



**HAL**  
open science

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

Eric Barrey, Veronica Burzio, Sophie Dhorne-Pollet, Jean-François Eléouët,  
Bernard Delmas

### ► To cite this version:

Eric Barrey, Veronica Burzio, Sophie Dhorne-Pollet, Jean-François Eléouët, Bernard Delmas. Think different with RNA therapy: can antisense oligonucleotides be used to inhibit replication and transcription of SARS-CoV-2?. 2023. hal-04106554

**HAL Id: hal-04106554**

**<https://hal.inrae.fr/hal-04106554>**

Preprint submitted on 25 May 2023

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

# Supplementary Materials

Barrey et al. 2020

Figure S1:

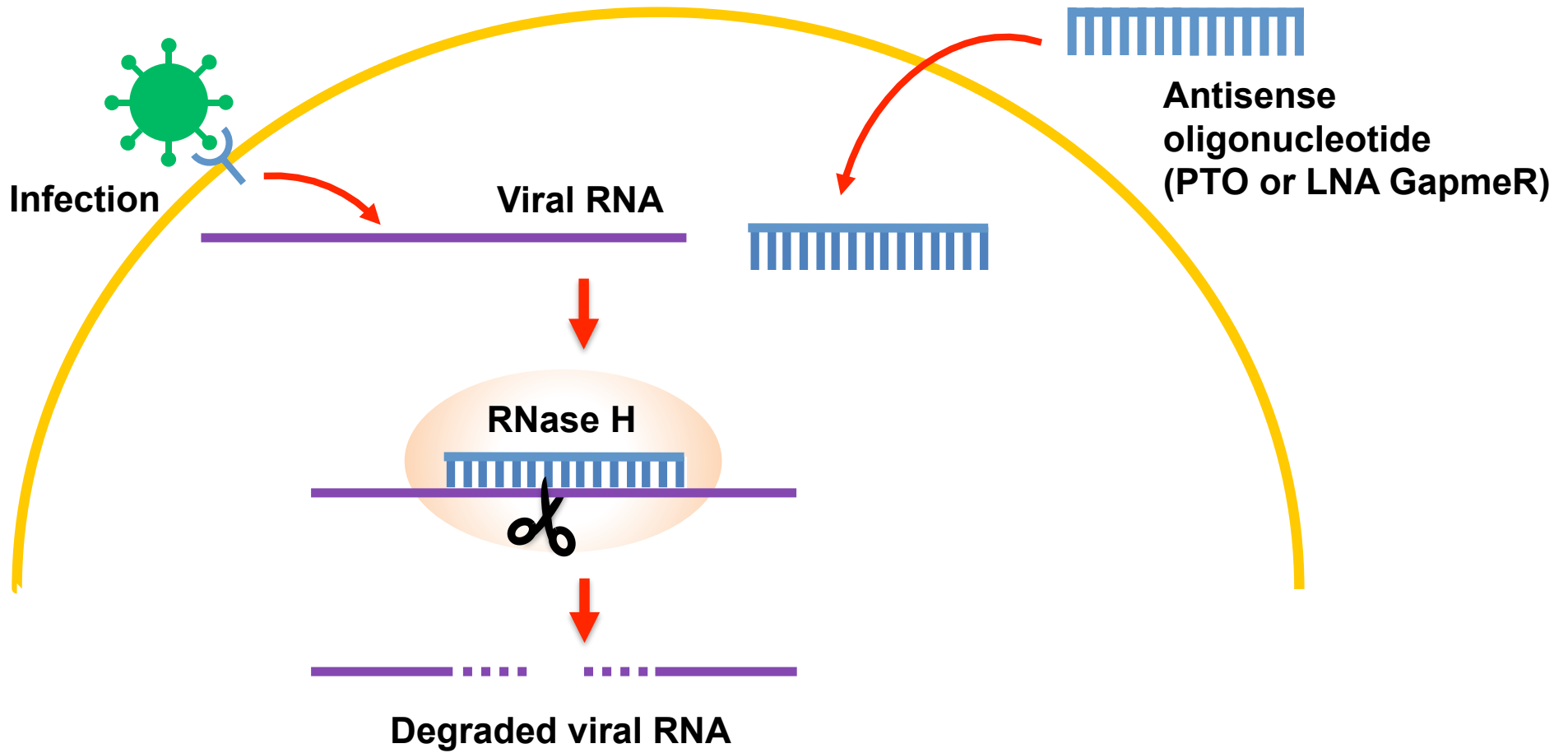


Figure S2:

