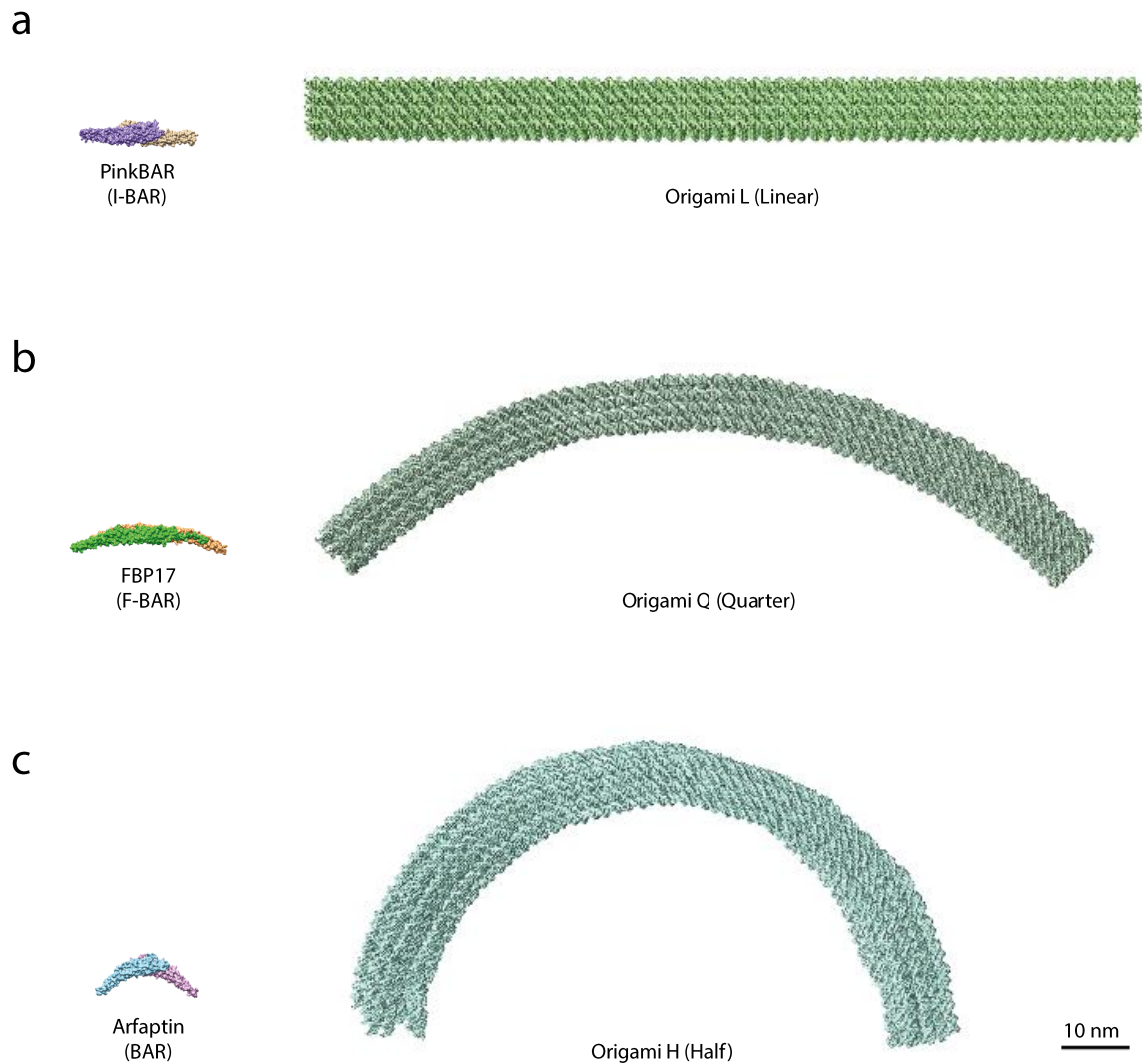
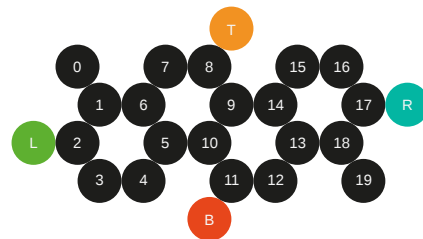


