

SUPPLEMENTARY INFORMATION

Supplemental Table 1: Histone enriched promoters (D1 array)

Go Category	Total Genes	Changed Genes	Enrichment	FDR
<i>Sequence-specific DNA binding</i>	425	32	4.601991	0
<i>Transcription factor activity</i>	755	38	3.076248	0
<i>Transcription regulator activity</i>	1090	46	2.579384	0
<i>Multicellular organismal development</i>	1620	59	2.225982	0
<i>DNA binding</i>	1522	54	2.168522	0
<i>Regulation of transcription DNA-dependent</i>	1467	51	2.124833	0
<i>Transcription DNA-dependent</i>	1510	52	2.104801	0
<i>RNA biosynthetic process</i>	1512	52	2.102017	0
<i>Regulation of transcription</i>	1580	52	2.011551	0
<i>Transcription</i>	1623	53	1.995915	0
<i>Developmental process</i>	1644	53	1.97042	0
<i>RNA metabolic process</i>	2265	73	1.969878	0
<i>Regulation of cellular metabolic process</i>	1827	58	1.940324	0
<i>Regulation of metabolic process</i>	1772	55	1.897071	0
<i>Regulation of cellular process</i>	1839	57	1.894427	0
<i>Regulation of biological process</i>	2889	84	1.777119	0
<i>Multicellular organismal process</i>	3134	89	1.735704	0
<i>Biological regulation</i>	2648	73	1.68496	0
<i>System development</i>	3396	93	1.673786	0
<i>Nucleobase nucleoside metabolic process</i>	1231	40	1.986034	0.0015
<i>Nucleic acid binding</i>	2489	66	1.620704	0.001905
<i>Transcription from RNA polymerase II promoter</i>	2348	63	1.639937	0.002174
<i>Anatomical structure development</i>	460	21	2.79027	0.002273
<i>Organ development</i>	1465	44	1.835692	0.0025
<i>Skeletal development</i>	869	31	2.180352	0.002692
<i>Urogenital system development</i>	174	12	4.215186	0.0028
<i>Kidney development</i>	31	5	9.858096	0.004545
<i>Wnt receptor activity</i>	29	5	10.537964	0.005
<i>Growth factor activity</i>	7	3	26.194368	0.007941

Supplemental Table 2: D1 Histone-enriched loci (Illumina GAI FDR < 0.0001)

Go Category	Total Genes	Changed Genes	Enrichment	FDR
<i>Cell fate commitment</i>	75	60	1.59848	0
<i>Sequence-specific DNA binding</i>	424	337	1.588112	0
<i>Cellular morphogenesis during differentiation</i>	125	99	1.582495	0
<i>Cell projection organization and biogenesis</i>	169	131	1.548823	0
<i>Cell part morphogenesis</i>	169	131	1.548823	0
<i>Embryonic morphogenesis</i>	88	68	1.543986	0
<i>Regionalization</i>	82	63	1.535126	0
<i>Neurogenesis</i>	221	168	1.518918	0
<i>Wnt receptor signaling pathway</i>	107	80	1.493907	0
<i>Regulation of cell differentiation</i>	119	88	1.477587	0
<i>Regulation of transcription from RNA polymerase II promoter</i>	99	72	1.453164	0
<i>Organ morphogenesis</i>	304	221	1.452566	0
<i>Embryonic development</i>	226	164	1.449949	0
<i>Regulation of developmental process</i>	191	138	1.443653	0
<i>Voltage-gated ion channel activity</i>	171	123	1.43723	0
<i>Nervous system development</i>	604	433	1.432413	0
<i>Cation channel activity</i>	228	162	1.419703	0
<i>Transcription factor activity</i>	791	552	1.394376	0
<i>Muscle development</i>	136	94	1.38104	0
<i>Central nervous system development</i>	190	129	1.356605	0
<i>Skeletal development</i>	193	130	1.34587	0
<i>Anatomical structure morphogenesis</i>	855	575	1.343751	0
<i>System development</i>	1396	934	1.336838	0
<i>Multicellular organismal development</i>	1868	1248	1.334919	0
<i>Channel or pore class transporter activity</i>	363	242	1.332067	0
<i>Enzyme linked receptor protein signaling pathway</i>	228	152	1.332067	0
<i>Positive regulation of transcription DNA-dependent</i>	180	120	1.332067	0
<i>Cell morphogenesis</i>	374	249	1.330286	0
<i>Cell Differentiation</i>	1437	874	1.330286	0
<i>Positive regulation of transcription</i>	227	151	1.329133	0
<i>Anatomical structure development</i>	1679	1107	1.317389	0
<i>Positive regulation of cell proliferation</i>	192	126	1.311253	0
<i>Organ development</i>	996	650	1.303981	0
<i>Cell fate commitment</i>	75	60	1.59848	0
<i>Sequence-specific DNA binding</i>	424	337	1.588112	0
<i>Cellular morphogenesis during differentiation</i>	125	99	1.582495	0
<i>Positive regulation of biological process</i>	850	513	1.548823	0
<i>51674 localization of cell</i>	324	203	1.251896	0
<i>32502 developmental process</i>	2619	1639	1.250434	0
<i>06812 cation transport</i>	432	270	1.248812	0
<i>15075 ion transporter activity</i>	622	387	1.243191	0
<i>42127 regulation of cell proliferation</i>	383	238	1.241639	0
<i>65009 regulation of a molecular function</i>	400	246	1.228831	0
<i>06366 transcription from RNA polymerase II promoter</i>	532	326	1.2244	0
<i>50790 regulation of catalytic activity</i>	381	233	1.221935	0
<i>05576 extracellular region</i>	1056	596	1.127716	0
<i>06351 transcription DNA-dependent</i>	1866	1050	1.124333	0

Supplemental Table 2 continued: D1 Histone-enriched loci (Illumina GAI FDR < 0.0001)

Go Category	Total Genes	Changed Genes	Enrichment	FDR
<i>RNA biosynthetic process</i>	1869	1051	1.123597	0
<i>Extracellular region</i>	1056	596	1.127716	0
<i>Guanyl-nucleotide exchange factor activity</i>	123	84	1.364556	0.000073
<i>Blood vessel development</i>	133	90	1.352098	0.000074
<i>Ras protein signal transduction</i>	176	115	1.305577	0.000074
<i>Negative regulation of developmental process</i>	65	49	1.50626	0.000075
<i>Transport</i>	2094	1134	1.082066	0.000075
<i>Embryonic development ending in birth or egg hatching</i>	81	59	1.455406	0.000076
<i>Extracellular matrix structural constituent</i>	84	61	1.451001	0.000076
<i>Transporter activity</i>	1090	611	1.120036	0.000077
<i>Cyclic nucleotide metabolic process</i>	34	29	1.704262	0.000078
<i>Positive regulation of developmental process</i>	49	39	1.590324	0.000078
<i>Vasculature development</i>	135	92	1.361668	0.000079
<i>Anion transport</i>	161	107	1.32793	0.000079
<i>Extracellular matrix organization and biogenesis</i>	44	36	1.634809	0.00008
<i>Heart development</i>	80	59	1.473599	0.000081
<i>Extracellular matrix organization and biogenesis</i>	44	36	1.634809	0.00008
<i>Heart development</i>	80	59	1.473599	0.000081
<i>Voltage-gated potassium channel complex</i>	80	59	1.473599	0.000081
<i>Chordate embryonic development</i>	80	59	1.473599	0.000081
<i>Developmental maturation</i>	48	38	1.581829	0.000145
<i>Kidney development</i>	29	25	1.7225	0.000201
<i>Transcriptional activator activity</i>	243	152	1.24984	0.000203
<i>Anterior posterior pattern formation</i>	50	39	1.558518	0.000204
<i>Cyclic nucleotide biosynthetic process</i>	26	23	1.76755	0.000205
<i>Establishment of localization</i>	2154	1162	1.077898	0.000207
<i>Extracellular region part</i>	697	400	1.146686	0.000211
<i>Anatomical structure formation</i>	132	89	1.347204	0.000213
<i>Sensory organ development</i>	56	43	1.534255	0.000214
<i>Metanephros development</i>	23	21	1.824352	0.000216
<i>Blood vessel morphogenesis</i>	120	81	1.348717	0.00025
<i>Ionotropic glutamate receptor activity</i>	18	17	1.887094	0.000252
<i>Glutamate-gated ion channel activity</i>	18	17	1.887094	0.000252
<i>Muscle contraction</i>	149	98	1.314187	0.000255
<i>Brain development</i>	101	70	1.384822	0.000256

