

Table S3: Regression Models

Model	Chromatin Marks													Accuracy			
	H3K27me3	H3K9me3	H3K4me3	H3K9ac	FAIRE	H3K27ac	H3K4me2	H3K4me1	DNase	DF (DNase-FAIRE interaction term)	Motif	Intercept	R <sup>2</sup>	MSE	F value	P-value	
H3K27me3	0.1827											0.3435	0.008	0.3709	453.73	3e-100	
H3K9me3		0.4837										0.2688	0.020	0.3653	1166.256	<1e-200	
H3K4me3			1.0664									0.1467	0.290	0.2471	24664.98	<1e-200	
H3K9ac				1.0674								0.139	0.344	0.2322	31055.23	<1e-200	
FAIRE					2.609							-0.277	0.427	0.1858	48288.28	<1e-200	
H3K27ac						0.9162						0.1764	0.485	0.1872	54354.22	<1e-200	
H3K4me2							1.1938					0.0932	0.572	0.1432	83889.03	<1e-200	
H3K4me1								1.2704				0.071	0.655	0.1104	124600.5	<1e-200	
DNase									1.593			-0.059	0.665	0.1144	122062.2	<1e-200	
DF (DNase-FAIRE interaction term)										2.7255		0.1016	0.672	0.1163	121399.8	<1e-200	
Motif											0.0151	0.4871	0.140	0.3096	9531.949	<1e-200	
Best 3								0.6939	0.628	0.4981		-0.014	0.748	0.0828	63204.5	<1e-200	
Best 3 + motif								0.682	0.416	0.8247	0.0016	0.0241	0.749	0.0826	47599.55	<1e-200	
Full regression model	-0.0302	0.0237	-0.0707	-0.041	0.128	-0.089	0.213	0.5927	0.565	0.6438		-0.024	0.750	0.0817	19251.93	<1e-200	
Full Regression model + motif	-0.0484	-0.0087	-0.0667	-0.04	-0.02	-0.094	0.2153	0.5965	0.449	0.8691	0.0022	0.0495	0.744	0.0815	17432.86	<1e-200	