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## Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks

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2012	IL-33 markedly activates murine eosinophils by an NF- $\kappa$ B-dependent mechanism differentially dependent upon an IL-4-driven autoinflammatory loop. <b>2013</b> , 191, 4317-25	66
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2010	GeneScissors: a comprehensive approach to detecting and correcting spurious transcriptome inference owing to RNA-seq reads misalignment. <b>2013</b> , 29, i291-9	9
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1939	Comparative transcriptome analysis of climacteric fruit of Chinese pear ( <i>Pyrus ussuriensis</i> ) reveals new insights into fruit ripening. <b>2014</b> , 9, e107562	36
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1920	Notch signaling genes: myogenic DNA hypomethylation and 5-hydroxymethylcytosine. <b>2014</b> , 9, 842-50	35
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1901	Genome-wide analysis of the skeletogenic gene regulatory network of sea urchins. <b>2014</b> , 141, 2542-2542	7
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1899	Transcriptome profiling of CTLs regulated by rapamycin using RNA-Seq. <b>2014</b> , 66, 625-33	6
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1894	Study familial hypertrophic cardiomyopathy using patient-specific induced pluripotent stem cells. <b>2014</b> , 104, 258-69	127
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1891	Pachytene piRNAs instruct massive mRNA elimination during late spermiogenesis. <b>2014</b> , 24, 680-700	238
1890	Sex- and tissue-specific functions of <i>Drosophila</i> doublesex transcription factor target genes. <b>2014</b> , 31, 761-73	83
1889	A pituitary homeobox 2 (Pitx2):microRNA-200a-3p:β-catenin pathway converts mesenchymal cells to amelogenin-expressing dental epithelial cells. <b>2014</b> , 289, 27327-27341	30
1888	Maternal temperature history activates Flowering Locus T in fruits to control progeny dormancy according to time of year. <b>2014</b> , 111, 18787-92	106

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1881	Differentiation state-specific mitochondrial dynamic regulatory networks are revealed by global transcriptional analysis of the developing chicken lens. <b>2014</b> , 4, 1515-27	30
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1878	Bayesian phylogeny of sucrose transporters: ancient origins, differential expansion and convergent evolution in monocots and dicots. <b>2014</b> , 5, 615	34
1877	Characterization of a proposed dichorhavirus associated with the citrus leprosis disease and analysis of the host response. <b>2014</b> , 6, 2602-22	27
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1875	Ethylene-induced inhibition of root growth requires abscisic acid function in rice ( <i>Oryza sativa</i> L.) seedlings. <b>2014</b> , 10, e1004701	68
1874	Characterization of the Ca <sup>2+</sup> -gated and voltage-dependent K <sup>+</sup> -channel Slo-1 of nematodes and its interaction with emodepside. <b>2014</b> , 8, e3401	31
1873	Mapping and dynamics of regulatory DNA and transcription factor networks in <i>A. thaliana</i> . <b>2014</b> , 8, 2015-2030	191
1872	Transcriptomic analysis across nasal, temporal, and macular regions of human neural retina and RPE/choroid by RNA-Seq. <b>2014</b> , 129, 93-106	76
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1869	MultiRankSeq: multiperspective approach for RNAseq differential expression analysis and quality control. <b>2014</b> , 2014, 248090	44
1868	Next-Generation Sequencing. <b>2014</b> , 125-145	2
1867	Influence of ND10 components on epigenetic determinants of early KSHV latency establishment. <b>2014</b> , 10, e1004274	44
1866	Insights into the epigenomic landscape of the human malaria vector <i>Anopheles gambiae</i> . <b>2014</b> , 5, 277	15