Supplemental Table 3: Donor pool of histone-enriched loci (Illumina GAI FDR < 0.0001)

Go Category	Total Genes	Changed Genes	Enrichment	FDR
<i>RNA polymerase II transcription factor activity</i>	25	22	2.187319	0
<i>Cell fate commitment</i>	69	53	1.909221	0
<i>Regionalization</i>	86	60	1.734133	0
<i>Wnt receptor signaling pathway</i>	121	84	1.725534	0
<i>Pattern specification process</i>	123	85	1.717684	0
<i>Embryonic morphogenesis</i>	93	64	1.710514	0
<i>Sensory organ development</i>	80	55	1.708843	0
<i>Negative regulation of cell differentiation</i>	67	46	1.706525	0
<i>Cellular morphogenesis during differentiation</i>	124	85	1.703832	0
<i>Neurogenesis</i>	257	171	1.653836	0
<i>Embryonic development</i>	93	61	1.630333	0
<i>Chordate embryonic development</i>	93	61	1.630333	0
<i>Brain development</i>	133	87	1.625912	0
<i>Sequence-specific DNA binding</i>	488	311	1.584054	0
<i>Positive regulation of transcription from RNA polymerase II promoter</i>	145	92	1.577064	0
<i>Embryonic development</i>	221	140	1.574582	0
<i>Cell projection organization and biogenesis</i>	193	121	1.558323	0
<i>Cell part morphogenesis</i>	193	121	1.558323	0
<i>Regulation of cell differentiation</i>	157	98	1.551515	0
<i>Cell morphogenesis</i>	256	158	1.534075	0
<i>Cellular structure morphogenesis</i>	256	158	1.534075	0
<i>Central nervous system development</i>	227	140	1.532963	0
<i>Nervous system development</i>	675	408	1.502401	0
<i>Positive regulation of RNA metabolic process</i>	229	138	1.497867	0
<i>Skeletal development</i>	203	121	1.481559	0
<i>Vasculature development</i>	165	96	1.446162	0
<i>Organ morphogenesis</i>	355	205	1.435341	0
<i>Cell migration</i>	222	128	1.433133	0
<i>Anatomical structure morphogenesis</i>	823	457	1.380212	0
<i>Transcription activator activity</i>	284	157	1.374076	0
<i>System development</i>	1538	817	1.320369	0
<i>Multicellular organismal development</i>	2093	1104	1.31108	0
<i>Positive regulation of cellular process</i>	952	501	1.308068	0
<i>Anatomical structure development</i>	1768	930	1.307465	0
<i>Cell development</i>	1089	565	1.289585	0
<i>Cell differentiation</i>	1636	835	1.268623	0
<i>Cellular developmental process</i>	1636	835	1.268623	0
<i>Organ development</i>	1106	564	1.267516	0
<i>Developmental process</i>	2848	1443	1.259377	0
<i>Intracellular signaling cascade</i>	1291	653	1.257235	0
<i>Regulation of developmental process</i>	729	367	1.251319	0
<i>Regulation of RNA metabolic process</i>	2115	1049	1.232806	0
<i>Regulation of transcription DNA-dependent</i>	2103	1043	1.232749	0
<i>Regulation of transcription</i>	2228	1104	1.231639	0
<i>Regulation of gene expression</i>	2358	1159	1.221713	0
<i>Transcription DNA-dependent</i>	2159	1061	1.221497	0
<i>RNA biosynthetic process</i>	2163	1061	1.219238	0

Supplemental Table 3 continued: Donor pool of histone-enriched loci (Illumina GAI FDR < 0.0001)

Go Category	Total Genes	Changed Genes	Enrichment	FDR
<i>Regulation of metabolic process</i>	2629	1285	1.214904	0
<i>Transcription</i>	2315	1129	1.212195	0
<i>Anatomical structure formation</i>	152	89	1.455378	0.000072
<i>Transmembrane receptor protein tyrosine kinase activity</i>	62	43	1.723877	0.000074
<i>Small GTPase regulator activity</i>	201	112	1.385005	0.000136
<i>Respiratory tube development</i>	43	32	1.849741	0.000138
<i>Insulin receptor signaling pathway</i>	31	25	2.004508	0.000139
<i>Appendage morphogenesis</i>	37	28	1.880987	0.000189
<i>Limb morphogenesis</i>	37	28	1.880987	0.000189
<i>Appendage development</i>	37	28	1.880987	0.000189
<i>Limb development</i>	37	28	1.880987	0.000189
<i>Regulation of anatomical structure morphogenesis</i>	69	45	1.621037	0.000485
<i>Transcription corepressor activity</i>	106	64	1.500734	0.000491
<i>BMP signaling pathway</i>	18	16	2.209413	0.000539
<i>Regulation of neuron differentiation</i>	26	21	2.007592	0.000595
<i>Localization of cell</i>	365	184	1.25301	0.000694
<i>Protein-tyrosine kinase activity</i>	159	89	1.391305	0.000706
<i>Rho protein signal transduction</i>	101	61	1.501198	0.00071
<i>Small conjugating protein ligase activity</i>	137	78	1.415153	0.000769
<i>Forebrain development</i>	46	32	1.729106	0.000773
<i>Voltage-gated cation channel activity</i>	141	80	1.410264	0.000778
<i>Blood vessel morphogenesis</i>	145	82	1.405644	0.000787
<i>Tube development</i>	114	67	1.460829	0.000795
<i>Cartilage development</i>	35	26	1.846438	0.0008
<i>Regulation of cellular component organization and biogenesis</i>	241	127	1.309834	0.00082
<i>Mesoderm formation</i>	14	13	2.308048	0.000851
<i>Heart development</i>	93	56	1.496699	0.000947
<i>Regulation of neurogenesis</i>	41	29	1.7581	0.000952
<i>Negative regulation of developmental process</i>	314	159	1.258627	0.000964
<i>Regulation of cell proliferation</i>	456	223	1.215541	0.000984
<i>Voltage-gated ion channel activity</i>	189	102	1.34143	0.00099
<i>Voltage-gated channel activity</i>	189	102	1.34143	0.00099
<i>Actin filament-based process</i>	206	109	1.315191	0.001133
<i>Regulation of anatomical structure morphogenesis</i>	69	45	1.621037	0.000485
<i>Transcription corepressor activity</i>	106	64	1.500734	0.000491
<i>BMP signaling pathway</i>	18	16	2.209413	0.000539
<i>Regulation of neuron differentiation</i>	26	21	2.007592	0.000595
<i>Localization of cell</i>	365	184	1.25301	0.000694
<i>Protein-tyrosine kinase activity</i>	159	89	1.391305	0.000706
<i>Rho protein signal transduction</i>	101	61	1.501198	0.00071
<i>Small conjugating protein ligase activity</i>	137	78	1.415153	0.000769
<i>Forebrain development</i>	46	32	1.729106	0.000773
<i>Voltage-gated cation channel activity</i>	141	80	1.410264	0.000778
<i>Blood vessel morphogenesis</i>	145	82	1.405644	0.000787
<i>Tube development</i>	114	67	1.460829	0.000795
<i>Cartilage development</i>	35	26	1.846438	0.0008
<i>Regulation of cellular component organization and biogenesis</i>	241	127	1.309834	0.00082

