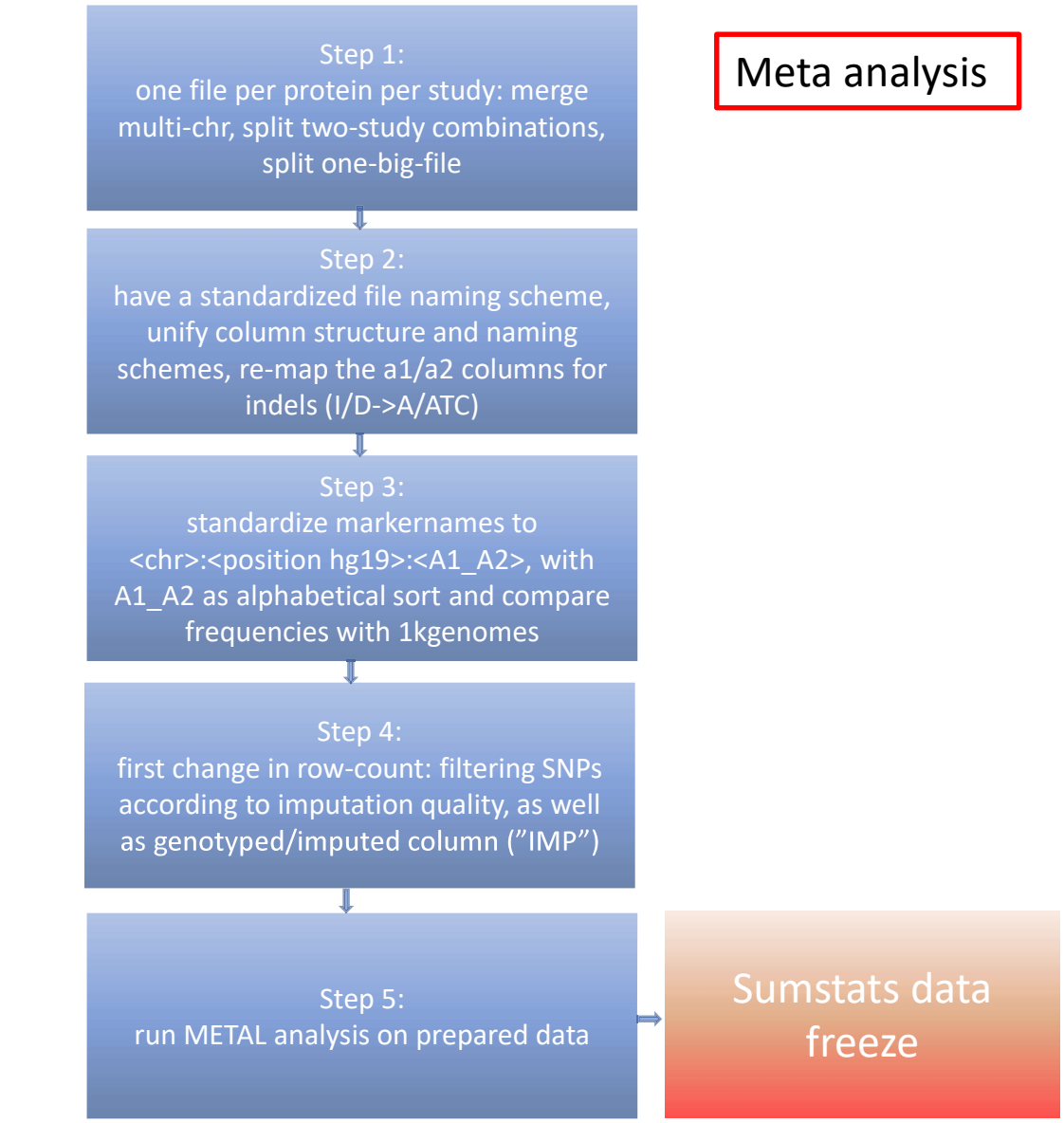
A)


Step 1:
one file per protein per study: merge multi-chr, split two-study combinations, split one-big-file
Step 2:
have a standardized file naming scheme, unify column structure and naming schemes, re-map the a1/a2 columns for indels (I/D->A/ATC)
Step 3:
standardize markernames to <chr>:<position hg19>:<A1_A2>, with A1_A2 as alphabetical sort and compare frequencies with 1kgenomes
Step 4:
first change in row-count: filtering SNPs according to imputation quality, as well as genotyped/imputed column (”IMP”)
Step 5:
run METAL analysis on prepared data
Meta analysis
Sumstats data freeze