

Table S4. Improvement of the prediction performance of NESmapper by incorporating the properties of the amino acids composing the NES-flanking sequences.

Flanking property	NESmapper threshold score	ValidNES data ^a		Sp-protein data ^b
		False negatives (Sensitivity)	False positives	False positives
–	1	44 (0.785)	1,033	2,059
+		47 (0.771)	970	1,931
–	2	53 (0.742)	788	1,655
+		51 (0.751)	850	1,646
–	3	63 (0.693)	618	1,298
+		55 (0.752)	738	1,383

^a ValidNES dataset consisting of proteins containing 205 LMB-sensitive NESs.

^b Sp-protein dataset consisting of 484 proteins from *S. pombe* whose subcellular localizations are not affected by LMB-treatment.

The prediction was performed with the untrained NES profiles.