	A	В	С	D	E	F	G	Н	T	J	K	L	M	N
1	chrom	chromstart	chromend	gene_name	promoter	CpG island	S00289 meth_ratio	S00289 total CpG	S00645 meth_ratio	S00645 total CpG	meth diff	pvalue	classificat	ion
2	chr5	75846750	75846751	IQGAP2			1	38	- 0	14	1	5.65E-13	stronglyHy	/permeth
3	chr16	88565056	88565057	ZFPM1			1	22	0	22	1	9.51E-13	stronglyHy	permeth
4	chr2	26110056	26110057				1	18	0	26	1	9.71E-13	stronglyHy	permeth
5	chr4	113143609	113143610				1	20	0	33	1	3.27E-12	stronglyHy	permeth
6	chr7	1399953	1399954				1	24	0	17	1	6.6E-12	stronglyHy	permeth
7	chr7	67075551	67075552				1	30	0	14	1	8.7E-12	stronglyHy	permeth
8	chr12	69228042	69228043	MDM2			1	22	0	18	1	8.82E-12	stronglyHy	permeth
9	chr17	73091151	73091152	SLC16A5			1	44	0	20	1	9.21E-12	stronglyHy	permeth
10	chr7	128167264	128167265				1	19	0	20	1	1.45E-11	stronglyHy	permeth
11	chr1	236495892	236495893				1	24	0	16	1	1.59E-11	stronglyHy	permeth
12	chr1	45262532	45262533				1	20	0	18	1	2.98E-11	stronglyHy	permeth
13	chr5	65558778	65558779				1	20	0	18	1	2.98E-11	stronglyHy	permeth
14	chr10	115350596	115350597	NRAP			1	14	0	26	1	4.31E-11	stronglyHy	permeth
15	chr19	539816	539817	CDC34			1	12	0	30	1	9.04E-11	stronglyHy	permeth
16	chr2	90279517	90279518				1	10	0	40	1	9.73E-11	stronglyHy	permeth
17	chr2	10928081	10928082	PDIA6			1	26	0	28	1	1.11E-10	stronglyHy	permeth
18	chr16	1495743	1495744	CLCN7	CCDC154		1	16	0	20	1	1.37E-10	stronglyHy	permeth
19	chr13	52151558	52151559				1	20	0	16	1	1.37E-10	stronglyHy	permeth
20	chr2	167406824	167406825				1	20	0	16	1	1.37E-10	stronglyHy	permeth
21	chr17	73091150	73091151	SLC16A5			1	18	0	18	1	2 2E-10	stronglyHy	permeth
22	chr20	60986957	60986958	C20orf151			1	34	0	10	1	4.03E-10	stronglyHy	permeth
23	chr3	94226411	94226412				1	16	0	18	1	4.54E-10	stronglyHy	permeth
24	chr20	59854714	59854715	CDH4			1	20	0	14	1	7 18E-10	stronglyHy	permeth
25	chr7	57218125	57218126				1	20	0	14	1	7.18E-10	stronglyHy	permeth
26	chr17	27615321	27615322	NUFIP2			1	22	0	12	1	1.82E-09	stronglyHy	permeth
27	chr9	94684858	94684859	ROR2			1	22	0	12	1	1 82E-09	stronglyHy	permeth
28	chr7	4174701	4174702	SDK1			1	18	0	14	1	2.12E-09	stronglyHy	permeth
29	chr22	48926628	48926629	EAM19A5			1	16	0	16	1	3.33E-09	stronglyHy	/permeth
30	chr20	286027	286028				1	20	0	12	1	4 43E-09	stronglyHy	permeth
31	chr4	8599465	8599466	CP7			1	20	0	12	1	4 43E-09	stronglyHy	permeth
32	chr12	6581803	6581804		VAMP1		1	16	0	14	1	6.88E-09	stronglyHy	permeth
33	chr19	36611282	36611283	TBCB			1	16	0	14	1	6 88F-09	stronglyHy	permeth
34	chr12	11700572	11700573		LOC338817		1	14	0	16	1	6.88E-09	stronglyHy	permeth
35	chr12	11700578	11700579		LOC338817		1	14	0	16	1	6.88E-09	stronglyHy	permeth
36	chr18	14393506	14393507			Y	1	14	0	16	1	6 88E-09	stronglyHy	permeth
37	chr19	542653	542654		GZMM		. 1	14	0	16	1	6 88E-09	stronglyHy	/permeth
20	1.0	440506406	410506107	DAIA				17		10		C.00E.00		

Result Tables

The Result Table, which indicates chromosomal positions and annotated **gene names**, **promoter regions** and **CpG islands**, is the best way for you to discover methylation changes at specific genomic sites. Using these annotations, you can quickly filter to find your regions of interest. Unlike other approaches which only provide average signals for enriched regions showing high levels of DNA methylation, our Next-Gen sequencing-based services are more sensitive, quantitative, and identify methylated cytosines with singlenucleotide resolution.



Browser Tracks

Two kinds of UCSC Genome Browser tracks are provided for you to visualize methylation data: Methylation track and Read track. The Methylation track shows methylation ratios (percent methylated) at each site, and the Read track shows where the reads align to the reference genomes. Simply copy and paste the provided track lines to UCSC Genome Browsers to load tracks, and you can utilize the many features available from the UCSC Genome Browser, such as gene annotations, detection of SNPs, localization of repetitive DNA elements, and comparison to results of the ENCODE project at each region.



Clustering Heatmap

The heatmap is one of the easiest ways to visualize and communicate how your samples or groups of samples are separated, in this example with regard to DNA methylation levels, using statistical methods. In this heatmap, Red represents individual CpG sites that are 0% methylated and Yellow represents sites with 100% methylation. Dendrograms of hierarchical clustering help you figure out how to group samples and determine which samples have similar methylation patterns by clustering based on methylation ratios.



Region Coverage Pie Chart

The coverage pie chart shows the fold read coverage at the indicated region, in this case, the CpG islands. Region coverage pie charts are also available for promoters, gene bodies.



Methylation Level Boxplot

The boxplot displays the median DNA methylation levels as well as the distribution of methylation levels within a sample. The boxplots show the 2nd quartile (median) as a yellow line, and 1st quartile and 3rd quartile as the bottom and upper bounds of the box, respectively.



Methylation Overview

The Methylation Overview plot shows the DNA methylation ratio (percent methylated) across the entire genome to quickly display the DNA methylation levels across all genomic regions.



Read Coverage Plot

The Read Coverage Plot shows the fold read coverage across entire genome to easily visualize the regions of the genome that were covered, and the extent of the coverage.



Methylation Histogram

The Methylation Histogram shows how CpGs were distributed in terms of methylation level. The x-axis is methylation level from non-methylated to full-methylated. The y-axis indicates CpG counts in certain methylation level.



Color Scatter Plot

The color scatter plot shows correlation between two samples in terms of methylation ratios of overlapped sites. The n value in the title is total number of overlapped sites, and the r value is Pearson's correlation coefficient. Yellow and green dots are strongly hypermethylated and strongly hypomethylated CpG sites, respectively, and blue dots are the other CpG sites.



Hexbin Plot

The hexbin plot is an updated version of the scatterplot that is better suited for analysis of very large data sets. It shows the correlation between two samples, and Pearson's R correlation coefficient and total number of overlapped sites (n) are displayed in the title. Colors represent densities of points, with Red showing points with many values and Blue showing points with few values at the indicated location on the plot. The color is calculated by log10(N). For example, if there are 1000 CpG sites in a data point on the plot, the color code of that data point is log10(1000) = 3. According to the color index on the right, the value of 3 would make the data point light green.