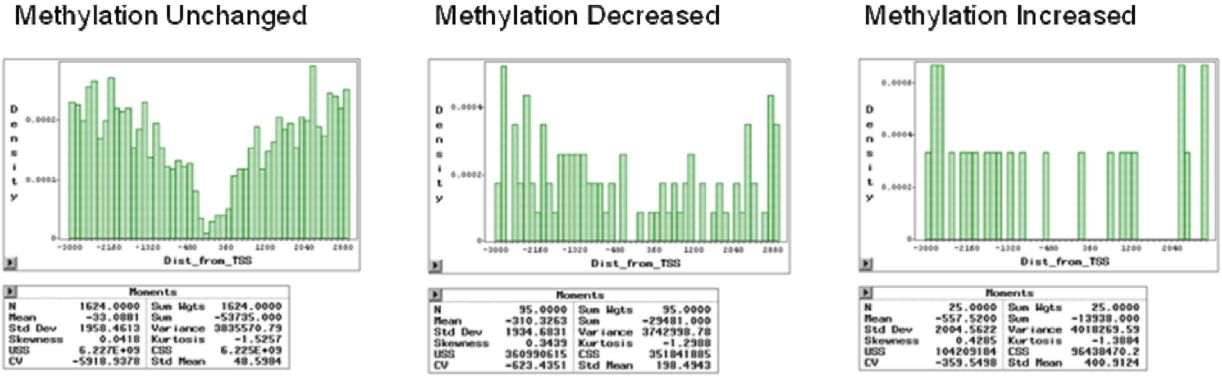
Figure S1: Distribution of (A) LINE elements, (B) SINE elements, (C) LTR retrotransposons, and (D) DNA tranposons near gene promoters at which methylation was unchanged, decreased, or increased from E17.5 to P21.

A. LINE elements



Methylation Unchanged

Moments			
N	1624.0000	Sum Wgts	1624.0000
Mean	-33.0881	Sum	-53735.000
Std Dev	1958.4613	Variance	3835570.79
Skewness	0.0418	Kurtosis	-1.5257
USS	6.227E+09	CSS	6.225E+09
CV	-5918.9378	Std Mean	48.5984

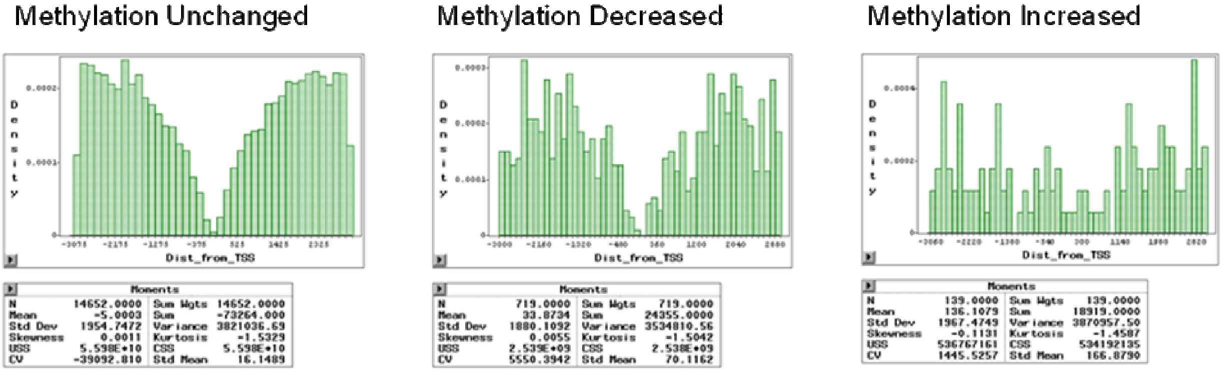
Methylation Decreased

Moments			
N	95.0000	Sum Wgts	95.0000
Mean	-310.3263	Sum	-29481.000
Std Dev	1934.6831	Variance	3742998.78
Skewness	0.3439	Kurtosis	-1.2988
USS	360990615	CSS	351841885
CV	-623.4351	Std Mean	198.4943

Methylation Increased

Moments			
N	25.0000	Sum Wgts	25.0000
Mean	-557.5200	Sum	-13938.000
Std Dev	2004.5622	Variance	4018269.59
Skewness	0.4285	Kurtosis	-1.3884
USS	104209184	CSS	96438470.2
CV	-359.5498	Std Mean	400.9124

B. SINE elements



Methylation Unchanged

Moments			
N	14652.0000	Sum Wgts	14652.0000
Mean	-5.0003	Sum	-73264.000
Std Dev	1954.7472	Variance	3821036.69
Skewness	0.0011	Kurtosis	-1.5329
USS	5.598E+10	CSS	5.598E+10
CV	-39092.810	Std Mean	16.1489

