Supporting Information for

Corresponding V-Target Lattice Structure to Enhance Selection Pressure for Aptamers Selection

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S.1 Detailed Parameters of the Three Structures

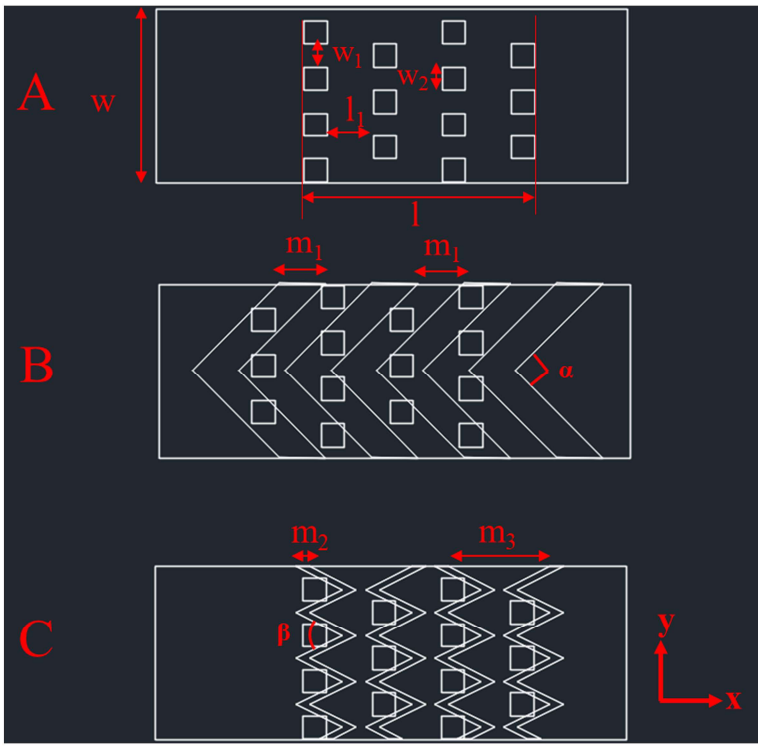

Fig. S1 Top views of the three channel models with no structure (A), with forward herringbone structure (B) and with corresponding V-shaped structure (C).

In Fig. S1, the width (w) of the chip with three channel structures is 800 μm and the height was 50 μm. The target array area of the three structures is consistent, containing 30×8 lattices, each of which is 50 μm long and wide and 20 μm high. The distance (w1) between two adjacent lattices on the Y- dimension is 50 μm, and the distance (l1) between two adjacent lattices on the X- dimension is 100μm, and the length (l) of the whole array area is 4.4 mm (Fig. S1A). The height of the forward herringbone structure is 20 μm, the width (m1) of the arms and the distance (m1) between the

arms are 100 μm, and the angle (α) between the two arms is 90° (Fig. S1B). The height of the corresponding V-shaped structure is 20 μm, the width (m2) of the arms is 30 μm, the distance (m3) between the arms is 120 μm, and the angle (β) between the two arms is 53° (Fig. S1C).

S.2. Velocity and Vorticity Distributions of Different Cross-sections with Different Structures

