

Table S13. Performance of consensus classifiers PON-P and PredictSNP with PMD-UNIPROT and MMP datasets.

	PMD-UNIPROT			MMP		
	PON-P	PredictSNP ^a	PredictSNP	PON-P	PredictSNP ^a	PredictSNP
True positives	362	523	714	1,461	2,743	3,773
False negatives	192	89	198	875	258	683
True negatives	268	159	298	4,152	2,619	4,291
False positives	65	116	220	522	1,390	3,247
Total	887	887	1,430	7,010	7,010	11,994
Sensitivity^b	0.653	0.855	0.783	0.625	0.914	0.847
Specificity^b	0.805	0.578	0.575	0.888	0.653	0.569
Precision^b	0.770	0.670	0.648	0.848	0.725	0.663
NPV^b	0.699	0.799	0.726	0.703	0.884	0.788
Accuracy^b	0.729	0.716	0.679	0.757	0.784	0.708
MCC^b	0.464	0.450	0.366	0.532	0.588	0.433
AUC^b	0.724	0.740	0.724	0.790	0.804	0.787

^a – PredictSNP set up to return predictions for the same number of mutations as PON-P; these mutations have the highest PredictSNP score reflecting the degree of confidence in its decision; ^b – these metrics were calculated with normalized numbers