

# Bulk RNA-Seq

This tutorial gives an overview of RNA-Seq analysis with Partek Flow. It will guide you through creating an RNA-Seq analysis pipeline. The goals of the analysis are to create a list of differentially expressed genes, visualize these gene expression signatures by hierarchical clustering, and interpret the gene lists using gene ontology (GO) enrichment.

This tutorial will illustrate:

- [Importing the tutorial data set](#)
- [Adding sample attributes](#)
- [Running pre-alignment QA/QC](#)
- [Trimming bases and filtering reads](#)
- [Aligning to a reference genome](#)
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## Description of the Data Set

This tutorial uses a subset of the data set published in Xu et al. 2013 (PMID: 23902433). In the experiment, mRNA was isolated from HT29 colon cancer cells treated with the drug 5-aza-deoxy-cytidine (5-aza) at three different doses: 0M (control), 5M, or 10M. The mRNA was sequenced using Illumina HiSeq (paired end reads). The goal of the experiment was to identify differentially expressed genes between the different treatment groups.

## Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



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