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## Think different with RNA therapy: can antisense oligonucleotides be used to inhibit replication and transcription of SARS-CoV-2?

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# Supplementary Materials

Barrey et al. 2020

Figure S1:

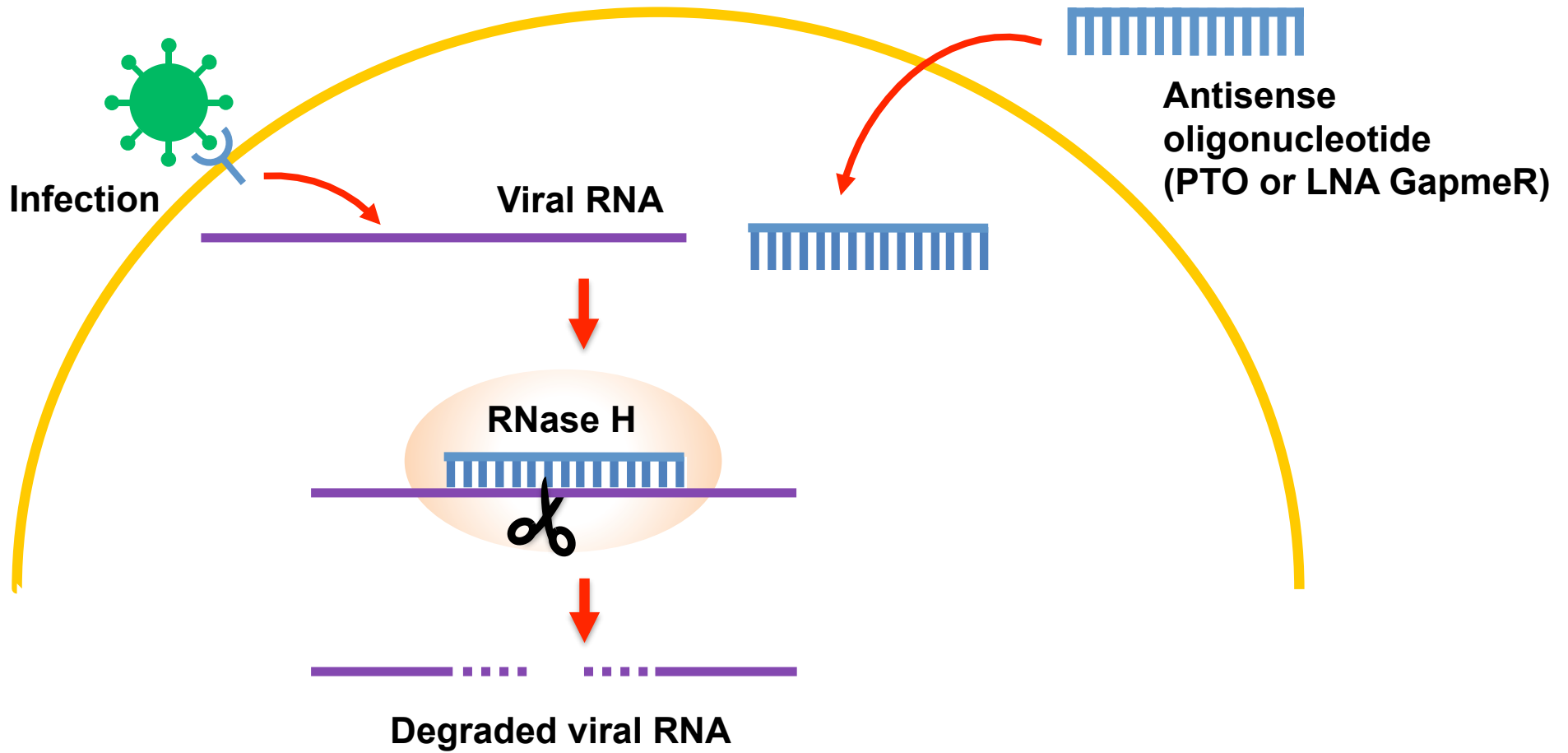


Figure S2:

