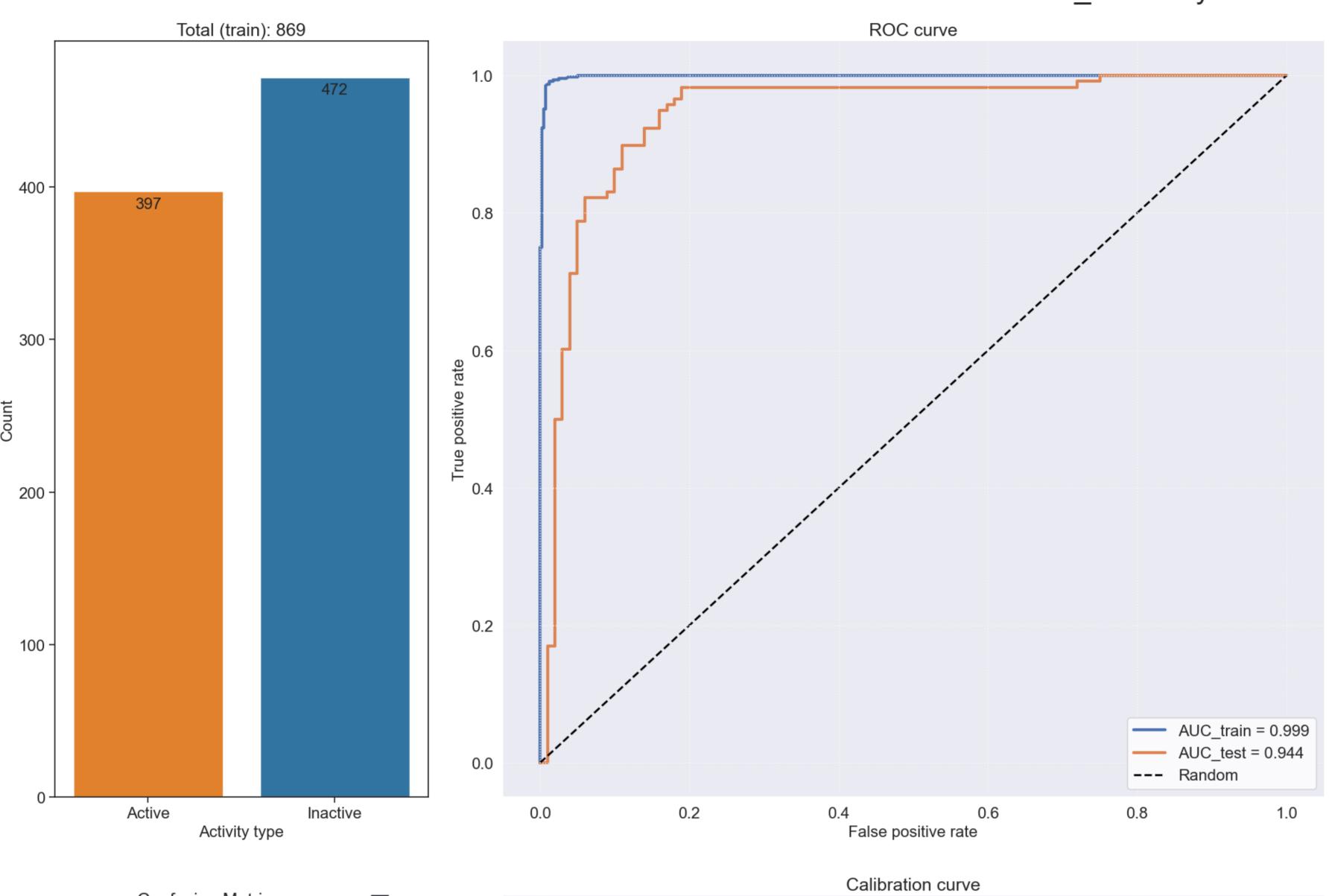
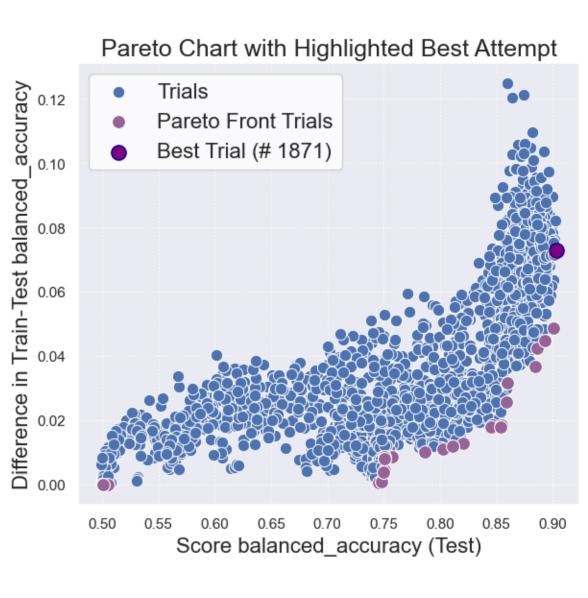
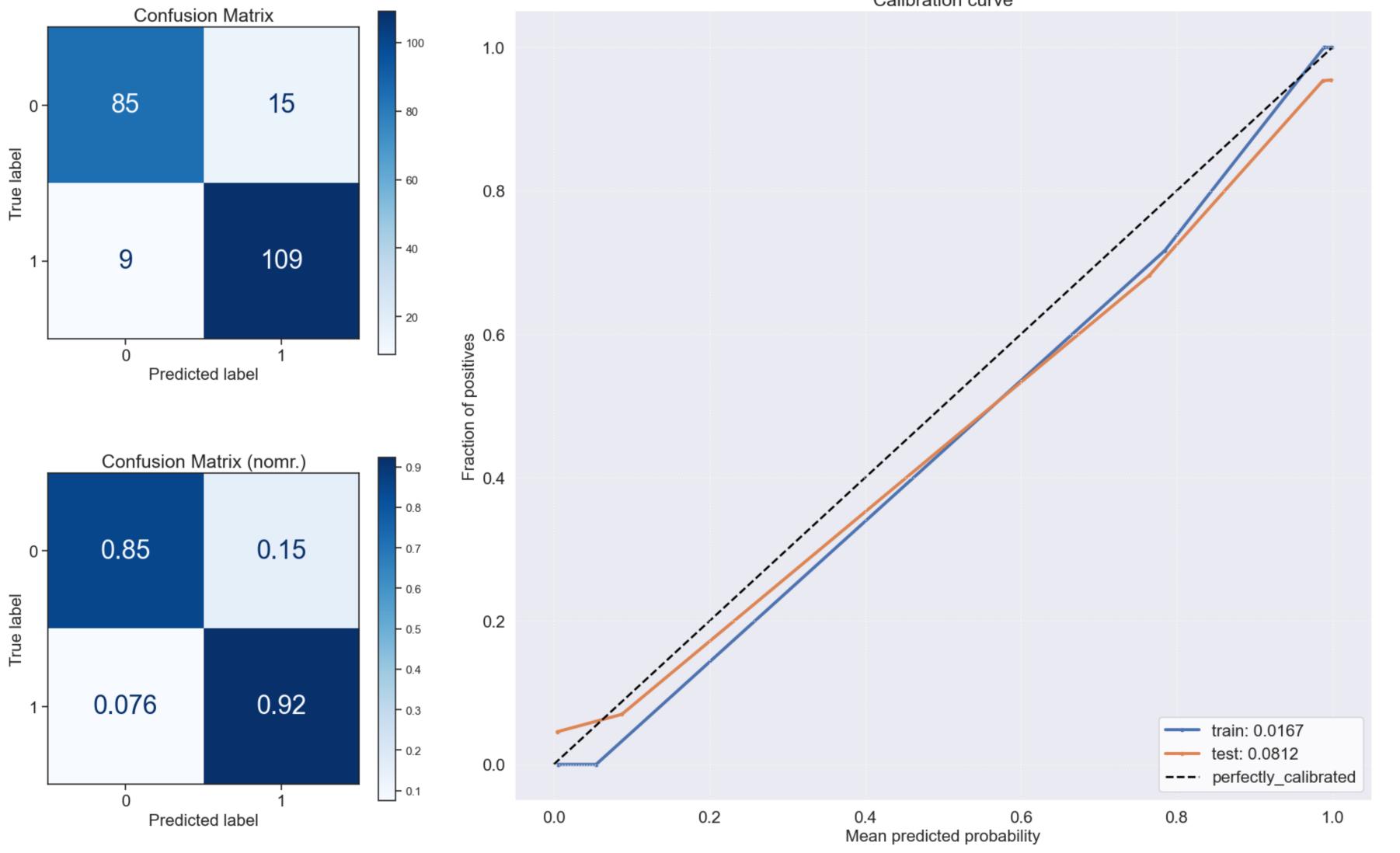
Protein: P30968 - metric: balanced_accuracy





