Supplementary Materials

Supplementary Table 1 - Log-odds nucleotide substitution with methyl-C as distinct base

	A	C	Methyl-C	G	T
A	1.3416	-1.5032	-1.4048	-1.5049	-1.9324
C	-1.5032	2.8936	2.4681	-1.3574	-1.0784
Methyl-C	-1.4048	2.4681	4.9673	-1.9300	-0.6387
G	-1.5049	-1.3574	-1.9300	1.7257	-2.1093
T	-1.9324	-1.0784	-0.6387	-2.1093	1.1555

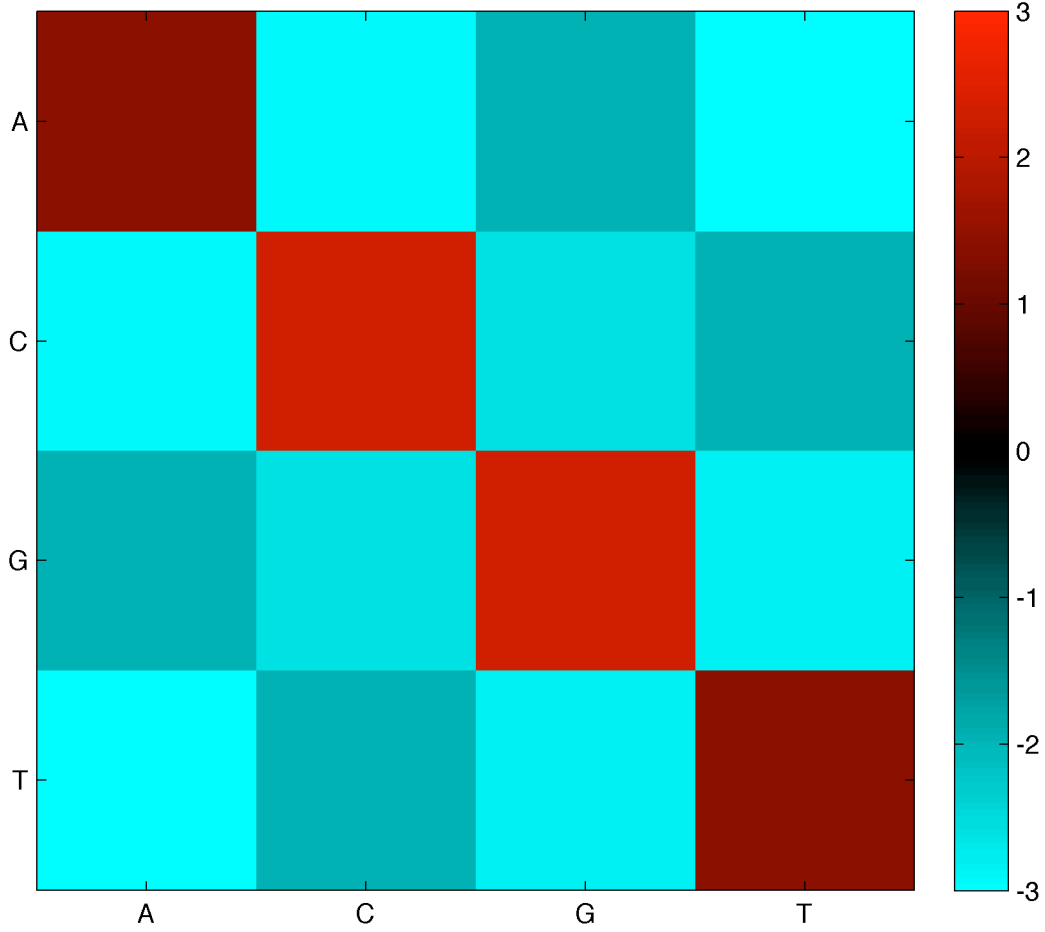**Supplementary Table 2 - Log-odds cytosine methylation transition levels**

Repeats	0-19%	20-39%	40-59%	60-79%	80-99%	100%
0-19%	0.3017	-0.5664	-1.2712	-1.7696	-2.0701	-2.4220
20-39%	-0.5664	1.3670	1.1491	0.6774	-0.1709	-0.8334
40-59%	-1.2712	1.1491	1.9743	1.7883	1.0841	0.1941
60-79%	-1.7696	0.6774	1.7883	2.2489	2.0475	1.1661
80-99%	-2.0701	-0.1709	1.0841	2.0475	2.3921	2.3447
100%	-2.4220	-0.8334	0.1941	1.1661	2.3447	3.0562

