

Pipeline

Raw reads



Alignment: reference Galgal4; BWA



Remove duplication: picard-tools



Call variants : GATK/freebayes/SAMtools



Select SNP: GATK



Hard filtering : DP & mapping quality



Separate brown and white layers: GATK



Exclude monomorphic SNPs



Improve the quality of genotype : Beagle



Imputation: minimac/FImpute/IMPUTE2