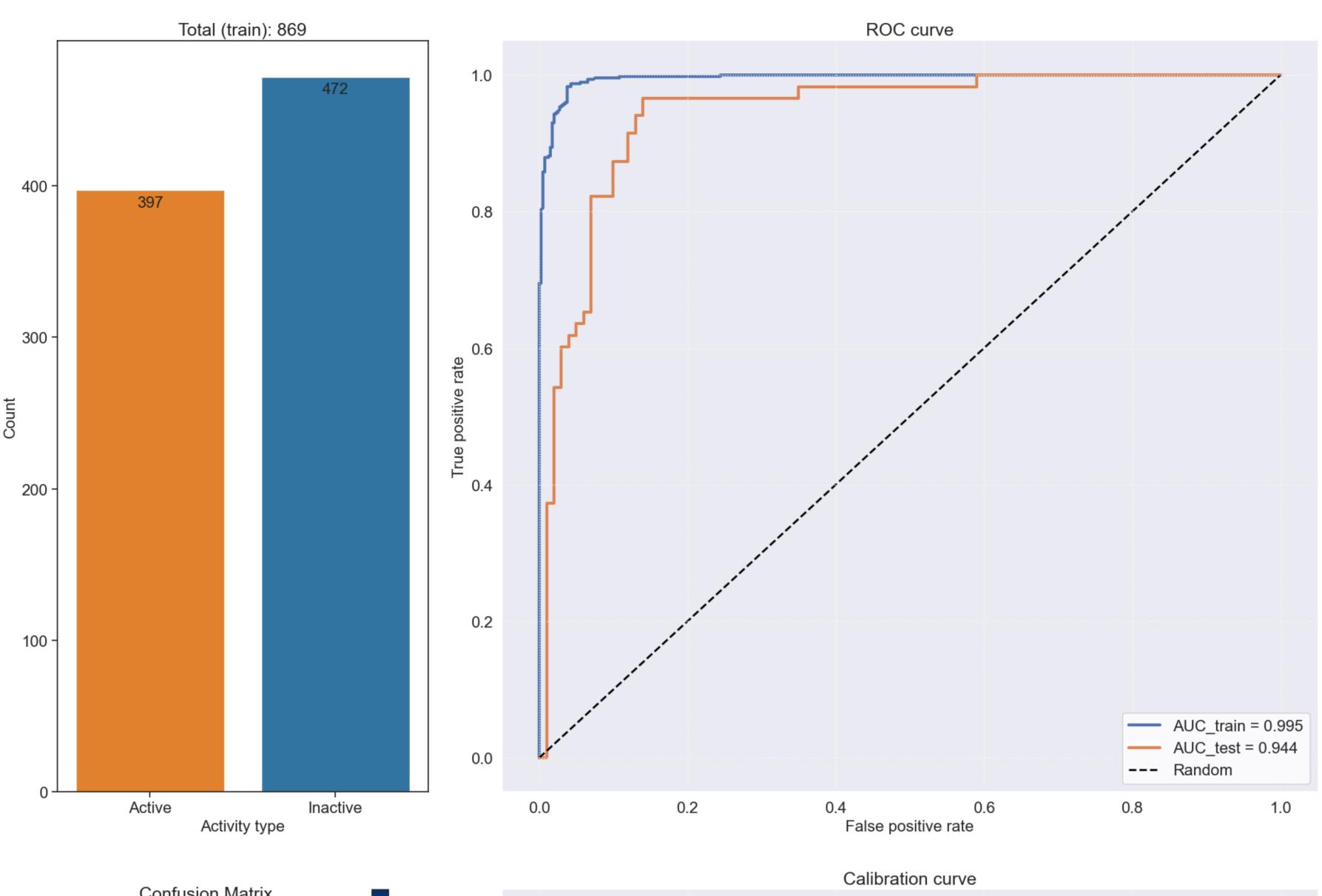
XGBoost Parameters	Value
alpha	2.0184
colsample_bytree	0.6806
gamma	0.4333
lambda	1.265
learning_rate	0.1182
max_depth	10.0
min_child_weight	4.0
n_estimators	754.0
reg_alpha	0.1122
reg_lambda	0.9539
scale_pos_weight	2.8235
subsample	0.6463

