

Tools

search tools

[Get Data](#)[Send Data](#)[ENCODE Tools](#)[Lift-Over](#)[Text Manipulation](#)[Filter and Sort](#)[Join, Subtract and Group](#)[Convert Formats](#)[Extract Features](#)[Fetch Sequences](#)[Fetch Alignments](#)[Get Genomic Scores](#)[Operate on Genomic Intervals](#)[Statistics](#)[Wavelet Analysis](#)[Graph/Display Data](#)[Regional Variation](#)[Multiple regression](#)[Multivariate Analysis](#)[Evolution](#)[Motif Tools](#)[Multiple Alignments](#)[Metagenomic analyses](#)[FASTA manipulation](#)[NGS: QC and manipulation](#)[NGS: Mapping](#)[NGS: Indel Analysis](#)[NGS: RNA Analysis](#)[NGS: SAM Tools](#)[NGS: GATK Tools \(beta\)](#)[NGS: Peak Calling](#)[NGS: Simulation](#)[SNP/WGA: Data; Filters](#)[SNP/WGA: QC; LD; Plots](#)[SNP/WGA: Statistical Models](#)[Phenotype Association](#)[VCF Tools](#)

Welcome to Galaxy on the Cloud

managed by CloudMan

History

Unnamed history

0 bytes

i Your history is empty. Click 'Get Data' on the left pane to start