Supplemental Table 4: TH2B Enriched Promoters (D1 array)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Beta DNA polymerase activity</i>	3	3	22.225524	0.018333
<i>Multidrug transport</i>	3	3	22.225524	0.018333
<i>Cation transport</i>	380	35	2.047088	0.023333
<i>Metal ion transport</i>	310	30	2.150857	0.0275
<i>Voltage-gated potassium channel</i>	72	11	3.395566	0.0325
<i>Potassium ion transport</i>	141	17	2.679673	0.03375
<i>Alpha-type channel activity</i>	333	32	2.135786	0.035
<i>Voltage-gated ion channel activity</i>	161	18	2.484841	0.035455
<i>Potassium ion binding</i>	106	14	2.935447	0.036
<i>Transporter activity</i>	1067	73	1.520584	0.037143
<i>Adenylate cyclase activity</i>	14	5	7.937687	0.04
<i>Channel or pore class transporter activity</i>	338	33	2.169948	0.06

Supplemental Table 5: H3K4me2 enriched promoters (D1 array)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Multicellular organismal development</i>	1620	148	1.394279	0.005
<i>Developmental process</i>	2265	197	1.327398	0.01
<i>Sequence-specific DNA binding</i>	425	50	1.795495	0.026667
<i>Anatomical structure development</i>	1465	132	1.375116	0.03
<i>System development</i>	1231	113	1.400953	0.031429
<i>Cell-cell signaling</i>	525	57	1.656985	0.035
<i>Organ development</i>	869	84	1.47524	0.035
<i>Menstrual cycle</i>	30	9	4.578511	0.04
<i>Multicellular organism reproduction</i>	45	10	3.39149	0.065294
<i>Reproductive process in a multicellular organism</i>	45	10	3.39149	0.065294
<i>Multicellular organismal process</i>	2648	212	1.221859	0.067333

Supplemental Table 6: H3K4me3 enriched promoters (D1 array)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Nuclear pore</i>	44	15	3.620699	0
<i>mRNA metabolic process</i>	198	44	2.36016	0
<i>mRNA processing</i>	165	35	2.25288	0
<i>Chromosome</i>	204	40	2.082494	0
<i>RNA processing</i>	266	51	2.036303	0
<i>Nuclear part</i>	596	109	1.94238	0
<i>RNA binding</i>	481	78	1.722279	0
<i>Cell cycle</i>	606	98	1.717542	0
<i>Cell cycle process</i>	530	82	1.643205	0
<i>RNA metabolic process</i>	1827	256	1.488179	0
<i>Transcription DNA-dependent</i>	1510	199	1.399684	0
<i>RNA biosynthetic process</i>	1512	199	1.397833	0
<i>Regulation of transcription DNA-dependent</i>	1467	193	1.397272	0
<i>Transcription</i>	1644	216	1.395423	0
<i>DNA binding</i>	1522	199	1.388648	0
<i>Regulation of transcription</i>	1580	206	1.384727	0
<i>Regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	1623	211	1.380759	0
<i>Regulation of cellular metabolic process</i>	1772	229	1.372542	0
<i>Regulation of metabolic process</i>	1839	237	1.368739	0
<i>Regulation of cellular process</i>	2889	341	1.253605	0
<i>Regulation of biological process</i>	3134	362	1.226771	0
<i>RNA splicing</i>	137	30	2.325705	0.000227
<i>Macromolecule localization</i>	548	83	1.608612	0.000233
<i>Intracellular transport</i>	494	75	1.612457	0.0004
<i>Cellular protein metabolic process</i>	2294	271	1.254671	0.000417
<i>RNA localization</i>	36	13	3.835259	0.000426
<i>Ligase activity</i>	238	42	1.874244	0.000727
<i>Establishment of cellular localization</i>	596	86	1.53252	0.000741
<i>Specific RNA polymerase II transcription factor activity</i>	29	11	4.028548	0.000755
<i>Translation initiation factor activity</i>	46	14	3.232393	0.000833
<i>Spliceosome</i>	88	21	2.53449	0.000847
<i>Nucleic acid transport</i>	35	12	3.641389	0.000862
<i>RNA transport</i>	35	12	3.641389	0.000862
<i>Establishment of RNA localization</i>	35	12	3.641389	0.000862
<i>Ribonucleoprotein complex</i>	328	53	1.716153	0.001475
<i>Nuclear membrane part</i>	54	15	2.9502	0.001791
<i>Pore complex</i>	54	15	2.9502	0.001791
<i>Tricarboxylic acid cycle</i>	22	9	4.344839	0.001846
<i>Acetyl-CoA catabolic process</i>	22	9	4.344839	0.001846
<i>Cellular localization</i>	611	86	1.494897	0.001905
<i>Ubiquitin cycle</i>	267	45	1.790009	0.001935
<i>Translation regulator activity</i>	99	21	2.25288	0.004405
<i>Spermatogenesis</i>	141	27	2.033755	0.004444
<i>Male gamete generation</i>	141	27	2.033755	0.004444

Supplemental Table 6 continued: H3K4me3 enriched promoters (D1)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Transcription regulator activity</i>	1090	136	1.325154	0.004458
<i>RNA export from nucleus</i>	20	8	4.248287	0.004512
<i>Translation factor activity nucleic acid binding</i>	86	19	2.346438	0.004828
<i>Protein transport</i>	460	66	1.523842	0.004884
<i>Microtubule-based process</i>	136	26	2.030431	0.005114
<i>Protein modification process</i>	1218	149	1.29925	0.006517
<i>Nuclear chromosome</i>	55	14	2.703456	0.007444
<i>Acetyl-CoA metabolic process</i>	27	9	3.540239	0.00828
<i>Transcription from RNA polymerase II promoter</i>	460	65	1.500754	0.00837
<i>Nucleobase nucleoside nucleotide and nucleic acid transport</i>	44	12	2.89656	0.008404
<i>Organelle organization and biogenesis</i>	711	93	1.389208	0.008438
<i>Microtubule cytoskeleton organization and biogenesis</i>	57	14	2.608598	0.008454
<i>Sexual reproduction</i>	218	36	1.75388	0.008526
<i>Meiotic recombination</i>	18	7	4.130279	0.010918
<i>Tricarboxylic acid cycle intermediate metabolic process</i>	23	8	3.694163	0.01101
<i>Nuclear export</i>	29	9	3.296085	0.018762
<i>Cofactor catabolic process</i>	29	9	3.296085	0.018762
<i>Gamete generation</i>	184	31	1.78936	0.018835
<i>Protein complex</i>	1361	161	1.256382	0.01902
<i>Intracellular protein transport</i>	289	44	1.616995	0.019208
<i>Endomembrane system</i>	331	49	1.572251	0.0194

