dataset: gene expression RNAseq - TOIL RSEM expected\_count

hub: https://toil.xenahubs.net

cohort [TCGA Pan-Cancer (PANCAN)](https://xenabrowser.net/datapages/?cohort=TCGA%20Pan-Cancer%20(PANCAN)&removeHub=https%3A%2F%2Fxena.treehouse.gi.ucsc.edu%3A443)  
dataset IDtcga\_gene\_expected\_count  
download

<https://toil-xena-hub.s3.us-east-1.amazonaws.com/download/tcga_gene_expected_count.gz>; [Full metadata](https://toil-xena-hub.s3.us-east-1.amazonaws.com/download/tcga_gene_expected_count.json)

samples10530  
version2016-09-01  
type of datagene expression RNAseq  
unitlog2(expected\_count+1)  
ID/Gene Mapping

<https://toil-xena-hub.s3.us-east-1.amazonaws.com/download/probeMap%2Fgencode.v23.annotation.gene.probemap>; [Full metadata](https://toil-xena-hub.s3.us-east-1.amazonaws.com/download/probeMap%2Fgencode.v23.annotation.gene.probemap.json)  
authorUCSC TOIL RNA-seq recompute  
wranglingData (file names: \*.rsem\_genes.results) are downloaded, expected\_count values are extracted, log2(x+1) transformed, and combined.  
input data formatROWs (identifiers) x COLUMNs (samples) (i.e. genomicMatrix)

**Data download**

Expression raw data: TCGAPanCancer\_tcgageneexpectedcount

Clinical raw data: Survival\_SupplementalTable\_S1\_20171025\_xena\_sp\_clinical\_data.rds

Gene annotation: probeMap\_gencode.v23.annotation.gene