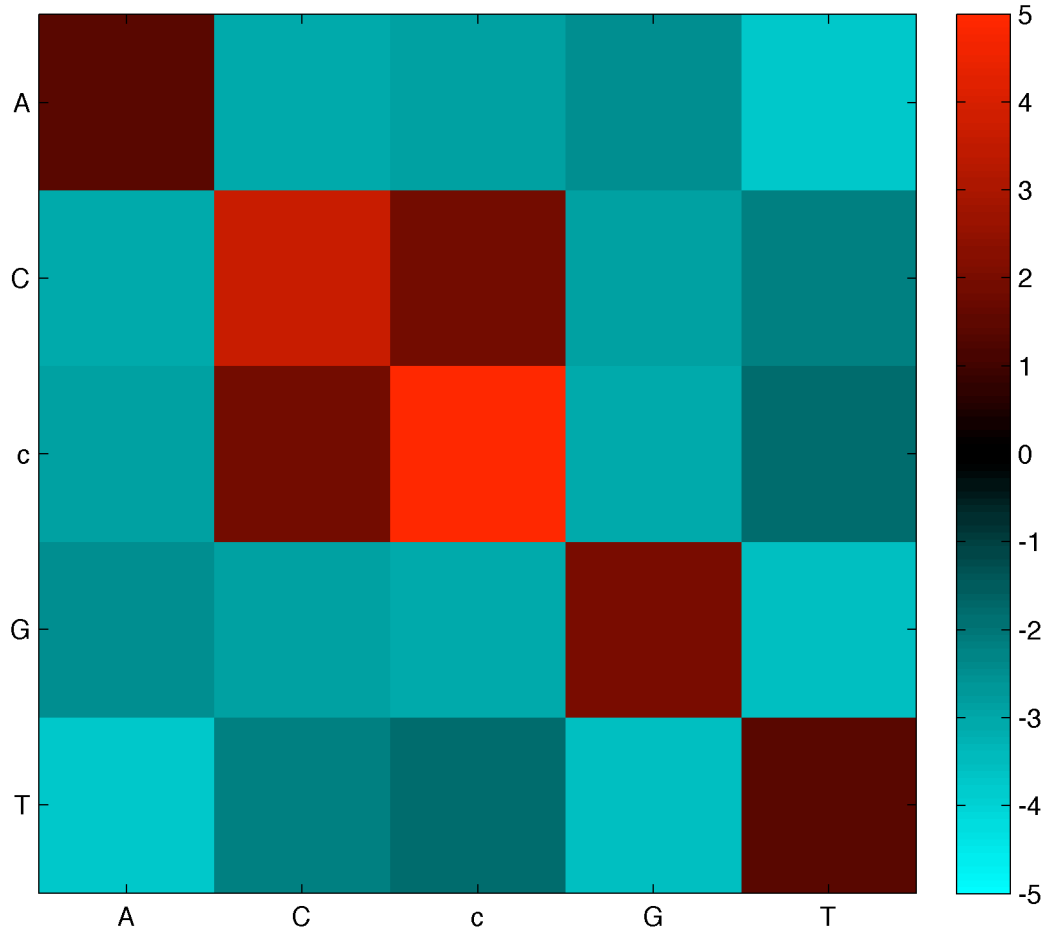**Supplementary Figure 1 - Log-Odds Ratio of Nucleotide Substitution: Duplicate Genes**
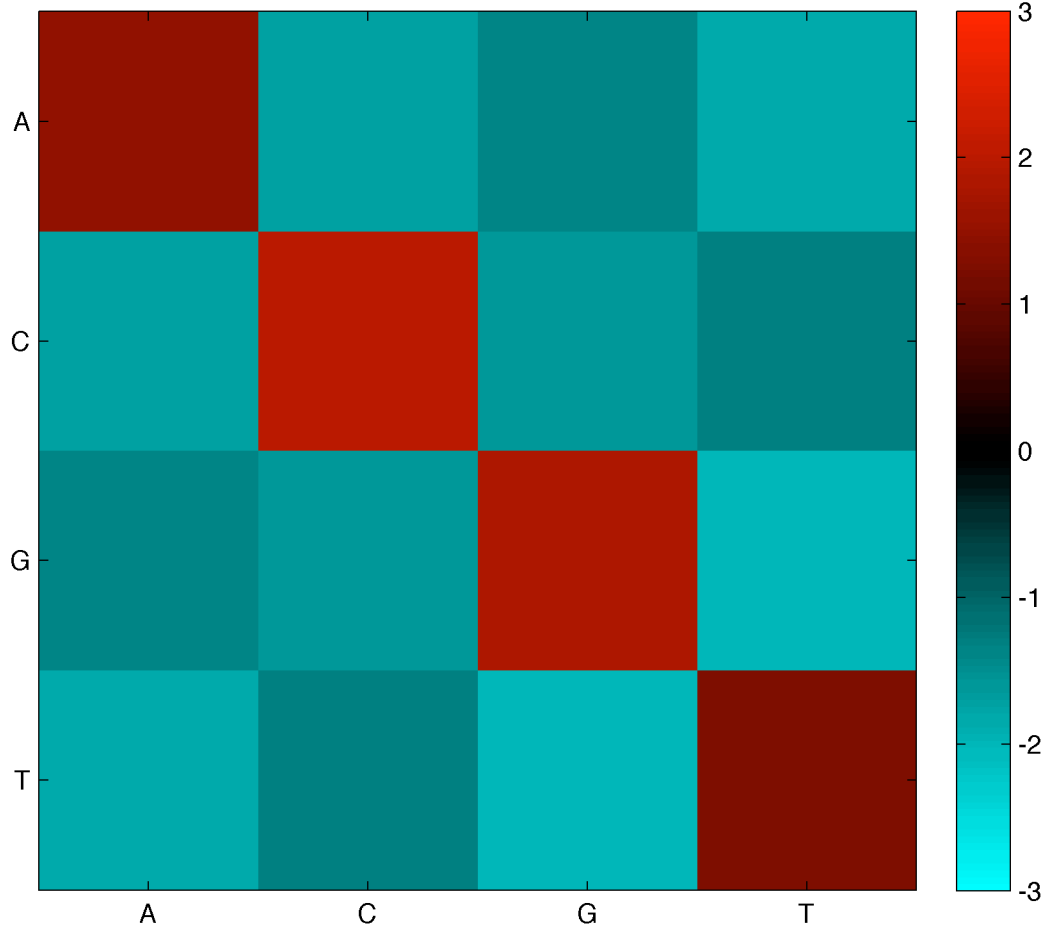
Log-odds substitution matrix of aligned duplicated gene bases (x-axis and y-axis) not considering cytosine methylation.

