Table S1. Models' performances evaluated on an additional human dataset, with MAE and BAE genes identified in monoclonal cell lines derived from GM12878 (Nag et al., 2013, Dataset S2).

Model	Recall (Sensitivity)	Specificity	Precision (PPV)	NPV	F1	Accuracy	Balanced Accuracy
ada	0.419	0.967	0.741	0.881	0.535	0.867	0.693
glmStepAIC	0.379	0.982	0.828	0.876	0.52	0.872	0.681
svmPoly	0.435	0.968	0.753	0.884	0.551	0.87	0.701
nnet	0.415	0.972	0.766	0.881	0.538	0.87	0.693
mlpML	0.443	0.959	0.709	0.885	0.545	0.864	0.701
rf	0.395	0.96	0.69	0.876	0.503	0.857	0.678
rpart	0.423	0.955	0.677	0.881	0.521	0.857	0.689
knn	0.379	0.97	0.738	0.874	0.501	0.862	0.675
evtree	0.423	0.955	0.677	0.881	0.521	0.857	0.689