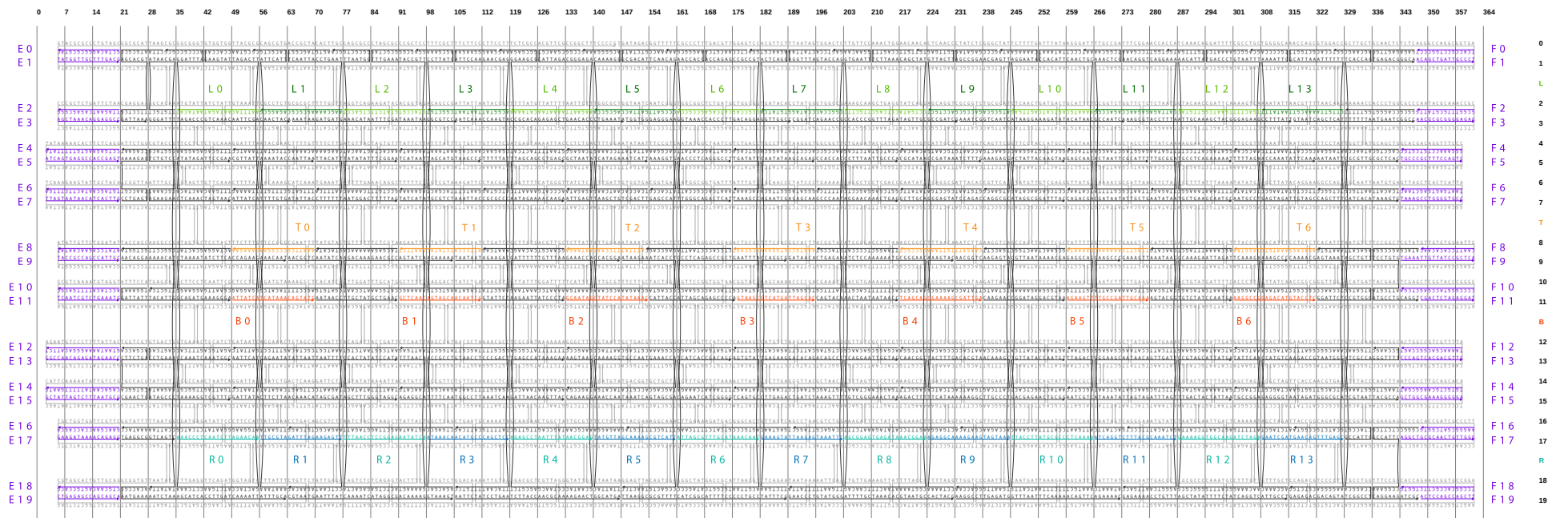


Supplementary Figure 1

Size comparison between BAR proteins and the designed BAR-mimicking DNA origami nanoscaffolds. (a) DNA origami L aims to mimic the shape of flat I-BAR domain proteins, such as PinkBAR; (b) origami Q aims to mimic the shape of moderately-curved F-BAR domain proteins, such as FBP17; and (c) origami H aims to mimic the shape of highly-curved BAR domain proteins, such as Arfaptin. When compared to BAR dimers, our DNA origami structures have at least a 5-fold increased length and 20-fold increased concave surface area. Scale bar: 10 nm.