Supplementary Figure 2 - Log-Odds Ratio of Nucleotide Substitution: Repeat Regions

Transition probability of repeat region bases (x-axis and y-axis) not considering cytosine methylation.
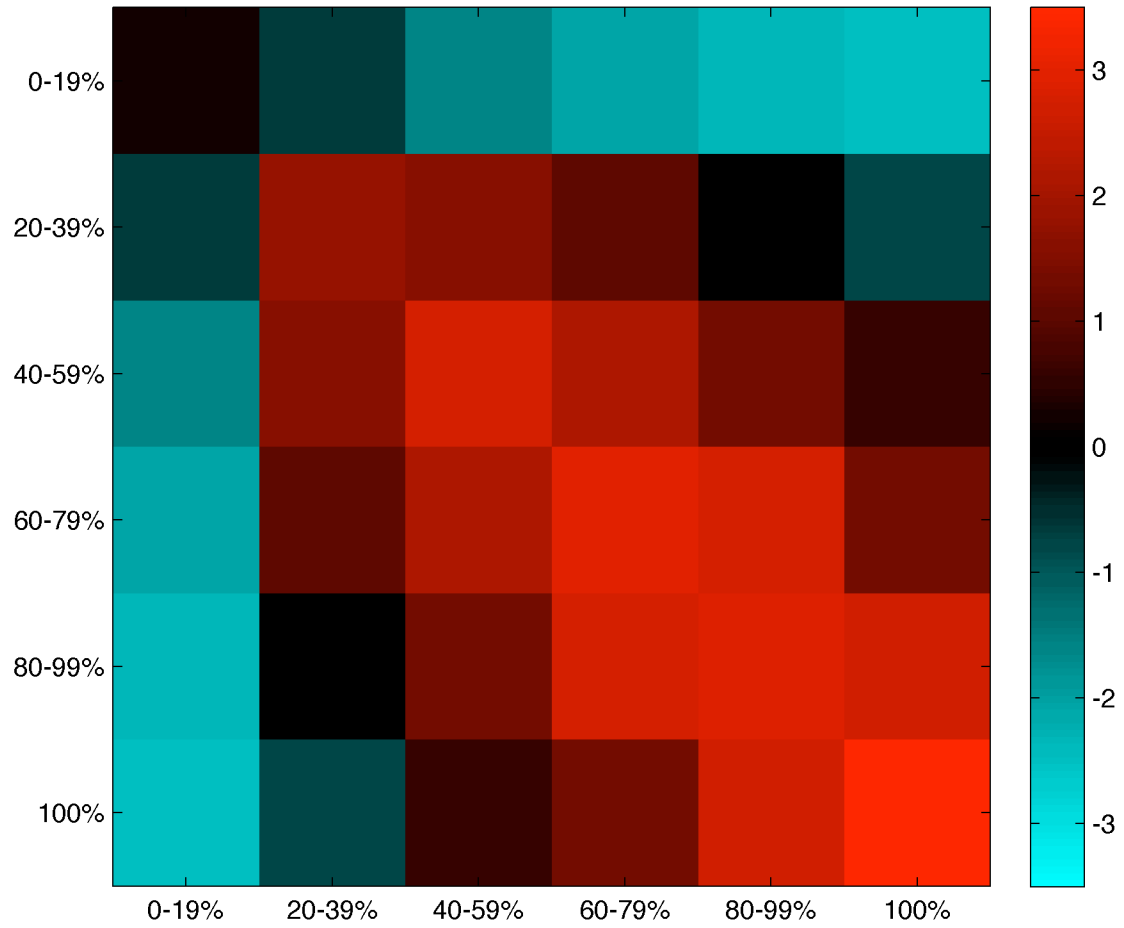
Supplementary Figure 3 - Log-odds Ratio of Nucleotide Base Transitions: Unique Tandem Repeats

