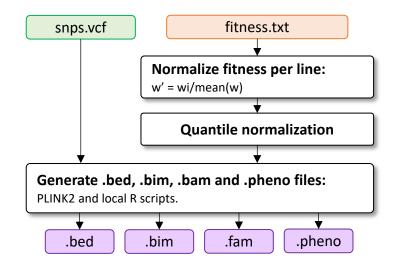
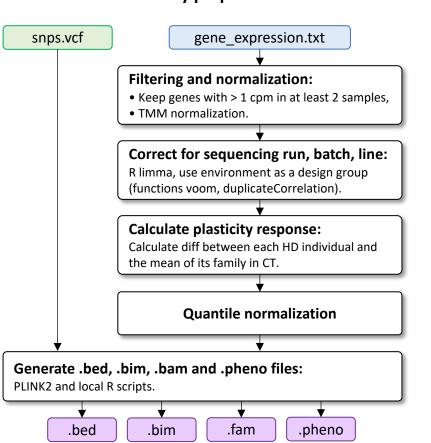
Expression levels preparation

Filtering and normalization: • Keep genes with > 1 cpm in at least 2 samples, • TMM normalization. Correct for sequencing run, batch, line: R limma (functions voom, duplicateCorrelation). Quantile normalization Generate .bed, .bim, .bam and .pheno files: PLINK2 and local R scripts. .bed .bim .fam .pheno

Fitness preparation



Plasticity preparation



eQTL mapping