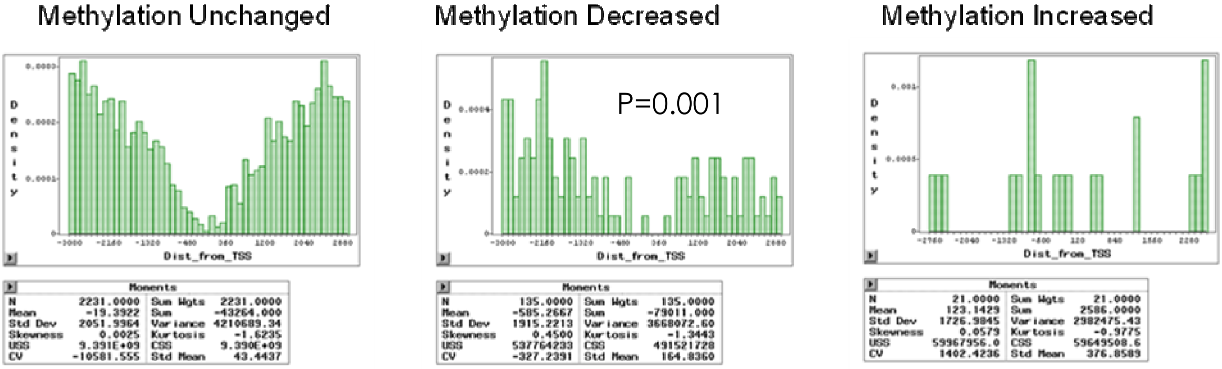
Methylation Decreased

Moments			
N	719.0000	Sum Wgts	719.0000
Mean	33.8734	Sum	24355.0000
Std Dev	1880.1092	Variance	3534810.56
Skewness	0.0055	Kurtosis	-1.5042
USS	2.539E+09	CSS	2.538E+09
CV	5550.3942	Std Mean	70.1162

Methylation Increased

Moments			
N	139.0000	Sum Wgts	139.0000
Mean	136.1079	Sum	18919.0000
Std Dev	1967.4749	Variance	3870957.50
Skewness	-0.1131	Kurtosis	-1.4587
USS	536767161	CSS	534192135
CV	1445.5257	Std Mean	166.8790

C. LTR retrotranposons



Methylation Unchanged

Moments			
N	2231.0000	Sum Wgts	2231.0000
Mean	-19.3922	Sum	-43264.000
Std Dev	2051.9964	Variance	4210689.34
Skewness	0.0025	Kurtosis	-1.6235
USS	9.391E+09	CSS	9.390E+09
CV	-10581.555	Std Mean	43.4437

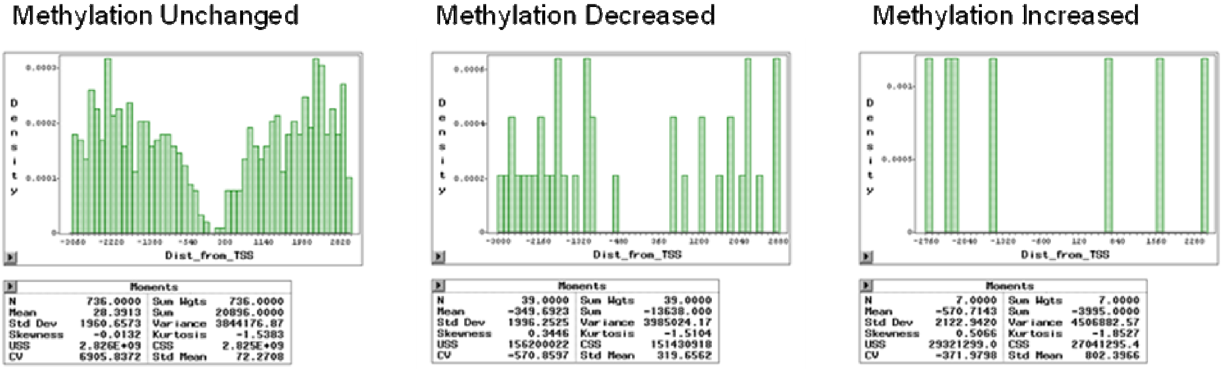
Methylation Decreased

Moments			
N	135.0000	Sum Wgts	135.0000
Mean	-585.2667	Sum	-79011.000
Std Dev	1915.2213	Variance	3668072.60
Skewness	0.4500	Kurtosis	-1.3443
USS	537764233	CSS	491521728
CV	-327.2391	Std Mean	164.8360

