Supporting Information

Selection of aptamers against live bacterial cells

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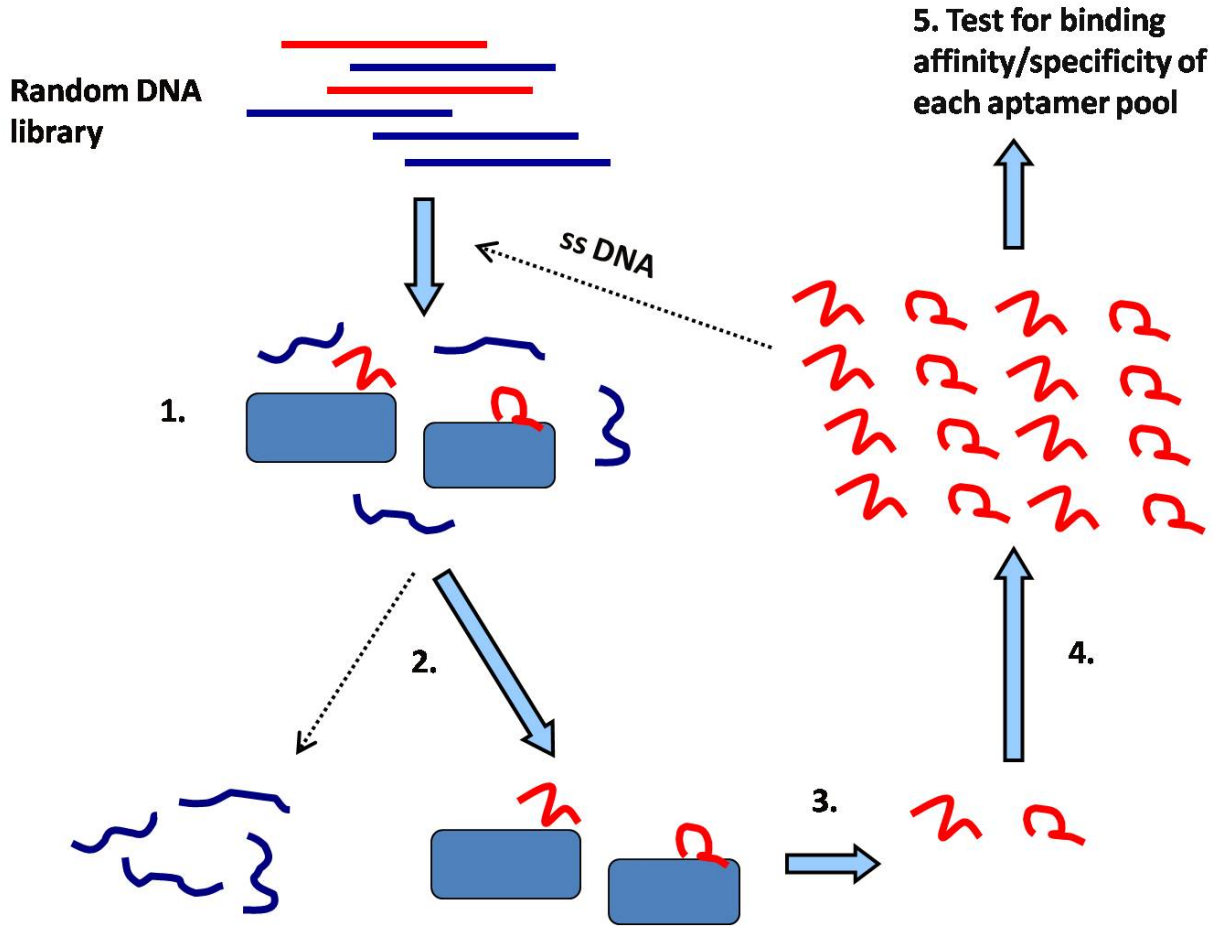


Figure S1. Schematic showing the main steps for the selection of aptamers against live bacterial cells. Step 1: Incubate a DNA library of 10^{15} random sequences with live bacterial cells. Step 2: Separate the DNA sequences bound to the cells from the unbound DNA sequences by centrifugation. Wash the cells three times to remove the weakly bound DNA sequences. Step 3: Release the bound DNA from the cell surface by heating and elution. Step 4: Amplify the DNA sequences eluted from the cells. Use this pool of DNA for the next round of selection starting from Step 1. Step 5: Test the binding of selected pool of DNA for the target cells prior to cloning and sequencing the selected DNA aptamers.

