

**Table S4. Correlation of the IUPRED short method used in the main survey with other predictive methods (see text).**

<b>Method</b>	<b>Mean</b>	<b>Spearman's rho</b>
IUPRED short	12.4	1.00
IUPRED long	12.3	0.96
ESPRITZ N	19.1	0.92
ESPRITZ X	11.0	0.94
IUPRED short, regions	21.8*	0.50
ESPRITZ N, regions	31.6*	0.62
ESPRITZ X, regions	24.1*	0.68

\* percentage of proteins in a virus that have at least one long disordered region of 30 or more residues.