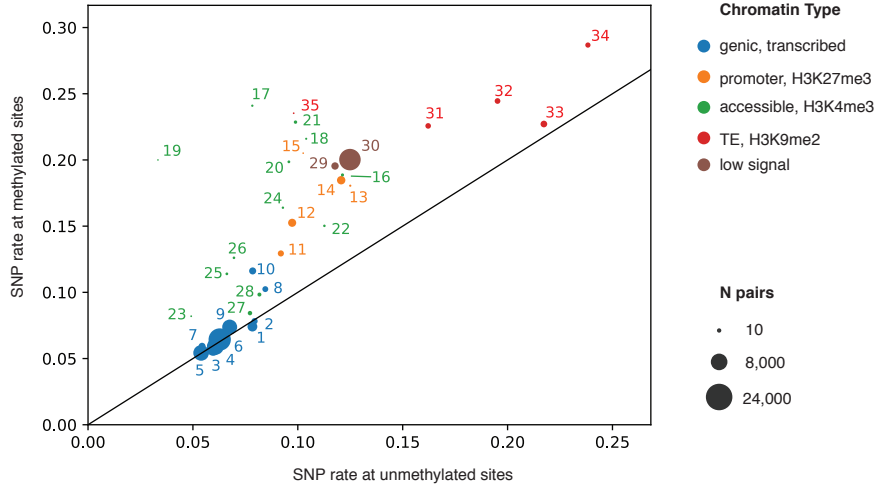
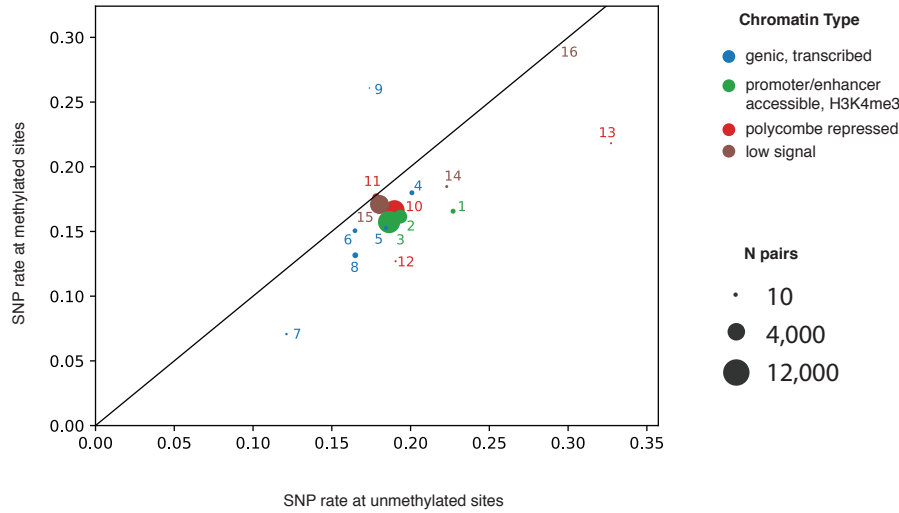


A. thaliana



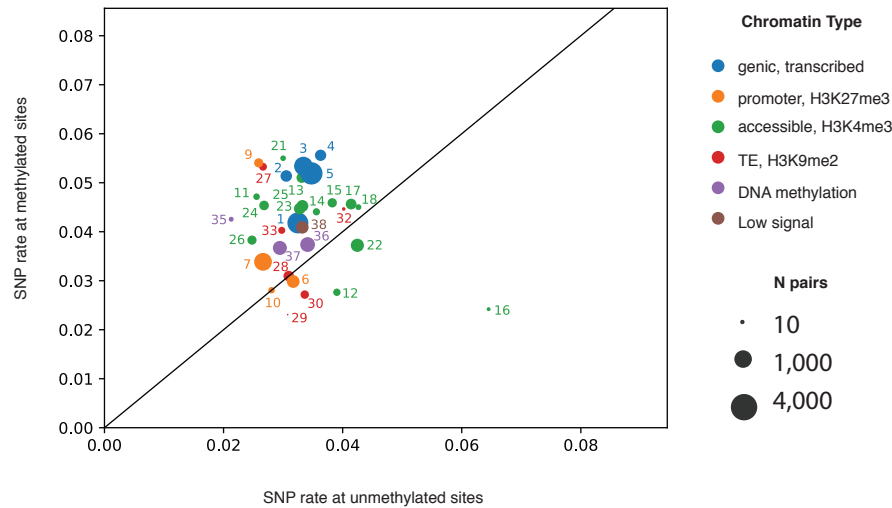
State	Preferential epigenetics marks	Preferential location
State 1	H3.3	3'UTR
State 2	H3.3, histone acetylation,H3K4me2,H2A.Z	CDS,3'UTR
State 3	H3K4me1,H3.3,H3.1	CDS
State 4	H3K4me1,H3.3	CDS,intron
State 5	H3K4me1,H3K36me3,H3.3,H3.1	CDS
State 6	H3K4me1,H3K36me3	intron
State 7	H3K4me1,H3K36me3,H3K4me2	CDS,intron
State 8	H3K4me1,H3K4me2,H2A.Z	CDS
State 9	H3K4me1	intron
State 10	H2A.Z	CDS,intron
State 11	H3K27me3,H2A.Z,H3K4me2	CDS
State 12	H3K27me3,H2A.Z	Promoter,CDS,intron,intergenic
State 13	H3K27me3,H2A.Z	Promoter,intergenic
State 14	H3K27me3	Promoter,intergenic
State 15	H3K27me3,accessible DNA	Promoter,intergenic
State 16	accessible DNA	Promoter,intergenic
State 17	accessible DNA	Promoter
State 18	accessible DNA	Promoter
State 19	accessible DNA	Promoter,snRNA
State 20	accessible DNA	Promoter
State 21	accessible DNA	Promoter
State 22	histone acetylation,H3K4me2	coding gene,miRNA,snRNA
State 23	accessible DNA,H3K36ac,H3K56ac,H4K16ac,H3K4me3	Promoter,5'UTR
State 24	accessible DNA,histone acetylation,H3K4me3	5'UTR,snRNA
State 25	histone acetylation,H3K4me3,H3K4me2,H2A.Z	intron
State 26	histone acetylation,H3K4me3,H3K4me2,H2A.Z	CDS
State 27	H3K4me2,histone acetylation,H3K4me3,H2A.Z	CDS
State 28	H3K4me3,H3K4me2,H2A.Z	intron
State 29	weak signal	intergenic
State 30	rare signal	intergenic
State 31	DNA methylation,H3K9me2,H3K27me3	intergenic,miRNA
State 32	DNA methylation,H3K9me2	intergenic,TE
State 33	H3K9me2,DNA methylation	TE
State 34	H3K9me2,DNA methylation,H3K27me1	TE,miRNA
State 35	H3K9me2,DNA methylation,H2A.X	intergenic,pericentromere
State 36	CENH3,H3K9me2,DNA methylation,accessible DNA	rRNA,rRNA,centromere

