

Table S2: Discriminant Models

Model	Chromatin Marks													Accuracy	
	H3K4me1	H3K27me3	DF (DNase-FAIRE interaction term)	FAIRE	H3K4me2	H3K4me3	H3K9ac	DNase	H3K27ac	H3K9me3	Motif	Intercept	Sensitivity	Specificity	
<b>Best 3</b>	30.96	-5.99	13.95									-25.09	89.08%	97.65%	
<b>Best 3 + motif</b>	31.69	-4.32	14.31							-0.04		-24.59	88.82%	97.64%	
<b>Regression 3</b>	29.49		11.08				1.64					-24.07	89.62%	97.54%	
<b>Regression 3 + motif</b>	32.81		-27.92				27.81			-0.17		-30.38	89.74%	97.23%	
<b>All significant chromatin marks</b>	28.4	-7.72	13.47		9.39	1.63	20.39	5.84	-8.76			-25.78	91.18%	96.99%	
<b>All significant chromatin marks + motif</b>	29.77	-5.95	-28.61		9.69	1.65	30.37	-5.79	-5.06	-0.11		-29.85	90.95%	96.90%	
<b>Full Discriminant Analysis model</b>	29.73	-7.03	-18.55	-8.73	9.79	2.17	25.2	-5.56	-6.69	-1.04		-25.65	90.84%	97.00%	
<b>Full Discriminant Analysis model + motif</b>	29.89	-5.91	-28.76	-1.57	9.73	2.1	30.73	-5.47	-5.02	-0.1		-29.54	90.90%	96.93%	