> , 40, 7416-29	377
1442	Fast CPU-based DNA exact sequence aligner. <b>2012</b> ,	1
1441	Mapping reads on a genomic sequence: an algorithmic overview and a practical comparative analysis. <b>2012</b> , 19, 796-813	58
1440	A message passing algorithm for reference-guided sequence assembly from high-throughput sequencing data. <b>2012</b> ,	1
1439	Using GPUs for the exact alignment of short-read genetic sequences by means of the Burrows-Wheeler transform. <b>2012</b> , 9, 1245-56	16
1438	Identifying core features of adaptive metabolic mechanisms for chronic heat stress attenuation contributing to systems robustness. <b>2012</b> , 4, 480-93	37
1437	Perturbation of FlhI interferes with <i>Proteus mirabilis</i> swarmer cell gene expression and differentiation. <b>2012</b> , 194, 437-47	39
1436	Hardware Acceleration of Short Read Mapping. <b>2012</b> ,	65
1435	An empirical Bayes mixture model for SNP detection in pooled sequencing data. <i>Bioinformatics</i> , <b>2012</b> , 28, 2569-75	7.2 6

1434	Identification of a chronic obstructive pulmonary disease genetic determinant that regulates HHIP. <b>2012</b> , 21, 1325-35	118
1433	BASplice: Bi-direction alignment for detecting splice junctions. <b>2012</b> ,	
1432	An FPGA aligner for short read mapping. <b>2012</b> ,	5
1431	A comparative study of methods for detecting small somatic variants in disease-normal paired next generation sequencing data. <b>2012</b> ,	1
1430	Large-scale discovery of enhancers from human heart tissue. <b>2011</b> , 44, 89-93	197
1429	Multiscale integration of -omic, imaging, and clinical data in biomedical informatics. <b>2012</b> , 5, 74-87	35
1428	Deep sequencing reveals persistence of intra- and inter-host genetic diversity in natural and greenhouse populations of zucchini yellow mosaic virus. <b>2012</b> , 93, 1831-1840	29
1427	Application of next-generation sequencing technologies in virology. <b>2012</b> , 93, 1853-1868	189
1426	A physical, genetic and functional sequence assembly of the barley genome. <b>2012</b> , 491, 711-6	1124
1425	Deletion of a conserved regulatory element required for Hmx1 expression in craniofacial mesenchyme in the dumbo rat: a newly identified cause of congenital ear malformation. <b>2012</b> , 5, 812-22	20
1424	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. <b>2012</b> , 44, 760-4	671
1423	Cloud Based Short Read Mapping Service. <b>2012</b> ,	3
1422	Whole-exome sequencing identifies mutations in the nucleoside transporter gene SLC29A3 in dysosteosclerosis, a form of osteopetrosis. <b>2012</b> , 21, 4904-9	63
1421	Heterozygous missense mutations in SMARCA2 cause Nicolaides-Baraitser syndrome. <b>2012</b> , 44, 445-9, S1	170
1420	Mutations in UVSSA cause UV-sensitive syndrome and impair RNA polymerase II processing in transcription-coupled nucleotide-excision repair. <b>2012</b> , 44, 586-92	123
1419	De novo mutations in the actin genes ACTB and ACTG1 cause Baraitser-Winter syndrome. <b>2012</b> , 44, 440-4, S1-2	181
1418	Nucleomorph genome sequence of the cryptophyte alga <i>Chroomonas mesostigmatica</i> CCMP1168 reveals lineage-specific gene loss and genome complexity. <b>2012</b> , 4, 1162-75	44
1417	Mutation of the parkinsonism gene ATP13A2 causes neuronal ceroid-lipofuscinosis. <b>2012</b> , 21, 2646-50	196

1416	RBFOX1 regulates both splicing and transcriptional networks in human neuronal development. <b>2012</b> , 21, 4171-86	140
1415	Mutations in DNMT1 cause autosomal dominant cerebellar ataxia, deafness and narcolepsy. <b>2012</b> , 21, 2205-10	190
1414	SQ109 targets MmpL3, a membrane transporter of trehalose monomycolate involved in mycolic acid donation to the cell wall core of Mycobacterium tuberculosis. <b>2012</b> , 56, 1797-809	351
1413	Predicting cell-type-specific gene expression from regions of open chromatin. <b>2012</b> , 22, 1711-22	175
1412	Ultrafast clustering algorithms for metagenomic sequence analysis. <b>2012</b> , 13, 656-68	294
1411	Identification of natural and artificial DNA substrates for light-activated LOV-HTH transcription factor EL222. <b>2012</b> , 51, 10024-34	42
1410	Analysis of a Streptococcus pyogenes puerperal sepsis cluster by use of whole-genome sequencing. <b>2012</b> , 50, 2224-8	47
1409	Retinal transcriptome profiling by directional next-generation sequencing using 100 ng of total RNA. <b>2012</b> , 884, 319-34	22
1408	Exome sequencing reveals an unexpected genetic cause of disease: NOTCH3 mutation in a Turkish family with Alzheimer's disease. <b>2012</b> , 33, 1008.e17-23	72
1407	De novo gene disruptions in children on the autistic spectrum. <b>2012</b> , 74, 285-99	1052
1406	Background mutations in parental cells account for most of the genetic heterogeneity of induced pluripotent stem cells. <b>2012</b> , 10, 570-82	165
1405	A computational index derived from whole-genome copy number analysis is a novel tool for prognosis in early stage lung squamous cell carcinoma. <b>2012</b> , 99, 18-24	13
1404	Detection, annotation and visualization of alternative splicing from RNA-Seq data with SplicingViewer. <b>2012</b> , 99, 178-82	29
1403	Identification of a mutation in LARS as a novel cause of infantile hepatopathy. <b>2012</b> , 106, 351-8	64
1402	Next-generation sequencing reveals phylogeographic structure and a species tree for recent bird divergences. <b>2012</b> , 62, 397-406	69
1401	Rate of de novo mutations and the importance of father's age to disease risk. <b>2012</b> , 488, 471-5	1417
1400	A direct characterization of human mutation based on microsatellites. <b>2012</b> , 44, 1161-5	219
1399	Counting absolute numbers of molecules using unique molecular identifiers. <b>2011</b> , 9, 72-4	637

1398	Methods and software in NGS for TE analysis. <b>2012</b> , 859, 105-14		6
1397	A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals. <b>2012</b> , 47, 810-22		299
1396	Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. <b>2012</b> , 488, 106-10		552
1395	Molecular and developmental contributions to divergent pigment patterns in marine and freshwater sticklebacks. <b>2012</b> , 14, 351-62		24
1394	Next-generation sequencing data interpretation: enhancing reproducibility and accessibility. <b>2012</b> , 13, 667-72		215
1393	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. <i>Bioinformatics</i> , <b>2012</b> , 28, 878-9	7.2	158
1392	Melanoma genome sequencing reveals frequent PREX2 mutations. <b>2012</b> , 485, 502-6		555
1391	Fast and accurate read alignment for resequencing. <i>Bioinformatics</i> , <b>2012</b> , 28, 2366-73	7.2	37
1390	Tracing the evolutionary history of the pandemic group A streptococcal M1T1 clone. <b>2012</b> , 26, 4675-84		41
1389	Accurate gene synthesis with tag-directed retrieval of sequence-verified DNA molecules. <b>2012</b> , 9, 913-5		48
1388	Exome sequencing identifies MVK mutations in disseminated superficial actinic porokeratosis. <b>2012</b> , 44, 1156-60		94
1387	Exome sequencing identifies a novel multiple sclerosis susceptibility variant in the TYK2 gene. <b>2012</b> , 79, 406-11		42
1386	Strain-dependent diversity in the <i>Pseudomonas aeruginosa</i> quorum-sensing regulon. <b>2012</b> , 109, E2823-31		81
1385	Transcriptomics using next generation sequencing technologies. <b>2012</b> , 917, 293-317		11
1384	Identification of somatic mutations in parathyroid tumors using whole-exome sequencing. <b>2012</b> , 97, E1774-81		112
1383	Comparing DNA Sequence Collections by Direct Comparison of Compressed Text Indexes. <b>2012</b> , 214-224		11
1382	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. <b>2012</b> , 44, 1006-14		887
1381	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. <b>2012</b> , 22, 2478-88		191

1380	Mutations in the neverland gene turned <i>Drosophila pachea</i> into an obligate specialist species. <b>2012</b> , 337, 1658-61	67
1379	Estimating the human mutation rate using autozygosity in a founder population. <b>2012</b> , 44, 1277-81	162
1378	Mapping single molecule sequencing reads using basic local alignment with successive refinement (BLASR): application and theory. <b>2012</b> , 13, 238	764
1377	From a single whole exome read to notions of clinical screening: primary ciliary dyskinesia and RSPH9 p.Lys268del in the Arabian Peninsula. <b>2012</b> , 76, 211-20	18
1376	Comparative transcriptome analysis of transporters, phytohormone and lipid metabolism pathways in response to arsenic stress in rice ( <i>Oryza sativa</i> ). <b>2012</b> , 195, 97-112	145
1375	Site-specific genome editing in <i>Plasmodium falciparum</i> using engineered zinc-finger nucleases. <b>2012</b> , 9, 993-8	126
1374	Intracontinental spread of human invasive <i>Salmonella</i> Typhimurium pathovariants in sub-Saharan Africa. <b>2012</b> , 44, 1215-21	279
1373	Mutations in the mechanotransduction protein PIEZO1 are associated with hereditary xerocytosis. <b>2012</b> , 120, 1908-15	273
1372	Paired-end sequencing of Fosmid libraries by Illumina. <b>2012</b> , 22, 2241-9	47
1371	RazerS 3: faster, fully sensitive read mapping. <i>Bioinformatics</i> , <b>2012</b> , 28, 2592-9	7.2 91
1370	Mutations in the TGF- $\beta$ repressor SKI cause Shprintzen-Goldberg syndrome with aortic aneurysm. <b>2012</b> , 44, 1249-54	199
1369	Exome sequencing of extreme phenotypes identifies DCTN4 as a modifier of chronic <i>Pseudomonas aeruginosa</i> infection in cystic fibrosis. <b>2012</b> , 44, 886-9	170
1368	Detection and quantification of alternative splicing variants using RNA-seq. <b>2012</b> , 883, 97-110	17
1367	Outer-membrane cytochrome-independent reduction of extracellular electron acceptors in <i>Shewanella oneidensis</i> . <b>2012</b> , 158, 2144-2157	32
1366	Using formaldehyde-assisted isolation of regulatory elements (FAIRE) to isolate active regulatory DNA. <b>2012</b> , 7, 256-67	230
1365	Spark: a navigational paradigm for genomic data exploration. <b>2012</b> , 22, 2262-9	26
1364	Differential expression--the next generation and beyond. <b>2012</b> , 11, 57-62	27
1363	The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. <b>2012</b> , 279, 4724-33	331

1362	Rainbow: an integrated tool for efficient clustering and assembling RAD-seq reads. <i>Bioinformatics</i> , <b>2012</b> , 28, 2732-7	7.2	78
1361	Spinal muscular atrophy associated with progressive myoclonic epilepsy is caused by mutations in <i>ASAH1</i> . <b>2012</b> , 91, 5-14		109
1360	Familial pityriasis rubra pilaris is caused by mutations in <i>CARD14</i> . <b>2012</b> , 91, 163-70		164
1359	A homozygous mutation in <i>KCTD7</i> links neuronal ceroid lipofuscinosis to the ubiquitin-proteasome system. <b>2012</b> , 91, 202-8		79
1358	Congenital asplenia in mice and humans with mutations in a Pbx/Nkx2-5/p15 module. <b>2012</b> , 22, 913-26		59
1357	Identification of transcriptome SNPs between <i>Xiphophorus</i> lines and species for assessing allele specific gene expression within F <sub>1</sub> interspecies hybrids. <b>2012</b> , 155, 102-8		31
1356	Genome sequencing and analysis of the Tasmanian devil and its transmissible cancer. <b>2012</b> , 148, 780-91		251
1355	Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. <b>2012</b> , 148, 59-71		600
1354	Personal omics profiling reveals dynamic molecular and medical phenotypes. <b>2012</b> , 148, 1293-307		921
1353	The GATA2 transcriptional network is requisite for RAS oncogene-driven non-small cell lung cancer. <b>2012</b> , 149, 642-55		216
1352	Sequencing chromosomal abnormalities reveals neurodevelopmental loci that confer risk across diagnostic boundaries. <b>2012</b> , 149, 525-37		441
1351	Genome-wide analysis of pre-mRNA 3' end processing reveals a decisive role of human cleavage factor I in the regulation of 3' UTR length. <b>2012</b> , 1, 753-63		247
1350	Severe ALG8-CDG (CDG-1h) associated with homozygosity for two novel missense mutations detected by exome sequencing of candidate genes. <b>2012</b> , 55, 196-202		12
1349	Extremely slow rate of evolution in the HOX cluster revealed by comparison between Tanzanian and Indonesian coelacanths. <b>2012</b> , 505, 324-32		8
1348	TWARIT: an extremely rapid and efficient approach for phylogenetic classification of metagenomic sequences. <b>2012</b> , 505, 259-65		12
1347	Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. <b>2012</b> , 109, E2382-90		243
1346	The population genomics of a fast evolver: high levels of diversity, functional constraint, and molecular adaptation in the tunicate <i>Ciona intestinalis</i> . <b>2012</b> , 4, 740-9		93
1345	Integrative genome analyses identify key somatic driver mutations of small-cell lung cancer. <b>2012</b> , 44, 1104-10		919

1344	Improving PacBio long read accuracy by short read alignment. <b>2012</b> , 7, e46679	229
1343	Genotype of a historic strain of <i>Mycobacterium tuberculosis</i> . <b>2012</b> , 109, 18511-6	76
1342	Prioritizing genetic variants for causality on the basis of preferential linkage disequilibrium. <b>2012</b> , 91, 422-34	17
1341	WDR35 mutation in siblings with Sensenbrenner syndrome: a ciliopathy with variable phenotype. <b>2012</b> , 158A, 2917-24	35
1340	Rare variants in TMEM132D in a case-control sample for panic disorder. <b>2012</b> , 159B, 896-907	21
1339	Error-correcting properties of the SOLiD Exact Call Chemistry. <b>2012</b> , 13, 145	9
1338	Oculus: faster sequence alignment by streaming read compression. <b>2012</b> , 13, 297	3
1337	High throughput whole rumen metagenome profiling using untargeted massively parallel sequencing. <b>2012</b> , 13, 53	55
1336	Genome-wide mRNA sequencing of a single canine cerebellar cortical degeneration case leads to the identification of a disease associated SPTBN2 mutation. <b>2012</b> , 13, 55	31
1335	Historically low mitochondrial DNA diversity in koalas ( <i>Phascolarctos cinereus</i> ). <b>2012</b> , 13, 92	21
1334	Quantitative genome re-sequencing defines multiple mutations conferring chloroquine resistance in rodent malaria. <b>2012</b> , 13, 106	24
1333	A genome-wide study of two-component signal transduction systems in eight newly sequenced mutans streptococci strains. <b>2012</b> , 13, 128	30
1332	A framework genetic map for <i>Miscanthus sinensis</i> from RNAseq-based markers shows recent tetraploidy. <b>2012</b> , 13, 142	75
1331	Improving the performance of true single molecule sequencing for ancient DNA. <b>2012</b> , 13, 177	32
1330	Improving ancient DNA read mapping against modern reference genomes. <b>2012</b> , 13, 178	178
1329	Exome sequencing generates high quality data in non-target regions. <b>2012</b> , 13, 194	95
1328	Whole genome sequencing analysis of <i>Plasmodium vivax</i> using whole genome capture. <b>2012</b> , 13, 262	34
1327	Elucidation of the molecular envenomation strategy of the cone snail <i>Conus geographus</i> through transcriptome sequencing of its venom duct. <b>2012</b> , 13, 284	74

1326	Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. <b>2012</b> , 13, 302	78
1325	Composition and organization of active centromere sequences in complex genomes. <b>2012</b> , 13, 324	19
1324	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. <b>2012</b> , 13, 34	50
1323	A tale of three next generation sequencing platforms: comparison of Ion Torrent, Pacific Biosciences and Illumina MiSeq sequencers. <b>2012</b> , 13, 341	1328
1322	Genome-wide SNP discovery in walnut with an AGSNP pipeline updated for SNP discovery in allogamous organisms. <b>2012</b> , 13, 354	34
1321	Optimizing de novo common wheat transcriptome assembly using short-read RNA-Seq data. <b>2012</b> , 13, 392	89
1320	Identification of common carp ( <i>Cyprinus carpio</i> ) microRNAs and microRNA-related SNPs. <b>2012</b> , 13, 413	47
1319	De novo sequence assembly and characterisation of a partial transcriptome for an evolutionarily distinct reptile, the tuatara ( <i>Sphenodon punctatus</i> ). <b>2012</b> , 13, 439	33
1318	Sequencing and analysis of a South Asian-Indian personal genome. <b>2012</b> , 13, 440	23
1317	NG6: Integrated next generation sequencing storage and processing environment. <b>2012</b> , 13, 462	48
1316	High depth, whole-genome sequencing of cholera isolates from Haiti and the Dominican Republic. <b>2012</b> , 13, 468	7
1315	Comparative genomic analysis of human infective <i>Trypanosoma cruzi</i> lineages with the bat-restricted subspecies <i>T. cruzi marinkellei</i> . <b>2012</b> , 13, 531	45
1314	De novo assembly of the pepper transcriptome ( <i>Capsicum annuum</i> ): a benchmark for in silico discovery of SNPs, SSRs and candidate genes. <b>2012</b> , 13, 571	93
1313	A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes. <b>2012</b> , 13, 583	64
1312	Sequencing of the needle transcriptome from Norway spruce ( <i>Picea abies</i> Karst L.) reveals lower substitution rates, but similar selective constraints in gymnosperms and angiosperms. <b>2012</b> , 13, 589	49
1311	Pre-capture multiplexing improves efficiency and cost-effectiveness of targeted genomic enrichment. <b>2012</b> , 13, 618	16
1310	Limitations and possibilities of low cell number ChIP-seq. <b>2012</b> , 13, 645	66
1309	Exon capture and bulk segregant analysis: rapid discovery of causative mutations using high-throughput sequencing. <b>2012</b> , 13, 649	13

1308	The effect of strand bias in Illumina short-read sequencing data. <b>2012</b> , 13, 666	85
1307	Genome wide SNP discovery in flax through next generation sequencing of reduced representation libraries. <b>2012</b> , 13, 684	53
1306	Targeted enrichment of the black cottonwood ( <i>Populus trichocarpa</i> ) gene space using sequence capture. <b>2012</b> , 13, 703	61
1305	Reference genome-independent assessment of mutation density using restriction enzyme-phased sequencing. <b>2012</b> , 13, 72	36
1304	Development of high-throughput SNP-based genotyping in <i>Acacia auriculiformis</i> x <i>A. mangium</i> hybrids using short-read transcriptome data. <b>2012</b> , 13, 726	11
1303	High-throughput sequencing of black pepper root transcriptome. <b>2012</b> , 12, 168	42
1302	<i>Scheffersomyces stipitis</i> : a comparative systems biology study with the Crabtree positive yeast <i>Saccharomyces cerevisiae</i> . <b>2012</b> , 11, 136	48
1301	De novo sequencing, assembly and analysis of the genome of the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D, a model for modern industrial biotechnology. <b>2012</b> , 11, 36	183
1300	Missense mutations in <i>ITPR1</i> cause autosomal dominant congenital nonprogressive spinocerebellar ataxia. <b>2012</b> , 7, 67	100
1299	Specific combination of compound heterozygous mutations in 17 $\beta$ -hydroxysteroid dehydrogenase type 4 ( <i>HSD17B4</i> ) defines a new subtype of D-bifunctional protein deficiency. <b>2012</b> , 7, 90	58
1298	Bio-samtools: Ruby bindings for SAMtools, a library for accessing BAM files containing high-throughput sequence alignments. <b>2012</b> , 7, 6	40
1297	A direct comparison of next generation sequencing enrichment methods using an aortopathy gene panel- clinical diagnostics perspective. <b>2012</b> , 5, 50	28
1296	How do alignment programs perform on sequencing data with varying qualities and from repetitive regions?. <b>2012</b> , 5, 6	28
1295	Efficient subtraction of insect rRNA prior to transcriptome analysis of <i>Wolbachia</i> - <i>Drosophila</i> lateral gene transfer. <b>2012</b> , 5, 230	26
1294	Genome sequencing and analysis of <i>Salmonella enterica</i> serovar Typhi strain CR0063 representing a carrier individual during an outbreak of typhoid fever in Kelantan, Malaysia. <b>2012</b> , 4, 20	7
1293	Strategies to identify long noncoding RNAs involved in gene regulation. <b>2012</b> , 2, 37	63
1292	Resources for methylome analysis suitable for gene knockout studies of potential epigenome modifiers. <b>2012</b> , 1, 3	35
1291	The GEM mapper: fast, accurate and versatile alignment by filtration. <b>2012</b> , 9, 1185-8	382

1290	A high-coverage genome sequence from an archaic Denisovan individual. <b>2012</b> , 338, 222-6	1276
1289	Comparative population genomics in <i>Collinsia</i> sister species reveals evidence for reduced effective population size, relaxed selection, and evolution of biased gene conversion with an ongoing mating system shift. <b>2013</b> , 67, 1263-78	32
1288	Clonal evolution of preleukemic hematopoietic stem cells precedes human acute myeloid leukemia. <b>2012</b> , 4, 149ra118	517
1287	The oyster genome reveals stress adaptation and complexity of shell formation. <b>2012</b> , 490, 49-54	1464
1286	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. <b>2011</b> , 44, 53-7	408
1285	DNA template strand sequencing of single-cells maps genomic rearrangements at high resolution. <b>2012</b> , 9, 1107-12	111
1284	Analysis of global transcriptional profiles of enterotoxigenic <i>Escherichia coli</i> isolate E24377A. <b>2012</b> , 80, 1232-42	38
1283	Fighting outbreaks with bacterial genomics: case review and workflow proposal. <b>2012</b> , 15, 341-51	10
1282	LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. <b>2012</b> , 40, 11189-201	666
1281	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. <b>2012</b> , 44, 1316-20	317
1280	Next-generation sequencing: impact of exome sequencing in characterizing Mendelian disorders. <b>2012</b> , 57, 621-32	155
1279	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. <b>2012</b> , 482, 226-31	1655
1278	De novo transcriptome assembly and SNP discovery in the wing polymorphic salt marsh beetle <i>Pogonus chalceus</i> (Coleoptera, Carabidae). <b>2012</b> , 7, e42605	48
1277	Exome sequencing of gastric adenocarcinoma identifies recurrent somatic mutations in cell adhesion and chromatin remodeling genes. <b>2012</b> , 44, 570-4	486
1276	Massively parallel sequencing approaches for characterization of structural variation. <b>2012</b> , 838, 369-84	38
1275	Autosomal dominant myofibrillar myopathy with arrhythmogenic right ventricular cardiomyopathy 7 is caused by a DES mutation. <b>2012</b> , 20, 984-5	44
1274	Prions are a common mechanism for phenotypic inheritance in wild yeasts. <b>2012</b> , 482, 363-8	308
1273	GEM: crystal-clear DNA alignment. <b>2012</b> , 9, 1159-61	1