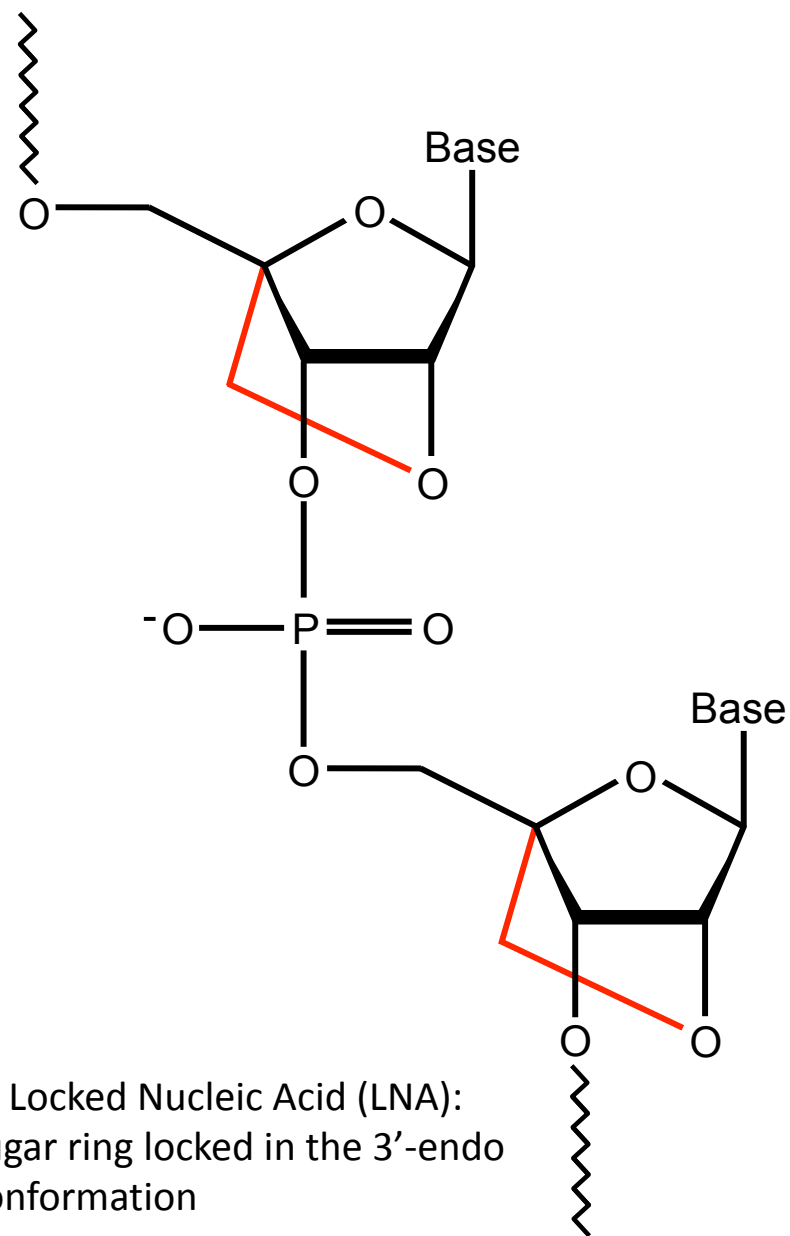
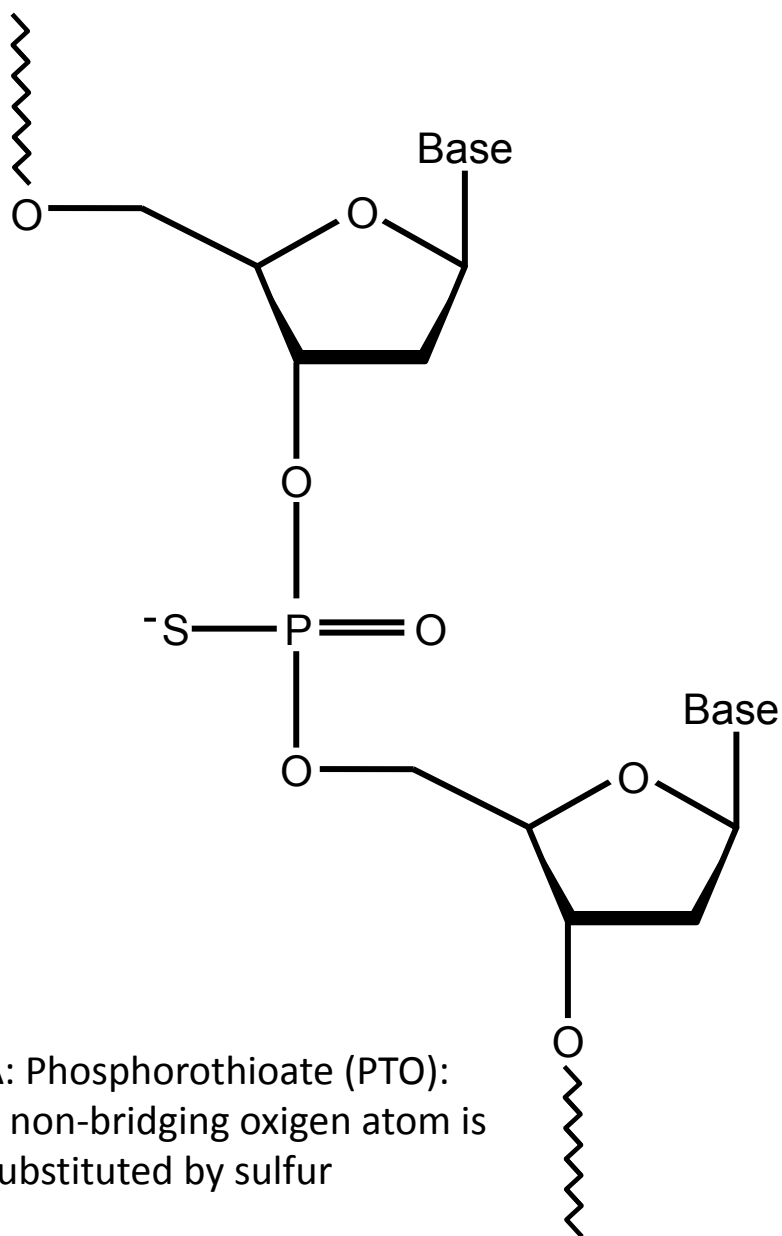
