

- H3K4me3 sequencing depth
- Expression-H3K4me3 overlapping
- TFBS frequency

Plot H3K4me4 peaks

Plot sequencing depth of H3K4me3 at one or a set of TSSs. The depth was the normalized average of 6 control or 6 SLE samples. By default, the plotted data is in log2 scale, so a difference of 1.0 is the same as 2 fold change. Plot options:

- "Plot unit": plot individual TSS or all TSSs mapped to a gene set.
- "Plot value": plot control and SLE data separately, or their difference (SLE - control).
- "Plot type": plot type (landscape vs. barplot).
- "Plot scale": plot data in log2 scale (default), or unlogged scale.
- "Plot range": plot range around TSS (-10kb to +10kb).

Select a TSS

Search:

ID	Gene	Gene_ID	Chr	Location	Strand	H3K4me3_Control	H3K4me3_SLE
chr1_1243269	ACAP3	116983	chr1	1243269	-	Both	Both
chr1_1709909	NADK	65220	chr1	1709909	-	Both	Both
chr1_1710297	NADK	65220	chr1	1710297	-	Both	Both
chr1_1822526	GNB1	2782	chr1	1822526	-	Both	Both
chr1_6052357	KCNAB2	8514	chr1	6052357	+	Both	Both

Showing 1 to 5 of 27,588 entries Previous Next

Select a gene set

BioSystems Clear selection

Search:

ID	Name	Size
GO:0002200_human	somatic diversification of immune receptors	47
GO:0002204_human	somatic recombination of immunoglobulin genes involved in immune response	18
GO:0002208_human	somatic diversification of immunoglobulins involved in immune response	18
GO:0002218_human	activation of innate immune response	156
GO:0002220_human	innate immune response activating cell surface receptor signaling pathway	7

Showing 1 to 5 of 150 entries (filtered from 19,440 total entries) Previous Next

Select plot unit

Individual TSS

Gene set average

Select plot value

Control/SLE separately

Control-SLE difference

Select plot type

Plot landscape

Plot bar

Select plot scale

Logged

Unlogged

Select plot range