Supplemental Table 7: H3K4me3-enriched loci as determined from donor pool (Illumina GAI FDR < 0.001)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>RNA splicing</i>	64	46	1.622	0
<i>spliceosome</i>	119	85	1.612	0
<i>ATP-dependent helicase activity</i>	88	62	1.59	0
<i>mRNA processing</i>	235	156	1.48	0
<i>Protein folding</i>	151	99	1.48	0
<i>Helicase activity</i>	129	84	1.4699	0
<i>ribonucleoprotein complex biogenesis and assembly</i>	186	134	1.468	0
<i>mRNA metabolic process</i>	272	177	1.463	0
<i>RNA processing</i>	404	253	1.413636	0
<i>Ribonucleoprotein complex</i>	400	250	1.41	0
<i>nucleolus</i>	158	97	1.385	0
<i>Microtubule-based process</i>	190	116	1.378	0
<i>Ligase activity</i>	338	204	1.362	0
<i>Translation</i>	351	210	1.350	0
<i>Mitotic cell cycle</i>	295	168	1.285	0
<i>Cell cycle phase</i>	323	183	1.285	0
<i>Nucleoplasm</i>	442	250	1.279302	0
<i>Nucleoplasm part</i>	381	215	1.272843	0
<i>Cell cycle process</i>	395	253	1.257553	0
<i>Transcription factor binding</i>	390	214	1.238	0
<i>RNA metabolic process</i>	2624	1411	1.213	0
<i>Transcription from RNA polymerase II promoter</i>	610	326	1.206	0
<i>Nucleobase nucleoside nucleotide metabolic process</i>	3279	1734	1.19	0
<i>DNA binding</i>	2080	1099	1.199734	0
<i>Cell cycle</i>	691	364	1.18	0
<i>Gene expression</i>	3028	1878	1.18	0
<i>Transcription</i>	2315	1207	1.173	0
<i>Transcription DNA-dependent</i>	2159	1121	1.172	0
<i>RNA biosynthetic process</i>	2163	1222	1.171	0
<i>Regulation of gene expression</i>	2358	1223	1.1698	0
<i>Transcription regulator activity</i>	1309	678	1.169	0
<i>Regulation of transcription DNA-dependent</i>	2103	1089	1.1689	0
<i>Regulation of transcription</i>	2228	1146	1.161	0
<i>Post-translational protein modification</i>	1346	777	1.133388	0
<i>Ribonucleotide binding</i>	1537	879	1.12284	0

Supplemental Table 7 continued: H3K4me3-enriched loci as determined from donor pool (Illumina GAI FDR < 0.001)

GO CATEGORY	Total Genes	Changed Genes	Enrichment	FDR
<i>M phase</i>	261	148	1.28	0.000098
<i>Mitochondrion</i>	807	413	1.15	0.00099
<i>Ribosome biogenesis and assembly</i>	86	57	1.49	0.0001
<i>Regulation of cell cycle</i>	272	154	1.278	0.000102
<i>Ubiquitin-dependent protein catabolic process</i>	164	98	1.3489	0.000185
<i>RNA helicase activity</i>	28	24	1.85	0.000187
<i>Protein RNA complex Assembly</i>	105	67	1.440	0.000189
<i>Spindle</i>	70	48	1.547	0.000192
<i>Spermatogenesis</i>	202	106	1.296	0.00082
<i>Male gamete generation</i>	202	106	1.296	0.00082
<i>Response to DNA damage stimulus</i>	278	152	1.234	0.003
<i>Mitosis</i>	198	112	1.276	0.003
<i>Flagellum</i>	30	23	1.73	0.00331
<i>Regulation of translation</i>	99	61	1.347	0.00349
<i>Centrosome</i>	124	74	1.347	0.00349
<i>Gamete generation</i>	247	136	1.24	0.00353
<i>Regulation of RNA cellular biosynthetic process</i>	128	76	1.3403	0.00357
<i>Negative regulation of cell cycle</i>	138	81	1.323143	0.00038
<i>mRNA splice site selection</i>	13	12	2.08	0.00397
<i>rRNA processing</i>	61	40	1.48839	0.00515
<i>nuclear chromosome part</i>	61	40	1.488	0.00515
<i>Translation initiation factor activity</i>	58	44	1.489455	0.0056
<i>Negative regulation of cellular process</i>	1023	579	1.111234	0.00057
<i>Chromosome organization and biogenesis</i>	345	211	1.200787	0.000606
<i>Regulation of protein metabolic process</i>	301	184	1.200201	0.001384
<i>RNA splicing via transesterification reactions</i>	64	47	1.441852	0.001392
<i>RNA splicing via transesterification reactions with bulged adenosine as nucleophile</i>	64	47	1.441852	0.001392
<i>Nuclear mRNA splicing via spliceosome</i>	64	47	1.441852	0.001392
<i>rRNA metabolic process</i>	64	47	1.441852	0.001392
<i>Establishment of cellular localization</i>	766	439	1.125223	0.0012
<i>Transcription factor complex</i>	161	105	1.28046	0.001208
<i>Establishment of protein localization</i>	674	389	1.133163	0.00125
<i>Regulation of cyclin-dependent protein kinase activity</i>	48	37	1.513433	0.001258
<i>Protein tyrosine phosphatase activity</i>	97	67	1.356144	0.001438
<i>Regulation of translation</i>	99	68	1.348579	0.001657
<i>Interphase of mitotic cell cycle</i>	84	59	1.379036	0.001667
<i>G1 S transition of mitotic cell cycle</i>	33	27	1.606396	0.001677
<i>Nucleolar part</i>	39	31	1.56063	0.001718
<i>Embryonic developmemt</i>	220	120	1.225	0.01

Supplemental Table 8: Donor pool H3K27me3-enriched loci (Illumina GAI FDR <0.0001)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Wnt receptor signaling</i>	20	18	2.706	0
<i>Embryonic organ development</i>	20	18	2.706	0
<i>Transmembrane receptor protein</i>	18	16	2.706	0
<i>Inner ear morphogenesis</i>	27	24	2.619	0
<i>Mesenchymal cell development and differentiation</i>	23	19	2.484	0
<i>Cell fate commitment</i>	69	54	2.353	0
<i>Embryonic morphogenesis</i>	93	71	2.295	0
<i>Lung development</i>	42	31	2.219	0
<i>Cyclic nucleotide metabolic process</i>	37	27	2.194	0
<i>Appendage morphogenesis</i>	37	27	2.1943	0
<i>Limb morphogenesis</i>	37	27	2.1943	0
<i>Appendage development</i>	37	27	2.1943	0
<i>Limb development</i>	37	27	2.1943	0
<i>Sensory organ development</i>	80	58	2.1800	0
<i>Potassium ion binding</i>	123	89	2.171	0
<i>Regionalization</i>	86	62	2.16	0
<i>Anterior posterior pattern formation</i>	54	38	2.116	0
<i>Axonogenesis</i>	112	77	2.06	0
<i>Pattern specification process</i>	123	84	2.0535	0
<i>Regulation of anatomical structure morphogenesis</i>	69	47	2.048	0
<i>Neuron differentiation</i>	206	139	2.029	0
<i>Forebrain development</i>	46	31	2.026	0
<i>Developmental maturation</i>	52	35	2.02	0
<i>Neuron morphogenesis during differentiation</i>	118	79	2.013	0
<i>Skeletal development</i>	203	133	1.970	0
<i>Neurite development</i>	133	87	1.966	0
<i>Neurogenesis</i>	265	165	1.930	0
<i>Cell migration</i>	222	142	1.9217	0
<i>Brain development</i>	133	85	1.921	0
<i>Embryonic development</i>	221	40	1.904	0
<i>Sequence specific DNA binding</i>	488	309	1.904	0
<i>Tube Development</i>	114	70	1.86	0
<i>Vasculature development</i>	165	101	1.846	0
<i>Organ morphogenesis</i>	335	215	1.821	0
<i>Blood vessel development</i>	162	98	1.819	0
<i>Central nervous system development</i>	227	137	1.814	0
<i>Heart development</i>	93	56	1.8106	0
<i>Anatomical structure formation</i>	152	91	1.8002	0
<i>Bone remodeling</i>	96	57	1.785	0
<i>Chordate embryonic development</i>	93	55	1.778	0