1272	A randomized Numerical Aligner (rNA). <b>2012</b> , 78, 1868-1882	5
1271	Identification of mutations in the prostaglandin transporter gene SLCO2A1 and its phenotype-genotype correlation in Japanese patients with pachydermoperiostosis. <b>2012</b> , 68, 36-44	60
1270	A mutation in the 5'-UTR of IFITM5 creates an in-frame start codon and causes autosomal-dominant osteogenesis imperfecta type V with hyperplastic callus. <b>2012</b> , 91, 349-57	176
1269	Exome sequencing followed by large-scale genotyping fails to identify single rare variants of large effect in idiopathic generalized epilepsy. <b>2012</b> , 91, 293-302	88
1268	Using ERDS to infer copy-number variants in high-coverage genomes. <b>2012</b> , 91, 408-21	91
1267	RBPJ mutations identified in two families affected by Adams-Oliver syndrome. <b>2012</b> , 91, 391-5	92
1266	Exome sequencing and functional validation in zebrafish identify GTDC2 mutations as a cause of Walker-Warburg syndrome. <b>2012</b> , 91, 541-7	144
1265	The TRK-fused gene is mutated in hereditary motor and sensory neuropathy with proximal dominant involvement. <b>2012</b> , 91, 320-9	76
1264	Burden of rare sarcomere gene variants in the Framingham and Jackson Heart Study cohorts. <b>2012</b> , 91, 513-9	88
1263	Discovery and statistical genotyping of copy-number variation from whole-exome sequencing depth. <b>2012</b> , 91, 597-607	391
1262	Recessive HYDIN mutations cause primary ciliary dyskinesia without randomization of left-right body asymmetry. <b>2012</b> , 91, 672-84	212
1261	Imputation of exome sequence variants into population- based samples and blood-cell-trait-associated loci in African Americans: NHLBI GO Exome Sequencing Project. <b>2012</b> , 91, 794-808	103
1260	Mutations in OTOGL, encoding the inner ear protein otogelin-like, cause moderate sensorineural hearing loss. <b>2012</b> , 91, 872-82	88
1259	Mutation in TECPR2 reveals a role for autophagy in hereditary spastic paraparesis. <b>2012</b> , 91, 1065-72	120
1258	Deficiency for the ubiquitin ligase UBE3B in a blepharophimosis-ptosis-intellectual-disability syndrome. <b>2012</b> , 91, 998-1010	62
1257	Disruption of a large intergenic noncoding RNA in subjects with neurodevelopmental disabilities. <b>2012</b> , 91, 1128-34	53
1256	A new mutational mechanism for hypertrophic cardiomyopathy. <b>2012</b> , 507, 165-9	9
1255	Comparison of genome diversity of Brucella spp. field isolates using Universal Bio-signature Detection Array and whole genome sequencing reveals limitations of current diagnostic methods. <b>2012</b> , 509, 142-8	6

1254	Effects of short-term exposure to 2,3,7,8-tetrachlorodibenzo-p-dioxin on microRNA expression in zebrafish embryos. <b>2012</b> , 264, 262-73	34
1253	miRSeqNovel: an R based workflow for analyzing miRNA sequencing data. <b>2012</b> , 26, 208-11	14
1252	Identifying ChIP-seq enrichment using MACS. <b>2012</b> , 7, 1728-40	857
1251	Deep sequencing of small RNAs in tomato for virus and viroid identification and strain differentiation. <b>2012</b> , 7, e37127	97
1250	Allele identification in assembled genomic sequence datasets. <b>2012</b> , 888, 197-211	1
1249	A survey of copy-number variation detection tools based on high-throughput sequencing data. <b>2012</b> , Chapter 7, Unit7.19	18
1248	Using cloud computing infrastructure with CloudBioLinux, CloudMan, and Galaxy. <b>2012</b> , Chapter 11, Unit11.9	21
1247	Genome-wide genetic changes during modern breeding of maize. <b>2012</b> , 44, 812-5	256
1246	Mutations in ABCD4 cause a new inborn error of vitamin B12 metabolism. <b>2012</b> , 44, 1152-5	157
1245	Case study: enrichment of ancient mitochondrial DNA by hybridization capture. <b>2012</b> , 840, 189-95	8
1244	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. <b>2012</b> , 44, 1111-6	712
1243	Investigating natural variation in Drosophila courtship song by the evolve and resequence approach. <b>2012</b> , 191, 633-42	89
1242	Discovery of common variants associated with low TSH levels and thyroid cancer risk. <b>2012</b> , 44, 319-22	167
1241	Next generation sequencing in clinical medicine: Challenges and lessons for pathology and biomedical informatics. <b>2012</b> , 3, 40	106
1240	Definition of Promotome  Transcriptome Architecture Using CAGEscan. <b>2012</b> , 47-61	
1239	Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. <b>2012</b> , 30, 777-82	1045
1238	Library preparation and data analysis packages for rapid genome sequencing. <b>2012</b> , 944, 1-22	16
1237	Next-generation sequencing-based genome-wide mutation analysis of L-lysine-producing <i>Corynebacterium glutamicum</i> ATCC 21300 strain. <b>2012</b> , 50, 860-3	11

1236	Xenopus Protocols. <b>2012,</b>	5
1235	Genomic islands of divergence in hybridizing Heliconius butterflies identified by large-scale targeted sequencing. <b>2012,</b> 367, 343-53	255
1234	Dominant missense mutations in ABCC9 cause Cantú syndrome. <b>2012,</b> 44, 793-6	139
1233	Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. <b>2012,</b> 481, 389-93	1011
1232	Insights into the bovine rumen plasmidome. <b>2012,</b> 109, 5452-7	96
1231	Molecular tracing of the emergence, adaptation, and transmission of hospital-associated methicillin-resistant Staphylococcus aureus. <b>2012,</b> 109, 9107-12	138
1230	Chromosome-scale selective sweeps shape Caenorhabditis elegans genomic diversity. <b>2012,</b> 44, 285-90	251
1229	Mice lacking a Myc enhancer that includes human SNP rs6983267 are resistant to intestinal tumors. <b>2012,</b> 338, 1360-3	171
1228	Detecting and annotating genetic variations using the HugeSeq pipeline. <b>2012,</b> 30, 226-9	90
1227	A Torrent of data: mapping chromatin organization using 5C and high-throughput sequencing. <b>2012,</b> 513, 113-41	20
1226	Gene Regulatory Networks. <b>2012,</b>	2
1225	Environmental DNA-encoded antibiotics fasamycins A and B inhibit FabF in type II fatty acid biosynthesis. <b>2012,</b> 134, 2981-7	69
1224	A comparative analysis of tissue gene expression data from high-throughput studies. <b>2012,</b> 57, 2920-2927	3
1223	Efficient alignment of next generation sequencing data using MapReduce on the cloud. <b>2012,</b>	
1222	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in Saccharomyces cerevisiae. <b>2012,</b> 40, 10084-97	222
1221	Hadoop Applications in Bioinformatics. <b>2012,</b>	1
1220	Reduced representation methods for subgenomic enrichment and next-generation sequencing. <b>2011,</b> 772, 85-103	19
1219	Omics Era in Stem Cell Research: Data Integration of Multi-regulatory Layers. <b>2012,</b> 119-137	

1218	A Model for Programming Data-Intensive Applications on FPGAs: A Genomics Case Study. <b>2012,</b>	2
1217	Molecular dynamics simulations of Ago silencing complexes reveal a large repertoire of admissible 'seed-less' targets. <b>2012, 2, 569</b>	54
1216	Genome-wide mapping of nucleosomes in yeast using paired-end sequencing. <b>2012, 513, 145-68</b>	27
1215	. <b>2012, 29, 89-97</b>	1
1214	MDAsim: A multiple displacement amplification simulator. <b>2012,</b>	4
1213	High throughput sequencing methods for microbiome profiling: application to food animal systems. <b>2012, 13, 40-53</b>	19
1212	De novo mutations in ATP1A3 cause alternating hemiplegia of childhood. <b>2012, 44, 1030-4</b>	280
1211	Compressive genomics. <b>2012, 30, 627-30</b>	83
1210	The malaria parasite <i>Plasmodium vivax</i> exhibits greater genetic diversity than <i>Plasmodium falciparum</i> . <b>2012, 44, 1046-50</b>	196
1209	Next generation sequence analysis and computational genomics using graphical pipeline workflows. <b>2012, 3, 545-75</b>	41
1208	Applied Computational Genomics. <b>2012,</b>	
1207	Multithreaded FPGA acceleration of DNA sequence mapping. <b>2012,</b>	15
1206	Effects of premature termination codon polymorphisms in the <i>Drosophila pseudoobscura</i> subclade. <b>2012, 75, 141-50</b>	5
1205	ChopSticks: High-resolution analysis of homozygous deletions by exploiting concordant read pairs. <b>2012, 13, 279</b>	1
1204	Evolution of cichlid vision via trans-regulatory divergence. <b>2012, 12, 251</b>	24
1203	Protein evolution in two co-occurring types of <i>Symbiodinium</i> : an exploration into the genetic basis of thermal tolerance in <i>Symbiodinium</i> clade D. <b>2012, 12, 217</b>	83
1202	Steps to ensure accuracy in genotype and SNP calling from Illumina sequencing data. <b>2012, 13 Suppl 8, S8</b>	80
1201	BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data. <b>2012, 13 Suppl 8, S9</b>	4

1200	snpTree--a web-server to identify and construct SNP trees from whole genome sequence data. <b>2012</b> , 13 Suppl 7, S6	76
1199	Effective normalization for copy number variation detection from whole genome sequencing. <b>2012</b> , 13 Suppl 6, S16	12
1198	A catalogue of putative unique transcripts from Douglas-fir ( <i>Pseudotsuga menziesii</i> ) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. <b>2012</b> , 13, 673	29
1197	Genomic resources for a model in adaptation and speciation research: characterization of the <i>Poecilia mexicana</i> transcriptome. <b>2012</b> , 13, 652	22
1196	Genetic structure of community acquired methicillin-resistant <i>Staphylococcus aureus</i> USA300. <b>2012</b> , 13, 508	18
1195	Improving mapping and SNP-calling performance in multiplexed targeted next-generation sequencing. <b>2012</b> , 13, 417	6
1194	Characterization of the transcriptome of an ecologically important avian species, the Vinous-throated Parrotbill <i>Paradoxornis webbianus bulomachus</i> (Paradoxornithidae; Aves). <b>2012</b> , 13, 149	12
1193	High yield derivation of enriched glutamatergic neurons from suspension-cultured mouse ESCs for neurotoxicology research. <b>2012</b> , 13, 127	24
1192	Optimizing hybrid assembly of next-generation sequence data from <i>Enterococcus faecium</i> : a microbe with highly divergent genome. <b>2012</b> , 6 Suppl 3, S21	13
1191	Retinal Development. <b>2012</b> ,	3
1190	Genome drafts of four phytoplasma strains of the ribosomal group 16SrIII. <b>2012</b> , 158, 2805-2814	44
1189	Pattern matching through Chaos Game Representation: bridging numerical and discrete data structures for biological sequence analysis. <b>2012</b> , 7, 10	29
1188	cnvHiTSeq: integrative models for high-resolution copy number variation detection and genotyping using population sequencing data. <b>2012</b> , 13, R120	24
1187	Microevolutionary analysis of <i>Clostridium difficile</i> genomes to investigate transmission. <b>2012</b> , 13, R118	151
1186	Derivation of HLA types from shotgun sequence datasets. <b>2012</b> , 4, 95	118
1185	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. <b>2012</b> , 4, 86	31
1184	AdapterRemoval: easy cleaning of next-generation sequencing reads. <b>2012</b> , 5, 337	388
1183	A mild form of SLC29A3 disorder: a frameshift deletion leads to the paradoxical translation of an otherwise noncoding mRNA splice variant. <b>2012</b> , 7, e29708	37

1182	Mutational signatures of de-differentiation in functional non-coding regions of melanoma genomes. <b>2012</b> , 8, e1002871	10
1181	CAPRG: sequence assembling pipeline for next generation sequencing of non-model organisms. <b>2012</b> , 7, e30370	4
1180	Genome features of "Dark-fly", a <i>Drosophila</i> line reared long-term in a dark environment. <b>2012</b> , 7, e33288	24
1179	Methylcap-seq reveals novel DNA methylation markers for the diagnosis and recurrence prediction of bladder cancer in a Chinese population. <b>2012</b> , 7, e35175	44
1178	Rare variants in ischemic stroke: an exome pilot study. <b>2012</b> , 7, e35591	30
1177	GHOSTM: a GPU-accelerated homology search tool for metagenomics. <b>2012</b> , 7, e36060	13
1176	Concordant signaling pathways produced by pesticide exposure in mice correspond to pathways identified in human Parkinson's disease. <b>2012</b> , 7, e36191	45
1175	Optimizing read mapping to reference genomes to determine composition and species prevalence in microbial communities. <b>2012</b> , 7, e36427	42
1174	Biased gene fractionation and dominant gene expression among the subgenomes of <i>Brassica rapa</i> . <b>2012</b> , 7, e36442	195
1173	Paired tumor and normal whole genome sequencing of metastatic olfactory neuroblastoma. <b>2012</b> , 7, e37029	29
1172	Response of sunflower ( <i>Helianthus annuus</i> L.) leaf surface defenses to exogenous methyl jasmonate. <b>2012</b> , 7, e37191	13
1171	Artificial polyploidy improves bacterial single cell genome recovery. <b>2012</b> , 7, e37387	22
1170	Transcriptome profiling of citrus fruit response to huanglongbing disease. <b>2012</b> , 7, e38039	124
1169	Comparative geno-plasticity analysis of <i>Mycoplasma bovis</i> HB0801 (Chinese isolate). <b>2012</b> , 7, e38239	55
1168	Consensus rules in variant detection from next-generation sequencing data. <b>2012</b> , 7, e38470	27
1167	A novel SND1-BRAF fusion confers resistance to c-Met inhibitor PF-04217903 in GTL16 cells through [corrected] MAPK activation. <b>2012</b> , 7, e39653	38
1166	Large-scale transcriptome analysis of retroelements in the migratory locust, <i>Locusta migratoria</i> . <b>2012</b> , 7, e40532	23
1165	Twist1 transcriptional targets in the developing atrio-ventricular canal of the mouse. <b>2012</b> , 7, e40815	8

1164	Discovery of genes related to insecticide resistance in <i>Bactrocera dorsalis</i> by functional genomic analysis of a de novo assembled transcriptome. <b>2012</b> , 7, e40950	37
1163	Genometa--a fast and accurate classifier for short metagenomic shotgun reads. <b>2012</b> , 7, e41224	29
1162	An integrated pipeline for de novo assembly of microbial genomes. <b>2012</b> , 7, e42304	330
1161	SAP--a sequence mapping and analyzing program for long sequence reads alignment and accurate variants discovery. <b>2012</b> , 7, e42887	0
1160	A deletion in the bovine FANCI gene compromises fertility by causing fetal death and brachyspina. <b>2012</b> , 7, e43085	64
1159	Genome-wide characterization of pancreatic adenocarcinoma patients using next generation sequencing. <b>2012</b> , 7, e43192	59
1158	Inherited MST1 deficiency underlies susceptibility to EV-HPV infections. <b>2012</b> , 7, e44010	101
1157	Pan-genomic analysis provides insights into the genomic variation and evolution of <i>Salmonella</i> Paratyphi A. <b>2012</b> , 7, e45346	23
1156	Choosing the best plant for the job: a cost-effective assay to prescreen ancient plant remains destined for shotgun sequencing. <b>2012</b> , 7, e45644	15
1155	A genome-wide identification analysis of small regulatory RNAs in <i>Mycobacterium tuberculosis</i> by RNA-Seq and conservation analysis. <b>2012</b> , 7, e32723	39
1154	MOCAT: a metagenomics assembly and gene prediction toolkit. <b>2012</b> , 7, e47656	143
1153	COPS: a sensitive and accurate tool for detecting somatic Copy Number Alterations using short-read sequence data from paired samples. <b>2012</b> , 7, e47812	12
1152	A streamlined method for detecting structural variants in cancer genomes by short read paired-end sequencing. <b>2012</b> , 7, e48314	19
1151	Library preparation and multiplex capture for massive parallel sequencing applications made efficient and easy. <b>2012</b> , 7, e48616	22
1150	Novel SNP Discovery in African Buffalo, <i>Syncerus caffer</i> , using high-throughput Sequencing. <b>2012</b> , 7, e48792	14
1149	Exome analysis of two limb-girdle muscular dystrophy families: mutations identified and challenges encountered. <b>2012</b> , 7, e48864	18
1148	A 3.7 Mb deletion encompassing ZEB2 causes a novel polled and multisystemic syndrome in the progeny of a somatic mosaic bull. <b>2012</b> , 7, e49084	18
1147	Exploring Pandora's box: potential and pitfalls of low coverage genome surveys for evolutionary biology. <b>2012</b> , 7, e49202	27

1146	Two different high throughput sequencing approaches identify thousands of de novo genomic markers for the genetically depleted Bornean elephant. <b>2012</b> , 7, e49533	18
1145	Whole genome sequence typing to investigate the Apophysomyces outbreak following a tornado in Joplin, Missouri, 2011. <b>2012</b> , 7, e49989	54
1144	Reevaluating assembly evaluations with feature response curves: GAGE and assemblathons. <b>2012</b> , 7, e52210	69
1143	FastUniq: a fast de novo duplicates removal tool for paired short reads. <b>2012</b> , 7, e52249	291
1142	Genotyping of fanconi anemia patients by whole exome sequencing: advantages and challenges. <b>2012</b> , 7, e52648	30
1141	A model-based clustering method for genomic structural variant prediction and genotyping using paired-end sequencing data. <b>2012</b> , 7, e52881	14
1140	Molecular epidemiologic investigation of an anthrax outbreak among heroin users, Europe. <b>2012</b> , 18, 1307-13	58
1139	Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for back fat thickness in Italian Large White pigs using a selective genotyping approach. <b>2012</b> , 90, 2450-64	59
1138	The Population Genomics of Sunflowers and Genomic Determinants of Protein Evolution Revealed by RNAseq. <b>2012</b> , 1, 575-96	30
1137	Case study of sequence capture enrichment technology: identification of variation underpinning developmental syndromes in an amniote model. <b>2012</b> , 3, 233-47	6
1136	The human transcriptome: an unfinished story. <b>2012</b> , 3, 344-60	80
1135	Genome-wide sequencing reveals two major sub-lineages in the genetically monomorphic pathogen xanthomonas campestris pathovar musacearum. <b>2012</b> , 3, 361-77	37
1134	Using Drosophila melanogaster as a Model for Genotoxic Chemical Mutational Studies with a New Program, SnpSift. <b>2012</b> , 3, 35	459
1133	Assessing the accuracy and power of population genetic inference from low-pass next-generation sequencing data. <b>2012</b> , 3, 66	37
1132	Bioinformatics of Cancer ncRNA in High Throughput Sequencing: Present State and Challenges. <b>2012</b> , 3, 287	7
1131	Deep Sequence Analysis of Non-Small Cell Lung Cancer: Integrated Analysis of Gene Expression, Alternative Splicing, and Single Nucleotide Variations in Lung Adenocarcinomas with and without Oncogenic KRAS Mutations. <b>2012</b> , 2, 12	38
1130	Recombination modulates how selection affects linked sites in Drosophila. <b>2012</b> ,	1
1129	Massively parallel sequencing of the mouse exome to accurately identify rare, induced mutations: an immediate source for thousands of new mouse models. <b>2012</b> , 2, 120061	81

1128	Preface. <b>2012</b> , xxv-xxvi	1
1127	TWIST represses estrogen receptor-alpha expression by recruiting the NuRD protein complex in breast cancer cells. <b>2012</b> , 8, 522-32	46
1126	Discovery of a large set of SNP and SSR genetic markers by high-throughput sequencing of pepper ( <i>Capsicum annuum</i> ). <b>2012</b> , 11, 2295-300	36
1125	BarraCUDA - a fast short read sequence aligner using graphics processing units. <b>2012</b> , 5, 27	86
1124	Concurrent CIC mutations, IDH mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <b>2012</b> , 226, 7-16	226
1123	Elevated coding mutation rate during the reprogramming of human somatic cells into induced pluripotent stem cells. <b>2012</b> , 30, 435-40	140
1122	Variations in the exome of the LNCaP prostate cancer cell line. <b>2012</b> , 72, 1317-27	18
1121	Performance comparison of whole-genome sequencing platforms. <b>2011</b> , 30, 78-82	241
1120	Cost-effective, high-throughput DNA sequencing libraries for multiplexed target capture. <b>2012</b> , 22, 939-46	637
1119	Fast gapped-read alignment with Bowtie 2. <b>2012</b> , 9, 357-9	24735
1118	Disentangling the relationship between sex-biased gene expression and X-linkage. <b>2012</b> , 22, 1255-65	91
1117	Mutational processes molding the genomes of 21 breast cancers. <b>2012</b> , 149, 979-93	1279
1116	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <b>2011</b> , 44, 47-52	752
1115	Whole-exome sequencing of pediatric acute lymphoblastic leukemia. <b>2012</b> , 26, 1602-7	27
1114	Evolution and functional impact of rare coding variation from deep sequencing of human exomes. <b>2012</b> , 337, 64-9	1280
1113	miRNA data analysis: next-gen sequencing. <b>2012</b> , 822, 273-88	25
1112	O-GlcNAc regulates pluripotency and reprogramming by directly acting on core components of the pluripotency network. <b>2012</b> , 11, 62-74	221
1111	rNA: a fast and accurate short reads numerical aligner. <i>Bioinformatics</i> , <b>2012</b> , 28, 123-4	7.2 32

1110	Complete genome sequence of the thermophilic bacterium <i>Thermus</i> sp. strain CCB_US3_UF1. <b>2012</b> , 194, 1240	9
1109	Detection of redundant fusion transcripts as biomarkers or disease-specific therapeutic targets in breast cancer. <b>2012</b> , 72, 1921-8	71
1108	Genomic Structural Variants. <b>2012</b> ,	1
1107	DeepBase: annotation and discovery of microRNAs and other noncoding RNAs from deep-sequencing data. <b>2012</b> , 822, 233-48	19
1106	RNA-SeQC: RNA-seq metrics for quality control and process optimization. <i>Bioinformatics</i> , <b>2012</b> , 28, 1530-22	538
1105	Sensitive mapping of recombination hotspots using sequencing-based detection of ssDNA. <b>2012</b> , 22, 957-65	78
1104	De novo mutations revealed by whole-exome sequencing are strongly associated with autism. <b>2012</b> , 485, 237-41	1470
1103	Mutation mapping and identification by whole-genome sequencing. <b>2012</b> , 22, 1541-8	101
1102	R-loop formation is a distinctive characteristic of unmethylated human CpG island promoters. <b>2012</b> , 45, 814-25	492
1101	Apoptotic cleavage of DNA in human lymphocyte chromatin shows high sequence specificity. <b>2012</b> , 30, 211-6	4
1100	The origin and evolution of mutations in acute myeloid leukemia. <b>2012</b> , 150, 264-78	1143
1099	Optimal enzymes for amplifying sequencing libraries. <b>2011</b> , 9, 10-1	164
1098	De Novo assembly of the Manila clam <i>Ruditapes philippinarum</i> transcriptome provides new insights into expression bias, mitochondrial doubly uniparental inheritance and sex determination. <b>2012</b> , 29, 771-86	80
1097	Use of mutation profiles to refine the classification of endometrial carcinomas. <b>2012</b> , 228, 20-30	227
1096	Association testing for next-generation sequencing data using score statistics. <b>2012</b> , 36, 430-7	34
1095	Biases and errors on allele frequency estimation and disease association tests of next-generation sequencing of pooled samples. <b>2012</b> , 36, 549-60	18
1094	Inhibition of the LSD1 (KDM1A) demethylase reactivates the all-trans-retinoic acid differentiation pathway in acute myeloid leukemia. <b>2012</b> , 18, 605-11	502
1093	Structure and mechanism of the CMR complex for CRISPR-mediated antiviral immunity. <b>2012</b> , 45, 303-13	251

1092	Chd2 interacts with H3.3 to determine myogenic cell fate. <b>2012</b> , 31, 2994-3007		88
1091	Cancer exome analysis reveals a T-cell-dependent mechanism of cancer immunoediting. <b>2012</b> , 482, 400-4		849
1090	BCL2 mutations in diffuse large B-cell lymphoma. <b>2012</b> , 26, 1383-90		97
1089	Genome sequencing reveals complex speciation in the <i>Drosophila simulans</i> clade. <b>2012</b> , 22, 1499-511		158
1088	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. <b>2012</b> , 44, 631-5		184
1087	Exome sequencing and the genetic basis of complex traits. <b>2012</b> , 44, 623-30		303
1086	Genomic dark matter: the reliability of short read mapping illustrated by the genome mappability score. <i>Bioinformatics</i> , <b>2012</b> , 28, 2097-105	7.2	86
1085	High-Throughput Sequencing Data Analysis Software: Current State and Future Developments. <b>2012</b> , 231-248		4
1084	Applications of High-Throughput Sequencing. <b>2012</b> , 27-53		1
1083	Small-molecule-induced DNA damage identifies alternative DNA structures in human genes. <b>2012</b> , 8, 301-10		467
1082	Short-Read Mapping. <b>2012</b> , 107-125		2
1081	Generation and Analysis of Genome-Wide DNA Methylation Maps. <b>2012</b> , 151-167		
1080	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. <b>2012</b> , 169-190		2
1079	MicroRNA Expression Profiling and Discovery. <b>2012</b> , 191-208		
1078	Designing a transcriptome next-generation sequencing project for a nonmodel plant species. <b>2012</b> , 99, 257-66		166
1077	Reference genome sequence of the model plant <i>Setaria</i> . <b>2012</b> , 30, 555-61		573
1076	Large-scale compression of genomic sequence databases with the Burrows-Wheeler transform. <i>Bioinformatics</i> , <b>2012</b> , 28, 1415-9	7.2	85
1075	SEQuel: improving the accuracy of genome assemblies. <i>Bioinformatics</i> , <b>2012</b> , 28, i188-96	7.2	46

