MultiQC

Sample MultiQC report: NHD13_GEO RNAseq

Project Type	RNA-seq
Library Preparation	
Sequencing Platform	
Data Formatting	bcltofastq-2.19.0
Data Cleaning	fastp 0.20.1, --in1 ../${SAMPLE}_R1.fastq.gz --out1 clt_${SAMPLE}_R1.fastq.gz --length_required 35 --cut_front_window_size 1 --cut_front_mean_quality 13 --cut_front --cut_tail_window_size 1 --cut_tail_mean_quality 13 --cut_tail -w 8 -y -r -j ${SAMPLE}_fastp.json
Genome Alignment	STAR_2.7.6a, --twopassMode Basic --runMode alignReads --genomeDir ${GENOME} --readFilesIn ${SAMPLE} --outSAMtype BAM Unsorted --outSAMstrandField intronMotif --outFilterIntronMotifs RemoveNoncanonical
Reference Genome	
Read Quantification1	subread-2.0.1, featurecounts, -s 2 -t exon -g gene_name
Read Quantification3	salmon-1.3.0, --seqBias --gcBias --posBias

Report generated on 2022-02-07, 13:31 based on data in: `/gpfs/fs2/scratch/grc_group/dalia_ongoing/Project_NHD13_GEO`

Welcome! Not sure where to start? Watch a tutorial video (6:08) don't show again

General Statistics

Copy table | Configure Columns | Plot | Showing $^{6}/_{6}$ rows and $^{10}/_{11}$ columns.

Sample Name	% Duplication	GC content	% PF	% Adapter	% Aligned	M Aligned	% Assigned	M Assigned	% Aligned	M Aligned
NHD13_1	31.6%	49.1%	96.3%		80.6%	13.5	50.2%	11.5	68.7%	14.9
NHD13_2	32.9%	48.8%	96.4%		81.4%	14.1	52.4%	12.3	91.3%	15.8
NHD13_3	32.9%	48.7%	96.5%	2.6%	81.4%	14.2	52.1%	12.3	90.8%	15.9
WT_1	31.7%	48.4%	96.5%		81.8%	12.5	52.7%	10.8	90.8%	13.9
WT_2	32.1%	48.8%	96.4%	2.7%	82.2%	13.4	53.5%	11.7	91.2%	14.9
WT_3	32.9%	48.2%	96.4%	2.5%	81.8%	14.2	52.7%	12.3	91.0%	15.8

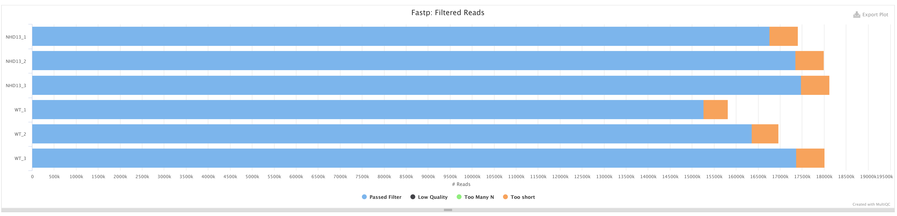
FastP

FastP An ultra-fast all-in-one FASTQ preprocessor (QC, adapters, trimming, filtering, splitting...)

Filtered Reads

Filtering statistics of sampled reads.

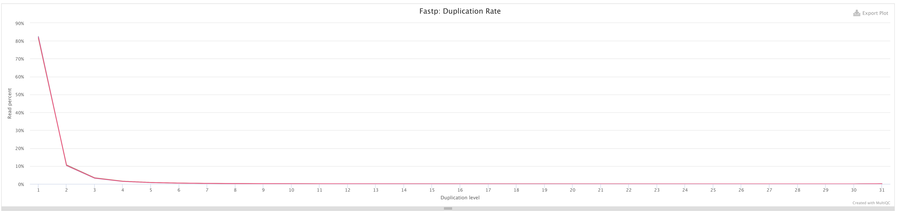
Number of Reads | Percentages



Duplication Rates

Duplication rates of sampled reads.

Y-Limits:

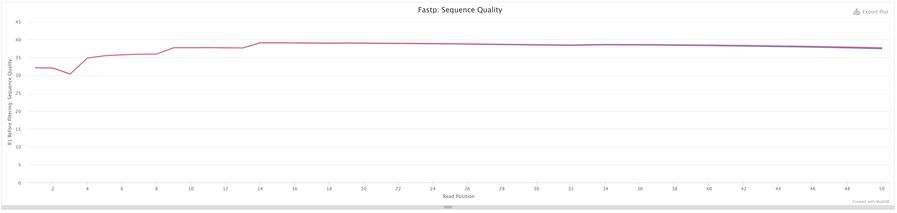


Sequence Quality

Average sequencing quality over each base of all reads.

Y-Limits:

Read 1: Before filtering | Read 1: After filtering

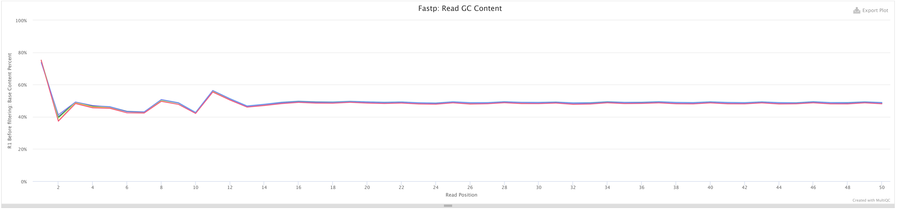


GC Content

Average GC content over each base of all reads.

Y-Limits:

Read 1: Before filtering | Read 1: After filtering



N content

Average N content over each base of all reads.

Y-Limits:

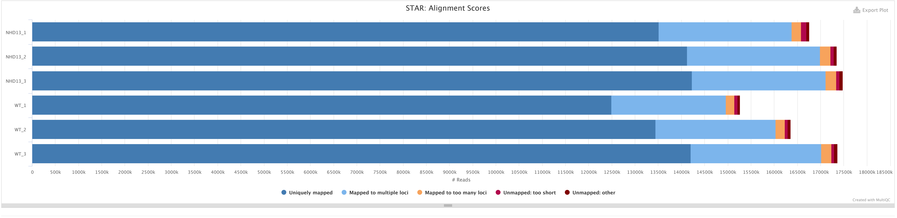
Read 1: Before filtering | Read 1: After filtering

STAR

STAR is an ultrafast universal RNA-seq aligner.

Alignment Scores

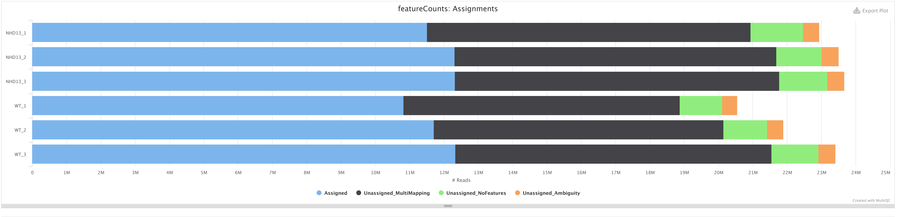
Number of Reads | Percentages



FeatureCounts (Unique Reads)

Subread featureCounts is a highly efficient general-purpose read summarization program that counts mapped reads for genomic features such as genes, exons, promoter, gene bodies, genomic bins and chromosomal locations.

Number of Reads | Percentages



Salmon

Salmon is a tool for quantifying the expression of transcripts using RNA-seq data.

Y-Limits: