

CITATION REPORT

List of articles citing

Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation

DOI: 10.1038/nbt.1621

Nature Biotechnology, 2010, 28, 511-5.

Source: <https://exaly.com/paper-pdf/49614091/citation-report.pdf>

Version: 2024-04-26

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
2266	Integrating Transcriptomic Data with Mechanistic Systems Pharmacology Models for Virtual Drug Combination Trials.		
2265	Identification of Blood Protein Biomarkers of Acute Liver Injury by Targeted Quantitative Proteomics in Acetaminophen- and Carbon-Tetrachloride-Treated Mouse Models and Acetaminophen Overdose Patients.		
2264	.		
2263	Abstract.		
2262	Abstract.		0
2261	Abstract.		
2260	Assessment of orthologous splicing isoforms in human and mouse orthologous genes. 2010 , 11, 534		27
2259	Rnnotator: an automated de novo transcriptome assembly pipeline from stranded RNA-Seq reads. 2010 , 11, 663		168
2258	De novo assembled expressed gene catalog of a fast-growing Eucalyptus tree produced by Illumina mRNA-Seq. 2010 , 11, 681		137
2257	Massive parallel sequencing of mRNA in identification of unannotated salinity stress-inducible transcripts in rice (<i>Oryza sativa</i> L.). 2010 , 11, 683		64
2256	Comparison of transcriptomic landscapes of bovine embryos using RNA-Seq. 2010 , 11, 711		63
2255	Transcriptome profiling in neurodegenerative disease. 2010 , 193, 189-202		50
2254	Nuclear envelope alterations generate an aging-like epigenetic pattern in mice deficient in Zmpste24 metalloprotease. 2010 , 9, 947-57		44
2253	Advancing RNA-Seq analysis. <i>Nature Biotechnology</i> , 2010 , 28, 421-3	44.5	158
2252	Haploidy with histones. <i>Nature Biotechnology</i> , 2010 , 28, 423-4	44.5	9
2251	Comprehensive comparative analysis of strand-specific RNA sequencing methods. 2010 , 7, 709-15		562
2250	Alternative expression analysis by RNA sequencing. 2010 , 7, 843-7		227

2249	De novo assembly and analysis of RNA-seq data. 2010 , 7, 909-12	701
2248	Analysis and design of RNA sequencing experiments for identifying isoform regulation. 2010 , 7, 1009-15	934
2247	Simplifying complexity. 2010 , 7, 793-5	1
2246	HMMSplicer: a tool for efficient and sensitive discovery of known and novel splice junctions in RNA-Seq data. 2010 , 5, e13875	44
2245	De novo transcriptome sequencing in Anopheles funestus using Illumina RNA-seq technology. 2010 , 5, e14202	117
2244	A dual platform approach to transcript discovery for the planarian Schmidtea mediterranea to establish RNAseq for stem cell and regeneration biology. 2010 , 5, e15617	54
2243	Transcribed dark matter: meaning or myth?. 2010 , 19, R162-8	220
2242	Global regulation of alternative splicing during myogenic differentiation. 2010 , 38, 7651-64	110
2241	Tissue-specific transcript annotation and expression profiling with complementary next-generation sequencing technologies. 2010 , 38, e165	30
2240	Changes in transcript abundance in Chlamydomonas reinhardtii following nitrogen deprivation predict diversion of metabolism. 2010 , 154, 1737-52	398
2239	Isoform abundance inference provides a more accurate estimation of gene expression levels in RNA-seq. 2010 , 8 Suppl 1, 177-92	27
2238	Noisy splicing drives mRNA isoform diversity in human cells. 2010 , 6, e1001236	203
2237	Statistical Issues in the Analysis of ChIP-Seq and RNA-Seq Data. 2010 , 1, 317-34	11
2236	Next-generation sequencing techniques for eukaryotic microorganisms: sequencing-based solutions to biological problems. 2010 , 9, 1300-10	106
2235	From RNA-seq reads to differential expression results. 2010 , 11, 220	471
2234	Large non-coding RNAs: missing links in cancer?. 2010 , 19, R152-61	416
2233	Algorithms in Bioinformatics. 2010 ,	
2232	Genomic SELEX: a discovery tool for genomic aptamers. 2010 , 52, 125-32	47

2231	Cloud-scale RNA-sequencing differential expression analysis with Myrna. 2010 , 11, R83	227
2230	Annotating conserved and novel features of primate transcriptomes using sequencing. 2010 , 11, 125	1
2229	Design and evaluation of genome-wide libraries for RNA interference screens. 2010 , 11, R61	59
2228	Data mining of mRNA-Seq and small RNA-Seq data to find microRNA targets. 2010 ,	
2227	The domestic dog: man's best friend in the genomic era. 2011 , 12, 216	87
2226	RNA-Seq and find: entering the RNA deep field. 2011 , 3, 74	18
2225	Epigenetic regulation of satellite cell activation during muscle regeneration. 2011 , 2, 18	48
2224	Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. 2011 ,	
2223	A novel framework for chimeric transcript detection based on accurate gene fusion model. 2011 ,	
2222	Workshop: Transcriptome assembly from RNA-Seq data: Objectives, algorithms and challenges. 2011 ,	2
2221	Analysis of transcriptome complexity through RNA sequencing in normal and failing murine hearts. 2011 , 109, 1332-41	160
2220	Comparative analysis of RNA-Seq alignment algorithms and the RNA-Seq unified mapper (RUM). 2011 , 27, 2518-28	261
2219	Chromatin signature analysis and prediction of genome-wide novel promoters using finite mixture model. 2011 ,	1
2218	iQuant: A fast yet accurate GUI tool for transcript quantification. 2011 ,	1
2217	SPATA: A highly accurate GUI tool for de novo transcriptome assembly. 2011 ,	
2216	Discovering regulatory overlapping RNA transcripts. 2011 , 18, 295-303	1
2215	RNA-sequence analysis of human B-cells. 2011 , 21, 991-8	112
2214	Differential expression in RNA-seq: a matter of depth. 2011 , 21, 2213-23	1072

2213	De novo assembly of expressed transcripts and global analysis of the <i>Phalaenopsis aphrodite</i> transcriptome. 2011 , 52, 1501-14	92
2212	. 2011 ,	1
2211	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. 2011 , 25, 1915-27	2492
2210	Alternative transcription exceeds alternative splicing in generating the transcriptome diversity of cerebellar development. 2011 , 21, 1260-72	142
2209	Protocol dependence of sequencing-based gene expression measurements. 2011 , 6, e19287	73
2208	IsoLasso: a LASSO regression approach to RNA-Seq based transcriptome assembly. 2011 , 18, 1693-707	100
2207	Genome sequence and analysis of the tuber crop potato. 2011 , 475, 189-95	1438
2206	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. 2011 , 10, 322-33	30
2205	Deep proteome and transcriptome mapping of a human cancer cell line. 2011 , 7, 548	723
2204	ReadDB provides efficient storage for mapped short reads. 2011 , 12, 278	
2203	Transcriptome sequencing across a prostate cancer cohort identifies PCAT-1, an unannotated lincRNA implicated in disease progression. <i>Nature Biotechnology</i> , 2011 , 29, 742-9	44.5 824
2202	Comparative genomics of the pathogenic ciliate <i>Ichthyophthirius multifiliis</i> , its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. 2011 , 12, R100	89
2201	TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. 2011 , 12, R72	547
2200	Haplotype and isoform specific expression estimation using multi-mapping RNA-seq reads. 2011 , 12, R13	179
2199	Targeted protein-omic methods are bridging the gap between proteomic and hypothesis-driven protein analysis approaches. 2011 , 8, 565-75	20
2198	The human mitochondrial transcriptome. 2011 , 146, 645-58	561
2197	Control of embryonic stem cell lineage commitment by core promoter factor, TAF3. 2011 , 146, 720-31	132
2196	The monarch butterfly genome yields insights into long-distance migration. 2011 , 147, 1171-85	410

2195	Combinatorial patterning of chromatin regulators uncovered by genome-wide location analysis in human cells. 2011 , 147, 1628-39	265
2194	Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution. 2011 , 147, 1537-50	882
2193	Decoding muscle alternative splicing. 2011 , 21, 380-7	40
2192	Identification of novel transcripts in annotated genomes using RNA-Seq. 2011 , 27, 2325-9	716
2191	Synthetic spike-in standards for RNA-seq experiments. 2011 , 21, 1543-51	437
2190	Genome-wide regulation of 5hmC, 5mC, and gene expression by Tet1 hydroxylase in mouse embryonic stem cells. 2011 , 42, 451-64	493
2189	A Dictyostelium SH2 adaptor protein required for correct DIF-1 signaling and pattern formation. 2011 , 353, 290-301	3
2188	DNA methylation and SETDB1/H3K9me3 regulate predominantly distinct sets of genes, retroelements, and chimeric transcripts in mESCs. 2011 , 8, 676-87	309
2187	A transcriptomic atlas of mouse neocortical layers. 2011 , 71, 605-16	224
2186	Introduction and Historical Overview of DNA Sequencing. 2011 , 96, 7.0.1	1
2185	Construction of normalized RNA-seq libraries for next-generation sequencing using the crab duplex-specific nuclease. 2011 , Chapter 4, Unit4.12	65
2184	SNP discovery in black cottonwood (<i>Populus trichocarpa</i>) by population transcriptome resequencing. 2011 , 11 Suppl 1, 81-92	96
2183	Improving RNA-Seq expression estimates by correcting for fragment bias. 2011 , 12, R22	804
2182	ExpressionPlot: a web-based framework for analysis of RNA-Seq and microarray gene expression data. 2011 , 12, R69	31
2181	An introduction to the informatics of "next-generation" sequencing. 2011 , Chapter 11, Unit 11.1.	11
2180	RNA-Seq for Plant Pathogenic Bacteria. 2011 , 2, 689-705	6
2179	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011 , 29, 922-7	44.5 324
2178	Identification and correction of systematic error in high-throughput sequence data. 2011 ,	1

2177	Gene Expression Analysis Using RNA-Seq from Organisms Lacking Substantial Genomic Resources. 2011,	
2176	Utility of RNA Sequencing for Analysis of Maize Reproductive Transcriptomes. 2011, 4, 191-203	100
2175	Next generation quantitative genetics in plants. 2011, 2, 77	10
2174	SOAPsplice: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. 2011, 2, 46	82
2173	Thousands of Novel Transcripts Identified in Mouse Cerebrum, Testis, and ES Cells Based on ribo-minus RNA Sequencing. 2011, 2, 93	12
2172	Genome-Wide Gene Expression Profiling of Nucleus Accumbens Neurons Projecting to Ventral Pallidum Using both Microarray and Transcriptome Sequencing. 2011, 5, 98	28
2171	Noncanonical compensation of zygotic X transcription in early <i>Drosophila melanogaster</i> development revealed through single-embryo RNA-seq. 2011, 9, e1000590	141
2170	Mayday SeaSight: combined analysis of deep sequencing and microarray data. 2011, 6, e16345	16
2169	Differential gene expression in the siphonophore <i>Nanomia bijuga</i> (Cnidaria) assessed with multiple next-generation sequencing workflows. 2011, 6, e22953	34
2168	GENE-counter: a computational pipeline for the analysis of RNA-Seq data for gene expression differences. 2011, 6, e25279	50
2167	Transcriptional profiling of endocrine cerebro-osteodysplasia using microarray and next-generation sequencing. 2011, 6, e25400	8
2166	The post-apoptotic fate of RNAs identified through high-throughput sequencing of human hair. 2011, 6, e27603	9
2165	Statistical Modeling of RNA-Seq Data. 2011, 26,	53
2164	Identification of Common Carp Innate Immune Genes with Whole-Genome Sequencing and RNA-Seq Data. 2011, 8, 165-175	18
2163	Transcriptomic Technologies and Statistical Data Analysis. 2011, 133-162	
2162	The next generation: using new sequencing technologies to analyse gene regulation. 2011, 16, 210-22	37
2161	Transcription factor genes of <i>Schizophyllum commune</i> involved in regulation of mushroom formation. 2011, 81, 1433-45	96
2160	Understanding the pathogenesis of Alzheimer's disease: will RNA-Seq realize the promise of transcriptomics?. 2011, 116, 937-46	49

2159	Deep RNA sequencing improved the structural annotation of the Tuber melanosporum transcriptome. 2011 , 189, 883-891	46
2158	Regulatory mechanisms underlying C4 photosynthesis. 2011 , 190, 9-20	35
2157	BM-map: Bayesian mapping of multireads for next-generation sequencing data. 2011 , 67, 1215-24	22
2156	Development and applications of single-cell transcriptome analysis. 2011 , 8, S6-11	230
2155	Computational methods for transcriptome annotation and quantification using RNA-seq. 2011 , 8, 469-77	711
2154	RNA sequencing: advances, challenges and opportunities. 2011 , 12, 87-98	1432
2153	Heart failure: advances through genomics. 2011 , 12, 357-62	55
2152	Genotype and SNP calling from next-generation sequencing data. 2011 , 12, 443-51	959
2151	Next-generation transcriptome assembly. 2011 , 12, 671-82	878
2150	The developmental transcriptome of <i>Drosophila melanogaster</i> . 2011 , 471, 473-9	1094
2149	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. 2011 , 471, 68-73	1241
2148	Trends in computational biology 2010. <i>Nature Biotechnology</i> , 2011 , 29, 45-9	44.5 7
2147	Full-length transcriptome assembly from RNA-Seq data without a reference genome. <i>Nature Biotechnology</i> , 2011 , 29, 644-52	44.5 11785
2146	Advances in bacterial transcriptome and transposon insertion-site profiling using second-generation sequencing. 2011 , 29, 586-94	23
2145	The study of eQTL variations by RNA-seq: from SNPs to phenotypes. 2011 , 27, 72-9	176
2144	Identification and correction of systematic error in high-throughput sequence data. 2011 , 12, 451	173
2143	MAKER2: an annotation pipeline and genome-database management tool for second-generation genome projects. 2011 , 12, 491	1008
2142	De novo sequence assembly and characterization of the floral transcriptome in cross- and self-fertilizing plants. 2011 , 12, 298	71

2141	Revealing the missing expressed genes beyond the human reference genome by RNA-Seq. 2011 , 12, 590	23
2140	Using RNA-seq to determine the transcriptional landscape and the hypoxic response of the pathogenic yeast <i>Candida parapsilosis</i> . 2011 , 12, 628	59
2139	Widespread RNA and DNA sequence differences in the human transcriptome. 2011 , 333, 53-8	328
2138	IsoLasso: A LASSO Regression Approach to RNA-Seq Based Transcriptome Assembly. 2011 , 168-188	14
2137	The emergence of lncRNAs in cancer biology. 2011 , 1, 391-407	1384
2136	<i>Ascaris suum</i> draft genome. 2011 , 479, 529-33	217
2135	Applications of high-throughput sequencing to symbiotic nematodes of the genus <i>Heterorhabditis</i> . 2011 , 55, 111-118	8
2134	Next-generation sequencing and its applications in molecular diagnostics. 2011 , 11, 333-43	125
2133	In vivo and transcriptome-wide identification of RNA binding protein target sites. 2011 , 44, 828-40	124
2132	Local and global factors affecting RNA sequencing analysis. 2011 , 419, 317-22	41
2131	mRNA-Seq Reveals a Comprehensive Transcriptome Profile of Rice under Phosphate Stress. 2011 , 4, 50-65	36
2130	Overview of available methods for diverse RNA-Seq data analyses. 2011 , 54, 1121-8	49
2129	De novo transcriptome assembly of RNA-Seq reads with different strategies. 2011 , 54, 1129-33	14
2128	Microarrays, deep sequencing and the true measure of the transcriptome. 2011 , 9, 34	370
2127	Estimation of alternative splicing isoform frequencies from RNA-Seq data. 2011 , 6, 9	125
2126	An integrative analysis of DNA methylation and RNA-Seq data for human heart, kidney and liver. 2011 , 5 Suppl 3, S4	30
2125	Experimental design, preprocessing, normalization and differential expression analysis of small RNA sequencing experiments. 2011 , 2, 2	74
2124	Differentiation and fiber type-specific activity of a muscle creatine kinase intronic enhancer. 2011 , 1, 25	18

2123	NSMAP: a method for spliced isoforms identification and quantification from RNA-Seq. 2011 , 12, 162	26
2122	rnaSeqMap: a Bioconductor package for RNA sequencing data exploration. 2011 , 12, 200	10
2121	Querying large read collections in main memory: a versatile data structure. 2011 , 12, 242	10
2120	Bias detection and correction in RNA-Sequencing data. 2011 , 12, 290	110
2119	IsoformEx: isoform level gene expression estimation using weighted non-negative least squares from mRNA-Seq data. 2011 , 12, 305	21
2118	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. 2011 , 12, 323	9564
2117	ReCount: a multi-experiment resource of analysis-ready RNA-seq gene count datasets. 2011 , 12, 449	115
2116	Analysis of cancer metabolism with high-throughput technologies. 2011 , 12 Suppl 10, S8	9
2115	Rice-Map: a new-generation rice genome browser. 2011 , 12, 165	9
2114	RNA-seq: technical variability and sampling. 2011 , 12, 293	195
2113	A tissue-specific landscape of sense/antisense transcription in the mouse intestine. 2011 , 12, 305	17
2112	Directional RNA deep sequencing sheds new light on the transcriptional response of <i>Anabaena</i> sp. strain PCC 7120 to combined-nitrogen deprivation. 2011 , 12, 332	127
2111	Somatic sex-specific transcriptome differences in <i>Drosophila</i> revealed by whole transcriptome sequencing. 2011 , 12, 364	66
2110	Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. 2011 , 12, 441	25
2109	Comparative analysis of neural transcriptomes and functional implication of unannotated intronic expression. 2011 , 12, 494	3
2108	False negative rates in <i>Drosophila</i> cell-based RNAi screens: a case study. 2011 , 12, 50	36
2107	De novo sequence assembly of <i>Albugo candida</i> reveals a small genome relative to other biotrophic oomycetes. 2011 , 12, 503	94
2106	The classification of mRNA expression levels by the phosphorylation state of RNAPII CTD based on a combined genome-wide approach. 2011 , 12, 516	29

2105	RNA-Seq improves annotation of protein-coding genes in the cucumber genome. 2011 , 12, 540	134
2104	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. 2011 , 12, 552	72
2103	Directional gene expression and antisense transcripts in sexual and asexual stages of <i>Plasmodium falciparum</i> . 2011 , 12, 587	221
2102	Whole transcriptome analysis: what are we still missing?. 2011 , 3, 527-43	21
2101	Conservation of an RNA regulatory map between <i>Drosophila</i> and mammals. 2011 , 21, 193-202	165
2100	Next-generation sequence analysis. <i>Nature Biotechnology</i> , 2011 , 29, 45-46	44.5 10
2099	A comparison of analog and Next-Generation transcriptomic tools for mammalian studies. 2011 , 10, 135-50	48
2098	SPATA: A seeding and patching algorithm for de novo transcriptome assembly. 2011 ,	1
2097	Systematic reconstruction of splicing regulatory modules by integrating many RNA-seq datasets. 2011 ,	
2096	Accurate estimation of expression levels of homologous genes in RNA-seq experiments. 2011 , 18, 459-68	28
2095	RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes. 2011 ,	1
2094	SpliceTrap: a method to quantify alternative splicing under single cellular conditions. 2011 , 27, 3010-6	73
2093	FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. 2011 , 27, 2633-40	42
2092	Nonrandom gene loss from the <i>Drosophila miranda</i> neo-Y chromosome. 2011 , 3, 1329-37	41
2091	Pyicos: a versatile toolkit for the analysis of high-throughput sequencing data. 2011 , 27, 3333-40	76
2090	Genome-wide mapping of RNA Pol-II promoter usage in mouse tissues by ChIP-seq. 2011 , 39, 190-201	62
2089	Genome-wide in silico identification of new conserved and functional retinoic acid receptor response elements (direct repeats separated by 5 bp). 2011 , 286, 33322-34	63
2088	Characterizing the impact of smoking and lung cancer on the airway transcriptome using RNA-Seq. 2011 , 4, 803-17	117

2087	RSEQtools: a modular framework to analyze RNA-Seq data using compact, anonymized data summaries. 2011 , 27, 281-3	89
2086	Direct and indirect effects of H-NS and Fis on global gene expression control in <i>Escherichia coli</i> . 2011 , 39, 2073-91	196
2085	Zebrafish mRNA sequencing deciphers novelties in transcriptome dynamics during maternal to zygotic transition. 2011 , 21, 1328-38	211
2084	Comparative analysis of proteome and transcriptome variation in mouse. 2011 , 7, e1001393	417
2083	Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the <i>Arabidopsis</i> Transcriptome. 2011 , 1, 559-70	58
2082	Isoform-level microRNA-155 target prediction using RNA-seq. 2011 , 39, e61	26
2081	The genome of the leaf-cutting ant <i>Acromyrmex echinatior</i> suggests key adaptations to advanced social life and fungus farming. 2011 , 21, 1339-48	183
2080	Accurate quantification of transcriptome from RNA-Seq data by effective length normalization. 2011 , 39, e9	91
2079	Modeling and automation of sequencing-based characterization of RNA structure. 2011 , 108, 11069-74	95
2078	A pipeline for RNA-seq data processing and quality assessment. 2011 , 27, 867-9	48
2077	Using non-uniform read distribution models to improve isoform expression inference in RNA-Seq. 2011 , 27, 502-8	72
2076	RISC RNA sequencing for context-specific identification of in vivo microRNA targets. 2011 , 108, 18-26	87
2075	Loss of cerebral cavernous malformation 3 (Ccm3) in neuroglia leads to CCM and vascular pathology. 2011 , 108, 3737-42	78
2074	Whole transcriptome sequencing reveals gene expression and splicing differences in brain regions affected by Alzheimer's disease. 2011 , 6, e16266	213
2073	Next-generation sequencing reveals HIV-1-mediated suppression of T cell activation and RNA processing and regulation of noncoding RNA expression in a CD4+ T cell line. 2011 , 2,	54
2072	Efficiently identifying genome-wide changes with next-generation sequencing data. 2011 , 39, e130	27
2071	Parent-of-origin effects on gene expression and DNA methylation in the maize endosperm. 2011 , 23, 4221-33	160
2070	Differentiation of the maize subgenomes by genome dominance and both ancient and ongoing gene loss. 2011 , 108, 4069-74	462

2069	Sparse linear modeling of next-generation mRNA sequencing (RNA-Seq) data for isoform discovery and abundance estimation. 2011 , 108, 19867-72	98
2068	Cryptococcal titan cell formation is regulated by G-protein signaling in response to multiple stimuli. 2011 , 10, 1306-16	80
2067	Nuclear effects of G-protein receptor kinase 5 on histone deacetylase 5-regulated gene transcription in heart failure. 2011 , 4, 659-68	37
2066	Evidence for compensatory upregulation of expressed X-linked genes in mammals, <i>Caenorhabditis elegans</i> and <i>Drosophila melanogaster</i> . 2011 , 43, 1179-85	206
2065	De novo assembly and validation of planaria transcriptome by massive parallel sequencing and shotgun proteomics. 2011 , 21, 1193-200	90
2064	Transcriptional programs in transient embryonic zones of the cerebral cortex defined by high-resolution mRNA sequencing. 2011 , 108, 14950-5	115
2063	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . 2011 , 477, 419-23	495
2062	The reality of pervasive transcription. 2011 , 9, e1000625; discussion e1001102	325
2061	Sex chromosome-specific regulation in the <i>Drosophila</i> male germline but little evidence for chromosomal dosage compensation or meiotic inactivation. 2011 , 9, e1001126	98
2060	MicroRNA-driven developmental remodeling in the brain distinguishes humans from other primates. 2011 , 9, e1001214	159
2059	Over-expression of DSCAM and COL6A2 cooperatively generates congenital heart defects. 2011 , 7, e1002344	53
2058	Characterization and improvement of RNA-Seq precision in quantitative transcript expression profiling. 2011 , 27, i383-91	108
2057	Sequencing-based expression profiling in zebrafish. 2011 , 104, 379-99	1
2056	Discovery from data repositories. <i>Nature Biotechnology</i> , 2011 , 29, 46-47	44.5 2
2055	Toward an integrated model of capsule regulation in <i>Cryptococcus neoformans</i> . 2011 , 7, e1002411	71
2054	Transcriptome analysis of rice mature root tissue and root tips in early development by massive parallel sequencing. 2012 , 63, 2141-57	37
2053	Essential role for miR-196a in brown adipogenesis of white fat progenitor cells. 2012 , 10, e1001314	177
2052	Genome, functional gene annotation, and nuclear transformation of the heterokont oleaginous alga <i>Nannochloropsis oceanica</i> CCMP1779. 2012 , 8, e1003064	306

2051	RNA-sequencing analysis of 5' capped RNAs identifies many new differentially expressed genes in acute hepatitis C virus infection. 2012 , 4, 581-612	32
2050	Escape from preferential retention following repeated whole genome duplications in plants. 2012 , 3, 94	52
2049	Rapid turnover of long noncoding RNAs and the evolution of gene expression. 2012 , 8, e1002841	238
2048	Phylogenetic and transcriptomic analysis of chemosensory receptors in a pair of divergent ant species reveals sex-specific signatures of odor coding. 2012 , 8, e1002930	150
2047	Tackling skeletal muscle cells epigenome in the next-generation sequencing era. 2012 , 2012, 979168	2
2046	Discovering chimeric transcripts in paired-end RNA-seq data by using EricScript. 2012 , 28, 3232-9	108
2045	WormBase: Annotating many nematode genomes. 2012 , 1, 15-21	11
2044	A comparison of brain gene expression levels in domesticated and wild animals. 2012 , 8, e1002962	91
2043	Calpain-5 mutations cause autoimmune uveitis, retinal neovascularization, and photoreceptor degeneration. 2012 , 8, e1003001	58
2042	A histone deacetylase adjusts transcription kinetics at coding sequences during <i>Candida albicans</i> morphogenesis. 2012 , 8, e1003118	67
2041	RNAseq analysis of the parasitic nematode <i>Strongyloides stercoralis</i> reveals divergent regulation of canonical dauer pathways. 2012 , 6, e1854	63
2040	A systematically improved high quality genome and transcriptome of the human blood fluke <i>Schistosoma mansoni</i> . 2012 , 6, e1455	306
2039	Genome-wide transcriptional profiling of appressorium development by the rice blast fungus <i>Magnaporthe oryzae</i> . 2012 , 8, e1002514	132
2038	Evidence for widespread positive and purifying selection across the European rabbit (<i>Oryctolagus cuniculus</i>) genome. 2012 , 29, 1837-49	57
2037	Transcription factor Amr1 induces melanin biosynthesis and suppresses virulence in <i>Alternaria brassicicola</i> . 2012 , 8, e1002974	57
2036	Spreading of heterochromatin is limited to specific families of maize retrotransposons. 2012 , 8, e1003127	124
2035	Positional correlation analysis improves reconstruction of full-length transcripts and alternative isoforms from noisy array signals or short reads. 2012 , 28, 929-37	6
2034	Enrichment of HP1a on <i>Drosophila</i> chromosome 4 genes creates an alternate chromatin structure critical for regulation in this heterochromatic domain. 2012 , 8, e1002954	45

2033	Bellerophon: an RNA-Seq data analysis framework for chimeric transcripts discovery based on accurate fusion model. 2012 , 28, 2114-21	33
2032	Dynamic deposition of histone variant H3.3 accompanies developmental remodeling of the Arabidopsis transcriptome. 2012 , 8, e1002658	93
2031	Persistent androgen receptor-mediated transcription in castration-resistant prostate cancer under androgen-deprived conditions. 2012 , 40, 10765-79	80
2030	The genome of <i>Prunus mume</i> . 2012 , 3, 1318	295
2029	BRAFV600E remodels the melanocyte transcriptome and induces BANC1 to regulate melanoma cell migration. 2012 , 22, 1006-14	218
2028	Computational inference of mRNA stability from histone modification and transcriptome profiles. 2012 , 40, 6414-23	16
2027	Trade-off between selection for dosage compensation and masculinization on the avian Z chromosome. 2012 , 192, 1433-45	57
2026	Age-related changes of gene expression in the neocortex: preliminary data on RNA-Seq of the transcriptome in three functionally distinct cortical areas. 2012 , 24, 1427-42	18
2025	Identification of putative candidate genes involved in cuticle formation in <i>Prunus avium</i> (sweet cherry) fruit. 2012 , 110, 101-12	55
2024	Savant Genome Browser 2: visualization and analysis for population-scale genomics. 2012 , 40, W615-21	42
2023	Whole genome expression differences in human left and right atria ascertained by RNA sequencing. 2012 , 5, 327-35	43
2022	Transcriptomes of mouse olfactory epithelium reveal sexual differences in odorant detection. 2012 , 4, 703-12	34
2021	Postexposure treatment with the live-attenuated rabies virus (RV) vaccine TriGAS triggers the clearance of wild-type RV from the Central Nervous System (CNS) through the rapid induction of genes relevant to adaptive immunity in CNS tissues. 2012 , 86, 3200-10	45
2020	Pinstripe: a suite of programs for integrating transcriptomic and proteomic datasets identifies novel proteins and improves differentiation of protein-coding and non-coding genes. 2012 , 28, 3042-50	59
2019	The central role of the host cell in symbiotic nitrogen metabolism. 2012 , 279, 2965-73	57
2018	VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. 2012 , 40, D729-34	134
2017	Transcriptome survey reveals increased complexity of the alternative splicing landscape in Arabidopsis. 2012 , 22, 1184-95	520
2016	Cell type-specific genomics of <i>Drosophila</i> neurons. 2012 , 40, 9691-704	114

2015	Preferred analysis methods for single genomic regions in RNA sequencing revealed by processing the shape of coverage. 2012 , 40, e63	4
2014	A new approach to bias correction in RNA-Seq. 2012 , 28, 921-8	22
2013	Transcription factor TEAD4 regulates expression of myogenin and the unfolded protein response genes during C2C12 cell differentiation. 2012 , 19, 220-31	58
2012	Circadian changes in long noncoding RNAs in the pineal gland. 2012 , 109, 13319-24	68
2011	RNA-Seq mapping and detection of gene fusions with a suffix array algorithm. 2012 , 8, e1002464	40
2010	H2B monoubiquitylation is a 5'-enriched active transcription mark and correlates with exon-intron structure in human cells. 2012 , 22, 1026-35	50
2009	Direct and indirect involvement of microRNA-499 in clinical and experimental cardiomyopathy. 2012 , 111, 521-31	105
2008	The grapevine expression atlas reveals a deep transcriptome shift driving the entire plant into a maturation program. 2012 , 24, 3489-505	252
2007	Extensive alternative polyadenylation during zebrafish development. 2012 , 22, 2054-66	220
2006	Cyber-T web server: differential analysis of high-throughput data. 2012 , 40, W553-9	120
2005	fus/TLS orchestrates splicing of developmental regulators during gastrulation. 2012 , 26, 1351-63	35
2004	An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads. 2012 ,	12
2003	Research resource: RNA-Seq reveals unique features of the pancreatic β cell transcriptome. 2012 , 26, 1783-92	87
2002	shutdown is a component of the Drosophila piRNA biogenesis machinery. 2012 , 18, 1446-57	66
2001	Estimation of alternative splicing variability in human populations. 2012 , 22, 528-38	49
2000	Unexpected diversity and expression of avian endogenous retroviruses. 2012 , 3, e00344-12	42
1999	Characterization of the longissimus lumborum transcriptome response to adding propionate to the diet of growing Angus beef steers. 2012 , 44, 543-50	18
1998	RNA sequencing: platform selection, experimental design, and data interpretation. 2012 , 22, 271-4	140

1997	Long noncoding RNAs in <i>C. elegans</i> . 2012 , 22, 2529-40	157
1996	Genome-wide identification of enhancers in skeletal muscle: the role of MyoD1. 2012 , 26, 2763-79	115
1995	Novel roles for KLF1 in erythropoiesis revealed by mRNA-seq. 2012 , 22, 2385-98	65
1994	Loss of miR-29 in myoblasts contributes to dystrophic muscle pathogenesis. 2012 , 20, 1222-33	90
1993	SPLOOCE: a new portal for the analysis of human splicing variants. 2012 , 9, 1339-43	7
1992	Algorithm to identify frequent coupled modules from two-layered network series: application to study transcription and splicing coupling. 2012 , 19, 710-30	14
1991	Removing technical variability in RNA-seq data using conditional quantile normalization. 2012 , 13, 204-16	378
1990	Reconstructing isoform graphs from RNA-Seq data. 2012 ,	1
1989	Genome-wide identification of regulatory DNA elements and protein-binding footprints using signatures of open chromatin in <i>Arabidopsis</i> . 2012 , 24, 2719-31	164
1988	Incorporating RNA-seq data into the zebrafish Ensembl genebuild. 2012 , 22, 2067-78	72
1987	Effects of drought on gene expression in maize reproductive and leaf meristem tissue revealed by RNA-Seq. 2012 , 160, 846-67	228
1986	Transcriptome assembly and isoform expression level estimation from biased RNA-Seq reads. 2012 , 28, 2914-21	68
1985	Sex-biased transcriptome evolution in <i>Drosophila</i> . 2012 , 4, 1189-200	125
1984	Cold-inducible RNA-binding protein modulates circadian gene expression posttranscriptionally. 2012 , 338, 379-83	188
1983	Detecting differential usage of exons from RNA-seq data. 2012 , 22, 2008-17	882
1982	Modelling and simulating generic RNA-Seq experiments with the flux simulator. 2012 , 40, 10073-83	200
1981	X-chromosome hyperactivation in mammals via nonlinear relationships between chromatin states and transcription. 2011 , 19, 56-61	67
1980	Cutaneous retinoic acid levels determine hair follicle development and downgrowth. 2012 , 287, 39304-15	17

1979	Integration of Hi-C and ChIP-seq data reveals distinct types of chromatin linkages. 2012 , 40, 7690-704	76
1978	Reduced DICER1 elicits an interferon response in endometrial cancer cells. 2012 , 10, 316-25	12
1977	Genome sequence of the oleaginous red yeast <i>Rhodospiridium toruloides</i> MTCC 457. 2012 , 11, 1083-4	51
1976	W chromosome expression responds to female-specific selection. 2012 , 109, 8207-11	76
1975	The role of CYP3A4 mRNA transcript with shortened 3'-untranslated region in hepatocyte differentiation, liver development, and response to drug induction. 2012 , 81, 86-96	10
1974	Identification and properties of 1,119 candidate lincRNA loci in the <i>Drosophila melanogaster</i> genome. 2012 , 4, 427-42	165
1973	A genome-wide regulatory framework identifies maize pericarp color1 controlled genes. 2012 , 24, 2745-64	120
1972	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. 2012 , 22, 2315-27	158
1971	Quantification of Transcriptome Responses of the Rumen Epithelium to Butyrate Infusion using RNA-seq Technology. 2012 , 6, 67-80	37
1970	A systems approach and skeletal myogenesis. 2012 , 2012, 759407	6
1969	Modulation of NF- κ B-dependent gene transcription using programmable DNA minor groove binders. 2012 , 109, 1023-8	104
1968	Retinoic acid receptors recognize the mouse genome through binding elements with diverse spacing and topology. 2012 , 287, 26328-41	100
1967	Using Poisson mixed-effects model to quantify transcript-level gene expression in RNA-Seq. 2012 , 28, 63-8	25
1966	Xenome--a tool for classifying reads from xenograft samples. 2012 , 28, i172-8	149
1965	Bayesian assignment of gene ontology terms to gene expression experiments. 2012 , 28, i603-i610	4
1964	AutismKB: an evidence-based knowledgebase of autism genetics. 2012 , 40, D1016-22	129
1963	RNASEQR--a streamlined and accurate RNA-seq sequence analysis program. 2012 , 40, e42	25
1962	SAVoR: a server for sequencing annotation and visualization of RNA structures. 2012 , 40, W59-64	14

1961	The super elongation complex family of RNA polymerase II elongation factors: gene target specificity and transcriptional output. 2012 , 32, 2608-17	126
1960	Expression dynamics of the <i>Medicago truncatula</i> transcriptome during the symbiotic interaction with <i>Sinorhizobium meliloti</i> : which role for nitric oxide?. 2013 , 161, 425-39	73
1959	Transcriptomic landscape of breast cancers through mRNA sequencing. 2012 , 2, 264	67
1958	Comparative transcriptome analyses of deltamethrin-resistant and -susceptible <i>Anopheles gambiae</i> mosquitoes from Kenya by RNA-Seq. 2012 , 7, e44607	69
1957	Characterizing regulatory and functional differentiation between maize mesophyll and bundle sheath cells by transcriptomic analysis. 2012 , 160, 165-77	111
1956	Characteristics and significance of intergenic polyadenylated RNA transcription in <i>Arabidopsis</i> . 2013 , 161, 210-24	18
1955	sizzled function and secreted factor network dynamics. 2012 , 1, 286-94	
1954	Computational Biology. 2012 ,	1
1953	GenomicTools: an open source platform for developing high-throughput analytics in genomics. 2012 , 189-220	
1952	A Method for Isoform Prediction from RNA-Seq Data by Iterative Mapping. 2012 , 5, 27-33	
1951	COMPARATIVE RNA-SEQ FOR THE INVESTIGATION OF RESISTANCE TO PHYTOPHTHORA ROOT ROT IN THE RED RASPBERRY 'LATHAM'. 2012 , 67-72	3
1950	Genome-wide analysis of STAT3 binding in vivo predicts effectors of the anti-inflammatory response in macrophages. 2012 , 119, e110-9	94
1949	MKL1 and MKL2 play redundant and crucial roles in megakaryocyte maturation and platelet formation. 2012 , 120, 2317-29	46
1948	The biology of nematode- and IL4R β -dependent murine macrophage polarization in vivo as defined by RNA-Seq and targeted lipidomics. 2012 , 120, e93-e104	44
1947	A zinc-finger-family transcription factor, AbVf19, is required for the induction of a gene subset important for virulence in <i>Alternaria brassicicola</i> . 2012 , 25, 443-52	24
1946	Chromatin modification by SUMO-1 stimulates the promoters of translation machinery genes. 2012 , 40, 10172-86	52
1945	RNA sequencing reveals dynamic changes of mRNA abundance of cytochromes P450 and their alternative transcripts during mouse liver development. 2012 , 40, 1198-209	46
1944	Promoter-specific transcription inhibition in <i>Staphylococcus aureus</i> by a phage protein. 2012 , 151, 1005-16	19

