

# GenePattern

## ExprToGct Documentation

**Description:** Converts an EXPR file to GCT format.

**Contact:** GenePattern Help, [gp-help@broadinstitute.org](mailto:gp-help@broadinstitute.org)

### Summary

This module converts a file in EXPR format to GCT format.

The EXPR file format is a tab-delimited format produced by the [Cufflinks](#) module. The ExprToGct module extracts expression data from an EXPR file and writes it to a GCT file. For each transcript or gene ID, the EXPR file contains Fragments Per Kilobase of exon model per Million mapped fragments (FPKM). The FPKM values are written to the data column of the GCT file, while the chromosome name and left and right coordinates are written to the Description column of the GCT file. Finally, the first column of the EXPR file is used for the Name column, or row identifiers, in the GCT file.

The GCT format is a tab-delimited file format that describes an expression dataset commonly used in GenePattern and other tools. More information can be found here: [http://www.broadinstitute.org/cancer/software/genepattern/tutorial/gp\\_fileformats.html](http://www.broadinstitute.org/cancer/software/genepattern/tutorial/gp_fileformats.html).

### Links

Cufflinks documentation: <http://cufflinks.cbcn.umd.edu/>

### Parameters

Name	Description
input.file	The input file in EXPR format.
output.prefix	A label that will be used to name the GCT output file.

### Output Files

1. <output.prefix>.gct

This GCT file contains the row identifiers, chromosome names, left and right coordinates and FPKM values from the EXPR file.

### Platform Dependencies

**Module type:** Data Format Conversion

**CPU type:** any

**OS:** any

**Language:** Perl