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**TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions**

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1831	Runx1 Transcription Factor Is Required for Myoblasts Proliferation during Muscle Regeneration. <b>2015</b> , 11, e1005457	45
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1819	Vitamin D Modulates Expression of the Airway Smooth Muscle Transcriptome in Fatal Asthma. <b>2015</b> , 10, e0134057	26
1818	RNA-Seq Analysis of Abdominal Fat Reveals Differences between Modern Commercial Broiler Chickens with High and Low Feed Efficiencies. <b>2015</b> , 10, e0135810	42
1817	Identification of Distinct Tumor Subpopulations in Lung Adenocarcinoma via Single-Cell RNA-seq. <b>2015</b> , 10, e0135817	45
1816	Allele-Selective Transcriptome Recruitment to Polysomes Primed for Translation: Protein-Coding and Noncoding RNAs, and RNA Isoforms. <b>2015</b> , 10, e0136798	9
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1665	Neuronal CRTG-1 governs systemic mitochondrial metabolism and lifespan via a catecholamine signal. <b>2015</b> , 160, 842-855	115
1664	The Sweden Cancerome Analysis Network - Breast (SCAN-B) Initiative: a large-scale multicenter infrastructure towards implementation of breast cancer genomic analyses in the clinical routine. <b>2015</b> , 7, 20	70
1663	A generalized dSpliceType framework to detect differential splicing and differential expression events using RNA-Seq. <b>2015</b> , 14, 192-202	10
1662	Genomic Characterization Reveals Insights Into Patulin Biosynthesis and Pathogenicity in <i>Penicillium</i> Species. <b>2015</b> , 28, 635-47	104
1661	Coupling of T cell receptor specificity to natural killer T cell development by bivalent histone H3 methylation. <b>2015</b> , 212, 297-306	34

1660	ADAR1 is required for differentiation and neural induction by regulating microRNA processing in a catalytically independent manner. <b>2015</b> , 25, 459-76	60
1659	Genetic blueprint of the zoonotic pathogen <i>Toxocara canis</i> . <b>2015</b> , 6, 6145	77
1658	Analysis of RNAseq datasets from a comparative infectious disease zebrafish model using GeneTiles bioinformatics. <b>2015</b> , 67, 135-47	12
1657	Sphingolipids, Transcription Factors, and Conserved Toolkit Genes: Developmental Plasticity in the Ant Cardiocondyla obscurior. <b>2015</b> , 32, 1474-86	31
1656	Overlapping and unique signatures in the proteomic and transcriptomic responses of the nematode <i>Caenorhabditis elegans</i> toward pathogenic <i>Bacillus thuringiensis</i> . <b>2015</b> , 51, 1-9	28
1655	<i>Arabidopsis</i> chloroplast mini-ribonuclease III participates in rRNA maturation and intron recycling. <b>2015</b> , 27, 724-40	33
1654	Quantitative gene profiling of long noncoding RNAs with targeted RNA sequencing. <b>2015</b> , 12, 339-42	119
1653	HISAT: a fast spliced aligner with low memory requirements. <b>2015</b> , 12, 357-60	8026
1652	RNA toxicity and missplicing in the common eye disease fuchs endothelial corneal dystrophy. <b>2015</b> , 290, 5979-90	80
1651	Functional annotation of the <i>Ophiostoma novo-ulmi</i> genome: insights into the phytopathogenicity of the fungal agent of Dutch elm disease. <b>2014</b> , 7, 410-30	44
1650	Ballgown bridges the gap between transcriptome assembly and expression analysis. <b>2015</b> , 33, 243-6	413
1649	Comparative analysis of the silk gland transcriptomes between the domestic and wild silkworms. <b>2015</b> , 16, 60	56
1648	miR-503 represses human cell proliferation and directly targets the oncogene DDHD2 by non-canonical target pairing. <b>2015</b> , 16, 40	19
1647	Transcriptome analysis of nitrogen-starvation-responsive genes in rice. <b>2015</b> , 15, 31	79
1646	The KRAB zinc finger protein ZFP809 is required to initiate epigenetic silencing of endogenous retroviruses. <b>2015</b> , 29, 538-54	105
1645	Analytical workflow profiling gene expression in murine macrophages. <b>2015</b> , 13, 1550010	7
1644	ARGONAUTE2 cooperates with SWI/SNF complex to determine nucleosome occupancy at human Transcription Start Sites. <b>2015</b> , 43, 1498-512	33
1643	Spatiotemporal expression and transcriptional perturbations by long noncoding RNAs in the mouse brain. <b>2015</b> , 112, 6855-62	114

1642	MSProGene: integrative proteogenomics beyond six-frames and single nucleotide polymorphisms. <b>2015</b> , 31, i106-15	38
1641	Transcriptome analysis reveals a classical interferon signature induced by IFN $\beta$ in human primary cells. <b>2015</b> , 16, 414-21	31
1640	ERG Activates the YAP1 Transcriptional Program and Induces the Development of Age-Related Prostate Tumors. <b>2015</b> , 27, 797-808	75
1639	Single-cell RNA-seq transcriptome analysis of linear and circular RNAs in mouse preimplantation embryos. <i>Genome Biology</i> , <b>2015</b> , 16, 148	18.3 243
1638	Evolution of dosage compensation under sexual selection differs between X and Z chromosomes. <b>2015</b> , 6, 7720	35
1637	Discovery, Annotation, and Functional Analysis of Long Noncoding RNAs Controlling Cell-Cycle Gene Expression and Proliferation in Breast Cancer Cells. <b>2015</b> , 59, 698-711	137
1636	LncRNA analysis of mouse spermatogonial stem cells following glial cell-derived neurotrophic factor treatment. <b>2015</b> , 5, 275-8	3
1635	Genome analysis of rice-blast fungus <i>Magnaporthe oryzae</i> field isolates from southern India. <b>2015</b> , 5, 284-91	18
1634	Deep sequencing-generated modules demonstrate coherent expression patterns for various cardiac diseases. <b>2015</b> , 574, 53-60	1
1633	Enhanced biological processes associated with alopecia in polar bears ( <i>Ursus maritimus</i> ). <b>2015</b> , 529, 114-20	14
1632	Self-renewing diploid Axin2(+) cells fuel homeostatic renewal of the liver. <b>2015</b> , 524, 180-5	459
1631	Mistargeted mitochondrial proteins activate a proteostatic response in the cytosol. <b>2015</b> , 524, 485-8	250
1630	Statistical models for RNA-seq data derived from a two-condition 48-replicate experiment. <b>2015</b> , 31, 3625-30	54
1629	Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. <i>Genome Biology</i> , <b>2015</b> , 16, 150	18.3 104
1628	Exploiting genome variation to improve next-generation sequencing data analysis and genome editing efficiency in <i>Populus tremula</i> lba 717-1B4. <b>2015</b> , 11, 1	22
1627	Pseudo-Seq: Genome-Wide Detection of Pseudouridine Modifications in RNA. <b>2015</b> , 560, 219-45	31
1626	Molecular characterization of 7 new established cell lines from high grade serous ovarian cancer. <b>2015</b> , 362, 218-28	17
1625	Nerves Regulate Cardiomyocyte Proliferation and Heart Regeneration. <b>2015</b> , 34, 387-99	162