1943	STATs shape the active enhancer landscape of T cell populations. 2012 , 151, 981-93	269
1942	Proteomics-directed cloning of circulating antiviral human monoclonal antibodies. <i>Nature Biotechnology</i> , 2012 , 30, 1039-43	44-5 45
1941	Suppression of progenitor differentiation requires the long noncoding RNA ANCR. 2012 , 26, 338-43	321
1940	An atlas of the Epstein-Barr virus transcriptome and epigenome reveals host-virus regulatory interactions. 2012 , 12, 233-45	175
1939	Transcriptional reprogramming by root knot and migratory nematode infection in rice. 2012 , 196, 887-900	117
1938	Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. 2012 , 40, 4288-97	2691
1937	Circadian oscillations of protein-coding and regulatory RNAs in a highly dynamic mammalian liver epigenome. 2012 , 16, 833-45	199
1936	Evolutionary dynamics of gene and isoform regulation in Mammalian tissues. 2012 , 338, 1593-9	587
1935	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. 2012 , 28, 1923-4	52
1934	Activating transcription factor 3 regulates immune and metabolic homeostasis. 2012 , 32, 3949-62	54
1933	FX: an RNA-Seq analysis tool on the cloud. 2012 , 28, 721-3	57
1932	Bioinformatics tools and databases for analysis of next-generation sequence data. 2012 , 11, 12-24	59
1931	Morphine epigenomically regulates behavior through alterations in histone H3 lysine 9 dimethylation in the nucleus accumbens. 2012 , 32, 17454-64	101
1930	The histone deacetylase SIRT6 is a tumor suppressor that controls cancer metabolism. 2012 , 151, 1185-99	476
1929	Genome sequence of the model medicinal mushroom <i>Ganoderma lucidum</i> . 2012 , 3, 913	307
1928	How to analyze gene expression using RNA-sequencing data. 2012 , 802, 259-74	22
1927	Stable intronic sequence RNA (sisRNA), a new class of noncoding RNA from the oocyte nucleus of <i>Xenopus tropicalis</i> . 2012 , 26, 2550-9	98
1926	Adiponectin regulates expression of hepatic genes critical for glucose and lipid metabolism. 2012 , 109, 14568-73	95

1925	Retrograde signaling and photoprotection in a gun4 mutant of <i>Chlamydomonas reinhardtii</i> . 2012 , 5, 1242-62	42
1924	Towards accurate detection and genotyping of expressed variants from whole transcriptome sequencing data. 2012 , 13 Suppl 2, S6	31
1923	SpliceGrapher: detecting patterns of alternative splicing from RNA-Seq data in the context of gene models and EST data. 2012 , 13, R4	101
1922	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. 2012 , 13, R102	51
1921	The genomic landscape shaped by selection on transposable elements across 18 mouse strains. 2012 , 13, R45	124
1920	Human histone H3K79 methyltransferase DOT1L protein [corrected] binds actively transcribing RNA polymerase II to regulate gene expression. 2012 , 287, 39698-709	62
1919	Introns in UTRs: why we should stop ignoring them. 2012 , 34, 1025-34	89
1918	Development of a molecular test to determine the vitality status of Norway spruce (<i>Picea abies</i>) seedlings during frozen storage. 2012 , 43, 665-678	21
1917	A validated regulatory network for Th17 cell specification. 2012 , 151, 289-303	794
1916	Genome-wide analysis reveals extensive functional interaction between DNA replication initiation and transcription in the genome of <i>Trypanosoma brucei</i> . 2012 , 2, 185-97	71
1915	Transcriptome analysis of the planarian eye identifies ovo as a specific regulator of eye regeneration. 2012 , 2, 294-307	134
1914	FACS purification and transcriptome analysis of drosophila neural stem cells reveals a role for Klumpfuss in self-renewal. 2012 , 2, 407-18	98
1913	The microtubule plus-end tracking protein CLASP2 is required for hematopoiesis and hematopoietic stem cell maintenance. 2012 , 2, 781-8	12
1912	Exploring the host transcriptome for mechanisms underlying protective immunity and resistance to nematode infections in ruminants. 2012 , 190, 1-11	10
1911	Transcriptome analysis of <i>Drosophila</i> CNS midline cells reveals diverse peptidergic properties and a role for castor in neuronal differentiation. 2012 , 372, 131-42	18
1910	Discovery and characterization of new transcripts from RNA-seq data in mouse CD4(+) T cells. 2012 , 100, 303-13	10
1909	RNA-seq transcriptome analysis of male and female zebra finch cell lines. 2012 , 100, 363-9	20
1908	Poised RNA polymerase II changes over developmental time and prepares genes for future expression. 2012 , 2, 1670-83	74

1907	Biclustering of linear patterns in gene expression data. 2012 , 19, 619-31	4
1906	Workshop: Novel transcript reconstruction from paired-end RNA-Seq reads using fragment length distribution. 2012 ,	
1905	Perturbation of FliL interferes with <i>Proteus mirabilis</i> swarmer cell gene expression and differentiation. 2012 , 194, 437-47	39
1904	A multi-omic map of the lipid-producing yeast <i>Rhodospiridium toruloides</i> . 2012 , 3, 1112	244
1903	MonarchBase: the monarch butterfly genome database. 2013 , 41, D758-63	69
1902	Linking photoreceptor excitation to changes in plant architecture. 2012 , 26, 785-90	334
1901	R-SAP: a multi-threading computational pipeline for the characterization of high-throughput RNA-sequencing data. 2012 , 40, e67	6
1900	A physical, genetic and functional sequence assembly of the barley genome. 2012 , 491, 711-6	1124
1899	Next-generation sequencing technologies for gene expression profiling in plants. 2012 , 11, 63-70	100
1898	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. 2012 , 22, 577-91	590
1897	Identifying differentially expressed transcripts from RNA-seq data with biological variation. 2012 , 28, 1721-8	148
1896	Comparative analysis of protein-coding genes and long non-coding RNAs of prostate cancer between Caucasian and Chinese populations. 2012 ,	1
1895	Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. 2012 , 28, 1086-92	1129
1894	Application of the Gini correlation coefficient to infer regulatory relationships in transcriptome analysis. 2012 , 160, 192-203	46
1893	Analysis of gene expression from the <i>Wolbachia</i> genome of a filarial nematode supports both metabolic and defensive roles within the symbiosis. 2012 , 22, 2467-77	140
1892	Retinal transcriptome profiling by directional next-generation sequencing using 100 ng of total RNA. 2012 , 884, 319-34	22
1891	Alternative splicing: enhancing ability to cope with stress via transcriptome plasticity. 2012 , 185-186, 40-9	168
1890	Basic leucine zipper transcription factor OsbZIP16 positively regulates drought resistance in rice. 2012 , 193-194, 8-17	75

1889	Genome-wide transcriptome analysis in murine neural retina using high-throughput RNA sequencing. 2012 , 99, 44-51	35
1888	Identification of long non-protein coding RNAs in chicken skeletal muscle using next generation sequencing. 2012 , 99, 292-8	119
1887	Methods and software in NGS for TE analysis. 2012 , 859, 105-14	6
1886	Technical considerations for functional sequencing assays. 2012 , 13, 802-7	32
1885	Binding profiles of chromatin-modifying proteins are predictive for transcriptional activity and promoter-proximal pausing. 2012 , 19, 126-38	8
1884	GFOLD: a generalized fold change for ranking differentially expressed genes from RNA-seq data. 2012 , 28, 2782-8	273
1883	mRNA-Seq reveals complex patterns of gene regulation and expression in the mouse skeletal muscle transcriptome associated with calorie restriction. 2012 , 44, 331-44	12
1882	The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. 2012 , 7, 1534-50	742
1881	Polycomb associates genome-wide with a specific RNA polymerase II variant, and regulates metabolic genes in ESCs. 2012 , 10, 157-70	221
1880	Dual RNA-seq of pathogen and host. 2012 , 10, 618-30	484
1879	Microsporidian genome analysis reveals evolutionary strategies for obligate intracellular growth. 2012 , 22, 2478-88	191
1878	Detection and quantification of alternative splicing variants using RNA-seq. 2012 , 883, 97-110	17
1877	Differential expression--the next generation and beyond. 2012 , 11, 57-62	27
1876	Strategies for transcriptome analysis in nonmodel plants. 2012 , 99, 267-76	103
1875	Massively parallel sequencing technology in pathogenic microbes. 2012 , 835, 271-94	5
1874	Intragenic enhancers act as alternative promoters. 2012 , 45, 447-58	193
1873	Transcriptome analyses during fruiting body formation in <i>Fusarium graminearum</i> and <i>Fusarium verticillioides</i> reflect species life history and ecology. 2012 , 49, 663-73	56
1872	Base-resolution analyses of sequence and parent-of-origin dependent DNA methylation in the mouse genome. 2012 , 148, 816-31	396

1871	Personal omics profiling reveals dynamic molecular and medical phenotypes. 2012 , 148, 1293-307	921
1870	The pan-ErbB negative regulator Lrig1 is an intestinal stem cell marker that functions as a tumor suppressor. 2012 , 149, 146-58	486
1869	Cell-free formation of RNA granules: bound RNAs identify features and components of cellular assemblies. 2012 , 149, 768-79	564
1868	Noncanonical Wnt signaling maintains hematopoietic stem cells in the niche. 2012 , 150, 351-65	218
1867	Transcript dynamics of proinflammatory genes revealed by sequence analysis of subcellular RNA fractions. 2012 , 150, 279-90	338
1866	Improving PacBio long read accuracy by short read alignment. 2012 , 7, e46679	229
1865	Efficient direct reprogramming of mature amniotic cells into endothelial cells by ETS factors and TGF β suppression. 2012 , 151, 559-75	170
1864	Regulation and expression of the ATP-binding cassette transporter ABCG2 in human embryonic stem cells. 2012 , 30, 2175-87	33
1863	Computational analysis of noncoding RNAs. 2012 , 3, 759-78	44
1862	A genome resource to address mechanisms of developmental programming: determination of the fetal sheep heart transcriptome. 2012 , 590, 2873-84	13
1861	Genetic dissection of growth, wood basic density and gene expression in interspecific backcrosses of <i>Eucalyptus grandis</i> and <i>E. urophylla</i> . 2012 , 13, 60	24
1860	Transcriptome landscape of the human placenta. 2012 , 13, 115	65
1859	RNA-Seq analysis uncovers transcriptomic variations between morphologically similar in vivo- and in vitro-derived bovine blastocysts. 2012 , 13, 118	82
1858	Elucidation of the molecular envenomation strategy of the cone snail <i>Conus geographus</i> through transcriptome sequencing of its venom duct. 2012 , 13, 284	74
1857	Oomycete Transcriptomics Database: a resource for oomycete transcriptomes. 2012 , 13, 303	7
1856	Quantitative RNA-Seq analysis in non-model species: assessing transcriptome assemblies as a scaffold and the utility of evolutionary divergent genomic reference species. 2012 , 13, 361	72
1855	Transcriptome sequencing of <i>Eucalyptus camaldulensis</i> seedlings subjected to water stress reveals functional single nucleotide polymorphisms and genes under selection. 2012 , 13, 364	47
1854	A draft of the genome and four transcriptomes of a medicinal and pesticidal angiosperm <i>Azadirachta indica</i> . 2012 , 13, 464	62

1853	Whole transcriptome analyses of six thoroughbred horses before and after exercise using RNA-Seq. 2012 , 13, 473	56
1852	Genome-wide association between DNA methylation and alternative splicing in an invertebrate. 2012 , 13, 480	115
1851	Combining laser microdissection and RNA-seq to chart the transcriptional landscape of fungal development. 2012 , 13, 511	54
1850	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. 2012 , 13, 547	89
1849	Resolving candidate genes of mouse skeletal muscle QTL via RNA-Seq and expression network analyses. 2012 , 13, 592	17
1848	Genomic consequences of transitions from cross- to self-fertilization on the efficacy of selection in three independently derived selfing plants. 2012 , 13, 611	28
1847	RNA-seq and microarray complement each other in transcriptome profiling. 2012 , 13, 629	109
1846	Downy mildew resistance induced by <i>Trichoderma harzianum</i> T39 in susceptible grapevines partially mimics transcriptional changes of resistant genotypes. 2012 , 13, 660	108
1845	De novo reconstruction of the <i>Toxoplasma gondii</i> transcriptome improves on the current genome annotation and reveals alternatively spliced transcripts and putative long non-coding RNAs. 2012 , 13, 696	36
1844	Strand-specific RNA-seq reveals widespread occurrence of novel cis-natural antisense transcripts in rice. 2012 , 13, 721	62
1843	Global transcriptome analysis reveals distinct expression among duplicated genes during sorghum-interaction. 2012 , 12, 121	37
1842	Genistein cooperates with the histone deacetylase inhibitor vorinostat to induce cell death in prostate cancer cells. 2012 , 12, 145	47
1841	<i>Scheffersomyces stipitis</i> : a comparative systems biology study with the Crabtree positive yeast <i>Saccharomyces cerevisiae</i> . 2012 , 11, 136	48
1840	Pathway-based classification of cancer subtypes. 2012 , 7, 21	75
1839	Analysis of the swine tracheobronchial lymph node transcriptomic response to infection with a Chinese highly pathogenic strain of porcine reproductive and respiratory syndrome virus. 2012 , 8, 208	24
1838	Improving metabolic flux predictions using absolute gene expression data. 2012 , 6, 73	107
1837	Potential role of multiple carbon fixation pathways during lipid accumulation in <i>Phaeodactylum tricornutum</i> . 2012 , 5, 40	147
1836	Adipose co-expression networks across Finns and Mexicans identify novel triglyceride-associated genes. 2012 , 5, 61	24

1835	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. 2012 , 5, 6	13
1834	Statistical methods for identifying differentially expressed genes in RNA-Seq experiments. 2012 , 2, 26	32
1833	Strategies to identify long noncoding RNAs involved in gene regulation. 2012 , 2, 37	63
1832	Metalloproteinases and their associated genes contribute to the functional integrity and noise-induced damage in the cochlear sensory epithelium. 2012 , 32, 14927-41	34
1831	Genomics of Volvocine Algae. 2012 , 64, 185-243	35
1830	Next Generation Microarray Bioinformatics. 2012 ,	6
1829	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. 2013 , 67, 1263-78	32
1828	Time Course RNA-seq: A Potential Avenue with Somewhat Different Approach in Tandem of Differential Analysis. 2012 ,	
1827	The diverse applications of RNA-seq for functional genomic studies in <i>Aspergillus fumigatus</i> . 2012 , 1273, 25-34	14
1826	Expression of <i>lec-1</i> , a mycobiont gene encoding a galectin-like protein in the lichen <i>Peltigera membranacea</i> . 2012 , 57, 23-31	25
1825	Tag Sequencing. 2012 ,	
1824	Gene structure in the sea urchin <i>Strongylocentrotus purpuratus</i> based on transcriptome analysis. 2012 , 22, 2079-87	113
1823	Deciphering the plant splicing code: experimental and computational approaches for predicting alternative splicing and splicing regulatory elements. 2012 , 3, 18	61
1822	Gene expression in mouse oocytes by RNA-Seq. 2012 , 825, 237-51	5
1821	De novo derivation of proteomes from transcriptomes for transcript and protein identification. 2012 , 9, 1207-11	131
1820	'Omics investigations of HIV and SIV pathogenesis and innate immunity. 2013 , 363, 87-116	2
1819	Single-neuron RNA-Seq: technical feasibility and reproducibility. 2012 , 3, 124	52
1818	Total RNA-Seq: Complete Analysis of the Transcriptome Using Illumina Sequencing-By-Synthesis Sequencing. 2012 , 367-381	1

1817 Stranded RNA-Seq: Strand-Specific Shotgun Sequencing of RNA. **2012**, 91-108

1816 Tracing the genesis of human embryonic stem cells. *Nature Biotechnology*, **2012**, 30, 247-9 44.5

1815 MicroRNA signature in patients with eosinophilic esophagitis, reversibility with glucocorticoids, and assessment as disease biomarkers. **2012**, 129, 1064-75.e9 122

1814 Engineering C4 photosynthetic regulatory networks. **2012**, 23, 298-304 15

1813 Simplification and desexualization of gene expression in self-fertile nematodes. **2012**, 22, 2167-72 53

1812 The physiology of sterol nutrition in the pea aphid *Acyrtosiphon pisum*. **2012**, 58, 1383-9 22

1811 Structural analysis of the quaking homodimerization interface. **2012**, 423, 766-81 24

1810 Beyond the Pipelines: Cloud Computing Facilitates Management, Distribution, Security, and Analysis of High-Speed Sequencer Data. **2012**, 449-468 3

1809 Genome-wide mapping of nucleosome occupancy, histone modifications, and gene expression using next-generation sequencing technology. **2012**, 513, 297-313 23

1808 Using cloud computing infrastructure with CloudBioLinux, CloudMan, and Galaxy. **2012**, Chapter 11, Unit11.9 21

1807 Normalization, bias correction, and peak calling for ChIP-seq. **2012**, 11, Article 9 66

1806 NGS analyses by visualization with Trackster. *Nature Biotechnology*, **2012**, 30, 1036-9 44.5 22

1805 Next-generation sequencing technologies and fragment assembly algorithms. **2012**, 855, 155-74 19

1804 Gene prediction. **2012**, 855, 175-201 11

1803 Definition of Promotome and Transcriptome Architecture Using CAGEscan. **2012**, 47-61

1802 Tag-Seq: Next-Generation Tag Sequencing for Gene Expression Profiling. **2012**, 211-241 2

1801 Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells. *Nature Biotechnology*, **2012**, 30, 777-82 44.5 1045

1800 Library preparation and data analysis packages for rapid genome sequencing. **2012**, 944, 1-22 16

1799	The Arabidopsis Information Resource (TAIR): improved gene annotation and new tools. 2012 , 40, D1202-10	1348
1798	Modeling RNA degradation for RNA-Seq with applications. 2012 , 13, 734-47	17
1797	Application of genomic and molecular methods to fundamental questions in canine and feline reproductive health. 2012 , 47 Suppl 6, 309-12	1
1796	Current status and future perspectives for sequencing livestock genomes. 2012 , 3, 8	30
1795	A closer look at RNA editing. <i>Nature Biotechnology</i> , 2012 , 30, 246-7	44-5 5
1794	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in <i>Saccharomyces cerevisiae</i> . 2012 , 40, 10084-97	222
1793	Genomic approaches for interrogating the biochemistry of medicinal plant species. 2012 , 517, 139-59	41
1792	Hadoop Applications in Bioinformatics. 2012 ,	1
1791	Direct isolation and RNA-seq reveal environment-dependent properties of engrafted neural stem/progenitor cells. 2012 , 3, 1140	50
1790	Improving the Flexibility of RNA-Seq Data Analysis Pipelines. 2012 , 2012, 70-73	1
1789	RBM20, a gene for hereditary cardiomyopathy, regulates titin splicing. 2012 , 18, 766-73	337
1788	RNA Abundance Analysis. 2012 ,	2
1787	Utilizing RNA-Seq data for cancer network inference. 2012 ,	4
1786	Transcriptome analyses of <i>Bactericera cockerelli</i> adults in response to " <i>Candidatus Liberibacter solanacearum</i> " infection. 2012 , 287, 803-17	38
1785	RNA-seq analysis of synovial fibroblasts brings new insights into rheumatoid arthritis. 2012 , 2, 43	34
1784	Transcriptome profile of a bovine respiratory disease pathogen: <i>Mannheimia haemolytica</i> PHL213. 2012 , 13 Suppl 15, S4	10
1783	Accuracy of RNA-Seq and its dependence on sequencing depth. 2012 , 13 Suppl 13, S5	20
1782	Prediction of novel long non-coding RNAs based on RNA-Seq data of mouse Klf1 knockout study. 2012 , 13, 331	93

1781	Alt Event Finder: a tool for extracting alternative splicing events from RNA-seq data. 2012 , 13 Suppl 8, S10	19
1780	Steps to ensure accuracy in genotype and SNP calling from Illumina sequencing data. 2012 , 13 Suppl 8, S8	80
1779	DFI: gene feature discovery in RNA-seq experiments from multiple sources. 2012 , 13 Suppl 8, S11	3
1778	RNA-Seq analysis implicates dysregulation of the immune system in schizophrenia. 2012 , 13 Suppl 8, S2	48
1777	Efficient experimental design and analysis strategies for the detection of differential expression using RNA-Sequencing. 2012 , 13, 484	139
1776	The regulatory effect of miRNAs is a heritable genetic trait in humans. 2012 , 13, 383	21
1775	Retinal Development. 2012 ,	3
1774	A normalization strategy for comparing tag count data. 2012 , 7, 5	57
1773	Transposable elements reveal a stem cell-specific class of long noncoding RNAs. 2012 , 13, R107	361
1772	Transcriptome walking: a laboratory-oriented GUI-based approach to mRNA identification from deep-sequenced data. 2012 , 5, 673	11
1771	Maize (<i>Zea mays</i> L.) genome diversity as revealed by RNA-sequencing. 2012 , 7, e33071	123
1770	A powerful method for transcriptional profiling of specific cell types in eukaryotes: laser-assisted microdissection and RNA sequencing. 2012 , 7, e29685	88
1769	Characterization and comparison of the leukocyte transcriptomes of three cattle breeds. 2012 , 7, e30244	25
1768	Inhibition of miR-29 by TGF-beta-Smad3 signaling through dual mechanisms promotes transdifferentiation of mouse myoblasts into myofibroblasts. 2012 , 7, e33766	102
1767	Population differences in transcript-regulator expression quantitative trait loci. 2012 , 7, e34286	6
1766	Transcriptome analysis reveals strain-specific and conserved stemness genes in <i>Schmidtea mediterranea</i> . 2012 , 7, e34447	44
1765	Transcriptome responses of insect fat body cells to tissue culture environment. 2012 , 7, e34940	10
1764	Expression profiling of <i>Cucumis sativus</i> in response to infection by <i>Pseudoperonospora cubensis</i> . 2012 , 7, e34954	43

1763	mRNA-Seq analysis of the <i>Pseudoperonospora cubensis</i> transcriptome during cucumber (<i>Cucumis sativus</i> L.) infection. 2012 , 7, e35796	47
1762	Transcriptome characterization by RNA-seq unravels the mechanisms of butyrate-induced epigenomic regulation in bovine cells. 2012 , 7, e36940	39
1761	Gene isoform specificity through enhancer-associated antisense transcription. 2012 , 7, e43511	22
1760	High-resolution transcriptome of human macrophages. 2012 , 7, e45466	168
1759	Comparative transcriptional analysis of homologous pathogenic and non-pathogenic <i>Lawsonia intracellularis</i> isolates in infected porcine cells. 2012 , 7, e46708	15
1758	Transcriptome analysis of the Asian honey bee <i>Apis cerana cerana</i> . 2012 , 7, e47954	27
1757	Complex modulation of the <i>Aedes aegypti</i> transcriptome in response to dengue virus infection. 2012 , 7, e50512	96
1756	Evaluating de Bruijn graph assemblers on 454 transcriptomic data. 2012 , 7, e51188	20
1755	Comparative transcriptome profiling of the early response to <i>Magnaporthe oryzae</i> in durable resistant vs susceptible rice (<i>Oryza sativa</i> L.) genotypes. 2012 , 7, e51609	105
1754	Development of transcriptomic resources for interrogating the biosynthesis of monoterpene indole alkaloids in medicinal plant species. 2012 , 7, e52506	121
1753	Splicing programs and cancer. 2012 , 2012, 269570	38
1752	Alternative splicing regulated by butyrate in bovine epithelial cells. 2012 , 7, e39182	10
1751	The human transcriptome: an unfinished story. 2012 , 3, 344-60	80
1750	A central role for long non-coding RNA in cancer. 2012 , 3, 17	130
1749	Improving RNA-Seq Precision with MapAl. 2012 , 3, 28	2
1748	Global Approaches to the Role of miRNAs in Drug-Induced Changes in Gene Expression. 2012 , 3, 109	20
1747	Big (sequencing) future of non-coding RNA research for the understanding of cocaine. 2012 , 3, 158	1
1746	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. 2012 , 2, 12	38

1745	Detecting differential usage of exons from RNA-Seq data. 2012,	11
1744	Detecting differential usage of exons from RNA-Seq data. 2012,	8
1743	HELLP babies link a novel lincRNA to the trophoblast cell cycle. 2012, 122, 4003-11	53
1742	Identification of artifactual microarray probe signals constantly present in multiple sample types. 2012, 53, 91-8	5
1741	The Tissue Specific Role of Estrogen and Progesterone in Human Endometrium and Mammary Gland. 2012,	1
1740	Computational approaches to discovering noncoding RNA. 2012, 3, 567-79	15
1739	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. 2012, 7, 562-78	8342
1738	Fast gapped-read alignment with Bowtie 2. 2012, 9, 357-9	24735
1737	Disentangling the relationship between sex-biased gene expression and X-linkage. 2012, 22, 1255-65	91
1736	Unbiased approach to profile the variety of small non-coding RNA of human blood plasma with massively parallel sequencing technology. 2012, 12 Suppl 1, S43-51	25
1735	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. 2012, 22, 246-58	385
1734	JETTA: junction and exon toolkits for transcriptome analysis. 2012, 28, 1274-5	19
1733	Evolutionary Genomics. 2012,	4
1732	A beginner's guide to eukaryotic genome annotation. 2012, 13, 329-42	416
1731	Integrating genomes. 2012, 336, 179-82	18
1730	Nprl3 is required for normal development of the cardiovascular system. 2012, 23, 404-15	25
1729	Studying and modelling dynamic biological processes using time-series gene expression data. 2012, 13, 552-64	307
1728	Global assembly of expressed sequence tags. 2012, 883, 193-9	

1727	Sex-specific adaptation drives early sex chromosome evolution in <i>Drosophila</i> . 2012 , 337, 341-5		135
1726	The origin and evolution of mutations in acute myeloid leukemia. 2012 , 150, 264-78		1143
1725	Targeted enrichment strategies for next-generation plant biology. 2012 , 99, 291-311		149
1724	Effects of sequence variation on differential allelic transcription factor occupancy and gene expression. 2012 , 22, 860-9		113
1723	"Calling cards" for DNA-binding proteins in mammalian cells. 2012 , 190, 941-9		41
1722	Integrated genome analysis suggests that most conserved non-coding sequences are regulatory factor binding sites. 2012 , 40, 7858-69		26
1721	Applications of High-Throughput Sequencing. 2012 , 27-53		1
1720	Differential Expression for RNA Sequencing (RNA-Seq) Data: Mapping, Summarization, Statistical Analysis, and Experimental Design. 2012 , 169-190		2
1719	Designing a transcriptome next-generation sequencing project for a nonmodel plant species. 2012 , 99, 257-66		166
1718	Next generation RNA-sequencing in prognostic subsets of chronic lymphocytic leukemia. 2012 , 87, 737-40		21
1717	Genome sequence of foxtail millet (<i>Setaria italica</i>) provides insights into grass evolution and biofuel potential. <i>Nature Biotechnology</i> , 2012 , 30, 549-54	44.5	447
1716	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012 , 30, 555-61	44.5	573
1715	The yak genome and adaptation to life at high altitude. 2012 , 44, 946-9		472
1714	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012 , 30, 693-700	44.5	758
1713	Macro lncRNAs: a new layer of cis-regulatory information in the mammalian genome. 2012 , 9, 731-41		56
1712	Nutritional control of mRNA isoform expression during developmental arrest and recovery in <i>C. elegans</i> . 2012 , 22, 1920-9		31
1711	Computational analysis of RNA-seq. 2012 , 883, 201-19		9
1710	Widespread dynamic DNA methylation in response to biotic stress. 2012 , 109, E2183-91		640

1709	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. <i>Nature Biotechnology</i> , 2011 , 30, 99-104	44.5	356
1708	Deeply dissecting stemness: making sense to non-coding RNAs in stem cells. 2012 , 8, 78-86		12
1707	Repetitive DNA and next-generation sequencing: computational challenges and solutions. 2011 , 13, 36-46		1053
1706	Transcriptome sequencing of <i>Salmonella enterica</i> serovar Enteritidis under desiccation and starvation stress in peanut oil. 2012 , 30, 311-5		86
1705	A de novo transcriptome assembly of <i>Lucilia sericata</i> (Diptera: Calliphoridae) with predicted alternative splices, single nucleotide polymorphisms and transcript expression estimates. 2012 , 21, 205-21		43
1704	Confirmation of an epilepsy modifier locus on mouse chromosome 11 and candidate gene analysis by RNA-Seq. 2012 , 11, 452-60		20
1703	Fractionation mutagenesis and similar consequences of mechanisms removing dispensable or less-expressed DNA in plants. 2012 , 15, 131-9		145
1702	Genomics and transcriptomics across the diversity of the Nematoda. 2012 , 34, 108-20		18
1701	Advances in plant genome sequencing. 2012 , 70, 177-90		128
1700	Analysis of plant germline development by high-throughput RNA profiling: technical advances and new insights. 2012 , 70, 18-29		36
1699	Comparative transcriptomics of three Poaceae species reveals patterns of gene expression evolution. 2012 , 71, 492-502		144
1698	Parental genome imbalance in <i>Brassica oleracea</i> causes asymmetric triploid block. 2012 , 71, 503-16		32
1697	Isoform diversity and its importance for axon regeneration. 2012 , 32, 420-31		3
1696	Challenges in estimating percent inclusion of alternatively spliced junctions from RNA-seq data. 2012 , 13 Suppl 6, S11		36
1695	MGMR: leveraging RNA-Seq population data to optimize expression estimation. 2012 , 13 Suppl 6, S2		3
1694	Integrating many co-splicing networks to reconstruct splicing regulatory modules. 2012 , 6 Suppl 1, S17		14
1693	Annotation of the domestic dog genome sequence: finding the missing genes. 2012 , 23, 124-31		10
1692	eQTL Mapping Using RNA-seq Data. 2013 , 5, 198-219		51

1691	High throughput investigative Dermatology in 2012 and beyond: A new era beckons. 2013 , 54, 1-8	2
1690	Hyperosmotic priming of Arabidopsis seedlings establishes a long-term somatic memory accompanied by specific changes of the epigenome. 2013 , 14, R59	200
1689	RNA sequencing reveals sexually dimorphic gene expression before gonadal differentiation in chicken and allows comprehensive annotation of the W-chromosome. 2013 , 14, R26	72
1688	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. 2013 , 14, R28	227
1687	Computational purification of individual tumor gene expression profiles leads to significant improvements in prognostic prediction. 2013 , 5, 29	70
1686	Characteristics of cross-hybridization and cross-alignment of expression in pseudo-xenograft samples by RNA-Seq and microarrays. 2013 , 3, 8	3
1685	The Mll2 branch of the COMPASS family regulates bivalent promoters in mouse embryonic stem cells. 2013 , 20, 1093-7	131
1684	Gene expression analysis following olfactory learning in <i>Apis mellifera</i> . 2013 , 40, 1631-9	12
1683	Diversity in the complexity of phosphate starvation transcriptomes among rice cultivars based on RNA-Seq profiles. 2013 , 83, 523-37	42
1682	Independent specialization of the human and mouse X chromosomes for the male germ line. 2013 , 45, 1083-7	111
1681	Human housekeeping genes, revisited. 2013 , 29, 569-74	716
1680	High-throughput RNA sequencing of a formalin-fixed, paraffin-embedded autopsy lung tissue sample from the 1918 influenza pandemic. 2013 , 229, 535-45	48
1679	Deep Sequencing Data Analysis. 2013 ,	4
1678	Decoding the <i>Ascaris suum</i> Genome using Massively Parallel Sequencing and Advanced Bioinformatic Methods [Unprecedented Prospects for Fundamental and Applied Research]. 2013 , 287-314	
1677	Prioritization of retinal disease genes: an integrative approach. 2013 , 34, 853-9	6
1676	Orchestrated intron retention regulates normal granulocyte differentiation. 2013 , 154, 583-95	290
1675	Genome-wide annotation of genes and noncoding RNAs of foxtail millet in response to simulated drought stress by deep sequencing. 2013 , 83, 459-73	132
1674	Pairwise comparisons of ten porcine tissues identify differential transcriptional regulation at the gene, isoform, promoter and transcription start site level. 2013 , 438, 346-52	11

1673	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , 2013 , 31, 759-65	44.5	289
1672	Whole transcriptome sequencing of the aging rat brain reveals dynamic RNA changes in the dark matter of the genome. 2013 , 35, 763-76		82
1671	Transcriptomic profiling of <i>Aspergillus flavus</i> in response to 5-azacytidine. 2013 , 56, 78-86		58
1670	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. 2013 , 8, 1494-512		4563
1669	Maternal imprinting at the H19-Igf2 locus maintains adult haematopoietic stem cell quiescence. 2013 , 500, 345-9		201
1668	The evolution and pathogenic mechanisms of the rice sheath blight pathogen. 2013 , 4, 1424		177
1667	PM-Seq: Using Finite Poisson Mixture Models for RNA-Seq Data Analysis and Transcript Expression Level Quantification. 2013 , 5, 71-87		2
1666	Statistical and Computational Methods for High-Throughput Sequencing Data Analysis of Alternative Splicing. 2013 , 5, 138-155		10
1665	Parallel comparison of Illumina RNA-Seq and Affymetrix microarray platforms on transcriptomic profiles generated from 5-aza-deoxy-cytidine treated HT-29 colon cancer cells and simulated datasets. 2013 , 14 Suppl 9, S1		69
1664	CLASS: constrained transcript assembly of RNA-seq reads. 2013 , 14 Suppl 5, S14		20
1663	A mixture model for expression deconvolution from RNA-seq in heterogeneous tissues. 2013 , 14 Suppl 5, S11		25
1662	A novel min-cost flow method for estimating transcript expression with RNA-Seq. 2013 , 14 Suppl 5, S15		48
1661	Gene set enrichment analysis of RNA-Seq data: integrating differential expression and splicing. 2013 , 14 Suppl 5, S16		40
1660	NURD: an implementation of a new method to estimate isoform expression from non-uniform RNA-seq data. 2013 , 14, 220		12
1659	Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. 2013 , 14, 128		2715
1658	Differential expression analysis for paired RNA-Seq data. 2013 , 14, 110		18
1657	A comparison of methods for differential expression analysis of RNA-seq data. 2013 , 14, 91		552
1656	Estimation of data-specific constitutive exons with RNA-Seq data. 2013 , 14, 31		4

1655	Alternative splicing tends to avoid partial removals of protein-protein interaction sites. 2013 , 14, 379	3
1654	The developing xylem transcriptome and genome-wide analysis of alternative splicing in <i>Populus trichocarpa</i> (black cottonwood) populations. 2013 , 14, 359	51
1653	RNA-seq analysis of single bovine blastocysts. 2013 , 14, 350	53
1652	Behavioral and neurogenomic transcriptome changes in wild-derived zebrafish with fluoxetine treatment. 2013 , 14, 348	85
1651	Insights into organ-specific pathogen defense responses in plants: RNA-seq analysis of potato tuber- <i>Phytophthora infestans</i> interactions. 2013 , 14, 340	83
1650	Differential transcript isoform usage pre- and post-zygotic genome activation in zebrafish. 2013 , 14, 331	27
1649	Discovering chromatin motifs using FAIRE sequencing and the human diploid genome. 2013 , 14, 310	4
1648	Functional transcriptomic analysis of the role of MAB-5/Hox in Q neuroblast migration in <i>Caenorhabditis elegans</i> . 2013 , 14, 304	8
1647	The transcriptome of <i>Leishmania major</i> in the axenic promastigote stage: transcript annotation and relative expression levels by RNA-seq. 2013 , 14, 223	64
1646	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. 2013 , 14, 204	53
1645	The transcript catalogue of the short-lived fish <i>Nothobranchius furzeri</i> provides insights into age-dependent changes of mRNA levels. 2013 , 14, 185	45
1644	Determination of dosage compensation of the mammalian X chromosome by RNA-seq is dependent on analytical approach. 2013 , 14, 150	25
1643	Systematic analysis of palatal transcriptome to identify cleft palate genes within TGFB-knockout mice alleles: RNA-Seq analysis of TGFB Mice. 2013 , 14, 113	26
1642	Genome reannotation of the lizard <i>Anolis carolinensis</i> based on 14 adult and embryonic deep transcriptomes. 2013 , 14, 49	45
1641	<i>Saccharopolyspora erythraea</i> 's genome is organised in high-order transcriptional regions mediated by targeted degradation at the metabolic switch. 2013 , 14, 15	23
1640	Improved moderation for gene-wise variance estimation in RNA-Seq via the exploitation of external information. 2013 , 14 Suppl 1, S9	1
1639	Potential roles of microRNAs in regulating long intergenic noncoding RNAs. 2013 , 6 Suppl 1, S7	63
1638	Personal genomes, quantitative dynamic omics and personalized medicine. 2013 , 1, 71-90	26