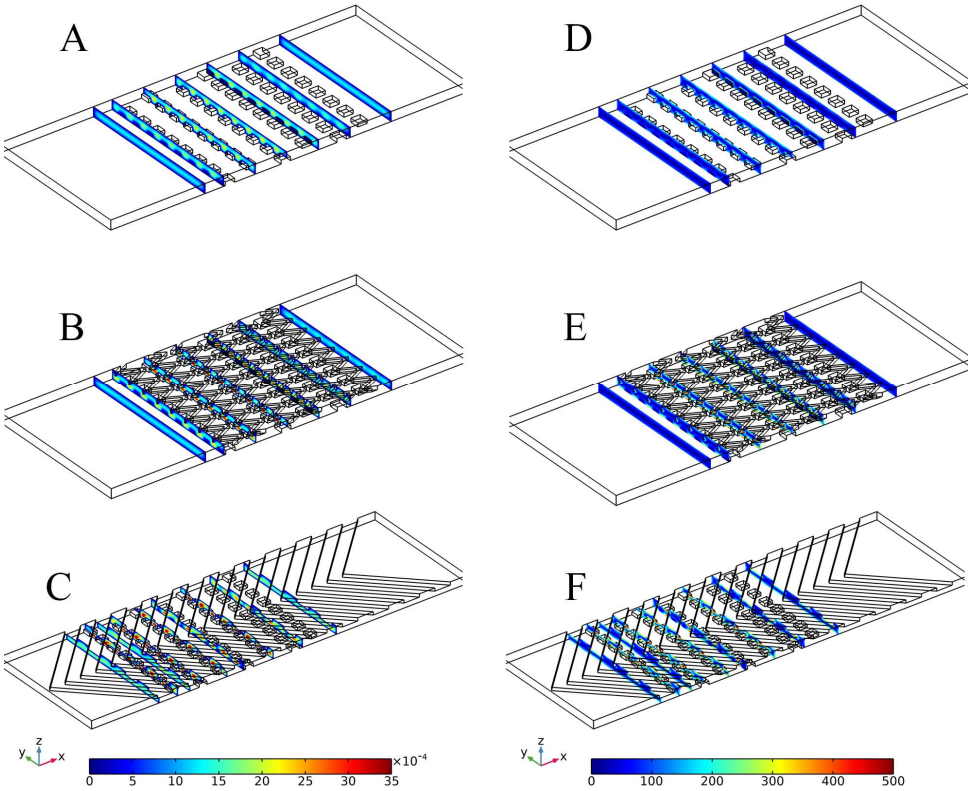

Fig. S2 Velocity field distribution of different cross-sections in the channel with no superstructure (A), with the corresponding V-shaped structure (B) and with the forward herringbone structure (C). The scale unit of velocity field is $m \cdot s^{-1}$. Vorticity field distribution of different cross-sections in the channel with no superstructure (D), with the corresponding V-shaped structure (E) and with the forward herringbone structure (F). The scale unit of vorticity field is s^{-1}.

S.3 Characterization of the Microfluidic Chip with the Corresponding V-Lattice Structure

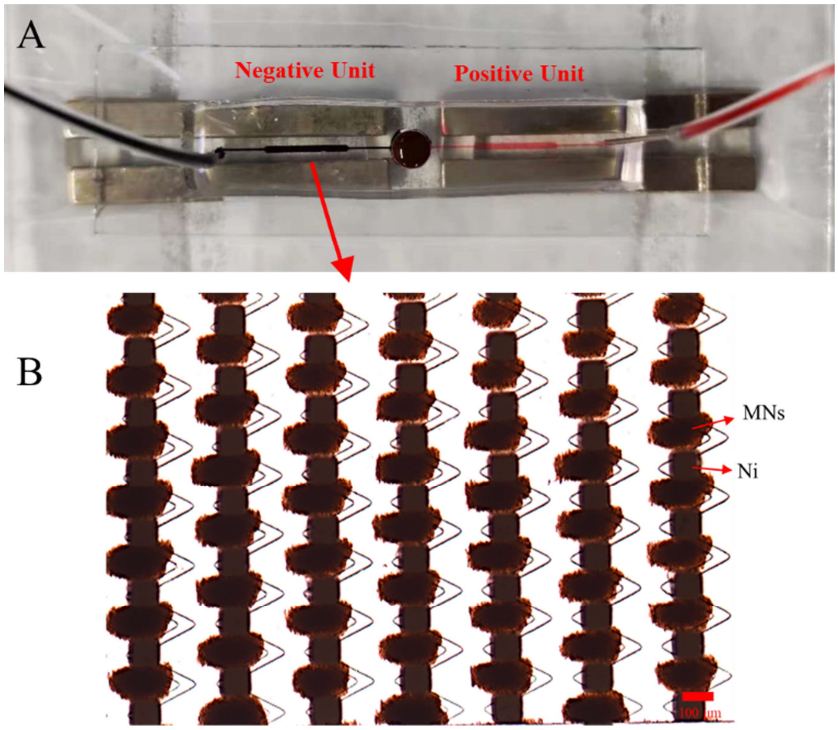

Fig. S3 (A) Photograph of the microfluidic chip with the corresponding V-lattice structure. (B) Microscopic image of MNs-HA captured by the microfluidic chip with the corresponding V-lattice structure.

