# Selection and preliminary application of a single stranded DNA 

## aptamer targeted colorectal cancer serum

 Zhao ${ }^{\text {ab }}$

Table S1. Screening parameters of aptamers against the serum targets of colorectal cancer patients through SELEX technique

| Round | Volume of | Amount of | Total amount of | ssDNA |  | Number | Amount of |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | magnetic | the initial | mixed serum | library | Washing buffer | of | recovery |
|  | beads (mL) | ssDNA | after treatment | incubation |  | washing | ssDNA |
|  |  | library ( $\mu \mathrm{g}$ ) | ( $\mu \mathrm{L}$ ) | time (min) |  |  | ( $\mu \mathrm{g}$ ) |
| 1 | 4 | 31.40 | 1000 | 60 | PBS | 3 | 0.52 |
| 2 | 2 | 28.95 | 600 | 60 | PBS | 5 | 0.86 |
| 3 | 2 | 26.49 | 350 | 50 | PBS+0.02\%Tween20 | 3 | 0.94 |
| 4 | 1.8 | 24.68 | 300 | 50 | PBS $+0.02 \%$ Tween 20 | 5 | 1.12 |
| 5 | 1.8 | 22.87 | 275 | 50 | PBS $+0.05 \%$ Tween 20 | 3 | 1.25 |
| 6 | 1.6 | 21.54 | 250 | 40 | PBS+1\%Tween 20 | 3 | 1.48 |
| 7 | 1.6 | 18.65 | 225 | 40 | PBS+1\%Tween20+ | 5 | 1.75 |
|  |  |  |  |  | 0.004\% SWCNT |  |  |
| 8 | 1.5 | 15.32 | 200 | 40 | PBS+1.5\%Tween20+ | 3 | 1.98 |
|  |  |  |  |  | 0.004\% SWCNT |  |  |
| 9 | 1.3 | 12.98 | 175 | 30 | PBS+2\%Tween20 | 5 | 2.55 |
|  |  |  |  |  | +0.008\% SWCNT |  |  |
| 10 | 1 | 12.69 | 150 | 30 | PBS $+2 \%$ Tween 20 | 5 | 2.48 |
|  |  |  |  |  | +0.008\% SWCNT |  |  |



Fig.S1 The recovery rate of each circle during the whole screening process. The amounts of ssDNA recovered in the first 9 rounds were rising up continuously, and there is no evident difference in the 10th round in comparison to the ninth round, which proved the success of the screening. Error bars represent standard deviation from triplicate analysis.


Fig.S2 Gel electrophoresis imaging of PCR amplification products of collected
ssDNA in round 10. The PCR amplification product of collected ssDNA in the colorectal cancer group ran in two parallel 10+ lanes and the PCR amplification product of collected ssDNA in the healthy group ran in two parallel 10- lanes .


Figure S3. Predicted secondary structure of four candidate aptamers in $37^{\circ} \mathrm{C}$
with IDT.