1074	Constitutional chromothripsis rearrangements involve clustered double-stranded DNA breaks and nonhomologous repair mechanisms. <b>2012</b> , 1, 648-55			159
1073	Targeted next generation sequencing of clinically significant gene mutations and translocations in leukemia. <b>2012</b> , 25, 795-804			72
1072	Analysis of high-throughput ancient DNA sequencing data. <b>2012</b> , 840, 197-228			129
1071	Genomic affinities of two 7,000-year-old Iberian hunter-gatherers. <b>2012</b> , 22, 1494-9			129
1070	Graph concordance of next-generation sequence assemblies. <i>Bioinformatics</i> , <b>2012</b> , 28, 13-6	7.2		39
1069	wANNOVAR: annotating genetic variants for personal genomes via the web. <b>2012</b> , 49, 433-6			293
1068	De novo germline and postzygotic mutations in AKT3, PIK3R2 and PIK3CA cause a spectrum of related megalencephaly syndromes. <b>2012</b> , 44, 934-40			521
1067	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <b>2012</b> , 486, 395-9			1417
1066	Dynamic transitions in RNA polymerase II density profiles during transcription termination. <b>2012</b> , 22, 1447-56			40
1065	GRASS: a generic algorithm for scaffolding next-generation sequencing assemblies. <i>Bioinformatics</i> , <b>2012</b> , 28, 1429-37	7.2		40
1064	Temporal and fluoride control of secondary metabolism regulates cellular organofluorine biosynthesis. <b>2012</b> , 7, 1576-85			17
1063	Cohesin regulates tissue-specific expression by stabilizing highly occupied cis-regulatory modules. <b>2012</b> , 22, 2163-75			117
1062	Methylome analysis using MeDIP-seq with low DNA concentrations. <b>2012</b> , 7, 617-36			209
1061	Ultra-low-input, tagmentation-based whole-genome bisulfite sequencing. <b>2012</b> , 22, 1139-43			98
1060	Next generation sequencing for molecular diagnosis of neuromuscular diseases. <b>2012</b> , 124, 273-83			70
1059	Mutations in EZH2 cause Weaver syndrome. <b>2012</b> , 90, 110-8			190
1058	Mutations in KAT6B, encoding a histone acetyltransferase, cause Genitopatellar syndrome. <b>2012</b> , 90, 282-9			99
1057	Haploinsufficiency of a spliceosomal GTPase encoded by EFTUD2 causes mandibulofacial dysostosis with microcephaly. <b>2012</b> , 90, 369-77			143

1056	Mutations in <i>ROGDI</i> Cause Kohlschütter-Törz Syndrome. <b>2012</b> , 90, 701-7	46
1055	Identification of <i>IRF8</i> , <i>TMEM39A</i> , and <i>IKZF3-ZPBP2</i> as susceptibility loci for systemic lupus erythematosus in a large-scale multiracial replication study. <b>2012</b> , 90, 648-60	134
1054	Exome sequencing identifies <i>PDE4D</i> mutations as another cause of acrodysostosis. <b>2012</b> , 90, 740-5	105
1053	A human homeotic transformation resulting from mutations in <i>PLCB4</i> and <i>GNAI3</i> causes auriculocondylar syndrome. <b>2012</b> , 90, 907-14	60
1052	Haploinsufficiency of <i>SF3B4</i> , a component of the pre-mRNA spliceosomal complex, causes Nager syndrome. <b>2012</b> , 90, 925-33	135
1051	High-throughput resequencing of target-captured cDNA in cancer cells. <b>2012</b> , 103, 131-5	14
1050	Genome-wide <i>LORE1</i> retrotransposon mutagenesis and high-throughput insertion detection in <i>Lotus japonicus</i> . <b>2012</b> , 69, 731-41	120
1049	Protein-RNA interactions: new genomic technologies and perspectives. <b>2012</b> , 13, 77-83	408
1048	Approximate all-pairs suffix/prefix overlaps. <b>2012</b> , 213, 49-58	12
1047	Next generation sequencing and bioinformatic bottlenecks: the current state of metagenomic data analysis. <b>2012</b> , 23, 9-15	243
1046	Textual data compression in computational biology: Algorithmic techniques. <b>2012</b> , 6, 1-25	18
1045	Genomic characterisation of acral melanoma cell lines. <b>2012</b> , 25, 488-92	35
1044	Strong selection against hybrids maintains a narrow contact zone between morphologically cryptic lineages in a rainforest lizard. <b>2012</b> , 66, 1474-89	35
1043	Genetic architecture and adaptive significance of the selfing syndrome in <i>Capsella</i> . <b>2012</b> , 66, 1360-74	63
1042	Evidence of adaptation from ancestral variation in young populations of beach mice. <b>2012</b> , 66, 3209-23	50
1041	Genomic basis of aging and life-history evolution in <i>Drosophila melanogaster</i> . <b>2012</b> , 66, 3390-403	93
1040	Laboratory evolution of new lactate transporter genes in a <i>jen1</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as <i>ADY2</i> alleles by whole-genome resequencing and transcriptome analysis. <b>2012</b> , 12, 359-374	44
1039	Turbidostat culture of <i>Saccharomyces cerevisiae</i> W303-1A under selective pressure elicited by ethanol selects for mutations in <i>SSD1</i> and <i>UTH1</i> . <b>2012</b> , 12, 521-33	25

1038	High Performance Multiple Sequence Alignment System for Pyrosequencing Reads from Multiple Reference Genomes. <b>2012</b> , 72, 83-93	8
1037	Direct mutation analysis by high-throughput sequencing: from germline to low-abundant, somatic variants. <b>2012</b> , 729, 1-15	67
1036	An algorithm for mapping short reads to a dynamically changing genomic sequence. <b>2012</b> , 10, 15-22	0
1035	Identification of a novel nidovirus associated with a neurological disease of the Australian brushtail possum ( <i>Trichosurus vulpecula</i> ). <b>2012</b> , 156, 418-24	36
1034	Forward genetics uncovers Transmembrane protein 107 as a novel factor required for ciliogenesis and Sonic hedgehog signaling. <b>2012</b> , 368, 382-92	28
1033	Effector identification in the lettuce downy mildew <i>Bremia lactucae</i> by massively parallel transcriptome sequencing. <b>2012</b> , 13, 719-31	39
1032	Search for an aetiological virus candidate in chronic lymphocytic leukaemia by extensive transcriptome analysis. <b>2012</b> , 157, 709-17	6
1031	Adaptation of <i>Drosophila</i> to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. <b>2012</b> , 21, 4931-41	152
1030	High-throughput and parallel SNP discovery in selected candidate genes in <i>Eucalyptus camaldulensis</i> using Illumina NGS platform. <b>2012</b> , 10, 646-56	20
1029	Targeted re-sequencing of the allohexaploid wheat exome. <b>2012</b> , 10, 733-42	108
1028	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <b>2012</b> , 10, 703-8	39
1027	<i>Plasmodium falciparum</i> centromeres display a unique epigenetic makeup and cluster prior to and during schizogony. <b>2012</b> , 14, 1391-401	56
1026	An improved approach for accurate and efficient calling of structural variations with low-coverage sequence data. <b>2012</b> , 13 Suppl 6, S6	36
1025	PAIR: polymorphic Alu insertion recognition. <b>2012</b> , 13 Suppl 6, S7	4
1024	Optimizing Illumina next-generation sequencing library preparation for extremely AT-biased genomes. <b>2012</b> , 13, 1	434
1023	Polymorphism discovery and allele frequency estimation using high-throughput DNA sequencing of target-enriched pooled DNA samples. <b>2012</b> , 13, 16	13
1022	miRviewer: a multispecies microRNA homologous viewer. <b>2012</b> , 5, 92	56
1021	Detecting false-positive signals in exome sequencing. <b>2012</b> , 33, 609-13	112

1020	Haploinsufficiency of SOX5 at 12p12.1 is associated with developmental delays with prominent language delay, behavior problems, and mild dysmorphic features. <b>2012</b> , 33, 728-40	62
1019	Genetic diagnosis of neuroacanthocytosis disorders using exome sequencing. <b>2012</b> , 27, 539-43	19
1018	High altitude adaptation in Daghestani populations from the Caucasus. <b>2012</b> , 131, 423-33	27
1017	Exome sequencing identifies GCDH (glutaryl-CoA dehydrogenase) mutations as a cause of a progressive form of early-onset generalized dystonia. <b>2012</b> , 131, 435-42	19
1016	Search for chromosome rearrangements: new approaches toward discovery of novel translocations in head and neck squamous cell carcinoma. <b>2013</b> , 35, 831-5	1
1015	A survey of error-correction methods for next-generation sequencing. <b>2013</b> , 14, 56-66	162
1014	Toll-like receptor alterations in myelodysplastic syndrome. <b>2013</b> , 27, 1832-40	105
1013	TNPO3 protects HIV-1 replication from CPSF6-mediated capsid stabilization in the host cell cytoplasm. <b>2013</b> , 10, 20	105
1012	Newborn screening for SCID identifies patients with ataxia telangiectasia. <b>2013</b> , 33, 540-9	69
1011	Genetic diversity among pandemic 2009 influenza viruses isolated from a transmission chain. <b>2013</b> , 10, 116	14
1010	Using an ensemble of statistical metrics to quantify large sets of plant transcription factor binding sites. <b>2013</b> , 9, 12	2
1009	Mutations in ALDH6A1 encoding methylmalonate semialdehyde dehydrogenase are associated with dysmyelination and transient methylmalonic aciduria. <b>2013</b> , 8, 98	28
1008	Intellectual disability associated with a homozygous missense mutation in THOC6. <b>2013</b> , 8, 62	34
1007	MRI characterisation of adult onset alpha-methylacyl-coA racemase deficiency diagnosed by exome sequencing. <b>2013</b> , 8, 1	61
1006	RECOT: a tool for the coordinate transformation of next-generation sequencing reads for comparative genomics and transcriptomics. <b>2013</b> , 8, 6	1
1005	Genome-wide analysis of functional sirtuin chromatin targets in yeast. <b>2013</b> , 14, R48	43
1004	Characterizing and measuring bias in sequence data. <b>2013</b> , 14, R51	534
1003	Systematic biases in DNA copy number originate from isolation procedures. <b>2013</b> , 14, R33	35

1002	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <b>2013</b> , 14, R28	227
1001	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <b>2013</b> , 14, R27	212
1000	Retrotransposition of gene transcripts leads to structural variation in mammalian genomes. <b>2013</b> , 14, R22	82
999	SOAPfuse: an algorithm for identifying fusion transcripts from paired-end RNA-Seq data. <b>2013</b> , 14, R12	147
998	CGAL: computing genome assembly likelihoods. <b>2013</b> , 14, R8	59
997	Genome-scale analyses of butanol tolerance in <i>Saccharomyces cerevisiae</i> reveal an essential role of protein degradation. <b>2013</b> , 6, 48	63
996	Distinct roles of KAP1, HP1 and G9a/GLP in silencing of the two-cell-specific retrotransposon MERVL in mouse ES cells. <b>2013</b> , 6, 15	107
995	Nucleosomal DNA binding drives the recognition of H3K36-methylated nucleosomes by the PSIP1-PWWP domain. <b>2013</b> , 6, 12	103
994	Tumor-associated copy number changes in the circulation of patients with prostate cancer identified through whole-genome sequencing. <b>2013</b> , 5, 30	246
993	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. <b>2013</b> , 5, 28	315
992	Identification and functional validation of HPV-mediated hypermethylation in head and neck squamous cell carcinoma. <b>2013</b> , 5, 15	99
991	Next-Generation Sequencing as a Tool for Detailed Molecular Characterisation of Genomic Insertions and Flanking Regions in Genetically Modified Plants: a Pilot Study Using a Rice Event Unauthorised in the EU. <b>2013</b> , 6, 1718-1727	45
990	An efficient rRNA removal method for RNA sequencing in GC-rich bacteria. <b>2013</b> , 3, 1	35
989	Lessons learned from implementing a national infrastructure in Sweden for storage and analysis of next-generation sequencing data. <b>2013</b> , 2, 9	59
988	DNA unmethylome profiling by covalent capture of CpG sites. <b>2013</b> , 4, 2190	41
987	Diagnosis of copy number variation by Illumina next generation sequencing is comparable in performance to oligonucleotide array comparative genomic hybridisation. <b>2013</b> , 102, 174-81	44
986	Simultaneous and complete genome sequencing of influenza A and B with high coverage by Illumina MiSeq Platform. <b>2013</b> , 193, 394-404	41
985	53BP1 alters the landscape of DNA rearrangements and suppresses AID-induced B cell lymphoma. <b>2013</b> , 49, 623-31	31

984	First evidence of <i>Equus asinus</i> L. in the Chalcolithic disputes the Phoenicians as the first to introduce donkeys into the Iberian Peninsula. <b>2013</b> , 40, 4483-4490	14
983	Deep Sequencing Data Analysis. <b>2013</b> ,	4
982	Genetic programs in human and mouse early embryos revealed by single-cell RNA sequencing. <b>2013</b> , 500, 593-7	622
981	Anaerobic oxidation of methane coupled to nitrate reduction in a novel archaeal lineage. <b>2013</b> , 500, 567-70	750
980	Investigating the effect of two methane-mitigating diets on the rumen microbiome using massively parallel sequencing. <b>2013</b> , 96, 6030-46	36
979	Emulsion PCR-coupled target enrichment: an effective fishing method for high-throughput sequencing of poorly preserved ancient DNA. <b>2013</b> , 528, 347-51	10
978	Prioritization of retinal disease genes: an integrative approach. <b>2013</b> , 34, 853-9	6
977	Massively parallel decoding of mammalian regulatory sequences supports a flexible organizational model. <b>2013</b> , 45, 1021-1028	155
976	Bioinformatics Research and Applications. <b>2013</b> ,	
975	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. <b>2013</b> , 76, 494-505	191
974	Cooperativity and rapid evolution of cobound transcription factors in closely related mammals. <b>2013</b> , 154, 530-40	107
973	Development of a rifampicin-resistant <i>Bacillus subtilis</i> strain for natto-fermentation showing enhanced exoenzyme production. <b>2013</b> , 115, 654-7	10
972	Radiation resistance of sequencing chips for in situ life detection. <b>2013</b> , 13, 560-9	7
971	Homoeolog expression bias and expression level dominance in allopolyploid cotton. <b>2013</b> , 110, 171-80	230
970	Recurrent somatic alterations of <i>FGFR1</i> and <i>NTRK2</i> in pilocytic astrocytoma. <b>2013</b> , 45, 927-32	550
969	MicroRNA Cancer Regulation. <b>2013</b> ,	17
968	Model selection as a tool for phylogeographic inference: an example from the willow <i>Salix melanopsis</i> . <b>2013</b> , 22, 4014-28	50
967	A tripartite transcription factor network regulates primordial germ cell specification in mice. <b>2013</b> , 15, 905-15	187

966	Accurate sex identification of ancient human remains using DNA shotgun sequencing. <b>2013</b> , 40, 4477-4482	212
965	RUNX1 is a key target in t(4;11) leukemias that contributes to gene activation through an AF4-MLL complex interaction. <b>2013</b> , 3, 116-27	103
964	The evolution and pathogenic mechanisms of the rice sheath blight pathogen. <b>2013</b> , 4, 1424	177
963	The haplotype-resolved genome and epigenome of the aneuploid HeLa cancer cell line. <b>2013</b> , 500, 207-11	236
962	Zucchini yellow mosaic virus (ZYMV, Potyvirus): vertical transmission, seed infection and cryptic infections. <b>2013</b> , 176, 259-64	38
961	Single Nucleotide Polymorphism (SNP) Detection and Genotype Calling from Massively Parallel Sequencing (MPS) Data. <b>2013</b> , 5, 3-25	14
960	Statistical Challenges in Sequence-Based Association Studies with Population- and Family-Based Designs. <b>2013</b> , 5, 54-70	8
959	Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing. <b>2013</b> , 5, 138-155	10
958	Next generation sequencing in cancer research and clinical application. <b>2013</b> , 15, 4	76
957	WEP: a high-performance analysis pipeline for whole-exome data. <b>2013</b> , 14 Suppl 7, S11	38
956	GAM-NGS: genomic assemblies merger for next generation sequencing. <b>2013</b> , 14 Suppl 7, S6	59
955	metaBEETL: high-throughput analysis of heterogeneous microbial populations from shotgun DNA sequences. <b>2013</b> , 14 Suppl 5, S2	12
954	Bellerophon: a hybrid method for detecting interchromosomal rearrangements at base pair resolution using next-generation sequencing data. <b>2013</b> , 14 Suppl 5, S6	12
953	A random-permutations-based approach to fast read alignment. <b>2013</b> , 14 Suppl 5, S8	4
952	Quantifying single nucleotide variant detection sensitivity in exome sequencing. <b>2013</b> , 14, 195	63
951	QualComp: a new lossy compressor for quality scores based on rate distortion theory. <b>2013</b> , 14, 187	37
950	Benchmarking short sequence mapping tools. <b>2013</b> , 14, 184	140
949	CUDASW++ 3.0: accelerating Smith-Waterman protein database search by coupling CPU and GPU SIMD instructions. <b>2013</b> , 14, 117	133

948	A hybrid short read mapping accelerator. <b>2013</b> , 14, 67	16
947	Inferring the evolutionary histories of divergences in <i>Hylobates</i> and <i>Nomascus gibbons</i> through multilocus sequence data. <b>2013</b> , 13, 82	27
946	Evolution of a horizontally acquired legume gene, albumin 1, in the parasitic plant <i>Phelipanche aegyptiaca</i> and related species. <b>2013</b> , 13, 48	37
945	Identifying Mendelian disease genes with the variant effect scoring tool. <b>2013</b> , 14 Suppl 3, S3	240
944	Transposon fingerprinting using low coverage whole genome shotgun sequencing in cacao ( <i>Theobroma cacao</i> L.) and related species. <b>2013</b> , 14, 502	15
943	A systematic evaluation of hybridization-based mouse exome capture system. <b>2013</b> , 14, 492	5
942	Assessment of the genomic variation in a cattle population by re-sequencing of key animals at low to medium coverage. <b>2013</b> , 14, 446	52
941	Rainbow: a tool for large-scale whole-genome sequencing data analysis using cloud computing. <b>2013</b> , 14, 425	38
940	A unique nucleosome arrangement, maintained actively by chromatin remodelers facilitates transcription of yeast tRNA genes. <b>2013</b> , 14, 402	40
939	RNA-seq analysis reveals extensive transcriptional plasticity to temperature stress in a freshwater fish species. <b>2013</b> , 14, 375	123
938	Phase-defined complete sequencing of the HLA genes by next-generation sequencing. <b>2013</b> , 14, 355	87
937	Comparative analysis of 4C-Seq data generated from enzyme-based and sonication-based methods. <b>2013</b> , 14, 345	11
936	Genome-scale transcriptional analyses of first-generation interspecific sunflower hybrids reveals broad regulatory compatibility. <b>2013</b> , 14, 342	12
935	Differential transcript isoform usage pre- and post-zygotic genome activation in zebrafish. <b>2013</b> , 14, 331	27
934	ContigScape: a Cytoscape plugin facilitating microbial genome gap closing. <b>2013</b> , 14, 289	30
933	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. <b>2013</b> , 14, 257	23
932	Integration of mate pair sequences to improve shotgun assemblies of flow-sorted chromosome arms of hexaploid wheat. <b>2013</b> , 14, 222	13
931	Prediction of constitutive A-to-I editing sites from human transcriptomes in the absence of genomic sequences. <b>2013</b> , 14, 206	27

930	The transcript catalogue of the short-lived fish <i>Nothobranchius furzeri</i> provides insights into age-dependent changes of mRNA levels. <b>2013</b> , 14, 185	45
929	Population-genomic variation within RNA viruses of the Western honey bee, <i>Apis mellifera</i> , inferred from deep sequencing. <b>2013</b> , 14, 154	26
928	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <b>2013</b> , 14, 148	40
927	A hybrid next generation transcript sequencing-based approach to identify allelic and homeolog-specific single nucleotide polymorphisms in allotetraploid white clover. <b>2013</b> , 14, 100	15
926	Combined CHIP-Seq and transcriptome analysis identifies AP-1/JunD as a primary regulator of oxidative stress and IL-1 $\beta$ synthesis in macrophages. <b>2013</b> , 14, 92	17
925	Comparative genomic analyses of <i>Mycoplasma hyopneumoniae</i> pathogenic 168 strain and its high-passaged attenuated strain. <b>2013</b> , 14, 80	38
924	Analysis of the leaf transcriptome of <i>Musa acuminata</i> during interaction with <i>Mycosphaerella musicola</i> : gene assembly, annotation and marker development. <b>2013</b> , 14, 78	34
923	Development of a high density 600K SNP genotyping array for chicken. <b>2013</b> , 14, 59	230
922	Identification of medium-sized genomic deletions with low coverage, mate-paired restricted tags. <b>2013</b> , 14, 51	1
921	Comparative genome analysis of <i>Spiroplasma melliferum</i> IPMB4A, a honeybee-associated bacterium. <b>2013</b> , 14, 22	67
920	<i>Saccharopolyspora erythraea</i> 's genome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. <b>2013</b> , 14, 15	23
919	The complex transcriptional landscape of the anucleate human platelet. <b>2013</b> , 14, 1	480
918	Genome reassembly with high-throughput sequencing data. <b>2013</b> , 14 Suppl 1, S8	2
917	Accelerating read mapping with FastHASH. <b>2013</b> , 14 Suppl 1, S13	53
916	Unraveling overlapping deletions by agglomerative clustering. <b>2013</b> , 14 Suppl 1, S12	5
915	Mutation spectrum in human colorectal cancers and potential functional relevance. <b>2013</b> , 14, 32	8
914	Exome profiling of primary, metastatic and recurrent ovarian carcinomas in a BRCA1-positive patient. <b>2013</b> , 13, 146	14
913	Mitochondrial genome sequences reveal deep divergences among <i>Anopheles punctulatus</i> sibling species in Papua New Guinea. <b>2013</b> , 12, 64	29

912	Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. <b>2013</b> , 500, 571-4	380
911	High resolution genotyping by restriction enzyme-phased sequencing of advanced backcross lines of rice exhibiting differential cold stress recovery. <b>2013</b> , 192, 107-115	2
910	An evaluation of the hybrid speciation hypothesis for <i>Xiphophorus clemenciae</i> based on whole genome sequences. <b>2013</b> , 67, 1155-68	21
909	Tiling Arrays. <b>2013</b> ,	1
908	A reversible gene trap collection empowers haploid genetics in human cells. <b>2013</b> , 10, 965-71	76
907	A novel method to predict regulatory regions based on histone mark landscapes in macrophages. <b>2013</b> , 218, 1416-27	11
906	Detecting rare variants for psychiatric disorders using next generation sequencing: a methods primer. <b>2013</b> , 15, 333	1
905	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <b>2013</b> , 1, 156-174	22
904	Computational methodology for ChIP-seq analysis. <b>2013</b> , 1, 54-70	20
903	Personal genomes, quantitative dynamic omics and personalized medicine. <b>2013</b> , 1, 71-90	26
902	Spatial and temporal mapping of de novo mutations in schizophrenia to a fetal prefrontal cortical network. <b>2013</b> , 154, 518-29	406
901	A novel rearrangement of occludin causes brain calcification and renal dysfunction. <b>2013</b> , 132, 1223-34	21
900	Clinical and mutation data in 12 patients with the clinical diagnosis of Nager syndrome. <b>2013</b> , 132, 885-98	54
899	Haploinsufficiency of KDM6A is associated with severe psychomotor retardation, global growth restriction, seizures and cleft palate. <b>2013</b> , 132, 537-52	48
898	Identification of COL6A2 mutations in progressive myoclonus epilepsy syndrome. <b>2013</b> , 132, 275-83	17
897	Variants in GATA4 are a rare cause of familial and sporadic congenital diaphragmatic hernia. <b>2013</b> , 132, 285-92	67
896	MutMap-Gap: whole-genome resequencing of mutant F2 progeny bulk combined with de novo assembly of gap regions identifies the rice blast resistance gene Pii. <b>2013</b> , 200, 276-283	149
895	Dynamic genetic features of chromosomes revealed by comparison of soybean genetic and sequence-based physical maps. <b>2013</b> , 126, 1103-19	17