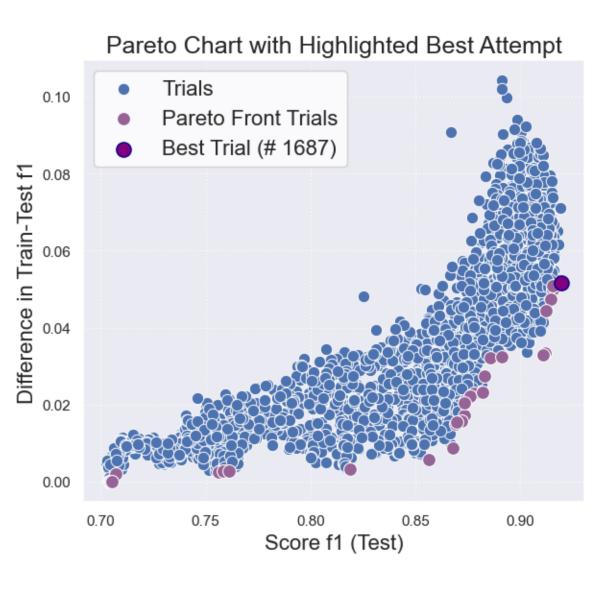


	Active/Inactive probability						
50	Inacti	ve zone		Active zone	type active (118) inactive (100) decoy (218)		
40	–						
Percent 08							
20							
0							
O	0.0 0.2	0.4	0.6	0.8	1.0		
	Probability						