1637	Comprehensively identifying and characterizing the missing gene sequences in human reference genome with integrated analytic approaches. 2013 , 132, 899-911	10
1636	Genomic inversion caused by gamma irradiation contributes to downregulation of a WBC11 homolog in bloomless sorghum. 2013 , 126, 1513-20	10
1635	Long noncoding RNA: a new player of heart failure?. 2013 , 6, 876-83	90
1634	Directional RNA-seq reveals highly complex condition-dependent transcriptomes in E. coli K12 through accurate full-length transcripts assembling. 2013 , 14, 520	29
1633	Strategies and future trends to identify the mode of action of phytotoxic compounds. 2013 , 212, 60-71	11
1632	Single-cell RNA-Seq profiling of human preimplantation embryos and embryonic stem cells. 2013 , 20, 1131-9	983
1631	Next Generation Sequencing in Cancer Research. 2013 ,	4
1630	Comprehensive analyses of microRNA gene evolution in paleopolyploid soybean genome. 2013 , 76, 332-44	16
1629	The sacred lotus genome provides insights into the evolution of flowering plants. 2013 , 76, 557-67	55
1628	High-resolution transcriptional analysis of the regulatory influence of cell-to-cell signalling reveals novel genes that contribute to Xanthomonas phytopathogenesis. 2013 , 88, 1058-69	43
1627	A glimpse into past, present, and future DNA sequencing. 2013 , 110, 3-24	106
1626	Genome-wide identification of cancer-related polyadenylated and non-polyadenylated RNAs in human breast and lung cell lines. 2013 , 56, 503-12	1
1625	Comparative study of de novo assembly and genome-guided assembly strategies for transcriptome reconstruction based on RNA-Seq. 2013 , 56, 143-55	40
1624	RNA-Seq for transcriptome analysis in non-model plants. 2013 , 1069, 43-58	46
1623	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. 2013 , 45, 1226-1231	205
1622	Count-based differential expression analysis of RNA sequencing data using R and Bioconductor. 2013 , 8, 1765-86	788
1621	Common fragile site profiling in epithelial and erythroid cells reveals that most recurrent cancer deletions lie in fragile sites hosting large genes. 2013 , 4, 420-8	134
1620	Assessing differential expression measurements by highly parallel pyrosequencing and DNA microarrays: a comparative study. 2013 , 17, 53-9	2

1619	RNA-Seq analysis of the parietal cortex in Alzheimer's disease reveals alternatively spliced isoforms related to lipid metabolism. 2013 , 536, 90-5	55
1618	Chromatin position effects assayed by thousands of reporters integrated in parallel. 2013 , 154, 914-27	219
1617	Genome-wide survey by ChIP-seq reveals YY1 regulation of lincRNAs in skeletal myogenesis. 2013 , 32, 2575-88	115
1616	Mutations in KARS, encoding lysyl-tRNA synthetase, cause autosomal-recessive nonsyndromic hearing impairment DFNB89. 2013 , 93, 132-40	80
1615	Selective suppression of endothelial cytokine production by progesterone receptor. 2013 , 59, 36-43	19
1614	SSP: an interval integer linear programming for de novo transcriptome assembly and isoform discovery of RNA-seq reads. 2013 , 102, 507-14	9
1613	CAST-ChIP maps cell-type-specific chromatin states in the Drosophila central nervous system. 2013 , 5, 271-82	26
1612	Genome-wide association of Yorkie with chromatin and chromatin-remodeling complexes. 2013 , 3, 309-18	100
1611	Methylmercury exposure increases lipocalin related (lpr) and decreases activated in blocked unfolded protein response (abu) genes and specific miRNAs in Caenorhabditis elegans. 2013 , 222, 189-96	18
1610	Enabling systems biology approaches through microfabricated systems. 2013 , 85, 8882-94	11
1609	Predicting enhancer transcription and activity from chromatin modifications. 2013 , 41, 10032-43	95
1608	Genetic control of primary microRNA insight into cis- and trans-regulatory variations by RNA-seq. 2013 , 517, 224-9	1
1607	Genome-wide analysis of histone modifications: H3K4me2, H3K4me3, H3K9ac, and H3K27ac in <i>Oryza sativa</i> L. Japonica. 2013 , 6, 1463-72	81
1606	Next-Generation Sequencing (NGS): A Revolutionary Technology in Pharmacogenomics and Personalized Medicine. 2013 , 39-61	2
1605	BRANCH: boosting RNA-Seq assemblies with partial or related genomic sequences. 2013 , 29, 1250-9	24
1604	Benchmarking RNA-Seq quantification tools. 2013 , 2013, 647-50	23
1603	Image-based transcriptomics in thousands of single human cells at single-molecule resolution. 2013 , 10, 1127-33	194
1602	Expression and regulation of intergenic long noncoding RNAs during T cell development and differentiation. 2013 , 14, 1190-8	315

1601	DNMT1-interacting RNAs block gene-specific DNA methylation. 2013 , 503, 371-6	379
1600	Classification of topological domains based on gene expression and regulation. 2013 , 56, 415-23	2
1599	SON connects the splicing-regulatory network with pluripotency in human embryonic stem cells. 2013 , 15, 1141-1152	62
1598	An epigenetic trap stabilizes singular olfactory receptor expression. 2013 , 154, 325-36	114
1597	Assessment of transcript reconstruction methods for RNA-seq. 2013 , 10, 1177-84	477
1596	Systematic evaluation of spliced alignment programs for RNA-seq data. 2013 , 10, 1185-91	371
1595	Systems biological approaches to measure and understand vaccine immunity in humans. 2013 , 25, 209-18	46
1594	Co-opting the unfolded protein response to elicit olfactory receptor feedback. 2013 , 155, 321-32	102
1593	The high polyphenol content of grapevine cultivar tannat berries is conferred primarily by genes that are not shared with the reference genome. 2013 , 25, 4777-88	88
1592	Whole-transcriptome analysis of hepatocellular carcinoma. 2013 , 30, 736	4
1591	Genomic insights into salt adaptation in a desert poplar. 2013 , 4, 2797	183
1590	Analysis of the canine brain transcriptome with an emphasis on the hypothalamus and cerebral cortex. 2013 , 24, 484-99	16
1589	An introduction to high-throughput sequencing experiments: design and bioinformatics analysis. 2013 , 1038, 1-26	8
1588	Study of <i>Candida albicans</i> and its interactions with the host: A mini review. 2013 , 3, 51-64	26
1587	SplicingCompass: differential splicing detection using RNA-seq data. 2013 , 29, 1141-8	48
1586	RNA sequencing of cancer reveals novel splicing alterations. 2013 , 3, 1689	134
1585	Dynamic expression of 3' UTRs revealed by Poisson hidden Markov modeling of RNA-Seq: implications in gene expression profiling. 2013 , 527, 616-23	18
1584	The genome of the ctenophore <i>Mnemiopsis leidyi</i> and its implications for cell type evolution. 2013 , 342, 1242592	466

1583	Genome-wide binding analysis of the transcription activator ideal plant architecture1 reveals a complex network regulating rice plant architecture. 2013 , 25, 3743-59	417
1582	Rapid and pervasive changes in genome-wide enhancer usage during mammalian development. 2013 , 155, 1521-31	256
1581	The presence, role and clinical use of spermatozoal RNAs. 2013 , 19, 604-24	238
1580	Interactome maps of mouse gene regulatory domains reveal basic principles of transcriptional regulation. 2013 , 155, 1507-20	255
1579	Functional implications of splicing polymorphisms in the human genome. 2013 , 22, 3449-59	13
1578	A heterozygous moth genome provides insights into herbivory and detoxification. 2013 , 45, 220-5	366
1577	Jasmonate Signaling. 2013 ,	3
1576	Enhanced expression of codon optimized interferon gamma in CHO cells. 2013 , 167, 326-33	27
1575	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. 2013 , 14, 671-83	775
1574	Transcriptome analysis of mouse brain infected with <i>Toxoplasma gondii</i> . 2013 , 81, 3609-19	63
1573	RNA-Seq analysis of <i>Citrus reticulata</i> in the early stages of <i>Xylella fastidiosa</i> infection reveals auxin-related genes as a defense response. 2013 , 14, 676	49
1572	RNA-seq analyses of gene expression in the microsclerotia of <i>Verticillium dahliae</i> . 2013 , 14, 607	55
1571	Characterization and modelling of interspecies electron transfer mechanisms and microbial community dynamics of a syntrophic association. 2013 , 4, 2809	82
1570	Accurate identification of polyadenylation sites from 3' end deep sequencing using a naive Bayes classifier. 2013 , 29, 2564-71	17
1569	Integrated detection of natural antisense transcripts using strand-specific RNA sequencing data. 2013 , 23, 1730-9	45
1568	Deep transcriptome profiling of ovarian cancer cells using next-generation sequencing approach. 2013 , 1049, 139-69	3
1567	Global analyses of UPF1 binding and function reveal expanded scope of nonsense-mediated mRNA decay. 2013 , 23, 1636-50	167
1566	Coupling deep transcriptome analysis with untargeted metabolic profiling in <i>Ophiorrhiza pumila</i> to further the understanding of the biosynthesis of the anti-cancer alkaloid camptothecin and anthraquinones. 2013 , 54, 686-96	67

1565	Investigating the physiological response of <i>Pichia (Komagataella) pastoris</i> GS115 to the heterologous expression of misfolded proteins using chemostat cultures. 2013 , 97, 9747-9762	39
1564	Whole transcriptome sequencing reveals genes involved in plastid/chloroplast division and development are regulated by the HP1/DDB1 at an early stage of tomato fruit development. 2013 , 238, 923-36	13
1563	Comprehensive analysis of RNA-seq data reveals the complexity of the transcriptome in <i>Brassica rapa</i> . 2013 , 14, 689	125
1562	<i>Histoplasma</i> yeast and mycelial transcriptomes reveal pathogenic-phase and lineage-specific gene expression profiles. 2013 , 14, 695	43
1561	Systematically profiling and annotating long intergenic non-coding RNAs in human embryonic stem cell. 2013 , 14 Suppl 5, S3	8
1560	Expression of non-protein-coding antisense RNAs in genomic regions related to autism spectrum disorders. 2013 , 4, 32	39
1559	Towards the integration, annotation and association of historical microarray experiments with RNA-seq. 2013 , 14 Suppl 14, S4	12
1558	Transcriptome analysis of human tissues and cell lines reveals one dominant transcript per gene. 2013 , 14, R70	175
1557	The genome and transcriptome of the enteric parasite <i>Entamoeba invadens</i> , a model for encystation. 2013 , 14, R77	68
1556	RNA-Seq effectively monitors gene expression in <i>Eutrema salsugineum</i> plants growing in an extreme natural habitat and in controlled growth cabinet conditions. 2013 , 14, 578	35
1555	Comparative studies of differential gene calling using RNA-Seq data. 2013 , 14 Suppl 13, S7	15
1554	HIV latency and integration site placement in five cell-based models. 2013 , 10, 90	85
1553	Transcriptomics: advances and approaches. 2013 , 56, 960-7	44
1552	Transcriptomic characterization of cold acclimation in larval zebrafish. 2013 , 14, 612	102
1551	NPEBseq: nonparametric empirical bayesian-based procedure for differential expression analysis of RNA-seq data. 2013 , 14, 262	25
1550	Gene-based single nucleotide polymorphism discovery in bovine muscle using next-generation transcriptomic sequencing. 2013 , 14, 307	27
1549	Transcriptome deep-sequencing and clustering of expressed isoforms from <i>Favia</i> corals. 2013 , 14, 546	20
1548	CRAC: an integrated approach to the analysis of RNA-seq reads. 2013 , 14, R30	54

1547	Assessing De Novo transcriptome assembly metrics for consistency and utility. 2013 , 14, 465	90
1546	Obligate mutualism within a host drives the extreme specialization of a fig wasp genome. 2013 , 14, R141	59
1545	Assessment of hematopoietic failure due to Rpl11 deficiency in a zebrafish model of Diamond-Blackfan anemia by deep sequencing. 2013 , 14, 896	18
1544	Divergent transcription is associated with promoters of transcriptional regulators. 2013 , 14, 914	83
1543	Fragment assignment in the cloud with eXpress-D. 2013 , 14, 358	18
1542	Chromatin signatures at transcriptional start sites separate two equally populated yet distinct classes of intergenic long noncoding RNAs. 2013 , 14, R131	135
1541	Analysis of porcine adipose tissue transcriptome reveals differences in de novo fatty acid synthesis in pigs with divergent muscle fatty acid composition. 2013 , 14, 843	58
1540	Analysis of banana transcriptome and global gene expression profiles in banana roots in response to infection by race 1 and tropical race 4 of <i>Fusarium oxysporum</i> f. sp. <i>cubense</i> . 2013 , 14, 851	84
1539	Transcriptome analysis of the filamentous fungus <i>Aspergillus nidulans</i> directed to the global identification of promoters. 2013 , 14, 847	43
1538	Sequencing the transcriptome of milk production: milk trumps mammary tissue. 2013 , 14, 872	35
1537	Sample size calculation based on exact test for assessing differential expression analysis in RNA-seq data. 2013 , 14, 357	26
1536	Gene and isoform expression signatures associated with tumor stage in kidney renal clear cell carcinoma. 2013 , 7 Suppl 5, S7	13
1535	Clustering of transcriptional profiles identifies changes to insulin signaling as an early event in a mouse model of Alzheimer's disease. 2013 , 14, 831	24
1534	Comparative transcriptome analysis of tomato (<i>Solanum lycopersicum</i>) in response to exogenous abscisic acid. 2013 , 14, 841	67
1533	Evaluation of read count based RNAseq analysis methods. 2013 , 14 Suppl 8, S2	47
1532	DNA from dead cancer cells induces TLR9-mediated invasion and inflammation in living cancer cells. 2013 , 142, 477-87	28
1531	Finding the active genes in deep RNA-seq gene expression studies. 2013 , 14, 778	125
1530	Expression analysis and in silico characterization of intronic long noncoding RNAs in renal cell carcinoma: emerging functional associations. 2013 , 12, 140	48

1529	Identification of novel transcripts and noncoding RNAs in bovine skin by deep next generation sequencing. 2013 , 14, 789	96
1528	Design of RNA splicing analysis null models for post hoc filtering of Drosophila head RNA-Seq data with the splicing analysis kit (Spanki). 2013 , 14, 320	35
1527	Assessing the impact of human genome annotation choice on RNA-seq expression estimates. 2013 , 14 Suppl 11, S8	30
1526	eRNAs promote transcription by establishing chromatin accessibility at defined genomic loci. 2013 , 51, 606-17	342
1525	A patient tumor transplant model of squamous cell cancer identifies PI3K inhibitors as candidate therapeutics in defined molecular bins. 2013 , 7, 776-90	116
1524	SILAC-based proteome analysis of <i>Starmerella bombicola</i> sophorolipid production. 2013 , 12, 4376-92	20
1523	Circular intronic long noncoding RNAs. 2013 , 51, 792-806	1352
1522	Functionalization-dependent induction of cellular survival pathways by CdSe quantum dots in primary normal human bronchial epithelial cells. 2013 , 7, 8397-411	43
1521	RNAi screens in mice identify physiological regulators of oncogenic growth. 2013 , 501, 185-90	117
1520	A Gro/TLE-NuRD corepressor complex facilitates Tbx20-dependent transcriptional repression. 2013 , 12, 5395-409	24
1519	Sequencing of mRNA identifies re-expression of fetal splice variants in cardiac hypertrophy. 2013 , 62, 99-107	28
1518	DNA methylation and differentiation: silencing, upregulation and modulation of gene expression. 2013 , 5, 553-68	116
1517	Hira-dependent histone H3.3 deposition facilitates PRC2 recruitment at developmental loci in ES cells. 2013 , 155, 107-20	185
1516	Smart-seq2 for sensitive full-length transcriptome profiling in single cells. 2013 , 10, 1096-8	1335
1515	Reliable identification of genomic variants from RNA-seq data. 2013 , 93, 641-51	247
1514	Genetically engineered transvestites reveal novel mating genes in budding yeast. 2013 , 195, 1277-90	8
1513	Machine learning and genome annotation: a match meant to be?. 2013 , 14, 205	56
1512	microRNA-9 targets the long non-coding RNA MALAT1 for degradation in the nucleus. 2013 , 3, 2535	185

1511	RNA-sequencing quantification of hepatic ontogeny of phase-I enzymes in mice. 2013 , 41, 2175-86	25
1510	Maize LAZY1 mediates shoot gravitropism and inflorescence development through regulating auxin transport, auxin signaling, and light response. 2013 , 163, 1306-22	88
1509	RNA-seq data analysis at the gene and CDS levels provides a comprehensive view of transcriptome responses induced by 4-hydroxynonenal. 2013 , 9, 3036-46	10
1508	Complexity of the alternative splicing landscape in plants. 2013 , 25, 3657-83	453
1507	IDBA-tran: a more robust de novo de Bruijn graph assembler for transcriptomes with uneven expression levels. 2013 , 29, i326-34	139
1506	Nfatc1 orchestrates aging in hair follicle stem cells. 2013 , 110, E4950-9	104
1505	A Bayesian adaptive dose selection procedure with an overdispersed count endpoint. 2013 , 32, 5008-27	4
1504	Genome-wide analysis of the rat colon reveals proximal-distal differences in histone modifications and proto-oncogene expression. 2013 , 45, 1229-43	19
1503	An Approach for Assessing RNA-seq Quantification Algorithms in Replication Studies. 2013 , 2013, 15-18	2
1502	SpliceGrapherXT. 2013 ,	0
1501	Differential analysis of gene regulation at transcript resolution with RNA-seq. <i>Nature Biotechnology</i> , 2013 , 31, 46-53	44.5 2465
1500	Bias Correction in RNA-Seq Short-Read Counts Using Penalized Regression. 2013 , 5, 88-99	1
1499	Use of Metabolomics and Transcriptomics to Gain Insights into the Regulation and Biosynthesis of Medicinal Compounds: Hypericum as a Model. 2013 , 395-411	3
1498	Analysis of alternative cleavage and polyadenylation by 3' region extraction and deep sequencing. 2013 , 10, 133-9	286
1497	Transcriptomics in the RNA-seq era. 2013 , 17, 4-11	211
1496	Latent enhancers activated by stimulation in differentiated cells. 2013 , 152, 157-71	552
1495	Regional activation of the cancer genome by long-range epigenetic remodeling. 2013 , 23, 9-22	150
1494	The blue light receptor complex WC-1/2 of <i>Schizophyllum commune</i> is involved in mushroom formation and protection against phototoxicity. 2013 , 15, 943-55	44

1493	Challenges and strategies in transcriptome assembly and differential gene expression quantification. A comprehensive in silico assessment of RNA-seq experiments. 2013 , 22, 620-34	178
1492	Streaming fragment assignment for real-time analysis of sequencing experiments. 2013 , 10, 71-3	649
1491	Peptidomic discovery of short open reading frame-encoded peptides in human cells. 2013 , 9, 59-64	407
1490	Next-generation sequencing in the clinic: promises and challenges. 2013 , 340, 284-95	206
1489	ALKBH5 is a mammalian RNA demethylase that impacts RNA metabolism and mouse fertility. 2013 , 49, 18-29	1627
1488	RNA sequencing reveals a diverse and dynamic repertoire of the <i>Xenopus tropicalis</i> transcriptome over development. 2013 , 23, 201-16	107
1487	iReckon: simultaneous isoform discovery and abundance estimation from RNA-seq data. 2013 , 23, 519-29	92
1486	Achieving high throughput sequencing of a cDNA library utilizing an alternative protocol for the bench top next-generation sequencing system. 2013 , 92, 122-6	2
1485	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. 2013 , 23, 169-80	133
1484	Transcriptome-wide identification of A > I RNA editing sites by inosine specific cleavage. 2013 , 19, 257-70	47
1483	Small open reading frames associated with morphogenesis are hidden in plant genomes. 2013 , 110, 2395-400	116
1482	Genome-wide analysis of human SNPs at long intergenic noncoding RNAs. 2013 , 34, 338-44	41
1481	Systems biology approaches to finding novel pain mediators. 2013 , 5, 11-35	20
1480	Long noncoding RNAs regulate adipogenesis. 2013 , 110, 3387-92	315
1479	Whole-genome methylation sequencing reveals distinct impact of differential methylations on gene transcription in prostate cancer. 2013 , 183, 1960-1970	33
1478	Genome-wide, whole mount in situ analysis of transcriptional regulators in zebrafish embryos. 2013 , 380, 351-62	43
1477	Analysis of in vitro insulin-resistance models and their physiological relevance to in vivo diet-induced adipose insulin resistance. 2013 , 5, 259-70	66
1476	Cell-cycle control of developmentally regulated transcription factors accounts for heterogeneity in human pluripotent cells. 2013 , 1, 532-44	98

1475	Establishment and interpretation of the genome sequence of the phytopathogenic fungus <i>Rhizoctonia solani</i> AG1-IB isolate 7/3/14. 2013 , 167, 142-55	68
1474	Cell-specific expression profiling of rare cell types as exemplified by its impact on our understanding of female gametophyte development. 2013 , 16, 41-9	10
1473	Expression profile analyses of human HCT-116 colon cancer cell line before and after serum induction. 2013 , 517, 236-9	
1472	Social insect genomes exhibit dramatic evolution in gene composition and regulation while preserving regulatory features linked to sociality. 2013 , 23, 1235-47	166
1471	Global analysis of the haematopoietic and endothelial transcriptome during zebrafish development. 2013 , 130, 122-31	19
1470	A tiered hidden Markov model characterizes multi-scale chromatin states. 2013 , 102, 1-7	7
1469	Incorporate gene signature profiling into routine molecular testing. 2013 , 2, 28-33	3
1468	Zinc-mediated RNA fragmentation allows robust transcript reassembly upon whole transcriptome RNA-Seq. 2013 , 63, 25-31	18
1467	Transcriptome characterization by RNA-Seq reveals the involvement of the complement components in noise-traumatized rat cochleae. 2013 , 248, 1-16	27
1466	A bird's-eye view on the modern genetics workflow and its potential applicability to the locust problem. 2013 , 336, 375-83	5
1465	Multiple regulatory variants modulate expression of 5-hydroxytryptamine 2A receptors in human cortex. 2013 , 73, 546-54	50
1464	Cancer genome sequencing: understanding malignancy as a disease of the genome, its conformation, and its evolution. 2013 , 340, 152-60	16
1463	Alternative splicing switching in stem cell lineages. 2013 , 8, 50-59	17
1462	In the spotlight: Bioinformatics. 2013 , 6, 3-8	1
1461	Recoding RNA editing of AZIN1 predisposes to hepatocellular carcinoma. 2013 , 19, 209-16	313
1460	Direct competition between hnRNP C and U2AF65 protects the transcriptome from the exonization of Alu elements. 2013 , 152, 453-66	285
1459	Divergent transcription of long noncoding RNA/mRNA gene pairs in embryonic stem cells. 2013 , 110, 2876-81	345
1458	Two new and distinct roles for <i>Drosophila</i> Argonaute-2 in the nucleus: alternative pre-mRNA splicing and transcriptional repression. 2013 , 27, 378-89	81

1457	A role for the RNA-binding protein MOS2 in microRNA maturation in Arabidopsis. 2013 , 23, 645-57	75
1456	Comparative study of RNA-seq- and microarray-derived coexpression networks in Arabidopsis thaliana. 2013 , 29, 717-24	76
1455	Genes, behavior and next-generation RNA sequencing. 2013 , 12, 1-12	65
1454	Sigma factor-mediated plastid retrograde signals control nuclear gene expression. 2013 , 73, 1-13	117
1453	De novo transcriptome characterization of Vitis vinifera cv. Corvina unveils varietal diversity. 2013 , 14, 41	82
1452	ASAP: an environment for automated preprocessing of sequencing data. 2013 , 6, 5	3
1451	The RNA Pol II elongation factor Ell3 marks enhancers in ES cells and primes future gene activation. 2013 , 152, 144-56	73
1450	The Coding and the Non-coding Transcriptome. 2013 , 27-41	2
1449	Application of next generation qPCR and sequencing platforms to mRNA biomarker analysis. 2013 , 59, 89-100	48
1448	RNA-Seq: revelation of the messengers. 2013 , 18, 175-9	108
1447	NFIB is a governor of epithelial-melanocyte stem cell behaviour in a shared niche. 2013 , 495, 98-102	116
1446	Hepatocyte nuclear factor 4 alpha deletion promotes diethylnitrosamine-induced hepatocellular carcinoma in rodents. 2013 , 57, 2480-90	81
1445	Identifying differentially spliced genes from two groups of RNA-seq samples. 2013 , 518, 164-70	39
1444	Effects of cocaine and withdrawal on the mouse nucleus accumbens transcriptome. 2013 , 12, 21-33	38
1443	LBR and lamin A/C sequentially tether peripheral heterochromatin and inversely regulate differentiation. 2013 , 152, 584-98	541
1442	Proteomic workflow for analysis of archival formalin-fixed and paraffin-embedded clinical samples to a depth of 10 000 proteins. 2013 , 7, 225-33	117
1441	Bioinformatics challenges in de novo transcriptome assembly using short read sequences in the absence of a reference genome sequence. 2013 , 30, 490-500	54
1440	Braveheart, a long noncoding RNA required for cardiovascular lineage commitment. 2013 , 152, 570-83	701

1439	Transcriptome analysis of Inbred Long Sleep and Inbred Short Sleep mice. 2013 , 12, 263-74	12
1438	Circular RNAs are a large class of animal RNAs with regulatory potency. 2013 , 495, 333-8	4603
1437	Genomic diversity and evolution of the head crest in the rock pigeon. 2013 , 339, 1063-7	169
1436	The lipid mediator protectin D1 inhibits influenza virus replication and improves severe influenza. 2013 , 153, 112-25	315
1435	Opportunities and methods for studying alternative splicing in cancer with RNA-Seq. 2013 , 340, 179-91	77
1434	A robust method for transcript quantification with RNA-seq data. 2013 , 20, 167-87	11
1433	An ancient transcription factor initiates the burst of piRNA production during early meiosis in mouse testes. 2013 , 50, 67-81	243
1432	Whole transcriptome analysis using next-generation sequencing of model species <i>Setaria viridis</i> to support C4 photosynthesis research. 2013 , 83, 77-87	49
1431	Peregrine: A rapid and unbiased method to produce strand-specific RNA-Seq libraries from small quantities of starting material. 2013 , 10, 502-15	31
1430	Integration of genome-wide approaches identifies lncRNAs of adult neural stem cells and their progeny in vivo. 2013 , 12, 616-28	193
1429	Reverse vaccinology in the 21st century: improvements over the original design. 2013 , 1285, 115-32	59
1428	Genome-wide profiling of 5-formylcytosine reveals its roles in epigenetic priming. 2013 , 153, 678-91	453
1427	Characterizing the interplay between multiple levels of organization within bacterial sigma factor regulatory networks. 2013 , 4, 1755	11
1426	A new method for stranded whole transcriptome RNA-seq. 2013 , 63, 126-34	39
1425	Loss of the six3/6 controlling pathways might have resulted in pinhole-eye evolution in <i>Nautilus</i> . 2013 , 3, 1432	20
1424	Predicting long non-coding RNAs using RNA sequencing. 2013 , 63, 50-9	82
1423	ADAR1 forms a complex with Dicer to promote microRNA processing and RNA-induced gene silencing. 2013 , 153, 575-89	226
1422	Systematic study of human long intergenic non-coding RNAs and their impact on cancer. 2013 , 56, 324-34	34

1421	Exploring the sampling universe of RNA-seq. 2013 , 12, 175-88	4
1420	DAF-16 employs the chromatin remodeller SWI/SNF to promote stress resistance and longevity. 2013 , 15, 491-501	145
1419	Correlates of relative resistance against low-dose rectal simian immunodeficiency virus challenges in peripheral blood mononuclear cells of vaccinated rhesus macaques. 2013 , 93, 437-48	6
1418	Guard cell purification and RNA isolation suitable for high-throughput transcriptional analysis of cell-type responses to biotic stresses. 2013 , 26, 844-9	28
1417	Human corneal epithelial subpopulations: oxygen dependent ex vivo expansion and transcriptional profiling. 2013 , 91 Thesis 4, 1-34	5
1416	Targeting long non-coding RNAs in cancers: progress and prospects. 2013 , 45, 1895-910	383
1415	Dynamics of 5-hydroxymethylcytosine during mouse spermatogenesis. 2013 , 4, 1995	139
1414	Global regulation of promoter melting in naive lymphocytes. 2013 , 153, 988-99	111
1413	RNA-Seq reveals differentially expressed isoforms and novel splice variants in buccal mucosal cancer. 2013 , 516, 24-32	10
1412	BACH2 represses effector programs to stabilize T(reg)-mediated immune homeostasis. 2013 , 498, 506-10	264
1411	New insight into transcription of human endogenous retroviral elements. 2013 , 30, 314-8	14
1410	Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer. 2013 , 20, 908-13	432
1409	Comparative RNA-seq analysis of early-infected peach leaves by the invasive phytopathogen <i>Xanthomonas arboricola</i> pv. <i>pruni</i> . 2013 , 8, e54196	42
1408	Senescence-associated lncRNAs: senescence-associated long noncoding RNAs. 2013 , 12, 890-900	147
1407	Horizontal gene transfer from diverse bacteria to an insect genome enables a tripartite nested mealybug symbiosis. 2013 , 153, 1567-78	285
1406	Uniform, optimal signal processing of mapped deep-sequencing data. <i>Nature Biotechnology</i> , 2013 , 31, 615-22	44.5 105
1405	Identification of novel exons and transcripts by comprehensive RNA-Seq of horn cancer transcriptome in <i>Bos indicus</i> . 2013 , 165, 37-44	11
1404	Genome-wide annotation and quantitation of translation by ribosome profiling. 2013 , Chapter 4, Unit 4.18	45

1403	lincRNAs: genomics, evolution, and mechanisms. 2013 , 154, 26-46	1841
1402	Production of high oleic rice grains by suppressing the expression of the OsFAD2-1 gene. 2013 , 40, 996-1004	33
1401	Characterizing the Genetic Basis for Nicotine Induced Cancer Development: A Transcriptome Sequencing Study. 2013 , 8, e67252	17
1400	Analysis of RNA-Seq data with TopHat and Cufflinks for genome-wide expression analysis of jasmonate-treated plants and plant cultures. 2013 , 1011, 305-15	54
1399	Transcriptomics in the Age of Ultra High-Throughput Sequencing. 2013 , 145-154	
1398	Using the iPlant collaborative discovery environment. 2013 , Chapter 1, Unit1.22	20
1397	Non-coding transcription at cis-regulatory elements: computational and experimental approaches. 2013 , 63, 66-75	4
1396	Genome-wide characterization and expression analysis of genetic variants in sweet orange. 2013 , 75, 954-64	20
1395	Contribution of antibody-based protein profiling to the human Chromosome-centric Proteome Project (C-HPP). 2013 , 12, 2439-48	44
1394	An integrative approach to understanding the combinatorial histone code at functional elements. 2013 , 29, 2231-7	6
1393	Targeting the endothelial progenitor cell surface proteome to identify novel mechanisms that mediate angiogenic efficacy in a rodent model of vascular disease. 2013 , 45, 999-1011	17
1392	Transcriptome analysis of the sulfate deficiency response in the marine microalga <i>Emiliana huxleyi</i> . 2013 , 199, 650-62	53
1391	Characterizing acetogenic metabolism using a genome-scale metabolic reconstruction of <i>Clostridium ljungdahlii</i> . 2013 , 12, 118	106
1390	The genome of the platyfish, <i>Xiphophorus maculatus</i> , provides insights into evolutionary adaptation and several complex traits. 2013 , 45, 567-72	201
1389	High occurrence of functional new chimeric genes in survey of rice chromosome 3 short arm genome sequences. 2013 , 5, 1038-48	8
1388	CathaCyc, a metabolic pathway database built from <i>Catharanthus roseus</i> RNA-Seq data. 2013 , 54, 673-85	95
1387	Preclinical vaccines against mammary carcinoma. 2013 , 12, 1449-63	9
1386	Common fusion transcripts identified in colorectal cancer cell lines by high-throughput RNA sequencing. 2013 , 6, 546-53	22

1385	Comprehensive evaluation of differential gene expression analysis methods for RNA-seq data. 2013 , 14, R95	461
1384	Whole-genome DNA/RNA sequencing identifies truncating mutations in RBCK1 in a novel Mendelian disease with neuromuscular and cardiac involvement. 2013 , 5, 67	66
1383	Identification of the zebrafish maternal and paternal transcriptomes. 2013 , 140, 2703-10	127
1382	Transcriptional analysis through RNA sequencing of giant cells induced by <i>Meloidogyne graminicola</i> in rice roots. 2013 , 64, 3885-98	98
1381	Exome RNA sequencing reveals rare and novel alternative transcripts. 2013 , 41, e6	38
1380	A transcript perspective on evolution. 2013 , 10, 1403-11	3
1379	Genome-guided transcriptome assembly in the age of next-generation sequencing. 2013 , 10, 1234-40	12
1378	The challenges of delivering bioinformatics training in the analysis of high-throughput data. 2013 , 14, 538-47	9
1377	Mass fingerprinting of complex mixtures: protein inference from high-resolution peptide masses and predicted retention times. 2013 , 12, 5730-41	12
1376	Simultaneous isoform discovery and quantification from RNA-seq. 2013 , 5, 100-118	16
1375	Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. 2013 , 14, 486	123
1374	Sample size calculation for differential expression analysis of RNA-seq data under Poisson distribution. 2013 , 6, 358-75	16
1373	Genome sequences of six wheat-infecting fusarium species isolates. 2013 , 1,	23
1372	c-Src modulates estrogen-induced stress and apoptosis in estrogen-deprived breast cancer cells. 2013 , 73, 4510-20	65
1371	Genome of <i>Drosophila suzukii</i> , the spotted wing drosophila. 2013 , 3, 2257-71	83
1370	Rat retinal transcriptome: effects of aging and AMD-like retinopathy. 2013 , 12, 1745-61	51
1369	<i>Cryptococcus neoformans</i> Rim101 is associated with cell wall remodeling and evasion of the host immune responses. 2013 , 4,	76
1368	<i>Clostridium scindens</i> : a human gut microbe with a high potential to convert glucocorticoids into androgens. 2013 , 54, 2437-49	128

1367	Female-specific induction of rat pituitary dentin matrix protein-1 by GnRH. 2013 , 27, 1840-55	14
1366	Epithelial splicing regulator protein 1 and alternative splicing in somatotroph adenomas. 2013 , 154, 3331-43	7
1365	Updating RNA-Seq analyses after re-annotation. 2013 , 29, 1631-7	18
1364	Inference of alternative splicing from RNA-Seq data with probabilistic splice graphs. 2013 , 29, 2300-10	18
1363	Tissue-specific splicing of a ubiquitously expressed transcription factor is essential for muscle differentiation. 2013 , 27, 1247-59	73
1362	Characterization of the rat developmental liver transcriptome. 2013 , 45, 301-11	15
1361	Functional DNA methylation differences between tissues, cell types, and across individuals discovered using the M&M algorithm. 2013 , 23, 1522-40	119
1360	Functional transcriptomics in the post-ENCODE era. 2013 , 23, 1961-73	49
1359	Systematic Assessment of RNA-Seq Quantification Tools Using Simulated Sequence Data. 2013 , 2013,	2
1358	Transforming Genomes Using MOD Files with Applications. 2013 ,	7
1357	An Island-Based Approach for Differential Expression Analysis. 2013 , 2013, 419-429	0
1356	Old world monkeys and new age science: the evolution of nonhuman primate systems virology. 2013 , 54, 166-80	14
1355	Depletion of stromal cells expressing fibroblast activation protein-1 from skeletal muscle and bone marrow results in cachexia and anemia. 2013 , 210, 1137-51	219
1354	Computational analysis of bacterial RNA-Seq data. 2013 , 41, e140	393
1353	Spatio-temporal transcript profiling of rice roots and shoots in response to phosphate starvation and recovery. 2013 , 25, 4285-304	201
1352	Host cell transcriptome profile during wild-type and attenuated dengue virus infection. 2013 , 7, e2107	50
1351	Function and evolution of DNA methylation in <i>Nasonia vitripennis</i> . 2013 , 9, e1003872	133
1350	A contribution to the study of plant development evolution based on gene co-expression networks. 2013 , 4, 291	18

1349	Improved Time Complexities for Learning Boolean Networks. 2013 , 15, 3762-3795	2
1348	Identification of genes critical for resistance to infection by West Nile virus using RNA-Seq analysis. 2013 , 5, 1664-81	18
1347	DDBJ read annotation pipeline: a cloud computing-based pipeline for high-throughput analysis of next-generation sequencing data. 2013 , 20, 383-90	63
1346	Transcription of the major neurospora crassa microRNA-like small RNAs relies on RNA polymerase III. 2013 , 9, e1003227	25
1345	An essential role for zygotic expression in the pre-cellular Drosophila embryo. 2013 , 9, e1003428	44
1344	The Fusarium graminearum histone H3 K27 methyltransferase KMT6 regulates development and expression of secondary metabolite gene clusters. 2013 , 9, e1003916	170
1343	Extensive chromosomal reshuffling drives evolution of virulence in an asexual pathogen. 2013 , 23, 1271-82	221
1342	Causes and consequences of chromatin variation between inbred mice. 2013 , 9, e1003570	16
1341	PolyCat: a resource for genome categorization of sequencing reads from allopolyploid organisms. 2013 , 3, 517-25	65
1340	Post-transcriptional regulation of myotube elongation and myogenesis by Hoi Polloi. 2013 , 140, 3645-56	25
1339	Female behaviour drives expression and evolution of gustatory receptors in butterflies. 2013 , 9, e1003620	108
1338	PNUTS/PP1 regulates RNAPII-mediated gene expression and is necessary for developmental growth. 2013 , 9, e1003885	29
1337	A KH-domain RNA-binding protein interacts with FIERY2/CTD phosphatase-like 1 and splicing factors and is important for pre-mRNA splicing in Arabidopsis. 2013 , 9, e1003875	62
1336	A chromatin link to caste identity in the carpenter ant Camponotus floridanus. 2013 , 23, 486-96	104
1335	Time series expression analyses using RNA-seq: a statistical approach. 2013 , 2013, 203681	18
1334	Analysis of the RelA:CBP/p300 interaction reveals its involvement in NF- κ B-driven transcription. 2013 , 11, e1001647	81
1333	The conserved SKN-1/Nrf2 stress response pathway regulates synaptic function in Caenorhabditis elegans. 2013 , 9, e1003354	47
1332	A conserved upstream motif orchestrates autonomous, germline-enriched expression of Caenorhabditis elegans piRNAs. 2013 , 9, e1003392	33