1624	Coordination between <i>Drosophila</i> Arc1 and a specific population of brain neurons regulates organismal fat. <b>2015</b> , 405, 280-90	8
1623	Genomics and drug profiling of fatal TCF3-HLF-positive acute lymphoblastic leukemia identifies recurrent mutation patterns and therapeutic options. <b>2015</b> , 47, 1020-1029	127
1622	Robust gene expression and mutation analyses of RNA-sequencing of formalin-fixed diagnostic tumor samples. <b>2015</b> , 5, 12335	43
1621	Nonuniform gene expression pattern detected along the longitudinal axis in the matured rice leaf. <b>2015</b> , 5, 8015	8
1620	Early maturation and distinct tau pathology in induced pluripotent stem cell-derived neurons from patients with MAPT mutations. <b>2015</b> , 138, 3345-59	87
1619	Early embryonic-like cells are induced by downregulating replication-dependent chromatin assembly. <b>2015</b> , 22, 662-71	195
1618	Identification, by systematic RNA sequencing, of novel candidate biomarkers and therapeutic targets in human soft tissue tumors. <b>2015</b> , 95, 1077-88	10
1617	Transgenic expression of the dicotyledonous pattern recognition receptor EFR in rice leads to ligand-dependent activation of defense responses. <b>2015</b> , 11, e1004809	73
1616	Complete Dosage Compensation in <i>Anopheles stephensi</i> and the Evolution of Sex-Biased Genes in Mosquitoes. <b>2015</b> , 7, 1914-24	30
1615	CSR-1 and P granules suppress sperm-specific transcription in the <i>C. elegans</i> germline. <b>2015</b> , 142, 1745-55	45
1614	Genetic and epigenetic architecture of sex-biased expression in the jewel wasps <i>Nasonia vitripennis</i> and <i>giraulti</i> . <b>2015</b> , 112, E3545-54	38
1613	Gene fusion detection in formalin-fixed paraffin-embedded benign fibrous histiocytomas using fluorescence in situ hybridization and RNA sequencing. <b>2015</b> , 95, 1071-6	54
1612	Differential expression of HERV-K (HML-2) proviruses in cells and virions of the teratocarcinoma cell line Tera-1. <b>2015</b> , 7, 939-68	43
1611	PPLine: An Automated Pipeline for SNP, SAP, and Splice Variant Detection in the Context of Proteogenomics. <b>2015</b> , 14, 3729-37	46
1610	RASA: Robust Alternative Splicing Analysis for Human Transcriptome Arrays. <b>2015</b> , 5, 11917	10
1609	Tumor Necrosis Factor Receptor 2 Restricts the Pathogenicity of CD8(+) T Cells in Mice With Colitis. <b>2015</b> , 149, 993-1005.e2	33
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1607	Exome and transcriptome sequencing of <i>Aedes aegypti</i> identifies a locus that confers resistance to <i>Brugia malayi</i> and alters the immune response. <b>2015</b> , 11, e1004765	25

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1605	Repair of DNA Damage Induced by the Cytidine Analog Zebularine Requires ATR and ATM in Arabidopsis. <b>2015</b> , 27, 1788-800	36
1604	Pharmacoethnicity in Paclitaxel-Induced Sensory Peripheral Neuropathy. <b>2015</b> , 21, 4337-46	26
1603	Integrative genomic analysis reveals widespread enhancer regulation by p53 in response to DNA damage. <b>2015</b> , 43, 4447-62	66
1602	Widespread Inducible Transcription Downstream of Human Genes. <b>2015</b> , 59, 449-61	90
1601	RNA helicase HEL-1 promotes longevity by specifically activating DAF-16/FOXO transcription factor signaling in <i>Caenorhabditis elegans</i> . <b>2015</b> , 112, E4246-55	27
1600	A Comparative Epigenomic Analysis of Polyploidy-Derived Genes in Soybean and Common Bean. <b>2015</b> , 168, 1433-47	67
1599	Expression of the CTCFL Gene during Mouse Embryogenesis Causes Growth Retardation, Postnatal Lethality, and Dysregulation of the Transforming Growth Factor $\beta$ Pathway. <b>2015</b> , 35, 3436-45	8
1598	Proteotoxic stress reprograms the chromatin landscape of SUMO modification. <b>2015</b> , 8, rs7	56
1597	Dnmt3l-knockout donor cells improve somatic cell nuclear transfer reprogramming efficiency. <b>2015</b> , 150, 245-56	10
1596	Natural selection constrains neutral diversity across a wide range of species. <b>2015</b> , 13, e1002112	187
1595	Identification of RNA polymerase III-transcribed Alu loci by computational screening of RNA-Seq data. <b>2015</b> , 43, 817-35	45
1594	Enhancer of Rudimentary Homolog Affects the Replication Stress Response through Regulation of RNA Processing. <b>2015</b> , 35, 2979-90	15
1593	Examining the evolution of the regulatory circuit controlling secondary metabolism and development in the fungal genus <i>Aspergillus</i> . <b>2015</b> , 11, e1005096	48
1592	Century-scale methylome stability in a recently diverged <i>Arabidopsis thaliana</i> lineage. <b>2015</b> , 11, e1004920	104
1591	Maternal and zygotic transcriptomes in the appendicularian, <i>Oikopleura dioica</i> : novel protein-encoding genes, intra-species sequence variations, and trans-spliced RNA leader. <b>2015</b> , 225, 149-59	17
1590	Essential Role for endogenous siRNAs during meiosis in mouse oocytes. <b>2015</b> , 11, e1005013	72
1589	Quantification of co-transcriptional splicing from RNA-Seq data. <b>2015</b> , 85, 36-43	19