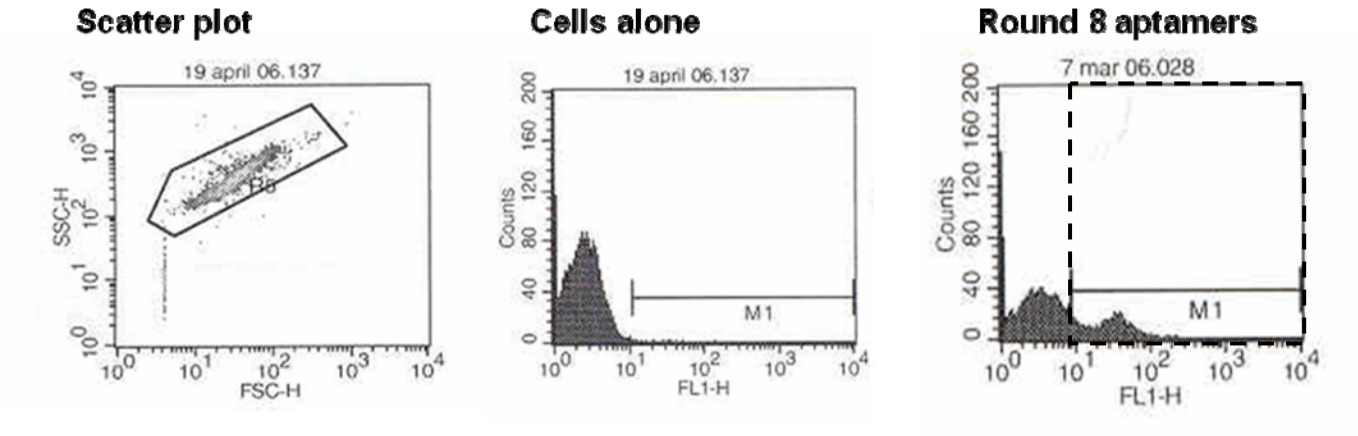


Figure S2. Typical flow cytometry outputs from screening of aptamer pools, showing increase in gated fluorescence intensity above background (boxed area) following incubation with round 8 aptamer pool. The aptamer pools were fluorescently-labeled via PCR amplification with 5'-FAM and were heat denatured. Approximately 10^7 *L. acidophilus* 4356 cells were either suspended in the binding buffer (central graph) or incubated with 100 pmol of fluorescently-labeled aptamer pool (from round 8) for 45 min in the binding buffer (right graph). The cells were washed once in the binding buffer containing 0.05% BSA prior to resuspension in the binding buffer for immediate flow cytometric analysis. Forward scatter (FSC-H), side scatter (SSC-H), and fluorescence intensity (FL1-H) were measured. The central graph shows the background fluorescence from the cells without incubation with the aptamer pool. The gated fluorescence intensity above background (the boxed area in the right graph) from the analysis of the cells incubated with the fluorescently-labeled aptamer pool was quantified.

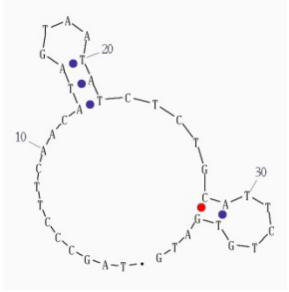
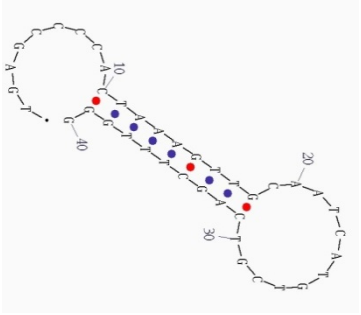
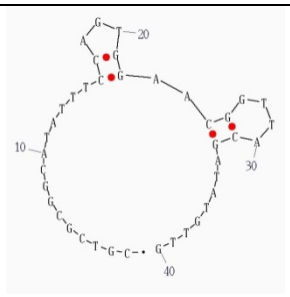
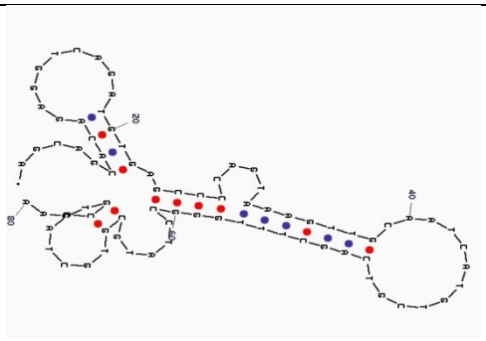
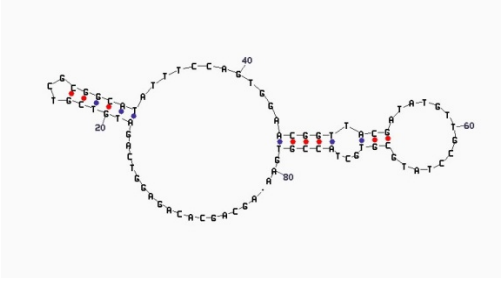
hemag1	
mag1	
hemag3	
mag1P	
hemag3P	