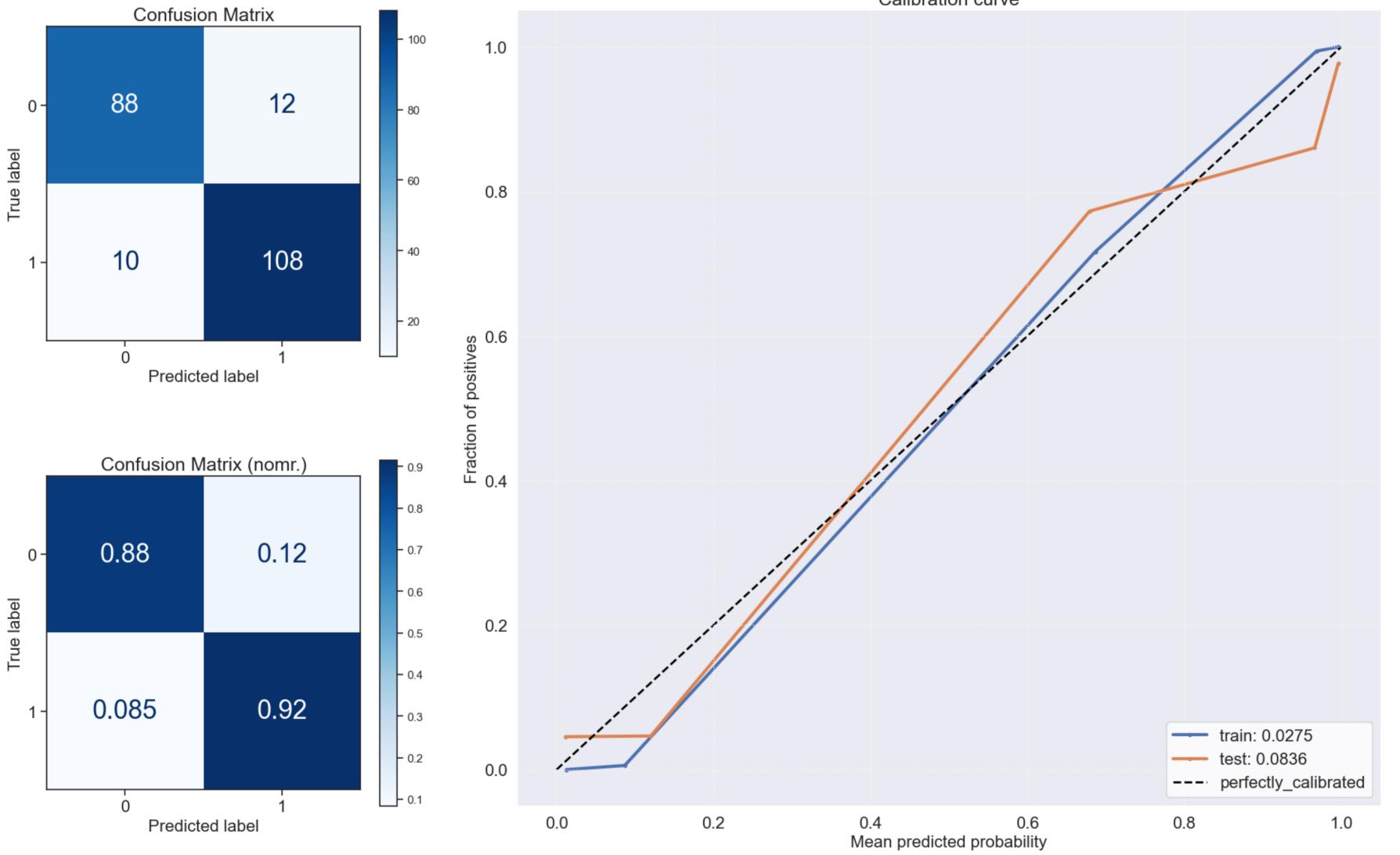
Metric	Train	Test
AUC	0.9988	0.9442
accuracy	0.9804	0.8899
balanced accuracy	0.9788	0.8869
recall_(sens)	0.9979	0.9237
specificity	0.9597	0.85
precision	0.9671	0.879
f1_score	0.9804	0.8896

