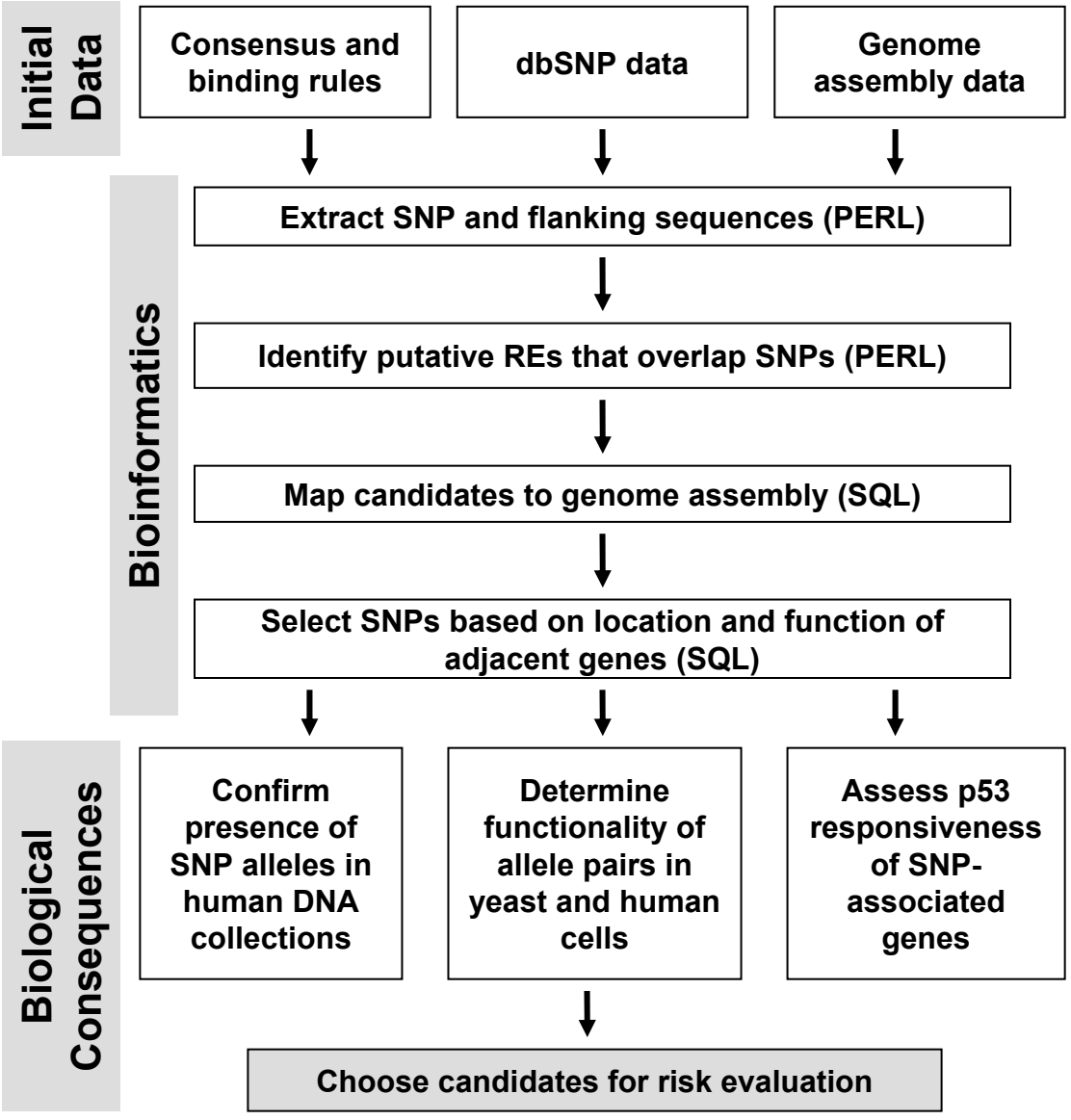
Initial Data
Consensus and binding rules
dbSNP data
Genome assembly data
Bioinformatics
Extract SNP and flanking sequences (PERL)
Identify putative REs that overlap SNPs (PERL)
Map candidates to genome assembly (SQL)
Select SNPs based on location and function of adjacent genes (SQL)
Biological Consequences
Confirm presence of SNP alleles in human DNA collections
Determine functionality of allele pairs in yeast and human cells
Assess p53 responsiveness of SNP-associated genes
Choose candidates for risk evaluation