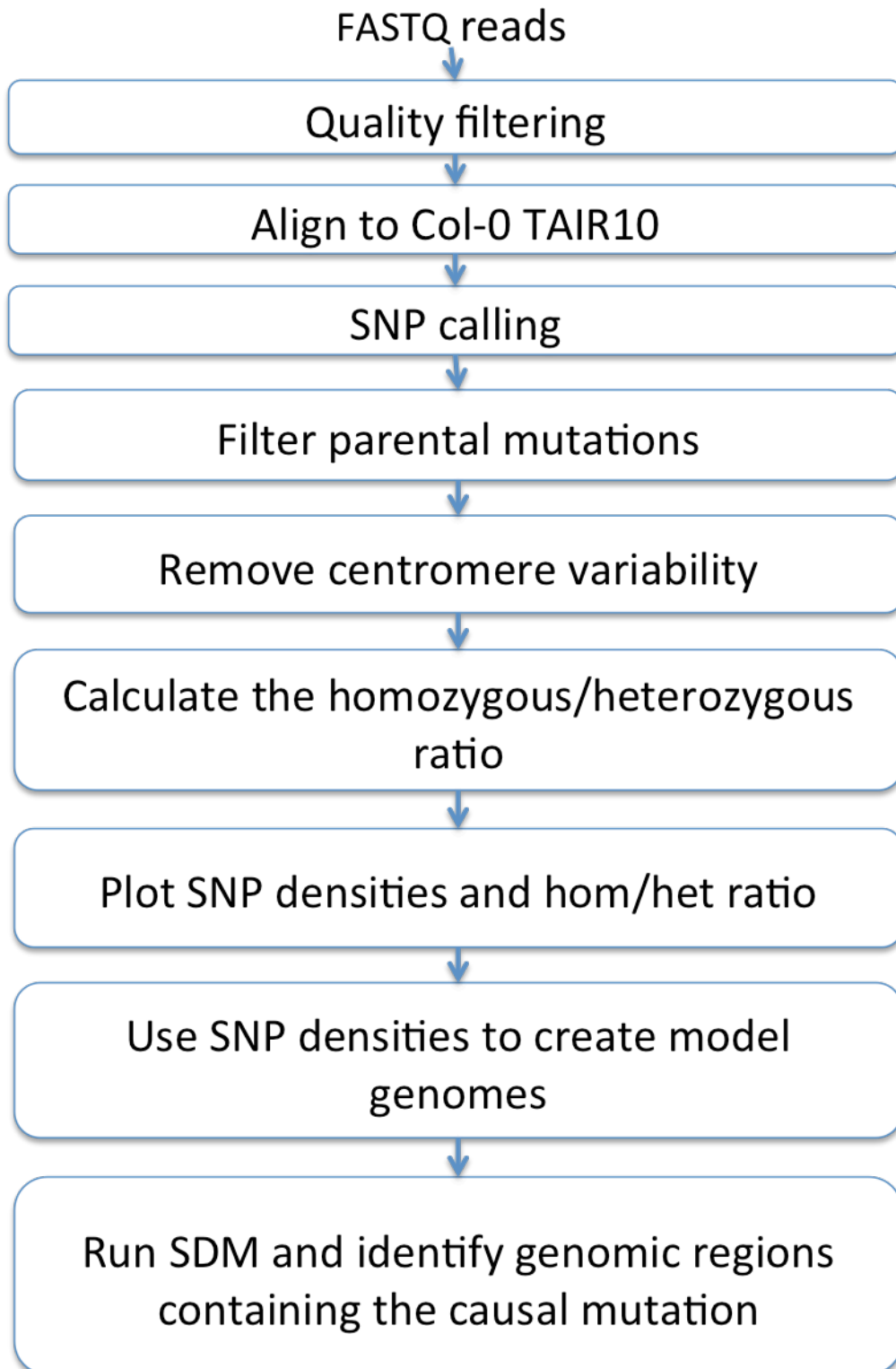# Additional figures

Additional figure 1 Standard pipeline for sequence alignment and SNP calling in forward genetic screens in *Arabipdopsis thaliana*.

Additional figure 2 Importance of the filtering step. Homozygous SNP distribution before filtering, after background SNPs filtering and after centromere removal.

FASTQ reads

Quality filtering

Align to Col-0 TAIR10

SNP calling

Filter parental mutations

Remove centromere variability

Calculate the homozygous/heterozygous ratio

Plot SNP densities and hom/het ratio

Use SNP densities to create model genomes

Run SDM and identify genomic regions containing the causal mutation

Additional Figure 2

Pre-filtering SNP distributions

Parental SNP filtering

Centromere removal