Table S1: Primer Sequences and Annealing temperatures, PCR for sequencing analysis

Gene	Forward	Reverse	T_a
HIST1H2BC	CAAATAAAATTTGGCGTCTG	TAGCAGAAATCCGCTCTTTA	55
HIST1H2BE	AACTGCAGAACAGCAAAGAT	TAGCTCCAATTGTGAAAAGG	55
HIST1H2BF	TTAGGTTGTGGACGAAGTGT	GAAAATATGCAGGTAATTACAACTC	55
HIST1H2BG	TTCCCTAGAAAACGGTGAA	TCATTCTCACTGCTGTTATTGT	55
HIST1H2BI	CTGTGGTCATTTGACGGTAT	TGCCAAGTCTGGAAAATTAC	55

Table S2: Primer Sequences and Annealing temperatures, Bisulfite Sequencing

Gene	Forward	Reverse	T_a
HIST1H2BE_ CpG 1 -179 to +184	TTTTAGGATATGATTAATGGGAGAGTAG	TCCCCATAACTTTAAAAAAATACC	54
HIST1H2BE_ CpG 2 +179 to +545	TGGGGATTATGAATTTTTTTGTTAA	CACCAACCCAAACAATAAATACC	54

Table S3: Primer Sequences, Q-RT-PCR

Gene	Forward	Reverse
HIST1H2BC	ACAAGGTGCTGAAACAGGTC	CGATGCGCTCAAATATGTCG
HIS1HIST1H2BE	AAGCACGCTGTGTCAGAG	CAGTTGCAGGGACAAGTTTAC
HIST1H2BF	TCCAGGGAGATCCAGACG	TTGGGATTGGGTATGAAGACG
HIST1H2BG	ATGCCTGAACCAGCTAAGTC	GTGAACCTGTTTTAGCACCTTG
HIST1H2BI	ACGTGTACAAGGTGCTGAAG	GGAGTTCATAATCCCCATAGCC
HIST1H3A	TCGTAAACTACCTTTCCAGCG	GTCCTCAAATAGCCCTACCAAG
HIST1H3C	AAGAAACCTCATCGCTACCG	AGGTCGGTTTTGAAGTCCTG
HIST1H4D	GGAAAATGTAATCCGCGATGC	CCATAAAGAGTGCGTCCCTG
Beta Actin	CCCTGGCACCCAGCAC	GCCGATCCACACGGAGTAC
RPS11	CTACAAGAACATCGGTCTGGG	ATGGTCCTCTGCATCTTCATC
UBB	TTGGTGATTGGCAGGATCC	TTTCGATGGTGTCACTGGG
GAPDH	ACATCGCTCAGACACCATG	TGTAGTTGAGGTCAATGAAGGG

Table S4: Target Sequences for stable clones

Stable Clone	Forward Target Sequence	Reverse Target Sequence
sh1	CGGCATCTCCTCTAAAGCCAT	
sh2	CGTGACCAAGGCGCAGAAGAA	
sh3	GAATTCCTTTGTCAACGACAT	
CDS HIST1H2BE	AAAGCGGCCGCAACTTGGAGCTGGTGTACTTGGTAACG	AAAGGATCCATGCCTGAGCCAGCGAAATCCG

Table S5: Histone variants queried in Nanostring analysis.

