Electronic Supplementary Information (ESI)

Cell-SELEX based selection and optimization of DNA aptamers for specifically recognition of human cholangiocarcinoma QBC-939 cells

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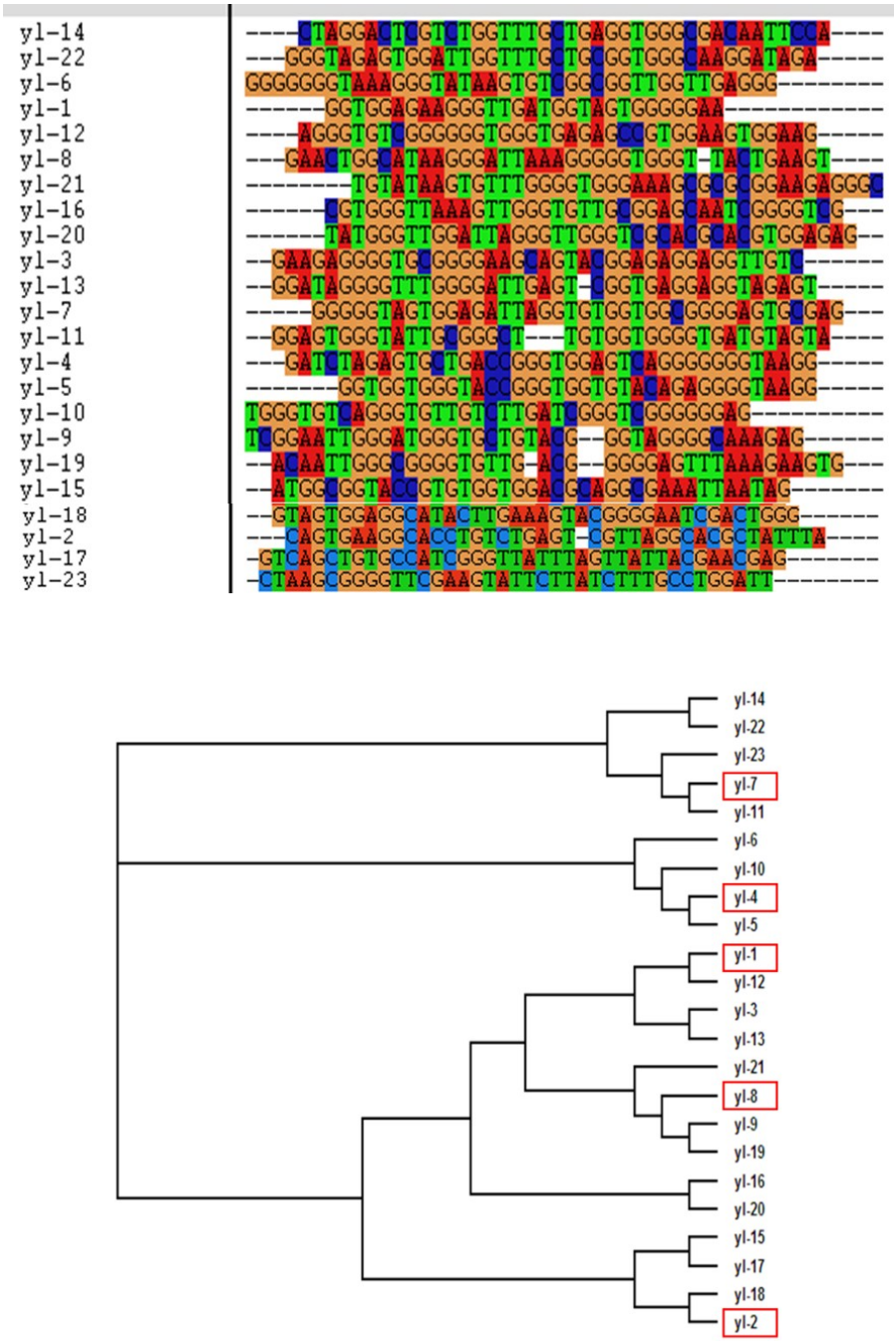

Fig. S1. Homology analysis of sequences using Clustal X. Sequences with the highest abundance in each family, yl1, yl2, yl4, yl7 and yl8 (marked with red box), were chosen as representatives and synthesized for further analysis.

