

<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>	2.4	0.42	1.4×10^{-12}
<i>Chga</i>	<i>siRNA-Chga.2</i>	3.55	0.41	3.7×10^{-18}
<i>Iqgap2</i>	<i>siRNA-Iqgap2.1</i>	2.33	0.86	4.3×10^{-11}
<i>IL11ra1</i>	<i>siRNA-IL11ra1.1</i>	2.20	0.43	1.6×10^{-10}
<i>Lrrn4</i>	<i>siRNA-Lrrn4.2</i>	2.01	0.45	1.7×10^{-8}
<i>Micalcl</i>	<i>siRNA-Micalcl.1</i>	2.64	1.11	1.8×10^{-12}
<i>Igsf5</i>	<i>siRNA-Igsf5.2</i>	1.37	0.18	4.5×10^{-4}
<i>Itga8</i>	<i>siRNA-Itga8.2</i>	1.56	0.30	1.7×10^{-5}
<i>Papss2</i>	<i>siRNA-Papss2.1</i>	2.19	0.35	7.4×10^{-10}

Supplementary Table S8: Effects of gene candidate knockdown on the number of PrP^{Sc}-infected cells in RML-chronically infected cells (iS7). Cells were transiently transfected with siRNA against the specified gene candidates. After three days, cells were counted using a Coulter counter and 2×10^4 cells/well transferred onto Elispot plates and the number of PrP^{Sc}-positive cells was determined. Relative numbers of PrP^{Sc}-positive cells expressed as fold change (FC) to controls (NSC) $\pm$ SD for three independent experiments are shown. Statistical significance was computed using a two-tailed Student's t-test.