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1863	A 660-Kb deletion with antagonistic effects on fertility and milk production segregates at high frequency in Nordic Red cattle: additional evidence for the common occurrence of balancing selection in livestock. <b>2014</b> , 10, e1004049	96
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1860	Inflammasome sensor NLRP1 controls rat macrophage susceptibility to <i>Toxoplasma gondii</i> . <b>2014</b> , 10, e1003927	96
1859	Papillomavirus genomes associate with BRD4 to replicate at fragile sites in the host genome. <b>2014</b> , 10, e1004117	73
1858	Evolutionary analysis of the cystatin family in three <i>Schistosoma</i> species. <b>2014</b> , 5, 206	11
1857	RNA sequencing analysis reveals transcriptomic variations in tobacco ( <i>Nicotiana tabacum</i> ) leaves affected by climate, soil, and tillage factors. <b>2014</b> , 15, 6137-60	14
1856	Evolutionary interrogation of human biology in well-annotated genomic framework of rhesus macaque. <b>2014</b> , 31, 1309-24	30
1855	A comparison of transcriptional patterns and mycological phenotypes following infection of <i>Fusarium graminearum</i> by four mycoviruses. <b>2014</b> , 9, e100989	34
1854	Altered chromatin occupancy of master regulators underlies evolutionary divergence in the transcriptional landscape of erythroid differentiation. <b>2014</b> , 10, e1004890	33
1853	RNA-Seq identifies key reproductive gene expression alterations in response to cadmium exposure. <b>2014</b> , 2014, 529271	14
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1848	Simultaneous characterization of somatic events and HPV-18 integration in a metastatic cervical carcinoma patient using DNA and RNA sequencing. <b>2014</b> , 24, 329-38	13
1847	A pathway switch directs BAFF signaling to distinct NF $\kappa$ B transcription factors in maturing and proliferating B cells. <b>2014</b> , 9, 2098-111	27
1846	Endogenous WNT signaling regulates hPSC-derived neural progenitor cell heterogeneity and specifies their regional identity. <b>2014</b> , 3, 1015-28	48
1845	Sox17-mediated XEN cell conversion identifies dynamic networks controlling cell-fate decisions in embryo-derived stem cells. <b>2014</b> , 9, 780-93	35
1844	Genome-wide identification and functional analysis of Apobec-1-mediated C-to-U RNA editing in mouse small intestine and liver. <b>2014</b> , 15, R79	70
1843	svaseq: removing batch effects and other unwanted noise from sequencing data. <b>2014</b> , 42,	270
1842	High-resolution profiling of novel transcribed regions during rat spermatogenesis. <b>2014</b> , 91, 5	40
1841	RNA-seq gene and transcript expression analysis using the BioExtract server and iPlant collaborative. <b>2014</b> ,	1
1840	Recent advances in candidate-gene and whole-genome approaches to the discovery of anthelmintic resistance markers and the description of drug/receptor interactions. <b>2014</b> , 4, 164-84	125
1839	From root to fruit: RNA-Seq analysis shows that arbuscular mycorrhizal symbiosis may affect tomato fruit metabolism. <b>2014</b> , 15, 221	103
1838	Identification of genes regulating growth and fatness traits in pig through hypothalamic transcriptome analysis. <b>2014</b> , 46, 195-206	19
1837	Ancient homology underlies adaptive mimetic diversity across butterflies. <b>2014</b> , 5, 4817	56
1836	Evolution of H3K27me3-marked chromatin is linked to gene expression evolution and to patterns of gene duplication and diversification. <b>2014</b> , 24, 1115-24	16
1835	Topoisomerase IIbeta is required for proper retinal development and survival of postmitotic cells. <b>2014</b> , 3, 172-84	16
1834	PseudoLasso. <b>2014</b> ,	

1833	Targeted chromatin profiling reveals novel enhancers in Ig H and Ig L chain Loci. <b>2014</b> , 192, 1064-70	18
1832	Apoptotic caspases prevent the induction of type I interferons by mitochondrial DNA. <b>2014</b> , 159, 1563-77	434
1831	Transcriptome meta-analysis of lung cancer reveals recurrent aberrations in NRG1 and Hippo pathway genes. <b>2014</b> , 5, 5893	100
1830	Genome-wide analysis of the human p53 transcriptional network unveils a lncRNA tumour suppressor signature. <b>2014</b> , 5, 5812	137