Protein: P30968 - metric: f1





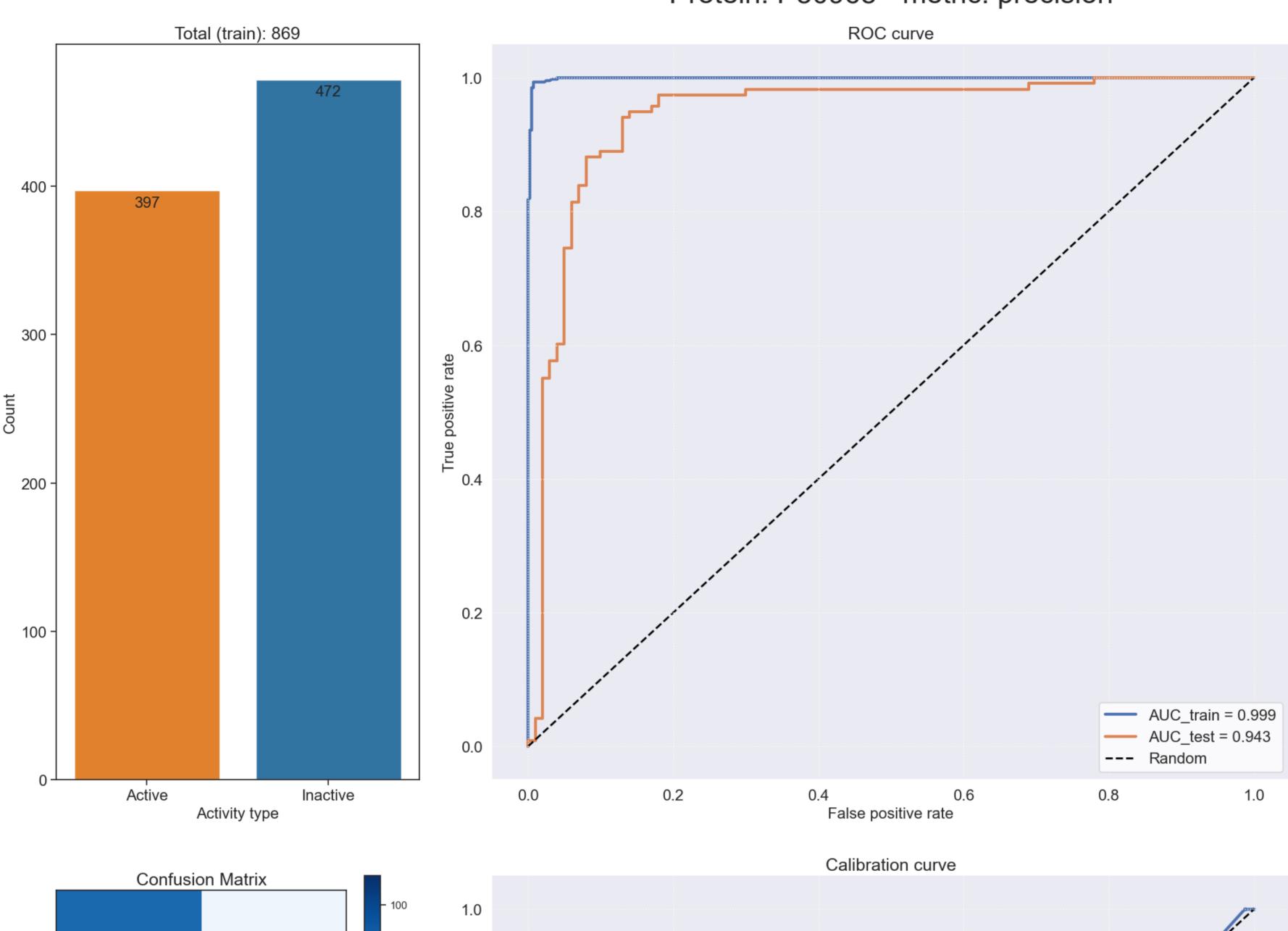
XGBoost Parameters	Value
alpha	1.1175
colsample_bytree	0.9541
gamma	0.6335
lambda	3.3643
learning_rate	0.2813
max_depth	5.0
min_child_weight	2.0
n_estimators	524.0
reg_alpha	0.623
reg_lambda	0.7736
scale_pos_weight	1.1844
subsample	0.8865

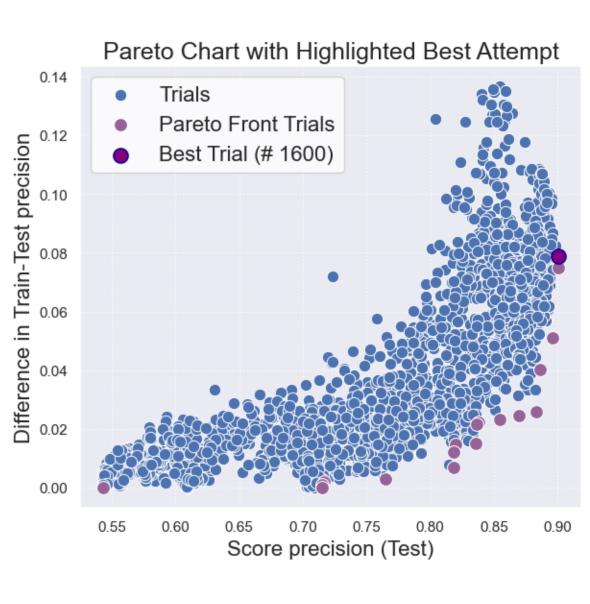


			Active/Inactiv	e probability		
40		Inactive zone			Active zone	type active (118) inactive (100) decoy (218)
30						
Percent 05						
10						
0 —						
	0.0	0.2	0.4 Proba	0.6 bility	0.8	1.0

