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


Dataset

<table>
<thead>
<tr>
<th></th>
<th>CD4+ T cells</th>
<th>Monocytes</th>
<th>Neutrophils</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotype data (WGS)</td>
<td>24,037,541</td>
<td>23,941,843</td>
<td>25,483,031</td>
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<tr>
<td>Genotype data (WGS)</td>
<td>8,951,822</td>
<td>8,945,669</td>
<td>8,792,880</td>
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<tr>
<td>Gene expression data (RNA-seq)</td>
<td>16,789</td>
<td>18,894</td>
<td>14,534</td>
</tr>
</tbody>
</table>

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

Contact

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