894	Improvement of the <i>Oryza sativa</i> Nipponbare reference genome using next generation sequence and optical map data. <b>2013</b> , 6, 4	1110
893	Cloud-based uniform ChIP-Seq processing tools for modENCODE and ENCODE. <b>2013</b> , 14, 494	5
892	Finding the lost treasures in exome sequencing data. <b>2013</b> , 29, 593-9	105
891	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. <b>2013</b> , 20, 1131-9	983
890	Transcription factor binding in human cells occurs in dense clusters formed around cohesin anchor sites. <b>2013</b> , 154, 801-13	253
889	Whole-genome sequencing uncovers the genetic basis of chronic mountain sickness in Andean highlanders. <b>2013</b> , 93, 452-62	90
888	Olfactory Receptors. <b>2013</b> ,	1
887	NGSPE: A pipeline for end-to-end analysis of DNA sequencing data and comparison between different platforms. <b>2013</b> , 43, 1171-6	2
886	AlienTrimmer: a tool to quickly and accurately trim off multiple short contaminant sequences from high-throughput sequencing reads. <b>2013</b> , 102, 500-6	117
885	Mass production of SNP markers in a nonmodel passerine bird through RAD sequencing and contig mapping to the zebra finch genome. <b>2013</b> , 13, 899-907	22
884	Next Generation Sequencing in Cancer Research. <b>2013</b> ,	4
883	Comprehensive analyses of microRNA gene evolution in paleopolyploid soybean genome. <b>2013</b> , 76, 332-44	16
882	Contribution of subgenomes to the transcriptome and their intertwined regulation in the allopolyploid <i>Coffea arabica</i> grown at contrasted temperatures. <b>2013</b> , 200, 251-260	52
881	Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. <b>2013</b> , 76, 530-44	247
880	Technical and implementation issues in using next-generation sequencing of cancers in clinical practice. <b>2013</b> , 109, 827-35	79
879	Coverage theories for metagenomic DNA sequencing based on a generalization of Stevens' theorem. <b>2013</b> , 67, 1141-61	24
878	Critical role of bioinformatics in translating huge amounts of next-generation sequencing data into personalized medicine. <b>2013</b> , 56, 110-8	23
877	Secretory meningiomas are defined by combined KLF4 K409Q and TRAF7 mutations. <b>2013</b> , 125, 351-8	158

876	Reconfigurable Computing: Architectures, Tools and Applications. <b>2013</b> ,	
875	BMP9 mutations cause a vascular-anomaly syndrome with phenotypic overlap with hereditary hemorrhagic telangiectasia. <b>2013</b> , 93, 530-7	204
874	Insights into the immuno-molecular biology of <i>Angiostrongylus vasorum</i> through transcriptomics--prospects for new interventions. <b>2013</b> , 31, 1486-500	16
873	An X-linked cobalamin disorder caused by mutations in transcriptional coregulator HCFC1. <b>2013</b> , 93, 506-14	90
872	DNA sequence motif: a jack of all trades for ChIP-Seq data. <b>2013</b> , 91, 135-71	6
871	Targeted sequence capture and resequencing implies a predominant role of regulatory regions in the divergence of a sympatric lake whitefish species pair ( <i>Coregonus clupeaformis</i> ). <b>2013</b> , 22, 4896-914	33
870	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. <b>2013</b> , 45, 1226-1231	205
869	The genomic landscape of oesophagogastric junctional adenocarcinoma. <b>2013</b> , 231, 301-10	31
868	Genome sequencing of mucosal melanomas reveals that they are driven by distinct mechanisms from cutaneous melanoma. <b>2013</b> , 230, 261-9	136
867	Mutations in COQ2 in familial and sporadic multiple-system atrophy. <b>2013</b> , 369, 233-44	251
866	Mutations in KARS, encoding lysyl-tRNA synthetase, cause autosomal-recessive nonsyndromic hearing impairment DFNB89. <b>2013</b> , 93, 132-40	80
865	Mouse SAMHD1 has antiretroviral activity and suppresses a spontaneous cell-intrinsic antiviral response. <b>2013</b> , 4, 689-96	113
864	Loss of function of glucocerebrosidase GBA2 is responsible for motor neuron defects in hereditary spastic paraplegia. <b>2013</b> , 92, 238-44	133
863	Constitutive activation of the calcium sensor STIM1 causes tubular-aggregate myopathy. <b>2013</b> , 92, 271-8	133
862	NDUFA4 mutations underlie dysfunction of a cytochrome c oxidase subunit linked to human neurological disease. <b>2013</b> , 3, 1795-805	85
861	Higher-order looping and nuclear organization of Tcra facilitate targeted rag cleavage and regulated rearrangement in recombination centers. <b>2013</b> , 3, 359-70	31
860	Identification of KLHL41 Mutations Implicates BTB-Kelch-Mediated Ubiquitination as an Alternate Pathway to Myofibrillar Disruption in Nemaline Myopathy. <b>2013</b> , 93, 1108-17	120
859	Whole-exome sequencing identifies tetratricopeptide repeat domain 7A (TTC7A) mutations for combined immunodeficiency with intestinal atresias. <b>2013</b> , 132, 656-664.e17	109

858	Complete <i>Arabidopsis thaliana</i> chloroplast genome sequence and insight into its polymorphism. <b>2013</b> , 1, 65-75	14
857	Genome-wide association of Yorkie with chromatin and chromatin-remodeling complexes. <b>2013</b> , 3, 309-18	100
856	Mutations in KCTD1 cause scalp-ear-nipple syndrome. <b>2013</b> , 92, 621-6	48
855	Mutations in ECEL1 cause distal arthrogryposis type 5D. <b>2013</b> , 92, 150-6	55
854	Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes. <b>2013</b> , 3, 1569	77
853	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. <b>2013</b> , 41, 6119-38	125
852	Mutations in WNT1 are a cause of osteogenesis imperfecta. <b>2013</b> , 50, 345-8	141
851	The linkage method: a novel approach for SNP detection and haplotype reconstruction from a single diploid individual using next-generation sequence data. <b>2013</b> , 30, 2187-96	7
850	Computing the longest common prefix array based on the Burrows-Wheeler transform. <b>2013</b> , 18, 22-31	28
849	Genome-wide analysis of histone modifications: H3K4me2, H3K4me3, H3K9ac, and H3K27ac in <i>Oryza sativa</i> L. Japonica. <b>2013</b> , 6, 1463-72	81
848	Infection structure-specific expression of $\beta$ 1,3-glucan synthase is essential for pathogenicity of <i>Colletotrichum graminicola</i> and evasion of $\beta$ glucan-triggered immunity in maize. <b>2013</b> , 25, 2356-78	64
847	Extensive intra-host genetic diversity uncovered in <i>Cryptosporidium parvum</i> using Next Generation Sequencing. <b>2013</b> , 15, 18-24	28
846	Exome analysis reveals a Japanese family with spinocerebellar ataxia, autosomal recessive 1. <b>2013</b> , 331, 158-60	2
845	<i>Salmonella Gallinarum</i> field isolates from laying hens are related to the vaccine strain SG9R. <b>2013</b> , 31, 4940-5	23
844	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. <b>2013</b> , 39-61	2
843	Deficiency of asparagine synthetase causes congenital microcephaly and a progressive form of encephalopathy. <b>2013</b> , 80, 429-41	100
842	A clinically validated diagnostic second-generation sequencing assay for detection of hereditary BRCA1 and BRCA2 mutations. <b>2013</b> , 15, 796-809	27
841	The exomes of the NCI-60 panel: a genomic resource for cancer biology and systems pharmacology. <b>2013</b> , 73, 4372-82	207

840	The long noncoding RNA SchLAP1 promotes aggressive prostate cancer and antagonizes the SWI/SNF complex. <b>2013</b> , 45, 1392-8	515
839	Clinical whole-exome sequencing for the diagnosis of mendelian disorders. <b>2013</b> , 369, 1502-11	1393
838	Exome sequencing identifies secondary mutations of SETBP1 and JAK3 in juvenile myelomonocytic leukemia. <b>2013</b> , 45, 937-41	175
837	Condensin I associates with structural and gene regulatory regions in vertebrate chromosomes. <b>2013</b> , 4, 2537	51
836	Exome sequencing identifies recurrent somatic mutations in EIF1AX and SF3B1 in uveal melanoma with disomy 3. <b>2013</b> , 45, 933-6	330
835	DNMT1-interacting RNAs block gene-specific DNA methylation. <b>2013</b> , 503, 371-6	379
834	Hypermutation of the inactive X chromosome is a frequent event in cancer. <b>2013</b> , 155, 567-81	50
833	Next-generation sequencing in schizophrenia and other neuropsychiatric disorders. <b>2013</b> , 162B, 671-8	21
832	Encore: Genetic Association Interaction Network centrality pipeline and application to SLE exome data. <b>2013</b> , 37, 614-21	18
831	Whole-genome and whole-exome sequencing of bladder cancer identifies frequent alterations in genes involved in sister chromatid cohesion and segregation. <b>2013</b> , 45, 1459-63	326
830	Mutations in DARS cause hypomyelination with brain stem and spinal cord involvement and leg spasticity. <b>2013</b> , 92, 774-80	127
829	A de novo mutation in the $\beta$ -tubulin gene TUBB4A results in the leukoencephalopathy hypomyelination with atrophy of the basal ganglia and cerebellum. <b>2013</b> , 92, 767-73	133
828	Stochastic ERK activation induced by noise and cell-to-cell propagation regulates cell density-dependent proliferation. <b>2013</b> , 52, 529-40	207
827	High-throughput identification of antigen-specific TCRs by TCR gene capture. <b>2013</b> , 19, 1534-41	127
826	Assessing the phenotypic effects in the general population of rare variants in genes for a dominant Mendelian form of diabetes. <b>2013</b> , 45, 1380-5	103
825	Accurately identifying low-allelic fraction variants in single samples with next-generation sequencing: applications in tumor subclone resolution. <b>2013</b> , 34, 1432-8	45
824	An ACT1 mutation selectively abolishes interleukin-17 responses in humans with chronic mucocutaneous candidiasis. <b>2013</b> , 39, 676-86	204
823	Pulling out the 1%: whole-genome capture for the targeted enrichment of ancient DNA sequencing libraries. <b>2013</b> , 93, 852-64	221

822	Consed: a graphical editor for next-generation sequencing. <i>Bioinformatics</i> , <b>2013</b> , 29, 2936-7	7.2	153
821	Identification of novel variants in colorectal cancer families by high-throughput exome sequencing. <b>2013</b> , 22, 1239-51		36
820	RACER: Rapid and accurate correction of errors in reads. <i>Bioinformatics</i> , <b>2013</b> , 29, 2490-3	7.2	51
819	Large-scale detection of in vivo transcription errors. <b>2013</b> , 110, 18584-9		76
818	Sequencing Y chromosomes resolves discrepancy in time to common ancestor of males versus females. <b>2013</b> , 341, 562-5		181
817	Mosaic copy number variation in human neurons. <b>2013</b> , 342, 632-7		404
816	Identification of candidate oncogenes in human colorectal cancers with microsatellite instability. <b>2013</b> , 145, 540-3.e22		40
815	Genetic incompatibilities are widespread within species. <b>2013</b> , 504, 135-7		136
814	Identification of genetic variants that affect histone modifications in human cells. <b>2013</b> , 342, 747-9		331
813	Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments. <b>2013</b> , 110, 15758-63		759
812	ESR1 ligand-binding domain mutations in hormone-resistant breast cancer. <b>2013</b> , 45, 1439-45		754
811	Isolated central hypothyroidism in young siblings as a manifestation of PROP1 deficiency: clinical impact of whole exome sequencing. <b>2013</b> , 79, 379-86		12
810	Genomic analysis of non-NF2 meningiomas reveals mutations in TRAF7, KLF4, AKT1, and SMO. <b>2013</b> , 339, 1077-80		508
809	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <b>2013</b> , 23, 2066-77		232
808	A New Method for Genome-wide Marker Development and Genotyping Holds Great Promise for Molecular Primatology. <b>2013</b> , 34, 303-314		17
807	A genome-wide map of CTCF multivalency redefines the CTCF code. <b>2013</b> , 3, 1678-1689		200
806	Efficient identification of Y chromosome sequences in the human and Drosophila genomes. <b>2013</b> , 23, 1894-907		68
805	Lep-MAP: fast and accurate linkage map construction for large SNP datasets. <i>Bioinformatics</i> , <b>2013</b> , 29, 3128-34	7.2	97

804	Suitability of Illumina deep mRNA sequencing for reliable gene expression profiling in a non-model conifer species ( <i>Pseudotsuga menziesii</i> ). <b>2013</b> , 9, 1513-1527		2
803	MicroRNA-128 governs neuronal excitability and motor behavior in mice. <b>2013</b> , 342, 1254-8		203
802	Cell-type, allelic, and genetic signatures in the human pancreatic beta cell transcriptome. <b>2013</b> , 23, 1554-62		140
801	Tmem88a mediates GATA-dependent specification of cardiomyocyte progenitors by restricting WNT signaling. <b>2013</b> , 140, 3787-98		15
800	Clinical application of amplicon-based next-generation sequencing in cancer. <b>2013</b> , 206, 413-9		85
799	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. <b>2013</b> , 110, 13481-6		127
798	A statistical variant calling approach from pedigree information and local haplotyping with phase informative reads. <i>Bioinformatics</i> , <b>2013</b> , 29, 2835-43	7.2	12
797	Very low-level heteroplasmy mtDNA variations are inherited in humans. <b>2013</b> , 40, 607-15		45
796	ERBB4 mutations that disrupt the neuregulin-ErbB4 pathway cause amyotrophic lateral sclerosis type 19. <b>2013</b> , 93, 900-5		95
795	Next-generation sequencing reveals high concordance of recurrent somatic alterations between primary tumor and metastases from patients with non-small-cell lung cancer. <b>2013</b> , 31, 2167-72		143
794	miR-9a minimizes the phenotypic impact of genomic diversity by buffering a transcription factor. <b>2013</b> , 155, 1556-67		70
793	Bubble-seq analysis of the human genome reveals distinct chromatin-mediated mechanisms for regulating early- and late-firing origins. <b>2013</b> , 23, 1774-88		65
792	Indoleamides are active against drug-resistant <i>Mycobacterium tuberculosis</i> . <b>2013</b> , 4, 2907		101
791	Isaac: ultra-fast whole-genome secondary analysis on Illumina sequencing platforms. <i>Bioinformatics</i> , <b>2013</b> , 29, 2041-3	7.2	210
790	The Sac1 domain of SYNJ1 identified mutated in a family with early-onset progressive Parkinsonism with generalized seizures. <b>2013</b> , 34, 1200-7		228
789	Coexpression networks implicate human midfetal deep cortical projection neurons in the pathogenesis of autism. <b>2013</b> , 155, 997-1007		591
788	Genome-wide mapping of transcriptional start sites defines an extensive leaderless transcriptome in <i>Mycobacterium tuberculosis</i> . <b>2013</b> , 5, 1121-31		206
787	The landscape of microsatellite instability in colorectal and endometrial cancer genomes. <b>2013</b> , 155, 858-68		247

786	Temporal response of the human virome to immunosuppression and antiviral therapy. <b>2013</b> , 155, 1178-87	285
785	Histone deacetylase inhibition promotes osteoblast maturation by altering the histone H4 epigenome and reduces Akt phosphorylation. <b>2013</b> , 288, 28783-91	65
784	Exome sequencing identifies distinct mutational patterns in liver fluke-related and non-infection-related bile duct cancers. <b>2013</b> , 45, 1474-8	334
783	Evidence for sex and recombination in the choanoflagellate <i>Salpingoeca rosetta</i> . <b>2013</b> , 23, 2176-80	70
782	Efficacy of chemotherapy in BRCA1/2 mutation carrier ovarian cancer in the setting of PARP inhibitor resistance: a multi-institutional study. <b>2013</b> , 19, 5485-93	103
781	RNA-DNA differences in human mitochondria restore ancestral form of 16S ribosomal RNA. <b>2013</b> , 23, 1789-96	42
780	An introduction to high-throughput sequencing experiments: design and bioinformatics analysis. <b>2013</b> , 1038, 1-26	8
779	ERF115 controls root quiescent center cell division and stem cell replenishment. <b>2013</b> , 342, 860-3	193
778	The eukaryotic genome, its reads, and the unfinished assembly. <b>2013</b> , 587, 2090-3	3
777	Aging as accelerated accumulation of somatic variants: whole-genome sequencing of centenarian and middle-aged monozygotic twin pairs. <b>2013</b> , 16, 1026-32	30
776	Single nucleotide variants (SNVs) define senescence-accelerated SAMP8 mice, a model of a geriatric condition. <b>2013</b> , 36, 349-63	6
775	mtDNA lineage expansions in Sherpa population suggest adaptive evolution in Tibetan highlands. <b>2013</b> , 30, 2579-87	37
774	Next Generation Sequencing. <b>2013</b> ,	10
773	Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. <b>2013</b> , 155, 1521-31	256
772	Systematic identification of molecular subtype-selective vulnerabilities in non-small-cell lung cancer. <b>2013</b> , 155, 552-66	129
771	A support vector machine for identification of single-nucleotide polymorphisms from next-generation sequencing data. <i>Bioinformatics</i> , <b>2013</b> , 29, 1361-6	7.2 26
770	Analysis of the DNA-binding profile and function of TALE homeoproteins reveals their specialization and specific interactions with Hox genes/proteins. <b>2013</b> , 3, 1321-33	90
769	Disentangling homeologous contigs in allo-tetraploid assembly: application to durum wheat. <b>2013</b> , 14 Suppl 15, S15	12

768	Heterogeneity in the entire genome for three genotypes of peach [ <i>Prunus persica</i> (L.) Batsch] as distinguished from sequence analysis of genomic variants. <b>2013</b> , 14, 750		15
767	Characterizing workflow-based activity on a production e-infrastructure using provenance data. <b>2013</b> , 29, 1931-1942		7
766	Region of difference 4 in alpine <i>Mycobacterium caprae</i> isolates indicates three variants. <b>2013</b> , 51, 1381-8		41
765	MATE-CLEVER: Mendelian-inheritance-aware discovery and genotyping of midsize and long indels. <i>Bioinformatics</i> , <b>2013</b> , 29, 3143-50	7.2	35
764	Population-scale analysis of human microsatellites reveals novel sources of exonic variation. <b>2013</b> , 516, 328-34		25
763	Morphological and genetic evidence for early Holocene cattle management in northeastern China. <b>2013</b> , 4, 2755		59
762	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. <i>Bioinformatics</i> , <b>2013</b> , 29, 2790-1	7.2	246
761	Transcriptome-wide identification of RNA binding sites by CLIP-seq. <b>2013</b> , 63, 32-40		25
760	FUS regulates genes coding for RNA-binding proteins in neurons by binding to their highly conserved introns. <b>2013</b> , 19, 498-509		77
759	Recent diversification of a marine genus ( <i>Tursiops</i> spp.) tracks habitat preference and environmental change. <b>2013</b> , 62, 865-77		64
758	Induced pluripotent stem cells are sensitive to DNA damage. <b>2013</b> , 11, 320-6		14
757	REDIttools: high-throughput RNA editing detection made easy. <i>Bioinformatics</i> , <b>2013</b> , 29, 1813-4	7.2	157
756	Pseudo-Sanger sequencing: massively parallel production of long and near error-free reads using NGS technology. <b>2013</b> , 14, 711		11
755	Deep sequencing reveals increased DNA methylation in chronic rat epilepsy. <b>2013</b> , 126, 741-56		134
754	A simple consensus approach improves somatic mutation prediction accuracy. <b>2013</b> , 5, 90		29
753	Fine mapping and identification of a candidate gene for a major locus controlling maturity date in peach. <b>2013</b> , 13, 166		79
752	Genomic diversity and adaptation of <i>Salmonella enterica</i> serovar Typhimurium from analysis of six genomes of different phage types. <b>2013</b> , 14, 718		31
751	Aneuploidy in neuroblastoma tumors is not associated with inactivating point mutations in the STAG2 gene. <b>2013</b> , 14, 102		4

750	BreakTrans: uncovering the genomic architecture of gene fusions. <b>2013</b> , 14, R87	18
749	Intraspecific variation of recombination rate in maize. <b>2013</b> , 14, R103	134
748	Combinational analysis of linkage and exome sequencing identifies the causative mutation in a Chinese family with congenital cataract. <b>2013</b> , 14, 107	8
747	An integrated transcriptome and epigenome analysis identifies a novel candidate gene for pancreatic cancer. <b>2013</b> , 6, 33	28
746	Assembly of a phased diploid <i>Candida albicans</i> genome facilitates allele-specific measurements and provides a simple model for repeat and indel structure. <b>2013</b> , 14, R97	88
745	Retrospective genomic analysis of sorghum adaptation to temperate-zone grain production. <b>2013</b> , 14, R68	82
744	Centroid based clustering of high throughput sequencing reads based on n-mer counts. <b>2013</b> , 14, 268	14
743	A new locus on chromosome 22q13.31 linked to recessive genetic epilepsy with febrile seizures plus (GEFS+) in a Tunisian consanguineous family. <b>2013</b> , 14, 93	7
742	Intronic non-CG DNA hydroxymethylation and alternative mRNA splicing in honey bees. <b>2013</b> , 14, 666	49
741	Ontogeny, distribution and potential roles of 5-hydroxymethylcytosine in human liver function. <b>2013</b> , 14, R83	54
740	An ENU mutagenesis screen identifies novel and known genes involved in epigenetic processes in the mouse. <b>2013</b> , 14, R96	60
739	Mutation in MEOX1 gene causes a recessive Klippel-Feil syndrome subtype. <b>2013</b> , 14, 95	35
738	HANDS: a tool for genome-wide discovery of subgenome-specific base-identity in polyploids. <b>2013</b> , 14, 653	9
737	Estimating exome genotyping accuracy by comparing to data from large scale sequencing projects. <b>2013</b> , 5, 69	20
736	Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial <i>Wolbachia</i> endosymbiont to its host filarial nematode <i>Brugia malayi</i> . <b>2013</b> , 14, 639	31
735	Distinct polyadenylation landscapes of diverse human tissues revealed by a modified PA-seq strategy. <b>2013</b> , 14, 615	35
734	BSTA: a targeted approach combines bulked segregant analysis with next-generation sequencing and de novo transcriptome assembly for SNP discovery in sunflower. <b>2013</b> , 14, 628	33
733	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <b>2013</b> , 2, 10	461

732	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <b>2013</b> , 14, 550	10
731	De novo transcriptome assembly of drought tolerant CAM plants, <i>Agave deserti</i> and <i>Agave tequilana</i> . <b>2013</b> , 14, 563	79
730	The root transcriptome for North American ginseng assembled and profiled across seasonal development. <b>2013</b> , 14, 564	28
729	Identification of piggyBac-mediated insertions in <i>Plasmodium berghei</i> by next generation sequencing. <b>2013</b> , 12, 287	2
728	Genetic variability of mutans streptococci revealed by wide whole-genome sequencing. <b>2013</b> , 14, 430	24
727	Exome sequencing of a patient with suspected mitochondrial disease reveals a likely multigenic etiology. <b>2013</b> , 14, 83	10
726	Gene-based single nucleotide polymorphism discovery in bovine muscle using next-generation transcriptomic sequencing. <b>2013</b> , 14, 307	27
725	Targeted next-generation sequencing of head and neck squamous cell carcinoma identifies novel genetic alterations in HPV+ and HPV- tumors. <b>2013</b> , 5, 49	158
724	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia</i> corals. <b>2013</b> , 14, 546	20
723	CRAC: an integrated approach to the analysis of RNA-seq reads. <b>2013</b> , 14, R30	54
722	Detection of phase-dependent transcriptomic changes and Rubisco-mediated CO <sub>2</sub> fixation into poly (3-hydroxybutyrate) under heterotrophic condition in <i>Ralstonia eutropha</i> H16 based on RNA-seq and gene deletion analyses. <b>2013</b> , 13, 169	45
721	Rapid and robust phylotyping of spa t003, a dominant MRSA clone in Luxembourg and other European countries. <b>2013</b> , 13, 339	11
720	Transcriptomic and genomic evidence for <i>Streptococcus agalactiae</i> adaptation to the bovine environment. <b>2013</b> , 14, 920	31
719	Fragment assignment in the cloud with eXpress-D. <b>2013</b> , 14, 358	18
718	A multi-omic analysis of an <i>Enterococcus faecium</i> mutant reveals specific genetic mutations and dramatic changes in mRNA and protein expression. <b>2013</b> , 13, 304	11
717	Population genomics of the endangered giant Galápagos tortoise. <b>2013</b> , 14, R136	24
716	Rapid microsatellite development for tree peony and its implications. <b>2013</b> , 14, 886	32
715	Viral expression associated with gastrointestinal adenocarcinomas in TCGA high-throughput sequencing data. <b>2013</b> , 7, 23	41

