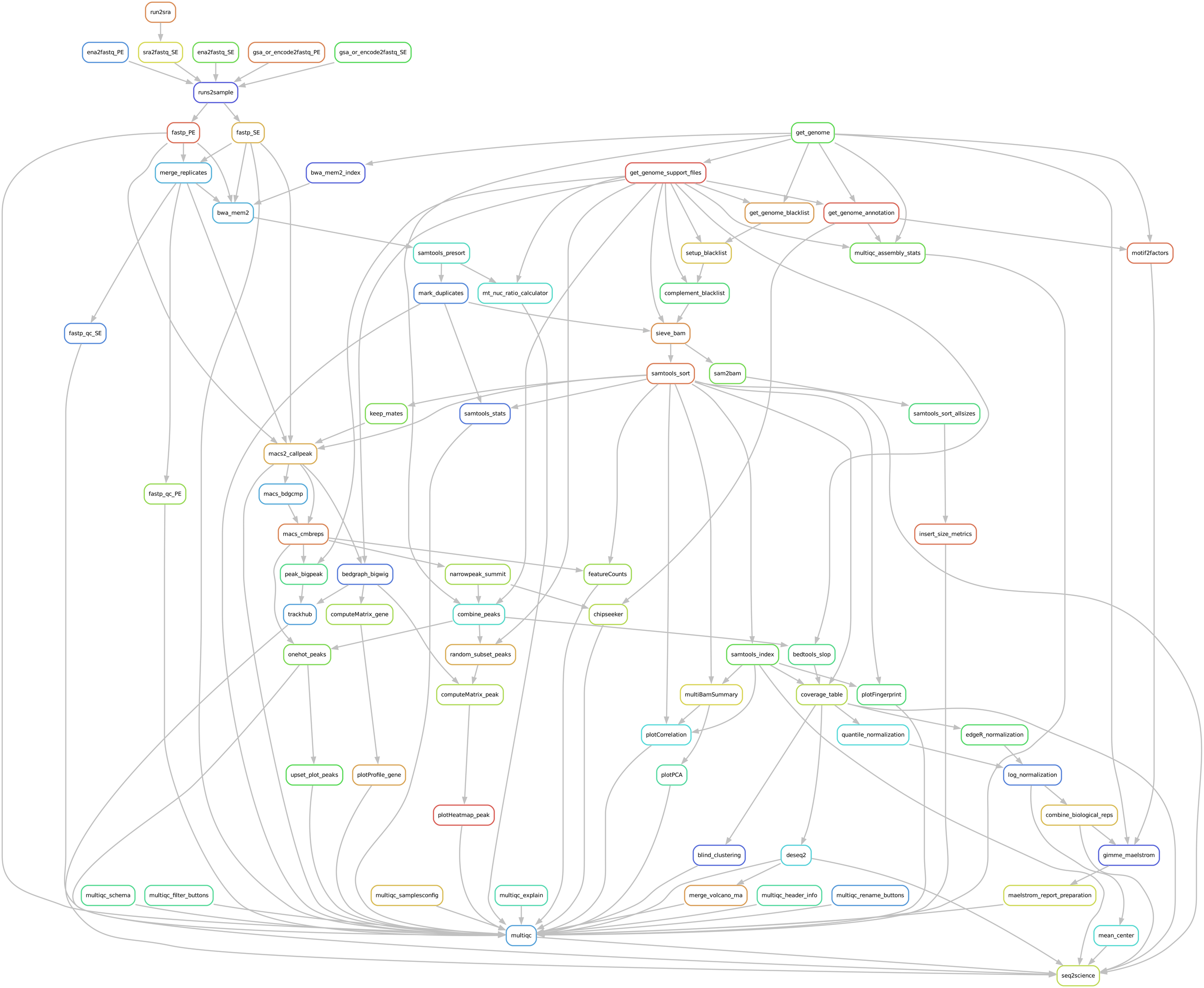
run2sra
ena2fastq_PE
sra2fastq_SE
ena2fastq_SE
gsa_or_encode2fastq_PE
gsa_or_encode2fastq_SE
runs2sample
fastp_PE
fastp_SE
get_genome
merge_replicates
bwa_mem2_index
get_genome_support_files
bwa_mem2
get_genome_blacklist
get_genome_annotation
samtools_presort
setup_blacklist
multiqc_assembly_stats
motif2factors
mark_duplicates
mt_nuc_ratio_calculator
complement_blacklist
fastp_qc_SE
sieve_bam
samtools_sort
sam2bam
keep_mates
samtools_stats
samtools_sort_allsizes
macs2_callpeak
fastp_qc_PE
macs_bdgcmp
macs_cmbreps
insert_size_metrics
peak_bigpeak
bedgraph_bigwig
narrowpeak_summit
featureCounts
trackhub
computeMatrix_gene
combine_peaks
chipseeker
onehot_peaks
random_subset_peaks
samtools_index
bedtools_slop
computeMatrix_peak
multiBamSummary
coverage_table
plotFingerprint
plotCorrelation
quantile_normalization
edgeR_normalization
upset_plot_peaks
plotProfile_gene
plotPCA
log_normalization
plotHeatmap_peak
combine_biological_reps
blind_clustering
deseq2
gimme_maelstrom
multiqc_schema
multiqc_filter_buttons
multiqc_samplesconfig
multiqc_explain
merge_volcano_ma
multiqc_header_info
multiqc_rename_buttons
maelstrom_report_preparation
multiqc
mean_center
seq2science