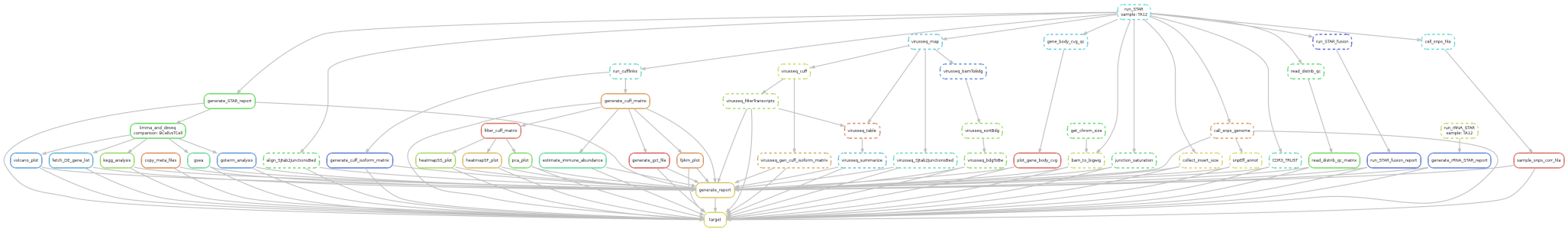
run_STAR
sample: TA12
virusseq_map
gene_body_cvg_qc
run_STAR_fusion
call_snps_hla
run_cufflinks
virusseq_cuff
virusseq_bam1bldg
read_distrib_qc
generate_STAR_report
generate_cuff_matrix
virusseq_filterTranscripts
limma_and_deseq
comparison: BCellvsTCell
filter_cuff_matrix
virusseq_table
virusseq_sortBdg
get_chrom_size
call_snps_genome
run_rRNA_STAR
sample: TA12
volcano_plot
fetch_DE_gene_list
kegg_analysis
copy_meta_files
gsea
goterm_analysis
align_STAR2junctionsBed
generate_cuff_isoform_matrix
heatmapSS_plot
heatmapST_plot
pca_plot
estimate_immune_abundance
generate_gct_file
fpkm_plot
virusseq_gen_cuff_isoform_matrix
virusseq_summarize
virusseq_STAR2junctionsBed
virusseq_bdgToBw
plot_gene_body_cvg
bam_to_bigwig
junction_saturation
collect_insert_size
snpEff_annot
CDR3_TRUST
read_distrib_qc_matrix
run_STAR_fusion_report
generate_rRNA_STAR_report
sample_snps_corr_hla
generate_report
target