

Supporting Information for
Selection and characterization of DNA aptamers to
crystal violet

Yang Chen^{1,2,†}, Jine Wang^{1,†}, Yajie Zhang¹, Lijun Xu¹, Tian Gao¹, Bing Wang², Renjun Pei^{1*}

¹CAS Key Laboratory of Nano-Bio Interface, Suzhou Institute of Nano-Tech and Nano-Bionics, Chinese Academy of Sciences, Suzhou, 215123, China

²School of Pharmacy, Xi'an Jiaotong University, Xi'an, 710061, China

†These authors contributed equally to this work.

*Corresponding author. CAS Key Laboratory of Nano-Bio Interface, Suzhou Institute of Nano-Tech and Nano-Bionics, Chinese Academy of Sciences, Suzhou, 215123, China.

Tel: +86-512-62872776, E-mail: rjpei2011@sinano.ac.cn.

Table S1 The detailed sequences of various G4 structures, i-motif structure, random dsDNA and ssDNA used in this paper.

Name	Sequence (5' to 3')
Hum21	GGGTTAGGGTTAGGGTTAGGG
PS2.M	GTGGGTAGGGCGGGTTGG
H22	AGGGTTAGGGTTAGGGTTAGGG
T30695	GGGTGGGTGGGTGGGT
G3TG4T	TGGGTGGGTGGGTGGGT
G3TG4TT	GGGTTTGGGTGGGTGGG
G3T4	GGGTTTGGGTTTGGGTTTGGG
C29	CCCCCTTCCCCCTTCCCCCTTCCCC
(dsDNA)	1st strand: TATAATACACGTAGCATCTGACA 2nd strand: TGTCAGATGCTACGTGTATTATA
random1	ATAATTCTATCTTATCTGGAATTATATATATATT
random2	TTTTTTTTCCCCCCCCCAAAAAAA
random3	AACGGGCAACGCAGTGACTGGATATCCCCGTT
random4	GCATATCGCCCCCCCCCGATATGCGCAATAA
random5	TATAATACACGTAGCATCTGACACTATAATCGTT

16 -CAAGGACAGTTAGTGAATGCA-CATTCCGGATC-
22 ---GGGCAACGGCAGTGACTGGA-TATCCCCCTGT-
17 ---CCCAAAGGGGTACGCACAGTGACCGGGAT-
20 ---CACCAGGTGGGTGAGCACAGTATTCAC-
26 ---GCCCAATGTGTTGAGCTGTACGGCAGTGT-
30 ---CACCGGTGCGCGCGTACAGGTAACTAGC-
9 ---CAGCCATATTGGGAGTATAACCCCTTOGCCT-
15 ---CCGGTAACGGCCAGTGTAACTTCCCCTGGT-
24 ---CACCGGTGGACATTGTTGTCTGGGCTA-
5 -----OGGAGTGTGATCCTCCGGTGTGGATAGAC-
19 -----CACAGAGGGAGCGGTGTCCCCAAGGTGGAA-
1 -----CCCACACCGTTCAAGGAGGATCAGGTAAAGCT-
12 -----ACACACACACTCTATATCATTAGCATGTACTCT-
4 -----CACCA-----CCCATGTCGCAGGGTACATAGTA-
6 -----CACCA-----AGGTCTCCGGCCAGTCGAGT-
23 **CAT**GGCACCCG-TATGCCCTCTGCTGTCTATC-
7 -----CCACAGCCTATGACGTGACATCGCGCAGTA-
29 -----CACAGGGGGCAGC-CAACGGGAAGTAGT-
8 -----CCCAGCGTAAAG---TCCACTCTCAGTGTGTGGC-
28 -----CCCCAGGGTCATGCTCAACTCCCCAATG-
27 GGGACGTTAGGCCTAAACCCAACACCCCTAG-
18 ---GGCTGTTCGCTCATGTGCCAACCTCOGTG-
3 -----GGGCTGGACCGTCATCAACCTTCCACATGCA-

Fig. S1 Sequence alignment result by Clustalx 1.8.3.



