RNA Data Processing

RAW RNA-seq Data of FASTA/FASTAQ Format

Map Reads to Reference Genome

Map Reads to Individual-specific haploid genomes

Mapped Reads as BAM files

DNA Data Processing

DNA genotype data in the study sample

haplotype data from reference panels

Phasing, e.g., by MACH or BEAGLE

phased, imputed haplotype data in the study sample

Counting

QC and counting
Remove reads with mapping ambiguity or low mapping quality
To count for allele-specific reads, remove those reads with low mapping quality at the SNP position.

eQTL Mapping

TReC per gene per sample
ASE per gene per sample per allele

Covariates, such as total reads per sample, batch, gender, age, etc.

PCs estimated from standardized TReC Data

eQTL mapping using TReC and ASE