1588	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. <b>2015</b> , 83, 118-27	22
1587	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. <b>2015</b> , 12, 519-22	443
1586	Transcriptomic Analysis of Yersinia enterocolitica Biovar 1B Infecting Murine Macrophages Reveals New Mechanisms of Extracellular and Intracellular Survival. <b>2015</b> , 83, 2672-85	11
1585	Mammalian NET-Seq Reveals Genome-wide Nascent Transcription Coupled to RNA Processing. <b>2015</b> , 161, 526-540	319
1584	DUSP4 deficiency caused by promoter hypermethylation drives JNK signaling and tumor cell survival in diffuse large B cell lymphoma. <b>2015</b> , 212, 775-92	45
1583	Maintenance and Loss of Duplicated Genes by Dosage Subfunctionalization. <b>2015</b> , 32, 2141-8	83
1582	AKI Recovery Induced by Mesenchymal Stromal Cell-Derived Extracellular Vesicles Carrying MicroRNAs. <b>2015</b> , 26, 2349-60	164
1581	Diurnal depression in leaf hydraulic conductance at ambient and elevated [CO <sub>2</sub> ] reveals anisohydric water management in field-grown soybean and possible involvement of aquaporins. <b>2015</b> , 116, 39-46	15
1580	Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation. <b>2015</b> , 523, 221-5	505
1579	Expression and functions of long noncoding RNAs during human T helper cell differentiation. <b>2015</b> , 6, 6932	124
1578	Deciphering poxvirus gene expression by RNA sequencing and ribosome profiling. <b>2015</b> , 89, 6874-86	41
1577	Transcriptomic analysis of degraded forensic body fluids. <b>2015</b> , 17, 35-42	19
1576	N6-methyladenine DNA modification in Drosophila. <b>2015</b> , 161, 893-906	401
1575	Genome-wide analysis of human global and transcription-coupled excision repair of UV damage at single-nucleotide resolution. <b>2015</b> , 29, 948-60	147
1574	RNA sequencing of sarcomas with simple karyotypes: identification and enrichment of fusion transcripts. <b>2015</b> , 95, 603-9	8
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1571	Antiviral gene expression in psoriasis. <b>2015</b> , 29, 1951-7	24

1570	Influence of sex on genetic regulation of "drinking in the dark" alcohol consumption. <b>2015</b> , 26, 43-56	13
1569	Rapid turnover of antimicrobial-type cysteine-rich protein genes in closely related <i>Oryza</i> genomes. <b>2015</b> , 290, 1753-70	6
1568	Gene expression profiling for seed protein and oil synthesis during early seed development in soybean. <b>2015</b> , 37, 409-418	9
1567	Combining RNA and protein profiling data with network interactions identifies genes associated with spermatogenesis in mouse and human. <b>2015</b> , 92, 71	17
1566	Comparative transcriptome profiling in human bicuspid aortic valve disease using RNA sequencing. <b>2015</b> , 47, 75-87	20
1565	Targeted gene mutation in tetraploid potato through transient TALEN expression in protoplasts. <b>2015</b> , 204, 17-24	78
1564	Native elongating transcript sequencing reveals human transcriptional activity at nucleotide resolution. <b>2015</b> , 161, 541-554	226
1563	Improved precision of QTL mapping using a nonlinear Bayesian method in a multi-breed population leads to greater accuracy of across-breed genomic predictions. <b>2015</b> , 47, 29	82
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1561	Genome-wide survey and expression analysis of F-box genes in chickpea. <b>2015</b> , 16, 67	41
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1559	A comprehensive evaluation of ensembl, RefSeq, and UCSC annotations in the context of RNA-seq read mapping and gene quantification. <b>2015</b> , 16, 97	81
1558	IPred - integrating ab initio and evidence based gene predictions to improve prediction accuracy. <b>2015</b> , 16, 134	10
1557	CodingQuarry: highly accurate hidden Markov model gene prediction in fungal genomes using RNA-seq transcripts. <b>2015</b> , 16, 170	98
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1555	Global gene expression patterns of grass carp following compensatory growth. <b>2015</b> , 16, 184	27
1554	Methamphetamine induces alterations in the long non-coding RNAs expression profile in the nucleus accumbens of the mouse. <b>2015</b> , 16, 18	30
1553	NexGenEx-Tom: a gene expression platform to investigate the functionalities of the tomato genome. <b>2015</b> , 15, 48	14

1552	Comparative metabolic and transcriptional analysis of a doubled diploid and its diploid citrus rootstock ( <i>C. junos</i> cv. Ziyang xiangcheng) suggests its potential value for stress resistance improvement. <b>2015</b> , 15, 89	82
1551	RNA sequencing reveals distinct mechanisms underlying BET inhibitor JQ1-mediated modulation of the LPS-induced activation of BV-2 microglial cells. <b>2015</b> , 12, 36	32
1550	Genome-wide analysis of the endoplasmic reticulum stress response during lignocellulase production in <i>Neurospora crassa</i> . <b>2015</b> , 8, 66	41
1549	Comparative methylome analysis identifies new tumour subtypes and biomarkers for transformation of nephrogenic rests into Wilms tumour. <b>2015</b> , 7, 11	34
1548	Transcriptome analysis of ageing in uninjured human Achilles tendon. <b>2015</b> , 17, 33	46
1547	An automated method for efficient, accurate and reproducible construction of RNA-seq libraries. <b>2015</b> , 8, 124	5
1546	Replicative senescence is associated with nuclear reorganization and with DNA methylation at specific transcription factor binding sites. <b>2015</b> , 7, 19	42
1545	RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. <b>2015</b> , 4, 5	87
1544	Single cell transcriptome amplification with MALBAC. <b>2015</b> , 10, e0120889	30
1543	Proteomic Validation of Transcript Isoforms, Including Those Assembled from RNA-Seq Data. <b>2015</b> , 14, 3541-54	10
1542	Mutant U2AF1 Expression Alters Hematopoiesis and Pre-mRNA Splicing In Vivo. <b>2015</b> , 27, 631-43	186
1541	Recursive splicing in long vertebrate genes. <b>2015</b> , 521, 371-375	88
1540	A novel member of the let-7 microRNA family is associated with developmental transitions in filarial nematode parasites. <b>2015</b> , 16, 331	20
1539	New signaling pathways govern the host response to <i>C. albicans</i> infection in various niches. <b>2015</b> , 25, 679-89	57
1538	Long non-coding RNA discovery across the genus anopheles reveals conserved secondary structures within and beyond the Gambiae complex. <b>2015</b> , 16, 337	56
1537	Integrated analysis of whole-exome sequencing and transcriptome profiling in males with autism spectrum disorders. <b>2015</b> , 6, 21	79
1536	Human disease modeling reveals integrated transcriptional and epigenetic mechanisms of NOTCH1 haploinsufficiency. <b>2015</b> , 160, 1072-86	138
1535	Implications of miR166 and miR159 induction to the basal response mechanisms of an andigena potato ( <i>Solanum tuberosum</i> subsp. andigena) to salinity stress, predicted from network models in <i>Arabidopsis</i> . <b>2015</b> , 58, 13-24	27