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1828	Cis-splicing and translation of the pre-trans-splicing molecule combine with efficiency in spliceosome-mediated RNA trans-splicing. <b>2014</b> , 22, 1176-1187	26
1827	Transcriptome analysis reveals a dynamic and differential transcriptional response to sulforaphane in normal and prostate cancer cells and suggests a role for Sp1 in chemoprevention. <b>2014</b> , 58, 2001-13	20
1826	Subsarcolemmal lipid droplet responses to a combined endurance and strength exercise intervention. <b>2014</b> , 2, e12187	40
1825	Atypical RNAs in the coelacanth transcriptome. <b>2014</b> , 322, 342-51	17
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1823	Global dissection of alternative splicing in paleopolyploid soybean. <b>2014</b> , 26, 996-1008	178
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1819	A plant-specific HUA2-LIKE (HULK) gene family in <i>Arabidopsis thaliana</i> is essential for development. <b>2014</b> , 80, 242-54	8
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1808	Next maSigPro: updating maSigPro bioconductor package for RNA-seq time series. <b>2014</b> , 30, 2598-602	168
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1436	The Genomic Basis of Postponed Senescence in <i>Drosophila melanogaster</i> . <b>2015</b> , 10, e0138569	26
1435	Genomics Virtual Laboratory: A Practical Bioinformatics Workbench for the Cloud. <b>2015</b> , 10, e0140829	80
1434	Deciphering Mineral Homeostasis in Barley Seed Transfer Cells at Transcriptional Level. <b>2015</b> , 10, e0141398	8
1433	The TrxG Complex Mediates Cytokine Induced De Novo Enhancer Formation in Islets. <b>2015</b> , 10, e0141470	7
1432	Interaction of Arabidopsis Trihelix-Domain Transcription Factors VFP3 and VFP5 with Agrobacterium Virulence Protein VirF. <b>2015</b> , 10, e0142128	8
1431	Transcriptome Analysis of Short Fiber Mutant Ligon lintless-1 (Li1) Reveals Critical Genes and Key Pathways in Cotton Fiber Elongation and Leaf Development. <b>2015</b> , 10, e0143503	18
1430	Comparative Transcriptome Analysis of Recessive Male Sterility (RGMS) in Sterile and Fertile Brassica napus Lines. <b>2015</b> , 10, e0144118	31
1429	Size of the Ovulatory Follicle Dictates Spatial Differences in the Oviductal Transcriptome in Cattle. <b>2015</b> , 10, e0145321	24
1428	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. <b>2015</b> , 11, e1004321	187
1427	A Computational Pipeline for Cross-Species Analysis of RNA-seq Data Using R and Bioconductor. <b>2015</b> , 9, 165-74	8
1426	Re-analysis of RNA-seq transcriptome data reveals new aspects of gene activity in Arabidopsis root hairs. <b>2015</b> , 6, 421	14
1425	Identification of heat-responsive genes in carnation ( <i>Dianthus caryophyllus</i> L.) by RNA-seq. <b>2015</b> , 6, 519	22
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1423	Transcriptomic analysis of fruit stored under cold conditions using controlled atmosphere in <i>Prunus persica</i> cv. "Red Pearl". <b>2015</b> , 6, 788	22
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1406	DYRK1A controls the transition from proliferation to quiescence during lymphoid development by destabilizing Cyclin D3. <b>2015</b> , 212, 953-70	44
1405	Splicing function of mitotic regulators links R-loop-mediated DNA damage to tumor cell killing. <b>2015</b> , 209, 235-46	39
1404	Improved integrative framework combining association data with gene expression features to prioritize Crohn's disease genes. <b>2015</b> , 24, 4147-57	16
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1400	agplus: a rapid and flexible tool for aggregation plots. <b>2015</b> , 31, 3046-7	11
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1374	Transcriptome profile of liver at different physiological stages reveals potential mode for lipid metabolism in laying hens. <b>2015</b> , 16, 763	57
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1372	Scrutinizing the immune defence inventory of <i>Camponotus floridanus</i> applying total transcriptome sequencing. <b>2015</b> , 16, 540	27
