

**Table S1. Intrinsic disorder in viral genomes classified by the hosts they interact with.**

<i>Host</i>	<i>N</i> <sup>a</sup>	<i>S</i> <sup>b</sup> (Kbp)		<i>D</i> <sup>c</sup> (%)		<i>Correlation</i> <sup>d</sup>		<i>R</i> <sup>2</sup> <sub>B</sub>	<i>R</i> <sup>2</sup> <sub>BS</sub>	<i>p</i> <sup>e</sup>
		$\mu$	$\sigma$	$\mu$	$\sigma$	$\rho$	<i>p</i>			
Plants	638	6.65	3.50	12.91	7.05	-0.73	<b>2.20 x 10<sup>-16</sup></b>	0.27	0.61	<b>&lt;2 x 10<sup>-16</sup></b>
Vertebrates	590	22.85	42.11	13.65	8.76	-0.35	<b>2.20 x 10<sup>-16</sup></b>	0.21	0.21	0.30
Vertebrates/Invertebrates	108	61.47	85.63	15.34	6.93	-0.77	<b>2.20 x 10<sup>-16</sup></b>	0.53	0.74	<b>2.09 x 10<sup>-15</sup></b>
Invertebrates	90	109.09	86.58	8.58	4.25	0.55	<b>2.97 x 10<sup>-8</sup></b>	0.17	0.40	<b>1.75 x 10<sup>-7</sup></b>
Bacteria	108	37.41	17.85	11.89	3.39	0.44	<b>2.34 x 10<sup>-6</sup></b>	0.19	0.41	<b>7.26 x 10<sup>-9</sup></b>
Bacteria, Archaea	346	65.88	49.05	12.36	3.95	0.19	<b>3.22 x 10<sup>-4</sup></b>	0.59	0.60	0.04
Plants, Fungi	71	6.54	2.86	11.90	4.80	0.31	8.81 x 10 <sup>-3</sup>	0.32	0.33	0.17
Fungi	19	6.23	4.40	6.33	5.59	0.57	0.01	0.65	0.66	0.32
Archaea	26	29.35	15.11	6.32	2.00	-0.37	0.06	-0.02	-0.05	0.57
Fungi, Protozoa	29	5.67	1.72	8.64	4.31	0.23	0.23	0.39	0.36	0.89
Vertebrates/Invertebrates, Plants	39	23.52	5.87	6.23	1.49	0.16	0.34	0.10	0.09	0.44
Bacteria, Mycoplasmas	26	7.29	1.08	10.43	4.19	-0.09	0.65	0.60	0.58	1.00
Vertebrates, Invertebrates, Plants	27	12.42	1.21	7.32	1.34	-0.08	0.69	-0.01	0.03	0.17
Vertebrates, Plants	25	13.98	2.70	2.90	1.22	0.06	0.77	-0.02	0.40	<b>7.01 x 10<sup>-4</sup></b>
Bacteria, Spiroplasmas	15	5.12	0.65	13.51	4.76	0.05	0.87	0.75	0.87	6.90 x 10 <sup>-3</sup>

<sup>a</sup>Number of genomes in the family.

<sup>b</sup>Genome size;  $\mu$  and  $\sigma$  represent the mean and standard deviation respectively.

<sup>c</sup>Percent protein disorder as defined in Materials & Methods.

<sup>d</sup>Correlation between disorder and genome size;  $\rho$  and *p* represent coefficient of correlation and probability respectively.

<sup>e</sup>Probability that genome size is a significant predictor of disorder, from an analysis of variance model including the composition of the four bases as covariates. Significant probabilities after Bonferroni correction are marked in bold.