Transition probability of unique tandem repeat bases (x-axis and y-axis) with methylated cytosine represented as a distinct base using lower-case c.
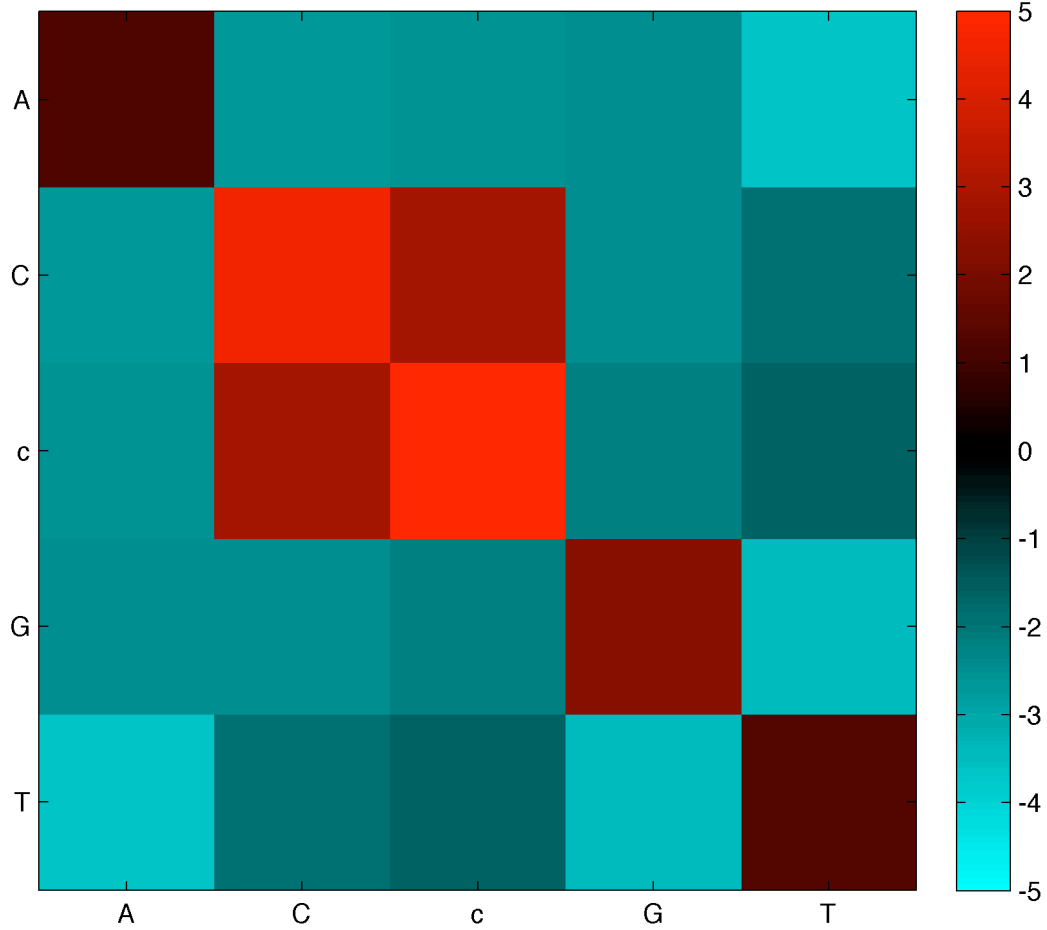
Supplementary Figure 4 - Log-odds Ratio of C-Methylation Percentage Transitions: Unique Tandem Repeats