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1367	Unraveling dual feeding associated molecular complexity of salivary glands in the mosquito <i>Anopheles culicifacies</i> . <b>2015</b> , 4, 1002-15	18
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1360	The contribution of cohesin-SA1 to gene expression and chromatin architecture in two murine tissues. <b>2015</b> , 43, 3056-67	20
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1352	PTEN deficiency reprogrammes human neural stem cells towards a glioblastoma stem cell-like phenotype. <b>2015</b> , 6, 10068	98
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1348	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . <b>2015</b> , 527, 508-11	208

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1340	Abasic pivot substitution harnesses target specificity of RNA interference. <b>2015</b> , 6, 10154	32
1339	Directional migration and transcriptional analysis of oligodendrocyte precursors subjected to stimulation of electrical signal. <b>2015</b> , 309, C532-40	18
1338	Comparative genomic analysis of <i>Leishmania</i> ( <i>Viannia</i> ) <i>peruviana</i> and <i>Leishmania</i> ( <i>Viannia</i> ) <i>braziliensis</i> . <b>2015</b> , 16, 715	37
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1333	Full-length single-cell RNA-seq applied to a viral human cancer: applications to HPV expression and splicing analysis in HeLa S3 cells. <b>2015</b> , 4, 51	42
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1330	Biased allelic expression in human primary fibroblast single cells. <b>2015</b> , 96, 70-80	88

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1328	Ten years of transcriptomics in wild populations: what have we learned about their ecology and evolution?. <b>2015</b> , 24, 710-25	140
1327	Enhancer sequence variants and transcription-factor deregulation synergize to construct pathogenic regulatory circuits in B-cell lymphoma. <b>2015</b> , 42, 186-98	47
1326	Data for chromosome contacts and matched transcription profiles at three cell cycle phases in the fission yeast. <b>2015</b> , 4, 12-6	
1325	The alternative splicing regulator Tra2b is required for somitogenesis and regulates splicing of an inhibitory Wnt11b isoform. <b>2015</b> , 10, 527-36	19
1324	Comparative interrogation of the developing xylem transcriptomes of two wood-forming species: <i>Populus trichocarpa</i> and <i>Eucalyptus grandis</i> . <b>2015</b> , 206, 1391-405	40
1323	Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development. <b>2015</b> , 290, 685-97	20
1322	A platform for rapid exploration of aging and diseases in a naturally short-lived vertebrate. <b>2015</b> , 160, 1013-1026	133
1321	Dosage and temporal thresholds in microRNA proteomics. <b>2015</b> , 14, 289-302	9
1320	A dual cis-regulatory code links IRF8 to constitutive and inducible gene expression in macrophages. <b>2015</b> , 29, 394-408	75
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1312	Gene expression defines natural changes in mammalian lifespan. <b>2015</b> , 14, 352-65	92

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1308	Genome-wide analysis of alternative splicing landscapes modulated during plant-virus interactions in <i>Brachypodium distachyon</i> . <b>2015</b> , 27, 71-85	106
1307	Massive parallel sequencing uncovers actionable FGFR2-PPHLN1 fusion and ARAF mutations in intrahepatic cholangiocarcinoma. <b>2015</b> , 6, 6087	183
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1304	Transcription factors GATA4 and HNF4A control distinct aspects of intestinal homeostasis in conjunction with transcription factor CDX2. <b>2015</b> , 290, 1850-60	35
1303	Transcriptomics of two evolutionary novelties: how to make a sperm-transfer organ out of an anal fin and a sexually selected "sword" out of a caudal fin. <b>2015</b> , 5, 848-64	8
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1297	An effective differential expression analysis of deep-sequencing data based on the Poisson log-normal model. <b>2015</b> , 13, 1550001	1
