

Additional file 22. Prediction of cNLSs using three different prediction algorithms Column A: set of proteins tested. Column B: Prediction algorithm used. Column C: Number of proteins with predicted NLS. Column D: number of proteins lacking a predicted NLS. Column E: percentage of proteins with predicted NLS in each set. Column F: p-value.

Protein set	NLS predictor	Positive predictions	Negative predictions	% positive	P-value (one sided Fisher's exact test; relative to all <i>P. falciparum</i> proteins)
All <i>P. falciparum</i> proteins	NLStradamus	2449	3042	45%	
	PredictNLS	1713	3778	31%	
	cNLS predictor	904	4548	17%	
Core nuclear proteome: 1 or more peptides	NLStradamus	409	386	51%	0.00828
	PredictNLS	296	499	37%	0.00647
	cNLS predictor	170	617	22%	0.00612
Core nuclear proteome: 2 or more peptides	NLStradamus	298	275	52%	0.007665
	PredictNLS	204	368	36%	0.0585
	cNLS predictor	121	445	21%	0.02433
Core nuclear proteome: nuclear fractions only	NLStradamus	238	185	56%	0.0004767
	PredictNLS	190	233	45%	0.0000263
	cNLS predictor	109	309	26%	0.0004754