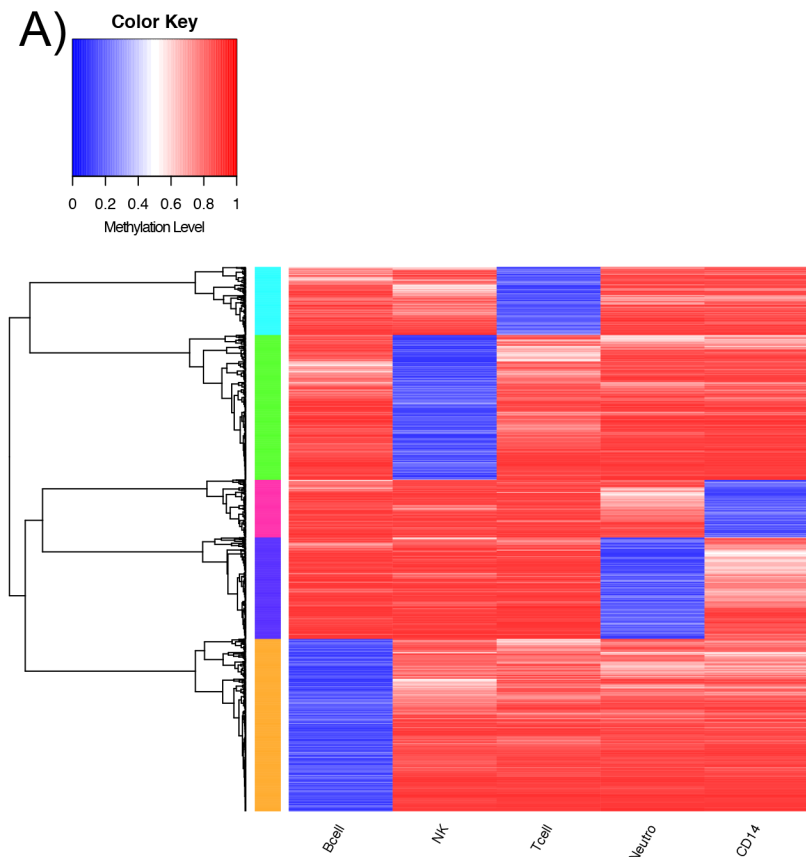


Suppl. Fig.1. Cell type- specific CpG sites

A) The average methylation level across the B cell, natural killer (NK), T cell, neutrophil (Neuro), and CD14+ (CD14) monocyte cell types. Red indicates high level of methylation at a cell type and blue indicates low levels of methylation. The 1739 CpG sites are clustered by their similarity using a Pearson's correlation coefficient into 5 groups indicated by the color: a) The light blue cluster contains 217 CpG sites uniquely low to T cells; b) the green cluster contains 463 CpG sites uniquely low to natural killer cells; c) the pink cluster contains 184 CpG sites uniquely low to CD14- positive cells; d) the purple cluster contains 324 CpG sites uniquely low to neutrophils; e) the orange cluster contains 551 CpG sites uniquely low to B cells. B) GREAT annotation of CD14+ CpG sites. The 184 CD14+ cell type- specific CpG sites were submitted to GREAT for enrichment of ontology terms available for the hg19 reference genome. C) GREAT annotation of T cell CpG sites. The 217 T cell type- specific CpG sites were submitted to GREAT for enrichment of ontology terms available for the hg19 reference genome. CpG sites were associated to a single proximal gene transcription start site within 100 kb.



B)

Ontology	CD14+ Signature Term Names	Hyper FDR Q-Val	Hyper Observed Gene Hits	Hyper Total Genes
MSigDB Perturbation	Genes with promoters occupied by PML-RARA fusion [GeneID=5371,5914] protein in acute promyelocytic leukemia(APL) cells NB4 and two APL primary blasts, based on Chip-seq data.	0.001	17	423
MSigDB Perturbation	Genes down-regulated in the urogenital sinus (UGS) of day E16 females exposed to the androgen dihydrotestosterone [PubChem=10635] for 6 h.	0.039	16	516
MSigDB Immunologic Signatures	Genes up-regulated in comparison of control conventional dendritic cells (cDC) at 0 h versus cDCs infected with Newcastle disease virus (NDV) at 18 h.	0.055	9	196
MSigDB Immunologic Signatures	Genes down-regulated in comparison of systemic lupus erythematosus B cells versus systemic lupus erythromatosus myeloid cells.	0.029	10	198
MSigDB Immunologic Signatures	Genes down-regulated in comparison of healthy B cells versus healthy myeloid cells.	0.035	9	198
MSigDB Immunologic Signatures	Genes down-regulated in comparison of naive T cells versus peripheral blood mononuclear cells (PBMC).	0.073	9	193
MSigDB Immunologic Signatures	Genes down-regulated in comparison of healthy CD4 [GeneID=920] T cells versus healthy myeloid cells.	0.043	9	197

C)

Ontology	Tcell Signature Term Name	Hyper FDR Q-Val	Hyper Observed Gene Hits	Hyper Total Genes
GO Biological Process	positive T cell selection	0.000	5	17
GO Biological Process	T cell activation	0.000	14	181
GO Biological Process	cell activation	0.000	21	566
GO Biological Process	lymphocyte activation	0.000	16	288
GO Biological Process	T cell selection	0.002	5	31
Disease Ontology	leukemia	0.042	19	1046
Disease Ontology	disease of anatomical entity	0.048	63	5897
Disease Ontology	immune system disease	0.065	42	3423
Disease Ontology	lymphoblastic leukemia	0.046	11	391
Disease Ontology	neutropenia	0.056	4	33
MSigDB Pathway	IL 17 Signaling Pathway	0.011	3	15
MSigDB Pathway	NO2-dependent IL 12 Pathway in NK cells	0.013	3	17
MSigDB Pathway	Dendritic cells in regulating TH1 and TH2 Development	0.002	4	22
MSigDB Pathway	Hematopoietic cell lineage	0.017	5	86