7 <sup>14</sup>	Phylogenomics of fescue grass-derived fungal endophytes based on selected nuclear genes and the mitochondrial gene complement. <b>2013</b> , 13, 270	13
7 <sup>13</sup>	Accurate detection of subclonal single nucleotide variants in whole genome amplified and pooled cancer samples using HaloPlex target enrichment. <b>2013</b> , 14, 856	19
7 <sup>12</sup>	iSVP: an integrated structural variant calling pipeline from high-throughput sequencing data. <b>2013</b> , 7 Suppl 6, S8	23
7 <sup>11</sup>	Whole genome resequencing in tomato reveals variation associated with introgression and breeding events. <b>2013</b> , 14, 791	98
7 <sup>10</sup>	Abnormal centrosome and spindle morphology in a patient with autosomal recessive primary microcephaly type 2 due to compound heterozygous WDR62 gene mutation. <b>2013</b> , 8, 178	29
7 <sup>09</sup>	Soil bacterial communities shaped by geochemical factors and land use in a less-explored area, Tibetan Plateau. <b>2013</b> , 14, 820	35
7 <sup>08</sup>	ChIP-seq in steatohepatitis and normal liver tissue identifies candidate disease mechanisms related to progression to cancer. <b>2013</b> , 6, 50	8
7 <sup>07</sup>	Targeted exome sequencing for mitochondrial disorders reveals high genetic heterogeneity. <b>2013</b> , 14, 118	46
7 <sup>06</sup>	Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. <b>2013</b> , 5, 91	125
7 <sup>05</sup>	Significant variance in genetic diversity among populations of <i>Schistosoma haematobium</i> detected using microsatellite DNA loci from a genome-wide database. <b>2013</b> , 6, 300	21
7 <sup>04</sup>	libgapmis: extending short-read alignments. <b>2013</b> , 14 Suppl 11, S4	5
7 <sup>03</sup>	Simple and efficient identification of rare recessive pathologically important sequence variants from next generation exome sequence data. <b>2013</b> , 34, 945-52	1
7 <sup>02</sup>	Deficiency in SLC25A1, encoding the mitochondrial citrate carrier, causes combined D-2- and L-2-hydroxyglutaric aciduria. <b>2013</b> , 92, 627-31	92
7 <sup>01</sup>	High throughput sequencing methods and analysis for microbiome research. <b>2013</b> , 95, 401-14	167
7 <sup>00</sup>	SWR-C and INO80 chromatin remodelers recognize nucleosome-free regions near +1 nucleosomes. <b>2013</b> , 154, 1246-56	138
6 <sup>99</sup>	Analysis of hepatitis B virus genotyping and drug resistance gene mutations based on massively parallel sequencing. <b>2013</b> , 193, 341-7	10
6 <sup>98</sup>	Genomic organization of human transcription initiation complexes. <b>2013</b> , 502, 53-8	49
6 <sup>97</sup>	A short-read multiplex sequencing method for reliable, cost-effective and high-throughput genotyping in large-scale studies. <b>2013</b> , 34, 1715-20	37

696	RNAi screens in mice identify physiological regulators of oncogenic growth. <b>2013</b> , 501, 185-90	117
695	Population genomic footprints of selection and associations with climate in natural populations of <i>Arabidopsis halleri</i> from the Alps. <b>2013</b> , 22, 5594-607	76
694	Anchoring and ordering NGS contig assemblies by population sequencing (POPSEQ). <b>2013</b> , 76, 718-27	219
693	Exome sequencing reveals FAM20c mutations associated with fibroblast growth factor 23-related hypophosphatemia, dental anomalies, and ectopic calcification. <b>2013</b> , 28, 1378-85	125
692	Massively-parallel sequencing assists the diagnosis and guided treatment of cancers of unknown primary. <b>2013</b> , 231, 413-23	73
691	Exome sequencing: an efficient diagnostic tool for complex neurodegenerative disorders. <b>2013</b> , 20, 486-492	20
690	Long runs of homozygosity are enriched for deleterious variation. <b>2013</b> , 93, 90-102	153
689	AMLs harboring DNMT3A-destabilizing variants show increased intratumor DNA methylation heterogeneity at bivalent chromatin domains.	0
688	The population genomic analyses of chloroplast genomes shed new insights on the complicated ploidy and evolutionary history in <i>Fragaria</i> . 13,	0
687	Rare genetic variants underlie outlying levels of DNA methylation and gene-expression.	0
686	N-Glycoprofiling of SLC35A2-CDG: Patient with a Novel Hemizygous Variant. <b>2023</b> , 11, 580	0
685	New Endothelial Corneal Dystrophy in a Chinese Family. <b>2023</b> , 42, 529-535	0
684	Whole Exome Sequencing Reveals Novel Candidate Genes in Familial Forms of Glaucomatous Neurodegeneration. <b>2023</b> , 14, 495	0
683	Paleogenetic analysis and radiocarbon dating on skeletal remains from the Roman necropolis of Contrada Diana (Lipari Island, Sicily). <b>2023</b> , 48, 103887	0
682	Spondyloocular Syndrome: A Report of an Additional Family and Phenotypic Spectrum Delineation. <b>2023</b> , 14, 497	0
681	Telomere-to-telomere assembly of diploid chromosomes with Verkko.	0
680	Massively parallel characterization of psychiatric disorder-associated and cell-type-specific regulatory elements in the developing human cortex.	0
679	Whole-genome sequencing identified novel mutations in a Chinese family with lynch syndrome. 13,	0

- 678 Genome-wide analysis of mutations induced by carbon ion beam irradiation in cotton. 14, ○
- 677 A phylogenetic study of dengue virus in urban Vietnam shows long-term persistence of endemic strains. **2023**, 9, ○
- 676 An Integrative Analysis of Nasopharyngeal Carcinoma Genomes Unraveled Unique Processes Driving a Viral-Positive Cancer. **2023**, 15, 1243 ○
- 675 Genomic diversity of SARS-CoV-2 can be accelerated by mutations in the nsp14 gene. **2023**, 26, 106210 ○
- 674 Dual specificity and target gene selection by the MADS-domain protein FRUITFULL. **2023**, 9, 473-485 ○
- 673 Natural variations of wheat EARLY FLOWERING 3 highlight their contributions to local adaptation through fine-tuning of heading time. ○
- 672 Clonal Hematopoiesis Mutations Are Present in Atherosclerotic Lesions in Peripheral Artery Disease. **2023**, 24, 3962 ○
- 671 The genome sequence of *Synechocystis* sp. PCC 6803 substrain GT-T and its implications for the evolution of PCC 6803 substrains. **2023**, 13, 701-712 ○
- 670 Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, *Quercus dentata*. ○
- 669 Low Gut Microbial Diversity Augments Estrogen-driven Pulmonary Fibrosis in Female-Predominant Interstitial Lung Disease. ○
- 668 Amazonian birds in more dynamic habitats have less population genetic structure and higher gene flow. ○
- 667 Whole Exome Sequencing of Hemiplegic Migraine Patients Shows an Increased Burden of Missense Variants in *CACNA1H* and *CACNA1I* Genes. ○
- 666 Widespread perturbation of ETS factor binding sites in cancer. **2023**, 14, ○
- 665 Benchmarking the Autoencoder Design for Imputing Single-Cell RNA Sequencing Data. ○
- 664 Tracking the evolution of esophageal squamous cell carcinoma under dynamic immune selection by multi-omics sequencing. **2023**, 14, ○
- 663 Genome, host genome integration, and gene expression in *Diadegma fenestrale* ichnovirus from the perspective of coevolutionary hosts. 14, ○
- 662 Predicting heterosis via genetic distance and the number of SNPs in selected segments of chromosomes in maize. 14, ○
- 661 Precipitation is the main axis of tropical plant phylogenetic turnover across space and time. **2023**, 9, ○

- 660 Insights into the Genetic Determination of the Autotetraploid Potato Plant Height. **2023**, 14, 507 ○
- 659 Parallel evolution and cryptic diversification in a common and widespread Amazonian tree, *Protium subserratum*. ○
- 658 NSD1 deposits histone H3 lysine 36 dimethylation to pattern non-CG DNA methylation in neurons. ○
- 657 Pangolin genomes offer key insights and resources for the world's most trafficked wild mammals. ○
- 656 SiHDA9 interacts with SiHAT3.1 and SiHDA19 to repress dehydration responses through H3K9 deacetylation in foxtail millet. ○
- 655 The idiosyncratic genome of Korean long-tailed chicken as a valuable genetic resource. **2023**, 26, 106236 ○
- 654 Multi-omics Investigation of Freeze Tolerance in the Amur Sleeper, an Aquatic Ectothermic Vertebrate. **2023**, 40, ○
- 653 Assessment of attenuation of varicella-zoster virus vaccines based on genomic comparison. **2023**, 95, ○
- 652 Transcriptome Dynamic Analysis Reveals New Candidate Genes Associated with Resistance to Fusarium Head Blight in Two Chinese Contrasting Wheat Genotypes. **2023**, 24, 4222 ○
- 651 Transcriptome-wide assessment of N6-methyladenosine modification identifies different gene expression and infection-associated pathways in *Treponema pallidum*-infected macrophage. **2023**, 109, 108-116 ○
- 650 Transcriptome-based variations effectively untangling the intraspecific relationships and selection signals in Xinyang Maojian tea population. 14, ○
- 649 Evolutionary History of the *Poecilia picta* Sex Chromosomes. **2023**, 15, ○
- 648 A Novel Preclinical In Vitro 3D Model of Oral Carcinogenesis for Biomarker Discovery and Drug Testing. **2023**, 24, 4096 ○
- 647 De Novo Assembly and Comparative Analysis of the Complete Mitochondrial Genome of *Chaenomeles speciosa* (Sweet) Nakai Revealed the Existence of Two Structural Isomers. **2023**, 14, 526 ○
- 646 Genome Polymorphism Analysis and Selected Sweep Regions Detection via the Genome Resequencing of 91 Cabbage (*Brassica oleracea*) Accessions. **2023**, 9, 283 ○
- 645 Tight genetic linkage of genes causing hybrid necrosis and pollinator isolation between young species. **2023**, 9, 420-432 ○
- 644 Pre- and Post-Zygotic Barriers Contribute to Reproductive Isolation and Correlate with Genetic Distance in *Cucumis*. **2023**, 12, 926 ○
- 643 Sweepstakes reproductive success via pervasive and recurrent selective sweeps. 12, ○

- 642 The genetic architecture of soybean photothermal adaptation to high latitudes. ○
- 641 Whole-Genome Comparison Reveals Structural Variations behind Heading Leaf Trait in Brassica oleracea. **2023**, 24, 4063 ○
- 640 Deciphering transcription factors and their corresponding regulatory elements during inhibitory interneuron differentiation using deep neural networks. 11, ○
- 639 Genetic Interaction of tRNA-Dependent Mistranslation with Fused in Sarcoma Protein Aggregates. **2023**, 14, 518 ○
- 638 Genome-Wide Genetic Structure of Henan Indigenous Chicken Breeds. **2023**, 13, 753 ○
- 637 Chromosome-level genome assembly and population genomics of Mongolian racerunner (*Eremias argus*) provide insights into high-altitude adaptation in lizards. **2023**, 21, ○
- 636 Impaired neurogenesis and neural progenitor fate choice in a human stem cell model of SETBP1 disorder. **2023**, 14, ○
- 635 FLI1 and FRA1 transcription factors drive the transcriptional regulatory networks characterizing muscle invasive bladder cancer. **2023**, 6, 1
- 634 A common genetic variation in GZMB may associate with cancer risk in patients with Lynch syndrome. 13, ○
- 633 Genomic analysis, trajectory tracking, and field surveys reveal sources and long-distance dispersal routes of wheat stripe rust pathogen in China. **2023**, 100563 ○
- 632 FrangiPANe, a tool for creating a panreference using left behind reads. **2023**, 5, ○
- 631 Genome-wide association study reveals markers and candidate genes associated with growth in the rice flower carp, an economic fish species of integrated rice-fish culture in China. 10, ○
- 630 Gene expression plasticity followed by genetic change during colonization a high-elevation environment. ○
- 629 Off-target piRNA gene silencing in *Drosophila melanogaster* rescued by a transposable element insertion. **2023**, 19, e1010598 ○
- 628 Bioinformatic Tools for NGS-Based Metagenomics to Improve the Clinical Diagnosis of Emerging, Re-Emerging and New Viruses. **2023**, 15, 587 ○
- 627 Single-cell whole-genome sequencing, haplotype analysis in prenatal diagnosis of monogenic diseases. **2023**, 6, e202201761 ○
- 626 A Comprehensive Genetic Analysis of Slovenian Families with Multiple Cases of Orofacial Clefts Reveals Novel Variants in the Genes IRF6, GRHL3, and TBX22. **2023**, 24, 4262 ○
- 625 Genomic, transcriptomic, and metabolomic analysis of *Oldenlandia corymbosa* reveals the biosynthesis and mode of action of anti-cancer metabolites. ○

- 624 Pan-genotypic probe-based enrichment to improve efficiency of Hepatitis B virus sequencing. ○
- 623 Genome assembly of *Musa beccari* shows extensive chromosomal rearrangements and genome expansion during evolution of Musaceae genomes. **2022**, 12, ○
- 622 Dietary butyrate ameliorates metabolic health associated with selective proliferation of gut Lachnospiraceae bacterium 28-4. **2023**, 8, ○
- 621 Identifying Targets of Selection in Laboratory Evolution Experiments. ○
- 620 FixItFelix: improving genomic analysis by fixing reference errors. **2023**, 24, ○
- 619 Whole-exome sequencing analysis of idiopathic hypogonadotropic hypogonadism: comparison of varicocele and non-obstructive azoospermia. ○
- 618 Structure of the human DICER3 pre-miRNA complex in a dicing state. **2023**, 615, 331-338 ○
- 617 Large-scale population structure and genetic architecture of agronomic traits of garlic. ○
- 616 Draft Genome Sequences of Three *Listeria monocytogenes* Strains Isolated from Chicken Carcasses in South Korea. **2023**, 12, ○
- 615 Community-wide collaboration is a must to reinstall trust in bioinformatics solutions and biomedical interpretation. **2023**, 20, ○
- 614 Autism-linked NLGN3 is a key regulator of gonadotropin-releasing hormone deficiency. **2023**, 16, ○
- 613 Drug Combination of Ciprofloxacin and Polymyxin B for the Treatment of Multidrug Resistant *Acinetobacter baumannii* Infections: A Drug Pair Limiting the Development of Resistance. **2023**, 15, 720 ○
- 612 A chromosome-level genome assembly for *Erianthus fulvus* provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. **2023**, 100562 ○
- 611 Regulatory mechanism of MeGI on sexuality in *Diospyros oleifera*. 14, ○
- 610 Improved Genomic Prediction of *Staphylococcus epidermidis* Isolation Sources with a Novel Polygenic Score. **2023**, 61, ○
- 609 Concerning the eXclusion in human genomics: The choice of sex chromosome representation in the human genome drastically affects number of identified variants. ○
- 608 Sequence determinant of small RNA production by DICER. **2023**, 615, 323-330 ○
- 607 CaV1 and CaV2 calcium channels mediate the release of distinct pools of synaptic vesicles. 12, ○

- 606 Lysosomal Storage Dysfunction, a Germline Variants Affecting Pancreatic Ductal Adenocarcinoma Development and Progression. ○
- 605 Chimera: The spoiler in multiple displacement amplification. **2023**, 21, 1688-1696 ○
- 604 Genomic prediction for complex traits across multiples harvests in alfalfa ( *Medicago sativa* L.) is enhanced by enviromics. ○
- 603 The AEGEAN-169 clade of bacterioplankton is synonymous with SAR11 subclade V (HIMB59) and metabolically distinct. ○
- 602 Targeted therapy for intractable cancer on the basis of molecular profiles: An open-label, phase II basket trial (Long March Pathway). 13, ○
- 601 Alteration of a Shiga toxin-encoding phage associated with a change in toxin production level and disease severity in *Escherichia coli*. **2023**, 9, ○
- 600 The Histone Variant H2A.Z C-Terminal Domain Has Locus-Specific Differential Effects on H2A.Z Occupancy and Nucleosome Localization. **2023**, 11, ○
- 599 ITDetect: a method to detect internal tandem duplication of FMS-like tyrosine kinase (FLT3) from next-generation sequencing data with high sensitivity and clinical application. **2023**, 24, ○
- 598 Genomic responses to parallel temperature gradients in the eelgrass *Zostera marina* in adjacent bays. ○
- 597 Highly accurate genome assembly of an improved high-yielding silkworm strain, Nichi01. **2023**, 13, ○
- 596 Genetic mapping of QTLs controlling brown seed coat traits by genome resequencing in sesame (*Sesamum indicum* L.). 14, ○
- 595 SSR identification and phylogenetic analysis in four plant species based on complete chloroplast genome sequences. **2023**, 125, 102670 ○
- 594 Phylogenetic challenges in a recently diversified and polyploid-rich *Alyssum* (Brassicaceae) lineage: low divergence, reticulation, and parallel polyploid speciation. ○
- 593 Highly conserved composite transposon harbouring aerobactin *iuc3* in *Klebsiella pneumoniae* from pigs. **2023**, 9, ○
- 592 A chromosome-level genome assembly of an early matured aromatic Japonica rice variety Qigeng10 to accelerate rice breeding for high grain quality in Northeast China. 14, ○
- 591 Computational methods and challenges in analyzing intratumoral microbiome data. **2023**, ○
- 590 Complete chloroplast genomes of six Neotropical palm tree species: genome structure comparison, identification of repeats sequences and evolutionary dynamic patterns. ○
- 589 The DNA damage response in advanced ovarian cancer: functional analysis combined with machine learning identifies signatures that correlate with chemotherapy sensitivity and patient outcome. ○

- 588 Sub genomic analysis of SARS-CoV-2 using short read amplicon-based sequencing. 14, ○
- 587 Inducible mismatch repair streamlines forward genetic approaches to target identification of cytotoxic small molecules. ○
- 586 Development and cytological characterization of wheat $\times$ thinopyrum intermedium translocation lines with novel stripe rust resistance gene. 14, ○
- 585 Comparative Analyses of Chloroplast Genomes for Parasitic Species of Santalales in the Light of Two Newly Sequenced Species, *Taxillus nigrans* and *Scurrula parasitica*. **2023**, 14, 560 ○
- 584 Highly-conserved regulatory activity of the ANR family in the virulence of diarrheagenic bacteria through interaction with Master and Global regulators. ○
- 583 Metagenomic analysis reveals patterns and hosts of antibiotic resistance in different pig farms. **2023**, 30, 52087-52106 ○
- 582 Genome-Wide Landscape of mRNAs, lncRNAs, and circRNAs during Testicular Development of Yak. **2023**, 24, 4420 ○
- 581 scCircle-seq unveils the diversity and complexity of circular DNAs in single cells. ○
- 580 Contrasting allelic effects for pistachio salinity tolerance in juvenile and mature trees. ○
- 579 Identification of a Novel Idiopathic Epilepsy Risk Locus and a Variant in the *CCDC85A* Gene in the Dutch Partridge Dog. **2023**, 13, 810 ○
- 578 Molecular Characterization of the First African Swine Fever Virus Genotype II Strains Identified from Mainland Italy, 2022. **2023**, 12, 372 ○
- 577 Whole genome sequencing of a wild swan goose population. 14, ○
- 576 Identification and characterization of extrachromosomal circular DNA in the silk gland of *Bombyx mori*. ○
- 575 Sample and library preparation approaches for the analysis of the virome of irrigation water. ○
- 574 Emergence, continuity, and evolution of *Yersinia pestis* throughout medieval and early modern Denmark. **2023**, 33, 1147-1152.e5 ○
- 573 Identification of MET fusions as novel therapeutic targets sensitive to MET inhibitors in lung cancer. **2023**, 21, ○
- 572 Clinical characteristics, diagnosis, outcomes and lung microbiome analysis of invasive pulmonary aspergillosis in the community-acquired pneumonia patients. **2023**, 10, e001358 ○
- 571 Climate-induced range shifts drive adaptive response via spatio-temporal sieving of alleles. **2023**, 14, ○

- 570 Weak range-wide population structure in the blackfin tuna (*Thunnus atlanticus*) revealed by analysis of genome-wide SNPs. ○
- 569 A minimal genome design to maximally guarantee fertile inter-subspecific hybrid rice. **2023**, 16, 726-738 1
- 568 Next-generation sequencing of pancreatic cyst wall specimens obtained using Moray micro-forceps for improving diagnostic accuracy. ○
- 567 Environmental drivers behind the genetic differentiation in mountain chickadees (*Poecile gambeli*). ○
- 566 A Cre-LoxP-based approach for combinatorial chromosome rearrangements in human HAP1 cells. **2023**, 31, ○
- 565 Exposure of *Shewanella oneidensis* MR-1 to Sublethal Doses of Ionizing Radiation Triggers Short-Term SOS Activation and Longer-Term Prophage Activation. **2023**, 89, ○
- 564 MeCP2 Represses the Activity of Topoisomerase II $\alpha$  in Long Neuronal Genes. ○
- 563 Conservation implications of elucidating the Korean wolf taxonomic ambiguity through whole-genome sequencing. ○
- 562 Novel Exon 7 Deletions in TSPAN12 in a Three-Generation FEVR Family: A Case Report and Literature Review. **2023**, 14, 587 ○
- 561 Short-Term Impact of Oxytetracycline Administration on the Fecal Microbiome, Resistome and Virulome of Grazing Cattle. **2023**, 12, 470 ○
- 560 Computational and mitochondrial functional studies of novel compound heterozygous variants in SPATA5 gene support a causal link with epileptogenic encephalopathy. **2023**, 17, ○
- 559 Core cellular and tissue-specific mechanisms enable desiccation tolerance in *Craterostigma*. **2023**, 114, 231-245 ○
- 558 An associative transcriptomics study on rice bean (*Vigna umbellata*) provides new insights into genetic basis and candidate genes governing flowering, maturity and seed weight. ○
- 557 Assessing the impacts of various factors on circular RNA reliability. **2023**, 6, e202201793 ○
- 556 Cancer vaccines based on whole-tumor lysate or neoepitopes with validated HLA binding outperform those with predicted HLA-binding affinity. **2023**, 26, 106288 ○
- 555 Whole-genome sequencing of ethnolinguistic diverse northwestern Chinese Hexi Corridor people from the 10K\_CPGDP project suggested the differentiated East-West genetic admixture along the Silk Road and their biological adaptations. ○
- 554 Phylogenomic insights into the origin and evolutionary history of evergreen broadleaved forests in East Asia under Cenozoic climate change. ○
- 553 cfSNV: a software tool for the sensitive detection of somatic mutations from cell-free DNA. ○

- 552 Evolutionary origin and establishment of a dioecious diploid-tetraploid complex. ○
- 551 The Colorectal Cancer Gut Environment Regulates Activity of the Microbiome and Promotes the Multidrug Resistant Phenotype of ESKAPE and Other Pathogens. **2023**, 8, 1
- 550 Screening of candidate genes related to differences in growth and development between Chinese indigenous and Western pig breeds. **2023**, 55, 147-153 ○
- 549 PCDH19 in Males: Are Hemizygous Variants Linked to Autism?. **2023**, 14, 598 ○
- 548 Genome-Wide Association Analysis of Fruit Shape-Related Traits in *Areca catechu*. **2023**, 24, 4686 ○
- 547 Genetic Basis of Early Onset Atrial Fibrillation in Patients without Risk Factors. **2023**, 10, 104 ○
- 546 Nanopore-Based Direct RNA Sequencing of the *Trypanosoma brucei* Transcriptome Identifies Novel lncRNAs. **2023**, 14, 610 ○
- 545 Unique Genomic Epidemiology of COVID-19 in the White Mountain Apache Tribe, April to August 2020, Arizona. **2023**, 8, ○
- 544 Regulatory de novo mutations underlying intellectual disability. **2023**, 6, e202201843 ○
- 543 Low Gut Microbial Diversity Augments Estrogen-Driven Pulmonary Fibrosis in Female-Predominant Interstitial Lung Disease. **2023**, 12, 766 ○
- 542 Human Genome Polymorphisms and Computational Intelligence Approach Revealed a Complex Genomic Signature for COVID-19 Severity in Brazilian Patients. **2023**, 15, 645 ○
- 541 QTL Mapping for Fiber Quality Based on Introgression Lines Population from *G. hirsutum* [G]. *tomentosum*. **2023**, 13, 579 ○
- 540 Genome assembly of the deep-sea coral *Lophelia pertusa*. ○
- 539 SMCHD1 loss triggers DUX4 expression by disrupting splicing in FSHD2. ○
- 538 An oligogenic architecture underlying ecological and reproductive divergence in sympatric populations. 12, ○
- 537 Building bridges from genome to physiology using machine learning and *Drosophila* experimental evolution. ○
- 536 Identification of SNP loci and candidate genes genetically controlling norisoprenoids in grape berry based on genome-wide association study. 14, ○
- 535 Chromosome-Length Assembly of the Baikal Seal (*Pusa sibirica*) Genome Reveals a Historically Large Population Prior to Isolation in Lake Baikal. **2023**, 14, 619 ○