Supplemental Table 8: Donor pool H3K27me3-enriched loci (Illumina GAI FDR <0.0001)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>System process</i>	1264	504	1.1989	0
<i>Ligand gated ion channel</i>	97	54	1.674	0
<i>Embryonic limb morphogenesis</i>	33	24	2.186	0.000044
<i>Embryonic appendage morphogenesis</i>	33	24	2.186	0.00044
<i>Neural crest cell development and differentiation</i>	14	13	2.792	0.00082
<i>Metanephros development</i>	23	18	2.3533	0.000114
<i>Voltage-gated calcium channel complex</i>	21	17	2.434	0.000115
<i>Eye morphogenesis</i>	21	17	2.434	0.000115
<i>Eye development</i>	42	28	2.004	0.000116
<i>Transcription</i>	2315	570	1.183421	0.000153
<i>Dorsal ventral pattern formation</i>	28	18	3.089797	0.000154
<i>Endoderm development</i>	9	9	4.806351	0.000155
<i>Negative regulation of cell differentiation</i>	67	32	2.295571	0.000155
<i>Developmental maturation</i>	52	27	2.495605	0.000156
<i>Ligand-gated ion channel activity</i>	97	42	2.081101	0.000158
<i>Morphogenesis of an epithelium</i>	63	29	2.212447	0.00018
<i>Neuron fate commitment</i>	14	11	3.776419	0.000181
<i>Regulation of heart contraction</i>	42	22	2.517613	0.000182
<i>Tube morphogenesis</i>	82	35	2.051491	0.000183
<i>Tissue remodeling</i>	105	42	1.92254	0.000183
<i>Positive regulation of transcription DNA-dependent</i>	227	76	1.609175	0.000184
<i>Somitogenesis</i>	16	12	3.604763	0.000185
<i>Biological process</i>	12711	2729	1.031904	0.000186
<i>Growth factor activity</i>	164	59	1.729114	0.000187

Supplemental Table 9: Loci enriched for H3K4me3 and H3k27me3 derived from donor pool sequencing data (Illumina GAI) FDR < 0.0001)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Cell fate determination</i>	27	14	4.239878	0
<i>Endocrine system development</i>	33	17	4.212346	0
<i>Cell fate commitment</i>	69	34	4.0292	0
<i>Neuron migration</i>	36	16	3.634181	0
<i>Embryonic morphogenesis</i>	93	41	3.604873	0
<i>Appendage morphogenesis</i>	37	16	3.53596	0
<i>Limb morphogenesis</i>	37	16	3.53596	0
<i>Appendage development</i>	37	16	3.53596	0
<i>Limb development</i>	37	16	3.53596	0
<i>Forebrain development</i>	46	19	3.377418	0
<i>Sensory organ development</i>	80	30	3.06634	0
<i>Anterior posterior pattern formation</i>	54	20	3.028484	0
<i>Brain development</i>	133	47	2.889584	0
<i>Regionalization</i>	86	30	2.852409	0
<i>Heart development</i>	93	32	2.813559	0
<i>Embryonic development</i>	221	74	2.737969	0
<i>Pattern specification process</i>	123	41	2.725636	0
<i>Homophilic cell adhesion</i>	133	43	2.643662	0
<i>Sequence-specific DNA binding</i>	488	155	2.597173	0
<i>Central nervous system development</i>	227	69	2.485491	0
<i>Chordate embryonic development</i>	93	28	2.461864	0
<i>Neurogenesis</i>	257	73	2.322623	0
<i>Tube development</i>	114	32	2.295272	0
<i>Skeletal development</i>	203	56	2.255698	0
<i>Organ morphogenesis</i>	355	97	2.234253	0
<i>Positive regulation of transcription from RNA polymerase II promoter</i>	145	39	2.199306	0
<i>Circulatory system process</i>	157	42	2.187453	0
<i>Blood circulation</i>	157	42	2.187453	0
<i>Regulation of cell differentiation</i>	157	42	2.187453	0
<i>Muscle development</i>	166	42	2.068856	0
<i>Transcription factor activity</i>	881	221	2.051188	0
<i>Neuron development</i>	152	38	2.044227	0
<i>Nervous system development</i>	675	168	2.035141	0
<i>Vasculature development</i>	165	41	2.031837	0
<i>Anatomical structure morphogenesis</i>	823	186	1.848001	0
<i>Organ development</i>	1106	249	1.840913	0
<i>Positive regulation of transcription DNA-dependent</i>	227	51	1.837102	0
<i>System development</i>	1538	340	1.807639	0
<i>Positive regulation of transcription</i>	278	60	1.7648	0
<i>Transcription regulator activity</i>	1309	281	1.755318	0
<i>Multicellular organismal development</i>	2093	446	1.742427	0
<i>Anatomical structure development</i>	1768	376	1.73898	0
<i>Positive regulation of metabolic process</i>	408	84	1.683481	0

Supplemental Table 9 continued: Loci enriched for H3K4me3 and H3k27me3 derived from donor pool sequencing data (Illumina GAI FDR < 0.0001)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Positive regulation of cellular metabolic process</i>	396	81	1.672549	0
<i>Regulation of transcription from RNA polymerase II promoter</i>	424	87	1.677809	0
<i>Biological adhesion</i>	683	139	1.664114	0
<i>Cell-cell signaling</i>	611	119	1.592556	0
<i>Developmental process</i>	2848	537	1.541783	0
<i>Transcription from RNA polymerase II promoter</i>	610	113	1.514738	0
<i>Cell differentiation</i>	1636	292	1.459448	0
<i>Cellular developmental process</i>	1636	292	1.459448	0
<i>Multicellular organismal process</i>	3267	567	1.419133	0
<i>Positive regulation of cellular process</i>	952	164	1.408627	0
<i>Cell development</i>	1089	186	1.396607	0
<i>Positive regulation of biological process</i>	1046	177	1.383664	0
<i>Negative regulation of cellular process</i>	1023	171	1.366814	0
<i>DNA binding</i>	2080	347	1.364128	0
<i>Regulation of transcription</i>	2228	368	1.350584	0
<i>Regulation of RNA metabolic process</i>	2115	348	1.34542	0
<i>Regulation of transcription DNA-dependent</i>	2103	346	1.345321	0
<i>Regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	2282	374	1.340124	0
<i>Transcription DNA-dependent</i>	2159	351	1.329363	0
<i>RNA biosynthetic process</i>	2163	351	1.326904	0
<i>Regulation of gene expression</i>	2358	382	1.324673	0
<i>Transcription</i>	2315	373	1.317489	0
<i>Biological regulation</i>	4522	682	1.233227	0
<i>Regulation of biological process</i>	4060	605	1.21848	0
<i>Cell communication</i>	3573	524	1.199188	0
<i>Positive regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	291	61	1.714059	0.000085
<i>Negative regulation of biological process</i>	1089	179	1.344046	0.000086
<i>Embryonic limb morphogenesis</i>	33	14	3.468991	0.000088
<i>Embryonic appendage morphogenesis</i>	33	14	3.468991	0.000088
<i>Positive regulation of RNA metabolic process</i>	229	51	1.821058	0.000089
<i>Substrate specific channel activity</i>	365	73	1.635381	0.00009
<i>Signal transduction</i>	3247	466	1.173526	0.000164
<i>Blood vessel development</i>	162	39	1.968515	0.000165
<i>Neurotransmitter binding</i>	101	28	2.266865	0.000167
<i>Positive regulation of heart contraction</i>	5	5	8.176907	0.000244
<i>Morphogenesis of an epithelium</i>	63	20	2.595843	0.000317
<i>Regulation of developmental process</i>	729	124	1.390859	0.000347
<i>Cellular morphogenesis during differentiation</i>	124	31	2.044227	0.00035
<i>Anatomical structure formation</i>	152	36	1.936636	0.000362