Transition probability of cytosine methylation levels (x-axis and y-axis) within unique tandem repeats.
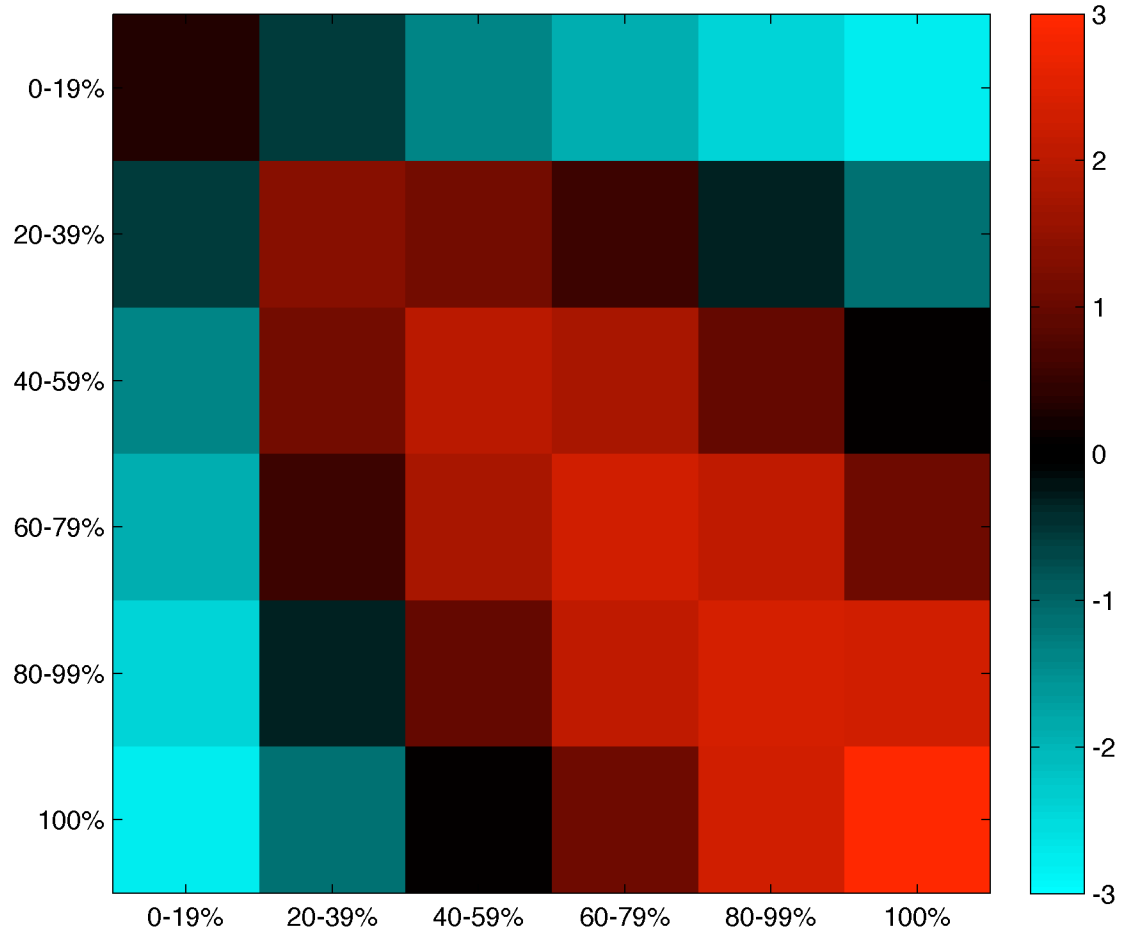
Supplementary Figure 5 - Log-odds Ratio of Nucleotide Base Transitions: Tandem Repeats