Name	p-value	Sites
5	2.72e-5	CGGAGTGTGAT CCTCCGGTGT
26	7.60e-5	G CCCAATGTGTT GAGCTGTACG
28	1.74e-4	C CCCAGGGTCAT GCTCAACTCC
20	5.41e-4	CAGGTGGGTG AGCACAGTATT CAC
19	6.00e-4	CACAGAG CGGAGCGTGTG CCCAAGGTGG
8	6.80e-4	CCCAGCGTAAG TCCACTCTCA
15	7.73e-4	CCGGTAACG GCCAGTGTAA TTCCCCCTGGT
12	8.68e-4	ACACACA CTCTATATCAT TAGCATGTAC
9	8.68e-4	CAGCCATATT GGGAGTATAAAC CCTTCGCCT
4	8.68e-4	CCATGTCGCA GGGTACATAGT A
29	9.74e-4	GGGCAGCCAA CGCGAAGTAGT
22	9.74e-4	G GGCAACGCAGT GACTGGATAT
16	1.34e-3	CA AGGACAGTAGT GAATGCACAT
17	1.70e-3	CAAAGGGTA CGCACAGTGAC CCGGGAT
30	1.97e-3	CAC CGGTGCGCCGT ACAGGTAAC
23	1.97e-3	CATGGCAC CGCTATGCC TGCTGTCTAT
6	2.57e-3	C ACCAAGGTCTC CGCGGCCAGT
24	2.82e-3	CAC CGGTGGACATT GTTGTCTGGG
3	3.88e-3	GGG CTGGACGTCAT CAACCTTCCA
1	4.85e-3	CACACCGTTC AGGAGGATCAG GTAAGCT
18	7.10e-3	GGCTGTT CGCTCCATGTG CCAACCTCCG
27	1.06e-2	TAGGCCTAAA CCCAACACCC AG
7	1.12e-2	CCACA GCCTATGACGT GACATCGCGC

Fig. S2 Sequence alignment result by MEME (<http://meme-suite.org/>).