Supplemental Table 10: Promoters deficient in DNA methylation (D2 and D4 array)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Embryonic development</i>	199	22	3.061998	0
<i>Multicellular organismal development</i>	1620	102	1.743896	0
<i>System development</i>	1231	83	1.867478	0
<i>Nucleus</i>	2828	153	1.498468	0
<i>RNA biosynthetic process</i>	1512	95	1.740232	0
<i>Transcription</i>	1644	202	1.70159	0
<i>Transcription regulator activity</i>	1090	75	1.905768	0
<i>Anatomical structure development</i>	1465	92	1.739344	0
<i>Regulation of transcription</i>	1580	97	1.700396	0
<i>RNA metabolic process</i>	1827	108	1.637271	0
<i>Nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	2489	136	1.513385	0
<i>Regulation of cellular metabolic process</i>	1772	105	1.641198	0
<i>Nucleic acid binding</i>	2348	130	1.533489	0
<i>Regulation of transcription DNA-dependent</i>	1467	91	1.718093	0
<i>DNA binding</i>	1522	93	1.692402	0
<i>Regulation of metabolic process</i>	1839	106	1.596465	0
<i>Organ development</i>	869	61	1.94422	0
<i>Biopolymer metabolic process</i>	3392	170	1.388125	0
<i>Developmental process</i>	2265	123	1.504085	0
<i>Transcription factor activity</i>	755	54	1.980989	0
<i>Transcription from RNA polymerase II promoter</i>	460	38	2.288027	0
<i>Regulation of transcription from RNA polymerase II promoter</i>	297	26	2.424668	0.000588
<i>Female pronucleus</i>	3	3	27.697168	0.001081
<i>Nervous system development</i>	553	39	1.953326	0.001053
<i>Central nervous system development</i>	179	18	2.78519	0.00125
<i>Dorsal ventral pattern formation</i>	22	6	7.553773	0.001463
<i>Positive regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	199	19	2.644453	0.002381
<i>Gamete generation</i>	184	18	2.709506	0.002558
<i>Anatomical structure formation</i>	122	14	3.178364	0.002727
<i>Anatomical structure morphogenesis</i>	730	46	1.745301	0.003556
<i>Notch signaling pathway</i>	34	7	5.702358	0.003478
<i>Pronucleus</i>	4	3	20.772876	0.004681
<i>M phase</i>	175	17	2.690582	0.005417
<i>Multicellular organismal process</i>	2648	127	1.328376	0.0054
<i>Regionalization</i>	72	10	3.846829	0.00549
<i>Cell cycle phase</i>	214	19	2.459094	0.005385
<i>Negative regulation of cellular process</i>	776	47	1.677535	0.006038
<i>Sequence-specific DNA binding</i>	425	30	1.955094	0.006667
<i>Negative regulation of cellular metabolic process</i>	256	21	2.272033	0.007636
<i>Cell cycle process</i>	530	35	1.829058	0.007544
<i>Negative regulation of biological process</i>	807	48	1.647415	0.007414
<i>Chromosome</i>	204	18	2.443868	0.007288
<i>Brain development</i>	93	11	3.276009	0.011
<i>Positive regulation of transcription</i>	192	17	2.452353	0.011148

Supplemental Table 10 continued : Promoters deficient in DNA methylation (D1 and D2 array)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Positive regulation of cellular metabolic process</i>	264	21	2.203184	0.010968
<i>Gastrulation</i>	31	6	5.360742	0.013492
<i>Positive regulation of transcription DNA- dependent</i>	147	14	2.637826	0.019692
<i>Meiosis</i>	44	7	4.406368	0.020149
<i>M phase of meiotic cell cycle</i>	44	7	4.406368	0.020149
<i>Sexual reproduction</i>	218	18	2.286922	0.021618
<i>Meiotic cell cycle</i>	45	7	4.308448	0.022754
<i>Mitosis</i>	135	13	2.667135	0.023714
<i>Cellular protein complex disassembly</i>	14	4	7.913477	0.026197
<i>Positive regulation of metabolic process</i>	280	21	2.077288	0.025833
<i>Male pronucleus</i>	2	2	27.697168	0.042405
<i>Regulation of translational elongation</i>	2	2	27.697168	0.042405
<i>Heart development</i>	75	9	3.32366	0.042683
<i>Heart morphogenesis</i>	7	3	11.870215	0.045833
<i>Vasculature development</i>	122	12	2.724312	0.045412
<i>Forebrain development</i>	25	5	5.539434	0.046292
<i>Spermatogenesis</i>	141	13	2.55364	0.045495
<i>Male gamete generation</i>	141	13	2.55364	0.045495

Supplemental Table 11: Promoters that share histone enrichment and DNA hypomethylation (array)

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Sequence-specific DNA binding</i>	425	35	5.037969	0
<i>Developmental process</i>	2265	37	2.186039	0
<i>Multicellular organismal development</i>	1620	30	2.478168	0
<i>DNA binding</i>	1522	27	2.373961	0
<i>Anatomical structure development</i>	1465	26	2.374981	0.002
<i>Transcription factor activity</i>	755	17	3.013189	0.003333
<i>RNA metabolic process</i>	1827	29	2.124144	0.002857
<i>Nucleic acid binding</i>	2348	34	1.937784	0.0025
<i>Regulation of transcription</i>	1467	25	2.280522	0.003333
<i>Neural tube patterning</i>	2	2	133.821053	0.006
<i>System development</i>	1231	22	2.391603	0.007273
<i>Transcription DNA-dependent</i>	1510	25	2.21558	0.0075
<i>RNA biosynthetic process</i>	1512	25	2.21265	0.006923
<i>Transcription regulator activity</i>	1090	20	2.455432	0.009286
<i>Transcription from RNA polymerase II promoter</i>	460	12	3.490984	0.008667
<i>Regulation of transcription</i>	1580	25	2.117422	0.0225
<i>Heart development</i>	75	5	8.921404	0.022353
<i>Regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	1623	25	2.061322	0.022778
<i>Regulation of metabolic process</i>	1839	27	1.964746	0.0235
<i>Skeletal development</i>	174	7	5.383606	0.023333
<i>Transcription</i>	1644	25	2.034992	0.022273
<i>Nucleobase and nucleic acid metabolic process</i>	2489	33	1.774245	0.032609
<i>Regulation of cellular metabolic process</i>	1772	26	1.963514	0.035
<i>Regulation of bone remodeling</i>	21	6	19.117293	0.0368
<i>Cell-cell signaling</i>	525	12	3.058767	0.035385
<i>Multicellular organismal process</i>	2648	34	1.718246	0.034074
<i>Voltage-gated potassium channel activity</i>	93	5	7.19468	0.040345
<i>Regulation of biological process</i>	3134	38	1.622591	0.039
<i>Biological regulation</i>	3396	40	1.57622	0.04
<i>Nervous system development</i>	553	12	2.903893	0.046875
<i>Alpha-type channel activity</i>	333	9	3.616785	0.045758
<i>Channel or pore class transporter activity</i>	338	9	3.563282	0.046176
<i>Anatomical structure morphogenesis</i>	730	14	2.566431	0.045143
<i>Positive regulation of cell differentiation</i>	28	3	14.33797	0.058056
<i>Regulation of cellular process</i>	2889	35	1.621231	0.057568
<i>Cellular morphogenesis during differentiation</i>	108	5	6.195419	0.056053
<i>Positive regulation of cellular process</i>	671	13	2.592658	0.056154
<i>Cell development</i>	859	15	2.336805	0.065854
<i>Potassium channel activity</i>	118	5	5.670384	0.067674
<i>Organ development</i>	869	15	2.309915	0.066136