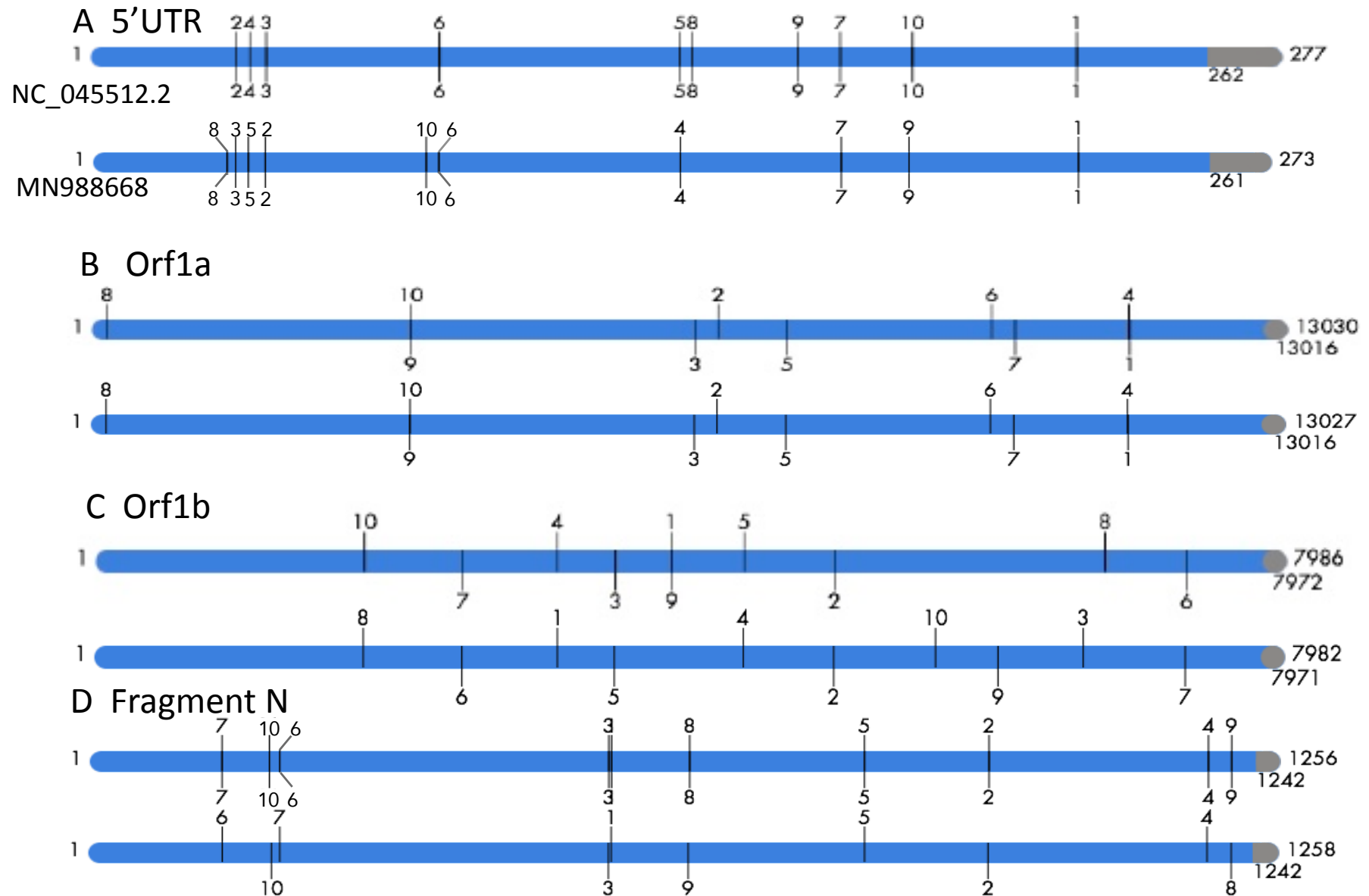