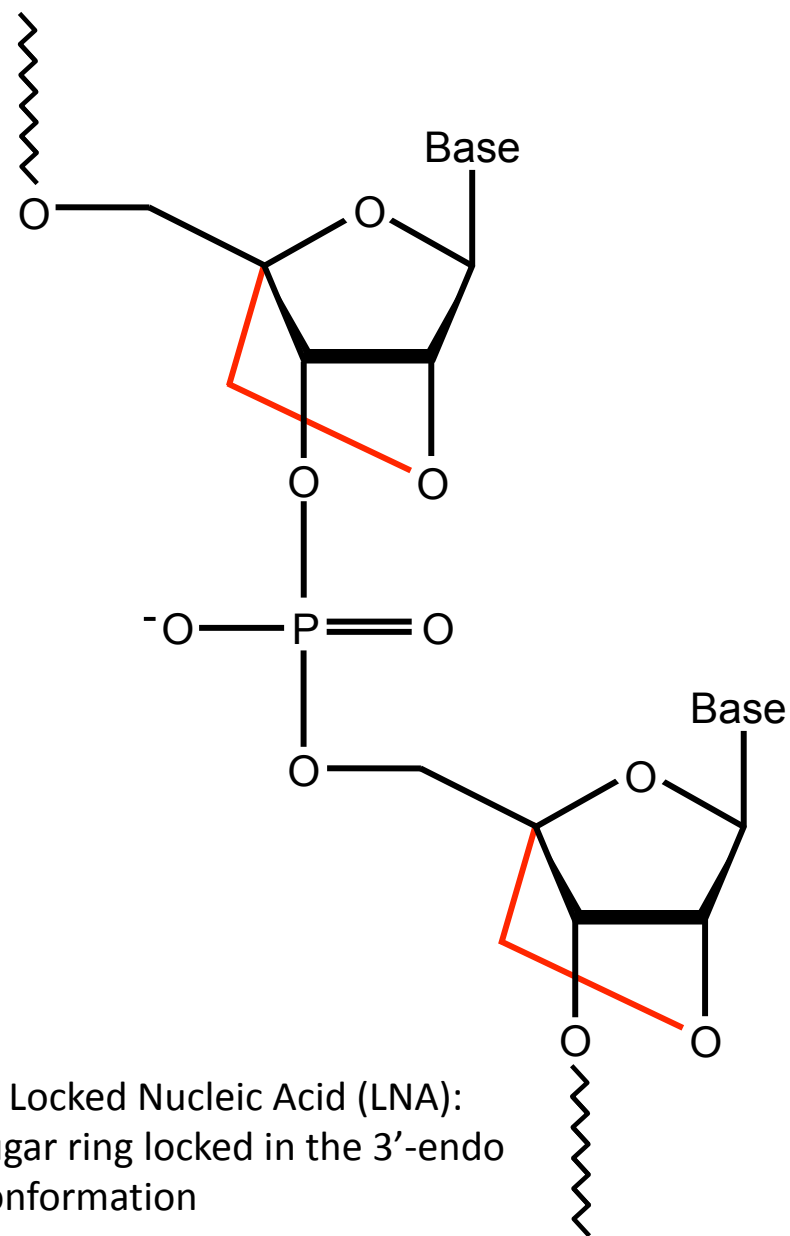
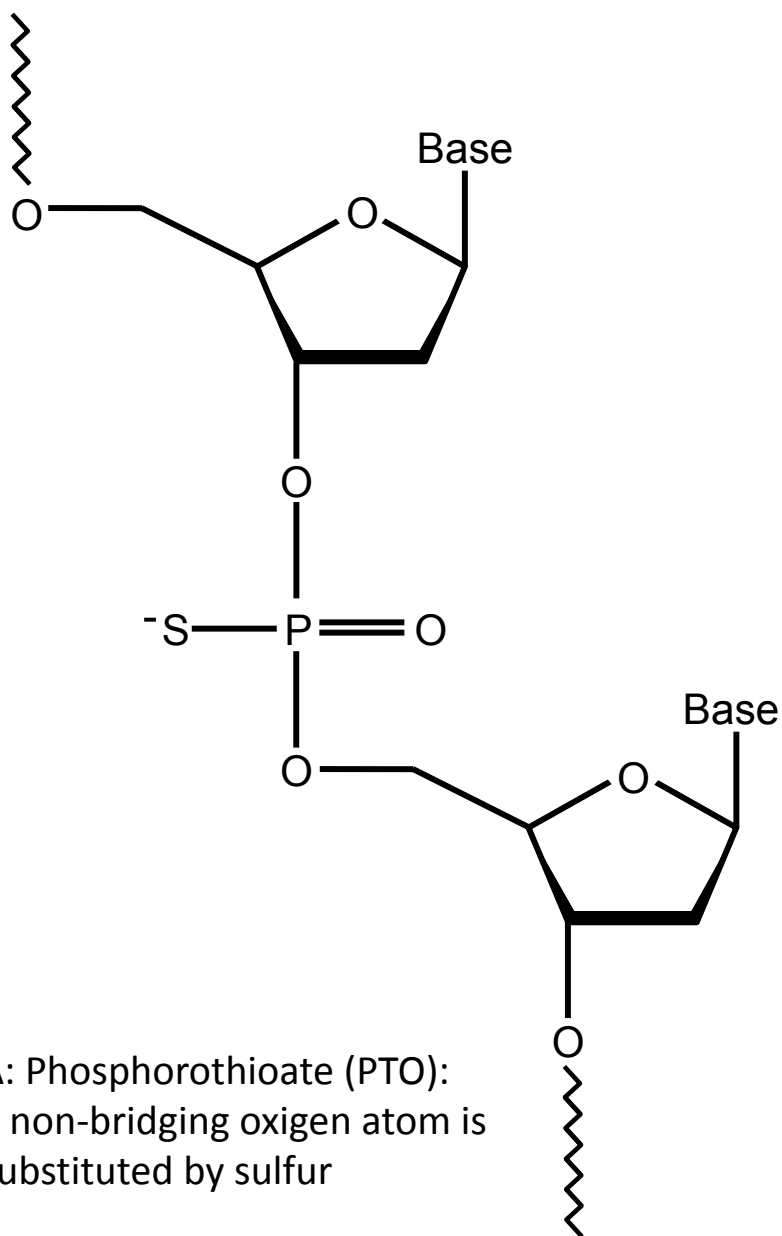
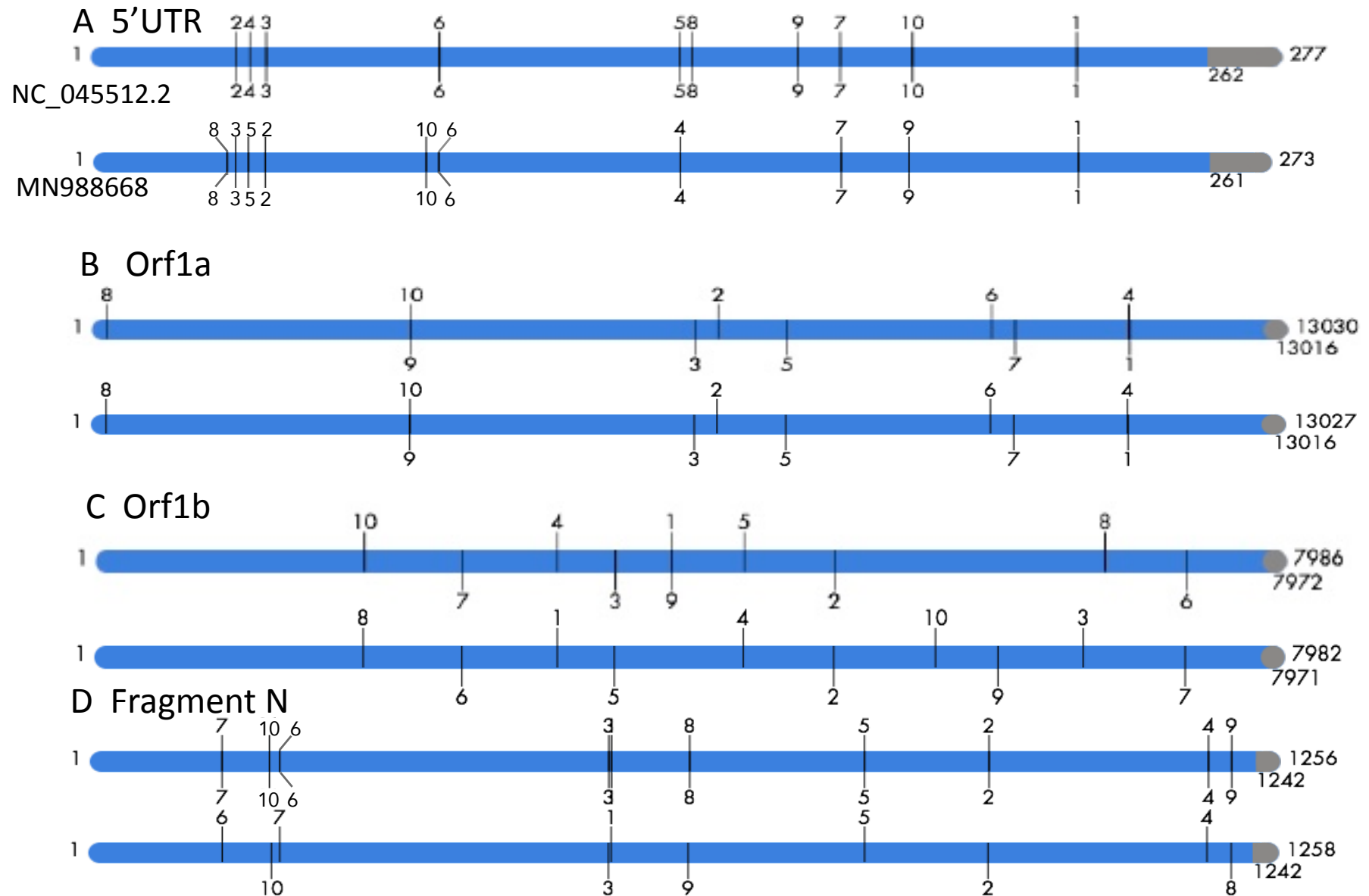


Figure S3: Comparison of relative positions of the antisense LNA GapmeRs obtained on two different SARS-Cov-2 sequences NC\_045512.2 (or MN908947, top) and MN988668 (bottom). The candidates are scored from 1 (best) to 10 on each sequence.



# 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