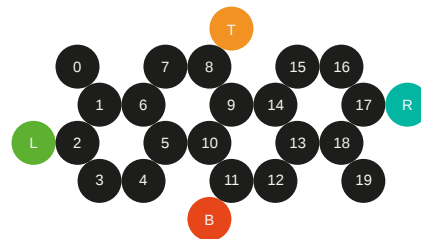


Origami L

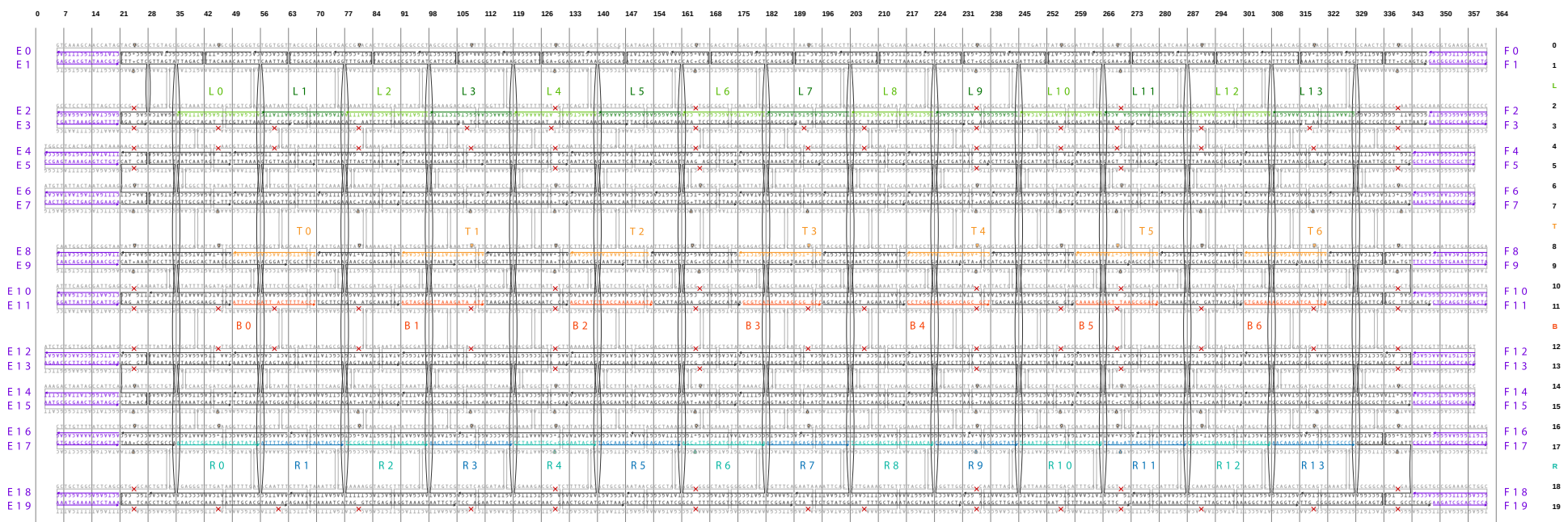


Supplementary Figure 2

Cadnano design and oligonucleotide sequences of the non-curved DNA origami structure L. Top positions T0-T7 are colored in gold, while bottom positions B0-B7 are colored in dark orange. Lateral positions L0-L13 and R0-R13 are colored in green and blue, respectively. Edge positions E0-E19 and F0-F19 are colored in purple. Core staples are colored in black; M13 p7249 scaffold is colored in grey. List of DNA staples can be found in Supplementary Table 1. Additional list of functional staples utilized can be found in appendix (see Supplementary Notes).

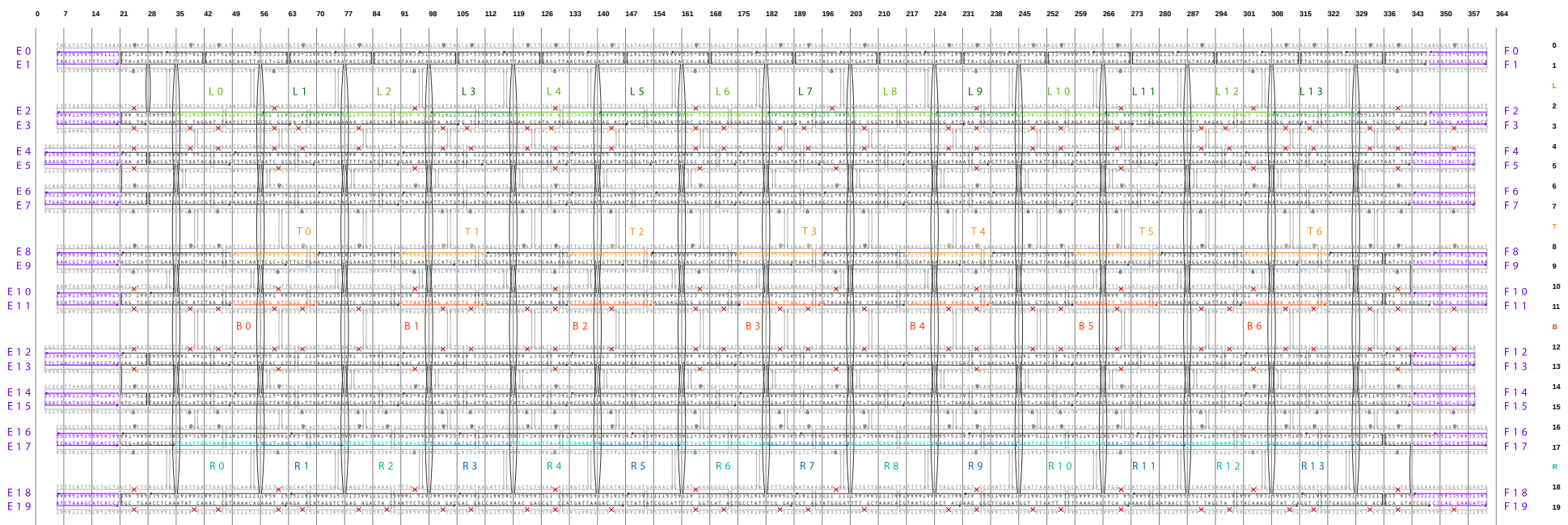
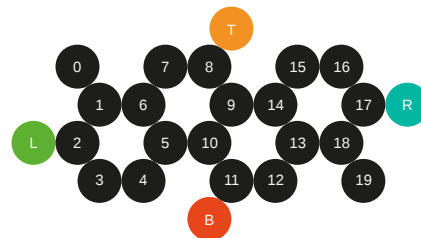