S.4 Characterization of HA Protein Coated MNs

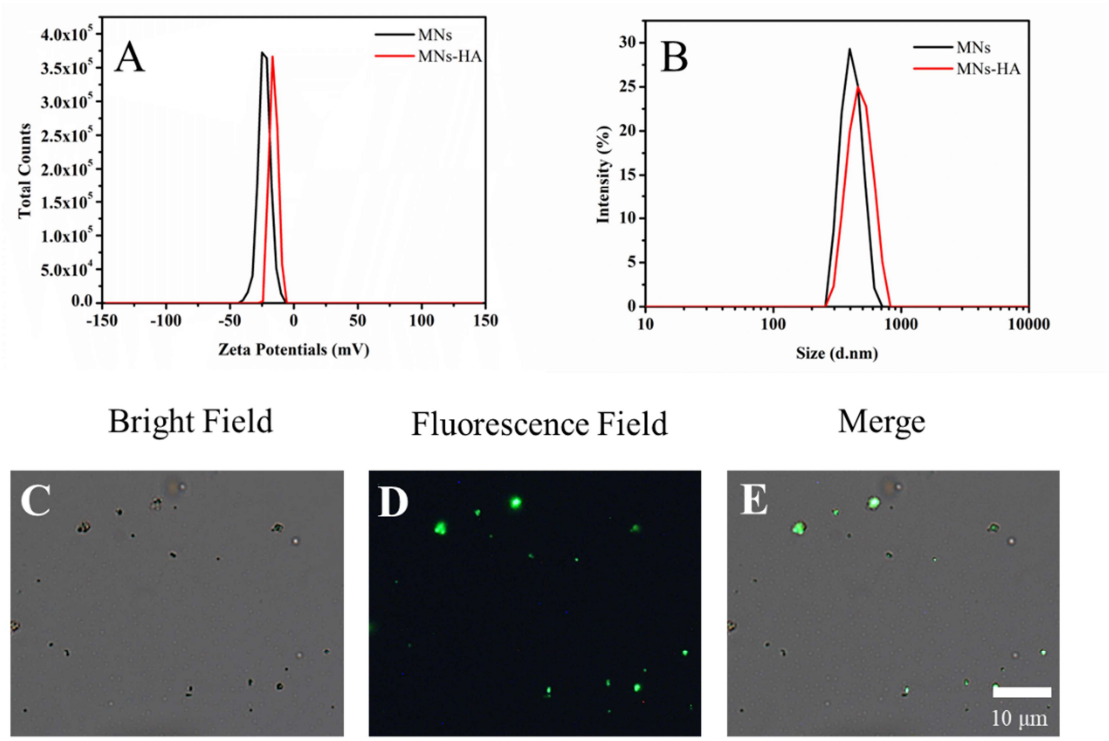

Fig. S4 (A) Zeta (ζ) potential of MNs and MNs-HA-H5N1. (B) Hydrodynamic size of MNs and MNs-HA-H5N1. (C-D) Microscopic image of MNs-HA-H5N1 incubating with influenza A H5N1 HA antibody (mouse Mab) and Goat Anti-Mouse IgG-Alexa Fluor 488.

