

iMETHYL

An integrative human DNA methylation variation and multi-omics database

<http://imethyl.iwate-megabank.org/>

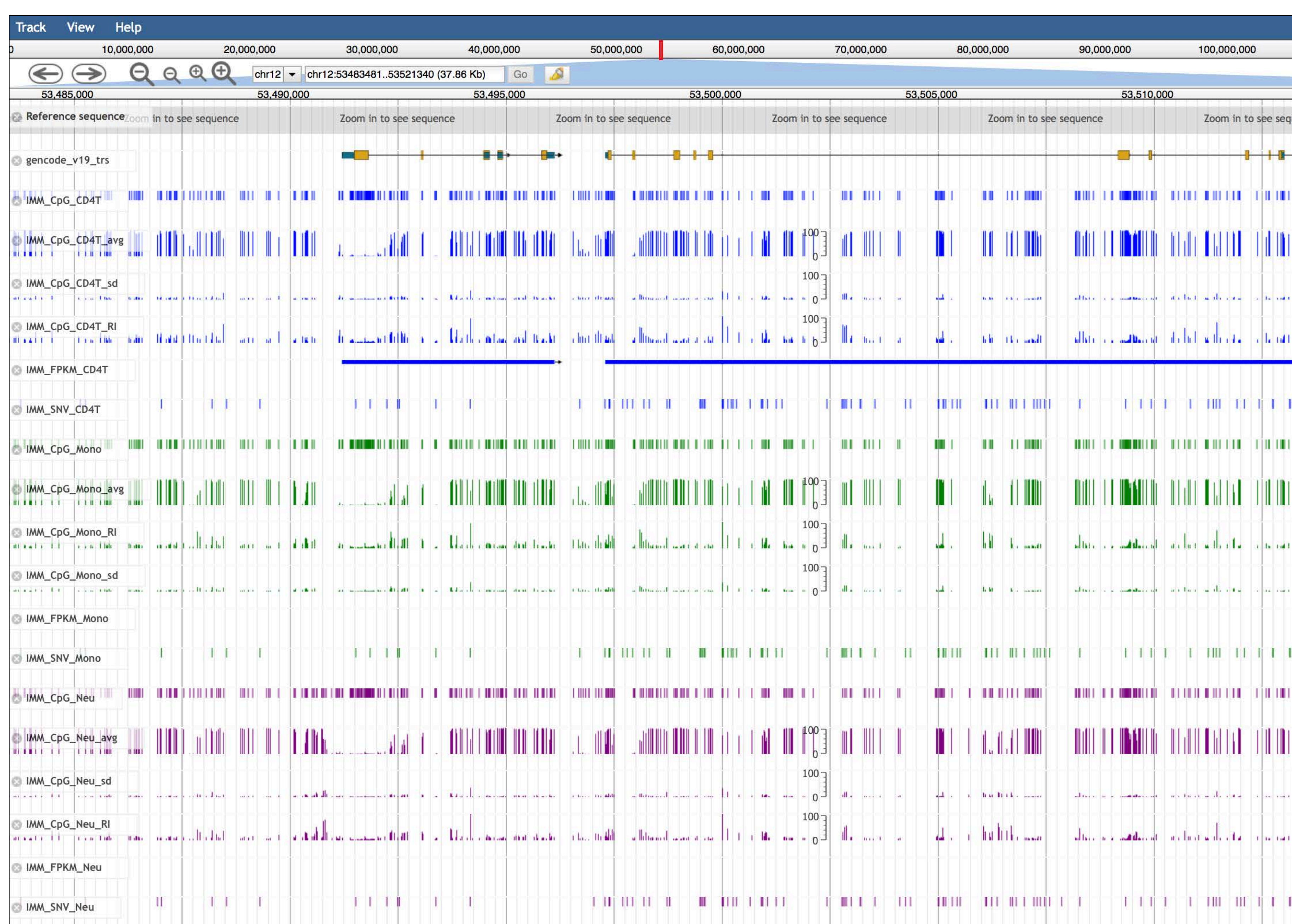
What is iMETHYL?

- The first database of DNA methylation (DNAm) variation based on high-coverage whole-genome bisulfite sequencing (WGBS) (covering ~90% of CpGs in the reference human genome).
- Integrates whole-genome DNA methylation, whole-genome, and whole-transcriptome analyses.
- Provides cell type-specific omics data: CD4⁺ T cells, monocytes, and neutrophils.
- Additional information will be released: expression and metabolomic quantitative trait loci (eQTL and mQTL) and expression quantitative trait methylation (eQTM).
- Summary data are downloadable.

iMETHYL genome browser

Komaki S., Sasaki M., Shimizu A., et al.: *Human Genome Variation, in press* (2018).

Genome browser



- Gene structure**
- CD4⁺ T cells**
 - CpG site
 - Mean DNAm level
 - SD of DNAm level
 - RI of DNAm level
 - Gene expression level
 - SNV
- Monocytes**
 - CpG site
 - Mean DNAm level
 - SD of DNAm level
 - RI of DNAm level
 - Gene expression level
 - SNV
- Neutrophils**
 - CpG site
 - Mean DNAm level
 - SD of DNAm level
 - RI of DNAm level
 - Gene expression level
 - SNV

Click CpG/Gene/SNV bars

Pop-up windows

DNA methylation level

Gene expression level

Allele frequency

- Details of methylation rate, gene expression, and allele frequency (mean and SD)

Dataset

		CD4 ⁺ T cells	Monocytes	Neutrophils
	<i>N</i> (Female)	102 (53)	102 (54)	94 (46)
DNA methylation data (WGBS)	# of CpGs ^{*1}	24,037,541	23,941,843	25,483,031
Genotype data (WGS ^{*2})	# of SNVs ^{*3}	8,951,822	8,945,669	8,792,880
Gene expression data (RNA-seq)	# of genes ^{*4}	16,789	18,894	14,534

^{*1}With an MAF of >1%. ^{*2}DNA extracted from buffy coats was used. ^{*3}With a call rate of ≥50%. ^{*4}With an FPKM ≥ 0.1 in ≥50% of subjects

Contact

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