

TCGA-OV genotype imputation log

Variant imputation

Michigan imputation server (<https://imputationserver.sph.umich.edu>) was used to impute for missing genotypes.

Autosomes (chr 1 – 22)

Chromosomes: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

SNPs: 868263

Chunks: 153

Datatype: unphased

Reference Panel: phase3

Phasing: eagle

Statistics:

Alternative allele frequency > 0.5 sites: 235,699

Reference Overlap: 99.67%

Match: 860,761

Allele switch: 0

Strand flip: 0

Strand flip and allele switch: 0

A/T, C/G genotypes: 0

Filtered sites:

Filter flag set: 0

Invalid alleles: 448

Duplicated sites: 2

NonSNP sites: 0

Monomorphic sites: 1,088

Allele mismatch: 3,105

SNPs call rate < 90%: 0

X chromosome

Chromosomes: X

SNPs: 36764

Chunks: 8

Datatype: unphased

Reference Panel: phase3

Phasing: shapeit

Statistics:

Alternative allele frequency > 0.5 sites: 0

Reference Overlap: 99.05%

Match: 26,353

Allele switch: 7,769

Strand flip: 0

Strand flip and allele switch: 0

A/T, C/G genotypes: 1,383

Filtered sites:

Filter flag set: 0

Invalid alleles: 0

Duplicated sites: 0

NonSNP sites: 0

Monomorphic sites: 785

Allele mismatch: 133

SNPs call rate < 90%: 0

Total number of variants

	Autosomes	X-chromosome
Before imputation	868,263	36,764
After imputation	46,181,723	1,778,607