- 534 Evolution of the germline mutation rate across vertebrates. **2023**, 615, 285-291 1
- 533 A novel mutation in ACS11 leads to androecy in cucumber. **2023**, 15, 650 0
- 532 Genetic Characterization of a Novel Equus caballus Papillomavirus Isolated from a Thoroughbred Mare. **2023**, 15, 650 0
- 531 A 23,000-year-old southern Iberian individual links human groups that lived in Western Europe before and after the Last Glacial Maximum. **2023**, 7, 597-609 0
- 530 No Increased Detection of Nucleic Acids of CNS-related Viruses in the Brains of Patients with Schizophrenia, Bipolar Disorder, and Autism Spectrum Disorder. 0
- 529 A spinal muscular atrophy modifier implicates the SMN protein in SNARE complex assembly at neuromuscular synapses. **2023**, 14, 884 0
- 528 Circulating tumor DNA reveals complex biological features with clinical relevance in metastatic breast cancer. **2023**, 14, 884 0
- 527 Non-Synonymous Variants in Fat QTL Genes among High- and Low-Milk-Yielding Indigenous Breeds. **2023**, 13, 884 0
- 526 Limited genetic variations of the Rh5-CyRPA-Ripr invasion complex in Plasmodium falciparum parasite population in selected malaria-endemic regions, Kenya. 4, 884 0
- 525 Whole-genome sequencing reveals a complex African population demographic history and signatures of local adaptation. **2023**, 186, 923-939.e14 1
- 524 Chromosomal Position of Ribosomal Protein Genes Affects Long-Term Evolution of Vibrio cholerae. 0
- 523 Robust Performance of SARS-CoV-2 Whole-Genome Sequencing from Wastewater with a Nonselective Virus Concentration Method. **2023**, 3, 954-962 0
- 522 Equine exploitation at Pompeii (AD 79). **2023**, 48, 103902 0
- 521 Prediction Model with HLA-A\*33:03 Reveals Number of Days to Develop Liver Cancer from Blood Test. **2023**, 24, 4761 0
- 520 Functional annotation of the animal genomes: An integrated annotation resource for the horse. **2023**, 19, e1010468 0
- 519 Adaptive laboratory evolution to hypersaline conditions of lactic acid bacteria isolated from seaweed. **2023**, 75, 21-30 0
- 518 Genetic Variants in Protein Tyrosine Phosphatase Non-Receptor Type 23 Are Responsible for Mesiodens Formation. **2023**, 12, 393 0
- 517 PGNneo: A Proteogenomics-Based Neoantigen Prediction Pipeline in Noncoding Regions. **2023**, 12, 782 0

- 516 Congenital hydrocephalus: new Mendelian mutations and evidence for oligogenic inheritance. **2023**, 17,
- 515 Identification of circular RNAs of *Cannabis sativa* L. potentially involved in the biosynthesis of cannabinoids. **2023**, 257,
- 514 hPSC-derived sacral neural crest enables rescue in a severe model of Hirschsprung's disease. **2023**, 30, 264-282.e9
- 513 Pangenomic analysis identifies structural variation associated with heat tolerance in pearl millet. **2023**, 55, 507-518
- 512 Point mutations of homologs as an adaptive solution to the gene loss. **2023**,
- 511 Characterization of Genes That Exhibit Genotype-Dependent Allele-Specific Expression and Its Implications for the Development of Maize Kernel. **2023**, 24, 4766
- 510 The enormous repetitive Antarctic krill genome reveals environmental adaptations and population insights. **2023**, 186, 1279-1294.e19
- 509 Whole exome sequencing in unexplained recurrent miscarriage families identified novel pathogenic genetic causes of euploid miscarriage.
- 508 Diversity and potential function of pig gut DNA viruses. **2023**, 9, e14020
- 507 Soluble Guanylate Cyclase  $\beta$  Subunit Represses Human Glioblastoma Growth. **2023**, 15, 1567
- 506 An autoimmune pleiotropic SNP modulates IRF5 alternative promoter usage through ZBTB3-mediated chromatin looping. **2023**, 14,
- 505 Population Structure Analysis and Genome-Wide Association Study of Tea (*Camellia sinensis* (L.) Kuntze) Germplasm in Qiannan, China, Based on SLAF-Seq Technology. **2022**, 91, 791-809
- 504 Identification and characterization analysis of candidate genes controlling mushroom leaf development in Chinese kale by BSA-seq. **2023**, 43,
- 503 Recessive pathogenic variants in MCAT cause combined oxidative phosphorylation deficiency. 12,
- 502 Exploring microbial functional biodiversity at the protein family level from metagenomic sequence reads to annotated protein clusters. 3,
- 501 Adulis and the transshipment of baboons during classical antiquity.
- 500 Microhomology-Mediated Circular DNA Formation from Oligonucleosomal Fragments During Spermatogenesis.
- 499 Genome-wide association study for the primary feather color trait in a native Chinese duck. 14,

- 498 Importance of genetic architecture in marker selection decisions for genomic prediction. ○
- 497 Enhancing urinary tract infection diagnosis for negative culture patients with metagenomic next-generation sequencing (mNGS). 13, ○
- 496 Structural variation of a sex-linked region confers monoecy and implicates GATA15 as a master regulator of sex in *Salix purpurea*. ○
- 495 Recombination Variation Shapes Phylogeny and Introgression in Wild Diploid Strawberries. **2023**, 40, ○
- 494 Developing Methods for Maintaining Genetic Diversity in Novel Aquaculture Species: The Case of *Seriola lalandi*. **2023**, 13, 913 ○
- 493 A scalable, GMP-compatible, autologous organotypic cell therapy for Dystrophic Epidermolysis Bullosa. ○
- 492 Comparative genomic epidemiology of serotype 3 IPD and carriage isolates from Southampton, UK between 2005 and 2017. **2023**, 9, ○
- 491 Computational genomics for understanding of DNA-DNA and protein-protein similarity. **2023**, 217-263 ○
- 490 Novel deleterious splicing variant in HFM1 causes gametogenesis defect and recurrent implantation failure: concerning the risk of chromosomal abnormalities in embryos. ○
- 489 Construction of a mini-RNA replicon in *Escherichia coli*. **2023**, 8, ○
- 488 The c.126C>A(p.Cys42Ter) SLC7A10 nonsense variant is a candidate causative variant for paradoxical pseudomyotonia in English Cocker and Springer Spaniels. ○
- 487 Systematic Identification of Post-Transcriptional Regulatory Modules. ○
- 486 Genome biology and evolution of mating type loci in four cereal rust fungi. ○
- 485 BRD9-SMAD2/3 orchestrates stemness and tumorigenesis in pancreatic ductal adenocarcinoma. ○
- 484 Phylogenomics sheds new light on the drivers behind a long-lasting systematic riddle: the figwort family Scrophulariaceae. ○
- 483 Stepwise use of genomics and transcriptomics technologies increases diagnostic yield in Mendelian disorders. 11, ○
- 482 Identification of putative regulatory single-nucleotide variants in NTN1 gene associated with NSCL/P. ○
- 481 Genomic epidemiology of SARS-CoV-2 during the first four waves in Mozambique. **2023**, 3, e0001593 ○

- 480 Genotype-phenotype mapping of a patient-derived lung cancer organoid biobank identifies NKX2-1-defined Wnt dependency in lung adenocarcinoma. **2023**, 42, 112212 ○
- 479 A genetic locus complements resistance to Bordetella pertussis-induced histamine sensitization. **2023**, 6, ○
- 478 Viral Metagenomic Analysis of the Fecal Samples in Domestic Dogs (*Canis lupus familiaris*). **2023**, 15, 685 ○
- 477 Population genetics of zig-zag eel (*Mastacembelus armatus*) uncover gene flow between an isolated island and the mainland China. 10, ○
- 476 Toward a global virus genomic surveillance network. **2023**, ○
- 475 Chromatin Remodeling via Retinoic Acid Action during Murine Spermatogonial Development. **2023**, 13, 690 ○
- 474 Evolution of synchronous female bilateral breast cancers and response to treatment. **2023**, 29, 646-655 ○
- 473 Genome Sequencing and Characterization of an Avian Orthoavulavirus 1 VG/GA-like Isolate with a Unique Fusion Cleavage Site Motif. **2023**, 67, ○
- 472 Fast and accurate DNaseSeq Variant Calling workflow composed of LUSH toolkit. ○
- 471 A key gene for the climatic adaptation of *Apis cerana* populations in China according to selective sweep analysis. **2023**, 24, ○
- 470 A comparative investigation of variant calling and genotyping for a single non-Caucasian whole genome. ○
- 469 Identification of exceptionally potent adenosine deaminases RNA editors from high body temperature organisms. **2023**, 19, e1010661 ○
- 468 Antifungal Tolerance and Resistance Emerge at Distinct Drug Concentrations and Rely upon Different Aneuploid Chromosomes. ○
- 467 LSD1 inhibition disrupts super-enhancer driven oncogenic transcriptional programs in castration-resistant prostate cancer. ○
- 466 Mutation Rate and Spectrum of the Silkworm in Normal and Temperature Stress Conditions. **2023**, 14, 649 ○
- 465 Shotgun metagenomics unravels higher antibiotic resistome profile in Bangladeshi gut microbiome. ○
- 464 The effects of mutations on gene expression and alternative splicing: a case study of EMS-induced heritable mutations in the microcrustacean *Daphnia*. ○
- 463 Genome-wide association study to identify SNPs and candidate genes associated with body size traits in donkeys. 14, ○

- 462 Recurrent neo-sex chromosome evolution in kiwifruit. **2023**, 9, 393-402 ○
- 461 Genomic analysis of *Leishmania turanica* strains from different regions of Central Asia. **2023**, 17, e0011145 ○
- 460 Somatic mutation landscape in a cohort of meningiomas that have undergone grade progression. **2023**, 23, ○
- 459 *Borrelia burgdorferi* Outer Surface Protein C Is Not the Sole Determinant of Dissemination in Mammals. **2023**, 91, ○
- 458 Next-generation sequencing analysis of hepatitis C virus resistance-associated substitutions in direct-acting antiviral failure in South Korea. **2023**, 29, 496-509 ○
- 457 Developing and reusing bioinformatics data analysis pipelines using scientific workflow systems. **2023**, 21, 2075-2085 ○
- 456 Integrating extracellular vesicle and circulating cell-free DNA analysis on a single plasma aliquot from breast cancer patients improves the detection of HER2 positivity. ○
- 455 Identification of de novo Mutations in the Chinese Autism Spectrum Disorder Cohort via Whole-Exome Sequencing Unveils Brain Regions Implicated in Autism. ○
- 454 PD-1 blockade plus chemoradiotherapy as preoperative therapy for patients with BRPC/LAPC: A biomolecular exploratory, phase II trial. **2023**, 4, 100972 ○
- 453 Genomics Insight into cfr-Mediated Linezolid-Resistant LA-MRSA in Italian Pig Holdings. **2023**, 12, 530 ○
- 452 A pseudo-outbreak of *Cyberlindnera fabianii* funguria: Implication from whole genome sequencing assay. 13, ○
- 451 Morphine Re-arranges Chromatin Spatial Architecture of Primate Cortical Neurons. ○
- 450 Multiple domestication events explain the origin of *Gossypium hirsutum* landraces in Mexico. **2023**, 13, ○
- 449 Whole genome analyses reveal weak signatures of population structure and environmentally associated local adaptation in an important North American pollinator, the bumble bee *Bombus vosnesenskii*. ○
- 448 De novo assembly of a chromosome-level reference genome of the ornamental butterfly *Sericanus montelus* based on nanopore sequencing and Hi-C analysis. 14, ○
- 447 Identification of Genetic Alterations in Rapid Progressive Glioblastoma by Use of Whole Exome Sequencing. **2023**, 13, 1017 ○
- 446 High performance imputation of structural and single nucleotide variants in Atlantic salmon using low-coverage whole genome sequencing. ○
- 445 Chromosome-level genome assembly of *Phrynocephalus forsythii* using third-generation DNA sequencing and Hi-C analysis. **2023**, 30, ○

- 444 genomepy: genes and genomes at your fingertips. **2023**, 39, ○
- 443 CTCF controls three-dimensional enhancer network underlying the inflammatory response of bone marrow-derived dendritic cells. **2023**, 14, ○
- 442 MC38 colorectal tumor cell lines from two different sources display substantial differences in transcriptome, mutanome and neoantigen expression. 14, ○
- 441 Campus Sewage Water Surveillance based dynamics and infection trends of SARS-CoV-2 variants during third wave of COVID-19 in Pune, India. ○
- 440 NPC1 variants are not associated with Parkinson's disease, REM-sleep behavior disorder or dementia with Lewy bodies in European cohorts. **2023**, ○
- 439 Emergence of Canonical and Noncanonical Genomic Variants following In Vitro Exposure of Clinical Mycobacterium tuberculosis Strains to Bedaquiline or Clofazimine. **2023**, 67, ○
- 438 ASGARD+: A New Modular Platform for Bacterial Antibiotic-Resistant Analysis. **2023**, 3, ○
- 437 A hydrogenotrophic Sulfurimonas is globally abundant in deep-sea oxygen-saturated hydrothermal plumes. **2023**, 8, 651-665 ○
- 436 Genus-Wide Genomic Characterization of Macrocooccus: Insights into Evolution, Population Structure, and Functional Potential. ○
- 435 Current sika deer effective population size is near to reaching its historically highest level in the Japanese archipelago by release from hunting rather than climate change and top predator extinction. 095968362311570 ○
- 434 A crowdsourcing database for the copy-number variation of the Spanish population. **2023**, 17, ○
- 433 Fine mapping of genes controlling pigment accumulation in oilseed rape (*Brassica napus* L.). **2023**, 43, ○
- 432 Genomic selection for agronomic traits in a winter wheat breeding program. **2023**, 136, ○
- 431 The impacts of bronze age in the gene pool of Chinese: Insights from phylogeographics of Y-chromosomal haplogroup N1a2a-F1101. 14, ○
- 430 Developing an integrated genomic selection approach beyond biomass for varietal protection and nutritive traits in perennial ryegrass (*Lolium perenne* L.). **2023**, 136, ○
- 429 Evolution of highly pathogenic H5N1 influenza A virus in the central nervous system of ferrets. **2023**, 19, e1011214 ○
- 428 Exploring the Relationship between Genomic Variation and Phenotype in Ornamental Pomegranate: A Study of Single and Double-Petal Varieties. **2023**, 9, 361 ○
- 427 Integrated metabolic and genetic analysis reveals distinct features of primary differentiated thyroid cancer and its metastatic potential in humans. ○

- 426 The Allele Catalog Tool: a web-based interactive tool for allele discovery and analysis. **2023**, 24, ○
- 425 Genetic Diversity and Phylogeography of a Turf-Forming Cosmopolitan Marine Alga, *Gelidium crinale* (Gelidiales, Rhodo-Phyta). **2023**, 24, 5263 ○
- 424 Upregulation of tandem duplicated BoFLC1 genes is associated with the non-flowering trait in *Brassica oleracea* var. *capitata*. **2023**, 136, ○
- 423 A hybrid and poly-polish workflow for the complete and accurate assembly of phage genomes: a case study of ten przondoviruses. ○
- 422 Long-B prokaryotic Argonaute systems employ various effectors to confer immunity via abortive infection. ○
- 421 Phenylalanine Ammonia-Lyase: A Key Gene for Color Discrimination of Edible Mushroom *Flammulina velutipes*. **2023**, 9, 339 ○
- 420 Clinical and biomarker analyses of sintilimab plus gemcitabine and cisplatin as first-line treatment for patients with advanced biliary tract cancer. **2023**, 14, ○
- 419 Chromosome-level genome of the three-spot damselfish, *Dascyllus trimaculatus*. **2023**, 13, ○
- 418 The chromosome-scale genome assembly of *Jasminum sambac* var. *unifoliatum* provides insights into the formation of floral fragrance. **2023**, ○
- 417 Weak reproductive isolation and extensive gene flow between *Mimulus glaucescens* and *M. guttatus* in northern California. ○
- 416 Phenotypic dimorphism between honeybee queen and worker is regulated by complicated epigenetic modifications. **2023**, 26, 106308 ○
- 415 In-silico Discovery of Genetic Diversity in *Cucumis sativus* var. *hardwickii*: A Wild Relative of Cultivated Cucumber. ○
- 414 Clinical isolates of *Candida auris* with enhanced adherence and biofilm formation due to genomic amplification of ALS4. **2023**, 19, e1011239 ○
- 413 Whole exome and transcript profiling of liver following aflatoxin B1 exposure in rats. ○
- 412 Ancient DNA of the Don-Hares Assumes the Existence of Two Distinct Mitochondrial Clades in Northeast Asia. **2023**, 14, 700 ○
- 411 Geographic-genomic and geographic-phenotypic differentiation of the *Aquilegia viridiflora* complex. ○
- 410 Mitochondrial Genome Sequence of *Salvia officinalis* (Lamiales: Lamiaceae) Suggests Diverse Genome Structures in Cogenetic Species and Finds the Stop Gain of Genes through RNA Editing Events. **2023**, 24, 5372 ○
- 409 Genetic structure and local adaptation of *Neptunea cumingii* crosse populations in China based on GBS technology. 11, ○

- 408 Deciphering the genetic basis of resistance to soybean cyst nematode combining IBD and association mapping. **2023**, 136, ○
- 407 Rare missense variants in the SH3 domain of PSTPIP1 are associated with hidradenitis suppurativa. **2023**, 4, 100187 ○
- 406 Characterization of viral pathogens associated with symptomatic upper respiratory tract infection in adults during a low COVID-19 transmission period. 11, e15008 ○
- 405 Characterization of the USDA Cucurbita pepo, C. moschata, and C. maxima germplasm collections. 14, ○
- 404 iGDP : An integrated genome decontamination pipeline for wild ciliated microeukaryotes. ○
- 403 Vaccination against swine influenza in pigs causes different drift evolutionary patterns upon swine influenza virus experimental infection and reduces the likelihood of genomic reassortments. 13, ○
- 402 Population Structure, Genetic Diversity and Candidate Genes for the Adaptation to Environmental Stress in Picea koraiensis. **2023**, 12, 1266 ○
- 401 C-Type Natriuretic Peptide Acts as a Microorganism-Activated Regulator of the Skin Commensals Staphylococcus epidermidis and Cutibacterium acnes in Dual-Species Biofilms. **2023**, 12, 436 ○
- 400 Multi-omics analysis uncovers tumor ecosystem dynamics during neoadjuvant toripalimab plus nab-paclitaxel and S-1 for esophageal squamous cell carcinoma: a single-center, open-label, single-arm phase 2 trial. **2023**, 90, 104515 ○
- 399 Co-Occurrence and Cooperation between Comammox and Anammox Bacteria in a Full-Scale Attached Growth Municipal Wastewater Treatment Process. **2023**, 57, 5013-5023 ○
- 398 Genome-Wide Association Study of Growth and Sex Traits Provides Insight into Heritable Mechanisms Underlying Growth Development of Macrobrachium nipponense (Oriental River Prawn). **2023**, 12, 429 ○
- 397 Association between Variants in the OCA2-HERC2 Region and Blue Eye Colour in HERC2 rs12913832 AA and AG Individuals. **2023**, 14, 698 ○
- 396 Comprehensive molecular phenotyping of ARID1A-deficient gastric cancer reveals pervasive epigenomic reprogramming and therapeutic opportunities. gutjnl-2022-328332 ○
- 395 A neomorphic mutation in the interferon activation domain of IRF4 causes a dominant primary immunodeficiency. **2023**, 220, ○
- 394 Fluoroquinolone Residues in the Environment Rapidly Induce Heritable Fluoroquinolone Resistance in Escherichia coli. **2023**, 57, 4784-4795 ○
- 393 Inferring biological kinship in ancient datasets: comparing the response of ancient DNA-specific software packages to low coverage data. **2023**, 24, ○
- 392 Bi-allelic mutation in SEC16B alters collagen trafficking and increases ER stress. **2023**, 15, ○
- 391 A Biallelic Truncating Variant in the TPR Domain of GEMIN5 Associated with Intellectual Disability and Cerebral Atrophy. **2023**, 14, 707 ○

- 390 Association of rare variants in ARSA with Parkinson disease. ○
- 389 First complete mitochondrial genome of the endemic goby, *Rhinogobius davidi* (Gobiiformes: Gobiidae: Gobionellinae), in China. **2023**, 8, 410-413 ○
- 388 BnIR: A multi-omics database with various tools for *Brassica napus* research and breeding. **2023**, 16, 775-789 ○
- 387 Survivin (BIRC5) Peptide Vaccine in the 4T1 Murine Mammary Tumor Model: A Potential Neoadjuvant T Cell Immunotherapy for Triple Negative Breast Cancer: A Preliminary Study. **2023**, 11, 644 ○
- 386 High Performance of a Dominant/X-Linked Gene Panel in Patients with Neurodevelopmental Disorders. **2023**, 14, 708 ○
- 385 The promise and challenges of characterizing genome-wide structural variants: A case study in a critically endangered parrot. ○
- 384 Immunogenetic metabolomics revealed key enzymes that modulate CAR-T metabolism and function. ○
- 383 Targeted engagement of Bcatenin-Ikaros complexes in refractory B-cell malignancies. ○
- 382 A Novel CovS Variant Harbored by a Colonization Strain Reduces *Streptococcus pyogenes* Virulence. ○
- 381 Microbial and Viral Genome and Proteome Nitrogen Demand Varies across Multiple Spatial Scales within a Marine Oxygen Minimum Zone. ○
- 380 Molecular Profile of MSH6-Associated Colorectal Carcinomas Shows Distinct Features From Other Lynch Syndrome-Associated Colorectal Carcinomas. **2023**, ○
- 379 Population genetics and geographic origins of mallards harvested in northwestern Ohio. **2023**, 18, e0282874 ○
- 378 The tissue-specific chromatin accessibility landscape of *Papaver somniferum*. 14, ○
- 377 An improved germline genome assembly for the sea lamprey *Petromyzon marinus* illuminates the evolution of germline-specific chromosomes. **2023**, 42, 112263 ○
- 376 Ancient mitogenomes from the Southern Pampas of Argentina reflect local differentiation and limited extra-regional linkages after rapid initial colonization. ○
- 375 Overexpression of Lmo2 initiates T-lymphoblastic leukemia via impaired thymocyte competition. **2023**, 220, ○
- 374 Population Structure and Genetic Diversity Analysis of Nufen 1H Line Chickens Using Whole-Genome Resequencing. **2023**, 13, 793 ○
- 373 Synthetic maize centromeres transmit chromosomes across generations. **2023**, 9, 433-441 ○

