

Workflow

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The disease we decided to investigate is breast cancer.

We would like to explore how different treatments effects MCF-7 breast cancer cell line.

We will analyze bulk RNA-seq expression data to run differential expression analysis to compare samples of MCF-7 cells after different treatments.

Accession ID	Location	Count matrix	Groups	Citation
E-GEOD-51403	E-GEOD-51403 < Browse < ArrayExpress < EMBL-EBI	yes	Treatment (10nM E2 treatment for 24h) and control MCF7 cells	Liu Y, Zhou J, White KP. RNA-seq differential expression studies: more sequence or more replication? <i>Bioinformatics</i> 2014 Feb 1;30(3):301-4. PMID: 24319002
E-GEOD-59251	E-GEOD-59251 < Browse < ArrayExpress < EMBL-EBI	yes	MCF-7 cells were treated with either ZNA (30 uM) or a vehicle control for 3 or 12 hours.	