Human (H1)



State	Preferential location
State 1_Pro	Promoter
State 2_Enh1	Enhancer
State 3_Enh1	Enhancer
State 4_Egn1	Expressed gene
State 5_Egn2	Expressed gene
State 6_Egn3	Expressed gene
State 7_Egn4	Expressed gene
State 8_Egn5	Expressed gene
State 9_Egn6	Expressed gene
State 10_Rep1	Polycomb repressed
State 11_Rep2	Polycomb repressed
State 12_Hel1	Heterochromatin
State 13_Hel2	Heterochromatin
State 14_Low1	Low signal
State 15_Low2	Low signal
State 16_Low3	Low signal

O. sativa



State	Preferential epigenetics marks	Preferential location
State 1	weak histone acetylation	intron,promoter,3'UTR,intergenic
State 2	H3K36me3,histone acetylation	promoter,3'UTR,intergenic
State 3	H3K36me3,histone acetylation	3'UTR
State 4	H3K36me3,H3K36me3,H3K4me2	exon
State 5	H3K36me3,H3K4me2	intron
State 6	H3K27me3	intergenic,intron,promoter
State 7	H3K27me3	intergenic,intron,promoter
State 8	H3K27me3	intergenic,intron,promoter
State 9	H3K27me3,H2A.Z	intergenic,intron,promoter
State 10	H3K27me3,H2A.Z,H3K36ac,H3K27ac,H3K4me3,H3K4me2	exon
State 11	H3K36ac,H3K27ac,H3K4me3,H3K4me2,H3K27me3,H2A.Z	exon,promoter
State 12	H2A.Z,histone acetylation,H3K4me2,H3K4me3	exon,promoter
State 13	histone acetylation,H3K4me3,H3K4me2,H3K36me3,H3K36me2,H2A.Z	3'UTR
State 14	H3K4me3,H3K4me3,H3K36me3,H2A.Z,histone acetylation	intron
State 15	H3K4me3,H3K4me3,H3K36me3	intron
State 16	H3K4me3,histone acetylation,H2A.Z	exon,promoter,3'UTR
State 17	histone acetylation,accessible DNA,H3K4me2,H3K4me3	promoter,axon,3'UTR
State 18	histone acetylation,accessible DNA,H2A.Z,H3K4me3	3'UTR,promoter,intergenic
State 19	DNA methylation,H3K4me3,H4K12ac,H4K16ac,CANF-YB1,CANF-YB1	exon,intron,promoter,intergenic
State 20	accessible DNA,H2A.Z,histone acetylation,H3K27me3,DNA methylation	intergenic,promoter,intron
State 21	accessible DNA	intergenic,promoter
State 22	accessible DNA	intergenic,promoter
State 23	accessible DNA	intergenic,promoter
State 24	accessible DNA	intergenic,promoter
State 25	H2A.Z,H3K4me2,H3K4me3,histone acetylation	promoter,intergenic,intron,3'UTR
State 26	DNA methylation,CANF-YB1	intergenic,promoter,intron
State 27	H3K9me2,DNA methylation,CANF-YB1	intergenic,TE,promoter,axon
State 28	H3K9me2,DNA methylation,Mnase	TE,axon,intron,promoter,axon
State 29	DNA methylation,H3K9me2,CENH3,Mnase	TE,axon,intron,promoter,intergenic
State 30	H3K9me2,DNA methylation	TE,axon,intron,promoter,intergenic
State 31	H3K9me2,CENH3,DNA methylation	TE,intron,intergenic,axon,promoter
State 32	H3K9me2,CENH3,DNA methylation,Mnase	TE,axon,intergenic,promoter,intron
State 33	DNA methylation,H3K4me2	intergenic,intron,promoter
State 34	DNA methylation,H3K36me3,H3K4me2	intergenic,promoter,intron
State 35	DNA methylation,H3K27me3,H3K36me3,H3K36me2,H3K36me3	intergenic,intron,promoter
State 36	DNA methylation,H3K36me3	intergenic,promoter,intron
State 37	DNA methylation	intergenic,promoter
State 38	rare signal	intergenic,promoter,intron

Figure S4. RR_{met} in *A. thaliana*, human, and rice for different chromatin states, deconstructed into SNP rates at methylated and unmethylated sites across pairs. Individual chromatin states, classified as described in the Methods, are labelled and grouped into broader chromatin state classes, indicated by colour, based on key shared characteristics/marks.