- 372 Mutations in ARHGEF15 cause autosomal dominant hereditary cerebral small vessel disease and osteoporotic fracture. **2023**, 145, 681-705 ○
- 371 Potential predictive value of circulating tumor DNA (ctDNA) mutations for the efficacy of immune checkpoint inhibitors in advanced triple-negative breast cancer. 14, ○
- 370 Maternal genetic history of ancient Tibetans over the past 4000 years. **2023**, ○
- 369 Hybrid zone or hybrid lineage: a genomic reevaluation of Sibley's classic species conundrum in *Pipilo towhees*. **2023**, 77, 852-869 1
- 368 Single substitution in H3.3G34 alters DNMT3A recruitment to cause progressive neurodegeneration. **2023**, 186, 1162-1178.e20 ○
- 367 Atorvastatin-pretreated mesenchymal stem cell-derived extracellular vesicles promote cardiac repair after myocardial infarction via shifting macrophage polarization by targeting microRNA-139-3p/Stat1 pathway. **2023**, 21, 1
- 366 Motif elucidation in ChIP-seq datasets with a knockout control. **2023**, 3, ○
- 365 Use of Next Generation Sequencing to Define the Origin of Primary Myelofibrosis. **2023**, 15, 1785 ○
- 364 Consolidating 23 years of historical data from an irrigated subtropical rice breeding program in Uruguay. ○
- 363 Comparative genomics reveals the diversification of triterpenoid biosynthesis and origin of ocotillol-type triterpenes in *Panax*. **2023**, 100591 ○
- 362 Synthetic regulatory genomics uncovers enhancer context dependence at the Sox2 locus. **2023**, 83, 1140-1152.e7 ○
- 361 Chromatin profiling identifies transcriptional readthrough as a conserved mechanism for piRNA biogenesis in mosquitoes. **2023**, 42, 112257 ○
- 360 Genome assembly of the deep-sea coral *Lophelia pertusa*. 2023, 1-12 ○
- 359 Verification of prognostic expression biomarkers is improved by examining enriched leukemic blasts rather than mononuclear cells from acute myeloid leukemia patients. **2023**, 11, ○
- 358 Intratumoral Bacteria Dysbiosis Is Associated with Human Papillary Thyroid Cancer and Correlated with Oncogenic Signaling Pathways. **2023**, ○
- 357 Multiomic analysis of malignant pleural mesothelioma identifies molecular axes and specialized tumor profiles driving intertumor heterogeneity. **2023**, 55, 607-618 ○
- 356 Whole Genome DNA Methylation and Mutational Profiles Identify Novel Changes in Proliferative Verrucous Leukoplakia. **2023**, ○
- 355 Antiviral immune response reveals host-specific virus infections in natural ant populations. 14, ○

- 354 Pharmacogenomic and Statistical Analysis. **2023**, 305-330 ○
- 353 Asexual male production by ZW recombination in *Artemia parthenogenetica*. **2023**, 77, 1-12 ○
- 352 Human genetic history on the Tibetan Plateau in the past 5100 years. **2023**, 9, ○
- 351 Assessment of the Genetic Diversity and Population Structure of the Peruvian Andean Legume, Tarwi (*Lupinus mutabilis*), with High Quality SNPs. **2023**, 15, 437 ○
- 350 Proteomic profiling of gastric cancer with peritoneal metastasis identifies a protein signature associated with immune microenvironment and patient outcome. ○
- 349 Assembly of novel microbial genomes from gut metagenomes of rhesus macaque (*Macaca mulatta*). **2023**, 15, ○
- 348 BRCA1-methylated triple negative breast cancers previously exposed to neoadjuvant chemotherapy form RAD51 foci and respond poorly to olaparib. 13, ○
- 347 Role of Histone Variant H2A.J in Fine-Tuning Chromatin Organization for the Establishment of Ionizing Radiation-Induced Senescence. **2023**, 12, 916 ○
- 346 Analysis of Genome Structure and Its Variations in Potato Cultivars Grown in Russia. **2023**, 24, 5713 ○
- 345 Identification and comparison of *Chlamydia psittaci*, *Legionella* and *Mycoplasma pneumonia* infection. ○
- 344 Evolution of the rice blast pathogen on spatially structured rice landraces maintains multiple generalist fungal lineages. ○
- 343 Chromosome-level de novo genome assembly of two conifer-parasitic wasps, *Megastigmus duclouxiana* and *Megastigmus sabinae*, reveals genomic imprints of adaptation to hosts. ○
- 342 Phylogenetic Analysis of Allotetraploid Species Using Polarized Genomic Sequences. ○
- 341 Metagenomic sequencing reveals swine lung microbial communities and metagenome-assembled genomes associated with lung lesions— pilot study. ○
- 340 Genomic epidemiology and antimicrobial resistance transmission of *Salmonella* Typhi and Paratyphi A at three urban sites in Africa and Asia. ○
- 339 Human Gut Microbial Sulfonolipids are linked to Inflammatory Bowel Diseases through Toll-Like Receptor 4 Signaling. ○
- 338 6mA-Sniper: Quantifying 6mA Sites in Eukaryotes at Single-Nucleotide Resolution. ○
- 337 NanoSquiggleVar: A method for direct analysis of targeted variants based on nanopore sequencing signals. ○

- 336 Pioneer factor ASCL1 cooperates with the mSWI/SNF complex at distal regulatory elements to regulate human neural differentiation. **2023**, 37, 218-242 ○
- 335 Rare Variants in Pharmacogenes Influence Clozapine Metabolism in Individuals with Schizophrenia. ○
- 334 Resistance in pea (*Pisum sativum*) genetic resources to the pea aphid, *Acyrtosiphon pisum*. ○
- 333 Genetic mapping of AhVt1, a novel genetic locus that confers the variegated testa color in cultivated peanut (*Arachis hypogaea* L.) and its utilization for marker-assisted selection. 14, ○
- 332 Dual impact of PTEN mutation on CSF dynamics and cortical networks via the dysregulation of neural precursors and their interneuron descendants. ○
- 331 Elucidating the genomic history of commercially used *Bacillus thuringiensis* subsp. *tenebrionis* strain NB176. 13, ○
- 330 Whole Genome Resequencing Revealed the Effect of Helicase yqhH Gene on Regulating *Bacillus thuringiensis* LLP29 against Ultraviolet Radiation Stress. **2023**, 24, 5810 1
- 329 Analysis of Genetic Diversity in *Coilia nasus* Based on 2b-RAD Simplified Genome Sequencing. **2023**, 15, 1173 ○
- 328 Single-cell transcriptomics identifies different immune signatures between macrophage activation-like syndrome and immune paralysis in sepsis. ○
- 327 Past Connectivity but Recent Inbreeding in Cross River Gorillas Determined Using Whole Genomes from Single Hairs. **2023**, 14, 743 ○
- 326 Complete mitochondrial genome sequence and annotation of *Rhinogobius lentiginis* (Gobiiformes: Gobiidae: Gobionellinae). **2023**, 8, 418-421 ○
- 325 Further evidence of an evolutionary continuum from a subset of lung carcinoids to aggressive neuroendocrine tumors. ○
- 324 Selective whole-genome amplification reveals population genetics of *Leishmania braziliensis* directly from patient skin biopsies. **2023**, 19, e1011230 ○
- 323 Parthenocarpy-related genes induced by naphthalene acetic acid in oil palm interspecific O<sub>1</sub> [Elaeis oleifera (Kunth) Cort<sup>1</sup>] [Elaeis guineensis Jacq.] hybrids. 14, ○
- 322 Mating systems and recombination landscape strongly shape genetic diversity and selection in wheat relatives. ○
- 321 Relatedness within colonies of three North American species of carpenter ants (Subgenus: *Camponotus*) and a comparison with relatedness estimates across Formicinae. ○
- 320 Analysis of Small Non-coding RNAs as Signaling Intermediates of Environmentally Integrated Responses to Abiotic Stress. **2023**, 403-427 ○
- 319 Evolutionary history of two evergreen *Rhododendron* species as revealed by chromosome-level genome assembly. 14, ○

- 318 Intraspecific Comparative Analysis Reveals Genomic Variation of *Didymella arachidicola* and Pathogenicity Factors Potentially Related to Lesion Phenotype. **2023**, 12, 476 ○
- 317 Genome-resolved metagenomics of milk microbiomes reveals the influence of maternal dietary fiber on neonatal inheritance of immunoregulatory traits. ○
- 316 Effects of oxycodone pharmacogenetics on postoperative analgesia and related clinical outcomes in children: a pilot prospective study. **2023**, 24, 187-197 ○
- 315 Co-segregation of recombinant chromatids maintains genome-wide heterozygosity in an asexual nematode. ○
- 314 Genomic analyses of hair from Ludwig van Beethoven. **2023**, ○
- 313 Native solitary bee reproductive success depends on early season precipitation and host plant richness. **2023**, 201, 965-978 ○
- 312 Comparative genomics of *Mycoplasma feriruminatoris*, a fast-growing pathogen of wild *Caprinae*. ○
- 311 Identification and characterization of extrachromosomal circular DNA in patients with high myopia and cataract. **2023**, 18, ○
- 310 A theoretical base for non-invasive prenatal paternity testing. **2023**, 346, 111649 ○
- 309 A view of the pan-genome of domesticated Cowpea (*Vigna unguiculata* [L.] Walp.). ○
- 308 Integrated analysis of genomic and transcriptomic data for the discovery of splice-associated variants in cancer. **2023**, 14, ○
- 307 Integration of GWAS, linkage analysis and transcriptome analysis to reveal the genetic basis of flowering time-related traits in maize. 14, ○
- 306 Recovery of metagenomic data from the *Aedes aegypti* microbiome using a reproducible snakemake pipeline: MINUUR. 8, 131 ○
- 305 Genomic clustering by geography not species in taxonomically complex British and Irish eyebrights (*Euphrasia*). ○
- 304 Identification of a suppressor for the wheat stripe rust resistance gene *Yr81* in Chinese wheat landrace Dahongpao. **2023**, 136, ○
- 303 Fine-mapping and candidate gene analysis of the *Mcgy1* locus responsible for gynoecy in bitter gourd (*Momordica* spp.). **2023**, 136, ○
- 302 Fine mapping and causal gene identification of a novel QTL for early flowering by QTL-seq, Target-seq and RNA-seq in spring oilseed rape. **2023**, 136, ○
- 301 Artificial selection footprints in domestic chicken genomes. ○

- 300 GWAS of grain color and tannin content in Chinese sorghum based on whole-genome sequencing. **2023**, 136, ○
- 299 Metagenomic analysis of coastal Kenya female *Aedes aegypti* mosquito RNA metaviromes reveal presence of diverse insect specific viruses. 8, 136 ○
- 298 A novel subclonal rearrangement of the STRN3::PDGFRB genes in de novo acute myeloid leukemia with NPM1 mutation and its leukemogenic effects. ○
- 297 Linkage and next generation sequencing (NGS) data in six large Danish families with dyslexia. ○
- 296 NVWa: Enhancing Sequence Alignment Accelerator Throughput via Hardware Scheduling. **2023**, ○
- 295 Vaginal microbiota of adolescents and their mothers: A preliminary study of vertical transmission and persistence. 2, ○
- 294 Investigating the Function of Predicted Proteins from RNA-Seq Data in Holstein and Cholistani Cattle Breeds. **2020**, 11, 121-135 ○
- 293 Competitive survival of clonal serial *Pseudomonas aeruginosa* isolates from cystic fibrosis airways in human neutrophils. **2023**, 26, 106475 ○
- 292 Patterns of Chromosomal Variation, Homoeologous Exchange, and Their Relationship with Genomic Features in Early Generations of a Synthetic Rice Segmental Allotetraploid. **2023**, 24, 6065 ○
- 291 Detection of Selection Signatures on the X Chromosome in Iranian Dromedary Camels using Whole Genome Sequencing Data. **2022**, 13, 155-161 ○
- 290 Identification of two unannotated miRNAs in classic Hodgkin lymphoma cell lines. **2023**, 18, e0283186 ○
- 289 A haplotype resolved chromosome-scale assembly of North American wild apple *Malus fusca* and comparative genomics of the fire blight *Mfu10* locus. Genome of the Pacific Crabapple *Malus fusca*. ○
- 288 An explainable deep learning classifier of bovine mastitis based on whole genome sequence data - circumventing the p&gt;&gt;&gt;n problem. ○
- 287 REXPERT: a machine learning tool to predict pathogenicity of tandem repeat loci. ○
- 286 Different molecular pathways are disrupted in Pyoderma gangrenosum patients and are associated with the severity of the disease. **2023**, 13, ○
- 285 Genome-wide analysis of a collective grave from Mentesh Tepe provides insight into the population structure of early neolithic population in the South Caucasus. **2023**, 6, ○
- 284 Clonal origin and development of high hyperdiploidy in childhood acute lymphoblastic leukaemia. **2023**, 14, ○
- 283 Molecular mapping and characterization of QTLs for grain quality traits in a RIL population of US rice under high nighttime temperature stress. **2023**, 13, ○

- 282 Intraspecific diversity in the mechanisms underlying abamectin resistance in a cosmopolitan pest. ○
- 281 Large-scale epidemiological study on feline autosomal dominant polycystic kidney disease and identification of novel PKD1 gene variants. ○
- 280 Generation of functional oocytes from male mice in vitro. **2023**, 615, 900-906 ○
- 279 Detection of Z-DNA Structures in Supercoiled Genome. **2023**, 179-193 ○
- 278 On the Multiple Pattern String Matching in DNA Databases. **2023**, 4, ○
- 277 Altered infective competence of the human gut microbiome in COVID-19. **2023**, 11, ○
- 276 Improved chromosomal-level genome assembly and re-annotation of leopard coral grouper. **2023**, 10, ○
- 275 Antimicrobial peptides act on the rumen microbiome and metabolome affecting the performance of castrated bulls. **2023**, 14, ○
- 274 POSMM: an efficient alignment-free metagenomic profiler that complements alignment-based profiling. **2023**, 18, ○
- 273 Massive genome reduction occurred prior to the origin of coral algal symbionts. ○
- 272 Genetic architecture of a pollinator shift and its fate in secondary hybrid zones of two *Petunia* species. **2023**, 21, ○
- 271 Pharmacogenomic profiling reveals molecular features of chemotherapy resistance in IDH wild-type primary glioblastoma. **2023**, 15, ○
- 270 Genetic mapping and molecular mechanism behind color variation in the Asian vine snake. **2023**, 24, ○
- 269 Multiancestry genomic and transcriptomic analysis of gastric cancer. **2023**, 55, 581-594 ○
- 268 Fine mapping and candidate gene analysis of CaFCD1 affecting cuticle biosynthesis in *Capsicum annuum* L.. **2023**, 136, ○
- 267 The *Torreya grandis* genome illuminates the origin and evolution of gymnosperm-specific sciadonic acid biosynthesis. **2023**, 14, ○
- 266 Characterization of stilbene synthase genes by comparative genome sequencing of *Vitis flexuosa* with high contents of stilbene compounds to *Vitis vinifera* genome. ○
- 265 *srdA* mutations suppress the *rseA/cpsA* deletion mutant conidiation defect in *Aspergillus nidulans*. **2023**, 13, ○

- 264 Genomic assessment reveals signal of adaptive selection in populations of the Spotted rose snapper *Lutjanus guttatus* from the Tropical Eastern Pacific. 11, e15029 ○
- 263 Weak gene-gene interaction facilitates the evolution of gene expression plasticity. **2023**, 21, ○
- 262 The garden asparagus (*Asparagus officinalis* L.) mitochondrial genome revealed rich sequence variation throughout whole sequencing data. 14, ○
- 261 Peruvian Amaranth (kiwicha) Accumulates Higher Levels of the Unsaturated Linoleic Acid. **2023**, 24, 6215 ○
- 260 Characterization of centromeric DNA of *Gossypium anomalum* reveals sequence-independent enrichment dynamics of centromeric repeats. **2023**, 31, ○
- 259 Discovery of SNP Molecular Markers and Candidate Genes Associated with Sacbrood Virus Resistance in *Apis cerana cerana* Larvae by Whole-Genome Resequencing. **2023**, 24, 6238 ○
- 258 Comparative Transcriptomic Analysis Reveals the Functionally Segmented Intestine in Tunicate Ascidian. **2023**, 24, 6270 ○
- 257 Introgression of morphological, phenological and productivity traits along with disease resistance from *Cicer pinnatifidum* into cultivated chickpea: a success story. **2023**, 219, ○
- 256 Increased flexibility of the SARS-CoV-2 RNA-binding site causes resistance to remdesivir. **2023**, 19, e1011231 ○
- 255 Dose rate dependent reduction in chromatin accessibility at transcriptional start sites long time after exposure to gamma radiation. **2023**, 18, ○
- 254 Multi-Knock $\downarrow$  multi-targeted genome-scale CRISPR toolbox to overcome functional redundancy in plants. **2023**, 9, 572-587 ○
- 253 Chromosome-scale de novo genome assembly and annotation of three representative *Casuarina* species: *C. equisetifolia*, *C. glauca*, and *C. cunninghamiana*. ○
- 252 Integrative epigenome profiling of 47XXY provides insights into whole genomic DNA hypermethylation and active chromatin accessibility. 10, ○
- 251 Integration of Selection Signatures and Protein Interactions Reveals NR6A1, PAPP2, and PIK3C2B as the Promising Candidate Genes Underlying the Characteristics of Licha Black Pig. **2023**, 12, 500 ○
- 250 Metagenomic Sequencing Identified Specific Bacteriophage Signature Discriminating between Healthy and Diarrheal Neonatal Piglets. **2023**, 15, 1616 ○
- 249 Cylindroma of the breast with CYLD gene mutation: a case report and review of the literature. ○
- 248 The DNA integrity number and concentration are useful parameters for successful comprehensive genomic profiling test for cancer using formalin-fixed paraffin embedded tissue. ○
- 247 Elucidating SNP-Based Population Structure and Genetic Diversity of *Bruguiera gymnorhiza* (L.) Savigny in Thailand. **2023**, 14, 693 ○

- 246 Beyond the spore, the exosporium sugar anthrose impacts vegetative *Bacillus anthracis* gene regulation in cis and trans. **2023**, 13, ○
- 245 Vaginal Microbiome Metagenome Inference Accuracy: Differential Measurement Error according to Community Composition. ○
- 244 Identification of CaPs locus involving in purple stripe formation on unripe fruit, reveals allelic variation and alternative splicing of R2R3-MYB transcription factor in pepper (*Capsicum annuum* L.). 14, ○
- 243 PRMT1 Inhibition Selectively Targets BNC1-Dependent Proliferation, but not Migration in Squamous Cell Carcinoma. ○
- 242 Community data-driven approach to identify pathogenic founder variants for pan-ethnic carrier screening panels. **2023**, 17, ○
- 241 Chromosome 11q13 amplification correlates with poor response and prognosis to PD-1 blockade in unresectable hepatocellular carcinoma. 14, ○
- 240 Genotype-phenotype pattern analysis of pathogenic PAX9 variants in Chinese Han families with non-syndromic oligodontia. 14, ○
- 239 Identification of HIR, EDS1 and PAD4 Genes Reveals Differences between *Coffea* Species That May Impact Disease Resistance. **2023**, 13, 992 ○
- 238 ScRNA-seq of Diverse Pheochromocytoma Patients Reveals Distinct Microenvironment Characteristics and Supports an Informative Molecular Classification System. ○
- 237 Insights into the genetic determination of tuber shape and eye depth in potato natural population based on autotetraploid potato genome. 14, ○
- 236 Comprehensive proteogenomic characterization of early duodenal cancer reveals the carcinogenesis tracks of different subtypes. **2023**, 14, ○
- 235 ULK4 and Fused/STK36 interact to mediate assembly of a motile flagellum. ○
- 234 Clonal hematopoiesis detection in patients with cancer using cell-free DNA sequencing. **2023**, 15, ○
- 233 A-MYB and BRDT-dependent RNA Polymerase II pause release orchestrates transcriptional regulation in mammalian meiosis. **2023**, 14, ○
- 232 The impact of damaging epilepsy and cardiac genetic variant burden in sudden death in the young. ○
- 231 k-mer-based GWAS enhances the discovery of causal variants and candidate genes in soybean. ○
- 230 A reference assembly for the legume cover crop, hairy vetch (*Vicia villosa*). ○
- 229 Whole-exome screening for primary congenital glaucoma in Lebanon. 1-12 ○

- 228 EVALUATION OF A METAGENOMIC NEXT-GENERATION SEQUENCING ASSAY WITH A NOVEL HOST DEPLETION METHOD FOR PATHOGEN IDENTIFICATION IN SEPTIC PATIENTS. ○
- 227 SARS-CoV-2 Variants Detection Strategies in Wastewater Samples Collected in the Bangkok Metropolitan Region. **2023**, 15, 876 ○
- 226 Genome structures resolve the early diversification of teleost fishes. **2023**, 379, 572-575 ○
- 225 Genome-wide analysis emancipates genomic diversity and signature of selection in Altay white-headed cattle of Xinjiang, China. 14, ○
- 224 Cytosine base editors induce off-target mutations and adverse phenotypic effects in transgenic mice. **2023**, 14, ○
- 223 Rare Coding Variants in Patients with Non-Syndromic Vestibular Dysfunction. **2023**, 14, 831 ○
- 222 APOBEC3B stratifies ovarian clear cell carcinoma with distinct immunophenotype and prognosis. ○
- 221 Phenotypic drought stress prediction of European beech (*Fagus sylvatica*) by genomic prediction and remote sensing. ○
- 220 Demographic fluctuations and selection during host-parasite co-evolution interactively increase genetic diversity. ○
- 219 Highly connected 3D chromatin networks established by an oncogenic fusion protein shape tumor cell identity. **2023**, 9, ○
- 218 GAGA-associated factor fosters loop formation in the *Drosophila* genome. **2023**, ○
- 217 Quantitative determination of SLC2A1 variant functional effects in GLUT1 deficiency syndrome. ○
- 216 No evidence for a common blood microbiome based on a population study of 9,770 healthy humans. ○
- 215 Genomics of the *Bumorigenes* clade of the family Rhizobiaceae and description of *Rhizobium rhododendri* sp. nov.. **2023**, 12, ○
- 214 Comparative genomics reveals unique features of two *Babesia motasi* subspecies: *Babesia motasi lintanensis* and *Babesia motasi hebeiensis*. **2023**, ○
- 213 Bursts in biosynthetic gene cluster transcription are accompanied by surges of natural compound production in the myxobacterium *Sorangium* sp.. ○
- 212 Three-dimensional and single-cell sequencing of liver cancer reveals comprehensive host-virus interactions in HBV infection. 14, ○
- 211 Whole Genome Sequencing Provides Information on the Genomic Architecture and Diversity of Cultivated Gilthead Seabream (*Sparus aurata*) Broodstock Nuclei. **2023**, 14, 839 ○

- 210 A highly contiguous genome assembly reveals sources of genomic novelty in the symbiotic fungus *Rhizophagus irregularis*. ○
- 209 Oral metagenomes from Native American Ancestors reveal distinct microbial lineages in the pre-contact era. ○
- 208 Sox11 is enriched in myogenic progenitors but dispensable for development and regeneration of skeletal muscle. ○
- 207 Dietary environmental factors shape the immune defence against infection with *Cryptosporidium*. ○
- 206 Does social antagonism facilitate supergene expansion? A novel region of suppressed recombination in a 4-haplotype supergene system. ○
- 205 Clinical usefulness of metagenomic next-generation sequencing for *Rickettsia* and *Coxiella burnetii* diagnosis. ○
- 204 Confounding factors in profiling of locus-specific human endogenous retrovirus (HERV) transcript signatures in primary T cells using multi-study-derived datasets. **2023**, 16, ○
- 203 Genomic insights of evolutionary divergence and life histories innovations in Antarctic brittle stars. ○
- 202 Characteristics, Comparative Analysis, and Phylogenetic Relationships of Chloroplast Genomes of Cultivars and Wild Relatives of Eggplant (*Solanum melongena*). **2023**, 45, 2832-2846 ○
- 201 A recurrent de novo variant in NUSAP1 escapes nonsense-mediated decay and leads to microcephaly, epilepsy, and developmental delay. ○
- 200 When does the female bias arise? Insights from the sex determination cascade of a flea beetle with a strongly skewed sex ratio. **2023**, 23, ○
- 199 Genomic characteristics and selection signals of Zhongshan ducks. **2023**, 100797 ○
- 198 Genome-Wide Association Study Reveals the Genetic Basis of Duck Plumage Colors. **2023**, 14, 856 ○
- 197 Uncovering the history of recombination and population structure in western Canadian stripe rust populations through mating-type alleles. ○
- 196 Genome-wide SNPs show hybridization of *Varroa* mites from different *Apis* hosts in Vietnam and Taiwan. **2023**, 54, ○
- 195 Genetic impacts on DNA methylation help elucidate regulatory genomic processes. ○
- 194 Major proliferation of transposable elements shaped the genome of the soybean rust pathogen *Phakopsora pachyrhizi*. **2023**, 14, ○
- 193 Ongoing introgression of a secondary sexual plumage trait in a stable avian hybrid zone. ○

