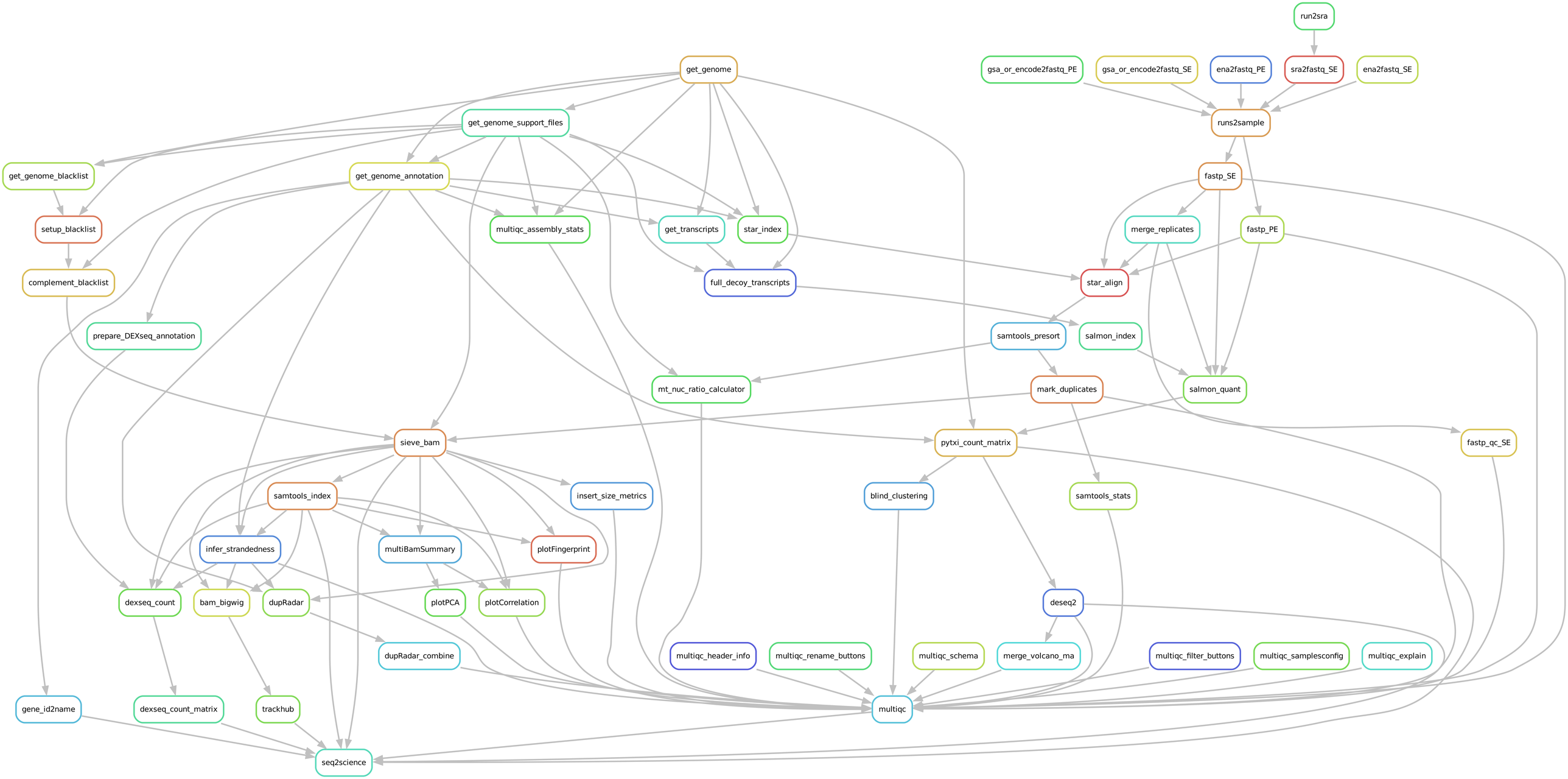
run2sra
get_genome
gsa_or_encode2fastq_PE
gsa_or_encode2fastq_SE
ena2fastq_PE
sra2fastq_SE
ena2fastq_SE
get_genome_support_files
runs2sample
get_genome_blacklist
get_genome_annotation
fastp_SE
setup_blacklist
multiqc_assembly_stats
get_transcripts
star_index
merge_replicates
fastp_PE
complement_blacklist
full_decoy_transcripts
star_align
prepare_DEXseq_annotation
samtools_presort
salmon_index
mt_nuc_ratio_calculator
mark_duplicates
salmon_quant
sieve_bam
pytxi_count_matrix
fastp_qc_SE
samtools_index
insert_size_metrics
blind_clustering
samtools_stats
infer_strandedness
multiBamSummary
plotFingerprint
dexseq_count
bam_bigwig
dupRadar
plotPCA
plotCorrelation
deseq2
dupRadar_combine
multiqc_header_info
multiqc_rename_buttons
multiqc_schema
merge_volcano_ma
multiqc_filter_buttons
multiqc_samplesconfig
multiqc_explain
gene_id2name
dexseq_count_matrix
trackhub
multiqc
seq2science