1534	Laser capture microdissection in <i>Ectocarpus siliculosus</i> : the pathway to cell-specific transcriptomics in brown algae. <b>2015</b> , 6, 54	8
1533	PROTEOFORMER: deep proteome coverage through ribosome profiling and MS integration. <b>2015</b> , 43, e29	100
1532	Multiplex single cell profiling of chromatin accessibility by combinatorial cellular indexing. <b>2015</b> , 348, 910-4	668
1531	Identification Exon Skipping Events From High-Throughput RNA Sequencing Data. <b>2015</b> , 14, 562-9	2
1530	Gender-specific postnatal demethylation and establishment of epigenetic memory. <b>2015</b> , 29, 923-33	57
1529	RNA exosome-regulated long non-coding RNA transcription controls super-enhancer activity. <b>2015</b> , 161, 774-89	280
1528	Activation of an endogenous retrovirus-associated long non-coding RNA in human adenocarcinoma. <b>2015</b> , 7, 22	40
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1526	Purifying Selection Maintains Dosage-Sensitive Genes during Degeneration of the Threespine Stickleback Y Chromosome. <b>2015</b> , 32, 1981-95	66
1525	Computational approaches towards understanding human long non-coding RNA biology. <b>2015</b> , 31, 2241-51	45
1524	A KAP1 phosphorylation switch controls MyoD function during skeletal muscle differentiation. <b>2015</b> , 29, 513-25	44
1523	Plant Omics Data Center: an integrated web repository for interspecies gene expression networks with NLP-based curation. <b>2015</b> , 56, e9	45
1522	The BRAF pseudogene functions as a competitive endogenous RNA and induces lymphoma in vivo. <b>2015</b> , 161, 319-32	233
1521	SRD: a <i>Staphylococcus</i> regulatory RNA database. <b>2015</b> , 21, 1005-17	40
1520	Current methods for automated annotation of protein-coding genes. <b>2015</b> , 7, 8-14	18
1519	AnimalTFDB 2.0: a resource for expression, prediction and functional study of animal transcription factors. <b>2015</b> , 43, D76-81	195
1518	Purification and Transcriptomic Analysis of Mouse Fetal Leydig Cells Reveals Candidate Genes for Specification of Gonadal Steroidogenic Cells. <b>2015</b> , 92, 145	28
1517	Comprehensive evaluation of the effectiveness of gene expression signatures to predict complete response to neoadjuvant chemoradiotherapy and guide surgical intervention in rectal cancer. <b>2015</b> , 208, 319-26	39

1516	Improving the gene structure annotation of the apicomplexan parasite <i>Neospora caninum</i> fulfils a vital requirement towards an in silico-derived vaccine. <b>2015</b> , 45, 305-18	10
1515	The CYP2C19 Intron 2 Branch Point SNP is the Ancestral Polymorphism Contributing to the Poor Metabolizer Phenotype in Livers with CYP2C19*35 and CYP2C19*2 Alleles. <b>2015</b> , 43, 1226-35	19
1514	Skipper genome sheds light on unique phenotypic traits and phylogeny. <b>2015</b> , 16, 639	32
1513	<i>Anopheles gambiae</i> Ag55 cell line as a model for <i>Lysinibacillus sphaericus</i> Bin toxin action. <b>2015</b> , 132, 105-110	3
1512	Expanded GAA repeats impede transcription elongation through the FXN gene and induce transcriptional silencing that is restricted to the FXN locus. <b>2015</b> , 24, 6932-43	40
1511	HIV-1 Nef promotes infection by excluding SERINC5 from virion incorporation. <b>2015</b> , 526, 212-7	269
1510	mRNA export through an additional cap-binding complex consisting of NCBP1 and NCBP3. <b>2015</b> , 6, 8192	47
1509	Transcriptional maturation of the mouse auditory forebrain. <b>2015</b> , 16, 606	21
1508	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. <b>2015</b> , 21, 1357-63	65
1507	Next-generation sequencing, assembly, and comparative analyses of the latex transcriptomes from two elite <i>Hevea brasiliensis</i> varieties. <b>2015</b> , 11, 1	9
1506	An <i>Arabidopsis</i> PWI and RRM motif-containing protein is critical for pre-mRNA splicing and ABA responses. <b>2015</b> , 6, 8139	62
1505	RNA sequencing reveals a unique fusion of the lysine (K)-specific methyltransferase 2A and smooth muscle myosin heavy chain 11 in myelodysplastic syndrome and acute myeloid leukemia. <b>2015</b> , 100, e1-3	4
1504	Genome-wide identification and characterization of tissue-specific RNA editing events in <i>D. melanogaster</i> and their potential role in regulating alternative splicing. <b>2015</b> , 12, 1391-401	26
1503	Cell type- and brain region-resolved mouse brain proteome. <b>2015</b> , 18, 1819-31	418
1502	Two-pass alignment improves novel splice junction quantification. <b>2016</b> , 32, 43-9	21
1501	Quality Control and Analysis of NGS RNA Sequencing Data. <b>2015</b> , 1326, 217-32	1
1500	The Central Region of the <i>Drosophila</i> Co-repressor Groucho as a Regulatory Hub. <b>2015</b> , 290, 30119-30	3
1499	The autism-associated gene chromodomain helicase DNA-binding protein 8 (CHD8) regulates noncoding RNAs and autism-related genes. <b>2015</b> , 5, e568	65

1498	i-cisTarget 2015 update: generalized cis-regulatory enrichment analysis in human, mouse and fly. <b>2015</b> , 43, W57-64	99
1497	SOX9 modulates the expression of key transcription factors required for heart valve development. <b>2015</b> , 142, 4340-50	37
1496	Early-late genes of the ecdysone cascade as models for transcriptional studies. <b>2015</b> , 14, 3593-601	14
1495	Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis. <b>2015</b> , 350, 1251-5	139
1494	QuickNGS elevates Next-Generation Sequencing data analysis to a new level of automation. <b>2015</b> , 16, 487	56
1493	Transcriptome sequencing of microglial cells stimulated with TLR3 and TLR4 ligands. <b>2015</b> , 16, 517	41
1492	Assessing the translational landscape of myogenic differentiation by ribosome profiling. <b>2015</b> , 43, 4408-28	38
1491	Cyclin-Dependent Kinase Regulation of Diurnal Transcription in <i>Chlamydomonas</i> . <b>2015</b> , 27, 2727-42	27
1490	Comparative genome analysis of <i>Pseudogymnoascus</i> spp. reveals primarily clonal evolution with small genome fragments exchanged between lineages. <b>2015</b> , 16, 400	6
1489	TARDIS, a targeted RNA directional sequencing method for rare RNA discovery. <b>2015</b> , 10, 1915-38	4
1488	Small RNA-mediated DNA (cytosine-5) methyltransferase 1 inhibition leads to aberrant DNA methylation. <b>2015</b> , 43, 6112-24	36
1487	The Genome and Methylome of a Beetle with Complex Social Behavior, <i>Nicrophorus vespilloides</i> (Coleoptera: Silphidae). <b>2015</b> , 7, 3383-96	65
1486	Focused human gene expression profiling using dual-color reverse transcriptase multiplex ligation-dependent probe amplification. <b>2015</b> , 33, 5282-8	15
1485	Genomic analysis of mycosis fungoides and Sézary syndrome identifies recurrent alterations in TNFR2. <b>2015</b> , 47, 1056-60	186
1484	RC3H1 post-transcriptionally regulates A20 mRNA and modulates the activity of the IKK/NF- $\kappa$ B pathway. <b>2015</b> , 6, 7367	74
1483	Improved binding site assignment by high-resolution mapping of RNA-protein interactions using iCLIP. <b>2015</b> , 6, 7921	23
1482	Sexual dimorphism and the evolution of sex-biased gene expression in the brown alga <i>ectocarpus</i> . <b>2015</b> , 32, 1581-97	68
1481	MUCOSAL IMMUNOLOGY. Individual intestinal symbionts induce a distinct population of ROR $\gamma$ regulatory T cells. <b>2015</b> , 349, 993-7	487