1331	Hsp70-Hsp40 chaperone complex functions in controlling polarized growth by repressing Hsf1-driven heat stress-associated transcription. 2013 , 9, e1003886	30
1330	The developmental transcriptome of the mosquito <i>Aedes aegypti</i> , an invasive species and major arbovirus vector. 2013 , 3, 1493-509	122
1329	Detecting and comparing non-coding RNAs in the high-throughput era. 2013 , 14, 15423-58	16
1328	The genome organization of <i>Thermotoga maritima</i> reflects its lifestyle. 2013 , 9, e1003485	31
1327	Extensive divergence of transcription factor binding in <i>Drosophila</i> embryos with highly conserved gene expression. 2013 , 9, e1003748	70
1326	Dystrophin-deficient pigs provide new insights into the hierarchy of physiological derangements of dystrophic muscle. 2013 , 22, 4368-82	94
1325	Grape RNA-Seq analysis pipeline environment. 2013 , 29, 614-21	23
1324	H3.3-H4 tetramer splitting events feature cell-type specific enhancers. 2013 , 9, e1003558	51
1323	Identification of novel target genes for safer and more specific control of root-knot nematodes from a pan-genome mining. 2013 , 9, e1003745	66
1322	Comprehensive analysis of transcriptome variation uncovers known and novel driver events in T-cell acute lymphoblastic leukemia. 2013 , 9, e1003997	94
1321	Systematically differentiating functions for alternatively spliced isoforms through integrating RNA-seq data. 2013 , 9, e1003314	58
1320	Quaking and PTB control overlapping splicing regulatory networks during muscle cell differentiation. 2013 , 19, 627-38	105
1319	TIGAR: transcript isoform abundance estimation method with gapped alignment of RNA-Seq data by variational Bayesian inference. 2013 , 29, 2292-9	29
1318	Identification of cilia genes that affect cell-cycle progression using whole-genome transcriptome analysis in <i>Chlamydomonas reinhardtii</i> . 2013 , 3, 979-91	42
1317	Accurate detection of differential RNA processing. 2013 , 41, 5189-98	30
1316	Phylogenomic distance method for analyzing transcriptome evolution based on RNA-seq data. 2013 , 5, 1746-53	12
1315	The yeast Snt2 protein coordinates the transcriptional response to hydrogen peroxide-mediated oxidative stress. 2013 , 33, 3735-48	26
1314	RNA-Seq analysis discloses early senescence and nucleolar dysfunction triggered by Tdp1 β depletion in <i>Medicago truncatula</i> . 2013 , 64, 1941-51	27

1313	Early de novo DNA methylation and prolonged demethylation in the muscle lineage. 2013 , 8, 317-32	63
1312	A TAF4 coactivator function for E proteins that involves enhanced TFIID binding. 2013 , 27, 1596-609	26
1311	Complex tissue-specific patterns and distribution of multiple RAGE splice variants in different mammals. 2013 , 5, 2420-35	29
1310	Characterization of the human ESC transcriptome by hybrid sequencing. 2013 , 110, E4821-30	222
1309	Bimodal quantitative relationships between histone modifications for X-linked and autosomal loci. 2013 , 110, 6949-54	8
1308	Transcriptome profiling of <i>Nasonia vitripennis</i> testis reveals novel transcripts expressed from the selfish B chromosome, paternal sex ratio. 2013 , 3, 1597-605	35
1307	The peptide-encoding CEP1 gene modulates lateral root and nodule numbers in <i>Medicago truncatula</i> . 2013 , 64, 5395-409	121
1306	Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features. 2013 , 41, 10044-61	56
1305	A known expressed sequence tag, BM742401, is a potent lincRNA inhibiting cancer metastasis. 2013 , 45, e31	45
1304	In vitro-differentiated neural cell cultures progress towards donor-identical brain tissue. 2013 , 22, 3534-46	16
1303	A discrete ubiquitin-mediated network regulates the strength of NOD2 signaling. 2013 , 33, 146-58	21
1302	Antisense transcripts enhanced by camptothecin at divergent CpG-island promoters associated with bursts of topoisomerase I-DNA cleavage complex and R-loop formation. 2013 , 41, 10110-23	46
1301	MITIE: Simultaneous RNA-Seq-based transcript identification and quantification in multiple samples. 2013 , 29, 2529-38	40
1300	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. 2013 , 41, e108	1489
1299	Differential splicing across immune system lineages. 2013 , 110, 14324-9	41
1298	Unraveling the molecular basis of temperature-dependent genetic regulation in <i>Penicillium marneffei</i> . 2013 , 12, 1214-24	17
1297	Overview of high throughput sequencing technologies to elucidate molecular pathways in cardiovascular diseases. 2013 , 112, 1613-23	77
1296	A dynamic H3K27ac signature identifies VEGFA-stimulated endothelial enhancers and requires EP300 activity. 2013 , 23, 917-27	64

1295	Histone methyltransferase SETD2 coordinates FACT recruitment with nucleosome dynamics during transcription. 2013 , 41, 2881-93	109
1294	The differential transcription network between embryo and endosperm in the early developing maize seed. 2013 , 162, 440-55	66
1293	TrueSight: a new algorithm for splice junction detection using RNA-seq. 2013 , 41, e51	28
1292	Higher order asymptotics for negative binomial regression inferences from RNA-sequencing data. 2013 , 12, 49-70	8
1291	Mutually exclusive signaling signatures define the hepatic and pancreatic progenitor cell lineage divergence. 2013 , 27, 1932-46	56
1290	CG methylated microarrays identify a novel methylated sequence bound by the CEBPB ATF4 heterodimer that is active in vivo. 2013 , 23, 988-97	77
1289	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. 2013 , 19, 479-89	16
1288	Program specificity for Ptf1a in pancreas versus neural tube development correlates with distinct collaborating cofactors and chromatin accessibility. 2013 , 33, 3166-79	23
1287	The maize methylome influences mRNA splice sites and reveals widespread paramutation-like switches guided by small RNA. 2013 , 23, 1651-62	199
1286	The intronic long noncoding RNA ANRASSF1 recruits PRC2 to the RASSF1A promoter, reducing the expression of RASSF1A and increasing cell proliferation. 2013 , 9, e1003705	138
1285	Peeling back the evolutionary layers of molecular mechanisms responsive to exercise-stress in the skeletal muscle of the racing horse. 2013 , 20, 287-98	18
1284	DEXUS: identifying differential expression in RNA-Seq studies with unknown conditions. 2013 , 41, e198	20
1283	CPAT: Coding-Potential Assessment Tool using an alignment-free logistic regression model. 2013 , 41, e74	969
1282	Selecting one of several mating types through gene segment joining and deletion in <i>Tetrahymena thermophila</i> . 2013 , 11, e1001518	64
1281	Cloud Computing with iPlant Atmosphere. 2013 , 43, 9.15.1-9.15.20	2
1280	IQdb: an intelligence quotient score-associated gene resource for human intelligence. 2013 , 2013, bat063	13
1279	Role of fat body lipogenesis in protection against the effects of caloric overload in <i>Drosophila</i> . 2013 , 288, 8028-8042	74
1278	Differential DNA methylation with age displays both common and dynamic features across human tissues that are influenced by CpG landscape. 2013 , 14, R102	239

1277	Developmental arrest of <i>Drosophila</i> survival motor neuron (Smn) mutants accounts for differences in expression of minor intron-containing genes. 2013 , 19, 1510-6	41
1276	RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments. 2013 , 41, e94	31
1275	Expression profiling of mouse subplate reveals a dynamic gene network and disease association with autism and schizophrenia. 2013 , 110, 3555-60	80
1274	Genomic architecture of adaptive color pattern divergence and convergence in <i>Heliconius</i> butterflies. 2013 , 23, 1248-57	57
1273	Pollen-specific, but not sperm-specific, genes show stronger purifying selection and higher rates of positive selection than sporophytic genes in <i>Capsella grandiflora</i> . 2013 , 30, 2475-86	62
1272	Next-generation sequencing of paired tyrosine kinase inhibitor-sensitive and -resistant EGFR mutant lung cancer cell lines identifies spectrum of DNA changes associated with drug resistance. 2013 , 23, 1434-45	41
1271	EDGE-pro: Estimated Degree of Gene Expression in Prokaryotic Genomes. 2013 , 9, 127-36	89
1270	Identification of a colonial chordate histocompatibility gene. 2013 , 341, 384-7	66
1269	GeneScissors: a comprehensive approach to detecting and correcting spurious transcriptome inference owing to RNA-seq reads misalignment. 2013 , 29, i291-9	9
1268	Global gene expression response of a population exposed to benzene: a pilot study exploring the use of RNA-sequencing technology. 2013 , 54, 566-73	9
1267	RAMPAGE: promoter activity profiling by paired-end sequencing of 5'-complete cDNAs. 2013 , 104, Unit 25B.11	44
1266	Therapeutic activities of engrafted neural stem/precursor cells are not dormant in the chronically injured spinal cord. 2013 , 31, 1535-47	43
1265	Trim24-repressed VL30 retrotransposons regulate gene expression by producing noncoding RNA. 2013 , 20, 339-46	52
1264	Orthology Guided Assembly in highly heterozygous crops: creating a reference transcriptome to uncover genetic diversity in <i>Lolium perenne</i> . 2013 , 11, 605-17	23
1263	Differential gene expression analysis using coexpression and RNA-Seq data. 2013 , 29, 2153-61	19
1262	Identification of novel point mutations in splicing sites integrating whole-exome and RNA-seq data in myeloproliferative diseases. 2013 , 1, 246-59	12
1261	Protective role of IL-6 in vascular remodeling in <i>Schistosoma</i> pulmonary hypertension. 2013 , 49, 951-9	38
1260	A meta-analysis of the genomic and transcriptomic composition of complex life. 2013 , 12, 2061-72	102

1259	Chronic ethanol exposure increases cytochrome P-450 and decreases activated in blocked unfolded protein response gene family transcripts in caenorhabditis elegans. 2013 , 27, 219-28	12
1258	Genome-wide profiling of chromosome interactions in Plasmodium falciparum characterizes nuclear architecture and reconfigurations associated with antigenic variation. 2013 , 90, 519-37	37
1257	Calculating sample size estimates for RNA sequencing data. 2013 , 20, 970-8	167
1256	Perturbations of Plasmodium Puf2 expression and RNA-seq of Puf2-deficient sporozoites reveal a critical role in maintaining RNA homeostasis and parasite transmissibility. 2013 , 15, 1266-83	56
1255	Allelic imbalance metre (Allim), a new tool for measuring allele-specific gene expression with RNA-seq data. 2013 , 13, 740-5	32
1254	Building localized bioinformatics platform based on Galaxy and high performance computing cluster. 2013 ,	1
1253	Thrombospondin 1 mediates high-fat diet-induced muscle fibrosis and insulin resistance in male mice. 2013 , 154, 4548-59	50
1252	Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. 2013 , 110, 19639-44	93
1251	High mobility group protein N5 (HMGN5) and lamina-associated polypeptide 2 (LAP2) interact and reciprocally affect their genome-wide chromatin organization. 2013 , 288, 18104-9	16
1250	Mechanisms and dynamics of orphan gene emergence in insect genomes. 2013 , 5, 439-55	97
1249	PrfA-like transcription factor gene lmo0753 contributes to L-rhamnose utilization in Listeria monocytogenes strains associated with human food-borne infections. 2013 , 79, 5584-92	8
1248	Stability, delivery and functions of human sperm RNAs at fertilization. 2013 , 41, 4104-17	210
1247	The shared genomic architecture of human nucleolar organizer regions. 2013 , 23, 2003-12	75
1246	Utilizing sequence intrinsic composition to classify protein-coding and long non-coding transcripts. 2013 , 41, e166	879
1245	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. 2013 , 41, e39	100
1244	EBSeq: an empirical Bayes hierarchical model for inference in RNA-seq experiments. 2013 , 29, 1035-43	805
1243	Glycyrrhiza uralensis transcriptome landscape and study of phytochemicals. 2013 , 54, 697-710	62
1242	High-Performance Computing In High-Throughput Sequencing. 2013 , 981-1002	1

1241	Comparison of normalization methods for differential gene expression analysis in RNA-Seq experiments: A matter of relative size of studied transcriptomes. 2013 , 6, e25849	52
1240	Amplitude modulation of androgen signaling by c-MYC. 2013 , 27, 734-48	62
1239	Long-term cultured mesenchymal stem cells frequently develop genomic mutations but do not undergo malignant transformation. 2013 , 4, e950	111
1238	Modulation of gene expression via overlapping binding sites exerted by ZNF143, Notch1 and THAP11. 2013 , 41, 4000-14	43
1237	Coevolution and life cycle specialization of plant cell wall degrading enzymes in a hemibiotrophic pathogen. 2013 , 30, 1337-47	68
1236	Extensive changes in DNA methylation are associated with expression of mutant huntingtin. 2013 , 110, 2354-9	121
1235	Genome-wide analysis of histone marks identifying an epigenetic signature of promoters and enhancers underlying cardiac hypertrophy. 2013 , 110, 20164-9	150
1234	The draft genome and transcriptome of <i>Panagrellus redivivus</i> are shaped by the harsh demands of a free-living lifestyle. 2013 , 193, 1279-95	41
1233	Noncoder: a web interface for exon array-based detection of long non-coding RNAs. 2013 , 41, e20	44
1232	The role of MyoD1 and histone modifications in the activation of muscle enhancers. 2013 , 8, 778-84	36
1231	Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. 2013 , 23, 1663-74	189
1230	Arabidopsis Root. 2013 , 2-1-2-17	
1229	Canonical Wnt signaling induces a primitive endoderm metastable state in mouse embryonic stem cells. 2013 , 31, 752-64	30
1228	Comprehensive whole-genome sequencing of an early-stage primary myelofibrosis patient defines low mutational burden and non-recurrent candidate genes. 2013 , 98, 1689-96	9
1227	CUX1 is a haploinsufficient tumor suppressor gene on chromosome 7 frequently inactivated in acute myeloid leukemia. 2013 , 121, 975-83	111
1226	Exome-wide association study of replicable nonsynonymous variants conferring risk for alcohol dependence. 2013 , 74, 622-5	5
1225	Transcriptome and proteome quantification of a tumor model provides novel insights into post-transcriptional gene regulation. 2013 , 14, r133	37
1224	The draft genome of a socially polymorphic halictid bee, <i>Lasioglossum albipes</i> . 2013 , 14, R142	58

1223	Genome-wide analysis of condensin binding in <i>Caenorhabditis elegans</i> . 2013 , 14, R112	58
1222	FusionQ: a novel approach for gene fusion detection and quantification from paired-end RNA-Seq. 2013 , 14, 193	25
1221	Probing functional polymorphisms in the dengue vector, <i>Aedes aegypti</i> . 2013 , 14, 739	9
1220	<i>Neurospora</i> and the dead-end hypothesis: genomic consequences of selfing in the model genus. 2013 , 67, 3600-16	24
1219	Expression of mRNA transcripts encoding membrane transporters detected with whole transcriptome sequencing of human brain and liver. 2013 , 23, 269-78	5
1218	RNA-seq analysis of transcriptomes in thrombin-treated and control human pulmonary microvascular endothelial cells. 2013 ,	8
1217	Improved use of a public good selects for the evolution of undifferentiated multicellularity. 2013 , 2, e00367	82
1216	Transposable elements become active and mobile in the genomes of aging mammalian somatic tissues. 2013 , 5, 867-83	205
1215	Dual functions of TAF7L in adipocyte differentiation. 2013 , 2, e00170	29
1214	Abiotic and Biotic Stress Responses in <i>Solanum tuberosum</i> Group Phureja DM1-3 516 R44 as Measured through Whole Transcriptome Sequencing. 2013 , 6, plantgenome2013.05.0014	25
1213	Efficient and comprehensive representation of uniqueness for next-generation sequencing by minimum unique length analyses. 2013 , 8, e53822	25
1212	Expression profile of ectopic olfactory receptors determined by deep sequencing. 2013 , 8, e55368	181
1211	The baboon kidney transcriptome: analysis of transcript sequence, splice variants, and abundance. 2013 , 8, e57563	9
1210	WNT5A inhibits metastasis and alters splicing of Cd44 in breast cancer cells. 2013 , 8, e58329	39
1209	Transcriptome analysis of artificial hybrid pufferfish Jiyun-1 and its parental species: implications for pufferfish heterosis. 2013 , 8, e58453	19
1208	De novo transcriptome sequence assembly and analysis of RNA silencing genes of <i>Nicotiana benthamiana</i> . 2013 , 8, e59534	132
1207	Functional impacts of NRXN1 knockdown on neurodevelopment in stem cell models. 2013 , 8, e59685	44
1206	RNA-Seq analysis of <i>Cocos nucifera</i> : transcriptome sequencing and de novo assembly for subsequent functional genomics approaches. 2013 , 8, e59997	63

1205	Maize gene atlas developed by RNA sequencing and comparative evaluation of transcriptomes based on RNA sequencing and microarrays. 2013 , 8, e61005	125
1204	RNA-Seq profiling reveals novel hepatic gene expression pattern in aflatoxin B1 treated rats. 2013 , 8, e61768	45
1203	Analysis of tumor heterogeneity and cancer gene networks using deep sequencing of MMTV-induced mouse mammary tumors. 2013 , 8, e62113	13
1202	Simultaneous transcriptome analysis of Sorghum and Bipolaris sorghicola by using RNA-seq in combination with de novo transcriptome assembly. 2013 , 8, e62460	68
1201	A novel approach for characterizing microsatellite instability in cancer cells. 2013 , 8, e63056	35
1200	Characterization of gonadal transcriptomes from Nile tilapia (<i>Oreochromis niloticus</i>) reveals differentially expressed genes. 2013 , 8, e63604	146
1199	Evaluating the impact of sequencing depth on transcriptome profiling in human adipose. 2013 , 8, e66883	44
1198	ANOVA-like differential expression (ALDEx) analysis for mixed population RNA-Seq. 2013 , 8, e67019	270
1197	RNA sequencing of the human milk fat layer transcriptome reveals distinct gene expression profiles at three stages of lactation. 2013 , 8, e67531	129
1196	LOCating non-unique matched tags (LONUT) to improve the detection of the enriched regions for ChIP-seq data. 2013 , 8, e67788	9
1195	Knockdown of CDKN1C (p57(kip2)) and PHLDA2 results in developmental changes in bovine pre-implantation embryos. 2013 , 8, e69490	19
1194	Global transcriptional responses of the toxic cyanobacterium, <i>Microcystis aeruginosa</i> , to nitrogen stress, phosphorus stress, and growth on organic matter. 2013 , 8, e69834	107
1193	Comprehensive characterization of 10,571 mouse large intergenic noncoding RNAs from whole transcriptome sequencing. 2013 , 8, e70835	46
1192	Identification and characterization of long non-coding RNAs related to mouse embryonic brain development from available transcriptomic data. 2013 , 8, e71152	38
1191	Transcriptome profile at different physiological stages reveals potential mode for curly fleece in Chinese tan sheep. 2013 , 8, e71763	37
1190	RNA-seq characterization of spinal cord injury transcriptome in acute/subacute phases: a resource for understanding the pathology at the systems level. 2013 , 8, e72567	48
1189	High-throughput RNA sequencing of pseudomonas-infected <i>Arabidopsis</i> reveals hidden transcriptome complexity and novel splice variants. 2013 , 8, e74183	49
1188	Gaucher disease: transcriptome analyses using microarray or mRNA sequencing in a <i>Gba1</i> mutant mouse model treated with velaglucerase alfa or imiglucerase. 2013 , 8, e74912	11

1187	Comparative genomics reveals insight into virulence strategies of plant pathogenic oomycetes. 2013 , 8, e75072	100
1186	Transcriptome sequencing and differential gene expression analysis of delayed gland morphogenesis in <i>Gossypium australe</i> during seed germination. 2013 , 8, e75323	19
1185	RNA-Seq reveals differential gene expression in <i>Staphylococcus aureus</i> with single-nucleotide resolution. 2013 , 8, e76572	12
1184	F11R is a novel monocyte prognostic biomarker for malignant glioma. 2013 , 8, e77571	32
1183	Optimal scaling of digital transcriptomes. 2013 , 8, e77885	20
1182	Identification of differentially expressed transcripts and pathways in blood one week and six months following implant of left ventricular assist devices. 2013 , 8, e77951	6
1181	Unique transcriptome patterns of the white and grey matter corroborate structural and functional heterogeneity in the human frontal lobe. 2013 , 8, e78480	35
1180	Inferring polymorphism-induced regulatory gene networks active in human lymphocyte cell lines by weighted linear mixed model analysis of multiple RNA-Seq datasets. 2013 , 8, e78868	4
1179	An integrated model of the transcriptome of HER2-positive breast cancer. 2013 , 8, e79298	16
1178	rSeqDiff: detecting differential isoform expression from RNA-Seq data using hierarchical likelihood ratio test. 2013 , 8, e79448	21
1177	Neuropsychological deficits in mice depleted of the schizophrenia susceptibility gene CSMD1. 2013 , 8, e79501	50
1176	RNA sequencing of the exercise transcriptome in equine athletes. 2013 , 8, e83504	32
1175	The genome sequence of the colonial chordate, <i>Botryllus schlosseri</i> . 2013 , 2, e00569	175
1174	Changes in RNA Splicing in Developing Soybean (<i>Glycine max</i>) Embryos. 2013 , 2, 1311-37	14
1173	A Comparison of Methods for RNA-Seq Differential Expression Analysis and a New Empirical Bayes Approach. 2013 , 3, 238-58	15
1172	Metabolic and Transcriptional Reprogramming in Developing Soybean (<i>Glycine max</i>) Embryos. 2013 , 3, 347-72	40
1171	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. 2013 , 2, e00348	148
1170	Minor introns are embedded molecular switches regulated by highly unstable U6atac snRNA. 2013 , 2, e00780	54

1169	Stormbow: A Cloud-Based Tool for Reads Mapping and Expression Quantification in Large-Scale RNA-Seq Studies. 2013 , 2013, 481545	9
1168	Deep sequencing of the transcriptome reveals inflammatory features of porcine visceral adipose tissue. 2013 , 9, 550-6	25
1167	Statistical Analysis of Mapped Reads from mRNA-Seq Data. 77-104	
1166	Model-Based Methods for Transcript Expression-Level Quantification in RNA-Seq. 105-125	
1165	Identifying differential expression genes and single nucleotide variations using RNA-seq in metastatic melanoma. 2014 , 13, 8153-62	4
1164	Pigtailed macaques as a model to study long-term safety of lentivirus vector-mediated gene therapy for hemoglobinopathies. 2014 , 1, 14055	9
1163	Genome-wide transcriptome analysis reveals that cadmium stress signaling controls the expression of genes in drought stress signal pathways in rice. 2014 , 9, e96946	83
1162	Whole transcriptome profiling of maize during early somatic embryogenesis reveals altered expression of stress factors and embryogenesis-related genes. 2014 , 9, e111407	62
1161	A comparative study of techniques for differential expression analysis on RNA-Seq data. 2014 , 9, e103207	152
1160	Construction of a public CHO cell line transcript database using versatile bioinformatics analysis pipelines. 2014 , 9, e85568	52
1159	Expression variants of the lipogenic AGPAT6 gene affect diverse milk composition phenotypes in <i>Bos taurus</i> . 2014 , 9, e85757	44
1158	A pan-cancer analysis of transcriptome changes associated with somatic mutations in U2AF1 reveals commonly altered splicing events. 2014 , 9, e87361	112
1157	Transcriptomics and identification of the chemoreceptor superfamily of the pupal parasitoid of the oriental fruit fly, <i>Spalangia endius</i> Walker (Hymenoptera: Pteromalidae). 2014 , 9, e87800	12
1156	MARIS: method for analyzing RNA following intracellular sorting. 2014 , 9, e89459	75
1155	The has-miR-526b binding-site rs8506G>a polymorphism in the lincRNA-NR_024015 exon identified by GWASs predispose to non-cardia gastric cancer risk. 2014 , 9, e90008	25
1154	RNA sequencing analysis and atrial natriuretic peptide production in patients with dilated and ischemic cardiomyopathy. 2014 , 9, e90157	17
1153	Natural antisense transcripts and long non-coding RNA in <i>Neurospora crassa</i> . 2014 , 9, e91353	35
1152	Transcriptome profiling of a multiple recurrent muscle-invasive urothelial carcinoma of the bladder by deep sequencing. 2014 , 9, e91466	24

1151	Sequencing degraded RNA addressed by 3' tag counting. 2014 , 9, e91851	60
1150	RNA-sequence analysis of primary alveolar macrophages after in vitro infection with porcine reproductive and respiratory syndrome virus strains of differing virulence. 2014 , 9, e91918	33
1149	Characterization of human pseudogene-derived non-coding RNAs for functional potential. 2014 , 9, e93972	42
1148	The impacts of read length and transcriptome complexity for de novo assembly: a simulation study. 2014 , 9, e94825	28
1147	The reference transcriptome of the adult female biting midge (<i>Culicoides sonorensis</i>) and differential gene expression profiling during teneral, blood, and sucrose feeding conditions. 2014 , 9, e98123	15
1146	Deep sequencing reveals new aspects of progesterone receptor signaling in breast cancer cells. 2014 , 9, e98404	9
1145	Transcriptome analysis of shade-induced inhibition on leaf size in relay intercropped soybean. 2014 , 9, e98465	33
1144	RNA-Seq transcriptome profiling identifies CRISPLD2 as a glucocorticoid responsive gene that modulates cytokine function in airway smooth muscle cells. 2014 , 9, e99625	101
1143	Nom1 mediates pancreas development by regulating ribosome biogenesis in zebrafish. 2014 , 9, e100796	12
1142	Meis1 regulates epidermal stem cells and is required for skin tumorigenesis. 2014 , 9, e102111	24
1141	Transcriptome wide identification and validation of calcium sensor gene family in the developing spikes of finger millet genotypes for elucidating its role in grain calcium accumulation. 2014 , 9, e103963	40
1140	Drug target mining and analysis of the Chinese tree shrew for pharmacological testing. 2014 , 9, e104191	16
1139	Transcriptomic analysis of tail regeneration in the lizard <i>Anolis carolinensis</i> reveals activation of conserved vertebrate developmental and repair mechanisms. 2014 , 9, e105004	90
1138	Genomic distribution of H3K9me2 and DNA methylation in a maize genome. 2014 , 9, e105267	108
1137	Transcriptome profiling of spinal muscular atrophy motor neurons derived from mouse embryonic stem cells. 2014 , 9, e106818	26
1136	Systemic suppression of the shoot metabolism upon rice root nematode infection. 2014 , 9, e106858	11
1135	RNA-Seq gene profiling--a systematic empirical comparison. 2014 , 9, e107026	61
1134	LncRBase: an enriched resource for lncRNA information. 2014 , 9, e108010	48

1133	High-resolution transcriptome analysis with long-read RNA sequencing. 2014 , 9, e108095	33
1132	De novo transcriptome sequencing analysis and comparison of differentially expressed genes (DEGs) in <i>Macrobrachium rosenbergii</i> in China. 2014 , 9, e109656	12
1131	Genome-wide identification and tissue-specific expression analysis of UDP-glycosyltransferases genes confirm their abundance in <i>Cicer arietinum</i> (Chickpea) genome. 2014 , 9, e109715	27
1130	DNA methylation and transcription in a distal region upstream from the bovine AlphaS1 casein gene after once or twice daily milking. 2014 , 9, e111556	14
1129	Long term storage of dry versus frozen RNA for next generation molecular studies. 2014 , 9, e111827	23
1128	Detection theory in identification of RNA-DNA sequence differences using RNA-sequencing. 2014 , 9, e112040	6
1127	Heart mitochondrial proteome study elucidates changes in cardiac energy metabolism and antioxidant PRDX3 in human dilated cardiomyopathy. 2014 , 9, e112971	14
1126	Characterization of X chromosome inactivation using integrated analysis of whole-exome and mRNA sequencing. 2014 , 9, e113036	12
1125	Developmental programming of long non-coding RNAs during postnatal liver maturation in mice. 2014 , 9, e114917	19
1124	The human pancreas proteome defined by transcriptomics and antibody-based profiling. 2014 , 9, e115421	25
1123	The kidney transcriptome and proteome defined by transcriptomics and antibody-based profiling. 2014 , 9, e116125	37
1122	Maternal experience with predation risk influences genome-wide embryonic gene expression in threespined sticklebacks (<i>Gasterosteus aculeatus</i>). 2014 , 9, e98564	35
1121	Pharmacological inhibition of cystine-glutamate exchange induces endoplasmic reticulum stress and ferroptosis. 2014 , 3, e02523	723
1120	The transcription factor Pou3f1 promotes neural fate commitment via activation of neural lineage genes and inhibition of external signaling pathways. 2014 , 3,	85
1119	Stratification of gene coexpression patterns and GO function mining for a RNA-Seq data series. 2014 , 2014, 969768	1
1118	Next-generation sequencing of genomic DNA fragments bound to a transcription factor in vitro reveals its regulatory potential. 2014 , 5, 1115-31	18
1117	Alternative splicing during <i>Arabidopsis</i> flower development results in constitutive and stage-regulated isoforms. 2014 , 5, 25	32
1116	The analytical landscape of static and temporal dynamics in transcriptome data. 2014 , 5, 35	24

1115	Brain-expressed 3'UTR extensions strengthen miRNA cross-talk between ion channel/transporter encoding mRNAs. 2014 , 5, 41	11
1114	Transcriptional responses of the Bdtf1-deletion mutant to the phytoalexin brassinin in the necrotrophic fungus <i>Alternaria brassicicola</i> . 2014 , 19, 10717-32	8
1113	Transcriptional Profiles of Mart-1(27-35) Epitope Specific TCReng Human CD8+ and CD4+ T Cells upon Epitope Encounter as Elucidated by RNASeq. 2014 , 01,	0
1112	The Future of Prenatal Diagnosis and Screening. 2014 , 3, 1291-301	6
1111	De novo Assembly and Analysis of the Northern Leopard Frog <i>Rana pipiens</i> Transcriptome. 2014 , 2, 141-9	10
1110	TAF7L modulates brown adipose tissue formation. 2014 , 3,	20
1109	Mapping Splicing Quantitative Trait Loci in RNA-Seq. 2014 , 13, 35-43	6
1108	Prediction of Gene Activity in Early B Cell Development Based on an Integrative Multi-Omics Analysis. 2014 , 7,	11
1107	Functional Implications of RNA Splicing for Human Long Intergenic Noncoding RNAs. 2014 , 10, 219-28	9
1106	Molecular mechanism of formation of cortical opacity in CRYAAN101D transgenic mice. 2014 , 55, 6398-408	6
1105	Differential transcriptome profile of peripheral white cells to identify biomarkers involved in oxaliplatin induced neuropathy. 2014 , 4, 282-96	8
1104	Using heterogeneity of the patient-derived xenograft model to identify the chemoresistant population in ovarian cancer. 2014 , 5, 8750-64	89
1103	Spud DB: A Resource for Mining Sequences, Genotypes, and Phenotypes to Accelerate Potato Breeding. 2014 , 7, plantgenome2013.12.0042	66
1102	ACF7 is a hair-bundle antecedent, positioned to integrate cuticular plate actin and somatic tubulin. 2014 , 34, 305-12	26
1101	Musashi-2 controls cell fate, lineage bias, and TGF- β signaling in HSCs. 2014 , 211, 71-87	99
1100	Defining the human gallbladder proteome by transcriptomics and affinity proteomics. 2014 , 14, 2498-507	17
1099	Phenotypic and Transcriptional Analysis of Divergently Selected Maize Populations Reveals the Role of Developmental Timing in Seed Size Determination. 2014 , 165, 658-669	33
1098	Human nonsense-mediated RNA decay initiates widely by endonucleolysis and targets snRNA host genes. 2014 , 28, 2498-517	119

1097	Data set for the genome-wide transcriptome analysis of human epidermal melanocytes. 2014 , 1, 70-2	3
1096	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. 2014 , 30, 3125-7	22
1095	Comparative analysis of RNA-seq data from polyA RNAs selection and ribosomal RNAs deletion protocol by strand-specific RNA sequencing technology. 2014 ,	
1094	Biological process annotation of proteins across the plant kingdom. 2014 , 1, 73-82	6
1093	CpG island-mediated global gene regulatory modes in mouse embryonic stem cells. 2014 , 5, 5490	21
1092	Deep sequencing of HIV-infected cells: insights into nascent transcription and host-directed therapy. 2014 , 88, 8768-82	31
1091	Transcriptomics in Health and Disease. 2014 ,	0
1090	Isoform Expression Analysis Based on RNA-seq Data. 2014 , 247-259	
1089	Identification of Biomarkers and Expression Signatures. 2014 , 69-78	
1088	Independent stratum formation on the avian sex chromosomes reveals inter-chromosomal gene conversion and predominance of purifying selection on the W chromosome. 2014 , 68, 3281-95	45
1087	Domestication of the dog from the wolf was promoted by enhanced excitatory synaptic plasticity: a hypothesis. 2014 , 6, 3115-21	23
1086	Mudskipper genomes provide insights into the terrestrial adaptation of amphibious fishes. 2014 , 5, 5594	89
1085	Molecular evolution of the Yap/Yorkie proto-oncogene and elucidation of its core transcriptional program. 2014 , 31, 1375-90	34
1084	Evaluation of de novo transcriptome assemblies from RNA-Seq data. 2014 ,	5
1083	Fungal Genomics. 2014 , 1-52	15
1082	Transcriptional analysis of endocrine disruption using zebrafish and massively parallel sequencing. 2014 , 52, R241-56	30
1081	Impact of ERBB2 mutations on in vitro sensitivity of bladder cancer to lapatinib. 2014 , 15, 1239-47	24
1080	Exploring the Transcriptome of Mycorrhizal Interactions. 2014 , 70, 53-78	6

1079	Parallel ionoregulatory adjustments underlie phenotypic plasticity and evolution of <i>Drosophila</i> cold tolerance. 2015 , 218, 423-32	51
1078	CLOCK-controlled polyphonic regulation of circadian rhythms through canonical and noncanonical E-boxes. 2014 , 34, 1776-87	77
1077	Breed-specific transcriptome response of spleen from six to eight week old piglet after infection with <i>Streptococcus suis</i> type 2. 2014 , 41, 7865-73	10
1076	Transcriptome analysis of <i>Gossypium hirsutum</i> flower buds infested by cotton boll weevil (<i>Anthonomus grandis</i>) larvae. 2014 , 15, 854	27
1075	Analysis of stranded information using an automated procedure for strand specific RNA sequencing. 2014 , 15, 631	25
1074	New gene models and alternative splicing in the maize pathogen <i>Colletotrichum graminicola</i> revealed by RNA-Seq analysis. 2014 , 15, 842	24
1073	Diversification of the C-TERMINALLY ENCODED PEPTIDE (CEP) gene family in angiosperms, and evolution of plant-family specific CEP genes. 2014 , 15, 870	40
1072	The parasite <i>Trichomonas vaginalis</i> expresses thousands of pseudogenes and long non-coding RNAs independently from functional neighbouring genes. 2014 , 15, 906	27
1071	Transposable elements modulate human RNA abundance and splicing via specific RNA-protein interactions. 2014 , 15, 537	64
1070	Site-specific genetic engineering of the <i>Anopheles gambiae</i> Y chromosome. 2014 , 111, 7600-5	51
1069	Set5 and Set1 cooperate to repress gene expression at telomeres and retrotransposons. 2014 , 9, 513-22	23
1068	Capture and Amplification by Tailing and Switching (CATS). An ultrasensitive ligation-independent method for generation of DNA libraries for deep sequencing from picogram amounts of DNA and RNA. 2014 , 11, 817-28	47
1067	The WNT receptor FZD7 is required for maintenance of the pluripotent state in human embryonic stem cells. 2014 , 111, 1409-14	88
1066	Dissecting the chromatin interactome of microRNA genes. 2014 , 42, 3028-43	22
1065	Improved structural annotation of protein-coding genes in the <i>Meloidogyne hapla</i> genome using RNA-Seq. 2014 , 3, e29158	6
1064	Genome-wide identification and functional prediction of novel and drought-responsive lincRNAs in <i>Populus trichocarpa</i> . 2014 , 65, 4975-83	200
1063	Temporal genomic evolution of bird sex chromosomes. 2014 , 14, 250	31
1062	Concurrent transcriptional profiling of <i>Dirofilaria immitis</i> and its <i>Wolbachia</i> endosymbiont throughout the nematode life cycle reveals coordinated gene expression. 2014 , 15, 1041	29

