

Supplementary figures

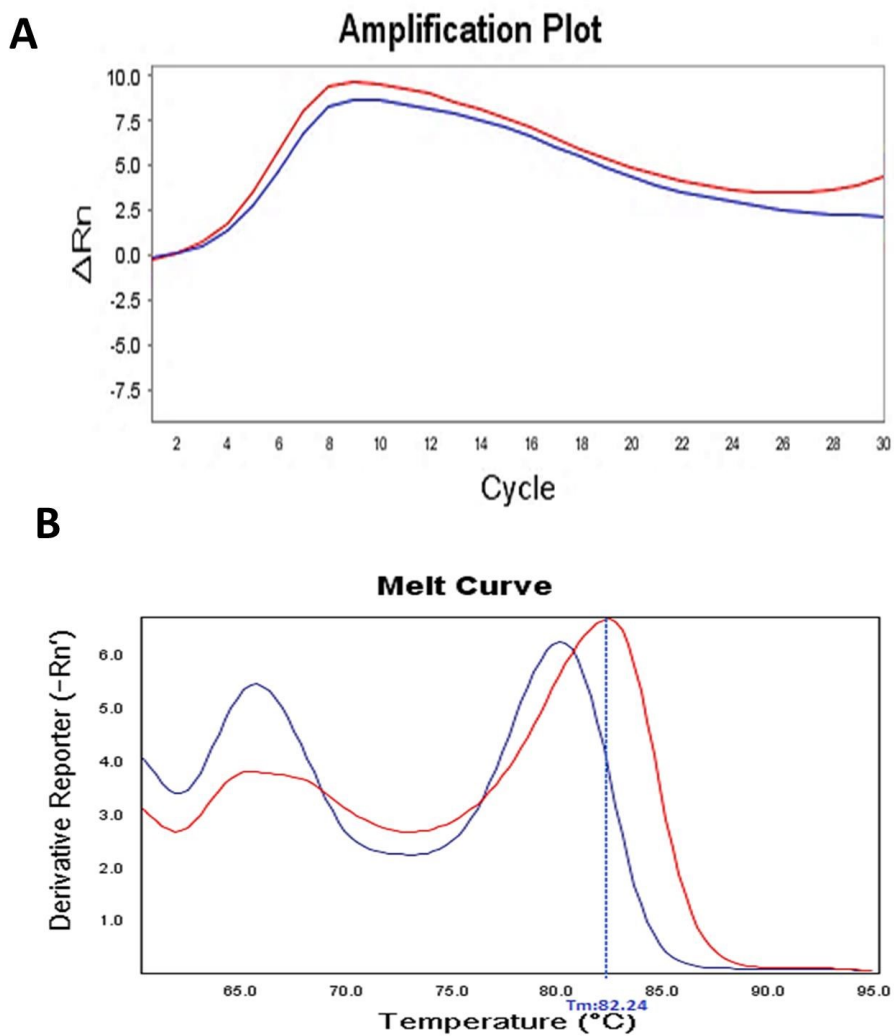


Fig. S1. Amplification (A) and melting (B) patterns of SELEX random library. Twenty-five nanogram of two different SELEX libraries was amplified in Real-Time PCR. The amplification plots of both libraries were characterized by a sudden fluorescent drop after ~ 8 cycles of PCR. The melting curve of both libraries was characterized by two broad and open picks with low T_m .

Supplementary Tables

Table S1. Raw data related to the screening of SELEX enrichment using the UV-Vis spectroscopy method. A defined amount of aptamer pool was used for the initiation of each round. After incubation time and washing steps, the bound aptamers to the immobilized target protein was eluted using 45 μ l of elution buffer. The concentration of the eluted aptamer pool at each round was measured spectrophotometrically at 260 nm using a Nanodrop instrument. The concentrations of recovered ssDNA pools were reasonably high and in the linear dynamic range of the implemented Nanodrop instrument (lower limit of 2.5 ng/ μ l).

SELEX Round	Before incubation	After incubation			
	The initial amount of used aptamer pool (ng)	The volume of elution buffer (μ l)	The concentration of eluted aptamer pool (ng/ μ l)	Total amount of eluted aptamer (ng)	Recovery percentage
1	49500	45	23	1035	2.1
2	1750	45	3	135	7.7
4	1750	45	6	270	15.4
6	1500	45	6	270	18
7	1500	45	8	360	24
8	1500	45	10	450	30
9	1250	45	7	315	25.2
10	1250	45	7	315	25.2

Table S2. Comparison of GC content of cloned aptamer fragments amplified by aptamer primers or pTG19 vector primers. The GC% difference in ~80 bp amplicons is higher compared to ~216 bp amplicons.

Aptamer group	Fragments amplified by aptamer primers		Fragments amplified by pTG19 vector primers	
	Size (bp)	GC %	Size (bp)	GC %
Ap-1	81	59	217	54
Ap-2	79	58	215	54
Ap-3	79	56	215	53
Ap-4	80	54	216	52
Ap-5	80	54	216	52