1480	Dynamic transition of transcription and chromatin landscape during fission yeast adaptation to glucose starvation. <b>2015</b> , 20, 392-407	18
1479	Chromatin and extracellular vesicle associated sperm RNAs. <b>2015</b> , 43, 6847-59	44
1478	Transcriptome sequencing reveals the roles of transcription factors in modulating genotype by nitrogen interaction in maize. <b>2015</b> , 34, 1761-71	19
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1476	Adaptive aneuploidy protects against thiol peroxidase deficiency by increasing respiration via key mitochondrial proteins. <b>2015</b> , 112, 10685-90	35
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1294	Identification and Analysis of NaHCO Stress Responsive Genes in Wild Soybean () Roots by RNA-seq. <b>2016</b> , 7, 1842	20
1293	Functional and RNA-Sequencing Analysis Revealed Expression of a Novel Stay-Green Gene from () Caused Chlorophyll Degradation and Accelerated Senescence in Arabidopsis. <b>2016</b> , 7, 1894	7
1292	OsSGL, a Novel DUF1645 Domain-Containing Protein, Confers Enhanced Drought Tolerance in Transgenic Rice and. <b>2016</b> , 7, 2001	32
1291	Transcriptional Response of Silkworm ( <i>Bombyx mori</i> ) Eggs to OBr HCl Treatment. <b>2016</b> , 17,	5
1290	From Big Data Analytics and Network Inference to Systems Modeling. <b>2016</b> , 113-144	
1289	Genome-wide identification and characterization of long non-coding RNAs in developmental skeletal muscle of fetal goat. <b>2016</b> , 17, 666	66
1288	eQTL mapping. 208-228	
1287	Boiler: lossy compression of RNA-seq alignments using coverage vectors. <b>2016</b> , 44, e133	2
1286	Bioinformatics Tools in Epigenomics Studies. <b>2016</b> , 73-107	1
1285	Sorafenib treatment during partial hepatectomy reduces tumorigenesis in an inflammation-associated liver cancer model. <b>2016</b> , 7, 4860-70	14
1284	Luminal long non-coding RNAs regulated by estrogen receptor alpha in a ligand-independent manner show functional roles in breast cancer. <b>2016</b> , 7, 3201-16	43
1283	Differential gene expression in dentate granule cells in mesial temporal lobe epilepsy with and without hippocampal sclerosis. <b>2016</b> , 57, 376-85	18

1282	Genomic analysis of snub-nosed monkeys ( <i>Rhinopithecus</i> ) identifies genes and processes related to high-altitude adaptation. <b>2016</b> , 48, 947-52	58
1281	Genetic and epigenetic methylation defects and implication of the <i>ERMN</i> gene in autism spectrum disorders. <b>2016</b> , 6, e855	22
1280	Developmental regulation of myeloerythroid progenitor function by the <i>Lin28b-let-7-Hmga2</i> axis. <b>2016</b> , 213, 1497-512	44
1279	<i>Phytophthora infestans</i> Argonaute 1 binds microRNA and small RNAs from effector genes and transposable elements. <b>2016</b> , 211, 993-1007	24
1278	SUSHI: an exquisite recipe for fully documented, reproducible and reusable NGS data analysis. <b>2016</b> , 17, 228	45
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1276	Identification and characterization of parasitism genes from the pinewood nematode <i>Bursaphelenchus xylophilus</i> reveals a multilayered detoxification strategy. <b>2016</b> , 17, 286-95	69
1275	Functional network analysis of genes differentially expressed during xylogenesis in <i>soc1</i> ful woody <i>Arabidopsis</i> plants. <b>2016</b> , 86, 376-90	22
1274	Fast neutron-induced structural rearrangements at a soybean <i>NAP1</i> locus result in gnarled trichomes. <b>2016</b> , 129, 1725-38	24
1273	<i>Rbm24</i> Regulates Alternative Splicing Switch in Embryonic Stem Cell Cardiac Lineage Differentiation. <b>2016</b> , 34, 1776-89	36
1272	Extensive ceRNA-ceRNA interaction networks mediated by miRNAs regulate development in multiple rhesus tissues. <b>2016</b> , 44, 9438-9451	38
1271	Melatonin and its receptor <i>MT1</i> are involved in the downstream reaction to luteinizing hormone and participate in the regulation of luteinization in different species. <b>2016</b> , 61, 279-90	50
1270	The Restorer-of-fertility-like 2 pentatricopeptide repeat protein and RNase P are required for the processing of mitochondrial <i>orf291</i> RNA in <i>Arabidopsis</i> . <b>2016</b> , 86, 504-13	22
1269	A targeted immunomic approach identifies diagnostic antigens in the human pathogen <i>Babesia microti</i> . <b>2016</b> , 56, 2085-99	20
1268	Transcriptome Analysis Reveals a Signature Profile for Tick-Borne Flavivirus Persistence in HEK 293T Cells. <b>2016</b> , 7,	19
1267	<i>Chd5</i> Regulates <i>MuERV-L/MERVL</i> Expression in Mouse Embryonic Stem Cells Via H3K27me3 Modification and Histone H3.1/H3.2. <b>2016</b> , 117, 780-92	22
1266	Status of dosage compensation of X chromosome in bovine genome. <b>2016</b> , 144, 435-44	3
1265	RNA-Seq Links the Transcription Factors <i>AINTEGUMENTA</i> and <i>AINTEGUMENTA-LIKE6</i> to Cell Wall Remodeling and Plant Defense Pathways. <b>2016</b> , 171, 2069-84	26