1061	Genome-wide screening and functional analysis identify a large number of long noncoding RNAs involved in the sexual reproduction of rice. 2014 , 15, 512	334
1060	Large-scale transcriptional response to hypoxia in <i>Aspergillus fumigatus</i> observed using RNAseq identifies a novel hypoxia regulated ncRNA. 2014 , 178, 331-9	21
1059	Evaluation of de novo transcriptome assemblies from RNA-Seq data. 2014 , 15, 553	170
1058	Olive fly transcriptomics analysis implicates energy metabolism genes in spinosad resistance. 2014 , 15, 714	20
1057	Methylome, transcriptome, and PPAR(α)cistrome analyses reveal two epigenetic transitions in fat cells. 2014 , 9, 1195-206	8
1056	Heterochromatin-mediated gene silencing facilitates the diversification of olfactory neurons. 2014 , 9, 884-92	48
1055	Transposable element-assisted evolution and adaptation to host plant within the <i>Leptosphaeria maculans</i> - <i>Leptosphaeria biglobosa</i> species complex of fungal pathogens. 2014 , 15, 891	111
1054	Piecing the puzzle together: a revisit to transcript reconstruction problem in RNA-seq. 2014 , 15 Suppl 9, S3	1
1053	Discovery of novel transcripts and gametophytic functions via RNA-seq analysis of maize gametophytic transcriptomes. 2014 , 15, 414	58
1052	The importance of study design for detecting differentially abundant features in high-throughput experiments. 2014 , 15, 527	11
1051	Conservation and functional influence of alternative splicing in wood formation of <i>Populus</i> and <i>Eucalyptus</i> . 2014 , 15, 780	23
1050	BADGE: a novel Bayesian model for accurate abundance quantification and differential analysis of RNA-Seq data. 2014 , 15 Suppl 9, S6	7
1049	Transcriptome profiling of CTLs regulated by rapamycin using RNA-Seq. 2014 , 66, 625-33	6
1048	Genomes of the rice pest brown planthopper and its endosymbionts reveal complex complementary contributions for host adaptation. 2014 , 15, 521	271
1047	DNA copy number evolution in <i>Drosophila</i> cell lines. 2014 , 15, R70	66
1046	Comparative transcriptome sequencing of tolerant rice introgression line and its parents in response to drought stress. 2014 , 15, 1026	80
1045	Overcoming endocrine resistance due to reduced PTEN levels in estrogen receptor-positive breast cancer by co-targeting mammalian target of rapamycin, protein kinase B, or mitogen-activated protein kinase kinase. 2014 , 16, 430	55
1044	Genomic characterization of the LEED..PEEDs, a gene family unique to the medicago lineage. 2014 , 4, 2003-12	10

1043	Alternative splicing at GYNNGY 5' splice sites: more noise, less regulation. 2014 , 42, 13969-80	15
1042	Variation in piRNA and transposable element content in strains of <i>Drosophila melanogaster</i> . 2014 , 6, 2786-98	29
1041	Genomic organization, transcriptomic analysis, and functional characterization of avian β and β keratins in diverse feather forms. 2014 , 6, 2258-73	44
1040	Tissue-specific RNA-Seq in human evoked inflammation identifies blood and adipose LincRNA signatures of cardiometabolic diseases. 2014 , 34, 902-12	60
1039	FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis. 2014 , 24, 1403-19	612
1038	Liver Med23 ablation improves glucose and lipid metabolism through modulating FOXO1 activity. 2014 , 24, 1250-65	36
1037	Methods to study splicing from high-throughput RNA sequencing data. 2014 , 1126, 357-97	58
1036	Genome-wide comparative analysis of flowering genes between <i>Arabidopsis</i> and mungbean. 2014 , 36, 799-808	11
1035	Mathematical Adventures in Performance Analysis. 2014 ,	4
1034	Stem Cell Transcriptional Networks. 2014 ,	3
1033	Reference genes for RT-qPCR studies in <i>Corynebacterium pseudotuberculosis</i> identified through analysis of RNA-seq data. 2014 , 106, 605-14	18
1032	The splicing activator DAZAP1 integrates splicing control into MEK/Erk-regulated cell proliferation and migration. 2014 , 5, 3078	42
1031	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. 2014 , 33, 1212-26	46
1030	Mammalian WTAP is a regulatory subunit of the RNA N6-methyladenosine methyltransferase. 2014 , 24, 177-89	1061
1029	A synthetic lethal screen identifies the Vitamin D receptor as a novel gemcitabine sensitizer in pancreatic cancer cells. 2014 , 13, 3839-56	23
1028	Defining a personal, allele-specific, and single-molecule long-read transcriptome. 2014 , 111, 9869-74	168
1027	Identification of mutant genes with high-frequency, high-risk, and high-expression in lung adenocarcinoma. 2014 , 5, 211-8	10
1026	SNAI2 controls the undifferentiated state of human epidermal progenitor cells. 2014 , 32, 3209-18	47

1025	Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. 2014 , 24, 743-50	440
1024	Engineering the anthocyanin regulatory complex of strawberry (<i>Fragaria vesca</i>). 2014 , 5, 651	70
1023	Inflammatory monocytes orchestrate innate antifungal immunity in the lung. 2014 , 10, e1003940	117
1022	Specific gene-regulation networks during the pre-implantation development of the pig embryo as revealed by deep sequencing. 2014 , 15, 4	79
1021	Transcriptome sequencing from diverse human populations reveals differentiated regulatory architecture. 2014 , 10, e1004549	35
1020	Perturbations in small molecule synthesis uncovers an iron-responsive secondary metabolite network in <i>Aspergillus fumigatus</i> . 2014 , 5, 530	36
1019	Bioinformatic Dissecting of TP53 Regulation Pathway Underlying Butyrate-induced Histone Modification in Epigenetic Regulation. 2014 , 6, 1-7	5
1018	Spatial regulation dominates gene function in the ganglia chain. 2014 , 30, 310-6	5
1017	Genetic background drives transcriptional variation in human induced pluripotent stem cells. 2014 , 10, e1004432	190
1016	Quality control on the frontier. 2014 , 5, 157	14
1015	Trp63 is regulated by STAT5 in mammary tissue and subject to differentiation in cancer. 2014 , 21, 443-57	5
1014	Differentiation state-specific mitochondrial dynamic regulatory networks are revealed by global transcriptional analysis of the developing chicken lens. 2014 , 4, 1515-27	30
1013	Characterization of a proposed dichorhavirus associated with the citrus leprosis disease and analysis of the host response. 2014 , 6, 2602-22	27
1012	Developmental regulation of ecdysone receptor (EcR) and EcR-controlled gene expression during pharate-adult development of honeybees (<i>Apis mellifera</i>). 2014 , 5, 445	36
1011	Reconstruction of the gene regulatory network involved in the sonic hedgehog pathway with a potential role in early development of the mouse brain. 2014 , 10, e1003884	10
1010	Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq. 2014 , 129, 93-106	76
1009	microRNA Profiling: An Overview of Current Technologies and Applications. 2014 , 64, 23-46	1
1008	FLI1 expression is correlated with breast cancer cellular growth, migration, and invasion and altered gene expression. 2014 , 16, 801-13	25

1007	Genetic analysis of DEFECTIVE KERNEL1 loop function in three-dimensional body patterning in <i>Physcomitrella patens</i> . 2014 , 166, 903-19	28
1006	Analysis of Deep Sequencing Data. 2014 , 325-354	
1005	metaseq: a Python package for integrative genome-wide analysis reveals relationships between chromatin insulators and associated nuclear mRNA. 2014 , 42, 9158-70	21
1004	Resistance to dual blockade of the kinases PI3K and mTOR in KRAS-mutant colorectal cancer models results in combined sensitivity to inhibition of the receptor tyrosine kinase EGFR. 2014 , 7, ra107	22
1003	MultiRankSeq: multiperspective approach for RNAseq differential expression analysis and quality control. 2014 , 2014, 248090	44
1002	Next-Generation Sequencing. 2014 , 125-145	2
1001	Two miRNA clusters, miR-34b/c and miR-449, are essential for normal brain development, motile ciliogenesis, and spermatogenesis. 2014 , 111, E2851-7	185
1000	Renal Gene Expression Database (RGED): a relational database of gene expression profiles in kidney disease. 2014 , 2014,	14
999	Possible loss of the chloroplast genome in the parasitic flowering plant <i>Rafflesia lagascae</i> (Rafflesiaceae). 2014 , 31, 793-803	131
998	The SET domain proteins SUVH2 and SUVH9 are required for Pol V occupancy at RNA-directed DNA methylation loci. 2014 , 10, e1003948	118
997	Regulation of synaptic nlg-1/neuroigin abundance by the skn-1/Nrf stress response pathway protects against oxidative stress. 2014 , 10, e1004100	34
996	Systematic analysis of Zn2Cys6 transcription factors required for development and pathogenicity by high-throughput gene knockout in the rice blast fungus. 2014 , 10, e1004432	99
995	RAN-binding protein 9 is involved in alternative splicing and is critical for male germ cell development and male fertility. 2014 , 10, e1004825	31
994	A scalable and accurate targeted gene assembly tool (SAT-Assembler) for next-generation sequencing data. 2014 , 10, e1003737	21
993	The Hmr and Lhr hybrid incompatibility genes suppress a broad range of heterochromatic repeats. 2014 , 10, e1004240	60
992	The genome of <i>Spironucleus salmonicida</i> highlights a fish pathogen adapted to fluctuating environments. 2014 , 10, e1004053	44
991	Sex-specific embryonic gene expression in species with newly evolved sex chromosomes. 2014 , 10, e1004159	15
990	Chromatin landscapes of retroviral and transposon integration profiles. 2014 , 10, e1004250	58

989	Allelic expression of deleterious protein-coding variants across human tissues. 2014 , 10, e1004304	43
988	The genomic landscape of the Ewing Sarcoma family of tumors reveals recurrent STAG2 mutation. 2014 , 10, e1004475	258
987	RNA sequencing analysis reveals transcriptomic variations in tobacco (<i>Nicotiana tabacum</i>) leaves affected by climate, soil, and tillage factors. 2014 , 15, 6137-60	14
986	"Out of pollen" hypothesis for origin of new genes in flowering plants: study from <i>Arabidopsis thaliana</i> . 2014 , 6, 2822-9	24
985	Dynamic DNA methylation orchestrates cardiomyocyte development, maturation and disease. 2014 , 5, 5288	202
984	The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. 2014 , 5, 4737	151
983	Efficient RNA isoform identification and quantification from RNA-Seq data with network flows. 2014 , 30, 2447-55	48
982	Protein-protein interaction and gene co-expression maps of ARFs and Aux/IAAs in <i>Arabidopsis</i> . 2014 , 5, 744	106
981	Evidence for widespread positive and negative selection in coding and conserved noncoding regions of <i>Capsella grandiflora</i> . 2014 , 10, e1004622	83
980	Comparative transcriptome analysis of leaves and roots in response to sudden increase in salinity in <i>Brassica napus</i> by RNA-seq. 2014 , 2014, 467395	38
979	Molecular mechanisms of hypoxic responses via unique roles of Ras1, Cdc24 and Ptp3 in a human fungal pathogen <i>Cryptococcus neoformans</i> . 2014 , 10, e1004292	13
978	Transcriptomic profiling of rat liver samples in a comprehensive study design by RNA-Seq. 2014 , 1, 140021	21
977	Altered Transcriptional Control Networks with Trans-Differentiation of Isogenic Mutant-KRas NSCLC Models. 2014 , 4, 344	13
976	Expanding and Vetting <i>Sorghum bicolor</i> Gene Annotations through Transcriptome and Methylome Sequencing. 2014 , 7, plantgenome2013.08.0025	22
975	SigFuge: single gene clustering of RNA-seq reveals differential isoform usage among cancer samples. 2014 , 42, e113	15
974	Mutations enabling displacement of tryptophan by 4-fluorotryptophan as a canonical amino acid of the genetic code. 2014 , 6, 629-41	21
973	Forty-four novel protein-coding loci discovered using a proteomics informed by transcriptomics (PIT) approach in rat male germ cells. 2014 , 91, 123	18
972	Bionimbus: a cloud for managing, analyzing and sharing large genomics datasets. 2014 , 21, 969-75	56

971	Insight into insulin secretion from transcriptome and genetic analysis of insulin-producing cells of <i>Drosophila</i> . 2014 , 197, 175-92	22
970	RNA-Seq alignment to individualized genomes improves transcript abundance estimates in multiparent populations. 2014 , 198, 59-73	55
969	Translational control of the oogenic program by components of OMA ribonucleoprotein particles in <i>Caenorhabditis elegans</i> . 2014 , 198, 1513-33	32
968	Genome-wide identification and functional analysis of Apobec-1-mediated C-to-U RNA editing in mouse small intestine and liver. 2014 , 15, R79	70
967	High-resolution profiling of novel transcribed regions during rat spermatogenesis. 2014 , 91, 5	40
966	Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. 2014 , 4, 164-84	125
965	Transcriptomic analysis of differentially expressed genes in the Ras1(CA)-overexpressed and wildtype posterior silk glands. 2014 , 15, 182	12
964	Transcriptome dynamics-based operon prediction in prokaryotes. 2014 , 15, 145	21
963	Sex- and tissue-specific profiles of chemosensory gene expression in a herbivorous gall-inducing fly (Diptera: Cecidomyiidae). 2014 , 15, 501	45
962	The discrepancies in the results of bioinformatics tools for genomic structural annotation. 2014 ,	
961	Identification of genetic variants associated with alternative splicing using sQTLseeker. 2014 , 5, 4698	77
960	Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. 2014 , 24, 1918-31	197
959	A comparison of combined p-value methods for gene differential expression using RNA-seq data. 2014 ,	
958	ORMAN: optimal resolution of ambiguous RNA-Seq multimappings in the presence of novel isoforms. 2014 , 30, 644-51	12
957	The <i>Cryptococcus neoformans</i> transcriptome at the site of human meningitis. 2014 , 5, e01087-13	85
956	Protease inhibitor 15, a candidate gene for abdominal aortic internal elastic lamina ruptures in the rat. 2014 , 46, 418-28	14
955	Topoisomerase IIbeta is required for proper retinal development and survival of postmitotic cells. 2014 , 3, 172-84	16
954	PseudoLasso. 2014 ,	

953	Identification of candidate genes involved in coronary artery calcification by transcriptome sequencing of cell lines. 2014 , 15, 198	8
952	The transcriptome of human pluripotent stem cells. 2014 , 28, 71-7	13
951	Insights into the maize pan-genome and pan-transcriptome. 2014 , 26, 121-35	336
950	High-resolution sequencing and modeling identifies distinct dynamic RNA regulatory strategies. 2014 , 159, 1698-710	136
949	Transdifferentiation of differentiated ovary into functional testis by long-term treatment of aromatase inhibitor in Nile tilapia. 2014 , 155, 1476-88	83
948	Fine-mapping nicotine resistance loci in <i>Drosophila</i> using a multiparent advanced generation inter-cross population. 2014 , 198, 45-57	37
947	Antigen-specific culture of memory-like CD8 T cells for adoptive immunotherapy. 2014 , 2, 839-45	4
946	Genome-wide study of KNOX regulatory network reveals brassinosteroid catabolic genes important for shoot meristem function in rice. 2014 , 26, 3488-500	77
945	Transcriptional targets of the schizophrenia risk gene MIR137. 2014 , 4, e404	42
944	The complex jujube genome provides insights into fruit tree biology. 2014 , 5, 5315	155
943	Novel synthetic Medea selfish genetic elements drive population replacement in <i>Drosophila</i> ; a theoretical exploration of Medea-dependent population suppression. 2014 , 3, 915-28	71
942	A highly conserved program of neuronal microexons is misregulated in autistic brains. 2014 , 159, 1511-23	356
941	Maize centromeres expand and adopt a uniform size in the genetic background of oat. 2014 , 24, 107-16	66
940	Decelerated genome evolution in modern vertebrates revealed by analysis of multiple lancelet genomes. 2014 , 5, 5896	99
939	Modeling chronic myeloid leukemia in immunodeficient mice reveals expansion of aberrant mast cells and accumulation of pre-B cells. 2014 , 4, e269	10
938	Integrative RNA-seq and microarray data analysis reveals GC content and gene length biases in the psoriasis transcriptome. 2014 , 46, 533-46	31
937	Genome-wide association discoveries of alcohol dependence. 2014 , 23, 526-39	29
936	Activation of muscle enhancers by MyoD and epigenetic modifiers. 2014 , 115, 1855-67	11

935	Cis-splicing and translation of the pre-trans-splicing molecule combine with efficiency in spliceosome-mediated RNA trans-splicing. 2014 , 22, 1176-1187		26
934	Lariat intronic RNAs in the cytoplasm of <i>Xenopus tropicalis</i> oocytes. 2014 , 20, 1476-87		90
933	Dynamic transcription factor activity and networks during ErbB2 breast oncogenesis and targeted therapy. 2014 , 6, 1170-82		10
932	Aldehyde dehydrogenase activity enriches for proximal airway basal stem cells and promotes their proliferation. 2014 , 23, 664-75		23
931	Gene expression profiling of replicative and induced senescence. 2014 , 13, 3927-37		66
930	Global dissection of alternative splicing in paleopolyploid soybean. 2014 , 26, 996-1008		178
929	The draft genome sequence of the ferret (<i>Mustela putorius furo</i>) facilitates study of human respiratory disease. <i>Nature Biotechnology</i> , 2014 , 32, 1250-5	44.5	81
928	Site-specific association with host and viral chromatin by Kaposi's sarcoma-associated herpesvirus LANA and its reversal during lytic reactivation. 2014 , 88, 6762-77		30
927	Ammonium induces differential expression of methane and nitrogen metabolism-related genes in <i>Methylocystis</i> sp. strain SC2. 2014 , 16, 3115-27		19
926	Prevalence, evolution, and cis-regulation of diel transcription in <i>Chlamydomonas reinhardtii</i> . 2014 , 4, 2461-71		21
925	Ionotropic GABA and glycine receptor subunit composition in human pluripotent stem cell-derived excitatory cortical neurones. 2014 , 592, 4353-63		13
924	An alternative, arginase-independent pathway for arginine metabolism in <i>Kluyveromyces lactis</i> involves guanidinobutyrase as a key enzyme. 2014 , 93, 369-89		14
923	A comparative systems analysis of polysaccharide-elicited responses in <i>Neurospora crassa</i> reveals carbon source-specific cellular adaptations. 2014 , 91, 275-99		70
922	Global discovery of erythroid long noncoding RNAs reveals novel regulators of red cell maturation. 2014 , 123, 570-81		135
921	Assessment and improvement of Indian-origin rhesus macaque and Mauritian-origin cynomolgus macaque genome annotations using deep transcriptome sequencing data. 2014 , 43, 317-28		4
920	Genome-guided transcript assembly by integrative analysis of RNA sequence data. <i>Nature Biotechnology</i> , 2014 , 32, 341-6	44.5	42
919	Genome-wide transcriptome analysis of human epidermal melanocytes. 2014 , 104, 482-9		25
918	Comparative genomics reveals insights into avian genome evolution and adaptation. 2014 , 346, 1311-20		628

917	Genome-wide identification of long intergenic noncoding RNA genes and their potential association with domestication in pigs. 2014 , 6, 1387-92	72
916	Mapping genetic modifiers of survival in a mouse model of Dravet syndrome. 2014 , 13, 163-72	89
915	Identification of species-specific novel transcripts in pig reproductive tissues using RNA-seq. 2014 , 45, 198-204	19
914	Answering the demands of digital genomics. 2014 , 26, 917-928	1
913	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. 2014 , 10, 737	31
912	Transcriptome-wide profiling and posttranscriptional analysis of hematopoietic stem/progenitor cell differentiation toward myeloid commitment. 2014 , 3, 858-75	25
911	Construction and assessment of individualized proteogenomic databases for large-scale analysis of nonsynonymous single nucleotide variants. 2014 , 14, 2699-708	13
910	A dynamic alternative splicing program regulates gene expression during terminal erythropoiesis. 2014 , 42, 4031-42	65
909	Chronic cocaine-regulated epigenomic changes in mouse nucleus accumbens. 2014 , 15, R65	108
908	NONCODEv4: exploring the world of long non-coding RNA genes. 2014 , 42, D98-103	342
907	AURA 2: Empowering discovery of post-transcriptional networks. 2014 , 2, e27738	57
906	Exon expression QTL (eeQTL) analysis highlights distant genomic variations associated with splicing regulation. 2014 , 2, 71-79	4
905	Global absolute quantification reveals tight regulation of protein expression in single <i>Xenopus</i> eggs. 2014 , 42, 9880-91	47
904	PLEK: a tool for predicting long non-coding RNAs and messenger RNAs based on an improved k-mer scheme. 2014 , 15, 311	317
903	Maternal nutrition induces gene expression changes in fetal muscle and adipose tissues in sheep. 2014 , 15, 1034	42
902	Transcriptome structure variability in <i>Saccharomyces cerevisiae</i> strains determined with a newly developed assembly software. 2014 , 15, 1045	8
901	Flower development and sex specification in wild grapevine. 2014 , 15, 1095	31
900	Evaluation and validation of a robust single cell RNA-amplification protocol through transcriptional profiling of enriched lung cancer initiating cells. 2014 , 15, 1129	16

899	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. 2014 , 15, 1148	9
898	A hyper-dynamic nature of bivalent promoter states underlies coordinated developmental gene expression modules. 2014 , 15, 1186	11
897	Systematic transcriptome analysis of the zebrafish model of diamond-blackfan anemia induced by RPS24 deficiency. 2014 , 15, 759	14
896	A transcriptome resource for the koala (<i>Phascolarctos cinereus</i>): insights into koala retrovirus transcription and sequence diversity. 2014 , 15, 786	42
895	Dual transcriptional profiling of mice and <i>Toxoplasma gondii</i> during acute and chronic infection. 2014 , 15, 806	111
894	Genes and signaling networks regulated during zebrafish optic vesicle morphogenesis. 2014 , 15, 825	17
893	Identification and functional analysis of long non-coding RNAs in mouse cleavage stage embryonic development based on single cell transcriptome data. 2014 , 15, 845	56
892	Transcriptome reconstruction and annotation of cynomolgus and African green monkey. 2014 , 15, 846	9
891	IUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. 2014 , 15, 862	18
890	Transcriptome sequencing of rhizome tissue of <i>Sinopodophyllum hexandrum</i> at two temperatures. 2014 , 15, 871	30
889	Transcriptomic portrait of human Mesenchymal Stromal/Stem Cells isolated from bone marrow and placenta. 2014 , 15, 910	43
888	RNA-sequencing analysis of <i>Trichophyton rubrum</i> transcriptome in response to sublethal doses of acriflavine. 2014 , 15 Suppl 7, S1	25
887	Genome-wide expression analysis of reactive oxygen species gene network in Mizuna plants grown in long-term spaceflight. 2014 , 14, 4	58
886	A new rhesus macaque assembly and annotation for next-generation sequencing analyses. 2014 , 9, 20	122
885	NF- κ B signaling and vesicle transport are correlated with the reactivation of the memory trace of morphine dependence. 2014 , 9, 142	7
884	Expression level of a flavonoid 3'-hydroxylase gene determines pathogen-induced color variation in sorghum. 2014 , 7, 761	17
883	Predicting expression: the complementary power of histone modification and transcription factor binding data. 2014 , 7, 36	31
882	A comprehensive resource of genomic, epigenomic and transcriptomic sequencing data for the black truffle <i>Tuber melanosporum</i> . 2014 , 3, 25	10

881	Comparisons of computational methods for differential alternative splicing detection using RNA-seq in plant systems. 2014 , 15, 364	63
880	VTBuilder: a tool for the assembly of multi isoform transcriptomes. 2014 , 15, 389	24
879	Cysteine protease and cystatin expression and activity during soybean nodule development and senescence. 2014 , 14, 294	39
878	Global identification of Smad2 and Eomesodermin targets in zebrafish identifies a conserved transcriptional network in mesendoderm and a novel role for Eomesodermin in repression of ectodermal gene expression. 2014 , 12, 81	30
877	Pegasus: a comprehensive annotation and prediction tool for detection of driver gene fusions in cancer. 2014 , 8, 97	47
876	Molecular profile of cochlear immunity in the resident cells of the organ of Corti. 2014 , 11, 173	38
875	HeatmapGenerator: high performance RNAseq and microarray visualization software suite to examine differential gene expression levels using an R and C++ hybrid computational pipeline. 2014 , 9, 30	32
874	Letting the data speak for themselves: a fully Bayesian approach to transcriptome assembly. 2014 , 15, 498	1
873	Bayesian transcriptome assembly. 2014 , 15, 501	43
872	High-resolution functional annotation of human transcriptome: predicting isoform functions by a novel multiple instance-based label propagation method. 2014 , 42, e39	32
871	PennSeq: accurate isoform-specific gene expression quantification in RNA-Seq by modeling non-uniform read distribution. 2014 , 42, e20	29
870	HIP1-ALK, a novel ALK fusion variant that responds to crizotinib. 2014 , 9, 285-94	68
869	Polymorphism identification and improved genome annotation of Brassica rapa through Deep RNA sequencing. 2014 , 4, 2065-78	25
868	RNA-Skim: a rapid method for RNA-Seq quantification at transcript level. 2014 , 30, i283-i292	34
867	ARH-seq: identification of differential splicing in RNA-seq data. 2014 , 42, e110	8
866	Integration of mapped RNA-Seq reads into automatic training of eukaryotic gene finding algorithm. 2014 , 42, e119	208
865	Spalt-like 4 promotes posterior neural fates via repression of pou5f3 family members in Xenopus. 2014 , 141, 1683-93	18
864	Modeling gene expression evolution with an extended Ornstein-Uhlenbeck process accounting for within-species variation. 2014 , 31, 201-11	68

863	De novo transcriptome sequencing of the Octopus vulgaris hemocytes using Illumina RNA-Seq technology: response to the infection by the gastrointestinal parasite <i>Aggregata octopiana</i> . 2014 , 9, e107873	44
862	RNA-Seq Data: A Complexity Journey. 2014 , 11, 123-30	15
861	Loss of NF1 in cutaneous melanoma is associated with RAS activation and MEK dependence. 2014 , 74, 2340-50	204
860	The genome sequence and effector complement of the flax rust pathogen <i>Melampsora lini</i> . 2014 , 5, 98	84
859	Two functionally distinct subsets of mast cells discriminated By IL-2-independent CD25 activities. 2014 , 193, 2196-206	8
858	A new dataset of spermatogenic vs. oogenic transcriptomes in the nematode <i>Caenorhabditis elegans</i> . 2014 , 4, 1765-72	96
857	The transcriptional co-repressor TLE3 suppresses basal signaling on a subset of estrogen receptor target genes. 2014 , 42, 11339-48	15
856	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. 2014 , 5, 5603	56
855	RNA-Seq using two populations reveals genes and alleles controlling wood traits and growth in <i>Eucalyptus nitens</i> . 2014 , 9, e101104	20
854	Genome diversity and divergence in <i>Drosophila mauritiana</i> : multiple signatures of faster X evolution. 2014 , 6, 2444-58	42
853	NRASG12V oncogene facilitates self-renewal in a murine model of acute myelogenous leukemia. 2014 , 124, 3274-83	20
852	Intragenic motifs regulate the transcriptional complexity of <i>Pkhd1/PKHD1</i> . 2014 , 92, 1045-56	26
851	Domestic dogs and cancer research: a breed-based genomics approach. 2014 , 55, 59-68	59
850	UnSplicer: mapping spliced RNA-Seq reads in compact genomes and filtering noisy splicing. 2014 , 42, e25	3
849	Computational analysis reveals a correlation of exon-skipping events with splicing, transcription and epigenetic factors. 2014 , 42, 2856-69	19
848	Integrated omics study delineates the dynamics of lipid droplets in <i>Rhodococcus opacus</i> PD630. 2014 , 42, 1052-64	67
847	Dietary and flight energetic adaptations in a salivary gland transcriptome of an insectivorous bat. 2014 , 9, e83512	9
846	A transcription factor network specifying inhibitory versus excitatory neurons in the dorsal spinal cord. 2014 , 141, 3102-3102	3

845	Comparison of <i>D. melanogaster</i> and <i>C. elegans</i> developmental stages, tissues, and cells by modENCODE RNA-seq data. 2014 , 24, 1086-101	59
844	Using RNA-seq Data to Detect Differentially Expressed Genes. 2014 , 25-49	3
843	Characterization of genetic diversity in the nematode <i>Pristionchus pacificus</i> from population-scale resequencing data. 2014 , 196, 1153-65	61
842	Specific adaptation of <i>Ustilagoidea virens</i> in occupying host florets revealed by comparative and functional genomics. 2014 , 5, 3849	122
841	Current challenges in the bioinformatics of single cell genomics. 2014 , 4, 7	35
840	<i>Arabidopsis</i> transcriptome analysis reveals key roles of melatonin in plant defense systems. 2014 , 9, e93462	185
839	Nova1 is a master regulator of alternative splicing in pancreatic beta cells. 2014 , 42, 11818-30	53
838	miRIAD-integrating microRNA inter- and intragenic data. 2014 , 2014,	58
837	Vespucci: a system for building annotated databases of nascent transcripts. 2014 , 42, 2433-47	14
836	Transcriptome analysis of the gill and swimbladder of <i>Takifugu rubripes</i> by RNA-Seq. 2014 , 9, e85505	19
835	Annexin A6 modifies muscular dystrophy by mediating sarcolemmal repair. 2014 , 111, 6004-9	90
834	Gene Expression and Gene Ontology Enrichment Analysis for H3K4me3 and H3K4me1 in Mouse Liver and Mouse Embryonic Stem Cell Using CHIP-Seq and RNA-Seq. 2014 , 8, 33-43	2
833	Genome-wide analysis of histone modifications in human endometrial stromal cells. 2014 , 28, 1656-69	38
832	Genetic influences on brain gene expression in rats selected for tameness and aggression. 2014 , 198, 1277-90	53
831	Protection of CpG islands against de novo DNA methylation during oogenesis is associated with the recognition site of E2f1 and E2f2. 2014 , 7, 26	16
830	Genome-wide discovery and characterization of maize long non-coding RNAs. 2014 , 15, R40	308
829	Fluctuation of Rac1 activity is associated with the phenotypic and transcriptional heterogeneity of glioma cells. 2014 , 127, 1805-15	16
828	Brf1 posttranscriptionally regulates pluripotency and differentiation responses downstream of Erk MAP kinase. 2014 , 111, E1740-8	18

827	Differentiating progressive from nonprogressive T1 bladder cancer by gene expression profiling: applying RNA-sequencing analysis on archived specimens. 2014 , 32, 327-36	15
826	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. 2014 ,	
825	Navigating and mining modENCODE data. 2014 , 68, 38-47	14
824	Identification of differentially expressed genes in hepatopancreas of oriental river prawn, <i>Macrobrachium nipponense</i> exposed to environmental hypoxia. 2014 , 534, 298-306	53
823	The earliest transcribed zygotic genes are short, newly evolved, and different across species. 2014 , 6, 285-92	121
822	PrimerSeq: Design and visualization of RT-PCR primers for alternative splicing using RNA-seq data. 2014 , 12, 105-9	10
821	A Comprehensive Analysis of CXCL12 Isoforms in Breast Cancer. 2014 , 7, 429-429	30
820	Genome-wide transcriptomic responses of the seagrasses <i>Zostera marina</i> and <i>Nanozostera noltii</i> under a simulated heatwave confirm functional types. 2014 , 15, 65-73	52
819	Transcriptome profiling to identify genes involved in pathogenicity of <i>Valsa mali</i> on apple tree. 2014 , 68, 31-8	40
818	The role of hyaluronic acid precursor concentrations in molecular weight control in <i>Streptococcus zooepidemicus</i> . 2014 , 56, 147-56	22
817	ncRNA-Protein Interactions in Development and Disease from the Perspective of High-Throughput Studies. 2014 , 87-115	
816	Pigmentation in sand pear (<i>Pyrus pyrifolia</i>) fruit: biochemical characterization, gene discovery and expression analysis with exocarp pigmentation mutant. 2014 , 85, 123-34	24
815	Structure and expression of <i>GSL1</i> and <i>GSL2</i> genes encoding gibberellin stimulated-like proteins in diploid and highly heterozygous tetraploid potato reveals their highly conserved and essential status. 2014 , 15, 2	23
814	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of <i>SULT2A1</i> in the testis. 2014 , 15, 4	6
813	Dynamic regulation of genome-wide pre-mRNA splicing and stress tolerance by the Sm-like protein <i>LSm5</i> in <i>Arabidopsis</i> . 2014 , 15, R1	386
812	Engineered chromosome-based genetic mapping establishes a 3.7 Mb critical genomic region for Down syndrome-associated heart defects in mice. 2014 , 133, 743-53	22
811	Characterizing the molecular basis of attenuation of Marek's disease virus via in vitro serial passage identifies de novo mutations in the helicase-primase subunit gene <i>UL5</i> and other candidates associated with reduced virulence. 2014 , 88, 6232-42	17
810	Differential transcriptomic analysis by RNA-Seq of GSNO-responsive genes between <i>Arabidopsis</i> roots and leaves. 2014 , 55, 1080-95	105

809	The iron stimulon and fur regulon of <i>Geobacter sulfurreducens</i> and their role in energy metabolism. 2014 , 80, 2918-27	20
808	Targeted sequencing for gene discovery and quantification using RNA CaptureSeq. 2014 , 9, 989-1009	116
807	Chronic LSD alters gene expression profiles in the mPFC relevant to schizophrenia. 2014 , 83, 1-8	36
806	RNA-sequencing analysis reveals new alterations in cardiomyocyte cytoskeletal genes in patients with heart failure. 2014 , 94, 645-53	27
805	From single-cell to cell-pool transcriptomes: stochasticity in gene expression and RNA splicing. 2014 , 24, 496-510	363
804	RNA-sequencing reveals previously unannotated protein- and microRNA-coding genes expressed in aleurone cells of rice seeds. 2014 , 103, 122-34	10
803	Discovery of human sORF-encoded polypeptides (SEPs) in cell lines and tissue. 2014 , 13, 1757-65	111
802	Towards an improved apple reference transcriptome using RNA-seq. 2014 , 289, 427-38	25
801	RNA-seq in the tetraploid <i>Xenopus laevis</i> enables genome-wide insight in a classic developmental biology model organism. 2014 , 66, 398-409	10
800	Dual RNA-seq of the plant pathogen <i>Phytophthora ramorum</i> and its tanoak host. 2014 , 10, 489-502	37
799	Pallial mucus of the oyster <i>Crassostrea virginica</i> regulates the expression of putative virulence genes of its pathogen <i>Perkinsus marinus</i> . 2014 , 44, 305-17	26
798	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. 2014 , 23, 2198-209	31
797	Identification and characterization of a galacturonic acid transporter from <i>Neurospora crassa</i> and its application for <i>Saccharomyces cerevisiae</i> fermentation processes. 2014 , 7, 20	44
796	RNA-seq analysis of bovine intramuscular, subcutaneous and perirenal adipose tissues. 2014 , 41, 1631-7	23
795	De novo sequencing and comparative analysis of three red algal species of Family Solieriaceae to discover putative genes associated with carrageenan biosynthesis. 2014 , 33, 45-53	2
794	Genome-wide identification and functional annotation of <i>Plasmodium falciparum</i> long noncoding RNAs from RNA-seq data. 2014 , 113, 1269-81	30
793	Bidirectional promoters are the major source of gene activation-associated non-coding RNAs in mammals. 2014 , 15, 35	78
792	Comprehensive analysis of gene expression in human retina and supporting tissues. 2014 , 23, 4001-14	86

791	An atlas of active enhancers across human cell types and tissues. 2014 , 507, 455-461	1595
790	CAGEExploreR: an R package for the analysis and visualization of promoter dynamics across multiple experiments. 2014 , 30, 1183-1184	5
789	Identification of putative insulin-like peptides and components of insulin signaling pathways in parasitic platyhelminths by the use of genome-wide screening. 2014 , 281, 877-93	18
788	Dissecting childhood asthma with nasal transcriptomics distinguishes subphenotypes of disease. 2014 , 133, 670-8.e12	144
787	RNA-Seq technology and its application in fish transcriptomics. 2014 , 18, 98-110	187
786	Time-series RNA-seq analysis package (TRAP) and its application to the analysis of rice, <i>Oryza sativa</i> L. ssp. Japonica, upon drought stress. 2014 , 67, 364-72	24
785	Modeling alternative splicing variants from RNA-Seq data with isoform graphs. 2014 , 21, 16-40	17
784	Alternative capture of noncoding RNAs or protein-coding genes by herpesviruses to alter host T cell function. 2014 , 54, 67-79	48
783	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014 , 32, 462-4	44.5 422
782	RRP1B is a metastasis modifier that regulates the expression of alternative mRNA isoforms through interactions with SRSF1. 2014 , 33, 1818-27	15
781	Origins and functional evolution of Y chromosomes across mammals. 2014 , 508, 488-93	339
780	Genome-wide analysis reveals a role for BRCA1 and PALB2 in transcriptional co-activation. 2014 , 33, 890-905	32
779	Deep RNA sequencing reveals dynamic regulation of myocardial noncoding RNAs in failing human heart and remodeling with mechanical circulatory support. 2014 , 129, 1009-21	297
778	Triplication of a 21q22 region contributes to B cell transformation through HMG1 overexpression and loss of histone H3 Lys27 trimethylation. 2014 , 46, 618-23	84
777	Integrative analysis of histone ChIP-seq and transcription data using Bayesian mixture models. 2014 , 30, 1154-1162	23
776	Single-cell genome and metatranscriptome sequencing reveal metabolic interactions of an alkane-degrading methanogenic community. 2014 , 8, 757-67	106
775	Magnesium availability regulates the development of root hairs in <i>Arabidopsis thaliana</i> (L.) Heynh. 2014 , 37, 2795-813	52
774	Global microRNA depletion suppresses tumor angiogenesis. 2014 , 28, 1054-67	52

