

# Genotype Imputation (Minimac4) 1.7.1

This is the new Michigan Imputation Server Pipeline using [Minimac4](#). Documentation can be found [here](#).

If your input data is **GRCh37/hg19** please ensure chromosomes are encoded without prefix (e.g. **20**).

If your input data is **GRCh38hg38** please ensure chromosomes are encoded with prefix 'chr' (e.g. **chr20**). [🔗](#)

<https://imputationserver.readthedocs.io>

▶ Run

Name

Biopsies

Reference Panel

TOPMed r2



[\(Details\)](#)

Input Files [\(VCF\)](#)

File Upload



- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr1.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr2.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr3.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr4.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr5.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr6.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr7.vcf.gz
- 📄 CEDAR-clean-snp-2\_mixed\_build\_chr8.vcf.gz

📁 Select Files

Multiple files can be selected by using the **ctrl** / **cmd** or **shift** keys.

Array Build

GRCh38/hg38



Please note that the final SNP coordinates always match the reference build.

rsq Filter

0.3



Phasing

Eagle v2.4 (phased output)



Population

vs. TOPMed Panel



Mode

Quality Control & Imputation



AES 256 encryption

Imputation Server encrypts all zip files by default. Please note that AES encryption does not work with standard unzip programs. Use 7z instead.

Generate Meta-imputation file

I will not attempt to re-identify or contact research participants.

I will report any inadvertent data release, security breach or other data management incident of which I become aware.

▶ Submit Job