Gene	Probe
H1F0	TTTGTTTTGCTATTAACCTACTTACGGGGTTAGGGATTTGCGGGGGGGGCTTGTGTGTTTTGTTGGCTTGTTTGCCATGAAGGTAGATGTGGGTGGGGAG
H1FOO	GGCTCCTGGGAGCGTCACCAGCGACATCTCACCCTCCTCGACTTCCACAGCAGGATCATCCAGGTCTCCTGAATCTGAAAAGCCAGGCCCGAGCCACGGC
H1FX	CCCACCCTCCTTGCCTTTGGGTGCGCGACAAACAATCGCTCCGGGCTCAGGGCTGCGCGGCTCTTCCCTTCATTCCATGGGCCTTTTTTTGGGCACAATA
H2AFB2	TGCTGGCGGCCGGGGGCGGACCTGCTCTCGCACCGTCCGAGCGGAGCTTTCGTTTTCAGTGAGCCAGGTGGAGCGCAGTCTACGGGAGGGCCACTACGCT
H2AFJ	CCCTGGGAAGATTCACAGGAATCTGTCCAGCTCTTATTACATGATGAGCAACATAGACAAGATACGAGGCATTGTAACTGCCCTGTCGCCACCCGCCTCT
H2AFV	TGCAGAGTGCTCTACTGACCAAGAAAGTTGTTGCTGCCACATTATAGATGTGGAGCCTAAGGGTCACAGAAATTGTGTGCTATGCCAAAAAACATTGAAC
H2AFX	CCGCCCCATTTCCCTTCCAGCAAACTCAACTCGGCAATCCAAGCACCTAGATACCAGCACAAGTCGGTTAATCCCTGTCTGGACTGAGCCTCCGTTGGCT
H2AFY	TGACCTAGGAAACACGCTGGAGAAGAAAGGTGGCAAGGAGTTTGTGGAAGCTGTCCTGGAACTCCGGAAAAAGAACGGGCCCTTGGAAGTAGCTGGAGCT
H2AFY2	ACAGAAGCTGTCCTTAACCCAGAGTGACATCAGCCATATTGGCTCCATGAGAGTGGAGGGCATTGTCCACCCAACCACAGCCGAAATTGACCTCAAAGAA
H2AFZ	GGTGGTGGGATCTCACCGTGGGTCCGATTAGCCTTTTCTCTGCCTTGCTTGCTTGAGCTTCAGCGGAATTCGAAATGGCTGGCGGTAAGGCTGGAAAGGA
H2BFS	AGCAGGTCCACCCCGACACCGGCATCTCCTCTAAGGCCATGGGAATCATGAACTCCTTCGTCAACGACATCTTCGAACGCATCGCAGGTGAGGCTTCCCG
H2BFWT	CGCTCTGGACGGTGCCGCCAGGTGACCCTACATGTCCGGAGCAACACTTTGAAAACCAAAGACGCTTGGCAGAACCCTGTTCCTTTCCAGAGACAGAGCT
HIST1H1A	GAGCGTCAAGACTCCGAAAAAGGCTAAAAAGCCTGCGGCAACAAGGAAATCCTCCAAGAATCCAAAAAAACCCAAAACTGTAAAGCCCAAGAAAGTAGCT
HIST1H1B	CCAAAGCCGCTAAGCCCAAAGCAGCAAAACCTAAAGCTGCAAAGGCCAAGAAGGCGGCTGCCAAAAAGAAGTAGGAAGCTGGCGTGTGAAAACCGCAACA
HIST1H1C	TTAAAAAGGCGGGCGGAACCAAACCTAAGAAGCCAGTTGGGGCAGCCAAGAAGCCCAAGAAGGCGGCTGGCGGCGCAACTCCGAAGAAGAGCGCTAAGAA
HIST1H1D	CTGCTCCACTTGCTCCTACCATTCCTGCACCCGCAGAAAAAACACCTGTGAAGAAAAAGGCGAAGAAGGCAGGCGCAACTGCTGGGAAACGCAAAGCATC
HIST1H2AA	ATCCATCGTCTGCTTCGTAAGGGAAACTATGCAGAGCGGATAGGGGCAGGCGCACCAGTGTATTTGGCGGCAGTGTTAGAGTATCTCACAGCAGAAATCC