773	Next-Generation Sequencing RNA-Seq Library Construction. 2014 , 106, 4.21.1-19	31
772	The histone H2A deubiquitinase Usp16 regulates embryonic stem cell gene expression and lineage commitment. 2014 , 5, 3818	48
771	Molecular Testing in Cancer. 2014 ,	1
770	Global transcriptome analyses of human and murine terminal erythroid differentiation. 2014 , 123, 3466-77	208
769	Genomics-Based Cancer Theranostics. 2014 , 9-20	0
768	Cancer Transcriptome Sequencing and Analysis. 2014 , 31-47	1
767	The Significance of Transcriptome Sequencing in Personalized Cancer Medicine. 2014 , 49-64	1
766	The high-quality genome of pummelo provides insights into the tissue-specific regulation of citric acid and anthocyanin during domestication.	
765	RALY regulate the proliferation and expression of immune/inflammatory response genes via alternative splicing of FOS.	0
764	De novo RNA sequencing for identification of growth-related genes in <i>Silurus lanzhouensis</i> muscle tissues.	
763	Ciliary Neurotrophic Factor Derived From Astrocytes Protects Retinal Ganglion Cells Through PI3K/AKT, JAK/STAT, and MAPK/ERK Pathways. 2022 , 63, 4	0
762	Prediction of the 3D cancer genome from genomic rearrangements using InfoHiC.	
761	An expanded role for the transcription factor WRINKLED1 in the biosynthesis of triacylglycerols during seed development. 13,	0
760	TcMYC2 regulates Pyrethrin biosynthesis in <i>Tanacetum cinerariifolium</i> .	2
759	Chronological attenuation of NPRA / PKG / AMPK signaling promotes vascular aging and elevates blood pressure.	0
758	Flnc: Machine Learning Improves the Identification of Novel Full-length Long Noncoding RNAs from RNA Sequencing Data Without Transcriptional Initiation Profiles.	
757	Elucidating the unknown transcriptional responses and PHR1 mediated biotic and abiotic stress tolerance during phosphorus-limitation.	
756	Transcriptome-wide analyses of RNA m6A methylation in hexaploid wheat reveal its roles in mRNA translation regulation. 13,	0

- 755 Preparation, characterization, and osteogenic activity mechanism of casein phosphopeptide-calcium chelate. 9, 0
- 754 Transcriptome analysis revealed gene expression feminization of testis after exogenous tetrodotoxin administration in pufferfish *Takifugu flavidus*. **2022**, 23, 1
- 753 High cysteine concentrations in cell culture media lead to oxidative stress and reduced bioprocess performance of recombinant CHO cells. 2200029 0
- 752 Post-transcriptional regulation of 2-acetyl-1-pyrroline (2-AP) biosynthesis pathway, silicon, and heavy metal transporters in response to Zn in fragrant rice. 13, 1
- 751 Novel estrogen-responsive genes (ERGs) for the evaluation of estrogenic activity. **2022**, 17, e0273164 0
- 750 Integrative analysis of circulating microRNAs and the placental transcriptome in recurrent pregnancy loss. 13, 1
- 749 Integrative transcriptomic and metabolomic analyses unveil tanshinone biosynthesis in *Salvia miltiorrhiza* root under N starvation stress. **2022**, 17, e0273495 1
- 748 Liver transcriptomics reveals features of the host response in a mouse model of dengue virus infection. 13, 0
- 747 Prkra Mutation Alters Long Noncoding RNA Expression During Embryonic External Ear Development. Publish Ahead of Print, 0
- 746 Translation control by maternal Nanog promotes oocyte maturation and early embryonic development. 0
- 745 METTL3 preferentially enhances non-m6A translation of epigenetic factors and promotes tumorigenesis. **2022**, 24, 1278-1290 1
- 744 D-Penicillamine Reveals the Amelioration of Seizure-Induced Neuronal Injury via Inhibiting Aqp11-Dependent Ferroptosis. **2022**, 11, 1602 0
- 743 Possible Contribution of Alternative Transcript Isoforms in Mature Biofilm Growth Phase of *Candida glabrata*. 0
- 742 Reduced calcium levels and accumulation of abnormal insulin granules in stem cell models of HNF1A deficiency. **2022**, 5, 1
- 741 Doxorubicin-Induced Cardiotoxicity May Be Alleviated by Bone Marrow Mesenchymal Stem Cell-Derived Exosomal lncRNA via Inhibiting Inflammation. Volume 15, 4467-4486 1
- 740 Comparative Transcriptome Profiling Reveals Potential Candidate Genes, Transcription Factors, and Biosynthetic Pathways for Phosphite Response in Potato (*Solanum tuberosum* L.). **2022**, 13, 1379 0
- 739 Tissue-specific mRNA profiling of the *Brassica napus*-*Sclerotinia sclerotiorum* interaction uncovers novel regulators of plant immunity. 0
- 738 Differential expression analysis of mRNAs, lncRNAs, and miRNAs expression profiles and construction of ceRNA networks in PEDV infection. **2022**, 23, 0

- 737 Bioinformatic analysis of circular RNA expression profiles in a rat lumbosacral spinal root avulsion model. 13,
- 736 Identification and expression analysis of the MADS-box genes of Kentucky bluegrass during inflorescence development.
- 735 Clostridium autoethanogenum isopropanol production via native plasmid pCA replicon. 10,
- 734 Transcriptomics and Genomics Analysis Uncover the Differentially Expressed Chlorophyll and Carotenoid-Related Genes in Celery. **2022**, 23, 8986 ○
- 733 Combined Transcriptomic and Metabolomic Analysis Reveals the Mechanism of Flavonoid Biosynthesis in Handroanthus chrysanthus (Jacq.) S.O.Grose. **2022**, 13, 1285
- 732 Humanized mice for investigating SARS-CoV-2 lung infection and associated human immune responses. ○
- 731 Physiological, Transcriptomic and Metabolomic Analyses of Overwintering Cryptomeria fortunei Needles. **2022**, 13, 1249 ○
- 730 Integrated genomic and transcriptomic elucidation of flowering in garlic. ○
- 729 Evidence of silk growth hampering in maize at high planting density using phenotypic and transcriptional analysis. **2022**,
- 728 Comparative Transcriptome Analysis Reveals Genes Associated with the Gossypol Synthesis and Gland Morphogenesis in Gossypium hirsutum. **2022**, 13, 1452
- 727 Integrated metabolomic and transcriptomic strategies to reveal adaptive mechanisms in castor plant during germination stage under alkali stress. **2022**, 105031 1
- 726 Differential expression and functional analysis of circRNA in the ovaries of Yili geese at different egg-laying stages.
- 725 Comprehensive analysis of RNA m6A methylation in pressure overload-induced cardiac hypertrophy. **2022**, 23,
- 724 Transcriptome sequencing reveals differences between leydig cells and sertoli cells of yak. 9,
- 723 satuRn: Scalable analysis of differential transcript usage for bulk and single-cell RNA-sequencing applications. 10, 374
- 722 Comprehensive analysis of differentially expressed profiles of mRNA, lncRNA, and miRNA of Yili geese ovary at different egg-laying stages. **2022**, 23, ○
- 721 The regulatory and transcriptional landscape associated with triterpenoid and lipid metabolisms by the bHLH-zip transcription factor SREBP in the medicinal fungus Ganoderma lingzhi. ○
- 720 The nearly complete assembly of Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. **2022**, 100422

7 ¹⁹	Comparison of de novo and reference genome-based transcriptome assembly pipelines for differential expression analysis of RNA sequencing data.	0
7 ¹⁸	DNA methylation affects freezing tolerance in winter rapeseed by mediating the expression of genes related to JA and CK pathways. 13,	
7 ¹⁷	Reduced Hypoxia Tolerance and Altered Gill Morphology at Elevated Temperatures May Limit the Survival of Tilapia (GIFT, <i>Oreochromis niloticus</i>) under Global Warming. 2022 , 7, 216	1
7 ¹⁶	NUCLEAR TRANSPORT FACTOR 2-LIKE improves drought tolerance by modulating leaf water loss in alfalfa (<i>Medicago sativa</i> L.).	1
7 ¹⁵	A reference-grade genome assembly for <i>Gossypium bickii</i> and insights into its genome evolution and formation of pigment gland and gossypol. 2022 , 100421	0
7 ¹⁴	Involvement of long non-coding RNAs in pear fruit senescence under high- and low-temperature conditions. 2022 ,	0
7 ¹³	Transcriptomic analysis reveals the defense mechanisms of citrus infested with <i>Diaphorina citri</i> . 2022 ,	0
7 ¹²	Hotspots of single-strand DNA Breakome are enriched at transcriptional start sites of genes. 9,	0
7 ¹¹	Identification of sex-biased and neurodevelopment genes via brain transcriptome in <i>Ostrinia furnacalis</i> . 13,	
7 ¹⁰	Functional Characterization of lncRNA152 as an Angiogenesis-Inhibiting Tumor Suppressor in Triple-Negative Breast Cancers.	1
7 ⁰⁹	Transcriptomes reveal the involved genes in the sea urchin <i>Mesocentrotus nudus</i> exposed to high flow velocities. 2022 , 12,	1
7 ⁰⁸	2 E ,4 E -Decadienoic Acid, a Novel Anti-Oomycete Agent from Coculture of <i>Bacillus subtilis</i> and <i>Trichoderma asperellum</i> .	0
7 ⁰⁷	Role of a ZF-HD Transcription Factor in miR157-Mediated Feed-Forward Regulatory Module That Determines Plant Architecture in <i>Arabidopsis</i> . 2022 , 23, 8665	
7 ⁰⁶	Improvement of S-adenosyl-L-methionine production in <i>Saccharomyces cerevisiae</i> by atmospheric and room temperature plasma-ultraviolet compound mutagenesis and droplet microfluidic adaptive evolution. 2022 , 12,	1
7 ⁰⁵	Advanced genes expression pattern greatly contributes to divergence in <i>Verticillium</i> wilt resistance between <i>Gossypium barbadense</i> and <i>Gossypium hirsutum</i> . 13,	
7 ⁰⁴	Aberrant RNA splicing of the phytic acid synthesis gene inositol-1,3,4 trisphosphate 5/6-kinase in a low phytic acid soybean line. 1-10	
7 ⁰³	Proliferation and Self-Renewal Are Differentially Sensitive to NRASG12V Oncogene Levels in an Acute Myeloid Leukemia Cell Line. OF1-OF13	0
7 ⁰²	A novel WRKY34-bZIP3 module regulates phenolic acid and tanshinone biosynthesis in <i>Salvia miltiorrhiza</i> . 2022 , 73, 182-191	1

701	Epigenomics of rats' liver and its cross-species functional annotation reveals key regulatory genes underlying short term heat-stress response. 2022 , 114, 110449	1
700	Rearrangement of T Cell genome architecture regulates GVHD. 2022 , 25, 104846	
699	Exogenous expression of barley HvWRKY6 in wheat improves broad-spectrum resistance to leaf rust, Fusarium crown rot, and sharp eyespot. 2022 , 218, 1002-1012	0
698	Regulation of myogenic gene expression. 2022 , 419, 113299	3
697	Identification of QTLs and candidate genes controlling berry size in table grape by integrating QTL and transcriptomic analysis. 2022 , 305, 111403	1
696	Transcriptional networks underlying a primary ovarian insufficiency disorder in alligators naturally exposed to EDCs. 2022 , 557, 111751	
695	Integrative analysis of transcriptomics and proteomics of longissimus thoracis of the Hu sheep compared with the Dorper sheep. 2022 , 193, 108930	0
694	Revealing the impacts on shaping scutate scales in goose skin. 2022 , 844, 146840	
693	New insights into vesicle granulation in <i>Citrus grandis</i> revealed by systematic analysis of sugar- and acid-related genes and metabolites. 2022 , 194, 112063	0
692	Hypoxia alters glucose and lipid metabolisms in golden pompano (<i>Trachinotus blochii</i>). 2023 , 562, 738747	
691	Hexane Extract of <i>Citrus sphaerocarpa</i> Suppresses the Accumulation of Lipid Droplets in 3T3-L1 Adipocytes. 2022 , 2, 1507-1516	0
690	Genome-wide identification and expression analysis of WRKY family genes under soft rot in Chinese cabbage. 13,	1
689	Pharmacogenomic landscape of head and neck squamous cell carcinoma informs precision oncology therapy. 2022 , 14,	0
688	Transcriptome Profiling of Different State Callus Induced from Immature Embryo in Maize. 2022 , 2022, 1-12	0
687	A Morbillivirus Infection Shifts DC Maturation Toward a Tolerogenic Phenotype to Suppress T Cell Activation.	0
686	Genome analysis of <i>Parmales</i> , a sister group of diatoms, reveals the evolutionary specialization of diatoms from phago-mixotrophs to photoautotrophs.	0
685	Comparison of two willow genotypes reveals potential roles of iron-regulated transporter 9 and heavy-metal ATPase 1 in cadmium accumulation and resistance in <i>Salix suchowensis</i> . 2022 , 244, 114065	0
684	Dufulin enhances salt resistance of rice. 2022 , 188, 105252	1

- 683 Comprehensive analysis of the lncRNAs, mRNAs, and miRNAs implicated in the immune response of *Pinctada fucata martensii* to *Vibrio parahaemolyticus*. **2022**, 130, 132-140 ○
- 682 The genetic adaptations of *Toxoptera aurantii* facilitated its rapid multiple plant hosts dispersal and invasion. **2022**, 114, 110472 ○
- 681 Comparative transcriptome reveals the effect of IFITM1 on differential resistance to duck hepatitis A virus genotype 3 in Pekin ducks. **2022**, 322, 198930 ○
- 680 Analysis of codon usage patterns in *Haloxylon ammodendron* based on genomic and transcriptomic data. **2022**, 845, 146842 ○
- 679 The pattern of DNA methylation alteration, and its association with the expression changes of non-coding RNAs and mRNAs in Moso bamboo under abiotic stress. **2022**, 325, 111451 1
- 678 Multi-omics reveals response mechanism of liver metabolism of hybrid sturgeon under ship noise stress. **2022**, 851, 158348 ○
- 677 RNA sequencing in parthenocarpic chili pepper (*Capsicum annuum*) fruit reveals genes involved in transcriptional regulation of capsaicinoid biosynthesis genes responsible for the fluctuation of pungency. **2022**, 306, 111456 ○
- 676 Techniques for Analyzing Genome-wide Expression of Non-coding RNA. **2023**, 163-184 ○
- 675 Circulating exosomal lncRNA contributes to the pathogenesis of spinal cord injury in rats. **2023**, 18, 889 ○
- 674 Metagenomics analysis of antibiotic resistance genes, the bacterial community and virulence factor genes of fouled filters and effluents from household water purifiers in drinking water. **2023**, 854, 158572 ○
- 673 Dufulin Upregulates Integral Membrane Protein Duf6 to Enhance Salt Resistance of Rice. ○
- 672 Cotton Microtubule-Associated Protein Ghmap2015 Mediates Fiber Elongation Through the Interaction with the Tubulin Ghtub13. ○
- 671 Small RNA-omics: Decoding the regulatory networks associated with horticultural traits. **2022**, 15-25 ○
- 670 Multiple time-series expression trajectories imply dynamic functional changes during cellular senescence. **2022**, 20, 4131-4137 ○
- 669 Integrated RNA-seq and RNAi Analysis of the Roles of the Hsp70 and SP Genes in Red-Shell *Meretrix meretrix* Tolerance to the Pathogen *Vibrio parahaemolyticus*. ○
- 668 Sequential And Directional Insulation By Conserved CTCF Sites Underlies The Hox Timer In Pseudo-Embryos. 1
- 667 TFAM Deficiency-Mediated Mitochondrial Disorder Affects Langerhans Cell Maintenance and Function. **2022**, ○
- 666 R2R3-MYB transcription factor GEMMA CUP-ASSOCIATED MYB1 mediates the cytokinin signal to achieve proper organ development in *Marchantia polymorpha*. ○

- 665 Transcriptomic signatures responding to PKM2 activator TEPP-46 in the hyperglycemic human renal proximal epithelial tubular cells. 13, ○
- 664 Identification of Novel Multi-Omics Expression Landscapes and Meta-Analysis of Landscape-Based Competitive Endogenous RNA Networks in ALDH+ Lung Adenocarcinoma Stem Cells. **2022**, 2022, 1-20 ○
- 663 Location and Identification on Chromosome 3B of Bread Wheat of Genes Affecting Chiasma Number. **2022**, 11, 2281 ○
- 662 Transcriptomic Analysis Reveals the Correlation between End-of-Day Far Red Light and Chilling Stress in *Setaria viridis*. **2022**, 13, 1565 ○
- 661 RNA-sequencing analysis of the Diquat-degrading yeast strain *Meyerozyma guilliermondii* Wyslmt and the discovery of Diquat degrading genes. 13, ○
- 660 Analysis of controlling genes for tiller growth of *Psathyrostachys juncea* based on transcriptome sequencing technology. **2022**, 22, ○
- 659 Effects of Low Temperature on Antioxidant and Heat Shock Protein Expression Profiles and Transcriptomic Responses in Crayfish (*Cherax destructor*). **2022**, 11, 1779 ○
- 658 Adaptive biomineralization in two morphotypes of Sternaspidae (Annelida) from the Northern China Seas. 9, ○
- 657 Investigation of chicken housekeeping genes using next-generation sequencing data. 13, ○
- 656 Runx2 regulates chromatin accessibility to direct the osteoblast program at neonatal stages. **2022**, 40, 111315 1
- 655 Comparative RNA-seq analysis reveals a critical role for ethylene in rose (*Rosa hybrida*) susceptible response to *Podosphaera pannosa*. 13, ○
- 654 Identification of stable housekeeping genes for induced pluripotent stem cells and -derived endothelial cells for drug testing. **2022**, 12, ○
- 653 Identification and function analysis of yellow-leaf mutant (YX-yl) of broomcorn millet. **2022**, 22, 1
- 652 Characterization of multitype colonies originating from porcine blastocysts produced in vitro. 10, ○
- 651 Comprehensive Analysis of Cuproptosis-related genes in prognosis, tumor microenvironment infiltration, and Immunotherapy response in gastric cancer. ○
- 650 DNA 6mA Demethylase ALKBH1 Orchestrates Fatty Acid Metabolism and Suppresses Diet-Induced Hepatic Steatosis. **2022**, ○
- 649 Genomics and epigenetics guided identification of tissue-specific genomic safe harbors. **2022**, 23, ○
- 648 Changes of the gene expression in silkworm larvae and *Cordyceps militaris* at late stages of the pathogenesis. ○

- 647 Immune Isoform Atlas: Landscape of alternative splicing in human immune cells. ○
- 646 Integrated multi-omics analysis and microbial recombinant protein system reveal hydroxylation and glycosylation involving nevadensin biosynthesis in *Lysionotus pauciflorus*. **2022**, 21, ○
- 645 Transcriptomic profiling of cotton leaves in response to cotton aphid damage. **2022**, 44, ○
- 644 Transcriptional sequencing analysis reveals the potential use of deer antler for bonifying the kidney and strengthening bone **2022**, 17, ○
- 643 Integrated analysis of transcriptome and metabolome reveals molecular mechanisms of salt tolerance in seedlings of upland rice landrace 17SM-19. 13, ○
- 642 Comparative transcriptome analysis of *Saposhnikovia divaricata* to reveal drought and rehydration adaption strategies. ○
- 641 Transcriptome characterization and profiling related to detoxification enzyme genes in *Chilo sacchariphagus* (Lepidoptera Crambidae). **2022**, 52, 404-427 ○
- 640 Transcriptome Analysis Revealed Hormone Pathways and bZIP Genes Responsive to Decapitation in Sunflower. **2022**, 13, 1737 ○
- 639 In Vitro Gene Expression Responses of Bovine Rumen Epithelial Cells to Different pH Stresses. **2022**, 12, 2621 ○
- 638 RNA sequencing and weighted gene co-expression network analysis uncover the hub genes controlling cold tolerance in *Helictotrichon virescens* seedlings. 13, ○
- 637 Single-cell RNA sequencing reveals dysregulation of spinal cord cell types in a severe spinal muscular atrophy mouse model. **2022**, 18, e1010392 ○
- 636 Transcriptome dynamics uncovers long non-coding RNAs response to salinity stress in *Chenopodium quinoa*. 13, ○
- 635 Bioinformatics study of expression from genomes of epidemiologically related MRSA CC398 isolates from human and wild animal samples. **2022**, 268, 104714 ○
- 634 Transcriptome reveals the candidate gene regulating leaf senescence induced by nitrogen deficiency. **2022**, 153822 1
- 633 Analysis of *Camellia oleifera* transcriptome reveals key pathways and hub genes involved during different photoperiods. **2022**, 22, ○
- 632 Comparative analysis of growth, physiological and transcriptomic response revealed mechanisms of waterlogging tolerance of hot pepper (*Capsicum annuum* var. *conoides*). ○
- 631 Smed-ETS-1 regulates cathepsin+ cell function and epidermal lineage landscape via basement membrane remodeling. ○
- 630 Combined physiological and transcriptome analysis revealed the response mechanism of *Pogostemon cablin* roots to p-hydroxybenzoic acid. 13, ○

- 629 On taming the effect of transcript level intra-condition count variation during differential expression analysis: A story of dogs, foxes and wolves. **2022**, 17, e0274591 ○
- 628 Comprehensive and scalable quantification of splicing differences with MntJULiP. **2022**, 23, ○
- 627 The function of a conidia specific transcription factor CsgA in *Aspergillus nidulans*. **2022**, 12, 1
- 626 Yeast NDI1 reconfigures neuronal metabolism and prevents the unfolded protein response in mitochondrial complex I deficiency. ○
- 625 Age-Associated Different Transcriptome Profiling in Zebrafish and Rats: an Insight into the Diversity of Vertebrate Aging. ○
- 624 Fluorous-Tagged Peptide Nanoparticles Ameliorate Acute Lung Injury via Lysosomal Stabilization and Inflammation Inhibition in Pulmonary Macrophages. **2022**, 18, 2203432 ○
- 623 Integrative metabolome and transcriptome analyses reveal the molecular mechanism underlying variation in floral scent during flower development of *Chrysanthemum indicum* var. aromaticum. 13, ○
- 622 RNA sequencing reveals lncRNA-mediated non-mendelian inheritance of feather growth change in chickens. ○
- 621 Changes in Transcriptome-Associated Co-Expression Profile of Embryonic External Ear Development After Prkra Gene Mutation. Publish Ahead of Print, ○
- 620 Single-nucleus RNA-seq reveals that MBD5, MBD6, and SILENZIO maintain silencing during epigenetic reprogramming in pollen. ○
- 619 Identification and Analysis of MADS-box, WRKY, NAC, and SBP-box Transcription Factor Families in *Diospyros oleifera* Cheng and Their Associations with Sex Differentiation. **2022**, 12, 2100 ○
- 618 Metabolome and Transcriptome Profiling Reveal Carbon Metabolic Flux Changes in *Yarrowia lipolytica* Cells to Rapamycin. **2022**, 8, 939 ○
- 617 Geographically Associated Fungus-Bacterium Interactions Contribute to the Formation of Geography-Dependent Flavor during High-Complexity Spontaneous Fermentation. 2
- 616 Sequence Data, Functional Annotation, and Relationship Analysis Between mRNAs and Long Noncoding RNAs from Tea Leaves During Infection by the Fungal Pathogen *Epicoccum sorghinum*. **2022**, 35, 875-879 ○
- 615 Outcomes of Low-Temperature Stress on Biological Alterations within Pothos (*Epipremnum aureum*) Leaves. **2022**, 12, 1432 ○
- 614 Effects of Drought and Host on the Growth of *Santalum album* Seedlings in Pot Culture. **2022**, 23, 11241 ○
- 613 Identification of four immune subtypes in locally advanced rectal cancer treated with neoadjuvant chemotherapy for predicting the efficacy of subsequent immune checkpoint blockade. 13, ○
- 612 Truncated CSF3 receptors induce pro-inflammatory responses in severe congenital neutropenia. ○

- 611 Histone H1 regulates non-coding RNA turnover on chromatin in a m6A-dependent manner. **2022**, 40, 111329 0
- 610 High-quality reference transcriptome construction improves RNA-seq quantification in *Oryza sativa indica*. 13, 0
- 609 Molecular Hydrogen Reduces Electromagnetic Pulse-Induced Male Rat Reproductive System Damage in a Rodent Model. **2022**, 2022, 1-23 0
- 608 Combined \square whole blood and skin fibroblasts- transcriptomic analysis in Psoriatic Arthritis reveals molecular signatures of activity, resistance and early response to treatment. 13, 0
- 607 Analysis of lncRNA in the skeletal muscle of rabbits at different developmental stages. 9, 0
- 606 A HST1 -like gene controlled tiller angle through regulating endogenous auxin in common wheat. 1
- 605 Identification of genes controlling compatible and incompatible reactions of pearl millet (*Pennisetum glaucum*) against blast (*Magnaporthe grisea*) pathogen through RNA-Seq. 13, 0
- 604 Functional Identification of *Arthrinium phaeospermum* Effectors Related to *Bambusa pervariabilis* \square *Dendrocalamopsis grandis* Shoot Blight. **2022**, 12, 1264 1
- 603 A family of unusual immunoglobulin superfamily genes in an invertebrate histocompatibility complex. **2022**, 119, 0
- 602 Comparative Expression Profile of Genes Encoding Intolerant Proteins in Bread vs. Durum Wheat During Grain Development. 0
- 601 Characterization of differentially expressed and lipid metabolism-related lncRNA-mRNA interaction networks during the growth of liver tissue through rabbit models. 9, 0
- 600 Temperature-sensitive male sterility in rice determined by the roles of AGO1d in reproductive phasiRNA biogenesis and function. 0
- 599 Survival of *Campylobacter jejuni* 11168H in *Acanthamoebae castellanii* Provides Mechanistic Insight into Host Pathogen Interactions. **2022**, 10, 1894 0
- 598 Polyadenylate-binding protein cytoplasmic 1 mediates alternative splicing events of immune-related genes in gastric cancer cells. 153537022211216 0
- 597 Analysis of the abomasal transcriptome of LDA affected cattle. 0
- 596 m1A and m6A modifications function cooperatively to facilitate rapid mRNA degradation. **2022**, 40, 111317 2
- 595 Characterization of the In Vitro Cultured Ovarian Cells in the Asian Yellow Pond Turtle (*Mauremys mutica*). **2022**, 11, 1404 0
- 594 A chronic signaling TGF β zebrafish reporter identifies immune response in melanoma. 0

593	Non-photoperiodic transition of female cannabis seedlings from juvenile to adult reproductive stage.	2
592	Matrix stiffness-induced transcriptome alterations and regulatory mechanisms revealed by RNA-seq in Endothelial cells.	0
591	Bmp5 Mutation Alters mRNA Expression During External Ear Development. Publish Ahead of Print,	0
590	Hedgehog signaling activates a mammalian heterochronic gene regulatory network controlling differentiation timing across lineages. 2022 , 57, 2181-2203.e9	0
589	Identification and characterization of candidate detoxification genes in <i>Pharsalia antennata</i> Gahan (Coleoptera: Cerambycidae). 13,	0
588	Characterization of lncRNA/circRNA-miRNA-mRNA network to reveal potential functional ceRNAs in the skeletal muscle of chicken. 13,	0
587	Establishment of a five-enzalutamide-resistance-related-gene-based classifier for recurrence-free survival predicting of prostate cancer.	0
586	Transcriptomic and iTRAQ-Based Quantitative Proteomic Analyses of inap CMS in <i>Brassica napus</i> L.. 2022 , 11, 2460	0
585	<i>Colletotrichum siamense</i> infection caused transcripts involved plant hormone signal transduction and phenylpropanoid biosynthesis varied in strawberry. 2022 , 50, 12791	0
584	Transcriptomic analysis of uterine receptivity in Guinea pigs. 2022 ,	0
583	Integrated Analysis of Transcriptome and Metabolome Reveals Distinct Responses of <i>Pelteobagrus fulvidraco</i> against <i>Aeromonas veronii</i> Infection at Invaded and Recovering Stage. 2022 , 23, 10121	0
582	Genomic Analysis of LEA Genes in <i>Carica papaya</i> and Insight into Lineage-Specific Family Evolution in Brassicales. 2022 , 12, 1453	1
581	DDX17 modulates the expression and alternative splicing of genes involved in apoptosis and proliferation in lung adenocarcinoma cells. 10, e13895	0
580	Expression profile of long non-coding RNA in inner Mongolian cashmere goat with putative roles in hair follicles development. 9,	0
579	Physiological and Molecular Characteristics of Southern Leaf Blight Resistance in Sweet Corn Inbred Lines. 2022 , 23, 10236	0
578	Genomic insights into the evolutionary history and diversification of bulb traits in garlic. 2022 , 23,	0
577	Integrated transcriptomics and metabolomics analysis of the hippocampus reveals altered neuroinflammation, downregulated metabolism and synapse in sepsis-associated encephalopathy. 13,	0
576	Characterization of lncRNAs in mycorrhizal tomato and elucidation of the role of lncRNA69908 in disease resistance. 2022 ,	0

575	Favine/CCDC3 deficiency accelerated atherosclerosis and thrombus formation is associated with decreased MEF2C-KLF2 pathway.. 2022 , 105252	0
574	JGI Plant Gene Atlas: An updateable transcriptome resource to improve structural annotations and functional gene descriptions across the plant kingdom.	0
573	Changes in the Transcriptome-Associated Co-Expression Profile of Embryonic External Ear Development After the BMP5 Gene Mutation. Publish Ahead of Print,	0
572	Translatome and transcriptome co-profiling reveals a role of TPRXs in human zygotic genome activation. 2022 , 378,	2
571	The global Protein-RNA interaction map of ESRP1 defines a post-transcriptional program that is essential for epithelial cell function. 2022 , 25, 105205	0
570	SERBP1 affects the apoptotic level by regulating the expression and alternative splicing of cellular and metabolic process genes in HeLa cells. 10, e14084	0
569	Biochemical and transcriptome analysis reveals pigment biosynthesis influenced chlorina leaf formation in <i>Anoectochilus roxburghii</i> (Wall.) Lindl.	0
568	Transcriptional changes in <i>Plasmodium falciparum</i> upon conditional knock down of mitochondrial ribosomal proteins RSM22 and L23. 2022 , 17, e0274993	0
567	KLF15 controls brown adipose tissue transcriptional flexibility and metabolism in response to various energetic demands. 2022 , 105292	0
566	Loss of endothelial EMCN drives tumor lung metastasis through the premetastatic niche. 2022 , 20,	0
565	Comparative genomics of <i>Sarcoptes scabiei</i> provide new insights into adaptation to permanent parasitism and within-host species divergence.	1
564	Transcriptomic insights into the molecular mechanism of wheat response to stripe rust fungus. 2022 , e10951	0
563	Transcriptomic and proteomic mechanisms underlying cold tolerance in plants. 66, 240-254	0
562	Transcriptome analysis and mining of genes related to shade tolerance in foxtail millet (<i>Setaria italica</i> (L.) P. Beauv.). 2022 , 9,	1
561	Bone marrow stromal cell antigen-1 (CD157) regulated by sphingosine kinase 2 mediates kidney fibrosis. 9,	0
560	Comparative analysis of two kinds of garlic seedings: qualities and transcriptional landscape.	0
559	Integrative analysis of transcriptomic and volatile compound profiles sheds new insights into the terpenoid biosynthesis in tree peony. 2022 , 188, 115672	0
558	Transcriptome analysis identifies TODL as a novel lncRNA associated with proliferation, differentiation, and tumorigenesis in liposarcoma through FOXM1. 2022 , 185, 106462	0

557	Systematic identification and characterization of lncRNAs and lncRNA-miRNA-mRNA networks in the liver of turbot (<i>Scophthalmus maximus</i> L.) induced with <i>Vibrio anguillarum</i> . 2022 , 131, 21-29	1
556	RNA Sequencing Reveals the Potential Adaptation Mechanism to Different Hosts of <i>Grapholita molesta</i> . 2022 , 13, 893	0
555	Transcriptomic-Metabolomic Profiling in Mouse Lung Tissues Reveals Sex- and Strain-Based Differences. 2022 , 12, 932	0
554	Developmental Potency and Metabolic Traits of Extended Pluripotency Are Faithfully Transferred to Somatic Cells via Cell Fusion-Induced Reprogramming. 2022 , 11, 3266	0
553	F1 Male Sterility in Cattle-Yak Examined through Changes in Testis Tissue and Transcriptome Profiles. 2022 , 12, 2711	1
552	Microglial debris is cleared by astrocytes via C4b-facilitated phagocytosis and degraded via RUBICON-dependent noncanonical autophagy in mice. 2022 , 13,	1
551	An integrative approach to assessing effects of a short-term Western diet on gene expression in rat liver. 13,	0
550	Transcriptome Analysis of <i>Kyoho</i> Grapevine Leaves Identifies Heat Response Genes Involved in the Transcriptional Regulation of Photosynthesis and Abscisic Acid. 2022 , 12, 2591	1
549	Lineage-selective super enhancers mediate core regulatory circuitry during adipogenic and osteogenic differentiation of human mesenchymal stem cells. 2022 , 13,	1
548	Long noncoding RNA IRF1-AS is associated with peste des petits ruminants infection. 2022 , 53,	0
547	Transcriptome analysis identifies novel gene(s) and pathways for salt stress responses in Dandi cultivar.	0
546	Weighted gene co-expression network analysis reveals key module and hub genes associated with the anthocyanin biosynthesis in maize pericarp. 13,	0
545	MINI-EX: Integrative inference of single-cell gene regulatory networks in plants. 2022 ,	0
544	Molecular phenotyping of malignant canine mammary tumours: Detection of high-risk group and its relationship with clinicomolecular characteristics.	0
543	Genome-wide identification and expression analysis of BrAGC genes in <i>Brassica rapa</i> reveal their potential roles in sexual reproduction and abiotic stress tolerance. 13,	0
542	hENT1 expression predicts response to gemcitabine and nab-paclitaxel in advanced pancreatic ductal adenocarcinoma (PDAC).	1
541	The m6A reader IGF2BP2 regulates glutamine metabolism and represents a therapeutic target in acute myeloid leukemia. 2022 ,	0
540	PNPO-PLP Axis Senses Prolonged Hypoxia by Regulating Lysosomal Activity.	0

539	Miniature inverted-repeat transposable elements drive rapid microRNA diversification in angiosperms.	1
538	Integrated Transcriptome and Metabolome Analysis of Color Change and Low-Temperature Response during Flowering of <i>Prunus mume</i> . 2022 , 23, 12831	0
537	Population genomics of an icefish reveals mechanisms of glacier-driven adaptive radiation in Antarctic notothenioids. 2022 , 20,	1
536	Molecular Biology, Genetics, and Translational Models of Human Cancer. 1-34	0
535	Genetic identification of SNP markers and candidate genes associated with sugarcane smut resistance using BSR-Seq. 13,	0
534	Flnc: Machine Learning Improves the Identification of Novel Long Noncoding RNAs From Stand-Alone RNA-Seq Data. 2022 , 8, 70	0
533	Irreversible Electroporation Mediates Glioma Apoptosis via Upregulation of AP-1 and Bim: Transcriptome Evidence. 2022 , 12, 1465	0
532	One novel ACOT7- <i>PHP4</i> fusion gene identified in one patient with acute lymphoblastic leukemia: a case report. 2022 , 15,	0
531	HBEGF-TNF induce a complex outer retinal pathology with photoreceptor cell extrusion in human organoids. 2022 , 13,	0
530	Transcriptomic analysis of succulent stem development of Chinese kale (<i>Brassica oleracea</i> var. <i>alboglabra</i> Bailey) and its synthetic allotetraploid via RNA sequencing. 13,	0
529	Efficient Minimum Flow Decomposition via Integer Linear Programming.	0
528	Improving RNA Assembly via Safety and Completeness in Flow Decompositions.	0
527	Effects of Sub-Minimum Inhibitory Concentrations of Imipenem and Colistin on Expression of Biofilm-Specific Antibiotic Resistance and Virulence Genes in <i>Acinetobacter baumannii</i> Sequence Type 1894. 2022 , 23, 12705	2
526	Diploid Chromosome-level Reference Genome and Population Genomic Analyses Provide Insights into Gypenoside Biosynthesis and Demographic Evolution of <i>Gynostemma pentaphyllum</i> (Cucurbitaceae).	0
525	Identification of Key Genes Involved in Resistance to Early Stage of BmNPV Infection in Silkworms. 2022 , 14, 2405	0
524	A full-length transcriptome and gene expression analysis of three detoxification gene families in a predatory stink bug, <i>Picromerus lewisi</i> . 13,	0
523	Genome-wide chromatin accessibility analysis unveils open chromatin convergent evolution during polyploidization in cotton. 2022 , 119,	1
522	Characterization of Abscisic Acid and Ethylene in Regulating the White Blush in Fresh-Cut Carrots. 2022 , 23, 12788	1

