

Table S1: Summary of MBD-seq, ChIP-seq, and MNase-seq primary data analysis (related to Figures 1 and 2).

Sample	# Reads (million)	# Reliable reads* (million)	# Peaks	Total bp covered by peaks	Ave. width of peak (bp)	Standard deviation	Min. length (bp)	Max. length (bp)
DNMT1-UD	21.6	17.1	20717	14745674	711.77	403.68	268	15617
DNMT1-DF	21.6	17.5	18272	12756408	698.14	388.67	280	15790
DNMT3A-UD	23.6	19.7	4660	3816013	818.89	827.9	219	19692
DNMT3A-DF	24.1	18.6	10708	9575563	894.24	1048.42	345	31111
DNMT3B-UD	46.9	30.5	21285	24415676	1147.08	905.52	343	13970
DNMT3B-DF	43.9	31.8	6237	6914694	1108.66	714.98	363	10388
DNA-Me UD	25.6	14.7	175761	174028114	990.14	609.34	212	19703
DNA-Me DF	14.9	12.3	51636	37776142	731.59	336.68	214	8211
H3K4me3-UD	24.1	19.7	47178	32156382	681.6	528.65	166	8489
H3K4 me3-DF	15.1	12.6	23231	30699129	1321.47	812.58	209	11486
H3K9me3-UD	28.5	22.2	69667	65466023	939.7	628.89	249	22925
H3K9me3 DF	28.1	21.4	52300	45675873	873.34	536.53	207	15574
H3K27me3-UD	22.0	17.1	100889	87811500	870	734.85	231	75765
H3K27me3-DF	28.1	22.8	42912	35804188	834.36	464.6	241	12094
H2AK119Ub-UD	20.6	16.2	67787	117211109	1729.11	1295.4	500	39025
H2AK119Ub-DF	46.3	36.8	41912	68413926	1632.32	1736.64	370	47113
H3K36me3-UD	24.9	21.8	27579	29289958	1062.04	885.04	254	28534
H3K36me3-DF	24.6	21.6	40641	44934868	1105.65	975.85	362	41689
ChIP Input	49.6	39.1						
MBD Input	22.4	14.4						
Nucleosome position-UD	459.1	359.4	9772482	1389263260	142.16	60.37	40	650
Nucleosome position-DF	371.2	328.5	10148750	1354218680	133.43	54.54	40	640
WA09 (H9) ES DNA-Me	95.9	65.2	180566	104444035	578.43	426.22	203	24176

UD - undifferentiated NCCIT

DF - RA differentiated NCCIT cells at day 7

*Reliable reads - reads mapped to a single location with a fixed number of mismatches and indels, as described in the Extended Experimental Procedures

Table S2: Sequences of quantitative RT-PCR primers used in this study (related to Figures 1, 2, S1, and S2).