Origami Q



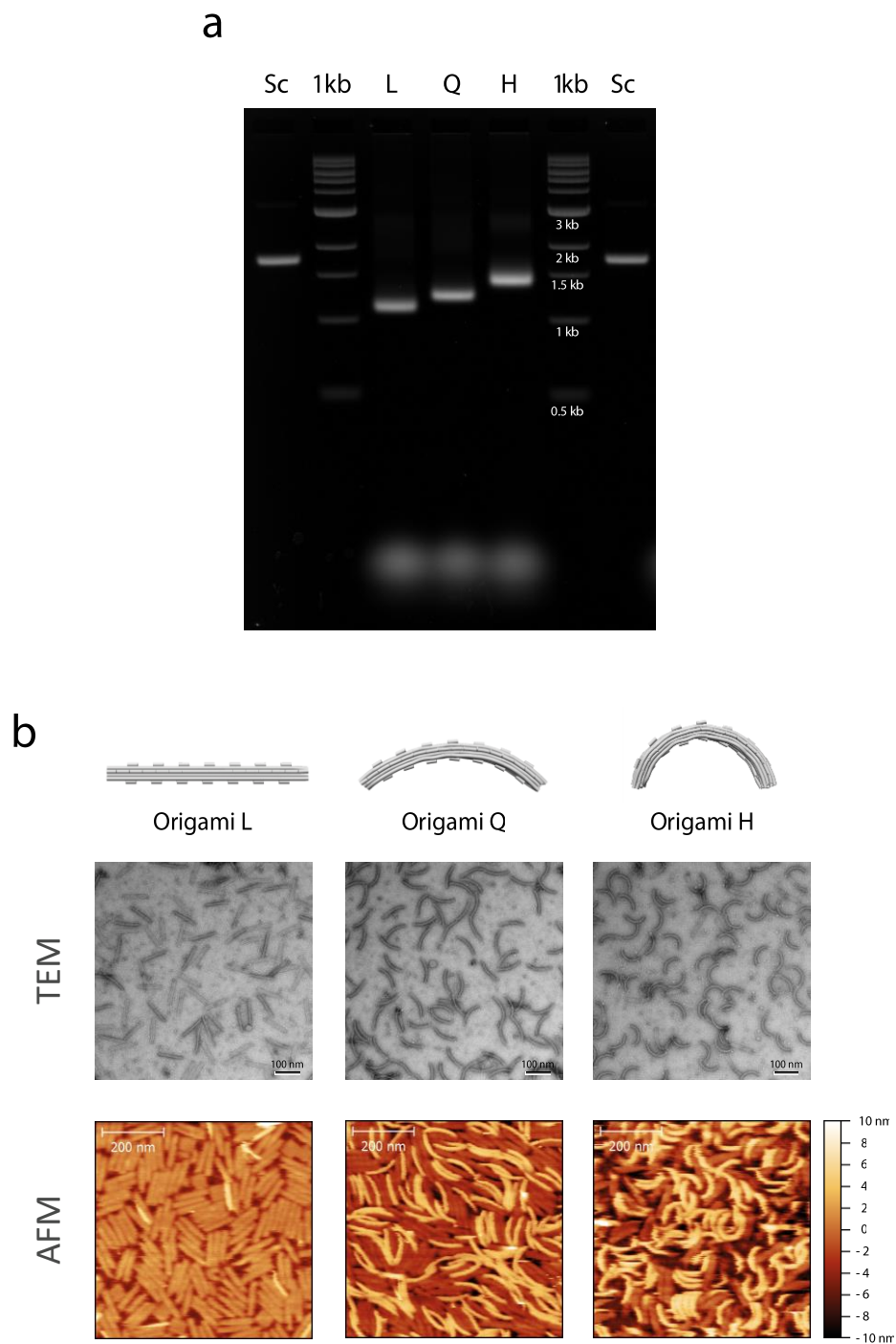
Supplementary Figure 3

Cadnano design and oligonucleotide sequences of the moderately-curved DNA origami structure Q. Top positions T0-T7 are colored in gold, while bottom positions B0-B7 are colored in dark orange. Lateral positions L0-L13 and R0-R13 are colored in green and blue, respectively. Edge positions E0-E19 and F0-F19 are colored in purple. Core staples are colored in black; M13 p7249 scaffold is colored in grey. List of DNA staples can be found in Supplementary Table 2. Additional list of functional staples utilized can be found in appendix (see Supplementary Notes).