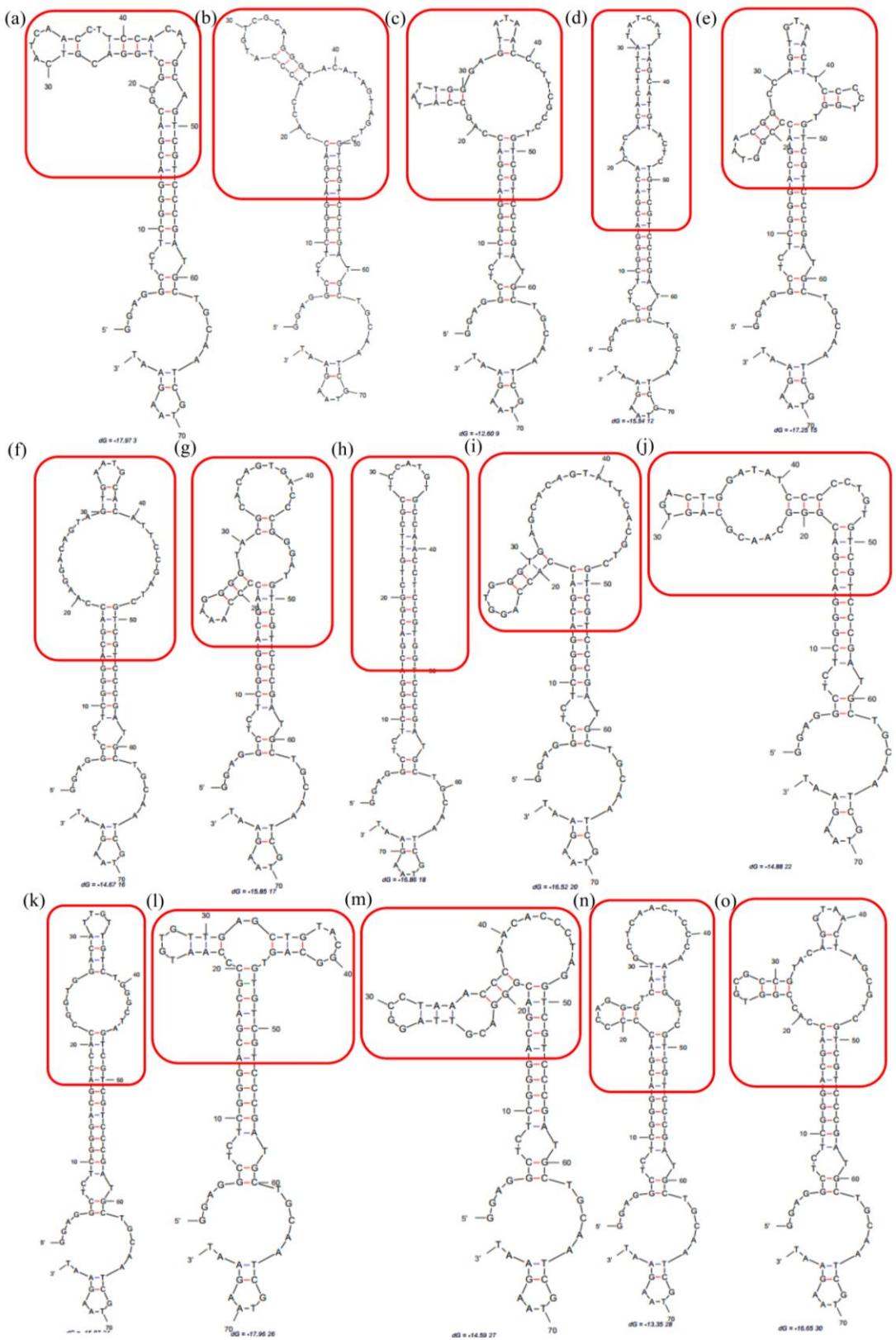


Fig. S3 Predicted secondary structures of CV3 (a), CV4 (b), CV9 (c), CV12 (d), CV15 (e), CV16 (f), CV17 (g), CV18 (h), CV20 (i), CV22 (j), CV24 (k), CV26 (l), CV27 (m), CV28 (n), and CV30 (o) by M-Fold (<http://mfold.rna.albany.edu/>). The

structures in red boxes were retained as their truncated aptamers and named as CV3S (a), CV4S (b), CV9S (c), CV12S (d), CV15S (e), CV16S (f), CV17S (g), CV18S (h), CV20S (i), CV22S (j), CV24S (k), CV26S (l), CV27S (m), CV28S (n), and CV30S (o), respectively.

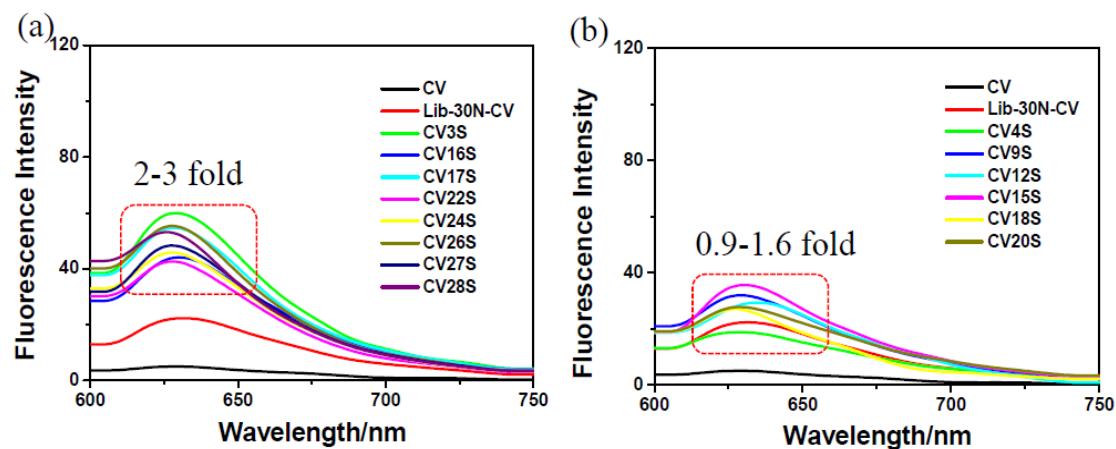


Fig. S4 Fluorescence spectra of crystal violet alone and in the presence of various truncated aptamers in SELEX buffer respectively. The concentrations of crystal violet and aptamers were both 2 μ M.