Table S4: Statistical analysis of C-enrichment and U-depletion at the first position of 21-nt reads

	C-enrichment at position 1 in the 5' end					
Virus	VSV					
Genotype	wildtype		*R2D2*		*loqs*	
Genome strand	plus	minus	plus	minus	plus	minus
p **value (vs genome composition)**	4.96E-08	4.50E-05	**0.374597356**	2.36E-04	1.50E-11	1.68E-14
p **value (vs read nt composition)**	3.47E-06	0.015226039	**0.999138769**	**0.980383249**	0.003972282	0.003742173
Virus	SINV					
Genotype	wildtype		R2D2		loqs	
Genome strand	plus	minus	plus	minus	plus	minus
p **value (vs genome composition)**	3.59E-05	1.79E-08	**0.241676722**	1.53E-10	0.000162761	0.00E+00
p **value (vs read nt composition)**	0.002804033	5.78E-06	**0.955041929**	0.000356005	0.030168561	1.10E-11

	U depletion at position 1 in the 5' end					
Virus	VSV					
Genotype	wildtype		*R2D2*		*loqs*	
Genome strand	plus	minus	plus	minus	plus	minus
p **value (vs genome composition)**	2.38E-10	3.49E-06	1.95E-18	4.21E-18	4.00E-13	4.32E-20
p **value (vs read nt composition)**	3.12E-08	0.001503414	1.29E-11	2.45E-10	4.31E-13	6.18E-20
Virus	SINV					
Genotype	wildtype		R2D2		loqs	
Genome strand	plus	minus	plus	minus	plus	minus
p **value (vs genome composition)**	0.049606029	0.038331565	**0.997226278**	**0.979822358**	**0.74128436**	0.034639679
p **value (vs read nt composition)**	**0.167905594**	**0.053154857**	**0.999999992**	**0.999955092**	**0.824744834**	0.008304462

Values above 0.05 are highlighted in bold.