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1295	Comparative genomic analysis of aspartic proteases in eight parasitic platyhelminths: insights into functions and evolution. <b>2015</b> , 559, 52-61	3
1294	Comparative transcriptomic analysis reveals novel genes and regulatory mechanisms of <i>Tetragenococcus halophilus</i> in response to salt stress. <b>2015</b> , 42, 601-16	34

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1292	Accounting for uncertainty in DNA sequencing data. <b>2015</b> , 31, 61-6	38
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1290	RNA-Sequencing and Methylome Analysis. <b>2015</b> , 77-88	0
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1268	Promoter hypermethylation of TERT is associated with hepatocellular carcinoma in the Han Chinese population. <b>2015</b> , 39, 600-9	26
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1266	Comprehensive miRNA sequence analysis reveals survival differences in diffuse large B-cell lymphoma patients. <b>2015</b> , 16, 18	71
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1259	Characterization of Cav1.4 complexes ( $\alpha 1.4$ , $\beta$ , and $\gamma$ ) in HEK293T cells and in the retina. <b>2015</b> , 290, 1505-21	41
1258	Analytical workflow profiling gene expression in murine macrophages. <b>2015</b> , 13, 1550010	7

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1253	The Chromatin and Transcriptional Landscape of Native Saccharomyces cerevisiae Telomeres and Subtelomeric Domains. <b>2015</b> , 200, 505-21	59
1252	Strand-specific RNA sequencing in Plasmodium falciparum malaria identifies developmentally regulated long non-coding RNA and circular RNA. <b>2015</b> , 16, 454	104
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1250	Tissue-specific epigenetics in gene neighborhoods: myogenic transcription factor genes. <b>2015</b> , 24, 4660-73	16
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1248	Potential Influence of Staphylococcus aureus Clonal Complex 30 Genotype and Transcriptome on Hematogenous Infections. <b>2015</b> , 2, ofv093	22
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- 454 Chromosome-level genome assembly of *Amomum tsao-ko* provides insights into the biosynthesis of flavor compounds. o
- 453 Sequestering microRNA396' expression enhanced alfalfa resistance to *Spodoptera* herbivory. o
- 452 Comparative transcriptomics of *Pinus massoniana* organs provides insights on terpene biosynthesis regulation. o
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- 440 A high-quality chromosome-level genome assembly of rohu carp, *Labeo rohita*, and its utilization in SNP-based exploration of gene flow and sex determination. ○
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- 437 An interplay between BRD4 and G9a regulates skeletal myogenesis. 10, ○
- 436 The heterogeneity in the landscape of gene dominance in maize is accompanied by unique chromatin environments. ○
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428	MtTRC-1, a Novel Transcription Factor, Regulates Cellulase Production via Directly Modulating the Genes Expression of the Mthac-1 and Mtcbh-1 in <i>Myceliophthora thermophila</i> .	o
427	Identification of a <i>Fusarium</i> ear rot resistance gene in maize by QTL mapping and RNA sequencing. 13,	o
426	<i>Colletotrichum siamense</i> infection caused transcripts involved plant hormone signal transduction and phenylpropanoid biosynthesis varied in strawberry. <b>2022</b> , 50, 12791	o
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424	Pericytes control vascular stability and auditory spiral ganglion neuron survival.	o
423	Alternative splicing in bladder cancer: potential strategies for cancer diagnosis, prognosis, and treatment.	o
422	Rapid and sensitive single-cell RNA sequencing with SHERRY2. <b>2022</b> , 20,	1
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420	The draft genome and multi-omics analyses reveal new insights into geo-herbalism properties of <i>Citrus grandis</i> 'Momentosa' <b>2022</b> , 111489	o
