

RSeQC: quality control of RNA-seq experiments

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Citation Report

#	ARTICLE	IF	CITATIONS
1	BSeQC: quality control of bisulfite sequencing experiments. <i>Bioinformatics</i> , 2013, 29, 3227-3229.	1.8	45
2	Jasmonate Signaling. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	5
3	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature Biotechnology</i> , 2013, 31, 1015-1022.	9.4	251
4	Smart-seq2 for sensitive full-length transcriptome profiling in single cells. <i>Nature Methods</i> , 2013, 10, 1096-1098.	9.0	2,022
5	In the Spotlight: Bioinformatics. <i>IEEE Reviews in Biomedical Engineering</i> , 2013, 6, 3-8.	13.1	2
6	Cryopreserved Bovine Spermatozoal Transcript Profile as Revealed by High-Throughput Ribonucleic Acid Sequencing1. <i>Biology of Reproduction</i> , 2013, 88, 49.	1.2	96
7	Analysis of RNA-Seq Data with TopHat and Cufflinks for Genome-Wide Expression Analysis of Jasmonate-Treated Plants and Plant Cultures. <i>Methods in Molecular Biology</i> , 2013, 1011, 305-315.	0.4	68
8	Distributed tools deployment and management for multiple galaxy instances in globus genomics. , 2013, , .		0
9	Decoding human gene expression signatures in the brain. <i>Transcription</i> , 2013, 4, 102-108.	1.7	9
10	Unique Transcriptome Patterns of the White and Grey Matter Corroborate Structural and Functional Heterogeneity in the Human Frontal Lobe. <i>PLoS ONE</i> , 2013, 8, e78480.	1.1	40
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16	Exploring the Transcriptome of Mycorrhizal Interactions. <i>Advances in Botanical Research</i> , 2014, 70, 53-78.	0.5	8
17	Analysis of stranded information using an automated procedure for strand specific RNA sequencing. <i>BMC Genomics</i> , 2014, 15, 631.	1.2	27
18	New gene models and alternative splicing in the maize pathogen <i>Colletotrichum graminicola</i> revealed by RNA-Seq analysis. <i>BMC Genomics</i> , 2014, 15, 842.	1.2	59

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19	FTO-dependent demethylation of N6-methyladenosine regulates mRNA splicing and is required for adipogenesis. <i>Cell Research</i> , 2014, 24, 1403-1419.	5.7	869
20	MultiRankSeq: Multiperspective Approach for RNAseq Differential Expression Analysis and Quality Control. <i>BioMed Research International</i> , 2014, 2014, 1-8.	0.9	50
21	Murine Leukemia Virus Uses NXF1 for Nuclear Export of Spliced and Unspliced Viral Transcripts. <i>Journal of Virology</i> , 2014, 88, 4069-4082.	1.5	36
22	Integrative RNA-seq and microarray data analysis reveals GC content and gene length biases in the psoriasis transcriptome. <i>Physiological Genomics</i> , 2014, 46, 533-546.	1.0	38
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30	Isolation and characterization of human osteoblasts from needle biopsies without in vitro culture. <i>Osteoporosis International</i> , 2014, 25, 887-895.	1.3	26
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56	A resource of ribosomal RNA-depleted RNA-Seq data from different normal adult and fetal human tissues. <i>Scientific Data</i> , 2015, 2, 150063.	2.4	24
57	Advanced Applications of RNA Sequencing and Challenges. <i>Bioinformatics and Biology Insights</i> , 2015, 9s1, BBI.S28991.	1.0	178
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