S.5 Preparation of the Evolved ssDNA Libraries

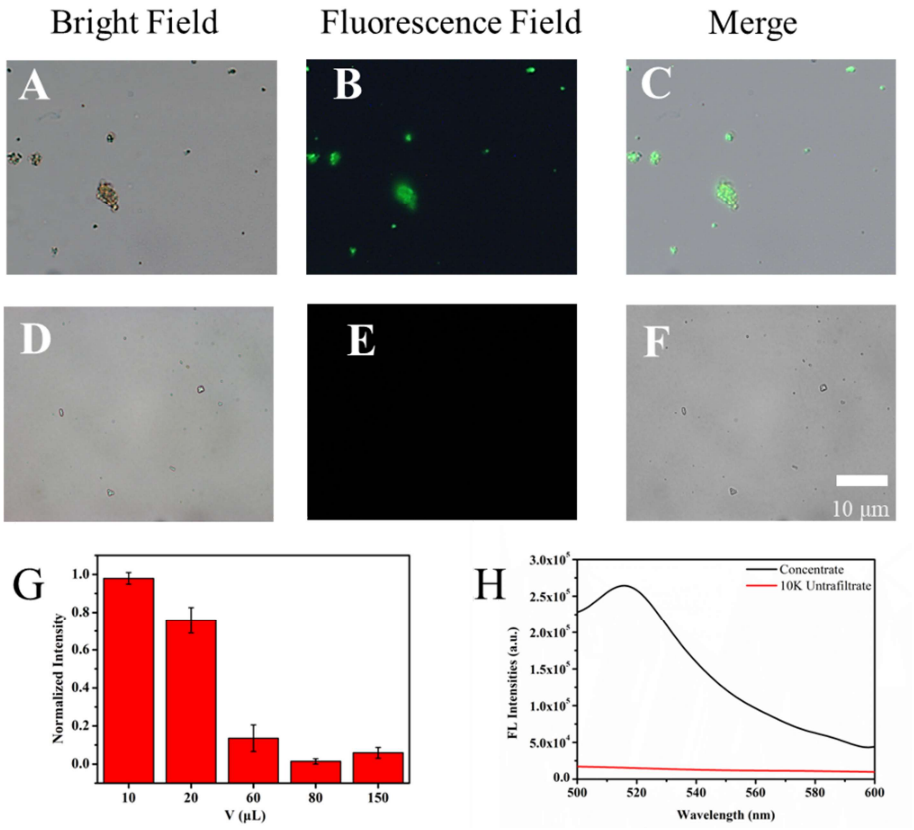

Fig. S5 (A-C) Microscopic image of amplification products captured by MNs-SA. (D-F) Microscopic image of MNs-SA-biotin-DNA treated with NaOH. (G) Optimization of MNs-SA amount during capturing the biotin modified PCR products. Error bars correspond to standard deviation (n=3) (H) Purification of the evolved libraries by a 10K ultrafiltration tube.