521	Identification of Candidate Genes and Regulatory Competitive Endogenous RNA (ceRNA) Networks Underlying Intramuscular Fat Content in Yorkshire Pigs with Extreme Fat Deposition Phenotypes. 2022 , 23, 12596	1
520	miRNA profiling of developing rat retina in the first three postnatal weeks.	0
519	Genome-wide analysis of MADS-box families and their expressions in flower organs development of pineapple (<i>Ananas comosus</i> (L.) Merr.). 13,	1
518	Response of Ruminal Microbiota Host Gene Interaction to High-Altitude Environments in Tibetan Sheep. 2022 , 23, 12430	0
517	A novel promising diagnostic candidate selected by screening the transcriptome of <i>Babesia gibsoni</i> (Wuhan isolate) asexual stages in infected beagles. 2022 , 15,	0
516	Lateral confined growth of cells activates Lef1 dependent pathways to regulate cell-state transitions. 2022 , 12,	0
515	Loss of NECTIN1 triggers melanoma dissemination upon local IGF1 depletion.	0
514	Oviduct Transcriptomic Reveals the Regulation of mRNAs and lncRNAs Related to Goat Prolificacy in the Luteal Phase. 2022 , 12, 2823	0
513	A web-based database server using 43,710 public RNA-seq samples for the analysis of gene expression and alternative splicing in livestock animals. 2022 , 23,	0
512	Transcriptome profile reveals novel candidate genes associated with bone strength in end-of-lay hens. 1-9	0
511	HIF-3 β -Induced miR-630 Expression Promotes Cancer Hallmarks in Cervical Cancer Cells by Forming a Positive Feedback Loop. 2022 , 2022, 1-19	0
510	Identification of long non-coding RNA-microRNA-mRNA regulatory modules and their potential roles in drought stress response in wheat (<i>Triticum aestivum</i> L.). 13,	0
509	Multi-Organ Transcriptome Response of Lumpfish (<i>Cyclopterus lumpus</i>) to <i>Aeromonas salmonicida</i> Subspecies <i>salmonicida</i> Systemic Infection. 2022 , 10, 2113	1
508	Identification of genes related to sexual differentiation and sterility in embryonic gonads of Mule ducks by transcriptome analysis. 13,	0
507	An in vivo avian model of human melanoma to perform rapid and robust preclinical studies.	0
506	Differentially Expressed mRNAs and Potential Mechanisms of Radiation-Induced T ₄ Esophageal Cell Injury. 2022 , 20, 155932582211368	0
505	Tumor-produced and aging-associated oncometabolite methylmalonic acid promotes cancer-associated fibroblast activation to drive metastatic progression. 2022 , 13,	0
504	The Effect of Knocked-Down Anti-Müllerian Hormone mRNA on Reproductive Characters of Male Nile Tilapia (<i>Oreochromis niloticus</i>) through Inhibition of the TGF- β Signaling Pathway. 2022 , 7, 299	2

- 503 Gut Microbiota and Transcriptome Analysis Reveals a Genetic Component to Dropping Moisture in Chickens. **2022**, 102242 ○
- 502 Arctic introgression and chromatin regulation facilitated rapid Qinghai-Tibet Plateau colonization by an avian predator. **2022**, 13, ○
- 501 UV-ARTP-DES compound mutagenesis breeding improves natamycin production of *Streptomyces natalensis* HW-2 and reveals transcriptional changes by RNA-seq. ○
- 500 Effect of Heat Starvation Stress on Physiological Immunity and Metabolism of *Mizuhopecten yessoensis*. **2022**, 14, 13217 ○
- 499 PIM3 kinase promotes tumor metastasis in hepatoblastoma by upregulating cell surface expression of chemokine receptor *cxcr4*. ○
- 498 Combined analysis of transcriptome and metabolome reveals the molecular mechanism and candidate genes of *Haloxylon* drought tolerance. 13, ○
- 497 Anthranilic acid accumulation in *Saccharomyces cerevisiae* induced by expression of a nonribosomal peptide synthetase gene from *Paecilomyces cinnamomeus* BCC 9616. ○
- 496 Integrated analysis of the whole transcriptome of skeletal muscle reveals the ceRNA regulatory network related to the formation of muscle fibers in Tan sheep. 13, ○
- 495 Monochloramine Induces Release of DNA and RNA from Bacterial Cells: Quantification, Sequencing Analyses, and Implications. ○
- 494 Alternative splicing reprogramming in fungal pathogen *Sclerotinia sclerotiorum* at different infection stages on *Brassica napus*. 13, ○
- 493 Molecular cloning and functional analysis of Chinese bayberry *MrSPL4* that enhances growth and flowering in transgenic tobacco. ○
- 492 Integration of transcriptome and metabolome analyses reveals key lodging-resistance-related genes and metabolic pathways in maize. 13, 1
- 491 Artificial optimization of bamboo *Ppmar2* transposase and host factors effects on *Ppmar2* transposition in yeast. 13, ○
- 490 Physiological and Transcriptional Analysis Reveals the Response Mechanism of *Camellia vietnamensis* Huang to Drought Stress. **2022**, 23, 11801 ○
- 489 Protein Kinase *RhCIPK6* Promotes Petal Senescence in Response to Ethylene in Rose (*Rosa Hybrida*). **2022**, 13, 1989 ○
- 488 Biochemical and Molecular Analysis of Field Resistance to Spirodiclofen in *Panonychus citri* (McGregor). **2022**, 13, 1011 ○
- 487 Identification of HLA class I-restricted immunogenic neoantigens in triple negative breast cancer. 13, ○
- 486 Combined transcriptome and metabolome analysis reveals the effects of light quality on maize hybrids. ○

- 485 RSV-induced Expanded Ciliated Cells Contribute to Bronchial Wall Thickening. ○
- 484 Transcription factor NtWRKY33a modulates the biosynthesis of polyphenols by targeting NtMYB4 and NtHCT genes in tobacco. **2022**, 111522 ○
- 483 Activin A promotes human trophoblast invasion by upregulating integrin β via ALK4-SMAD4 signaling. **2022**, 129, 62-69 ○
- 482 Identification of long non-coding RNA using single nucleotide epimutation analysis: a novel gene discovery approach. **2022**, 22, ○
- 481 Identification of sex-specific splicing via comparative transcriptome analysis of gonads from sea cucumber *Apostichopus japonicus*. **2022**, 101031 ○
- 480 De novo genome assembly and annotation of gall-forming medicinal plant *Pistacia chinensis* subsp. *integerrima* (J. L. Stewart ex Brandis) Rech. f.. **2022**, 101, ○
- 479 Whole genome sequencing of the fast-swimming Southern bluefin tuna (*Thunnus maccoyii*). 13, ○
- 478 Multiple tissue-specific epigenetic alterations regulate persistent gene expression changes following developmental DES exposure in mouse reproductive tissues. 1-21 2
- 477 Comparative transcriptome analysis of resistant and susceptible Kentucky bluegrass varieties in response to powdery mildew infection. **2022**, 22, ○
- 476 The expression of apoptosis related genes in HK-2 cells overexpressing PPM1K was determined by RNA-seq analysis. 13, ○
- 475 Multi-omics profiling reveals potential mechanisms of culture temperature modulating biosynthesis of carotenoids, lipids, and exopolysaccharides in oleaginous red yeast *Rhodotorula glutinis* ZHK. **2022**, 171, 114103 ○
- 474 Transcriptome analysis provides novel insights into the immune mechanisms of *Macrobrachium nipponense* during molting. **2022**, 131, 454-469 1
- 473 Watermelon responds to organic fertilizer by enhancing root-associated acid phosphatase activity to improve organic phosphorus utilization. **2022**, 279, 153838 ○
- 472 GATA6 regulates expression of annexin A10 (ANXA10) associated with epithelial-mesenchymal transition of oral squamous cell carcinoma. **2022**, 144, 105569 ○
- 471 Transcriptional analyses provide novel insights into the transgenerational effects of Poly (I:C) on chickens. **2022**, 247, 114216 ○
- 470 An integrative analysis of lncRNAs and mRNAs highlights the potential roles of lncRNAs in the process of follicle selection in Taihang chickens. **2023**, 195, 122-130 ○
- 469 Recent advances in transcriptomic biomarker detection for cancer. **2023**, 453-478 ○
- 468 Full-length transcriptome sequencing provides insights into flavonoid biosynthesis in *Camellia nitidissima* Petals. **2023**, 850, 146924 ○

- 467 Human transcriptome profiling: applications in health and disease. **2023**, 373-395 ○
- 466 Characterization of a new chlorimuron-ethyl-degrading strain *Cedecea* sp. LAM2020 and biodegradation pathway revealed by multiomics analysis. **2023**, 443, 130197 ○
- 465 Integrative metabolome and transcriptome analyses reveals the black fruit coloring mechanism of *Crataegus maximowiczii* C. K. Schneid. **2023**, 194, 111-121 ○
- 464 Prostate cancer resistance leads to a global deregulation of translation factors and unconventional translation. **2022**, 4, ○
- 463 Teaching Computational Genomics and Bioinformatics on a High Performance Computing Cluster - A Primer. ○
- 462 Increased chromatin accessibility facilitates intron retention in specific cell differentiation states. ○
- 461 Potential value of differentially expressed circular RNAs derived from circulating exosomes in the pathogenesis of rat spinal cord injury. 16, ○
- 460 Comparing adventitious root-formation and graft-unification abilities in clones of *Argania spinosa*. 13, ○
- 459 FINDEL: A Deep Learning Approach to Efficient Artifact Removal From Cancer Genomes. ○
- 458 Longer Duration of Active Oil Biosynthesis during Seed Development Is Crucial for High Oil Yield Lessons from Genome-Wide In Silico Mining and RNA-Seq Validation in Sesame. **2022**, 11, 2980 ○
- 457 Whole-genome assembly and annotation for the little yellow croaker (*Larimichthys polyactis*) provide insights into the evolution of hermaphroditism and gonochorism. ○
- 456 Transcriptome Analysis Reveals a Comprehensive Virus Resistance Response Mechanism in Pecan Infected by a Novel Badnavirus Pecan Virus. **2022**, 23, 13576 ○
- 455 Two newly-identified biological nitrification inhibitors in *Suaeda salsa*: synthetic pathways and influencing mechanisms. **2022**, 140172 ○
- 454 Transcriptome analysis of response strategy in *Hemerocallis fulva* under drought stress. ○
- 453 The dynamic changes of genes revealed that persistently overexpressed genes drive the evolution of cyflumetofen resistance in *Tetranychus cinnabarinus*. ○
- 452 A splicing site mutation in *FvePHP* gene is associated with leaf development and flowering time in woodland strawberry. ○
- 451 The grape powdery mildew resistance loci *Ren2*, *Ren3*, *Ren4D*, *Ren4U*, *Run1*, *Run1.2b*, *Run2.1*, and *Run2.2* activate different transcriptional responses to *Erysiphe necator*. ○
- 450 Comparative transcriptome sequencing analysis of female and male *Decapterus macrosoma*. 10, e14342 ○

- 449 Transcriptomic analysis supports a role for the nervous system in regulating growth and development of *Fasciola hepatica* juveniles. **2022**, 16, e0010854 ○
- 448 Genome-Wide Identification and Expression Analysis of the NAC Gene Family in *Kandelia obovata*, a Typical Mangrove Plant. **2022**, 44, 5622-5637 ○
- 447 Genome-wide transcriptome profiling revealed biological macromolecules respond to low temperature stress in *Brassica napus* L. 13, ○
- 446 Responses of transcriptome and metabolome in the roots of *Pugionium cornutum* (L.) Gaertn to exogenously applied phthalic acid. **2022**, 22, ○
- 445 Integrated Genomic and Transcriptomic Elucidation of Flowering in Garlic. **2022**, 23, 13876 ○
- 444 METTL14 is required for exercise-induced cardiac hypertrophy and protects against myocardial ischemia-reperfusion injury. **2022**, 13, ○
- 443 Genome-wide identification, organization, and expression profiles of the chicken fibroblast growth factor genes in public databases and Vietnamese indigenous Ri chickens against highly pathogenic avian influenza H5N1 virus infection. ○
- 442 Transcriptome analysis of *Citrus limon* infected with Citrus yellow vein clearing virus. ○
- 441 Transcription Factor VdCf2 Regulates Growth, Pathogenicity, and the Expression of a Putative Secondary Metabolism Gene Cluster in *Verticillium dahliae*. 1
- 440 Prostaglandin E2 receptor Ptger4b regulates female-specific peptidergic neurons and female sexual receptivity in medaka. **2022**, 5, 1
- 439 Differentially expressed long noncoding RNAs and mRNAs in PC12 cells under lysophosphatidylcholine stimulation. **2022**, 12, ○
- 438 Multi-omics analysis of the mechanisms behind flavonoid differences between purple and green tender shoots of *Camellia sinensis* var. *assamica*. ○
- 437 Chromosome-level genome and population genomics reveal evolutionary characteristics and conservation status of Chinese indigenous geese. **2022**, 5, 1
- 436 Transcriptional and biochemical analyses of *Planomicrobium* strain AX6 from Qinghai-Tibetan Plateau, China, reveal hydrogen peroxide scavenging potential. **2022**, 22, ○
- 435 DNA replication initiation shapes the mutational landscape and expression of the human genome. **2022**, 8, 1
- 434 Exogenous 24-epibrassinolide boosts plant growth under alkaline stress from physiological and transcriptomic perspectives: The case of broomcorn millet (*Panicum miliaceum* L.). **2022**, 248, 114298 ○
- 433 Revealing the Regulatory Mechanism of lncRNA-LMEP on Melanin Deposition Based on High-Throughput Sequencing in Xichuan Chicken Skin. **2022**, 13, 2143 ○
- 432 Low Temperature Inhibits the Defoliation Efficiency of Thidiazuron in Cotton by Regulating Plant Hormone Synthesis and the Signaling Pathway. **2022**, 23, 14208 1

- 431 Bioinformatics for Saffron-Omics and Crop Improvement. **2022**, 63-82 ○
- 430 Transcriptome sequencing reveals the effect of selenium nanoparticles on primary hepatocytes of rainbow trout. **2023**, 114, 109503 ○
- 429 Distinguish the toxic differentiations between acute exposure of micro- and nano-plastics on bivalves: An integrated study based on transcriptomic sequencing. **2023**, 254, 106367 ○
- 428 *Riemerella anatipestifer* GldG is necessary for secretion of effectors by type IX secretion system. **2023**, 276, 109628 ○
- 427 Temporal progress of gene expression analysis with RNA-Seq data: A review on the relationship between computational methods. **2023**, 21, 86-98 ○
- 426 Recent advances in machine learning applications in metabolic engineering. **2023**, 62, 108069 1
- 425 Integrated biochemical, transcriptomic and metabolomic analyses provide insight into heat stress response in Yangtze sturgeon (*Acipenser dabryanus*). **2023**, 249, 114366 ○
- 424 Transcriptomic insights into the effects of abscisic acid on the germination of *Magnolia sieboldii* K. Koch seed. **2023**, 853, 147066 ○
- 423 Metabolomics and transcriptomics analyses provides insights into S-alk(en)yl cysteine sulfoxides (CSOs) accumulation in onion (*Allium cepa*). **2023**, 310, 111727 ○
- 422 Cotton microtubule-associated protein GhMAP20L5 mediates fiber elongation through the interaction with the tubulin GhTUB13. **2023**, 327, 111545 1
- 421 Alternatively spliced exon 33 in *Dscam* controls antibacterial responses through regulating cellular endocytosis and regulation of actin cytoskeleton gene expression in the hemocytes of the Chinese mitten crab (*Eriocheir sinensis*). **2023**, 140, 104619 ○
- 420 Embryogenesis of a calanoid copepod analyzed by transcriptomics. **2023**, 45, 101054 ○
- 419 Matrix Stiffness-Induced Transcriptome Alterations and Regulatory Mechanisms Revealed by RNA-Seq in Endothelial Cells. **2022**, 13, 61-79 ○
- 418 The Use of Omics Technologies, Random Mutagenesis, and Genetic Transformation Techniques to Improve Algae for Biodiesel Industry. **2023**, 43-80 ○
- 417 Absence of Wee1 alters global transcriptional response to oxidative stress in *Schizosaccharomyces pombe*. **2022**, 369, ○
- 416 A comparative study of skin transcriptomes and histological observations for black and white hair colors of giant panda. 9, ○
- 415 Activation of pheromone-sensitive olfactory neurons by plant volatiles in the moth *Agrotis ipsilon* does not occur at the level of the pheromone receptor protein. 10, ○
- 414 SETD1A regulates transcriptional pause release of heme biosynthesis genes in leukemia. **2022**, 41, 111727 ○

- 413 Genes Associated with Biological Nitrogen Fixation Efficiency Identified Using RNA Sequencing in Red Clover (*Trifolium pratense* L.). **2022**, 12, 1975 ○
- 412 miR-18a-5p Is Involved in the Developmental Origin of Prostate Cancer in Maternally Malnourished Offspring Rats: A DOHaD Approach. **2022**, 23, 14855 ○
- 411 Identification of the Genes Encoding B3 Domain-Containing Proteins Related to Vernalization of *Beta vulgaris*. **2022**, 13, 2217 ○
- 410 Elacestrant demonstrates strong anti-estrogenic activity in PDX models of estrogen-receptor positive endocrine-resistant and fulvestrant-resistant breast cancer. **2022**, 8, ○
- 409 Transcriptome Profiling to Identify Genes Involved in Non-Target-Site-Based Resistance to Clodinafop-Propargyl in Asia Minor Bluegrass (*Polypogon fugax*). **2022**, 12, 2998 ○
- 408 Inhibition of GSK3 β Promotes Proliferation and Suppresses Apoptosis of Porcine Muscle Satellite Cells. **2022**, 12, 3328 ○
- 407 Beta cell dysfunction and dedifferentiation induced by Bone Morphogenetic Protein (BMP)-2 is associated with histone modifications and decreased NeuroD1 chromatin binding. ○
- 406 Comparison of CRISPR-Cas9-mediated megabase-scale genome deletion methods in mouse embryonic stem cells. ○
- 405 Whole transcriptome sequencing and competitive endogenous RNA regulation network construction analysis in benzo[a]pyrene-treated breast cancer cells. **2022**, 160564 ○
- 404 Chemical induction of splice-neoantigens attenuates tumor growth in a preclinical model of colorectal cancer. **2022**, 14, ○
- 403 Candidate genes and their alternative splicing may be potential biomarkers of acute myocardial infarction: a study of mouse model. **2022**, 22, ○
- 402 Effects of bepridil on early cardiac development of zebrafish. ○
- 401 Human Blood Extracellular Vesicles Activate Transcription of NF- κ B-Dependent Genes in A549 Lung Adenocarcinoma Cells. **2022**, 44, 6028-6045 ○
- 400 Comparative transcriptomic analysis provides insights into the molecular basis underlying pre-harvest sprouting in rice. **2022**, 23, 2
- 399 Physiological and transcriptomic analysis of antioxidant mechanisms in sweet sorghum seedling leaves in response to single and combined drought and salinity stress. **2022**, 17, 1006-1016 ○
- 398 Kinetics of mRNA nuclear export regulate innate immune response gene expression. **2022**, 13, ○
- 397 ThSCSP_12: Novel Effector in *Tilletia horrida* That Induces Cell Death and Defense Responses in Non-Host Plants. **2022**, 23, 14752 ○
- 396 Multiple-omics reveal the role of transcription factor bHLH130 during low nitrogen in apple rootstock. ○

395	Transcriptomic Analysis Revealed Candidate Genes Involved in Pseudomale Sperm Abnormalities in Chinese Tongue Sole (<i>Cynoglossus semilaevis</i>). 2022 , 11, 1716	1
394	RNA-Seq and Genome-Wide Association Studies Reveal Potential Genes for Rice Seed Shattering. 2022 , 23, 14633	0
393	Single-nucleus RNA-seq reveals that MBD5, MBD6, and SILENZIO maintain silencing in the vegetative cell of developing pollen. 2022 , 41, 111699	0
392	Cell Wall Matrix Polysaccharides Contribute to Salt&Alkali Tolerance in Rice. 2022 , 23, 15019	1
391	Establishment of a CRISPR/Cas9 knockout library for screening type I interferon-inducible antiviral effectors in pig cells. 13,	0
390	The nuclear factor of activated T cells 5 (NFAT5) contributes to the renal corticomedullary differences in gene expression. 2022 , 12,	0
389	A 163-bp insertion in the Capana10g000198 encoding a MYB transcription factor causes male sterility in pepper (<i>Capsicum annuum</i> L.).	0
388	Tyrosine phosphorylation controlled poly(A) polymerase I activity regulates general stress response in bacteria. 2023 , 6, e202101148	0
387	Laminarin ameliorates alcohol-induced liver damage and its molecular mechanism in mice.	0
386	POU1F1/Pou1f1 c.143-83A > G variant disrupts the branch site in pre-mRNA and leads dwarfism.	1
385	Stress Triggers Expression of Bovine Herpesvirus 1 Infected Cell Protein 4 (bICP4) RNA during Early Stages of Reactivation from Latency in Pharyngeal Tonsil. 2022 , 96,	2
384	Comprehensive analysis of cuproptosis-related genes in prognosis, tumor microenvironment infiltration, and immunotherapy response in gastric cancer.	0
383	Rapid induction and long-term self-renewal of neural crest-derived ectodermal chondrogenic cells from hPSCs. 2022 , 7,	0
382	Screening of Candidate Genes Associated with Brown Stripe Resistance in Sugarcane via BSR-seq Analysis. 2022 , 23, 15500	0
381	Divergence in interspecific and intersubspecific gene expression between two closely related horseshoe bats (<i>Rhinolophus</i>).	0
380	CaMYB12 -like underlies a major QTL for flavonoid content in pepper (<i>Capsicum annuum</i>) fruit.	0
379	The application of fatty acid synthesis inhibitors regulates the suberin biosynthesis in the exocarp of the russet mutant of Dangshansuli(<i>Pyrus bretschneideri</i> Rehd.). 2023 , 45,	0
378	Antiviral Activity of Oridonin Against Herpes Simplex Virus Type 1. Volume 16, 4311-4323	0

- 377 CRISPR-free, programmable RNA pseudouridylation to suppress premature termination codons. **2022,** ○
- 376 Biochemical activity is the default DNA state in eukaryotes. ○
- 375 Cholinergic control of Th17 cell pathogenicity in experimental autoimmune encephalomyelitis. ○
- 374 RdmA Is a Key Regulator in Autoinduction of DSF Quorum Quenching in *Pseudomonas nitroreducens* HS-18. ○
- 373 *Chlamydia trachomatis* infection co-operatively enhances HPV E6-E7 oncogenes mediated tumorigenesis and immunosuppression. **2022,** 105929 ○
- 372 The grape powdery mildew resistance loci *Ren2*, *Ren3*, *Ren4D*, *Ren4U*, *Run1*, *Run1.2b*, *Run2.1*, and *Run2.2* activate different transcriptional responses to *Erysiphe necator*. 13, ○
- 371 Defined Alginate Hydrogels Support Spinal Cord Organoid Derivation, Maturation, and Modeling of Spinal Cord Diseases. 2202342 ○
- 370 Metabolic changes of the acetogen *Clostridium* sp. AWRP through adaptation to acetate challenge. 13, ○
- 369 Molecular targeted therapy: A new avenue in glioblastoma treatment (Review). **2022,** 25, ○
- 368 Heat-inducible *SlWRKY3* confers thermotolerance by activating the *SlGRXS1* gene cluster in tomato. **2022,** ○
- 367 Rumen Epithelial Development- and Metabolism-Related Genes Regulate Their Micromorphology and VFAs Mediating Plateau Adaptability at Different Ages in Tibetan Sheep. **2022,** 23, 16078 ○
- 366 Context-dependent functions of mitochondria protein quality control in lung. ○
- 365 A Dietary Oxysterol, 7-Ketocholesterol, Exacerbates Imiquimod-Induced Psoriasis-like Dermatitis in Steatohepatic Mice. **2022,** 23, 15855 ○
- 364 Dynamic landscape of long noncoding RNAs during leaf aging in *Arabidopsis*. 13, ○
- 363 Extensive Adaptive Variation in Gene Expression within and between Closely Related Horseshoe Bats (Chiroptera, *Rhinolophus*) Revealed by Three Organs. **2022,** 12, 3432 ○
- 362 Establishment of quantitative nested-PCR of Abelson interactor 1 transcript variant-11. **2022,** 8, e12119 ○
- 361 High-resolution sequencing of nine elite upland cotton cultivars uncovers genic variations and breeding improvement targets. ○
- 360 Post-feeding molecular responses of cobia (*Rachycentron canadum*): RNA-sequencing as a tool to evaluate postprandial effects in hepatic lipid metabolism. ○

- 359 Translational control by maternal Nanog promotes oogenesis and early embryonic development. **2022**, 149, ○
- 358 Physiological changes and gene responses during *Ganoderma lucidum* growth with selenium supplementation. 10, e14488 ○
- 357 bHLH57 confers chilling tolerance and grain yield improvement in rice. 1
- 356 Alternative splicing and genetic variation of mhc-e: implications for rhesus cytomegalovirus-based vaccines. **2022**, 5, ○
- 355 Transcription and Metabolism Pathways of Anthocyanin in Purple Shamrock (*Oxalis triangularis* A.St.-Hil.). **2022**, 12, 1290 ○
- 354 Conservation of Nematocida microsporidia gene expression and host response in *Caenorhabditis* nematodes. **2022**, 17, e0279103 ○
- 353 Volatile organic compounds from *Lysinibacillus macroides* regulating the seedling growth of *Arabidopsis thaliana*. **2022**, 28, 1997-2009 ○
- 352 The molecular evolution of spermatogenesis across mammals. ○
- 351 The landscape of the long non-coding RNAs and circular RNAs of the abdominal fat tissues in the chicken lines divergently selected for fatness. **2022**, 23, ○
- 350 Human JAK1 gain of function causes dysregulated myelopoeisis and severe allergic inflammation. **2022**, 7, ○
- 349 Identification and Expression Analysis of MPK and MKK Gene Families in Pecan (*Carya illinoensis*). **2022**, 23, 15190 ○
- 348 Abundance of Ruminococcaceae is Associated with Claudin 22 Gene Expression and Body Weight in Mice. ○
- 347 Single-cell heterogeneity and dynamic evolution of Ph-like acute lymphoblastic leukemia patient with novel TPR-PDGFRB fusion gene. ○
- 346 Systematic Analysis of BELL Family Genes in *Zizania latifolia* and Functional Identification of ZlqSH1a/b in Rice Seed Shattering. **2022**, 23, 15939 ○
- 345 Halophyte *Nitraria billardieri* CIPK25 promotes photosynthesis in *Arabidopsis* under salt stress. 13, ○
- 344 Transcriptomic, histological and biochemical analyses of *Macrobrachium nipponense* response to acute heat stress. ○
- 343 Freddie: annotation-independent detection and discovery of transcriptomic alternative splicing isoforms using long-read sequencing. ○
- 342 INO80 Is Required for the Cell Cycle Control, Survival, and Differentiation of Mouse ESCs by Transcriptional Regulation. **2022**, 23, 15402 ○

- 341 Merging short and stranded long reads improves transcript assembly. ○
- 340 Identification of miRNA-mRNA regulatory network associated with the glutamatergic system in post-traumatic epilepsy rats. 13, 1
- 339 Influential factors and transcriptome analyses of immature diploid embryo anthocyanin accumulation in maize. 2022, 22, ○
- 338 Lhx2 is a progenitor-intrinsic modulator of Sonic Hedgehog signaling during early retinal neurogenesis. 11, ○
- 337 Asymmetric gene expression in grain development of reciprocal crosses between tetraploid and hexaploid wheats. 2022, 5, ○
- 336 Human Macrophage Long Intergenic Noncoding RNA, SIMALR , Suppresses Inflammatory Macrophage Apoptosis via NTN1 (Netrin-1). ○
- 335 Sugar-sweetened beverages exacerbate high-fat diet-induced inflammatory bowel disease by altering the gut microbiome. 2022, 109254 ○
- 334 R2R3-MYB transcription factor GEMMA CUP-ASSOCIATED MYB1 mediates the cytokinin signal to achieve proper organ development in *Marchantia polymorpha*. 2022, 12, ○
- 333 Chemotherapy-induced phlebitis via the GBP5/NLRP3 inflammasome axis and the therapeutic effect of aescin. ○
- 332 AHL-Priming Protein 1 mediates N-3-oxo-tetradecanoyl-homoserine lactone priming in *Arabidopsis*. 2022, 20, ○
- 331 Effects of Light Intensity on Physiological Characteristics and Expression of Genes in Coumarin Biosynthetic Pathway of *Angelica dahurica*. 2022, 23, 15912 ○
- 330 Comparative Analysis of mRNA and miRNA Expression between Dermal Papilla Cells and Hair Matrix Cells of Hair Follicles in Yak. 2022, 11, 3985 ○
- 329 Differentially expressed long noncoding RNAs in RAW264.7 macrophages during *Brucella* infection and functional analysis on the bacterial intracellular replication. 2022, 12, ○
- 328 LncRNA LENGa acts as a tumor suppressor in gastric cancer through BRD7/TP53 signaling. 2023, 80, ○
- 327 CYCLerR novel tool for the full isoform assembly and quantification of circRNAs. ○
- 326 ANRIL overexpression globally induces expression and alternative splicing of genes involved in inflammation in HUVECs. 2022, 27, ○
- 325 IMPDH inhibition activates TLR-VCAM1 pathway and suppresses the development of MLL-fusion leukemia. ○
- 324 Comparative transcriptome profiles of four sexually size dimorphic fish. 2022, 9, ○

- 323 TIPARP is involved in the regulation of intraocular pressure. **2022**, 5, 0
- 322 Alternative splicing of POUM2 regulates embryonic cuticular formation and tanning in *Bombyx mori*. 0
- 321 A novel steroid hydroxylase from *Nigrospora sphaerica* exhibiting broad substrate and stereo-specificity. **2022**, 106236 0
- 320 Tomato MED25 regulates fruit ripening by interacting with EIN3-like transcription factors. 0
- 319 Transcriptome analysis of PK-15 cells expressing CSFV NS4A. **2022**, 18, 0
- 318 Characterization of Multiple Alginate Lyases in a Highly Efficient Alginate-Degrading *Vibrio* Strain and Its Degradation Strategy. **2022**, 88, 0
- 317 Motility increase of adherent invasive *Escherichia coli* (AIEC) induced by a sub-inhibitory concentration of recombinant endolysin LysPA90. 13, 0
- 316 Impacts of DNA methylases and demethylases on the methylation and expression of *Arabidopsis* ethylene signal pathway genes. 0
- 315 Activation of the phenylpropanoid pathway in *Citrus sinensis* collapsed vesicles during segment drying revealed by physicochemical and targeted metabolomics analysis. **2022**, 135297 0
- 314 Transcriptome analysis of the muscle of fast- and slow-growing phoenix barb (*Spinibarbus denticulatus denticulatus*). 0
- 313 LncRNA EN-90756 promotes CPB2-induced proliferation and inhibits apoptosis in IPEC-J2 cells by affecting the JAK-STAT signaling pathway activation. 13, 1
- 312 A Flexible Automated Pipeline Engine for Transcript-Level Quantification from RNA-seq. **2022**, 45-54 0
- 311 Systematic analysis of photo/sko-regulated germination and post-germination development of shallow photodormant seeds in *Nicotiana tabacum* L.. 13, 0
- 310 Human IL-10 β producing Th1 cells exhibit a molecular signature distinct from Tr1 cells in malaria. **2023**, 133, 0
- 309 The bHLH-zip transcription factor SREBP regulates triterpenoid and lipid metabolisms in the medicinal fungus *Ganoderma lingzhi*. **2023**, 6, 0
- 308 Polycomb repressive complexes 1 and 2 are each essential for maintenance of X inactivation in extra-embryonic lineages. 1
- 307 High-quality haplotype-resolved genome assembly of cultivated octoploid strawberry. 0
- 306 Transcriptomics for Clinical and Experimental Biology Research: Hang on a Seq. 2200024 1

- 305 Reduced sphingolipid biosynthesis modulates proteostasis networks to enhance longevity. ○
- 304 Comparative transcriptomic analyzes of human lung epithelial cells infected with wild-type SARS-CoV-2 and its variant with a 12-bp missing in the E gene. 13, ○
- 303 Profiling mouse brown and white adipocytes to identify metabolically relevant small ORFs and functional microproteins. **2023**, 35, 166-183.e11 ○
- 302 Liver transcriptome analysis reveals the energy regulation and functional impairment of *Onychosoma sima* during starvation. ○
- 301 Integrative Analysis of Proteomics and Transcriptomics of *Longissimus dorsi* with Different Feeding Systems in Yaks. **2023**, 12, 257 ○
- 300 Genome sequencing and resequencing identified three horizontal gene transfers and uncovered the genetic mechanism on the intraspecies adaptive evolution of *Gastrodia elata* Blume. 13, ○
- 299 Identification and comparison of m6A modifications in glioblastoma non-coding RNAs with MeRIP-seq and Nanopore dRNA-seq. 1-14 ○
- 298 The Histone H3K27 Demethylase REF6 Is a Positive Regulator of Light-Initiated Seed Germination in *Arabidopsis*. **2023**, 12, 295 ○
- 297 Obacunone targets macrophage migration inhibitory factor (MIF) to impede osteoclastogenesis and alleviate ovariectomy-induced bone loss. **2023**, ○
- 296 Senescence in dahlia flowers is regulated by a complex interplay between flower age and floret position. 13, ○
- 295 CRISPR /Cas9-targeted mutagenesis of TaDCL4 , TaDCL5 and TaRDR6 induces male sterility in common wheat. ○
- 294 Physiological and transcriptomic analyses provide insight into thermotolerance in desert plant *Zygophyllum xanthoxylum*. **2023**, 23, ○
- 293 Type III Secretion System Repressor RhpR Induces Grp, a Glycine-Rich Outer Membrane Lipoprotein with Functions in Regulating the Periplasmic Space and Pleiotropic Responses. ○
- 292 NR3C1 overexpression regulates the expression and alternative splicing of inflammation-associated genes involved in PTSD. **2023**, 147199 ○
- 291 Genome-wide characterization of *Ficus carica* MADS-box transcription factors with a focus on their roles during fruit development. ○
- 290 Differentially expressed genes in head kidney of *Pelteobagrus fulvidraco* following *Vibrio cholerae* challenge. 13, ○
- 289 Gene Expression and Evolution in the Smalltooth Sawfish, *Pristis Pectinata*. ○
- 288 Gonad transcriptome analysis reveals the differences in gene expression related to sex-biased and reproduction of clam *Cyclina sinensis*. 9, ○

- 287 Wnt signaling regulates ion channel expression to promote smooth muscle and cartilage formation in developing mouse trachea. ○
- 286 Interactions between the gut micro-community and transcriptome of *Culex pipiens pallens* under low-temperature stress. **2023**, 16, ○
- 285 Genetic Underpinnings of Carotenogenesis and Light-Induced Transcriptome Remodeling in the Opportunistic Pathogen *Mycobacterium kansasii*. **2023**, 12, 86 ○
- 284 Systems biology's role in leveraging microalgal biomass potential: Current status and future perspectives. **2023**, 69, 102963 ○
- 283 Genome-Wide Identification and Analysis of the Heat-Shock Protein Gene in *L. edodes* and Expression Pattern Analysis under Heat Shock. **2023**, 45, 614-627 ○
- 282 Integrated transcriptome and proteome revealed that the declined expression of cell cycle-related genes associated with follicular atresia in geese. **2023**, 24, ○
- 281 Spatio-temporal expression pattern of Raffinose Synthase genes determine the levels of Raffinose Family Oligosaccharides in peanut (*Arachis hypogaea* L.) seed. **2023**, 13, ○
- 280 Transcriptomic Insights into Functions of LkABCG36 and LkABCG40 in *Nicotiana tabacum*. **2023**, 12, 227 ○
- 279 Transcriptome analysis and differential expression in *Arabidopsis thaliana* in response to rohitukine (a chromone alkaloid) treatment. **2023**, 23, ○
- 278 Comprehensive analysis of transcriptomics and metabolomics to understand tail-suspension-induced myocardial injury in rat. 9, ○
- 277 Tet-dependent 5-hydroxymethyl-Cytosine modification of mRNA regulates the axon guidance genes *robo2* and *slit1* in *Drosophila*. ○
- 276 Combined transcriptome and metabolome analysis reveals the effects of light quality on maize hybrids. **2023**, 23, ○
- 275 Integrated comparative transcriptome and weighted gene co-expression network analysis provide valuable insights into the response mechanisms of crayfish (*Procambarus clarkii*) to copper stress. **2023**, 130820 ○
- 274 Differential expression analysis of sugar accumulation-related genes during chestnut nut development. **2023**, 153918 ○
- 273 Transcriptome analysis and gene expression analysis related to salinity-alkalinity and low temperature adaptation of *Triplophysa yarkandensis*. 13, ○
- 272 Protein aggregation in plant mitochondria inhibits translation and induces an NAC017-dependent ethylene-associated unfolded protein response. ○
- 271 GeneMark-ETP: Automatic Gene Finding in Eukaryotic Genomes in Consistence with Extrinsic Data. ○
- 270 Regulation of *Helicobacter pylori* Urease and Acetone Carboxylase Genes by Nitric Oxide and the CrdRS Two-Component System. ○

- 269 The auxin signaling pathway contributes to phosphorus-mediated zinc homeostasis in maize. **2023**, 23, 1
- 268 Analysis of long noncoding RNAs and messenger RNAs expression profiles in the hearts of mice with acute viral myocarditis. **2023**, 95, 0
- 267 The MYB transcription factor Seed Shattering 11 controls seed shattering by repressing lignin synthesis in African rice. 0
- 266 The enhancement effect of low-dose dietary lipopolysaccharide on the growth and immunity of *Litopenaeus vannamei*, and transcriptome analysis. **2023**, 133, 108517 0
- 265 Multiomics analysis reveals the mechanisms underlying the different floral colors and fragrances of *Rosa hybrida* cultivars. **2023**, 195, 101-113 0
- 264 A computational pipeline to learn gene expression predictive models from epigenetic information at enhancers or promoters. **2023**, 4, 101948 0
- 263 Serverless computing for RNA-Seq data analysis. **2022**, 0
- 262 Pre-exposure cognitive performance variability is associated with severity of respiratory infection. **2022**, 12, 0
- 261 The Jasmine (*Jasminum sambac*) Genome Provides Insight into the Biosynthesis of Flower Fragrances and Jasmonates. **2022**, 1
- 260 Transcriptome analysis of the impact of diabetes as a comorbidity on tuberculosis. **2022**, 101, e31652 0
- 259 Chromosome-level assembly of triploid genome of sichuan pepper (*Zanthoxylum armatum*). **2022**, 0
- 258 Transcriptome analysis of a dog model of congestive heart failure shows that collagen-related 2-oxoglutarate-dependent dioxygenases contribute to heart failure. **2022**, 12, 0
- 257 Identification of the egusi seed trait locus (eg) and its suppressor gene associated with the thin seed coat trait in watermelon. 14, 0
- 256 Draft genome assembly for the colombian freshwater bocachico fish, *Prochilodus magdalenae*. 13, 0
- 255 Rapid genome functional annotation pipeline anchored to the House sparrow (*Passer domesticus*, Linnaeus 1758) genome reannotation. 0
- 254 Feeding Asian honeybee queens with European honeybee royal jelly alters body color and expression of related coding and non-coding RNAs. 14, 0
- 253 Prediction of transcript structure and concentration using RNA-Seq data. 0
- 252 Characterization of FLOWERING LOCUS C 5 in *Brassica rapa* L.. 0