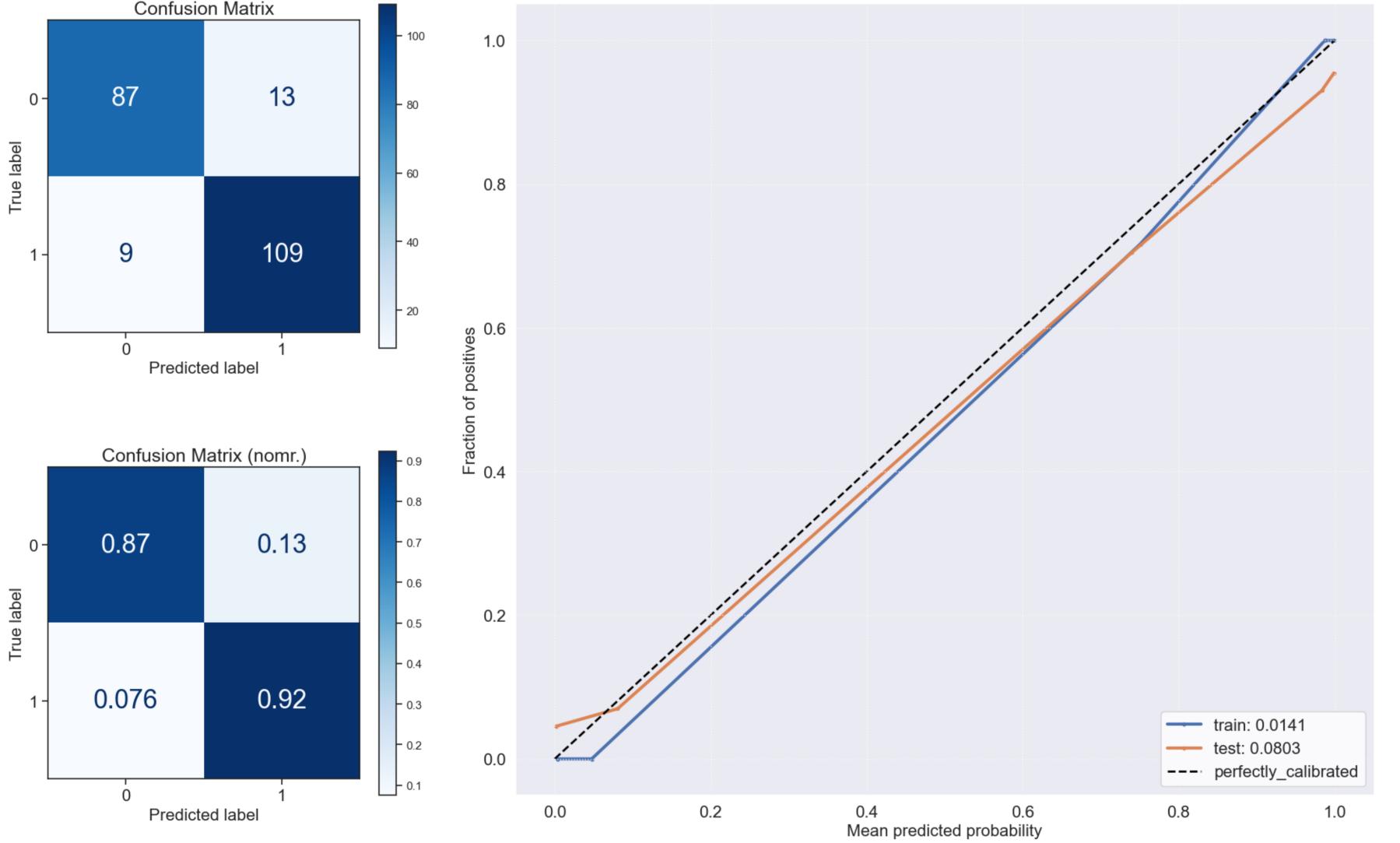
Metric	Train	Test
AUC	0.9953	0.9437
accuracy	0.9701	0.8991
balanced accuracy	0.9695	0.8976
recall_(sens)	0.9767	0.9153
specificity	0.9622	0.88
precision	0.9685	0.9
f1_score	0.9701	0.899

Protein: P30968 - metric: precision





XGBoost Parameters	Value
alpha	3.7643
colsample_bytree	0.7896
gamma	0.0411
lambda	3.531
learning_rate	0.3124
max_depth	3.0
min_child_weight	3.0
n_estimators	544.0
reg_alpha	0.5778
reg_lambda	0.9007
scale_pos_weight	1.7727
subsample	0.5807