1264	Genome-Wide Mapping of Targets of Maize Histone Deacetylase HDA101 Reveals Its Function and Regulatory Mechanism during Seed Development. <b>2016</b> , 28, 629-45	33
1263	Analysis of genes that influence sheep follicular development by different nutrition levels during the luteal phase using expression profiling. <b>2016</b> , 47, 354-64	5
1262	Oral secretions from <i>Mythimna separata</i> insects specifically induce defence responses in maize as revealed by high-dimensional biological data. <b>2016</b> , 39, 1749-1766	40
1261	ETV6-LPXN fusion transcript generated by t(11;12)(q12.1;p13) in a patient with relapsing acute myeloid leukemia with NUP98-HOXA9. <b>2016</b> , 55, 242-50	7
1260	Transcriptional landscape of trans-kingdom communication between <i>Candida albicans</i> and <i>Streptococcus gordonii</i> . <b>2016</b> , 31, 136-61	31
1259	RNA-seq analysis of clinical-grade osteochondral allografts reveals activation of early response genes. <b>2016</b> , 34, 1950-1959	22
1258	Diverse alternative back-splicing and alternative splicing landscape of circular RNAs. <b>2016</b> , 26, 1277-87	482
1257	Lineage-Specific Effector Signatures of Invariant NKT Cells Are Shared amongst $\gamma$ , Innate Lymphoid, and Th Cells. <b>2016</b> , 197, 1460-70	75
1256	Current analysis of host-parasite interactions with a focus on next generation sequencing data. <b>2016</b> , 119, 298-306	19
1255	CLAUSA Is a MYB Transcription Factor That Promotes Leaf Differentiation by Attenuating Cytokinin Signaling. <b>2016</b> , 28, 1602-15	27
1254	Human glioblastoma-associated microglia/monocytes express a distinct RNA profile compared to human control and murine samples. <b>2016</b> , 64, 1416-36	71
1253	The synovial microenvironment of osteoarthritic joints alters RNA-seq expression profiles of human primary articular chondrocytes. <b>2016</b> , 591, 456-64	14
1252	Morpholino-mediated Knockdown of DUX4 Toward Facioscapulohumeral Muscular Dystrophy Therapeutics. <b>2016</b> , 24, 1405-11	65
1251	Curation of the genome annotation of <i>Pichia pastoris</i> ( <i>Komagataella phaffii</i> ) CBS7435 from gene level to protein function. <b>2016</b> , 16,	47
1250	Myostatin in relation to physical activity and dysglycaemia and its effect on energy metabolism in human skeletal muscle cells. <b>2016</b> , 217, 45-60	30
1249	Transcriptomic Analysis Identifies Candidate Genes and Gene Sets Controlling the Response of Porcine Peripheral Blood Mononuclear Cells to Poly I:C Stimulation. <b>2016</b> , 6, 1267-75	7
1248	NPInter v3.0: an upgraded database of noncoding RNA-associated interactions. <b>2016</b> , 2016,	95
1247	Transcript level coordination of carbon pathways during silicon starvation-induced lipid accumulation in the diatom <i>Thalassiosira pseudonana</i> . <b>2016</b> , 210, 890-904	47



1246	Comparative metabolomic analysis reveals a reactive oxygen species-dominated dynamic model underlying chilling environment adaptation and tolerance in rice. <b>2016</b> , 211, 1295-310	63
1245	AsHSP17, a creeping bentgrass small heat shock protein modulates plant photosynthesis and ABA-dependent and independent signalling to attenuate plant response to abiotic stress. <b>2016</b> , 39, 1320-37	51
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1243	systemPipeR: NGS workflow and report generation environment. <b>2016</b> , 17, 388	98
1242	Improved Placement of Multi-mapping Small RNAs. <b>2016</b> , 6, 2103-11	132
1241	Dysregulated immune system networks in war veterans with PTSD is an outcome of altered miRNA expression and DNA methylation. <b>2016</b> , 6, 31209	58
1240	Comparative transcriptome analysis revealing dormant conidia and germination associated genes in <i>Aspergillus</i> species: an essential role for AtfA in conidial dormancy. <b>2016</b> , 17, 358	48
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1238	Loss of genetic diversity as a consequence of selection in response to high CO <sub>2</sub> . <b>2016</b> , 9, 1124-1132	12
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1236	Ecdysone signaling induces two phases of cell cycle exit in <i>Drosophila</i> cells. <b>2016</b> , 5, 1648-1661	22
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1231	Annotation of the Tomato Genome. <b>2016</b> , 159-171	
1230	Prediction of Gene Structures from RNA-seq Data Using Dual Decomposition. <b>2016</b> , 9, 1-6	2
1229	Transition of differential histone H3 methylation in photoreceptors and other retinal cells during retinal differentiation. <b>2016</b> , 6, 29264	23

1228	Circular RNAs are down-regulated in KRAS mutant colon cancer cells and can be transferred to exosomes. <b>2016</b> , 6, 37982	208
1227	The gene-expression profile of renal medulla in ISIAH rats with inherited stress-induced arterial hypertension. <b>2016</b> , 17, 151	6
1226	New insights into the Plasmodium vivax transcriptome using RNA-Seq. <b>2016</b> , 6, 20498	46
1225	Linear ubiquitination by LUBEL has a role in Drosophila heat stress response. <b>2016</b> , 17, 1624-1640	24
1224	POMP. <b>2016</b> ,	
1223	Isoform switching and exon skipping induced by the DNA methylation inhibitor 5-Aza-2'-deoxycytidine. <b>2016</b> , 6, 24545	9
1222	Transcriptome analysis of the fungal pathogen Fusarium oxysporum f. sp. medicaginis during colonisation of resistant and susceptible Medicago truncatula hosts identifies differential pathogenicity profiles and novel candidate effectors. <b>2016</b> , 17, 860	35
1221	The sorghum SWEET gene family: stem sucrose accumulation as revealed through transcriptome profiling. <b>2016</b> , 9, 127	63
1220	Reference-free comparison of microbial communities via de Bruijn graphs. <b>2016</b> ,	2
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1218	The hookworm Ancylostoma ceylanicum intestinal transcriptome provides a platform for selecting drug and vaccine candidates. <b>2016</b> , 9, 518	15
1217	Combinatory annotation of cell membrane receptors and signalling pathways of Bombyx mori prothoracic glands. <b>2016</b> , 3, 160073	4
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1215	Genome-wide long non-coding RNA screening, identification and characterization in a model microorganism Chlamydomonas reinhardtii. <b>2016</b> , 6, 34109	34
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1213	Identification of genes for engineering the male germline of Aedes aegypti and Ceratitis capitata. <b>2016</b> , 17, 948	5
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1211	Altered microRNA expression and pre-mRNA splicing events reveal new mechanisms associated with early stage Mycobacterium avium subspecies paratuberculosis infection. <b>2016</b> , 6, 24964	27