Gene	Forward	Reverse
HAND1	AAAGGCTCAGGACCCAAGAA	CAGCACGTCCATCAGGTAGG
MAP2	CAGGTGGCGGACGTGTGAAAATTGAGAGT G	CACGCTGGATCTGCCTGGGGACTGTG
FOXA2	TGGGAGCGGTGAAGATGGAAGGGCAC	TCATGCCAGCGCCCACGTACGACGAC
NANOG	TGAACCTCAGCTACAAACAGGTG	AACTGCATGCAGGACTGCAGAG
SOX2	ACAACCTCGGAGATCAGCA	GCAGCGTGTACTTATCCTTC
OCT4	CTTGCTGCAGAAGTGGGTGGAGGAA	CTGCAGTGTGGGTTTCGGGCA
DNMT1	GAGGCAGATGACGATGAGG	CAGTCTTGACGGCTTCTCC
DNMT3A	TATTGATGAGCGCACAAAGAGAGC	GGGTGTTCCAGGGTAACATTGAG
DNMT3B	TGTTTCTGTGTGGAGTGC	CAGCAATGGACTCCTCAC
HES7	GTCTAGGATTGTACTCTC	GGGATTTAATAACCACTTT
OTX2	CTCCAACACAGCCTCCAC	CTATAAAGTAGATGTGGCGAGTGA
EVX2	CATCAAGGTGTGGTTCCA	CGTCATCATGTAGGTGTAGA
HOXC5	GATGACCAAACACTGCACAT	TAGCGGTAAAGTGGAATT
HOXB8	GCAATTTCTACGGCTACGA	CGTACTGCACCAGGTCTG
HOXD1	CTACCCCAAGTCCGTCTC	TTACCTTTCTTAGAGGCATTC
HOXD10	CTGAGGTCTCCGTGTCCAGT	TTCTGCCACTCTTTGCAGTG
LEFTY1	TTCAAGTGGCCGTTTCTG	CTCCTTGATGCTGACGAT
EIF4G1	TATTCCAGCCAACTTGTC	CAACAGCCTCCTTCTTAT
ESPNP	GCAGCCAAAGGAGACTTC	CTTGGTTTGGGCATTCACT
ETV2	CAAATTAGGCTTCTGTTTCC	TACCTTTCCAGCATGTCT
CROCC	GAGGTGGAGCTGACACTAG	GCCCAAGCCTTTCTCCTG
DSP	AGCAGGATGTACTATTCTC	GATGGTGTCTGGTTCTG
NADK	ATCATGCTGTCACCTGAAG	ATGGCGGATCTCTTGCT
GAPDH	CTTTGGTATCGTGGAAGG	GATGATGTTCTGGAGAGC

Table S3: Sequences of primers used in quantitative ChIP and MBD enrichment experiments**(Related to Figures 1, 2, S2, and S4).**

Genomic loci	Forward	Reverse
HAND1	ACCTGTTTAACCCTTCTG	GGAGAGGTTGACATCAAA
NANOG	TGTTATTATCAACTAATCCTCTG	TGTGTCCCTCAACTCAAT
OCT4	TTGTCTCTTCGAAATCCA	GGTGTGTATCAACTGCTG
HES7	GAATCTGTCCGACTCAAC	TGAATGTAAGTGGCTTAGATAG
OTX2	AGTTCTATCTGTGAAGGA	AAGTGACTCTTGAAATCG
EVX2	CCGCTCGTCATTAAGGTA	ATCTATTTGTCTGCTCTGAAG
HOXC5	CTTGTGGGAACTATGGAT	TGGGAAAGTGATGCTTAA
HOXB8	CAACAAATCAAATACCTTC	TGACATTTAGAAAGACTC
HOXD1	CTACCCCAAGTCCGTCTC	TTACCTTTCTTAGAGGCATTC
HOXD10	GGCCCCTAGAGCTGAGACTT	CGGACAACAGCGACATCTAC
LEFTY1-Body	AATTAGGTGAGGTAAGTTGT	GATGACTGAACTGCTGAT
EIF4G1-Body	GGGTTATTAAGTTGGAAT	ACCATAGGAAGGAAGAAT
ESPNP	ATAGAGGCGAAGAGAATC	AGAGAAGAATCACCACAT
ETV2	TGAGCGATGAACTGAGGA	GCTTCTTGGGAGTCTAGTC
CROCC-Body	TTCATCTCTGGCTTAGTG	CCTTTCCACAACTTCAC
DSP	TGAGAAGTGCTATAATACGACAA	TCCAAACAATGCCGCTAA
NADK	ACGCAGACTACTCAGGAGAA	ACAACTGGGAGGGATGGT
UBE2B	CTCAGGGGTGGATTGTTGAC	TGTGGATTCAAAGACCACGA
PEX13	GCGTCTAGCAATTCTGTTCC	GTAGGGTGAGGTGGCAAAC
GPR109A	GCTGGAGCATTCACTAGG	TGAAGTCATCTCGGAACAC
OXT	TGTGCCAGACCATTAGC	AAGAGGTTGGTAGTATGATTGG
BRDT	CCCTTTGGCCTTACCAACTT	GCCCTCCCTGAAGAAAAAC