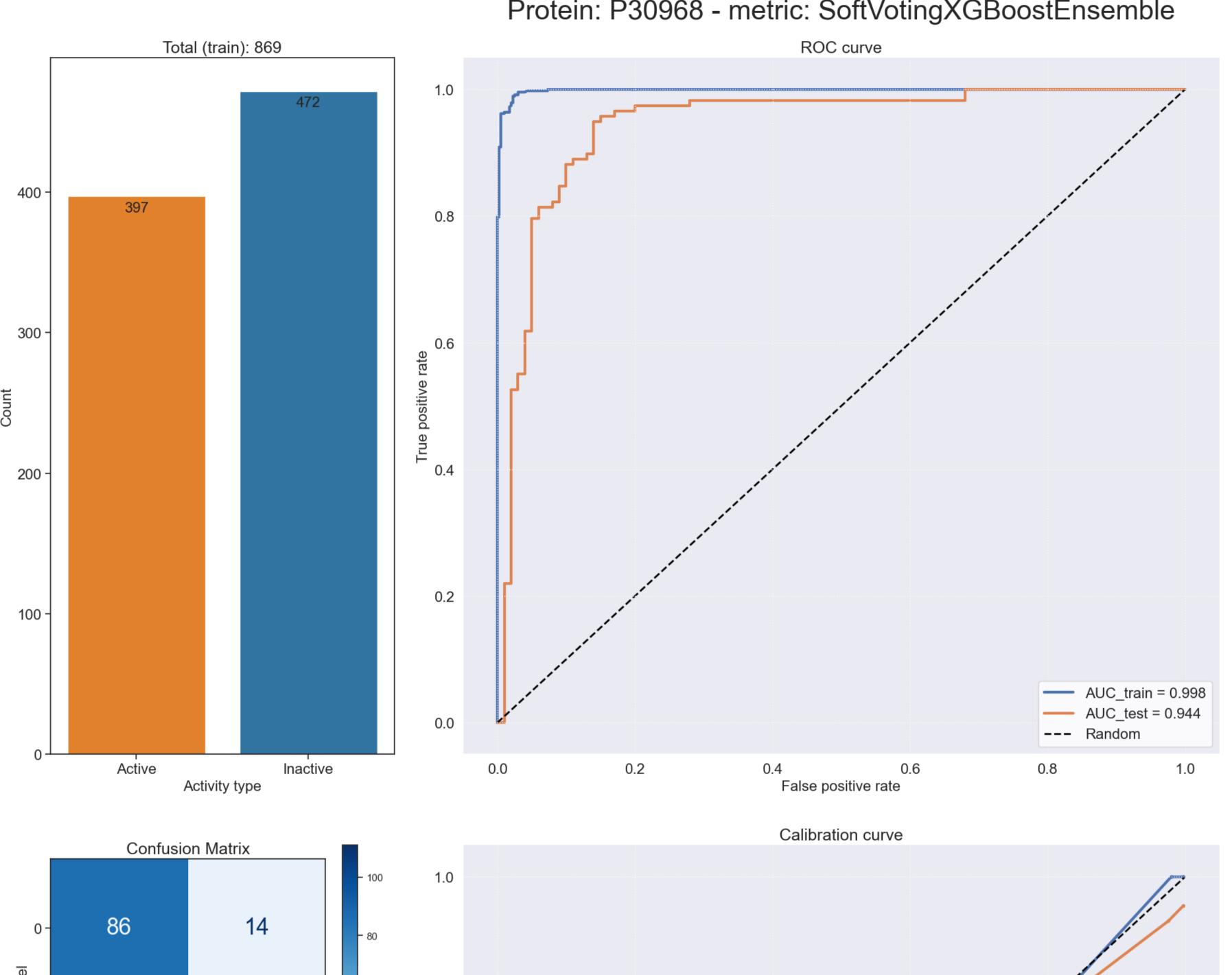


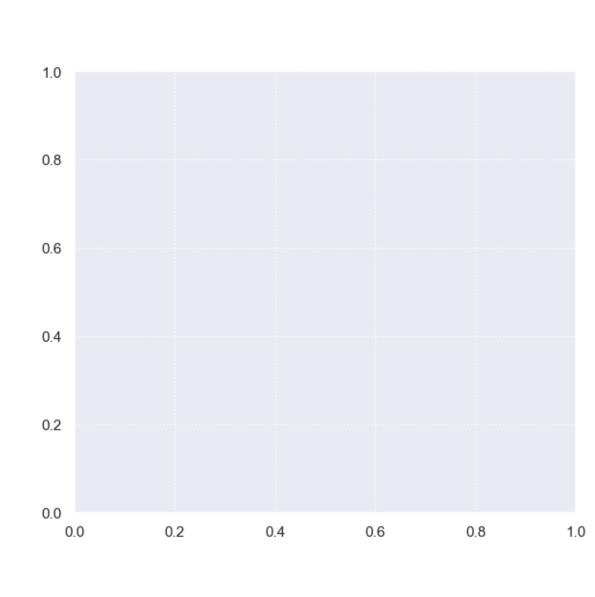
50 -	- In				Active zone	inactive (100) decoy (218)
Percent 08						
20						
10 	0.0	0.2	0.4 Proba	0.6	0.8	1.0