1210	Plastid: nucleotide-resolution analysis of next-generation sequencing and genomics data. <b>2016</b> , 17, 958	90
1209	A machine learning approach for the identification of key markers involved in brain development from single-cell transcriptomic data. <b>2016</b> , 17, 1025	20
1208	Genome-wide map of RNA degradation kinetics patterns in dendritic cells after LPS stimulation facilitates identification of primary sequence and secondary structure motifs in mRNAs. <b>2016</b> , 17, 1032	8
1207	MicroRNAs in Honey Bee Caste Determination. <b>2016</b> , 6, 18794	73
1206	An integrated analysis of cancer genes in thyroid cancer. <b>2016</b> , 35, 962-70	17
1205	Coexpression network analysis of the genes regulated by two types of resistance responses to powdery mildew in wheat. <b>2016</b> , 6, 23805	25
1204	An Inversion Disrupting FAM134B Is Associated with Sensory Neuropathy in the Border Collie Dog Breed. <b>2016</b> , 6, 2687-92	13
1203	Genome-wide DNA methylation analysis in multiple tissues in primary Sjögren's syndrome reveals regulatory effects at interferon-induced genes. <b>2016</b> , 75, 2029-2036	100
1202	Non-coding RNAs match the deleted genomic regions in humans. <b>2016</b> , 6, 37452	2
1201	Gene expression differences in Longissimus muscle of Nelore steers genetically divergent for residual feed intake. <b>2016</b> , 6, 39493	39
1200	Landscape and Fruit Developmental Regulation of Alternative Splicing in Tomato by Genome-Wide Analysis. <b>2016</b> , 2, 338-350	5
1199	Induction of Germ Cell-like Cells from Porcine Induced Pluripotent Stem Cells. <b>2016</b> , 6, 27256	24
1198	CD14 in the TLRs signaling pathway is associated with the resistance to E. coli F18 in Chinese domestic weaned piglets. <b>2016</b> , 6, 24611	8
1197	NOD-like receptor signaling and inflammasome-related pathways are highlighted in psoriatic epidermis. <b>2016</b> , 6, 22745	51
1196	Complete genomes of Hairstreak butterflies, their speciation, and nucleo-mitochondrial incongruence. <b>2016</b> , 6, 24863	35
1195	Comparative transcriptome assembly and genome-guided profiling for <i>Brettanomyces bruxellensis</i> LAMAP2480 during p-coumaric acid stress. <b>2016</b> , 6, 34304	9
1194	An IFIH1 gene polymorphism associated with risk for autoimmunity regulates canonical antiviral defence pathways in Cocksackievirus infected human pancreatic islets. <b>2016</b> , 6, 39378	34
1193	An expressed, endogenous Nodavirus-like element captured by a retrotransposon in the genome of the plant parasitic nematode <i>Bursaphelenchus xylophilus</i> . <b>2016</b> , 6, 39749	9

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1191	Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types. <b>2016</b> , 17, 178-87	148
1190	The venom gland transcriptome of the parasitoid wasp <i>Nasonia vitripennis</i> highlights the importance of novel genes in venom function. <b>2016</b> , 17, 571	14
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1187	JULiP: An efficient model for accurate intron selection from multiple RNA-seq samples. <b>2016</b> ,	
1186	Dissecting the expression relationships between RNA-binding proteins and their cognate targets in eukaryotic post-transcriptional regulatory networks. <b>2016</b> , 6, 25711	10
1185	TEtools facilitates big data expression analysis of transposable elements and reveals an antagonism between their activity and that of piRNA genes. <b>2017</b> , 45, e17	51
1184	Mitochondria are required for pro-ageing features of the senescent phenotype. <b>2016</b> , 35, 724-42	357
1183	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . <b>2016</b> , 17, 455-69	93
1182	Accelerated pseudogenization on the neo-X chromosome in <i>Drosophila miranda</i> . <b>2016</b> , 7, 13659	9
1181	Network analysis of psoriasis reveals biological pathways and roles for coding and long non-coding RNAs. <b>2016</b> , 17, 841	51
1180	Differential morphology and transcriptome profile between the incompletely fused carpels ovary and its wild-type in maize. <b>2016</b> , 6, 32652	3
1179	Robust Extracellular pH Modulation by <i>Candida albicans</i> during Growth in Carboxylic Acids. <b>2016</b> , 7,	40
1178	A novel brain tumour model in zebrafish reveals the role of YAP activation in MAPK- and PI3K-induced malignant growth. <b>2017</b> , 10, 15-28	35
1177	Global analysis of regulatory divergence in the evolution of mouse alternative polyadenylation. <b>2016</b> , 12, 890	15
1176	Expression profiling and functional annotation of noncoding genes across 11 distinct organs in rat development. <b>2016</b> , 6, 38575	4
1175	Multimodal stimulus coding by a gustatory sensory neuron in <i>Drosophila</i> larvae. <b>2016</b> , 7, 10687	20

1174	Stress-induced and epigenetic-mediated maize transcriptome regulation study by means of transcriptome reannotation and differential expression analysis. <b>2016</b> , 6, 30446	40
1173	The role of the poly(A) tract in the replication and virulence of tick-borne encephalitis virus. <b>2016</b> , 6, 39265	17
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1171	Transcriptome analysis revealed chimeric RNAs, single nucleotide polymorphisms and allele-specific expression in porcine prenatal skeletal muscle. <b>2016</b> , 6, 29039	8
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1168	Single-cell RNA sequencing reveals molecular and functional platelet bias of aged haematopoietic stem cells. <b>2016</b> , 7, 11075	153
1167	Development of single nucleotide polymorphism (SNP) markers from the mango ( <i>Mangifera indica</i> ) transcriptome for mapping and estimation of genetic diversity. <b>2016</b> , 315-322	7
1166	The acetyllysine reader BRD3R promotes human nuclear reprogramming and regulates mitosis. <b>2016</b> , 7, 10869	17
1165	The Composite Regulatory Basis of the Large X-Effect in Mouse Speciation. <b>2017</b> , 34, 282-295	29
1164	Genetic mosaics and time-lapse imaging identify functions of histone H3.3 residues in mouse oocytes and embryos. <b>2017</b> , 144, 519-528	6
1163	RBM5 reduces small cell lung cancer growth, increases cisplatin sensitivity and regulates key transformation-associated pathways. <b>2016</b> , 2, e00204	11
1162	Reassessing ecdysteroidogenic cells from the cell membrane receptors' perspective. <b>2016</b> , 6, 20229	9
1161	Differentially expressed genes in the locus associated with relative kidney weight and resting blood pressure in hypertensive rats of the ISIAH strain. <b>2016</b> , 50, 831-838	
1160	Principal component analysis based unsupervised feature extraction applied to publicly available gene expression profiles provides new insights into the mechanisms of action of histone deacetylase inhibitors. <b>2016</b> , 8, 1-18	16
1159	A proteogenomic approach for protein-level evidence of genomic variants in cancer cells. <b>2016</b> , 6, 35305	9
1158	Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation. <b>2016</b> , 30, 1731-46	68
1157	Zinc finger protein 407 overexpression upregulates PPAR target gene expression and improves glucose homeostasis in mice. <b>2016</b> , 311, E869-E880	9