Figure S3: Comparison of relative positions of the antisense LNA GapmeRs obtained on two different SARS-Cov-2 sequences NC\_045512.2 (or MN908947, top) and MN988668 (bottom). The candidates are scored from 1 (best) to 10 on each sequence.



# Table S1

ASO #	Sequence	Melt. temp.	Self annealing	Self annealing alignment	Self end-annealing	GC content (%)	Secondary structure score	Secondary structure
ASO1 *	CAAACAACACCATCC	48.15	4	CAAACAACACCATCC     CCTACCACAACAAAC	0	46.67	2	number of base pairs = 1, sequence = CAAACAACACCATCC, bracket notation = :::::(::):, score = 2
ASO2 *	ACAACACCATCAACT	47.91	8	ACAACACCATCAACT       TCAACTACCACAACA	2	40.00	4	number of base pairs = 2, sequence = ACAACACCATCAACT, bracket notation = :::(::):, score = 4
ASO3 *	TGGGTGGTTTATGTG	48.57	4	TGGGTGGTTTATGTG     GTGTATTGGTGGGT	0	46.67	2	number of base pairs = 1, sequence = TGGGTGGTTTATGTG, bracket notation = :::::(::):, score = 2
ASO4 *	TTGGGTTTGTCTGG	49.28	6	TTGGGTTTGTCTGG     GGTCTTGTGGGTT	3	46.67	3	number of base pairs = 1, sequence = TTGGGTTTGTCTGG, bracket notation = :::::(::):, score = 3
ASO5	AAAACACGCACAGAA	49.88	6	AAAACACGCACAGAA     AAGACACGCACAAAA	0	40.00	3	number of base pairs = 1, sequence = AAAACACGCACAGAA, bracket notation = :::::(::):, score = 3
ASO6	AGGAACGAGAAGAGG	50.01	6	AGGAACGAGAAGAGG     GGAGAAGAGCAAGGA	3	53.33	3	number of base pairs = 1, sequence = AGGAACGAGAAGAGG, bracket notation = :::(::):, score = 3
ASO7	CCTTCTTTCATCCT	47.96	4	CCTTCTTTCATCCT     TCCTACTTCTTCTCC	2	43.75	2	number of base pairs = 1, sequence = CCTTCTTTCATCCT, bracket notation = :::::(::):, score = 2
ASO8	GTTGGTTGGTTTGT	47.68	0	GTTGGTTGGTTTGT TTGTTTGGTTGGTTG	0	40.00	0	number of base pairs = 0, sequence = GTTGGTTGGTTTGT, bracket notation = :::::(::):, score = -1
ASO9	ACAGAACACACACAC	49.54	6	ACAGAACACACACAC    CACACACAAGACA	3	46.67	3	number of base pairs = 1, sequence = ACAGAACACACACAC, bracket notation = :::(::):, score = 3