Supplementary Information

Development of High Affinity Broadly Reactive Aptamers for Spike Protein of Multiple SARS-CoV-2 Variants

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Figure SI1: (a) Binding of aptamer K1 in Tris buffer and Hepes buffer. (b) Binding of aptamer M40 in Tris buffer and Hepes buffer.



Figure SI2: Control experiments. (a) Binding of aptamer K1 to BSA and ovalbumin. (b) Binding of aptamer M40 to BSA and ovalbumin.



Figure SI3: Binding of BG4 to biotinylated aptamer K1 (immobilised on plate) by ELISA. Aptamer K1 had a biotin tag at its 3'-end to facilitate its immobilisation on the streptavidin-coated microtiter plate.



Figure SI4: Predicted secondary structures of the aptamers using MFold¹ at in solution having 150 mM Na⁺ and 5 mM Mg²⁺ and 25°C. (a) Predicted structure of aptamer K1. (b) Predicted structure of aptamer M40.

Predicted	Position	Length	QGRS	G-Score
structure				
Sample	·			
P1	32	13	<u>GG</u> A <u>GG</u> AGAC <u>GGGG</u>	17
P2	32	14	<u>GG</u> A <u>GG</u> AGAC <u>GG</u> G <u>G</u>	18
Р3	32	14	<u>GG</u> AGGAGACG <u>GGGG</u>	16
P4	32	18	<u>GG</u> AGGAGACGGGGGCAGG	17
Р5	32	18	<u>GG</u> AGGAGACG <u>GG</u> GGCA <u>GG</u>	17
P6	32	18	<u>GG</u> AGGAGACGG <u>GG</u> GCA <u>GG</u>	16
P7	32	18	<u>GG</u> AGAGACGGGGGCAGG	15
P8	32	18	<u>GG</u> AGGAGAC <u>GGGG</u> GCA <u>GG</u>	14
Р9	32	18	<u>G</u> AGGAGAC <u>GG</u> G <u>GG</u> CA <u>GG</u>	15
P10	32	18	<u>GG</u> AGGAGACG <u>GGGG</u> CA <u>GG</u>	13
P11	32	19	<u>GG</u> AGGAGACGGGGGCAGGG	16
P12	32	19	<u>GG</u> AGGAGACG <u>GG</u> GGCAG <u>GG</u>	17
P13	32	19	<u>GG</u> A <u>GG</u> AGACGG <u>GG</u> GCAG <u>GG</u>	16
P14	32	19	<u>GG</u> A <u>GG</u> AGACGGG <u>GG</u> CAG <u>GG</u>	15
P15	32	19	<u>GG</u> AGGAGAC <u>GGGG</u> GCAG <u>GG</u>	14
P16	32	19	<u>GG</u> AGGAGAC <u>GG</u> G <u>GG</u> CAG <u>GG</u>	15
P17	32	19	<u>GG</u> AGGAGACG <u>GGGG</u> CAG <u>GG</u>	13
P18	35	15	<u>GG</u> AGAC <u>GGGG</u> GCA <u>GG</u>	17
P19	35	15	<u>GG</u> AGAC <u>GG</u> G <u>GG</u> CA <u>GG</u>	18
P20	35	15	<u>GG</u> AGACG <u>GGGG</u> CA <u>GG</u>	16
P21	35	16	<u>GG</u> AGAC <u>GGGG</u> GCAG <u>GG</u>	17
P22	35	16	<u>GG</u> AGAC <u>GG</u> G <u>GG</u> CAG <u>GG</u>	18
P23	35	16	<u>G</u> AGACG <u>GGGG</u> CAG <u>GG</u>	16

 Table SI1: A predicted G-quadruplex of aptamer K1 with its overlaps by QSGR-Mapper²

Table SI2: Sequences of the truncated oligos

Oligo14	CCACATCTACGA GCTCGAACGCCCGGAGGAGACGGGGGGGGGG
Oligo30	ACGA GCTCGAACGCCCGGAGGAGACGGGGGGCAGGGCGTG TTCACTGC

References

- 1 M. Zuker, Nucleic Acids Research, 2003. **31**(13): p. 3406-3415.
- 2 O. Kikin, L. D'Antonio, and P. S. Bagga, Nucleic Acids Research, 2006. **34**(suppl_2): p. W676-W682.