- 192 Genome-wide association study reveals that the IBSP locus affects ear size in cattle. ○
- 191 Back-to-Africa introductions of *Mycobacterium tuberculosis* as the main cause of tuberculosis in Dar es Salaam, Tanzania. **2023**, 19, e1010893 ○
- 190 Resolving the phylogeny of *Thladiantha* (Cucurbitaceae) with three different targeted-capture pipelines. ○
- 189 Titration-based normalization of antibody amount improves consistency of ChIP-seq experiments. **2023**, 24, ○
- 188 High-Quality Assembly and Comparative Analysis of *Actinidia latifolia* and *A. valvata* Mitogenomes. **2023**, 14, 863 ○
- 187 A minimally-invasive method for ancient DNA sampling of Prehistoric bone and antler tools and hunting weapons. ○
- 186 Dividing out quantification uncertainty allows efficient assessment of differential transcript expression. ○
- 185 Integrated analysis of biparental and natural populations reveals CRIB domain-containing protein underlying seed coat crack trait in watermelon. **2023**, 136, ○
- 184 The genomic architecture of a continuous color polymorphism in the European barn owl (*Tyto alba*). ○
- 183 Spurious intragenic transcription is a feature of mammalian cellular senescence and tissue aging. **2023**, 3, 402-417 ○
- 182 A compendium of stable hotspots in the CHO genome. ○
- 181 Cranberry fruit epicuticular wax benefits and identification of a wax-associated molecular marker. **2023**, 23, ○
- 180 The genetic basis of adaptation to copper pollution in *Drosophila melanogaster*. 14, ○
- 179 Test development, optimization and validation of a WGS pipeline for genetic disorders. **2023**, 16, ○
- 178 The Identification of a Yield-Related Gene Controlling Multiple Traits Using GWAS in Sorghum (*Sorghum bicolor* L.). **2023**, 12, 1557 ○
- 177 SPONDIŦOEPŦ(META) FŦYAL DŦPLAZINŦ TANILI BEŦTRK ERKEK HASTADAKŦGENETŦ ETYOLOJNŦ ARATIRILMASI. **2023**, 24, 184-189 ○
- 176 DNA methylation patterns suggest the involvement of DNMT3B and TET1 in osteosarcoma development. ○
- 175 Large-scale analysis of de novo mutations identifies risk genes for female infertility characterized by oocyte and early embryo defects. **2023**, 24, ○

- 174 Metastatic colorectal adenocarcinoma tumor purity assessment from whole exome sequencing data. **2023**, 18, e0271354 ○
- 173 Artificial intelligence in precision medicine. **2023**, 531-569 ○
- 172 GENOME REPORT: Chromosome-scale genome assembly of the African spiny mouse (*Acomys cahirinus*). ○
- 171 Genomic adaptation to extreme climate conditions in beef cattle as a consequence of cross-breeding program. **2023**, 24, ○
- 170 Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species. ○
- 169 Acetylation of histone H2B marks active enhancers and predicts CBP/p300 target genes. **2023**, 55, 679-692 ○
- 168 Unraveling the Genetic Population Structure of Mongolian Indigenous Cattle Breeds Using Whole Genome Sequencing Data. **2023**, 36-42 ○
- 167 Obligate chimerism in male yellow crazy ants. **2023**, 380, 55-58 ○
- 166 Genomic Relationships of *Glycine remota*, a Recently Discovered Perennial Relative of Soybean, within *Glycine*. **2023**, 48, 78-87 ○
- 165 Quantitative analysis of tRNA abundance and modifications by nanopore RNA sequencing. ○
- 164 Genomic and transcriptomic analysis of checkpoint blockade response in advanced non-small cell lung cancer. ○
- 163 Metagenomic insights into the composition and function of the gut microbiota of mice infected with *Toxoplasma gondii*. 14, ○
- 162 Sequential Antigen-loss and Branching Evolution in Lymphoma after Anti-CD19 and Anti-CD20 Targeted T Cell Redirecting Immunotherapy. ○
- 161 Echoes from the last Green Sahara: whole genome analysis of Fulani, a key population to unveil the genetic evolutionary history of Africa. ○
- 160 The ENCODE Uniform Analysis Pipelines. ○
- 159 Experimental characterization of de novo proteins and their unevolved random-sequence counterparts. **2023**, 7, 570-580 ○
- 158 Homologous recombination deficiency derived from whole-genome sequencing predicts platinum response in triple-negative breast cancers. **2023**, 14, ○
- 157 Resolution of structural variation in diverse mouse genomes reveals chromatin remodeling due to transposable elements. **2023**, 100291 ○

- 156 Population structure and genome-wide evolutionary signatures reveal putative climate-driven habitat change and local adaptation in the large yellow croaker. ○
- 155 The Allen Ancient DNA Resource (AADR): A curated compendium of ancient human genomes. ○
- 154 Tumor-Naïve Circulating Tumor DNA as an Early Response Biomarker for Patients Treated With Immunotherapy in Early Phase Clinical Trials. **2023**, ○
- 153 Genomics of adaptive evolution in the woolly mammoth. **2023**, ○
- 152 Topographic barriers drive the pronounced genetic subdivision of a range-limited fossorial rodent. ○
- 151 Molecular characterization stratifies VQ myeloma cells into two clusters with distinct risk signatures and drug responses. ○
- 150 The evolution and international spread of extensively drug resistant *Shigella sonnei*. **2023**, 14, ○
- 149 Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria mosquito species of the *Maculipennis* Group. **2023**, 21, ○
- 148 Genetic Screening of Targeted Region on the Chromosome 22q11.2 in Patients with Microtia and Congenital Heart Defect. **2023**, 14, 879 ○
- 147 AmelHap: Leveraging drone whole-genome sequence data to create a honey bee HapMap. **2023**, 10, ○
- 146 Molecular fingerprints of nuclear genome and mitochondrial genome for early diagnosis of lung adenocarcinoma. **2023**, 21, ○
- 145 Revisiting Genetic Epidemiology with a Refined Targeted Gene Panel for Hereditary Hearing Impairment in the Taiwanese Population. **2023**, 14, 880 ○
- 144 Identification of copy number variations in the genome of Dairy Gir cattle. **2023**, 18, e0284085 ○
- 143 Expanding known viral diversity in the healthy infant gut. ○
- 142 DisP-seq reveals the genome-wide functional organization of DNA-associated disordered proteins. ○
- 141 Differential Hsp90-dependent gene expression is strain-specific and common among yeast strains. **2023**, 106635 ○
- 140 Simplified algorithm for genetic subtyping in diffuse large B-cell lymphoma. **2023**, 8, ○
- 139 Small extracellular vesicles from spared nerve injury model and sham control mice differentially regulate gene expression in primary microglia. **2023**, ○

- 138 Genome-wide association reveals host-specific genomic traits in *Escherichia coli*. **2023**, 21, ○
- 137 Capture Methylation-Sensitive Restriction Enzyme Sequencing (Capture MRE-Seq) for Methylation Analysis of Highly Degraded DNA Samples. **2023**, 73-89 ○
- 136 FOXI3 pathogenic variants cause one form of craniofacial microsomia. **2023**, 14, ○
- 135 A potent allele marker related to low bull conception rate in Japanese Black bulls. **2023**, 100804 ○
- 134 Mate Pair Sequencing: Next-Generation Sequencing for Structural Variant Detection. **2023**, 127-149 ○
- 133 Genomic surveillance uncovers a pandemic clonal lineage of the wheat blast fungus. **2023**, 21, e3002052 ○
- 132 A chromosome 16 deletion conferring a high sucrose phenotype in soybean. **2023**, 136, ○
- 131 A late Neanderthal reveals genetic isolation in their populations before extinction. ○
- 130 Genomic, transcriptomic, and metabolic characterization of 2-Phenylethanol-resistant *Saccharomyces cerevisiae* obtained by evolutionary engineering. 14, ○
- 129 GWAS using low-pass whole genome sequence reveals a novel locus in canine congenital idiopathic megaesophagus. ○
- 128 Delineation of genes for a major QTL governing heat stress tolerance in chickpea. ○
- 127 On-person adaptive evolution of *Staphylococcus aureus* during treatment for atopic dermatitis. **2023**, 31, 593-603.e7 ○
- 126 The evolution of lung cancer and impact of subclonal selection in TRACERx. **2023**, 616, 525-533 ○
- 125 Staphylococcal diversity in atopic dermatitis from an individual to a global scale. **2023**, 31, 578-592.e6 ○
- 124 Genomic and transcriptomic analysis of sacred fig (*Ficus religiosa*). **2023**, 24, ○
- 123 Chromosome-length genome assemblies and cytogenomic analyses of pangolins reveal remarkable chromosome counts and plasticity. **2023**, 31, ○
- 122 Clonal evolution analyses of a chronic myeloid leukemia patient with hematopoietic stem cell transplantation based on deep sequencing. **2023**, 2, ○
- 121 A Novel Variant in VPS13B Underlying Cohen Syndrome. **2023**, 2023, 1-7 ○

- 120 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 ○
- 119 Tracing the spatiotemporal phylogenetics of Japanese encephalitis virus genotype I throughout Asia and the western Pacific. **2023**, 17, e0011192 ○
- 118 The origins and functional effects of postzygotic mutations throughout the human life span. **2023**, 380, ○
- 117 Chromatin context-dependent regulation and epigenetic manipulation of prime editing. ○
- 116 Fine-scale adaptive divergence of *Aedes aegypti* in heterogeneous landscapes and among climatic conditions in Metropolitan Manila, Philippines. ○
- 115 Transcriptional Mechanisms of Thermal Acclimation in *Prochlorococcus*. ○
- 114 An immunogenic and oncogenic feature-based classification for chemotherapy plus PD-1 blockade in advanced esophageal squamous cell carcinoma. **2023**, ○
- 113 Meiotic Behaviors of Allotetraploid Citrus Drive the Interspecific Recombination Landscape, the Genetic Structures, and Traits Inheritance in Tetrazyg Progenies Aiming to Select New Rootstocks. **2023**, 12, 1630 ○
- 112 Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF inactivating mutations in acute T cell leukemia. **2023**, 42, 112373 ○
- 111 Plasma cell-free DNA promise monitoring and tissue injury assessment of COVID-19. ○
- 110 Children with autism show differences in the gut DNA virome compared to non-autistic children: a case control study. **2023**, 23, ○
- 109 Sequence-Based Platforms for Discovering Biomarkers in Liquid Biopsy of Non-Small-Cell Lung Cancer. **2023**, 15, 2275 ○
- 108 Design and validation of *Dolosigranulum pigrum* specific PCR primers using the bacterial core genome. **2023**, 13, ○
- 107 Haplotyping interspecific hybrids by dual alignment to both parental genomes. ○
- 106 An In Silico Functional Analysis of Non-Synonymous Single-Nucleotide Polymorphisms of Bovine CMAH Gene and Potential Implication in Pathogenesis. **2023**, 12, 591 ○
- 105 Myeloid NGS Analyses of Paired Samples from Bone Marrow and Peripheral Blood Yield Concordant Results: A Prospective Cohort Analysis of the AGMT Study Group. **2023**, 15, 2305 ○
- 104 Genetic population structure of the Xiongnu Empire at imperial and local scales. **2023**, 9, ○
- 103 Validation of the Labcorp Plasma Focus Test to Facilitate Precision Oncology Through Cell-free DNA Genomic Profiling of Solid Tumors. **2023**, ○

- 102 Disturbances of purine and lipid metabolism in the microbiota-gut-brain axis in male adolescent nonhuman primates with depressive-like behaviors. **2023**, ○
- 101 The performance of metagenomic next-generation sequencing in diagnosing pulmonary infectious diseases using authentic clinical specimens: The Illumina platform versus the Beijing Genomics Institute platform. 14, ○
- 100 Never judge a bird by its feathers: genetics unveils the true target of trafficking in morphologically similar *Copsychus* species. ○
- 99 Paired yeast one-hybrid assays to detect DNA-binding cooperativity and antagonism across transcription factors. ○
- 98 Phylogenomics of the *Olea europaea* complex using 15 whole genomes supports recurrent genetic admixture together with differentiation into seven subspecies. **2023**, 21, ○
- 97 Genome-Wide Mapping of the *Escherichia coli* PhoB Regulon Reveals Many Transcriptionally Inert, Intragenic Binding Sites. ○
- 96 High Genetic Diversity of Carbapenem-Resistant *Acinetobacter baumannii* Isolates Recovered in Nigerian Hospitals in 2016 to 2020. ○
- 95 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 ○
- 94 The chromosome-level genome of *Cherax quadricarinatus*. **2023**, 10, ○
- 93 Integration of non-additive genome-wide association study with a multi-tissue transcriptome analysis of growth and carcass traits in Duroc pigs. **2023**, 100817 ○
- 92 Domesticating *Vigna stipulacea*: Chromosome-Level genome assembly reveals *VsPSAT1* as a candidate gene decreasing hard-seededness. 14, ○
- 91 Combinatorial genetic strategy accelerates the discovery of cancer genotype-phenotype associations. ○
- 90 A chromosome-level genome assembly of the yellow-throated marten (*Martes flavigula*). **2023**, 10, ○
- 89 Haplotype mapping of H3K27me3-associated chromatin interactions defines topological regulation of gene silencing in rice. **2023**, 42, 112350 ○
- 88 Redefining rock doves, *Columba livia*, using historical whole genome sequences. ○
- 87 Variant-specific introduction and dispersal dynamics of SARS-CoV-2 in New York City from Alpha to Omicron. **2023**, 19, e1011348 ○
- 86 Exposure to microbial products followed by loss of Tet2 promotes myelodysplastic syndrome via remodeling HSCs. **2023**, 220, ○
- 85 Genomics reveals broad hybridization in deeply divergent Palearctic grass and water snakes (*Natrix* spp.). **2023**, 107787 ○

- 84 A weaponized phage suppresses competitors in historical and modern metapopulations of pathogenic bacteria. ○
- 83 Analysis of the Complete Mitochondrial Genome of the Bitter Gourd (*Momordica charantia*). **2023**, 12, 1686 ○
- 82 Complete Genome Sequence of *Citrobacter braakii* GW-Imi-1b1, Isolated from Hospital Wastewater in Greifswald, Germany. ○
- 81 Whole-genome selective scans detect genes associated with important phenotypic traits in goat (*Capra hircus*). 14, ○
- 80 A robust reprogramming strategy for generating hepatocyte-like cells usable in pharmaco-toxicological studies. **2023**, 14, ○
- 79 KaryoCreate: A CRISPR-based technology to study chromosome-specific aneuploidy by targeting human centromeres. **2023**, ○
- 78 Lamin B1 overexpression alters chromatin organization and gene expression. **2023**, 14, ○
- 77 The ENCODE Imputation Challenge: a critical assessment of methods for cross-cell type imputation of epigenomic profiles. **2023**, 24, ○
- 76 Peritoneal cell-free DNA as a sensitive biomarker for detection of peritoneal metastasis in colorectal cancer: a prospective diagnostic study: A prospective diagnostic study. **2023**, 15, ○
- 75 Novel Sources of Biodiversity and Biomolecules from Bacteria Isolated from a High Middle Ages Soil Sample in Palermo (Sicily, Italy). ○
- 74 A systems biology approach uncovers novel disease mechanisms in age-related macular degeneration. **2023**, 100302 ○
- 73 Genomic Insights into Bacterial Resistance to Proline-Rich Antimicrobial Peptide Bac7. **2023**, 13, 438 ○
- 72 Bladder cancer organoids as a functional system to model different disease stages and therapy response. **2023**, 14, ○
- 71 First mitogenome phylogeny of the sun bear *Helarctos malayanus* reveals a deep split between Indochinese and Sundaic lineages. **2023**, 13, ○
- 70 Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. **2023**, 21, ○
- 69 Unique Salt-Tolerance-Related QTLs, Evolved in *Vigna riukiensis* (Na<sup>+</sup> Includer) and *V. nakashimae* (Na<sup>+</sup> Excluder), Shed Light on the Development of Super-Salt-Tolerant Azuki Bean (*V. angularis*) Cultivars. **2023**, 12, 1680 ○
- 68 Longitudinal large-scale changes in maternal circulating microRNAs associated with gestation-related compartments, fetal sex, and growth during and post-pregnancy. **2023**, 110628 ○
- 67 Histone divergence in *Trypanosoma brucei* results in unique alterations to nucleosome structure. ○

- 66 Identification and characterisation of de novo germline structural variants in two commercial pig lines using trio-based whole genome sequencing. **2023**, 24, ○
- 65 Evaluation of variant calling algorithms for wastewater-based epidemiology using mixed populations of SARS-CoV-2 variants in synthetic and wastewater samples. **2023**, 9, ○
- 64 Identifying climatic drivers of hybridization with a new ancestral niche reconstruction method. ○
- 63 Identifying novel regulatory effects for clinically relevant genes through the study of the Greek population. ○
- 62 Novel QTL for Lateral Root Density and Length improve Phosphorus Uptake in Rice (*Oryza sativa* L.). ○
- 61 Cell Type-Specific Regulation by a Heptad of Transcription Factors in Human Hematopoietic Stem and Progenitor Cells. ○
- 60 Optimization of Electroporation and Adeno-Associated Virus-Mediated Generation of 2.7 kb Knock-In Livestock Blastocysts. **2023**, 2, 120-132 ○
- 59 The hagfish genome and the evolution of vertebrates. ○
- 58 Mirusviruses link herpesviruses to giant viruses. ○
- 57 Genomics of severe and treatment-resistant obsessive-compulsive disorder treated with deep brain stimulation: a preliminary investigation. ○
- 56 De novo transcriptome sequencing and gene co-expression reveal a genomic basis for drought sensitivity and evidence of a rapid local adaptation on Atlas cedar (*Cedrus atlantica*). 14, ○
- 55 Identifying high-impact variants and genes in exomes of Ashkenazi Jewish inflammatory bowel disease patients. **2023**, 14, ○
- 54 Analytical Performance of a Highly Sensitive System to Detect Gene Variants Using Next-Generation Sequencing for Lung Cancer Companion Diagnostics. **2023**, 13, 1476 ○
- 53 Long-read sequencing reveals the complex structure of extra dic(21;21) chromosome and its biological changes. ○
- 52 Purifying Selection and Persistent Polymorphism among Nuclei in the Multinucleate Arbuscular Mycorrhizal (AM) Fungi. ○
- 51 Biallelic NPR1 loss of function variants are responsible for neonatal systemic hypertension. jmg-2023-109176 ○
- 50 A small RNA system ensures accurate homologous pairing and unpaired silencing of meiotic chromosomes. ○
- 49 The evolution of two transmissible cancers in Tasmanian devils. **2023**, 380, 283-293 ○

- 48 Attack of the clones: Population genetics reveals clonality of *Colletotrichum lupini*, the causal agent of lupin anthracnose. ○
- 47 RAPIDprep: A Simple, Fast Protocol for RNA Metagenomic Sequencing of Clinical Samples. **2023**, 15, 1006 ○
- 46 ACT-Discover: identifying karyotype heterogeneity in pancreatic cancer evolution using ctDNA. **2023**, 15, ○
- 45 Mapping a leaf rust resistance gene LrOft in durum wheat Ofanto and its suppressor SuLrOft in common wheat. 14, ○
- 44 3D genome mapping identifies subgroup-specific chromosome conformations and tumor-dependency genes in ependymoma. **2023**, 14, ○
- 43 Mapping and characterization of the recessive leaf rust resistance gene Lr83 on wheat chromosome arm 1DS. **2023**, 136, ○
- 42 Contribution of LRP1 in Human Congenital Heart Disease Correlates with Its Roles in the Outflow Tract and Atrioventricular Cushion Development. **2023**, 14, 947 ○
- 41 Fine mapping and identifying candidate gene of Y underlying yellow peel in *Cucurbita pepo*. 14, ○
- 40 CasKAS: direct profiling of genome-wide dCas9 and Cas9 specificity using ssDNA mapping. **2023**, 24, ○
- 39 Origin and diversification of a Himalayan orchid genus *Pleione*. **2023**, 107797 ○
- 38 Transcription factor binding site orientation and order are major drivers of gene regulatory activity. **2023**, 14, ○
- 37 Identifying novel risk conferring genes involved in glycosylation processes with familial schizophrenia in an Indian cohort: Prediction of ADAMTS9 gene variant for structural stability. **2023**, 872, 147443 ○
- 36 The mitochondrial genome of the diploid oat *Avena longiglumis*. **2023**, 23, ○
- 35 Carryover Contamination-Controlled Amplicon Sequencing Workflow for Accurate Qualitative and Quantitative Detection of Pathogens: a Case Study on SARS-CoV-2. ○
- 34 Epigenetically-regulated RNA-binding proteins signify malaria hypnozoite dormancy. ○
- 33 Genetic structure of an endangered species *Ormosia henryi* in southern China, and implications for conservation. **2023**, 23, ○
- 32 Characteristics of a Temperature-Sensitive Mutant Strain of *Salmonella Enteritidis* and Its Potential as a Live Vaccine Candidate. **2023**, 10, 313 ○
- 31 A multiomic approach to defining the essential genome of the globally important pathogen *Corynebacterium diphtheriae*. **2023**, 19, e1010737 ○

- 30 Identification of Candidate Genes Associated with Yak Body Size Using a Genome-Wide Association Study and Multiple Populations of Information. **2023**, 13, 1470 ○
- 29 Mitochondrial Genome Uncovered Hidden Genetic Diversity in *Microdous chalmersi* (Teleostei: Odontobutidae). **2023**, 8, 228 ○
- 28 Metatranscriptomic analysis of the gut microbiome of black soldier fly larvae reared on lignocellulose-rich fiber diets unveils key lignocellulolytic enzymes. 14, ○
- 27 Esrrb guides naive pluripotent cells through the formative transcriptional programme. **2023**, 25, 643-657 ○
- 26 Association between vascular ultrasound features and DNA sequencing in breast cancer: a preliminary study. **2023**, 14, ○
- 25 The R2R3-MYB transcription factor GaPC controls petal coloration in cotton. **2023**, ○
- 24 Highly structured genomic sequences mediate the function of a RNA virus polymerase. ○
- 23 Genetic, clinical, and pathological study of patients with severe hypertension-associated renal microangiopathy. ○
- 22 The Western Lake Erie culture collection: A promising resource for evaluating the physiological and genetic diversity of *Microcystis* and its associated microbiome. **2023**, 126, 102440 ○
- 21 Spatial transcriptomics reveal topological immune landscapes of Asian head and neck angiosarcoma. **2023**, 6, ○
- 20 Disruption of FBN1 by an Alu element insertion: A novel genetic cause of Marfan syndrome. **2023**, 66, 104775 ○
- 19 Two transects reveal remarkable variation in gene flow on opposite ends of a European toad hybrid zone. ○
- 18 Meeting in Liguria: Hybridisation between Apennine endemic *Euphorbia barrelieri* and western Mediterranean *E. nicaeensis* led to the allopolyploid origin of *E. ligustica*. **2023**, 185, 107805 ○
- 17 Integrated genomic analysis reveals aberrations in WNT signaling in germ cell tumors of childhood and adolescence. **2023**, 14, ○
- 16 Temperature and day length drive local adaptation in the Patagonian foundation tree species *Nothofagus pumilio*. ○
- 15 iBP-seq: an efficient and low-cost multiplex targeted genotyping and epigenotyping system. **2023**, ○
- 14 Strategies to improve genomic predictions for 35 duck carcass traits in an F2 population. **2023**, 14, ○
- 13 Human macroH2A1 drives nucleosome dephasing and genome instability in histone-humanized yeast. ○

- 12 Genomic analyses provide insights into the polyploidization-driven herbicide adaptation in *Leptochloa* weeds. ○
- 11 Application of 1993 Single Nucleotide Polymorphism Loci in Forensic Pairwise Kinship Identifications and Inference. **2023**, 102889 ○
- 10 Integrated microbiome-metabolome-genome axis data of Laiwu and Lulai pigs. **2023**, 10, ○
- 9 Analysis of the Plasmid-Based *ts*-Mutant *f*fabA/pTS-fabA Reveals Its Lethality under Aerobic Growth Conditions That Is Suppressed by Mild Overexpression of *desA* at a Restrictive Temperature in *Pseudomonas aeruginosa*. ○
- 8 Virological characteristics of the SARS-CoV-2 XBB variant derived from recombination of two Omicron subvariants. **2023**, 14, ○
- 7 Genetic differences of dengue virus 2 in patients with distinct clinical outcome. ○
- 6 Complete genome analysis of Tequatrovirus *ufvareg1*, a Tequatrovirus species inhibiting *Escherichia coli* O157:H7. 13, ○
- 5 Identification of Runs of Homozygosity Islands and Functional Variants in Wenchang Chicken. **2023**, 13, 1645 ○
- 4 Genetic Diversity and Breeding Signatures for Regional Indica Rice Improvement in Guangdong of Southern China. **2023**, 16, ○
- 3 Genotyping-by-sequencing provides new genetic and taxonomic insights in the critical group of *Centaurea tenorei*. 14, ○
- 2 Genomic landscape and its prognostic significance in stage III colorectal cancer: JCOG1506A1 , an ancillary of JCOG0910. ○
- 1 Genomics of Aminoglycoside Resistance in *Pseudomonas aeruginosa* Bloodstream Infections at a United States Academic Hospital. ○