419	Identification of long non-coding RNAs involved in floral scent of <i>Rosa hybrida</i> . 13,	1
418	Reprisal of <i>Schima superba</i> to Mn stress and exploration of its defense mechanism through transcriptomic analysis. 13,	o
417	Isolation of ferret astrocytes reveals their morphological, transcriptional, and functional differences from mouse astrocytes. 16,	o
416	Chromatin remodeler <i>Znhit1</i> controls bone morphogenetic protein signaling in embryonic lung tissue branching. <b>2022</b> , 298, 102490	o
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414	NHA1 is a cation/proton antiporter essential for the water-conserving functions of the rectal complex in <i>Tribolium castaneum</i> .	o
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404	Whole genome and transcriptome reveal flavone accumulation in <i>Scutellaria baicalensis</i> roots. 13,	0
403	Molecular Biology, Genetics, and Translational Models of Human Cancer. 1-34	0
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400	Identification of Candidate mRNA Isoforms for Prostate Cancer-Risk SNPs Utilizing Iso-eQTL and sQTL Methods. <b>2022</b> , 23, 12406	0
399	Fine mapping of genes controlling pigments accumulation in oilseed rape ( <i>Brassica napus</i> L.).	0
398	Interplay between the microalgae <i>Micrasterias radians</i> and its symbiont <i>Dyadobacter</i> sp. HH091. 13,	2
397	Mirror proteases of Ac-Trypsin and Ac-LysargiNase precisely improve novel event identifications in <i>Mycobacterium smegmatis</i> MC2 155 by proteogenomic analysis. 13,	0
396	The Effect of Salinity Stress on Enzyme Activities, Histology, and Transcriptome of Silver Carp ( <i>Hypophthalmichthys molitrix</i> ). <b>2022</b> , 11, 1580	1
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394	Transcriptome-Wide lncRNA and mRNA Profiling of Spleens from Meishan Pigs at Different Development Stages. <b>2022</b> , 12, 2676	0

393	Transcriptome analysis during fruit developmental stages in durian ( <i>Durio zibethinus</i> Murr.) var. D24.	0
392	Identification of Novel Transcripts and Exons by RNA-Seq of Transcriptome in <i>Durio zibethinus</i> Murr.	0
391	Genome-Wide Identification, Characterization and Expression Analysis of Mango ( <i>Mangifera indica</i> L.) chalcone synthase (CHS) Genes in Response to Light. <b>2022</b> , 8, 968	1
390	Integrated analysis of lncRNA-mediated ceRNA network involved in immune regulation in the spleen of Meishan piglets. 9,	0
389	Global transcriptome and coexpression network analyses reveal cultivar-specific molecular signatures associated with different rooting depth responses to drought stress in potato. 13,	0
388	Transcriptomic Dynamics of Active and Inactive States of Rho GTPase MoRho3 in <i>Magnaporthe oryzae</i> . <b>2022</b> , 8, 1060	0
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383	PGC-1 $\alpha$ and ERR $\beta$ Promote Glutamine Metabolism and Colorectal Cancer Survival via Transcriptional Upregulation of PCK2. <b>2022</b> , 14, 4879	0
382	Transcriptome Analysis of Hong Yang Kiwifruit in Response to <i>Bactrocera dorsalis</i> (Diptera: Tephritidae) Larval Feeding. <b>2022</b> , 57, 488-501	0
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380	Massive genome investigations reveal insights of prevalent introgression for environmental adaptation and triterpene biosynthesis in <i>Ganoderma</i> .	0
379	TaERF87 and TaAKS1 synergistically regulate TaP5CS1 / TaP5CR1 -mediated proline biosynthesis to enhance drought tolerance in wheat.	3
378	Transcriptome Analysis Reveals the Genes Related to Pollen Abortion in a Cytoplasmic Male-Sterile Soybean ( <i>Glycine max</i> (L.) Merr.). <b>2022</b> , 23, 12227	0
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352	Transcriptome Profiling of Stem-Differentiating Xylem in Response to Abiotic Stresses Based on Hybrid Sequencing in Cunninghamia lanceolata. <b>2022</b> , 23, 13986	0
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