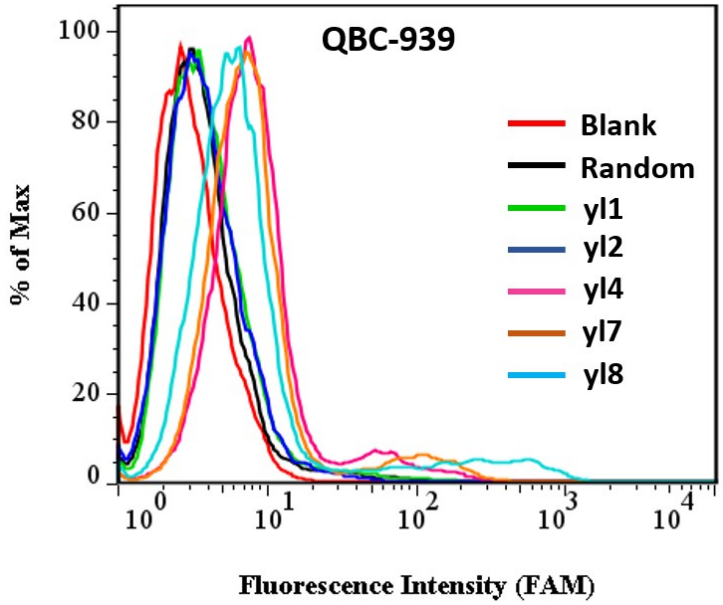

Fig. S2. Recognition of the QBC-939 cells with aptamer candidates. Flow cytometry was used to evaluate the binding ability of selected sequences (yl1, yl2, yl4, yl7 and yl8) to target cell line QBC-939, random sequence was used as control. These five sequences exhibited no binding ability or only very weak binding capacity to target QBC-939 cells.