Supplemental Table 12: Sperm DNA demethylation extends beyond CpGs

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Nucleus</i>	2665	103	1.668257	0
<i>Transcription DNA-dependent</i>	1398	64	1.97604	0
<i>RNA biosynthetic process</i>	1399	64	1.974627	0
<i>Regulation of transcription DNA-dependent</i>	1353	62	1.977957	0
<i>Regulation of RNA metabolic process</i>	1365	62	1.960568	0
<i>Transcription regulator activity</i>	996	50	2.166874	0
<i>Transcription</i>	1518	65	1.848266	0
<i>Regulation of transcription</i>	1457	63	1.866396	0
<i>RNA metabolic process</i>	1698	70	1.77944	0
<i>Regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	1500	64	1.841669	0
<i>Regulation of gene expression</i>	1540	65	1.821862	0
<i>Regulation of cellular process</i>	2683	97	1.560537	0
<i>Regulation of cellular metabolic process</i>	1708	69	1.74375	0
<i>Regulation of biological process</i>	2873	101	1.51743	0
<i>Intracellular</i>	6181	180	1.257004	0
<i>Gene expression</i>	2015	77	1.649448	0
<i>DNA binding</i>	1398	59	1.821662	0
<i>Biopolymer metabolic process</i>	3194	108	1.459526	0
<i>Regulation of metabolic process</i>	1757	69	1.695119	0
<i>Intracellular part</i>	5850	171	1.26172	0
<i>Nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	2249	82	1.573792	0
<i>Embryonic development</i>	183	15	3.538043	0.00037
<i>Transcription factor activity</i>	688	34	2.133111	0.000385
<i>Biological regulation</i>	3250	107	1.421096	0.0004
<i>Nucleic acid binding</i>	2071	76	1.584004	0.000417
<i>Embryonic morphogenesis</i>	78	10	5.533862	0.000435
<i>Macromolecule metabolic process</i>	4200	131	1.34631	0.000455
<i>Positive regulation of transcription</i>	214	16	3.227224	0.00069
<i>Anatomical structure morphogenesis</i>	643	32	2.148137	0.000714
<i>Positive regulation of nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	225	16	3.069449	0.000857
<i>Positive regulation of metabolic process</i>	324	20	2.664452	0.000882
<i>Cellular component organization and biogenesis</i>	1639	62	1.63281	0.000909
<i>Membrane-bounded organelle</i>	4209	129	1.32292	0.000938
<i>Intracellular membrane-bounded organelle</i>	4207	129	1.323549	0.000968
<i>Positive regulation of cellular metabolic process</i>	312	20	2.766931	0.001
<i>Positive regulation of RNA metabolic process</i>	171	13	3.281483	0.003864
<i>Primary metabolic process</i>	4979	145	1.257039	0.003902
<i>RNA polymerase II transcription factor activity</i>	170	13	3.300786	0.003953

Supplemental Table 12 continued: Sperm DNA demethylation extends beyond CpGs

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Positive regulation of transcription DNA-dependent</i>	170	13	3.300786	0.003953
<i>Embryonic development ending in birth or egg hatching</i>	83	9	4.680447	0.004
<i>Chordate embryonic development</i>	83	9	4.680447	0.004
<i>Transcription from RNA polymerase II promoter</i>	450	24	2.302087	0.004211
<i>Positive regulation of transcription from RNA polymerase II promoter</i>	109	10	3.960011	0.004222
<i>Pattern specification process</i>	102	10	4.231777	0.004324
<i>Anatomical structure development</i>	1378	52	1.628835	0.004681

Supplemental Table 13: Gene promoters occupied by Suz12 in ES cell are DNA demethylated and histone bound in sperm

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Sequence-specific DNA binding</i>	425	51	10.377959	0
<i>Transcription factor activity</i>	755	65	7.445556	0
<i>Transcription regulator activity</i>	1090	69	5.471537	0
<i>Multicellular organismal development</i>	1620	41	4.407517	0
<i>DNA binding</i>	1522	72	4.348046	0
<i>Regulation of transcription DNA-dependent</i>	1467	72	4.112349	0
<i>Transcription DNA-dependent</i>	1510	37	4.267268	0
<i>RNA biosynthetic process</i>	1512	37	4.261624	0
<i>developmental process</i>	2265	84	3.38306	0
<i>Regulation of transcription</i>	1580	72	4.078212	0
<i>RNA metabolic process</i>	1827	39	3.717502	0
<i>Regulation of nucleobase nucleoside</i>	1623	37	3.970163	0
<i>Nucleotide and nucleic acid metabolic process</i>				
<i>Regulation of metabolic process</i>	1839	39	3.693245	0
<i>Transcription</i>	1644	72	3.78945	0
<i>Regulation of cellular metabolic process</i>	1772	38	3.734608	0
<i>Nucleic acid binding</i>	2348	42	3.115132	0
<i>Regulation of biological process</i>	3134	48	2.667273	0
<i>Regulation of cellular process</i>	2889	45	2.712627	0
<i>Multicellular organismal process</i>	2648	43	2.827976	0
<i>Biological regulation</i>	3396	48	2.461494	0
<i>Nucleobase nucleoside nucleotide and nucleic acid metabolic process</i>	2489	40	2.798725	0
<i>System development</i>	1231	58	4.07	0
<i>Anatomical structure development</i>	1465	36	3.776226	0
<i>Organ development</i>	869	44	4.408878	0
<i>Nucleus</i>	2828	39	2.401654	0
<i>Nervous system development</i>	553	16	5.038718	0
<i>Transcription from RNA polymerase II promoter</i>	460	13	4.92165	0
<i>Anatomical structure morphogenesis</i>	730	36	4.264915	0
<i>Cellular metabolic process</i>	5390	50	1.615498	0
<i>Skeletal development</i>	174	8	8.006928	0
<i>Primary metabolic process</i>	5420	50	1.606556	0
<i>Lung development</i>	32	4	21.768836	0.00027
<i>Neural tube patterning</i>	2	2	174.150685	0.000263
<i>Respiratory tube development</i>	33	4	21.109174	0.000256
<i>Cellular process</i>	8815	65	1.284151	0.000476
<i>Central nervous system development</i>	179	7	6.810362	0.000465
<i>Positive regulation of transcription from RNA polymerase II promoter</i>	80	5	10.884418	0.000455
<i>Cell differentiation</i>	1210	38	2.590671	0.001957
<i>Cellular developmental process</i>	1210	18	2.590671	0.001957
<i>Brain development</i>	93	11	10.2294	0.00383
<i>Positive regulation of transcription DNA-dependent</i>	147	6	7.108191	0.00551
<i>Metabolic process</i>	6020	50	1.446434	0.0054

Supplemental Table 13: Gene promoters occupied by Suz12 in ES cell are DNA demethylated and histone bound in sperm

