Genotype Imputation (Minimac4) 1.6.6

This is the new Michigan Imputation Server Pipeline using <u>Minimac4</u>. Documentation can be found <u>here</u>.

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**). 🔗
<u>https://imputationserver.readthedocs.io</u>

▶ Run

Name	2023_01

Reference Panel (<u>Details</u>)	TOPMed r2 ⌄

Input Files (<u>VCF</u>)	File Upload ⌄
	📄 CEDAR-clean-snps-2_mixed_build_chr1.vcf.gz
	📄 CEDAR-clean-snps-2_mixed_build_chr2.vcf.gz
	📄 CEDAR-clean-snps-2_mixed_build_chr3.vcf.gz
	📄 CEDAR-clean-snps-2_mixed_build_chr4.vcf.gz
	📄 CEDAR-clean-snps-2_mixed_build_chr5.vcf.gz
	📄 CEDAR-clean-snps-2_mixed_build_chr6.vcf.gz
	📄 CEDAR-clean-snps-2_mixed_build_chr7.vcf.gz
	📄 CEDAR-clean-snps-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 & Imputatior ⌄

　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**