HIST1H2AB	GCCATCATAAGGCCAAGGGAAAGTGAAGAGTTAACGCTTCATGCACTGCTGTTTTTCTGTCAGCAGACAAAATCAGCCTAACAGCAAAGGCTCTTTTCAG
HIST1H2AC	ACTCGCATCATCCCGCGCCACTTGCAGCTGGCCATCCGCAACGACGAGGAGCTCAACAAACTGCTAGGCCGGGTGACCATTGCTCAGGGCGGCGTCCTTC
HIST1H2AE	ACTAGTCAAATCCGTCAGTGATCCCGAGTCCCAGAAACCAAAGGCTCTTTTCAGAGCCACCCACCTTTTCTGTAAAGTGCTGGAATACACATACGATGCC
HIST1H2AG	ACTGAGAGCCACCACAAGGCGAAGGGCAAGTAACTATCTGTACTAGTTTGTGGCAGCTCAAGTAAAATCGAGTCCAAACCAACGGCTCTTTTCAGGGCCA
HIST1H2AI	AAGAAGACCGAGAGCCACCACAAGGCGAAGGGCAAGTAGAAGCCTGGATTAGTTTGCAGCAACTCAATCCCAAAGGAACCAAAGGCTCTTTTCAGAGCCA
HIST1H2AJ	TGGCGTCCTGCCCAACATCCAGGCCGTGCTGCTGCCAAAGAAAACTGAGAGCCACCACAAGACTAAGTAAAGACCGAGTTGAAAAGCGCATAAAAACAAA
HIST1H2AK	ATCCAGGCCGTGCTGCTGCCTAAGAAAACTGAGAGCCACCACAAGGCCAAGGGCAAGTAGCGGGGCTGGAGCAGTTCATTACTCATACCTCGGTCCAAAC
HIST1H2AL	GCTACTGCCCAAGAAGACCGAGAGTCACCACAAGGCCAAAGGCAAATAATGTCTCCATAGAATCACTTTCCAATACAACGGCTCTTTTCAGAGCCACCTA
HIST1H2AM	CGGTGTTCTGCCTAACATCCAGGCCGTACTGCTCCCCAAGAAGACTGAGAGCCACCACAAAGCTAAGGGCAAGTAAGGGCTGAACTTTAAAAATGTAAAC
HIST1H2BB	CTGTGCGCCTGCTGCTGCCTGGGGAGCTGGCTAAGCATGCTGTGTCCGAGGGCACTAAGGCAGTTACCAAGTACACTAGCTCTAAATAAGTGCTTATGTA
HIST1H2BC	GCTGGCCAAGCACGCCGTGTCGGAGGGCACCAAGGCCGTCACCAAGTACACCAGCTCCAAGTAAACATTCCAAGTAAGCGTCTTAACACCTAACCCCAAA
HIST1H2BD	CTCAGGTGTTTGCAACAGTGTTCTAACTATTAACGCTACGATGCCTGAACCTACCAAGTCTGCTCCTGCCCCAAAGAAGGGCTCCAAGAAGGCGGTGACT
HIST1H2BE	GCCAAGCACGCTGTGTCAGAGGGCACCAAGGCCGTTACCAAGTACACCAGCTCCAAGTAAACTTGTCCCTGCAACTGCCTTAGTAAACCCAAAGGCTCTT
HIST1H2BF	GGGAGCTGGCTAAGCACGCCGTGTCAGAGGGCACCAAGGCCGTCACCAAGTACACCAGCTCTAAGTAATTCTAACGTCTTCATACCCAATCCCAAAGGCT
HIST1H2BG	GCTGGCCAAGCACGCAGTGTCCGAAGGTACCAAGGCTGTCACCAAGTATACAAGCTCCAAGTAAATGTGTGCTTAGGTGCTTTAAAACTCAAAGGCTCTT
HIST1H2BH	GGGGAACTGGCCAAGCACGCCGTGTCCGAGGGCACTAAGGCCGTCACCAAGTACACCAGCTCCAAATAAATGGACGCATGTTCAAACCCAAAGGCTCTTT

