
































Overview of CoBRA layout

A

 metasheet.csv	Comma Separated Spreadsheet (.csv)
 config.yaml	YAML
 Snakefile	File
 README.md	Markdown File
 scripts	Directory
 ref_files	Directory
 analysis	Directory

B

▼  analysis
▼  clustering_analysis
▼  rpkm.1_num_sample.0_scale.q_fliter.cov.2
▼  plots
▼  images
 heatmapSF_plot_2_percent
 heatmapSS_plot_2_percent
 pca_plot_2_percent
 read_counts
▶  rpkm.2_num_sample.3_scale.q_fliter.cov.2
▼  differential_peaks
▼  Met_over_Tumor
▼  GSEA
▶  C2_Curated.GseaPreranked.1587247351823
▶  H_Hallmark.GseaPreranked.1587247292750
 cistrome_toolkit
▼  logs
 clean_bam
 read_coutns
 remove_duplicates
 reorder
▼  preprocessed_files
▼  bam
 clean_bam
 remove_chrMY
 remove_duplicates
 reorder
 sorted_reads
▶  bed
▶  bigwig
▶  read_counts