

(a)

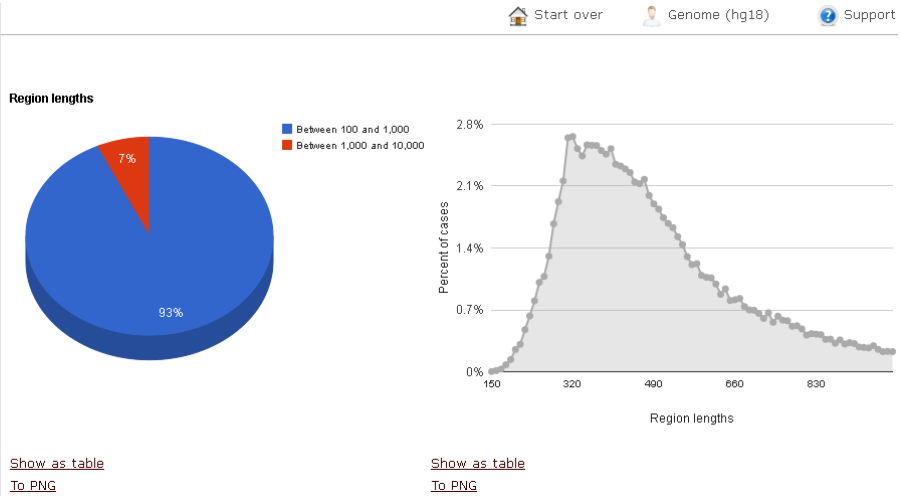
82,221 5hmC hotspots Szulwach

- Summary
- List the regions
- Region lengths**

Length of the region is between 1000 and 5700 for total of 5734 hits (7%)

Filter to this selection

- Region score
- DNA sequence
- Region location
- Histone modifications (ENCODE)
- DNaseI hypersensitive sites (ENCODE)
- DNA methylation (ROADMAP)



(b)

5,734 5hmC hotspots Szulwach

Length of the region is between 1000 and 5700

- Summary
- List the regions
- Region lengths
- Region score**

The region score is between 300 and 1000 for total of 2535 hits (44%)

Filter to this selection

(c)

Histone modifications (ENCODE)

- H3K4me1
- Neighborhood
- Overlapping**

H3K4me1 (GM12878)	597
H3K4me1 (H1hESC)	2,334
H3K4me1 (HMEC)	1,173
H3K4me1 (HSMM)	1,134
H3K4me1 (HUVEC)	850
H3K4me1 (K562)	810
H3K4me1 (NHEK)	768
H3K4me1 (NHLF)	1,004
H3K4me1 (any tissue)	2,418

- Not overlapping
- Distance to nearest

(d)

- Chromatin state segmentation**
- CpG islands (specific)
- CpG islands (sensitive)
- Conservation
- Repeat elements
- Genes and annotations
- Gene names (Ensembl)
- Gene ontology (terms)
- Gene ontology (words)**
- OMIM (terms)
- OMIM (words)
- Genes
- Gene promoters
- Gene transcription start sites
- Gene exons
- User annotations

Word	Number of GOs with such description
1 regulation	1608
2 activity	1066
3 process	835
4 cell	520
5 positive	482
6 binding	423
7 negative	389
8 metabolic	373
9 protein	362
10 response	343

(g)

- DNA methylation (ROADMAP)
- Fetal_lung
- hES_H1_p38
- Average CpG methylation ratio**

The average methylation ratio in hES_H1_p38 is between 0.2 and 0.5 for total of 16 hits (25%)

Filter to this selection

- Number of observed CpGs
- Deviation of the methylation ratios of CpGs
- Min methylation ratio of a CpG
- Max methylation ratio of a CpG

(f)

- DNA methylation (ROADMAP)
- Fetal_lung
- hES_H1_p38
- Average CpG methylation ratio**
- Number of observed CpGs**

The number of measured CpGs in hES_H1_p38 is between 5 and 72 for total of 65 hits (66%)

Filter to this selection

- Deviation of the methylation ratios of CpGs
- Min methylation ratio of a CpG
- Max methylation ratio of a CpG
- hES_H9_p58
- hFib_11_p8

(e)

- Chromatin state segmentation
- CpG islands (specific)
- CpG islands (sensitive)
- Conservation
- Repeat elements
- Genes and annotations
- User annotations
- 5hmC hotspots Stroud et al
- Overlapping**

Overlapping with d_5hmChotspotsStroudetal_258541 (50%)

- Not overlapping
- Distance to nearest

(h)

16 5hmC hotspots Szulwach

Length of the region is between 1000 and 5700

The region score is between 300 and 1000

The region overlaps with H3K4me1 sites in H1hESC tissue(50%)

Overlapping with genes annotated with GO described by 'regulation'

Overlapping with d_5hmChotspotsStroudetal_258541 (50%)

The number of measured CpGs in hES_H1_p38 is between 5 and 72

The average methylation ratio in hES_H1_p38 is between 0.23 and 0.5

[Export all](#)
[Download as text file](#)
[Export as custom track in UCSC Genome Browser](#)
[Export to Galaxy](#)
[Export to the Genomic HyperBrowser](#)

URL	chromosome	start	end
UCSC	chr1	154312318	154314236
UCSC	chr1	233871599	233873405
UCSC	chr1	10621968	10623311
UCSC	chr1	109598763	109600256
UCSC	chr1	53741128	53742573
UCSC	chr10	80652658	80653701
UCSC	chr11	69181564	69182875
UCSC	chr11	118693831	118695500
UCSC	chr13	113547903	113548942
UCSC	chr16	48082377	48083408

Listing all 16 regions
[Show full table](#)