S.6 Characterization of the Obtained Sequences

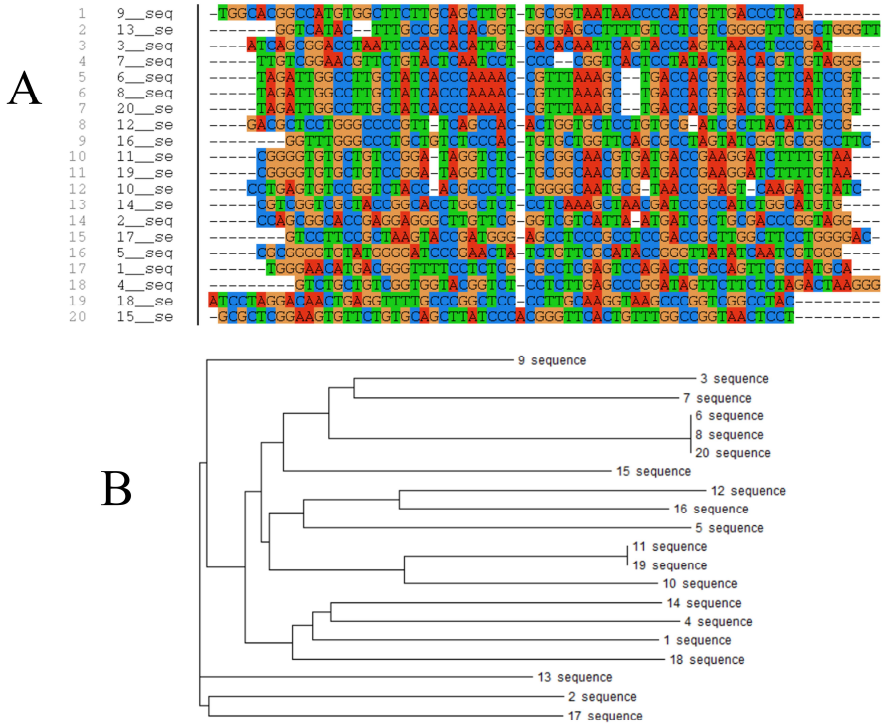

Fig. S6 (A) Sequences analysis after three rounds of selection. (B) Phylogenetic tree of the obtained sequences.

S.7 Characterization of Aptamers

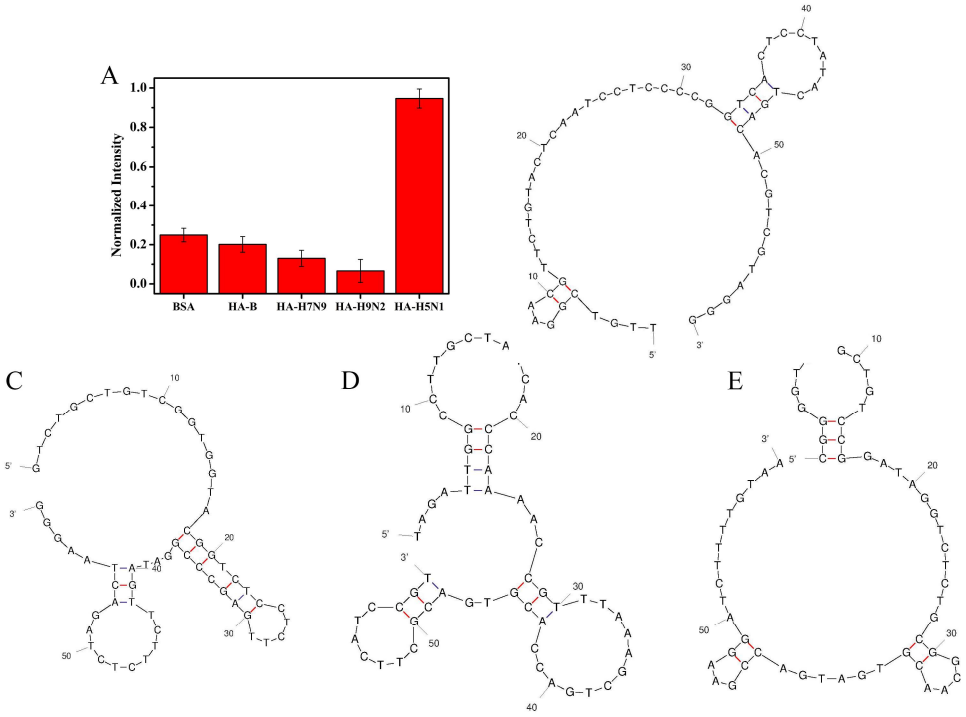

Fig. S7 (A) Specificity of 7-aptamer for HA-H5N1. Error bars correspond to standard deviation (n=3). (B-E) Secondary structure analysis of 7-aptamer, 4-aptamer, 6-aptamer, 11-aptamer.

Movie S1. Oblique View of the Particle Moving Trajectory without Superstructure

Movie S2. Side View of the Particle Moving Trajectory without Superstructure

Movie S3. Oblique View of the Particle Moving Trajectory with the Corresponding V-Lattice Structure

Movie S4. Side View of the Particle Moving Trajectory with the Corresponding V-Lattice Structure

By releasing 100 particles in the channel, velocity field and particle trajectories were coupled. Then the particle trajectories in the channel at different times were obtained by solving Navier-Stokes equations in transient state. An arrow represented a particle, the length of the arrow represented the particle of the velocity, and the direction of the arrow represented the direction in which the particle was moving.