## **Supplementary information**

## Clinical benefit of remdesivir in rhesus macaques infected with SARS-CoV-2

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## **Supplementary materials**

## Clinical benefit of remdesivir in rhesus macaques infected with SARS-CoV-2

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<sup>1</sup>Laboratory of Virology, <sup>2</sup>Rocky Mountain Veterinary Branch, <sup>3</sup>Laboratory of Bacteriology and <sup>4</sup>Research Technologies Branch, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, MT, United States of America; <sup>5</sup>Gilead Sciences, Foster City, CA, United States of America **Table S1. Deep sequencing results to confirm absence of known resistance mutations to remdesivir.** The timepoints for sequencing of BAL and swab samples were selected based on positivity in qRT-PCR to reflect the latest possible timepoints where the majority of animals were positive for that given sample type in qRT-PCR.

Treatment	Animal	Sample	Mean	F476	V553
	no.		sequencing	(nt 14,878-14,880)	(nt 15,109-15,111)
			coverage <sup>a</sup>		
Remdesivir	RM1	BAL <sup>b</sup>	197.27	no variants	no variants
		LLLL <sup>c</sup>	21.05	no variants	no variants
		Nose swab <sup>d</sup>	138.89	no variants	no variants
		RLLL <sup>e</sup>	11.22	no variants	no variants
	RM2	BAL	21.7	no variants	no variants
		LLLL	32.65	no variants	no variants
		Nose swab	187.29	no variants	no variants
		RLLL	19.37	no variants	no variants
	RM3	BAL	4.76	ND <sup>g</sup>	ND
		LLLL	5.43	ND	ND
		Nose swab	49.11	no variants	no variants
		RLLL	2.08	no variants	ND
		Rectal swab <sup>f</sup>	35.47	no variants	no variants
	RM4	BAL	421.43	no variants	no variants
		LLLL	81.65	no variants	no variants
		Nose swab	31.97	no variants	no variants
		RLLL	0.05	ND	ND
		Rectal swab	0.56	ND	ND
	RM5	BAL	25.37	no variants	no variants
		LLLL	0.02	ND	ND
		Nose swab	25.13	no variants	no variants
		RLLL	0.31	ND	ND
	RM6	BAL	17.1	no variants	no variants
		LLLL	5.39	no variants	ND
		Nose swab	25.27	ND	no variants
		RLLL	1.25	ND	no variants
		Rectal swab	0.42	ND	ND
Vehicle	RM7	BAL	352.51	no variants	no variants
		LLLL	123.92	no variants	no variants
		Nose swab	1.11	ND	no variants
		RLLL	229.79	no variants	no variants
		Rectal swab	17.72	no variants	no variants
	RM8	BAL	80.01	no variants	no variants
		LLLL	16.3	no variants	no variants
		Nose swab	0	ND	ND
		RLLL	4.28	ND	ND
		Rectal swab	1.39	ND	no variants
	RM9	BAL	258.39	no variants	no variants
		LLLL	1.34	ND	no variants
		Nose swab	0.87	ND	ND
		RLLL	26.65	no variants	no variants

RM10	BAL	250.71	no variants	no variants
	LLLL	7.12	no variants	no variants
	Nose swab	0.2	ND	ND
	RLLL	1210.31	no variants	no variants
	Rectal swab	5.17	ND	no variants
RM11	BAL	880.97	no variants	no variants
	LLLL	56.38	no variants	no variants
	Nose swab	2.63	ND	ND
	RLLL	597.65	no variants	no variants
	Rectal swab	0.1	ND	ND
RM12	BAL	415.3	no variants	no variants
	LLLL	0.43	ND	ND
	Nose swab	20.44	no variants	no variants
	RLLL	88.08	no variants	no variants
	Rectal swab	11.56	ND	no variants

<sup>a</sup> Mean sequencing coverage was calculated using the GATK version 3 DepthOfCoverage tool

<sup>b</sup> BAL: bronchoalveolar lavages collected at 3 dpi.

<sup>c</sup> LLLL: left lower lung lobe collected on 7 dpi

<sup>d</sup> collected on 5 dpi

<sup>e</sup> RLLL: right lower lung lobe collected on 7 dpi

<sup>f</sup> collected on 2 dpi

<sup>g</sup> No sequence coverage or coverage was too limited to call