Transition probability of tandem repeat bases (x-axis and y-axis) with methylated cytosine represented as a distinct base using lower-case c.
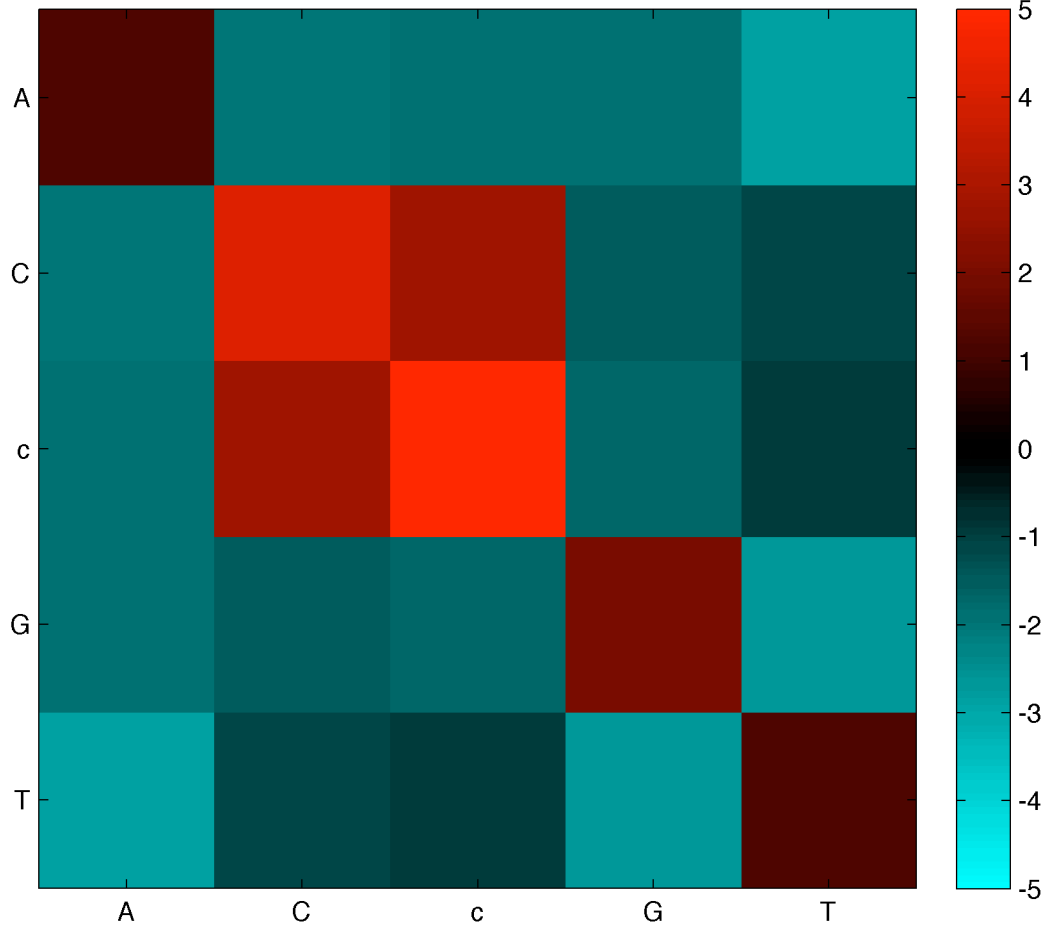
Supplementary Figure 6 - Log-odds Ratio of C-Methylation Percentage

