

Supplementary Materials

1. Figures legends

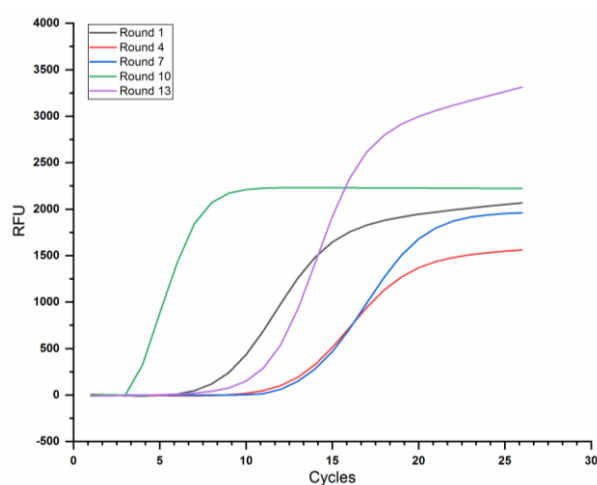


Figure S1 Amplification curve of qPCR for each round of selection.

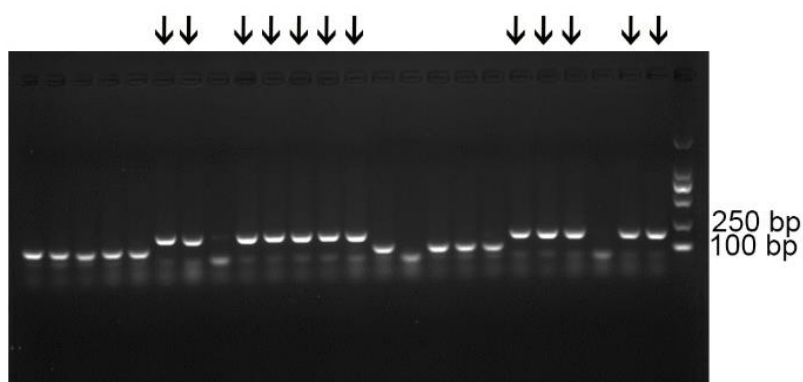


Figure S2 Identification of positive clones by electrophoresis. Arrows mean the clones with right insertions.

2. Table legend

Table S1 Seventeen of post round 13 library clones were sequenced and analyzed for consensus sequence family

Item	Sequence (5'-3')	dG (kcal/mol)
DDT_02	<u>TCCAGCACTCCACGCATAA</u> <u>AC</u> AGTTCGAGGCAACAAGGCTGATCAGTCTGATGTTGAAATGTTATGCGTGCGACGGTGAA	-41.3
DDT_03	<u>TCCAGCACTCCACGCATAA</u> <u>ACCGTCCACTGCTCGAATACAGCTTCGTCTCTTGCCAAGTGTGTTATGCGTGCGACGGTGAA</u>	-34.71
DDT_06	<u>TCCAGCACTCCACGCATAA</u> <u>ACCGCGCCACTCCAGAGAGTACATTCCAGTTCGGCCACATTTGGTTATGCGTGCGACGGTGAA</u>	-36.50
DDT_08	<u>TCCAGCACTCCACGCATAA</u> <u>CCACCACCGACAATAACCTTCGCGGAACAAACTGGGGTCTCGTTATGCGTGCGACGGTGAA</u>	-35.97
DDT_10	<u>TCCAGCACTCCACGCATAA</u> <u>CCCAGGCGCACACTCGTTCCACTCTCAGTTAAGCAAACCGTGTTATGCGTGCGACGGTGAA</u>	-32.15
DDT_13	<u>TCCAGCACTCCACGCATAA</u> <u>CGAATTGTGCTCAATGCGCCCCTGCAGTGAATGTGGAATTTGTTATGCGTGCGACGGTGAA</u>	-42.42
DDT_14	<u>TCCAGCACTCCACGCATAA</u> <u>CCACCCACGTAAGTGCATAAAGAATTGGTCATCGTTTCCCCGTTATGCGTGCGACGGTGAA</u>	-34.01
DDT_16	<u>TCCAGCACTCCACGCATAA</u> <u>CCACGCCGTCCGTCATACACGCTCCGTCAACACGTCCTTCTGGTTATGCGTGCGACGGTGAA</u>	-36.57
DDT_18	<u>TCCAGCACTCCACGCATAA</u> <u>CCGCCGTACTTACTACTCTGCCACCAATAACATGCACTACCCGTTATGCGTGCGACGGTGAA</u>	-29.32
DDT_19	<u>TCCAGCACTCCACGCATAA</u> <u>CCGACCAACTGTCTCGTGGTTGGTTCCGACTACTCAGCTCGGTTATGCGTGCGACGGTGAA</u>	-41.04
DDT_23	<u>TCCAGCACTCCACGCATAA</u> <u>CTGGCAACAACATTCGCTACGACCTGAAGCTCCTGACCTTTGTTATGCGTGCGACGGTGAA</u>	-34.38
DDT_24	<u>TCCAGCACTCCACGCATAA</u> <u>CCGCCAGATAGCCTGAACGATCGACAGTGAATCACCTCAGTTATGCGTGCGACGGTGAA</u>	-33.00
DDT_26	<u>TCCAGCACTCCACGCATAA</u> <u>CCGCAAGGTGGGTCCGACCTTTCCCCGTTATACAGACGTCGTTATGCGTGCGACGGTGAA</u>	-34.97
DDT_27	<u>TCCAGCACTCCACGCATAA</u> <u>CGAAGACATGCCCCGCAATGGATGTTGTTGGACCTGTTTGAGTTATGCGTGCGACGGTGAA</u>	-35.66
DDT_28	<u>TCCAGCACTCCACGCATAA</u> <u>CCGATCGCACCCTCGTGTCAATTGGATTCCACTAGGCCCGGTTATGCGTGCGACGGTGAA</u>	-39.08
DDT_34	<u>TCCAGCACTCCACGCATAA</u> <u>CCAGGACCGACCCCGCAGACTACAAAGTGTCACTAAGCAATGTTATGCGTGCGACGGTGAA</u>	-31.67
DDT_35	<u>TCCAGCACTCCACGCATAA</u> <u>CCCACAATCCAAGCCGTCCATCAATGCGGTTATCCATCCTGTTATGCGTGCGACGGTGAA</u>	-31.60

Notes: Sequence with under lines were primer binding sites; Sequences marked with Red color were selected for further analysis.