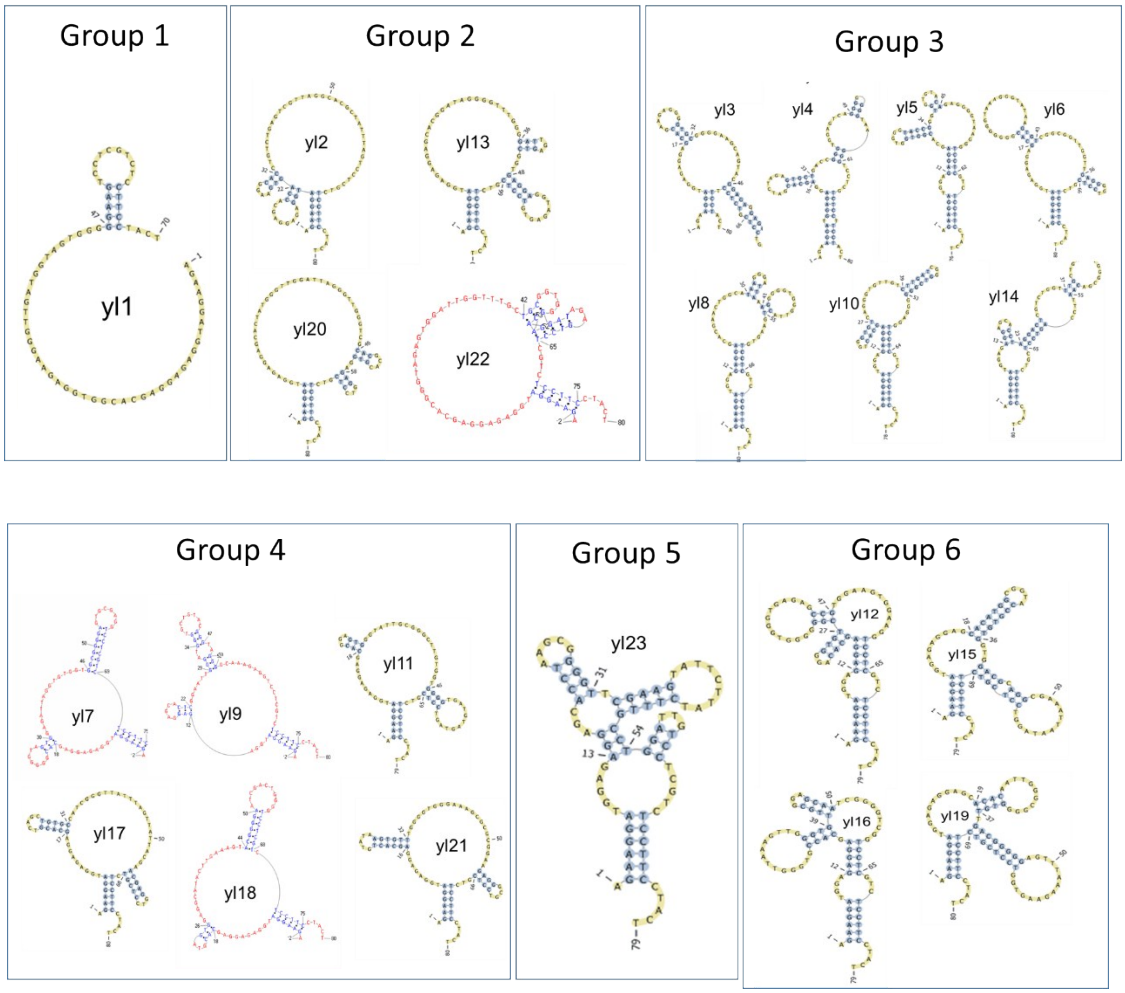

Fig. S3. Secondary structure analysis of the sequences. The 23 sequences were divided into six groups based on their presented motifs.

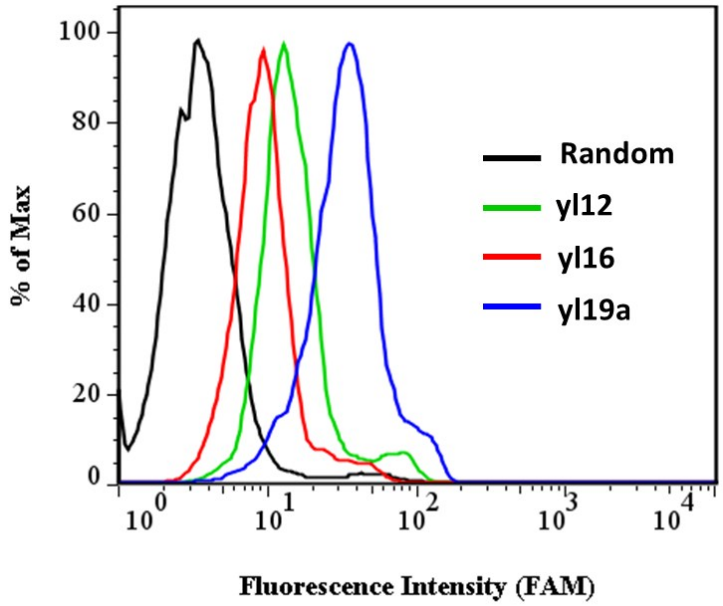

Fig. S4. Recognition of the QBC-939 cells with aptamer candidates. Sequences in Group 6 (yl12, yl16 and yl19) for their binding ability toward target QBC-939 cells. Comparing to yl19a, yl12 and yl16 only exhibited very weak target binding ability.

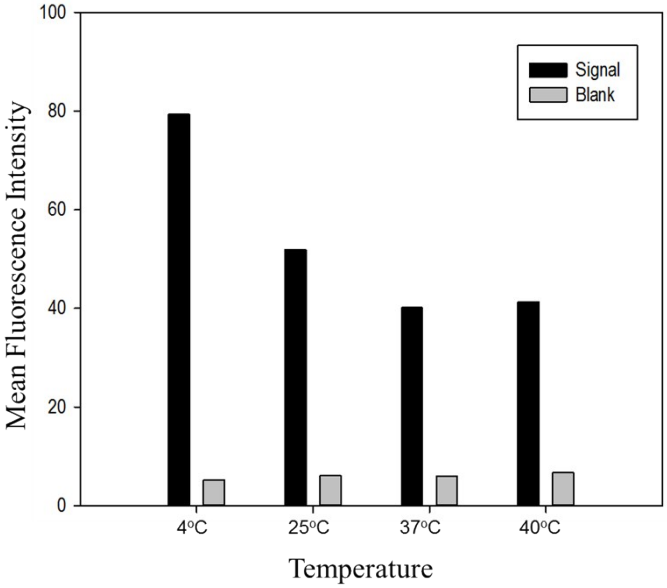

Fig. S5. Investigation on temperature's effect on the recognition ability of aptamer yl19a. The binding of the truncated sequence yl19a to target QBC-939 cells were tested at different temperatures 4 °C , 25 °C, 37 °C and 40 °C, fluorescence intensity was recorded using flow cytometry.