1156	Vine nitrogen status and volatile thiols and their precursors from plot to transcriptome level. <b>2016</b> , 16, 173	16
1155	Pervasive isoform-specific translational regulation via alternative transcription start sites in mammals. <b>2016</b> , 12, 875	55
1154	Disease Model of GATA4 Mutation Reveals Transcription Factor Cooperativity in Human Cardiogenesis. <b>2016</b> , 167, 1734-1749.e22	122
1153	Distal Limb Patterning Requires Modulation of cis-Regulatory Activities by HOX13. <b>2016</b> , 17, 2913-2926	46
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1151	Maintenance of leukemic cell identity by the activity of the Polycomb complex PRC1 in mice. <b>2016</b> , 2, e1600972	15
1150	Inhibition of DNA methylation promotes breast tumor sensitivity to netrin-1 interference. <b>2016</b> , 8, 863-77	15
1149	The <i>Evx1/Evx1as</i> gene locus regulates anterior-posterior patterning during gastrulation. <b>2016</b> , 6, 26657	16
1148	Transcriptome and long noncoding RNA sequencing of three extracellular vesicle subtypes released from the human colon cancer LIM1863 cell line. <b>2016</b> , 6, 38397	59
1147	The AS-RBM15 lncRNA enhances RBM15 protein translation during megakaryocyte differentiation. <b>2016</b> , 17, 887-900	46
1146	Global proteogenomic analysis of human MHC class I-associated peptides derived from non-canonical reading frames. <b>2016</b> , 7, 10238	127
1145	Sequence-based Association Analysis Reveals an MGST1 eQTL with Pleiotropic Effects on Bovine Milk Composition. <b>2016</b> , 6, 25376	65
1144	Delayed neurogenesis with respect to eye growth shapes the pigeon retina for high visual acuity. <b>2016</b> , 143, 4701-4712	12
1143	Single-cell sequencing maps gene expression to mutational phylogenies in PDGF- and EGF-driven gliomas. <b>2016</b> , 12, 889	67
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1141	<i>Dictyocaulus viviparus</i> genome, variome and transcriptome elucidate lungworm biology and support future intervention. <b>2016</b> , 6, 20316	17
1140	Comparative "Omics" of the <i>Fusarium fujikuroi</i> Species Complex Highlights Differences in Genetic Potential and Metabolite Synthesis. <b>2016</b> , 8, 3574-3599	81
1139	From yeast to hypha: defining transcriptomic signatures of the morphological switch in the dimorphic fungal pathogen <i>Ophiostoma novo-ulmi</i> . <b>2016</b> , 17, 920	14

1138	PHF20 Readers Link Methylation of Histone H3K4 and p53 with H4K16 Acetylation. <b>2016</b> , 17, 1158-1170	23
1137	A Comparative Analysis of 5-Azacytidine- and Zebularine-Induced DNA Demethylation. <b>2016</b> , 6, 2773-80	49
1136	Analysis of chromosomal aberrations and recombination by allelic bias in RNA-Seq. <b>2016</b> , 7, 12144	30
1135	Comparative transcriptome analysis among parental inbred and crosses reveals the role of dominance gene expression in heterosis in <i>Drosophila melanogaster</i> . <b>2016</b> , 6, 21124	7
1134	RNA sequencing of chorionic villi from recurrent pregnancy loss patients reveals impaired function of basic nuclear and cellular machinery. <b>2016</b> , 6, 38439	30
1133	The piggyBac transposon-derived genes TPB1 and TPB6 mediate essential transposon-like excision during the developmental rearrangement of key genes in <i>Tetrahymena thermophila</i> . <b>2016</b> , 30, 2724-2736	30
1132	Molecular and epigenetic features of melanomas and tumor immune microenvironment linked to durable remission to ipilimumab-based immunotherapy in metastatic patients. <b>2016</b> , 14, 232	24
1131	Redifferentiation of expanded human islet $\beta$ cells by inhibition of ARX. <b>2016</b> , 6, 20698	10
1130	Genomic and transcriptomic analyses of the tangerine pathotype of <i>Alternaria alternata</i> in response to oxidative stress. <b>2016</b> , 6, 32437	32
1129	Negative regulation of initial steps in skeletal myogenesis by mTOR and other kinases. <b>2016</b> , 6, 20376	4
1128	Transcriptome profiling of <i>Cucumis melo</i> fruit development and ripening. <b>2016</b> , 3, 16014	30
1127	DeepSplice: Deep classification of novel splice junctions revealed by RNA-seq. <b>2016</b> ,	10
1126	Construction and Annotation of a High Density SNP Linkage Map of the Atlantic Salmon ( <i>Salmo salar</i> ) Genome. <b>2016</b> , 6, 2173-9	33
1125	Development and Validation of <i>Thinopyrum elongatum</i> Expressed Molecular Markers Specific for the Long Arm of Chromosome 7E. <b>2016</b> , 56, 354-364	14
1124	Transcriptomic evidence for modulation of host inflammatory responses during febrile <i>Plasmodium falciparum</i> malaria. <b>2016</b> , 6, 31291	43
1123	Gene Regulatory Evolution During Speciation in a Songbird. <b>2016</b> , 6, 1357-64	21
1122	Exploring the Molecular Determinants of Tumor-Stroma Interaction in Non-small Cell Lung Cancer Through the Utilization of RNA-seq Data from Lung Biopsies. <b>2016</b> , 495-499	1
1121	Identification of a novel fusion transcript between human relaxin-1 (RLN1) and human relaxin-2 (RLN2) in prostate cancer. <b>2016</b> , 420, 159-68	12

1120	A comprehensive study of the genetic impact of rare variants in SORL1 in European early-onset Alzheimer's disease. <b>2016</b> , 132, 213-224	62
1119	Delineation of metabolic gene clusters in plant genomes by chromatin signatures. <b>2016</b> , 44, 2255-65	51
1118	Gene Expression and Profiling. <b>2016</b> , 59-82	
1117	Transcriptomic and epigenomic characterization of the developing bat wing. <b>2016</b> , 48, 528-36	45
1116	Different pathogenicities of Rice stripe virus from the insect vector and from viruliferous plants. <b>2016</b> , 210, 196-207	35
1115	DNMT3A Haploinsufficiency Transforms FLT3ITD Myeloproliferative Disease into a Rapid, Spontaneous, and Fully Penetrant Acute Myeloid Leukemia. <b>2016</b> , 6, 501-15	53
1114	SplAdder: identification, quantification and testing of alternative splicing events from RNA-Seq data. <b>2016</b> , 32, 1840-7	59
1113	Transcriptome analysis of cortical tissue reveals shared sets of downregulated genes in autism and schizophrenia. <b>2016</b> , 6, e817	25
1112	Gene expression changes in damaged osteoarthritic cartilage identify a signature of non-chondrogenic and mechanical responses. <b>2016</b> , 24, 1431-40	64
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1104	Induced Pluripotent Stem Cell-Derived Retinal Pigmented Epithelium: A Comparative Study Between Cell Lines and Differentiation Methods. <b>2016</b> , 32, 317-30	39
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