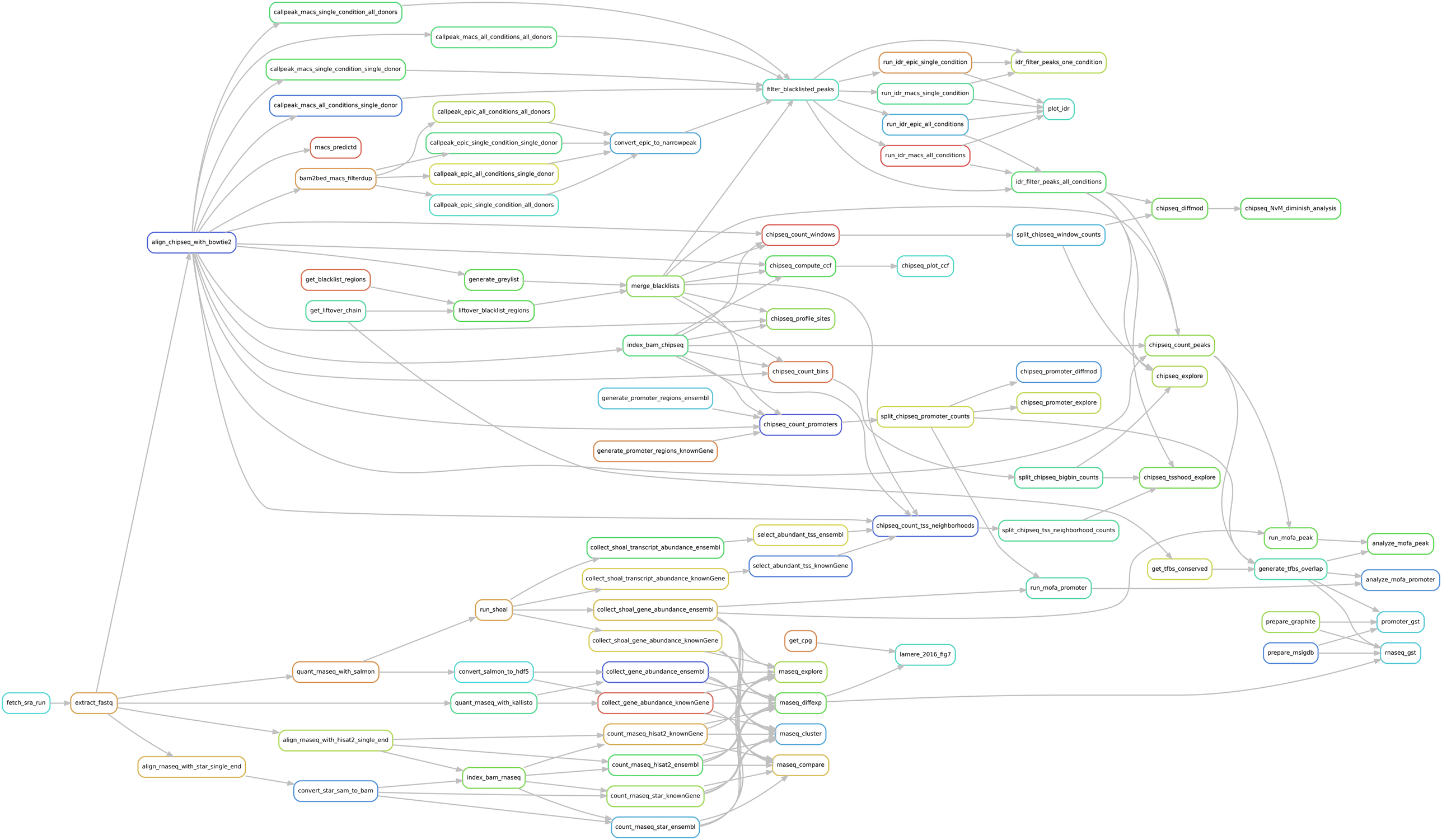
callpeak_macs_single_condition_all_donors
callpeak_macs_all_conditions_all_donors
callpeak_macs_single_condition_single_donor
callpeak_macs_all_conditions_single_donor
macs_predictd
bam2bed_macs_filterdup
callpeak_epic_all_conditions_all_donors
callpeak_epic_single_condition_single_donor
callpeak_epic_all_conditions_single_donor
callpeak_epic_single_condition_all_donors
convert_epic_to_narrowpeak
filter_blacklisted_peaks
run_idr_epic_single_condition
run_idr_macs_single_condition
run_idr_epic_all_conditions
run_idr_macs_all_conditions
idr_filter_peaks_one_condition
plot_idr
idr_filter_peaks_all_conditions
chipseq_diffmod
chipseq_NvM_diminish_analysis
align_chipseq_with_bowtie2
chipseq_count_windows
split_chipseq_window_counts
chipseq_compute_ccf
chipseq_plot_ccf
get_blacklist_regions
generate_greylist
merge_blacklists
get_liftover_chain
liftover_blacklist_regions
chipseq_profile_sites
index_bam_chipseq
chipseq_count_peaks
chipseq_count_bins
chipseq_explore
chipseq_promoter_diffmod
generate_promoter_regions_ensembl
chipseq_promoter_explore
split_chipseq_promoter_counts
chipseq_count_promoters
generate_promoter_regions_knownGene
split_chipseq_bigbin_counts
chipseq_tsshood_explore
chipseq_count_tss_neighborhoods
split_chipseq_tss_neighborhood_counts
select_abundant_tss_ensembl
run_mofa_peak
analyze_mofa_peak
collect_shoal_transcript_abundance_ensembl
select_abundant_tss_knownGene
get_tfbs_conserved
generate_tfbs_overlap
collect_shoal_transcript_abundance_knownGene
run_mofa_promoter
analyze_mofa_promoter
run_shoal
collect_shoal_gene_abundance_ensembl
prepare_graphite
promoter_gst
collect_shoal_gene_abundance_knownGene
get_cpg
lamere_2016_fig7
prepare_msigdb
rnaseq_gst
quant_rnaseq_with_salmon
convert_salmon_to_hdf5
collect_gene_abundance_ensembl
rnaseq_explore
fetch_sra_run
extract_fastq
quant_rnaseq_with_kallisto
collect_gene_abundance_knownGene
rnaseq_diffexp
align_rnaseq_with_hisat2_single_end
count_rnaseq_hisat2_knownGene
rnaseq_cluster
align_rnaseq_with_star_single_end
count_rnaseq_hisat2_ensembl
rnaseq_compare
index_bam_rnaseq
convert_star_sam_to_bam
count_rnaseq_star_knownGene
count_rnaseq_star_ensembl