- 251 Improved Annotation of the Peach (*Prunus persica*) Genome and Identification of Tissue- or Development Stage-Specific Alternative Splicing through the Integration of Iso-Seq and RNA-Seq Data. **2023**, 9, 175 ○
- 250 Identification and Functional Prediction of Long Non-Coding RNA in Longissimus Dorsi Muscle of Queshan Black and Large White Pigs. **2023**, 14, 197 ○
- 249 ESPRESSO: Robust discovery and quantification of transcript isoforms from error-prone long-read RNA-seq data. **2023**, 9, ○
- 248 Genome-Wide Characterization of B-Box Gene Family in *Salvia miltiorrhiza*. **2023**, 24, 2146 ○
- 247 Evolutionary transcriptomics reveals longevity mostly driven by polygenic and indirect selection in mammals. ○
- 246 Identification of genes associated with abiotic stress tolerance in sweetpotato using weighted gene co-expression network analysis. ○
- 245 An *in vivo* avian model of human melanoma to perform rapid and robust preclinical studies. ○
- 244 I-CONVEX: Fast and Accurate de Novo Transcriptome Recovery from Long Reads. **2023**, 339-363 ○
- 243 Transcriptome analysis and identification of genes associated with leaf crude protein content in foxtail millet [*Setaria italica* (L.) P. Beauv.]. 14, ○
- 242 Comparative susceptibility of SARS-CoV-2, SARS-CoV, and MERS-CoV across mammals. ○
- 241 Human zygotic genome activation is initiated from paternal genome. **2023**, 9, ○
- 240 A 21-bp InDel in the promoter of STP1 selected during tomato improvement accounts for soluble solid content in fruits. ○
- 239 Correlated evolution of social organization and lifespan in mammals. **2023**, 14, ○
- 238 scRNA-seq data analysis method to improve analysis performance. ○
- 237 Direct activation of microglia by β -glucosylceramide causes phagocytosis of neurons that exacerbates Gaucher disease. **2023**, ○
- 236 Barbel regeneration and function divergence in red-tail catfish (*Hemibagrus wyckioides*) based on the chromosome-level genomes and comparative transcriptomes. **2023**, 232, 123374 ○
- 235 Dysregulated lncRNAs are involved in the progress of myocardial infarction by constructing regulatory networks. **2023**, 18, ○
- 234 The interaction between the histone acetyltransferase complex Hat1-Hat2 and transcription factor AmyR provides a molecular brake to regulate amylase gene expression. **2023**, 119, 471-491 ○

- 233 Quantitative analysis of high-throughput biological data. ○
- 232 Human APOBEC3B promotes tumor heterogeneity in vivo including signature mutations and metastases. ○
- 231 Genome-wide-association study and transcriptome analysis reveal the genetic basis controlling the formation of leaf wax in *Brassica napus*. ○
- 230 Identification of the BcLEA Gene Family and Functional Analysis of the BcLEA73 Gene in Wucai (*Brassica campestris* L.). **2023**, 14, 415 ○
- 229 Integrative Transcriptome and Chlorophyll Fluorescence Test Analysis Shed New Light on the Leaf Senescence Mechanism of *Zoysia japonica*. **2023**, 13, 623 ○
- 228 Molecular cloning and functional analysis of Chinese bayberry MrSPL4 that enhances growth and flowering in transgenic tobacco. 14, ○
- 227 NQO1 regulates expression and alternative splicing of apoptotic genes associated with Alzheimer's disease in PC12 cells. ○
- 226 Transcriptome and proteome analyses reveal the potential mechanism of seed dormancy release in *Amomum tsaoko* during warm stratification. **2023**, 24, ○
- 225 Integrative Analysis of Blood Transcriptomics and Metabolomics Reveals Molecular Regulation of Backfat Thickness in Qinchuan Cattle. **2023**, 13, 1060 ○
- 224 Population-level annotation of lncRNA transcription in *Arabidopsis* reveals extensive variation associated with TE-like silencing. ○
- 223 Spectral light quality regulates the morphogenesis, architecture, and flowering in pepper (*Capsicum annuum* L.). **2023**, 241, 112673 ○
- 222 Characterization of Boxwood Shoot Bacterial Communities and Potential Impact from Fungicide Treatments. **2023**, 11, ○
- 221 Comparative transcriptome analysis revealed genes involved in the sexual size dimorphisms and expressed sequence tag-Simple Sequence Repeat loci validation in *Odonotermes formicarius*. 11, ○
- 220 Maternal diet alters long-term innate immune cell memory in fetal and juvenile hematopoietic stem and progenitor cells in nonhuman primate offspring. **2023**, 42, 112393 ○
- 219 Transcriptomic investigation reveals a physiological mechanism for *Beauveria bassiana* to survive under linoleic acid stress. **2023**, 26, 106551 ○
- 218 The landscape of cryptic antisense transcription in human cancers reveals an oncogenic noncoding RNA in lung cancer. **2023**, 9, ○
- 217 The effects of short-term dietary exposure to SiO₂ nanoparticle on the domesticated lepidopteran insect model silkworm (*Bombyx mori*): Evidence from the perspective of multi-omics. **2023**, 323, 138257 ○
- 216 Differentially-expressed genes related to glutathione metabolism and heavy metal transport reveals an adaptive, genotype-specific mechanism to Hg²⁺ exposure in rice (*Oryza sativa* L.). **2023**, 324, 121340 ○

- 215 Mechanisms of *Phaeocystis globosa* blooms in the Beibu Gulf revealed by metatranscriptome analysis. **2023**, 124, 102407 ○
- 214 The novel circular RNA CircMef2c is positively associated with muscle growth in Nile tilapia. **2023**, 115, 110598 ○
- 213 4-Vinyl Guaiacol exists widely in rhizosphere soil of Lanzhou lily (*Lilium davidii* var. *unicolor*) and has a strong negative effect on lily planting. **2023**, 315, 111959 ○
- 212 Lactate induces tumor-associated macrophage polarization independent of mitochondrial pyruvate carrier-mediated metabolism. **2023**, 237, 123810 ○
- 211 Transcriptome analysis of two bloom-forming *Prorocentrum* species reveals physiological changes related to light and temperature. **2023**, 125, 102421 ○
- 210 Hemocyte proliferation is associated with blood color shade variation in the blood clam, *Tegillarca granosa*. **2023**, 571, 739447 ○
- 209 Transcriptome analysis of chickpea during heat stress unveils the signatures of long intergenic non-coding RNAs (lincRNAs) and mRNAs in the heat-QTL region. **2023**, 2, 100026 ○
- 208 Proteomic, transcriptomic, biochemical, and physio-anatomical analyses provide insights into energy metabolism, light usage, and photosynthesis in cigar tobacco under different light intensities. **2023**, 198, 116651 ○
- 207 Comparative transcriptome analysis of interspecific CSSLs reveals candidate genes and pathways involved in verticillium wilt resistance in cotton (*Gossypium hirsutum* L.). **2023**, 197, 116560 ○
- 206 Gene expression profile of HCT-8 cells following single or co-infections with *Cryptosporidium parvum* and bovine coronavirus. 1
- 205 Hot spring distribution and survival mechanisms of thermophilic comammox *Nitrospira*. ○
- 204 Combined Study of Transcriptome and Metabolome Reveals Involvement of Metabolites and Candidate Genes in Flavonoid Biosynthesis in *Prunus avium* L.. **2023**, 9, 463 ○
- 203 Transcriptome analysis identifies differentially expressed genes involved in lignin biosynthesis in barley. **2023**, 236, 123940 ○
- 202 The diurnal salivary glands transcriptome of *Dermacentor nuttalli* from the first four days of blood feeding. **2023**, 14, 102178 ○
- 201 The molecular mechanisms and environmental effects of modified clay control algal blooms in aquacultural water. **2023**, 337, 117715 ○
- 200 The use of physiological and transcriptional analyses to examine molting regulatory mechanisms in juvenile horseshoe crab *Tachypleus tridentatus*. **2023**, 572, 739518 ○
- 199 Transcriptome Analysis of Reciprocal Hybrids Between *Crassostrea gigas* and *C. angulata* Reveals the Potential Mechanisms Underlying Thermo-Resistant Heterosis. ○
- 198 Class Discovery, Comparison, and Prediction Methods for RNA-Seq Data. **2022**, 2060-2084 ○

- 197 Transcriptomic analysis reveals the inhibition mechanism of pulsed light on fungal growth and ochratoxin A biosynthesis in *Aspergillus carbonarius*. **2023**, 165, 112501 ○
- 196 Natural methylation epialleles correlate with gene expression in maize. ○
- 195 Heat shock protein 70 and Cathepsin B genes are involved in the thermal tolerance of *Aphis gossypii*. ○
- 194 Physiological and Transcriptomic Analyses Revealed That Humic Acids Improve Low-Temperature Stress Tolerance in Zucchini (*Cucurbita pepo* L.) Seedlings. **2023**, 12, 548 ○
- 193 MAPKAPK2-centric transcriptome profiling reveals its major role in governing molecular crosstalk of IGFBP2, MUC4, and PRKAR2B during HNSCC pathogenesis. **2023**, 21, 1292-1311 ○
- 192 The complexity of EGFR exon 19 deletion and L858R mutant cells as assessed by proteomics, transcriptomics, and metabolomics. **2023**, 424, 113503 ○
- 191 High temperature aggravates mortalities of the Pacific oyster (*Crassostrea gigas*) infected with *Vibrio*: A perspective from homeostasis of digestive microbiota and immune response. **2023**, 568, 739309 ○
- 190 De Novo Assembly of an Allotetraploid *Artemisia argyi* Genome. **2023**, 13, 436 ○
- 189 New Insights on Endophytic Microbacterium-Assisted Blast Disease Suppression and Growth Promotion in Rice: Revelation by Polyphasic Functional Characterization and Transcriptomics. **2023**, 11, 362 ○
- 188 Skeletal Muscles of Sedentary and Physically Active Aged People Have Distinctive Genic Extrachromosomal Circular DNA Profiles. **2023**, 24, 2736 1
- 187 Comprehensive Transcriptome Analysis of *Arabidopsis thaliana* DNA Polymerase Epsilon Catalytic Subunit A and B Mutants. ○
- 186 A program of successive gene expression in mouse one-cell embryos. **2023**, 42, 112023 ○
- 185 Wilms tumor mutational subclasses converge to drive *CCND2* overexpression. ○
- 184 Pan-genome and transcriptome analyses provide insights into genomic variation and differential gene expression profiles related to disease resistance and fatty acid biosynthesis in eastern black walnut (*Juglans nigra*). **2023**, 10, ○
- 183 Whole-genome sequence of synthetically derived *Brassica napus* inbred cultivar Da-Ae. **2023**, 13, ○
- 182 Chromosome-Level Assembly of Flowering Cherry (*Prunus campanulata*) Provides Insight into Anthocyanin Accumulation. **2023**, 14, 389 ○
- 181 Resetting histone modifications during human prenatal germline development. **2023**, 9, ○
- 180 Differential gene expression analysis using RNA-seq in the blood of goats exposed to transportation stress. **2023**, 13, 1

- 179 RNA-seq analysis reveals the critical role of the novel lncRNA BIANCR in intramuscular adipogenesis through the ERK1/2 signaling pathway. **2023**, 14, ○
- 178 Self-supervised learning on millions of pre-mRNA sequences improves sequence-based RNA splicing prediction. ○
- 177 A chromosome-level genome assembly of the beet armyworm *Spodoptera exigua*. **2023**, 115, 110571 ○
- 176 Transcriptomic Analysis and Functional Gene Expression in Different Stages of Gonadal Development of *Macrobrachium rosenbergii*. **2023**, 8, 94 ○
- 175 Transcriptome analysis of the *Mizuhopecten yessoensis* gills under high temperature fluctuations. **2023**, 142, ○
- 174 A systematic and comprehensive analysis of T cell exhaustion related to therapy in lung adenocarcinoma tumor microenvironment. 14, ○
- 173 Integrated transcriptome and proteome analysis provides insights into the mechanism of cytoplasmic male sterility (CMS) in tobacco (*Nicotiana tabacum* L.). **2023**, 275, 104825 ○
- 172 Volatile Organic Compounds from *Pythium oligandrum* Play a Role in Its Parasitism on Plant-Pathogenic *Pythium myriotylum*. **2023**, 89, ○
- 171 Transcriptome analysis of Citrus limon infected with Citrus yellow vein clearing virus. **2023**, 24, ○
- 170 Identification of a new QTL underlying seminal root number in a maize-teosinte population. 14, ○
- 169 TET1 and TDG Suppress Inflammatory Response in Intestinal Tumorigenesis: Implications for Colorectal Tumors With the CpG Island Methylator Phenotype. **2023**, 164, 921-936.e1 ○
- 168 Development of homozygous tetraploid potato and whole genome doubling-induced the enrichment of H3K27ac and potentially enhanced resistance to cold-induced sweetening in tubers. **2023**, 10, ○
- 167 Transcriptome analysis of the hepatopancreas in *Penaeus vannamei* under experimental infection with *Enterocytozoon hepatopenaei* (EHP). **2023**, 134, 108605 ○
- 166 miR394 enhances WUSCHEL-induced somatic embryogenesis in *Arabidopsis thaliana*. **2023**, 238, 1059-1072 ○
- 165 NtMYB12 requires for competition between flavonol and (pro)anthocyanin biosynthesis in *Narcissus tazetta* tepals. **2023**, 3, ○
- 164 NFATc1 Is a Central Mediator of EGFR-Induced ARID1A Chromatin Dissociation During Acinar Cell Reprogramming. **2023**, 15, 1219-1246 ○
- 163 Genome and haplotype provide insights into the population differentiation and breeding improvement of *Gossypium barbadense*. **2023**, ○
- 162 ZBTB12 is a molecular barrier to dedifferentiation in human pluripotent stem cells. **2023**, 14, ○

- 161 Combination treatment of T1-44, a PRMT5 inhibitor with Vactosertib, an inhibitor of TGF- β signaling, inhibits invasion and prolongs survival in a mouse model of pancreatic tumors. **2023**, 14, 0
- 160 MiR-190a regulates milk protein biosynthesis through the mTOR and JAK2/STAT5 signaling pathways by targeting PTHLH in buffalo mammary epithelial cells. **2023**, 102, 105451 0
- 159 Transcriptome Analysis Reveals Regulatory Networks and Hub Genes in the Flavonoid Metabolism of *Rosa roxburghii*. **2023**, 9, 233 1
- 158 The genome of a vestimentiferan tubeworm (*Ridgeia piscesae*) provides insights into its adaptation to a deep-sea environment. **2023**, 24, 0
- 157 Effect and mechanism of NaHS on tobacco bacterial wilt caused by *Ralstonia solanacearum*. **2023**, 13, 0
- 156 Biosynthetic constraints on amino acid synthesis at the base of the food chain may determine their use in higher-order consumer genomes. **2023**, 19, e1010635 0
- 155 High temperature inhibited the accumulation of anthocyanin by promoting ABA catabolism in sweet cherry fruits. 14, 0
- 154 Comparative transcriptome analysis of *Saposhnikovia divaricata* to reveal drought and rehydration adaption strategies. **2023**, 50, 3493-3502 0
- 153 XY sex determination in a cnidarian. **2023**, 21, 0
- 152 The transcriptomic response of two basidiomycete fungi to plant biomass is modulated by temperature to a different extent. **2023**, 270, 127333 0
- 151 RSV-induced expanded ciliated cells contribute to bronchial wall thickening. **2023**, 327, 199060 0
- 150 The long noncoding RNA THBS1-AS1 promotes cardiac fibroblast activation in cardiac fibrosis by regulating TGFBR1. **2023**, 8, 0
- 149 Genome-wide analysis of long non-coding RNAs in sugar beet (*Beta vulgaris* L.) under drought stress. 14, 0
- 148 NFATc1 marks articular cartilage progenitors and negatively determines articular chondrocyte differentiation. 12, 1
- 147 Tidal emersion effects on universal metrics, elemental contents, and health conditions of Pacific oyster (*Crassostrea gigas*) on artificial reefs in Yellow River Delta, China. **2023**, 42, e02409 0
- 146 Integrating Transcriptomics and Hormones Dynamics Reveal Seed Germination and Emergence Process in *Polygonatum cyrtoneuma* Hua. **2023**, 24, 3792 0
- 145 Immunopathological mechanisms in the early stage of *Mycobacterium avium* subsp. paratuberculosis infection via different administration routes in a murine model. **2023**, 18, e0281880 0
- 144 Screening of lncRNA profiles during intramuscular adipogenic differentiation in longissimus dorsi and semitendinosus muscles in pigs. 1-11 0

- 143 Biological insights from multi-omics analysis strategies: Complex pleiotropic effects associated with autophagy. 14, ○
- 142 Chronological development of the morphological, physiological, biochemical, and transcriptomic changes provides insights into the mechanisms of gametogenesis in *Saccharina japonica*. **2023**, 35, 785-802 ○
- 141 Identification of lncRNAs and Their Regulatory Network Involved in Oil Biosynthesis in Developing Seeds of Yellowhorn (*Xanthoceras sorbifolium*). **2023**, 14, 407 ○
- 140 pCtFSG2, a flower-specific promoter with suitable promoter activity in safflower. ○
- 139 Liver Transcriptome Analysis Reveals Energy Regulation and Functional Impairment of *Onychostoma simalense* During Starvation. ○
- 138 Transcriptome sequencing and gene expression analysis revealed early ovule abortion of *Paeonia ludlowii*. **2023**, 24, ○
- 137 MBOAT7-driven lysophosphatidylinositol acylation in adipocytes contributes to systemic glucose homeostasis. **2023**, 64, 100349 ○
- 136 *Bacillus amyloliquefaciens* Induces Resistance in Tobacco Against Powdery Mildew Pathogen *Erysiphe cichoracearum*. ○
- 135 Transcriptome Dynamic Analysis Reveals New Candidate Genes Associated with Resistance to Fusarium Head Blight in Two Chinese Contrasting Wheat Genotypes. **2023**, 24, 4222 ○
- 134 A multimodal analysis of genomic and RNA splicing features in myeloid malignancies. **2023**, 26, 106238 1
- 133 Transcriptional Response of Multi-Stress-Tolerant *Saccharomyces cerevisiae* to Sequential Stresses. **2023**, 9, 195 ○
- 132 Multi-Omics Analysis Reveals the Regulatory and Metabolic Mechanisms Underlying Low-Nitrogen Tolerance at the Flowering Stage in Rice. **2023**, 13, 578 ○
- 131 Comprehensive physiological, transcriptomic, and metabolomic analysis of the response of *Panicum miliaceum* L. roots to alkaline stress. ○
- 130 Identification and analysis of long non-coding RNAs that are involved in response to GCRV infection in grass carp (*Ctenopharyngodon idella*). **2023**, 134, 108623 ○
- 129 On the gene expression landscape of cancer. **2023**, 18, e0277786 ○
- 128 Histone deacetylase OsHDA706 increases salt tolerance via H4K5/K8 deacetylation of OsPP2C49 in rice. ○
- 127 Optogenetic decoding of Akt2-regulated metabolic signaling pathways in skeletal muscle cells using transomics analysis. **2023**, 16, ○
- 126 The global regulator FpLaeB is required for the regulation of growth, development, and virulence in *Fusarium pseudograminearum*. 14, ○

- 125 Genome-wide identification and functional prediction of long non-coding RNAs associated with cold tolerance in japonica rice. ○
- 124 Transcriptome and Proteome Analysis Identifies Salt Stress Response Genes in Bottle Gourd Rootstock-Grafted Watermelon Seedlings. **2023**, 13, 618 ○
- 123 Field plus lab experiments help identify freezing tolerance and associated genes in subtropical evergreen broadleaf trees: A case study of *Camellia oleifera*. 14, ○
- 122 Transcriptional profiling analysis providing insights into desiccation tolerance mechanisms of the desert moss *Syntrichia caninervis*. 14, ○
- 121 Anti-aging Effects of Alu Antisense RNA on Human Fibroblast Senescence Through the MEK-ERK Pathway Mediated by KIF15. **2023**, 43, 35-47 ○
- 120 The TIR-Type NLR Protein Is Involved in the Regulation of *Phelipanche aegyptiaca* Resistance in *Cucumis melo*. **2023**, 13, 644 ○
- 119 Comparative analysis of two kinds of garlic seedings: qualities and transcriptional landscape. **2023**, 24, ○
- 118 Photosynthetic and transcriptomic responses of *Chlorella* sp. to tigecycline. **2023**, 71, 103033 ○
- 117 Revealing the History and Mystery of RNA-Seq. **2023**, 45, 1860-1874 ○
- 116 Analysis of lncRNA and mRNA expression profiling in immature and mature DeZhou donkey (equine *Taurus*) testes. ○
- 115 Altered expression of SELF-PRUNING disrupts homeostasis and facilitates signal delivery to meristems. ○
- 114 Comparative Transcriptome Analysis of the Differential Effects of Floryprauxifen-Benzyl Treatment on Phytohormone Transduction between Floryprauxifen-Benzyl-Resistant and -Susceptible Barnyard Grasses (*Echinochloa crus-galli* (L.) P. Beauv). **2023**, 13, 702 ○
- 113 RNA-seq analysis of soybean (*Glycine max*) responding to *Phytophthora sojae*. **2023**, 171, 180-188 ○
- 112 An updated *C. elegans* nuclear body muscle transcriptome for studies in muscle formation and function. **2023**, 13, ○
- 111 A virus-borne DNA damage signaling pathway controls the lysogeny-induction switch in a group of temperate pleolipoviruses. ○
- 110 Chromosome-level reference genome of *Tetrastigma hemsleyanum* (Vitaceae) provides insights into genomic evolution and the biosynthesis of phenylpropanoids and flavonoids. ○
- 109 Epigenome-wide association study in Chinese monozygotic twins identifies DNA methylation loci associated with blood pressure. **2023**, 15, ○
- 108 Simultaneous activation of Tor and suppression of ribosome biogenesis by TRIM-NHL proteins promotes terminal differentiation. **2023**, 42, 112181 ○

- 107 Transcriptomics and Proteomics of *Haemonchus contortus* in Response to Ivermectin Treatment. **2023**, 13, 919 ○
- 106 Olfactory and neuropeptide inputs to appetite neurons in the arcuate nucleus. ○
- 105 Different reoxygenation rates induce different metabolic, apoptotic and immune responses in Golden Pompano (*Trachinotus blochii*) after hypoxic stress. **2023**, 135, 108640 ○
- 104 Transcriptome Dynamics in *Triticum aestivum* Genotypes Associated with Resistance against the Wheat Dwarf Virus. **2023**, 15, 689 ○
- 103 Identification and Characterization of Long Non-Coding RNAs: Implicating Insights into Their Regulatory Role in Kiwifruit Ripening and Softening during Low-Temperature Storage. **2023**, 12, 1070 ○
- 102 Genome-Wide Analysis of lncRNA and mRNA Expression in the Uterus of Laying Hens during Aging. **2023**, 14, 639 ○
- 101 Human basal-like breast cancer is represented by one of the two mammary tumor subtypes in dogs. ○
- 100 Integrated analysis of metabolome and transcriptome reveals key candidate genes involved in flavonoid biosynthesis in *Pinellia ternata* under heat stress. ○
- 99 Differential requirements for different subfamilies of the mammalian SWI/SNF chromatin remodeling enzymes in myoblast differentiation. ○
- 98 Hypoxia-induced transcriptional differences in African and Asian versus European diabetic cybrids. **2023**, 13, ○
- 97 Transcriptome analysis and exploration of genes involved in the biosynthesis of secoiridoids in *Gentiana rhodantha*. 11, e14968 ○
- 96 IntS6 and the Integrator phosphatase module tune the efficiency of select premature transcription termination events. ○
- 95 Inhibition of Nonsense-Mediated Decay Induces Nociceptive Sensitization through Activation of the Integrated Stress Response. **2023**, 43, 2921-2933 ○
- 94 Change in Long Non-Coding RNA Expression Profile Related to the Antagonistic Effect of *Clostridium perfringens* Type C on Piglet Spleen. **2023**, 45, 2309-2325 ○
- 93 Comparative Analysis of Root Transcriptome of High-NUE Mutant and Wild-Type Barley under Low-Nitrogen Conditions. **2023**, 13, 806 ○
- 92 Transcriptional Inhibition of AGPAT2 Induces Abnormal Lipid Metabolism and Oxidative Stress in the Liver of Nile Tilapia *Oreochromis niloticus*. **2023**, 12, 700 ○
- 91 Knockout Mutants of OsPUB7 Generated Using CRISPR/Cas9 Revealed Abiotic Stress Tolerance in Rice. **2023**, 24, 5338 ○
- 90 Genome-wide identification and comparative analyses of key genes involved in C4 photosynthesis in five main gramineous crops. 14, ○

- 89 Recent advancements in identification and detection of saliva as forensic evidence: a review. **2023**, 13, ○
- 88 Identification of long noncoding RNAs involved in plumule-vernalization of Chinese cabbage. 14, ○
- 87 RSV infection does not induce EMT. ○
- 86 Begomoviral Ω 1 orchestrates organellar genomic instability to augment viral infection. ○
- 85 Bacteria require phase separation for fitness in the mammalian gut. **2023**, 379, 1149-1156 ○
- 84 Fetal hypoxia results in sex- and cell type-specific alterations in neonatal transcription in rat oligodendrocyte precursor cells, microglia, neurons, and oligodendrocytes. **2023**, 13, ○
- 83 Integrated transcriptome and metabolomic analysis of key metabolic pathways in response to cadmium stress in novel buckwheat and cultivated species. 14, ○
- 82 Transcriptome Analysis of Pecan (*Carya illinoensis*) Differentially Expressed Genes in Response to Drought Stress. **2023**, 14, 608 ○
- 81 Transcriptomics and metabolomics reveal the changes induced by arbuscular mycorrhizal fungi in *Panax quinquefolius* L.. ○
- 80 Transcriptome analysis of Lr19-virulent mutants provides clues for the AvrLr19 of *Puccinia triticina*. 14, ○
- 79 Evidence for a single, ancient origin of a genus-wide alternative life history strategy. **2023**, 9, ○
- 78 Floral Development Stage-Specific Transcriptomic Analysis Reveals the Formation Mechanism of Different Shapes of Ray Florets in *Chrysanthemum*. **2023**, 14, 766 ○
- 77 Bacteriophage antidefense genes that neutralize TIR and STING immune responses. **2023**, 42, 112305 ○
- 76 Adaptation of transgene mRNA translation boosts the anticancer efficacy of oncolytic HSV1. **2023**, 11, e006408 ○
- 75 The DREAM complex functions as conserved master regulator of somatic DNA-repair capacities. **2023**, 30, 475-488 ○
- 74 Functional differentiation of the ovine preadipocytes Insights from gene expression profiling. **2023**, 23, ○
- 73 Effects of Starvation on the Physiology and Liver Transcriptome of Yellowcheek (*Elopichthys bambusa*). **2023**, 8, 175 ○
- 72 Genome-Wide Characterization and Expression Analysis of Transcription Factor Families in Desert Moss *Syntrichia caninervis* under Abiotic Stresses. **2023**, 24, 6137 ○

- 71 Effects of branched-chain amino acids on Shiraia perylenequinone production in mycelium cultures. **2023**, 22, ○
- 70 Changes in the Long Noncoding RNA Expression Profile in the Development of the Embryonic External Ear After BMP5 Gene Mutation. Publish Ahead of Print, ○
- 69 Genome-Wide Effects on Gene Expression Between Parental and Filial Generations of Trisomy 11 and 12 of Rice. **2023**, 16, ○
- 68 Dynamics of histone acetylation during human early embryogenesis. **2023**, 9, ○
- 67 Discovery of Hippo signaling as a regulator of CSPG4 expression and as a therapeutic target for Clostridioides difficile disease. **2023**, 19, e1011272 ○
- 66 RNA-Seq Profiling between Commercial and Indigenous Iranian Chickens Highlights Differences in Innate Immune Gene Expression. **2023**, 14, 793 ○
- 65 Transcriptomic insights into the immune response of the intestine to Aeromonas veronii infection in northern snakehead (Channa argus). **2023**, 255, 114825 ○
- 64 An ancient testis-specific IQ motif-containing H gene regulates specific transcript isoform expression during spermatogenesis. **2023**, 150, ○
- 63 Bta-miR-206 and a Novel lncRNA-lncA2B1 Promote Myogenesis of Skeletal Muscle Satellite Cells via Common Binding Protein HNRNPA2B1. **2023**, 12, 1028 ○
- 62 Transcriptome Analysis Reveals the Immunoregulation of Replacing Fishmeal with Cottonseed Protein Concentrates on Litopenaeus vannamei. **2023**, 13, 1185 ○
- 61 Abnormalities in intron retention characterize patients with systemic lupus erythematosus. **2023**, 13, ○
- 60 Modulation of long noncoding RNA (lncRNA) and messenger RNA (mRNA) expression in the liver of Beagle dogs by Toxocara canis infection. **2023**, 16, ○
- 59 Transcriptome analysis reveals insight into the protective effect of N-acetylcysteine against cadmium toxicity in Ganoderma lucidum (Polyporales: Polyporaceae). ○
- 58 Regulatory Networks of lncRNAs, miRNAs, and mRNAs in Response to Heat Stress in Wheat (Triticum Aestivum L.): An Integrated Analysis. **2023**, 2023, 1-17 ○
- 57 Genome structures resolve the early diversification of teleost fishes. **2023**, 379, 572-575 ○
- 56 Transcriptome Profile in Dairy Cows Resistant or Sensitive to Milk Fat Depression. **2023**, 13, 1199 ○
- 55 Novel Transcriptomic Interactomes of Noncoding RNAs in the Heart under Altered Thyroid Hormonal States. **2023**, 24, 6560 ○
- 54 SLC38A10 Deficiency in Mice Affects Plasma Levels of Threonine and Histidine in Males but Not in Females: A Preliminary Characterization Study of SLC38A10^{-/-} Mice. **2023**, 14, 835 ○

- 53 The chromosome-level genome of *Eucommia ulmoides* provides insights into sex differentiation and linolenic acid biosynthesis. 14,
- 52 Combined lncRNA and mRNA Expression Profiles Identified the lncRNA-miRNA-mRNA Modules Regulating the Cold Stress Response in *Ammopiptanthus nanus*. **2023**, 24, 6502
- 51 Rhytidome- and cork-type barks of holm oak, cork oak and their hybrids highlight processes leading to cork formation.
- 50 *Plasmodium falciparum* gametocytes display global chromatin remodelling during sexual differentiation. **2023**, 21,
- 49 Identification of fertility restoration candidate genes from a restorer line R186 for *Gossypium harknessii* cytoplasmic male sterile cotton. **2023**, 23,
- 48 Comprehensive investigation of long non-coding RNAs in an endophytic fungus *Calcarisporium arbuscula* NRRL 3705. **2023**, 205,
- 47 *Leishmania infantum* (JPCM5) Transcriptome, Gene Models and Resources for an Active Curation of Gene Annotations. **2023**, 14, 866
- 46 Exploring body weight-influencing gut microbiota by elucidating the association with diet and host gene expression. **2023**, 13,
- 45 Contribution of A-to-I RNA editing, M6A RNA Methylation, and Alternative Splicing to physiological brain aging and neurodegenerative diseases.. **2023**, 111807
- 44 Super-pangenome analyses highlight genomic diversity and structural variation across wild and cultivated tomato species.
- 43 Auxin participates in regulating the leaf curl development of Wucai (*Brassica campestris* L.). **2023**, 175,
- 42 Hic1 identifies a specialized mesenchymal progenitor population in the embryonic limb responsible for bone superstructure formation. **2023**, 42, 112325
- 41 Sequential Antigen-loss and Branching Evolution in Lymphoma after Anti-CD19 and Anti-CD20 Targeted T Cell Redirecting Immunotherapy.
- 40 Expression profile analysis of lncRNA and mRNA in uterosacral ligaments of women with pelvic organ prolapse by RNA-seq. **2023**, 102, e33429
- 39 Standardization and Interpretation of RNA-sequencing for Transplantation. Publish Ahead of Print,
- 38 Jasminoidin and ursodeoxycholic acid exert synergistic effect against cerebral ischemia-reperfusion injury via Dectin-1-induced NF- κ B activation pathway. **2023**, 154817
- 37 FERONIA and wall-associated kinases coordinate defense induced by lignin modification in plant cell walls. **2023**, 9,
- 36 Symbiosis preservation: Putative regulation of fatty acyl-CoA reductase by miR-31a within the symbiont harboring bacteriome through tsetse evolution. 14,

- 35 Upregulation of RasGRF1 ameliorates spatial cognitive dysfunction in mice after chronic cerebral hypoperfusion. ○
- 34 Transcriptomics reveals the effects of NTRK1 on endoplasmic reticulum stress response-associated genes in human neuronal cell lines. 11, e15219 ○
- 33 Genomic and transcriptomic analysis of sacred fig (*Ficus religiosa*). **2023**, 24, ○
- 32 Microbial Niche Differentiation during Nitrite-Dependent Anaerobic Methane Oxidation. ○
- 31 Whole-Transcriptome Sequencing of Antler Tissue Reveals That circRNA2829 Regulates Chondrocyte Proliferation and Differentiation via the miR-4286-R+1/FOXO4 Axis. **2023**, 24, 7204 ○
- 30 Comparative study on abortion characteristics of Nsa CMS and Pol CMS and analysis of long non-coding RNAs related to pollen abortion in *Brassica napus*. **2023**, 18, e0284287 ○
- 29 IKK β Inhibition Attenuates Epithelial Mesenchymal Transition of Human Stem Cell-Derived Retinal Pigment Epithelium. **2023**, 12, 1155 ○
- 28 Integrated Analysis of Transcriptome Expression Profiles Reveals miRNA-326 β -IKK3.2-Regulated Porcine Chondrocyte Differentiation. **2023**, 24, 7257 ○
- 27 Moderate Salinity Stress Increases the Seedling Biomass in Oilseed Rape (*Brassica napus* L.). **2023**, 12, 1650 ○
- 26 TEAD1 trapping by the Q353R β -amin A/C causes dilated cardiomyopathy. **2023**, 9, ○
- 25 Early environmental exposure to oxytetracycline in *Danio rerio* may contribute to neurobehavioral abnormalities in adult zebrafish. **2023**, 882, 163482 ○
- 24 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 ○
- 23 Unexplored diversity and ecological functions of transposable phages. ○
- 22 First Draft Genome Assembly of Root-Lesion Nematode *Pratylenchus scribneri* Generated Using Long-Read Sequencing. **2023**, 24, 7311 ○
- 21 Identification of core cuproptosis-correlated biomarkers in abdominal aortic aneurysm immune microenvironment based on bioinformatics. 14, ○
- 20 Effect of Mechanical Tension on the Long-Chain Noncoding RNA Expression Profile of Human Skin Regeneration. Publish Ahead of Print, ○
- 19 Evolution of chemosensory tissues and cells across ecologically diverse *Drosophilids*. ○
- 18 Identification and expression analysis of heat shock protein family genes of gall fly (*Procecidochares utilis*) under temperature stress. ○

- 17 Cytological, transcriptome and miRNome temporal landscapes decode enhancement of rice grain size. **2023**, 21,
- 16 Monitoring Cultured Rat Hepatocytes Using RNA-Seq In Vitro. **2023**, 24, 7534
- 15 Effects of quercetin on granulosa cells from pre-hierarchical follicles by modulating MAPK signaling pathway in chicken. **2023**, 102736
- 14 A scoping review on deep learning for next-generation RNA-Seq. data analysis. **2023**, 23,
- 13 Overexpression of plastid lipid-associated protein in marine diatom enhances the xanthophyll synthesis and storage. 14,
- 12 Identification and sex-specific expression of chemosensory genes in the antennal transcriptomes of *Pachyrhinus yasumatsui* (Coleoptera: Curculionidae). **2023**, 23,
- 11 PAIP1 regulates expression of immune and inflammatory response associated genes at transcript level in liver cancer cell. 11, e15070
- 10 AUF1 modulates apoptosis via regulating transcription and alternative splicing of immune response genes in auditory hair cells.
- 9 miRNA Profiling of Developing Rat Retina in the First Three Postnatal Weeks.
- 8 Medaka (*Oryzias latipes*) *Olpax6.2* acquires maternal inheritance and germ cells expression, but was functionally degenerated in the eye. **2023**, 147439
- 7 Natural compounds ursolic acid and digoxin exhibit inhibitory activities to cancer cells in ROR α -dependent and -independent manner. 14,
- 6 Genome-wide analysis of RNA-binding proteins co-expression with alternative splicing events in mitral valve prolapse. 14,
- 5 Dynamics and stage-specificity of between-population gene expression divergence in the *Drosophila melanogaster* larval fat body. **2023**, 19, e1010730
- 4 Integrated genomic analysis reveals aberrations in WNT signaling in germ cell tumors of childhood and adolescence. **2023**, 14,
- 3 Integrated testis transcriptome and whole genome analysis of sexual maturity in Large White and Tongcheng pigs.
- 2 FAM46C-mediated tumor heterogeneity predicts extramedullary metastasis and poorer survival in multiple myeloma. **2023**, 15, 3644-3677
- 1 Transcriptome profiling of barley in response to mineral and organic fertilizers. **2023**, 23,