

Experimental validation of methods for differential gene pooling in RNA-seq

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Changes in C57BL6 Mouse Hippocampal Transcriptome Induced by Hypergravity Mimic Acute Corticosterone-Induced Stress. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 153.	1.4	10
2	Transcriptome Analysis Reveals Regulation of Gene Expression for Lipid Catabolism in Young Broilers by Butyrate Glycerides. <i>PLoS ONE</i> , 2016, 11, e0160751.	1.1	29
3	Studying Secondary Growth and Bast Fiber Development: The Hemp Hypocotyl Peeks behind the Wall. <i>Frontiers in Plant Science</i> , 2016, 7, 1733.	1.7	62
4	Homeopathy for wound healing? A question of scientific honesty. <i>Focus on Alternative and Complementary Therapies</i> , 2016, 21, 171-175.	0.1	0
5	Exploring the Molecular Determinants of Tumor-Stroma Interaction in Non-small Cell Lung Cancer Through the Utilization of RNA-seq Data from Lung Biopsies. <i>IFMBE Proceedings</i> , 2016, , 495-499.	0.2	1
6	Comparative Transcriptome Analysis between Low- and High-Cadmium-Accumulating Genotypes of Pakchoi (<i>Brassica chinensis</i> L.) in Response to Cadmium Stress. <i>Environmental Science & Technology</i> , 2016, 50, 6485-6494.	4.6	167
7	RNAontheBENCH: computational and empirical resources for benchmarking RNAseq quantification and differential expression methods. <i>Nucleic Acids Research</i> , 2016, 44, 5054-5067.	6.5	48
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14	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. <i>Nucleic Acids Research</i> , 2017, 45, e30-e30.	6.5	34
15	Nucleosome repositioning during differentiation of a human myeloid leukemia cell line. <i>Nucleus</i> , 2017, 8, 188-204.	0.6	21
16	Transcriptome profiling of <i>Eucalyptus nitens</i> reveals deeper insight into the molecular mechanism of cold acclimation and deacclimation process. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	17
17	De novo comparative transcriptome analysis of genes involved in fruit morphology of pumpkin cultivars with extreme size difference and development of EST-SSR markers. <i>Gene</i> , 2017, 622, 50-66.	1.0	29
18	Mice heterozygous for an inactivated allele of the schizophrenia associated <i>Brd1</i> gene display selective cognitive deficits with translational relevance to schizophrenia. <i>Neurobiology of Learning and Memory</i> , 2017, 141, 44-52.	1.0	16

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19	Candidate genes mediating magnetoreception in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Biology Letters</i> , 2017, 13, 20170142.	1.0	21
20	Transcriptional response after exposure to domoic acid-producing <i>Pseudo-nitzschia</i> in the digestive gland of the mussel <i>Mytilus galloprovincialis</i> . <i>Toxicon</i> , 2017, 140, 60-71.	0.8	31
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24	Oestrogen receptor beta isoform expression in sporadic colorectal cancer, familial adenomatous polyposis and progressive stages of colorectal cancer. <i>BMC Cancer</i> , 2017, 17, 754.	1.1	7
25	The flightless I protein interacts with RNA-binding proteins and is involved in the genome-wide mRNA post-transcriptional regulation in lung carcinoma cells. <i>International Journal of Oncology</i> , 2017, 51, 347-361.	1.4	5
26	Bias and misleading concepts in an <i>Arnica</i> research study. Comments to improve experimental Homeopathy. <i>Journal of Ayurveda and Integrative Medicine</i> , 2018, 9, 75-80.	0.9	3
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28	Transcriptome profiling and cataloging differential gene expression in floral buds of fertile and sterile lines of cotton (<i>Gossypium hirsutum</i> L.). <i>Gene</i> , 2018, 660, 80-91.	1.0	20
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34	Mouse-to-mouse variation in maturation heterogeneity of smooth muscle cells. <i>Lab on A Chip</i> , 2018, 18, 1875-1883.	3.1	12
35	Transcriptome analysis of differentially expressed genes involved in selenium accumulation in tea plant (<i>Camellia sinensis</i>). <i>PLoS ONE</i> , 2018, 13, e0197506.	1.1	44
36	Guidelines for RNA-seq projects: applications and opportunities in non-model decapod crustacean species. <i>Hydrobiologia</i> , 2018, 825, 5-27.	1.0	13

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44	Comparative transcriptome analysis of the transcriptional heterogeneity in different IgM+ cell subsets from peripheral blood of Nile tilapia (<i>Oreochromis niloticus</i>). <i>Fish and Shellfish Immunology</i> , 2019, 93, 612-622.	1.6	10
45	Comparative transcriptome analysis of two selenium-accumulating genotypes of <i>Aegilops tauschii</i> Coss. in response to selenium. <i>BMC Genetics</i> , 2019, 20, 9.	2.7	10
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54	Quantification of gene expression while taking into account RNA alternative splicing. <i>Genomics</i> , 2019, 111, 1517-1528.	1.3	39

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56	Signature of genome wide gene expression in classical swine fever virus infected macrophages and PBMCs of indigenous vis-a-vis crossbred pigs. <i>Gene</i> , 2020, 731, 144356.	1.0	6
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59	A tree frog (<i>Boana pugnax</i>) dataset of skin transcriptome for the identification of biomolecules with potential antimicrobial activities. <i>Data in Brief</i> , 2020, 32, 106084.	0.5	3
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118	Omics technologies for agricultural microbiology research. , 2022, , 343-394.		0
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