

<i>Gene symbol</i>	<i>siRNA construct</i>	Rel. rate of prion propagation		
		<i>FC</i>	<i>SD</i>	<i>t-test</i>
<i>Fn1</i>	<i>siRNA-Fn.2</i>	2.34	0.27	6.2×10^{-12}
<i>Chga</i>	<i>siRNA-Chga.2</i>	2.32	0.40	3.5×10^{-11}
<i>Iqgap2</i>	<i>siRNA-Iqgap2.1</i>	1.40	0.41	2.9×10^{-1}
<i>IL11ra1</i>	<i>siRNA-IL11ra1.1</i>	1.76	0.49	6.2×10^{-4}
<i>Lrrn4</i>	<i>siRNA-Lrrn4.1</i>	1.66	0.43	4.6×10^{-3}
<i>Micalcl</i>	<i>siRNA-Micalcl.1</i>	1.21	0.45	7.6×10^{-1}
<i>Chga</i>	<i>siRNA-Chga.2</i>	1.29	0.66	2.5×10^{-1}
<i>Igsf5</i>	<i>siRNA-Igsf5.2</i>	1.14	0.51	4.5×10^{-1}
<i>Itga8</i>	<i>siRNA-Itga8.2</i>	2.17	0.75	1.1×10^{-7}
<i>Papss2</i>	<i>siRNA-Papss2.1</i>	2.05	0.60	7.8×10^{-5}
<i>Galt</i>	<i>siRNA-Galt.1</i>	1.04	0.36	1.2×10^{-1}

Supplementary Table S9: Susceptibility of R7 cells to 22L prions after transient gene silencing of candidate genes. 1.5×10^4 R7 cells per well of a 96-well plate were transfected with siRNA followed by 22L prion infection (10^{-5} dilution) as described in Methods. Relative rates of prion propagation expressed as fold change (FC) to controls (NSC) $\pm$ SD are shown. Statistical significance was computed using a two-tailed Student's t-test.