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Regulation of transcription from RNA polymerase II promoter</i>	297	8	4.690928	0.006923
<i>Neuron fate specification</i>	5	2	69.660274	0.009811
<i>Pattern specification process</i>	111	15	7.844625	0.012321
<i>Kidney development</i>	29	3	18.015588	0.01614
<i>Tube development</i>	70	4	9.951468	0.019483
<i>Urogenital system development</i>	31	3	16.853292	0.020339
<i>Positive regulation of cellular metabolic process</i>	264	7	4.617632	0.020667
<i>positive regulation of transcription</i>	192	6	5.442209	0.020984
<i>Cell fate commitment</i>	74	7	8.13551	0.021452
<i>Embryonic limb morphogenesis</i>	34	3	15.366237	0.023231
<i>Embryonic appendage morphogenesis</i>	34	3	15.366237	0.023231
<i>Organ morphogenesis</i>	274	7	4.449105	0.022879
<i>Embryonic development</i>	199	36	15.250774	0.022206
<i>Positive regulation of nucleobase nucleoside</i>	199	6	5.250774	0.022206
<i>Nucleotide and nucleic acid metabolic process</i>				
<i>Cell development</i>	859	24	2.41575	0.022899
<i>Positive regulation of metabolic process</i>	280	7	4.353767	0.022571
<i>Appendage morphogenesis</i>	36	4	14.512557	0.022055
<i>Limb morphogenesis</i>	36	4	14.512557	0.022055

Supplemental Table 14: Promoters that acquire methylation in fibroblasts compared to sperm

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Embryonic development</i>	199	43	2.393575	0
<i>Anatomical structure morphogenesis</i>	730	105	1.593302	0
<i>Regulation of transcription DNA-dependent</i>	1467	205	1.547945	0
<i>Transcription DNA-dependent</i>	1510	208	1.525872	0
<i>RNA biosynthetic process</i>	1512	208	1.523854	0
<i>Regulation of transcription</i>	1580	216	1.514357	0
<i>Transcription</i>	1644	220	1.482356	0
<i>RNA metabolic process</i>	1827	241	1.461202	0
<i>Multicellular organismal development</i>	1620	201	1.374399	0
<i>Tube development</i>	70	20	3.164927	0.000526
<i>Negative regulation of cell differentiation</i>	49	15	3.390993	0.001034
<i>Transcription from RNA polymerase II promoter</i>	460	69	1.661587	0.001071
<i>Negative regulation of developmental process</i>	60	17	3.138553	0.001111
<i>Cellular component organization and biogenesis</i>	1763	209	1.313184	0.00125
<i>Developmental process</i>	2265	259	1.266669	0.001304
<i>System development</i>	1231	155	1.394779	0.001364
<i>Anatomical structure development</i>	1465	180	1.361027	0.001429
<i>Regulation of cell differentiation</i>	105	23	2.426444	0.001935
<i>Embryonic morphogenesis</i>	78	19	2.698303	0.002
<i>Organ morphogenesis</i>	274	45	1.819255	0.0025
<i>Nervous system development</i>	553	77	1.542401	0.003529
<i>Lung development</i>	32	11	3.807803	0.003636
<i>Synapse organization and biogenesis</i>	23	9	4.334574	0.003889
<i>Respiratory tube development</i>	33	11	3.692415	0.004
<i>Nucleosome assembly</i>	41	12	3.24212	0.005405
<i>Chromosome organization and biogenesis</i>	236	38	1.783624	0.005417
<i>Tube morphogenesis</i>	43	12	3.091324	0.005532
<i>Calcium-dependent cell-cell adhesion</i>	20	8	4.430898	0.005641
<i>Formation of primary germ layer</i>	21	8	4.219903	0.005652
<i>Gastrulation</i>	31	10	3.573305	0.005682
<i>Regulation of developmental process</i>	162	29	1.982963	0.005714
<i>Organ development</i>	869	108	1.376689	0.005778
<i>Branching morphogenesis of a tube</i>	30	10	3.692415	0.005789
<i>Chromosome organization and biogenesis</i>	226	37	1.813531	0.005814
<i>Chromatin assembly or disassembly</i>	87	19	2.419168	0.005854
<i>Macromolecular complex assembly</i>	359	53	1.635359	0.006
<i>Pattern specification process</i>	111	22	2.19549	0.006327
<i>Morphogenesis of a branching structure</i>	32	10	3.461639	0.0064
<i>Mesoderm morphogenesis</i>	22	8	4.028089	0.008039
<i>Protein-DNA complex assembly</i>	86	18	2.318493	0.008393
<i>Cellular component assembly</i>	389	55	1.566191	0.008462
<i>Positive regulation of cell differentiation</i>	28	9	3.560543	0.008491
<i>Regionalization</i>	72	16	2.46161	0.008545

Supplemental Table 14: Promoters that acquire methylation in fibroblasts compared to sperm

GO CATEGORY	TOTAL GENES	CHANGED GENES	ENRICHMENT	FDR
<i>Chromatin assembly</i>	52	13	2.769311	0.008704
<i>Synaptogenesis</i>	18	7	4.307817	0.009298
<i>DNA packaging</i>	180	30	1.846207	0.009483
<i>Embryonic arm morphogenesis</i>	3	3	11.077244	0.012623
<i>Arm morphogenesis</i>	3	3	11.077244	0.012623
<i>Positive regulation of osteoblast differentiation</i>	3	3	11.077244	0.012623
<i>Heart development</i>	75	16	2.363145	0.015625
<i>Response to hypoxia</i>	19	7	4.08109	0.016
<i>Chordate embryonic development</i>	69	15	2.408097	0.016866
<i>Anatomical structure formation</i>	122	22	1.997536	0.018169
<i>Mesoderm formation</i>	20	7	3.877035	0.018378
<i>Embryonic development ending in birth or egg hatching</i>	70	15	2.373695	0.018429
<i>Mitotic sister chromatid segregation</i>	15	6	4.430898	0.018933
<i>Sensory organ development</i>	57	13	2.526389	0.019211
<i>Mesoderm development</i>	44	11	2.769311	0.019221
<i>Cell cycle phase</i>	214	33	1.708173	0.019367
<i>Cell differentiation</i>	1210	138	1.263355	0.019634
<i>Cell cycle</i>	606	76	1.389225	0.020814
<i>Sister chromatid segregation</i>	16	6	4.153967	0.025057
<i>Cell fate determination</i>	27	8	3.282146	0.025455
<i>Protein catabolic process</i>	185	29	1.736433	0.025495
<i>Regulation of transcription from RNA polymerase II promoter</i>	297	42	1.566479	0.025556
<i>Cell fate commitment</i>	74	15	2.245387	0.02573
<i>Macromolecule catabolic process</i>	326	45	1.529067	0.025895
<i>Embryonic limb morphogenesis</i>	34	9	2.932212	0.025957
<i>Embryonic appendage morphogenesis</i>	34	9	2.932212	0.025957
<i>Dorsal ventral pattern formation</i>	22	7	3.524578	0.025978
<i>Regulation of gliogenesis</i>	4	3	8.307933	0.033469
<i>RNA interference</i>	4	3	8.307933	0.033469
<i>Regulation of glial cell differentiation</i>	4	3	8.307933	0.033469
<i>Tissue morphogenesis</i>	55	12	2.416853	0.0372
<i>Mesodermal cell fate commitment</i>	8	4	5.538622	0.04181
<i>Mitotic chromosome condensation</i>	8	4	5.538622	0.04181
<i>Pancreas development</i>	8	4	5.538622	0.04181
<i>Mesodermal cell differentiation</i>	8	4	5.538622	0.04181
<i>Appendage morphogenesis</i>	36	9	2.769311	0.042364
<i>Cell cycle process</i>	530	66	1.37943	0.044123
<i>Chromosome condensation</i>	13	5	4.260479	0.044554
<i>Positive regulation of developmental process</i>	43	10	2.576103	0.044696
<i>Anterior posterior pattern formation</i>	44	10	2.517556	0.048103
<i>Sex differentiation</i>	66	13	2.181881	0.050168
<i>Embryonic pattern specification</i>	25	7	3.101628	0.050339