

Duesselpore: Integrated Webserver for RNAseq analysis.

Before submission, please read [the instruction](#) carefully

Your submission

Upload your fastq files (all-in zip format, group by study group required)

Gene count method

Differential expression method

Number of top variance genes (For Gene Ontology)

Reference group (reference's sub-directory name)

Study group (study groups's sub-directory name)

Reference genes

Cluster replicate

ReadCountMinThreshold (Optional)

LfcThreshold (Optional)

AdjPValueThreshold (Optional)

KEGG id (for pathview)

Submit

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Test_name

Submission name, no space and special character

Choose File No file chosen

Rsubread/featureCounts (Liao et. al. 2014) for gene counts

Gene counting methods

DESeq2 (Love et. al. 2014)

Differential expression algorithm

30

Must be one of your study group, if not 1st group is used

first group

Must be one of your study group, if not 2nd group is used

second group

Human hg38 (Homo sapiens)

Cluster replica for heatmap plot

Yes

Minimum read count threshold for DESeq/edgeR filter

10

Logfold change threshold for gene ontology/pathway

1.0

AdjustPvalue threshold for gene set/ geneontology

0.05

KEGG id gene ontology plot, entry for pathview

hsa04144