Figure S3. Predicted most energetically favorable secondary structures of some selected aptamer sequences.

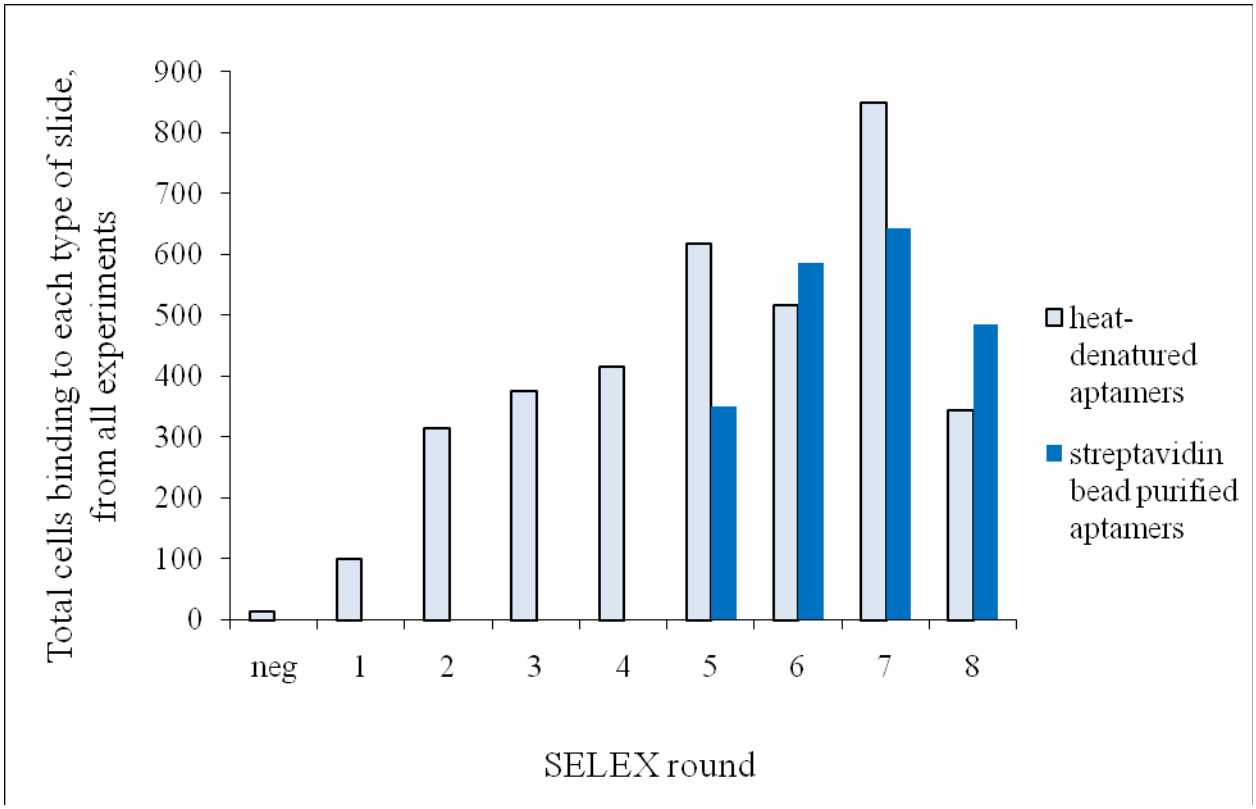


Figure S4. Total number of *L. acidophilus* 4356 cells binding to slides coated with aptamer pools. Each bar in the graph represents the sum of total cells counted from 10 separate microscope fields of view (5 fields of view from each of the duplicate slides). The area of each field of view is 2 cm^2 .