HIST1H2BJ	GCACGCCGTGTCCGAGGGTACTAAGGCCGTCACCAAGTACACCAGCGCTAAGTAAACAGTGAGTTGGTTGCAAACTCTCAACCCTAACGGCTCTTTTAAG
HIST1H2BK	CACAATTGCCTTCGGTTACCTCATTATCTACTGCAGAAAAGAAGACGAGAATGCAACCATACCTAGATGGACTTTTCCACAAGCTAAAGCTGGCCTCTTG
HIST1H2BL	CAAGCACGCGGTGTCGGAGGGCACCAAGGCCGTCACCAAGTACACCAGCTCCAAGTAAATTCTCAAGCTCTTGTCCAACCCAAAGGCTCTTTTCAGAGCC
HIST1H2BM	ATGCCTGAACCAGTCAAATCTGCTCCAGTCCCTAAAAAAGGCTCCAAGAAGGCCATTAACAAGGCTCAGAAGAAGGATGGAAAGAAGCGCAAACGCAGCC
HIST1H2BN	GGTGTCGGAGGGCACCAAGGCCGTCACCAAGTACACCAGTTCCAAGTGAGCCCGCCCACCGCGGAACGTTCGGTCAGTCTCGGCCCACACCCCAAAGGCT
HIST1H3A	GGCTCTGCGCGAGATCCGCCGTTATCAGAAGTCCACTGAACTGCTTATTCGTAAACTACCTTTCCAGCGCCTGGTGCGCGAGATTGCGCAGGACTTTAAA
HIST1H3B	CATCCATGCTAAGCGAGTGACTATTATGCCCAAAGACATCCAGCTCGCTCGCCGCATTCGCGGAGAAAGAGCGTAAATGTAAAGTCACTTTTTCATCAGT
HIST1H3D	ATCCAGGCTGTACTGCTCCCCAAGAAGACTGAGAGTCACCACAAGGCCAAGGCAGGTTTTAGAAGTTCGCAATGGCTCGTACCAAGCAGACTGCTCGCAA
HIST1H3E	TGACCATCATGCCTAAAGACATCCAGCTTGCCCGCCGCATTCGTGGGGAGAGGGCGTGAATTGTTTTGAGTACAAACCTTAAATCCAAAGGCTCTTCTCA
HIST1H3F	CCACCGCTACAGGCCTGGTACTGTCGCCCTCCGTGAAATCCGCCGCTATCAGAAATCGACTGAGCTACTGATTCGCAAGCTACCATTCCAGCGTCTGGTA
HIST1H3G	CGAGTGACTATCATGCCCAAGGACATTCAGCTCGCTCGCCGCATTCGTGGGGAGAGAGCGTAGAGGTTTCCGGGCAGTAATTCTATCCAACTTAAAAAGG
HIST1H3H	AAGCGGGTGACTATCATGCCCAAGGACATCCAGCTCGCACGTCGTATCCGCGGCGAGAGGGCTTGAGTCTCAAGGACTCACTGATTACATACCCAAAGGC
HIST1H3I	GTCACTATTATGCCTAAAGACATCCAGCTTGCGCGCCGCATCCGAGGGGAGAGGGCATAAATATTCCTATCAGCCCAAGAAGTCTGTCCAACCCCAAAAG
HIST1H3J	CTAAGGACATCCAGCTTGCGCGTCGTATCCGTGGCGAGCGAGCATAATCCCCTGCTCTATCTTGGGTTTCTTAATTGCTTCCAAGCTTCCAAAGGCTCTT
HIST1H4A	CAAGCGCCACCGCAAGGTGTTGCGTGACAACATCCAGGGCATCACCAAGCCGGCCATCCGGCGTCTGGCCCGGCGTGGCGGTGTGAAGCGGATCTCTGGT
HIST1H4B	TTTGGGTAAGGGAGGTGCCAAGCGTCACCGAAAAGTGCTGCGGGATAACATCCAAGGCATCACCAAACCGGCCATTCGGCGCCTTGCTAGGCGTGGTGGG
HIST1H4C	TTGGGGAAGGGTGGTGCTAAGCGCCATCGTAAGGTGCTCCGGGATAACATCCAGGGCATTACAAAACCGGCTATTCGCCGTTTGGCTCGGCGCGGTGGCG
HIST1H4D	CGGTAAGGGCGGAAAGGGTCTAGGTAAGGGTGGCGCCAAGCGTCACCGTAAGGTATTGCGTGACAATATCCAAGGAATCACCAAGCCCGCTATCCGCCGC
HIST1H4E	GGATGTGGTCTACGCGCTGAAGAGACAGGGACGCACTCTTTACGGCTTCGGCGGCTAATGCTACCGCTTAAACGACTCAGCATCTCGACTTCCCAAATCA
HIST1H4F	GTCTACGCGCTCAAGCGCCAGGGACGCACTCTGTACGGCTTTGGTGGCTGAGCCTCACCCCGGCTTTTTATTTAACAGCTCACCCATAAAAGGCCCTTTT
HIST1H4H	TGTGGTCTACGCGCTGAAGCGACAGGGACGCACTCTTTACGGCTTCGGTGGCTAAGGCTCCTGCTTGCTGCACTCTTATTTTCATTTTCAACCAAAGGCC
HIST1H4I	GCGTGAAGCGCATTTCTGGCCTCATCTATGAGGAGACCCGCGGAGTGTTGAAGGTGTTCCTGGAGAACGTGATCCGGGACGCCGTGACCTACACGGAGCA
HIST1H4K	AAGCGCAAGACGGTCACCGCCATGGATGTGGTCTACGCGCTCAAGCGCCAGGGCCGCACCCTCTACGGTTTCGGTGGTTGAGCGTCCCTTTCTATCAACA
HIST1H4L	CCGACGCCTGGCACGGCGTGGAGGCGTTAAGCGCATCTCAGGCCTTATATACGAGGAGACACGCGGAGTTCTTAAAGTGTTTTTGGAGAATGTAATCCGC
HIST2H2AA3	TAACATCCAGGCCGTACTGCTCCCTAAGAAGACGGAGAGTCACCACAAGGCAAAGGGCAAGTGAGGCTGACGTCCGGCCCAAGTGGGCCCAGCCCGGCCC
HIST2H2AC	CAGGCCGTTCTGTTACCAAAGAAAACCGAAAGCCACAAAGCCAAAAGCAAATAAATGCAGACAAACAAACCAAGACCAAAGGCTCTTTTTAGAGCCACCC
HIST2H2BE	TGCGAGGCACTTACCATGTAGATACGGGCTCAAAAGTCACCTCTCAGAGACCTACGTCATCCACTCAGGAATTCGCGCCTCTCATACTTGCCTGTCTCAT
HIST2H3C	CCAAGGACATCCAGCTGGCCCGCCGCATCCGTGGAGAGCGGGCTTAAGAAGTGGCGGTTCGGCCGGAGGTTCCATCGTATCCAAAAGGCTCTTTTCAGAG