Methylation Increased

Moments			
N	21.0000	Sum Wgts	21.0000
Mean	123.1429	Sum	2586.0000
Std Dev	1726.9845	Variance	2982475.43
Skewness	0.0579	Kurtosis	-0.9775
USS	59967956.0	CSS	59649508.6
CV	1402.4236	Std Mean	376.8589

D. DNA transposons



Methylation Unchanged

Moments			
N	736.0000	Sum Wgts	736.0000
Mean	28.3913	Sum	20896.0000
Std Dev	1960.6573	Variance	3844176.87
Skewness	-0.0132	Kurtosis	-1.5383
USS	2.826E+09	CSS	2.825E+09
CV	6905.8372	Std Mean	72.2708

Methylation Decreased

Moments			
N	39.0000	Sum Wgts	39.0000
Mean	-349.6923	Sum	-13638.000
Std Dev	1996.2525	Variance	3985024.17
Skewness	0.3446	Kurtosis	-1.5104
USS	156200022	CSS	151430918
CV	-570.8597	Std Mean	319.6562

Methylation Increased

Moments			
N	7.0000	Sum Wgts	7.0000
Mean	-570.7143	Sum	-3995.0000
Std Dev	2122.9420	Variance	4506882.57
Skewness	0.5066	Kurtosis	-1.8527
USS	29321299.0	CSS	27041295.4
CV	-371.9798	Std Mean	802.3966

Figure S2: Venn diagrams illustrating the prevalence of polycomb targets among genes in which methylation was gained, unchanged, or lost from E17.5 to P21.

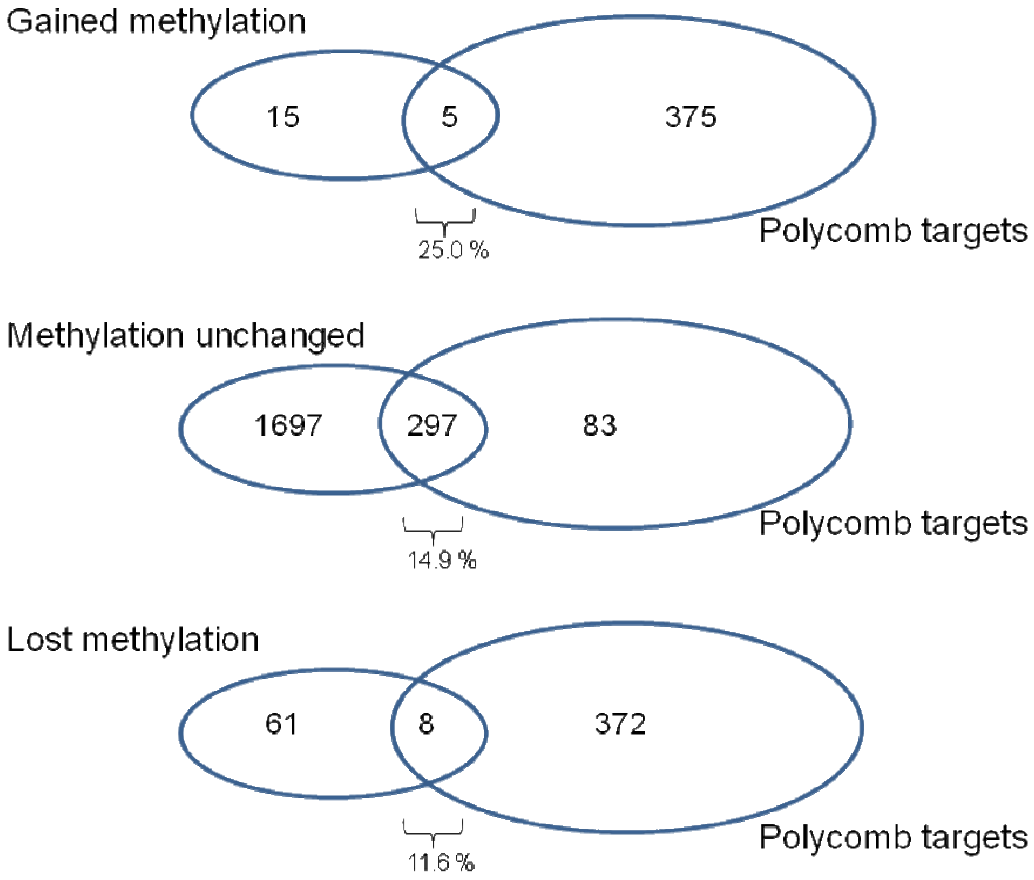


Figure S3: Percent methylation vs. age from P21 to P120, for the six genes evaluated for methylation dynamics from E17.5 to P21.