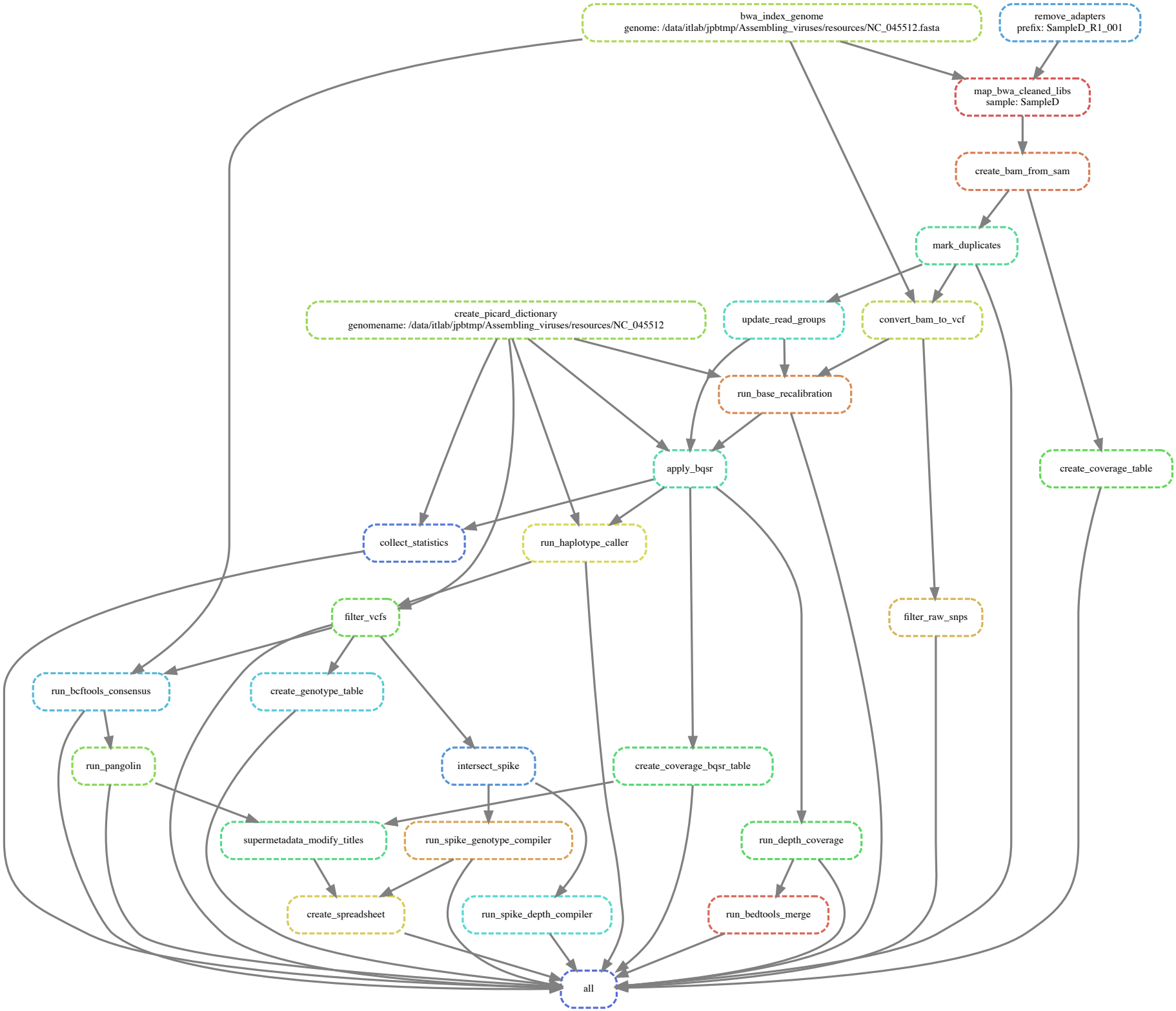
bwa_index_genome
genome: /data/itlab/jpbtmp/Assembling_viruses/resources/NC_045512.fasta
remove_adapters
prefix: SampleD_R1_001
map_bwa_cleaned_libs
sample: SampleD
create_bam_from_sam
mark_duplicates
create_picard_dictionary
genomename: /data/itlab/jpbtmp/Assembling_viruses/resources/NC_045512
update_read_groups
convert_bam_to_vcf
run_base_recalibration
apply_bqsr
create_coverage_table
collect_statistics
run_haplotype_caller
filter_vcfs
filter_raw_snps
run_bcftools_consensus
create_genotype_table
run_pangolin
intersect_spike
create_coverage_bqsr_table
supermetadata_modify_titles
run_spike_genotype_compiler
run_depth_coverage
create_spreadsheet
run_spike_depth_compiler
run_bedtools_merge
all