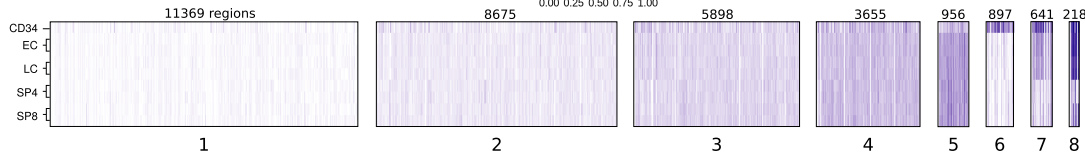
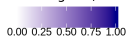


mean DNA methylation ratio on region (0: unmethylated; 1: methylated)

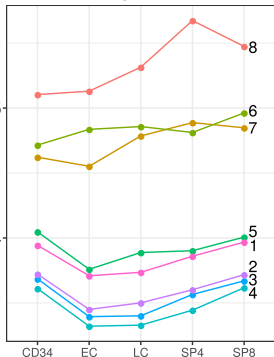


RNA-Seq

GREATR GO analysis

median of log2(RPKTMM + 1)

$-\log_{10}(\text{Binomial Benjamini-Hochberg-corrected P-value})$



1.9	1.4	0.4	1.5	2.4	0.3	1.3	0	- negative regulation of membrane protein ectodomain proteolysis
2.8	1.5	0.8	1.5	1.5	3.4	0.4	0.6	- B-1 B cell homeostasis
15	3.1	1.3	1.5	2.4	1.3	1.7	5.3	- mature B cell differentiation
5.8	8.4	2.5	1.3	1.3	2.2	2.5	0.5	- negative regulation of intracellular protein kinase cascade
2.3	5.4	0.4	0.9	0.4	0	0	0	- natural killer cell mediated cytotoxicity
0.2	1.7	0.4	2.6	0.5	0	0.6	0	- negative regulation of macrophage activation
6.1	6.2	10	1.8	1.5	0	1.1	0	- negative regulation of leukocyte degranulation

Other
hematopoietic
functions

1.2	1.4	0.4	1.2	1.6	4.1	2.1	7	- positive T cell selection
1.8	4.7	2.1	0.9	2.7	0.9	3.1	0.6	- alpha-beta T cell lineage commitment
1	2.1	3.8	1.2	1	0	0	0	- urinary bladder smooth muscle contraction
5.8	3.9	1.8	2.7	1.5	2.2	2.1	5.1	- response to laminar fluid shear stress
0.5	1.2	1	1	0.7	7.3	3.1	0.5	- maintenance of DNA repeat elements
2.7	4.8	4	2.3	2	0.2	3.1	0.3	- positive regulation of Rho GTPase activity
2.2	8	2.7	5.5	2.1	4.3	0	1.7	- positive regulation of transcription from RNA polymerase II promoter in response to stress
4.7	5.5	1	1.4	1.5	7.9	10.8	1.2	- positive regulation of nuclear-transcribed mRNA poly(A) tail shortening
4.7	6.6	1.3	1.5	1.9	6.7	9.3	1.7	- positive regulation of mRNA catabolic process
1	2	3	4	5	6	7	8	

T cell functions

GO Biological Process
Similarity filtered by best
binomial fold enrichment
and Wang distance of 0.1