Table S6: Hypomethylated Genes in C4-12 and LTED

Gene			C4-12			LTED		
Chromosome	Gene	Gene ID	Start	End	Fold change	Start	End	Fold change
20	znf217	nm_006526	51632123	51632723	0.25	51632060	51632660	0.47
20	dkfzp564p1772	al137703	45380801	45381401	0.22	45380793	45381393	0.13
17	bcas3	cr610433	56794836	56795436	0.23	56794761	56795361	0.42
13	adprhl1	nm_138430	113155015	113155615	0.38	113154872	113155472	0.49
8	dq574852	dq574852	141640763	141641363	0.42	99357363	99357963	0.47
6	hist1h2be	nm_003523	26291906	26292506	0.41	26291658	26292258	0.34
14	kiaa0325	ak023747	101568983	101569583	0.45	101579590	101580190	0.43
16	znf75a	nm_153028	3294447	3295047	0.37	3294395	3294995	0.38
15	dkfzp761d081	al157474	57158804	57159404	0.44	57158624	57159224	0.48
19	znf615	nm_198480	57209992	57210592	0.43	57202730	57203330	0.49
17	sirt7	nm_016538	77467994	77468594	0.46	77467995	77468595	0.45
20	sulf2	nm_018837	45731900	45732500	0.47	45730645	45731245	0.45
X	Znf157	nm_003446	47110480	47111080	0.48	47110445	47111045	0.45
6	Hist1h4d	nm_003539	26296523	26297123	0.4	26296523	26297123	0.4
21	Pred57	nm_001080845	45344128	45344728	0.47	45344172	45344772	0.47
20	dkfzp564p1772	al137703	45374362	45374962	0.41	45380793	45381393	0.13

Table S7: Significantly differentially methylated histone genes. Review of significantly differentially hypo-methylated genes in both C4-12 and LTED revealed a strong enrichment for histone genes. We mapped the methylation tracks for each cell line to the UCSC genome browser to visualize the methylation peaks to correlate the results to the MBD-PD array.

Gene	**Chromosomal location**	**MBD-PD array data**		**Visual Inspection of Peaks**	
		C4-12	**LTED**	**C4-12**	**LTED**
HIST1H1A	chr6:26,125,239-26,126,019	NA	HYPO	HYPO	HYPER
HIST1H2BB	chr6:26,151,326-26,151,972	NA	HYPO	HYPO	HYPER
HIST1H2BE	chr6:26,292,003-26,292,437	HYPO	HYPO	HYPO	HYPO
HIST1H3A	chr6:26,128,697-26,129,165	HYPO	NA	HYPO	HYPO
HIST1H3C	chr6:26,153,618-26,154,067		HYPO	HYPO	HYPO
HIST1H4D	chr6:26,296,917-26,297,283	HYPO	NA	HYPO	HYPO
HIST1H4F	chr6:26,348,633-26,349,000	HYPO	NA	HYPO	HYPER