Supporting Information

Programmable DNA Self-assemblies for Nanoscale Organization of Ligands and Proteins by Sung Ha Park, Peng Yin, Yan Liu, John H. Reif, Thomas H. LaBean, and Hao Yan.

Supporting Figures:

Figure S1. Strand structure and DNA sequences used in 2D nanogrid construction in Figure 1, (a) to (c) and Figure 2. Here, (a) and (b) are for the tile A and tile B, respectively. Each tile consists of nine different strands indicated by different colors. The black dots on the NG_A_loop and NG_B_loop strands indicate the site of biotin modification. Biotin functionalization was incorporated during oligonucleotide synthesis as an internal biotin-dT monomer (www.idtdna.com). For A and B tile, there is no biotin. For A* and B*, the loop strand contains biotin.



(a) NG A Tile



Figure S2. Strand structures and DNA sequences used for the 1D nanotrack construction used in Figures 1, (d) to (f) and Figure 3. Here, (a) and (b) are the structures of nanotrack A and B tiles containing base sequences, respectively. Each tile consists of nine different strands indicated by different colors. Black dots in the NT_A_loop and NT_B_loop strands indicate possible biotin sites. Biotin functionalization was incorporated during oligonucleotide synthesis as an internal biotin-dT monomer (www.idtdna.com). For A and B tile, there is no biotin. For A* and B*, the strand contains biotin.





Figure S3. (a) Schematic diagram of the unit tiles of the nanogrid. Here, the sticky-end *1* complements with *1'*, *2* to *2'* etc with pairs shown in matching colors. The center of the A tile is shown in blue and the B tile is shown in red. (b) Schematic drawing of the nanogrid showing the corrugation pattern and alternation of wide and narrow grid spacing. A tiles are in blue, B tiles in red, solid colors represent tiles facing in the orientation as in (a), while cross-hatched colors represent tiles which have been flipped over so the side which was facing into the page is now facing out of the page. It can be seen that neighboring tiles each need to be both flipped relative to the plane and rotated within the plane in order to properly match their sticky-end pairs. This arrangement results in a corrugation scheme in which A tiles and B tiles both occur in flipped orientations within the plane of the lattice. (c) Section profiles of AFM images of the nanogrid. After formation of the nanogrid, we observe alternating rows of different sized grid spacing, 19.3 and 17.6 nm which correspond to 4.5 full-turns and 4 full-turns, respectively, in excellent agreement with the designed structure.



Figure S4. (a) Schematic diagram of the unit tiles of the nanotrack. Here, the sticky-end complements with 1', 2 to 2' etc.. In contrast, a, b, c, and d are non-complementary sticky end pairs. Color coding and corrugation scheme are as described for Figure S3. (b) After formation of the nanotrack, we observe only one size of grid spacing 19.3 nm which corresponds to 4.5 full-turns of double helix. (c) Section profile of the nanotrack. Average spacing is about 19.5 nm, in very close agreement with the design.



Figure S5. Wider area AFM scans (2 x 2 micrometers) of AB nanogrid (left panel) and AB nanotrack (right panel) showing reproducibility of target structures. Following sample binding to mica, it was observed that DNA nanostructure was bound almost everywhere on the surface. These large area scans show that the vast majority of DNA in each sample could be found in the desired structure.

