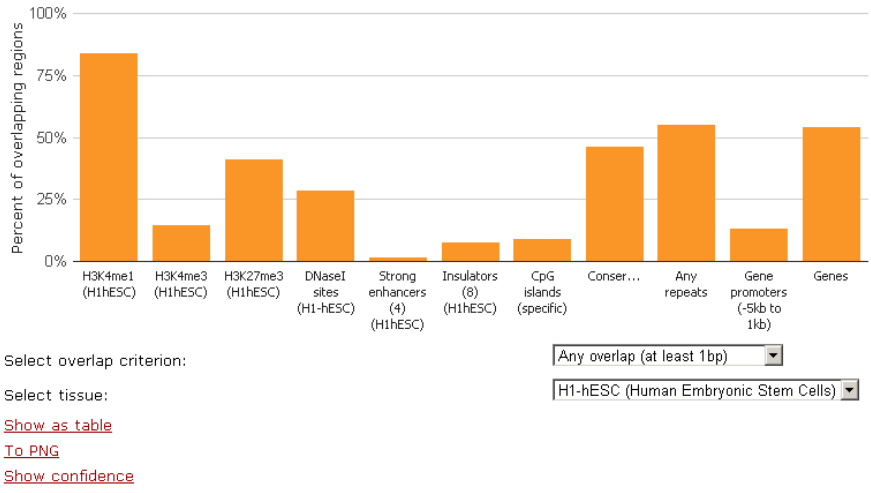


(a)

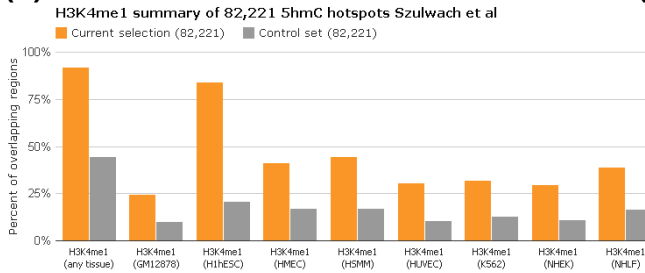
82,221 5hmC hotspots Szulwach et al

- Summary
 - List the regions
 - Region lengths
 - Region score
 - DNA sequence
 - Region location
- Histone modifications (ENCODE)
 - DNaseI hypersensitive sites (ENCODE)
 - DNA methylation (ROADMAP)
 - Chromatin state segmentation
 - Transcription factor binding sites (ENCODE)
 - CpG islands (specific)
 - CpG Islands (sensitive)
 - Lamina-associated domains
 - Conservation (28-way most conserved)
 - Strong enhancer candidates
 - Repeat elements
 - Genes and annotations
- User annotations

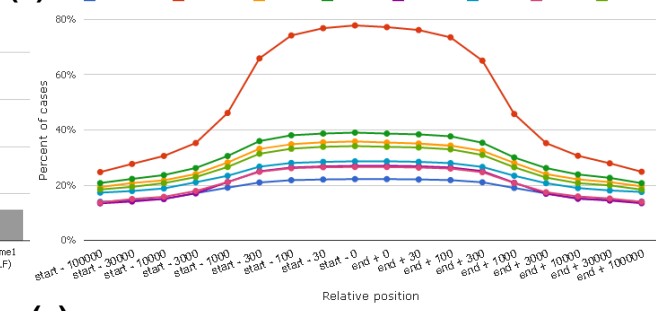
Summary of 82,221 5hmC hotspots Szulwach et al



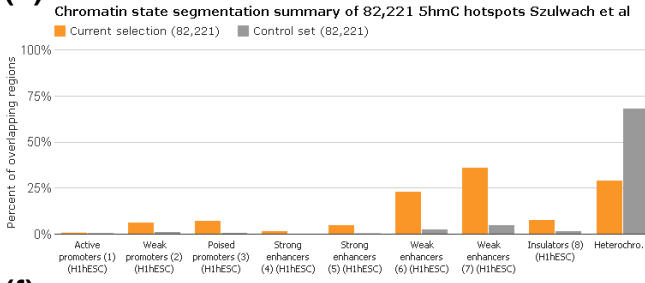
(b)



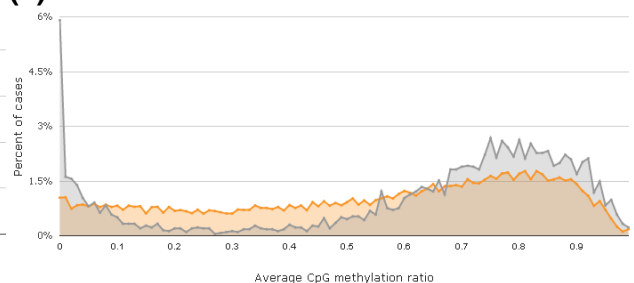
(c)



(d)



(e)



(f)

| GO | Number of regions | Number of genes | description | Ratio |
|-------------------------------|-------------------|-----------------|---|-------|
| 1 GO:0009966 | 1662 | 1120 | regulation of signal transduction | 1.48 |
| 2 GO:0023051 | 1891 | 1314 | regulation of signaling | 1.44 |
| 3 GO:0006357 | 1209 | 902 | regulation of transcription from RNA polymerase II promoter | 1.34 |
| 4 GO:0049583 | 1951 | 1490 | regulation of response to stimulus | 1.31 |
| 5 GO:0003653 | 1388 | 1058 | anatomical structure morphogenesis | 1.31 |
| 6 GO:0030234 | 1269 | 973 | enzyme regulator activity | 1.3 |
| 7 GO:0048869 | 2082 | 1643 | developmental process | 1.27 |
| 8 GO:0051239 | 1637 | 1266 | regulation of multicellular organismal process | 1.27 |
| 9 GO:0010646 | 1231 | 976 | regulation of cell communication | 1.26 |
| 10 GO:0030154 | 1570 | 1251 | cell differentiation | 1.25 |

Showing top 100 GOs (by number of regions) out of 1711 ([Show all 100](#))

macromolecule metabolic process regulation of signal transduction cellular developmental process nucleotide binding transferase activity positive regulation of biological process negative regulation of biological process metal ion binding regulation of macromolecule metabolic process response to organic substance protein complex intracellular non-membrane-bounded organelle protein metabolic process cytosol nuclear part signal transduction negative regulation of metabolic process positive regulation of metabolic process nitrogen compound metabolic process nucleic acid binding DNA binding intracellular cellular protein metabolic process regulation of cell communication cellular macromolecule metabolic process cellular component organization purine nucleotide binding regulation of molecular function regulation of biological quality ATP binding hydrolase activity regulation of catalytic activity nucleobase, nucleotide, nucleoside and nucleic acid metabolic process transport regulation of biosynthetic process macromolecule modification regulation of multicellular organismal process establishment of localization response to stress regulation of transcription, DNA-dependent regulation of macromolecule biosynthetic process adenylyl ribonucleotide binding purine ribonucleotide binding ribonucleotide binding purine ribonucleoside triphosphate binding cell differentiation cellular biosynthetic process cellular nitrogen compound metabolic process regulation of signaling anatomical structure morphogenesis cytoplasm cation binding organelle membrane ZINC ion binding ion binding regulation of cellular biosynthetic process plasma membrane part developmental process multicellular organismal process transporter activity adenylyl nucleotide binding regulation of RNA metabolic process macromolecule metabolic process non-membrane-bounded organelle cell fraction positive regulation of cellular metabolic process regulation of cellular metabolic process regulation of transcription receptor activity