Transitions: Tandem Repeats

Transition probability of cytosine methylation levels (x-axis and y-axis) within tandem repeats.
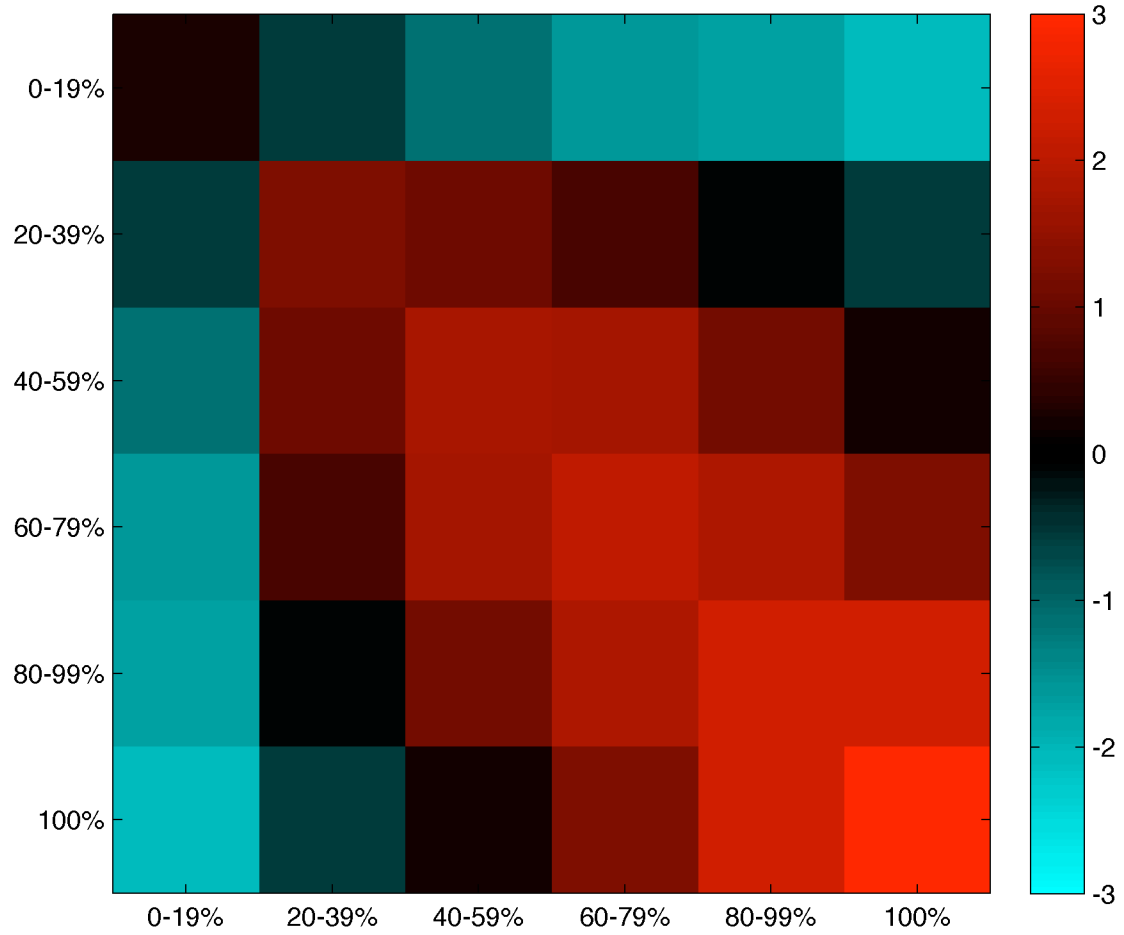
Supplementary Figure 7 - Log-odds Ratio of Nucleotide Base Transitions: Inverted Repeats

Transition probability of inverted repeat bases (x-axis and y-axis) with methylated cytosine represented as a distinct base using lower-case c.

Supplementary Figure 8 - Log-odds Ratio of C-Methylation Percentage

Transitions: Inverted Repeats

Transition probability of cytosine methylation levels (x-axis and y-axis) within inverted repeats.