A ROC Curve

True positive rate vs False positive rate

AUC = 0.7723

Features	Coeff
H3K27ac_CV	-0.0005
H3K27me3_CV	-0.009
H3K4me2_CV	0.011
H3K4me3_CV	0.017
H3K27ac_mean	0.035
H3K27me3_mean	-0.11
H3K4me2_mean	0.041
H3K4me3_mean	0.040

B

H3K4me1 — Fold change; legend: 0 h, 1 h, 4 h, 12 h; categories: CTR, S1(H0), S2(H0), S3(H1), S4(H1), S5(H4), S6(H4), S7(H12), S8(H12), S9(H0-1-4-12), S10(H0-1-4-12)

H3K27ac — Fold change; categories: CTR, S1(H0), S2(H0), S3(H1), S4(H1), S5(H4), S6(H4), S7(H12), S8(H12), S9(H0-1-4-12), S10(H0-1-4-12)

H3K27me3 — Fold change; categories: CTR, S1(H0), S2(H0), S3(H1), S4(H1), S7(H12), S8(H12), S9(H0-1-4-12), S10(H0-1-4-12)

C P-value < 2.2×10^{-16}; $\log_2$(EN number); DEG, nonDEG

D Poised enhancer (G1–G7; H0, H1, H4, H12); Repressive enhancer (G1–G7; H0, H1, H4, H12); $-\log_{10}$(P-value)

E H0, H0-1-12, H0-1-4-12, H1, H1-12, H12; legend: TTS, Promoter, Intron, Exon, Intergenic, non-coding, CpG, Repeats, 3'UTR, 5'UTR

Supplemental Fig. S3: Epigenetic state at TSS and distal regions. (A) ROC plot to evaluate the accuracy of the logistic regression on the prediction of DEG using Mean or CV of variable histone modifications. The coefficients of each model parameter are shown to the right. Mean histone mark signal strength was more heavily weighted than variation of the signal. (B) ChIP-qPCR validating the dynamic sites of AE, PE and RE. Column: Mean±SD, N=4. (C) Violin plot comparing the number of active enhancers within 100 kb of expressed DEGs and non-DEGs. The Wilcoxon rank sum test p-value is shown. (D) Enrichment of members of DEG clusters G1-G7 among PEs (right) or REs (left) that were present at a single time point (H0, H1, H4, or H12). We did not observe an obvious temporal relationship between regulatory elements and DEGs. Enrichment P-values were calculated by Fisher's exact test. (E) Location of REs with respect to genome annotations. Stable REs (H0-1-4-12) were more commonly found at promoters and CpG regions, whereas dynamic REs were more often found at distal and repetitive genomic regions.