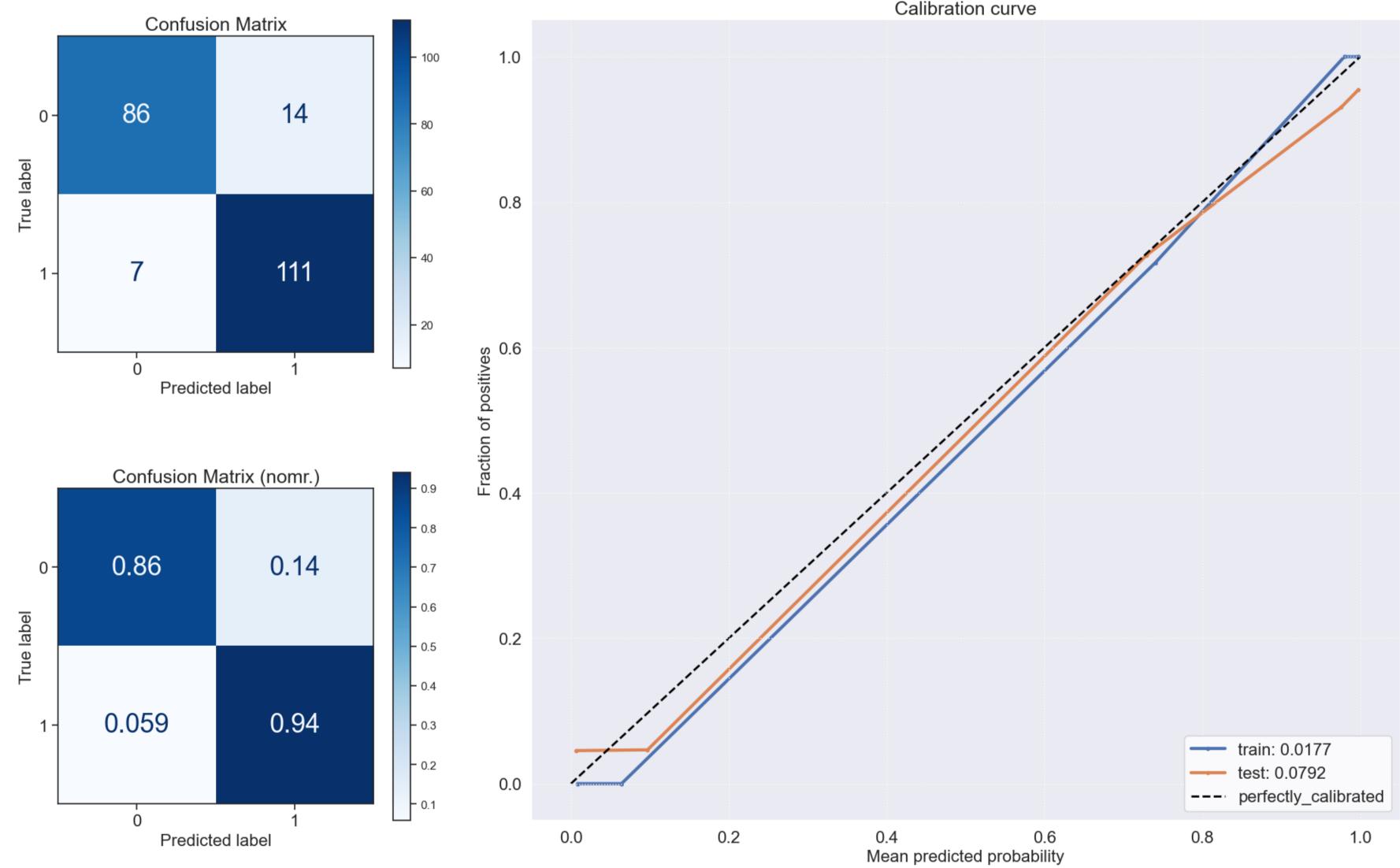
Active/Inactive probability

Metric	Train	Test
AUC	0.9992	0.9431
accuracy	0.9839	0.8991
balanced accuracy	0.9826	0.8969
recall_(sens)	0.9979	0.9237
specificity	0.9673	0.87
precision	0.9731	0.8934
f1_score	0.9839	0.8989

Protein: P30968 - metric: SoftVotingXGBoostEnsemble







40	lna	ctive zone			Active zone	type active (118) inactive (100) decoy (218)
30						
ercent						
20						
10						
0	0.0 0	.2 0	.4 Probability	0.6	0.8	1.0

Active/Inactive probability

Metric	Train	Test
AUC	0.9985	0.9445
accuracy	0.9816	0.9037
balanced accuracy	0.9802	0.9003
recall_(sens)	0.9958	0.9407
specificity	0.9647	0.86
precision	0.9711	0.888
f1_score	0.9816	0.9033