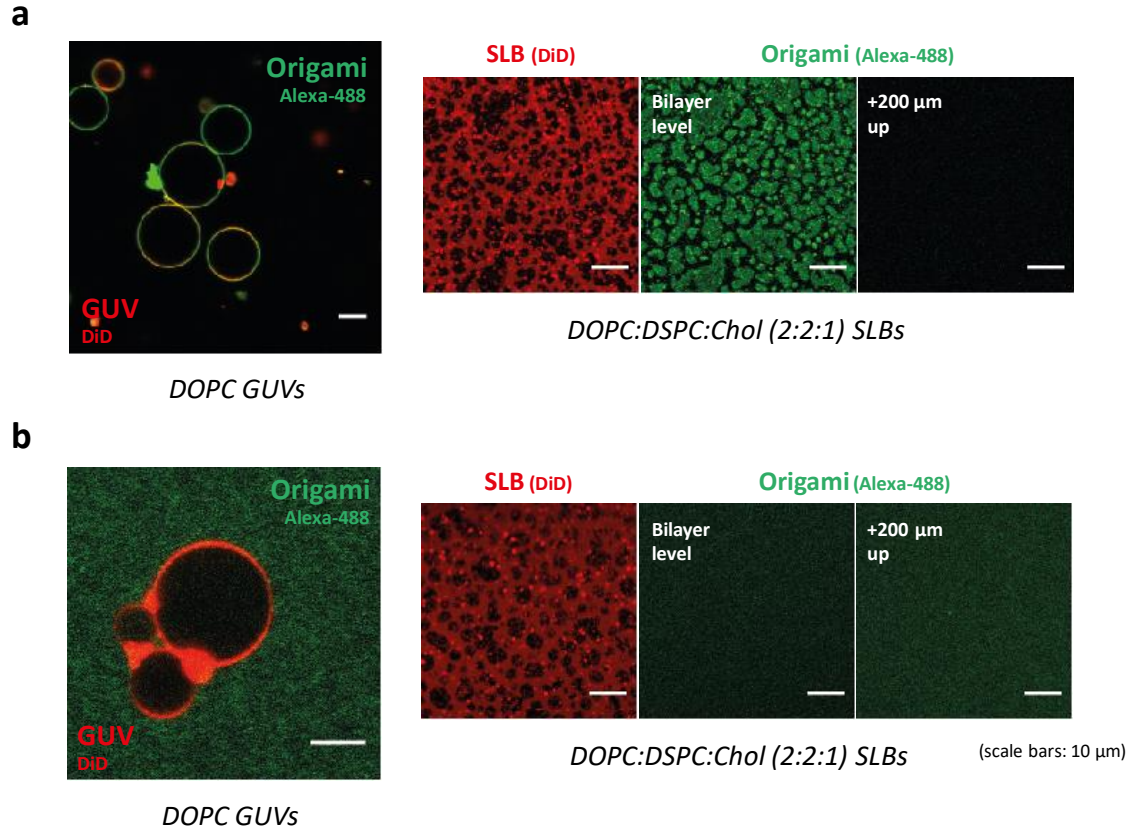
Supplementary Figure 4

Cadnano design and oligonucleotide sequences of the highly-curved DNA origami structure H. Top positions T0-T7 are colored in gold, while bottom positions B0-B7 are colored in dark orange. Lateral positions L0-L13 and R0-R13 are colored in green and blue, respectively. Edge positions E0-E19 and F0-F19 are colored in purple. Core staples are colored in black; M13 p7249 scaffold is colored in grey. List of DNA staples can be found in Supplementary Table 3. Additional list of functional staples utilized can be found in appendix (see Supplementary Notes).



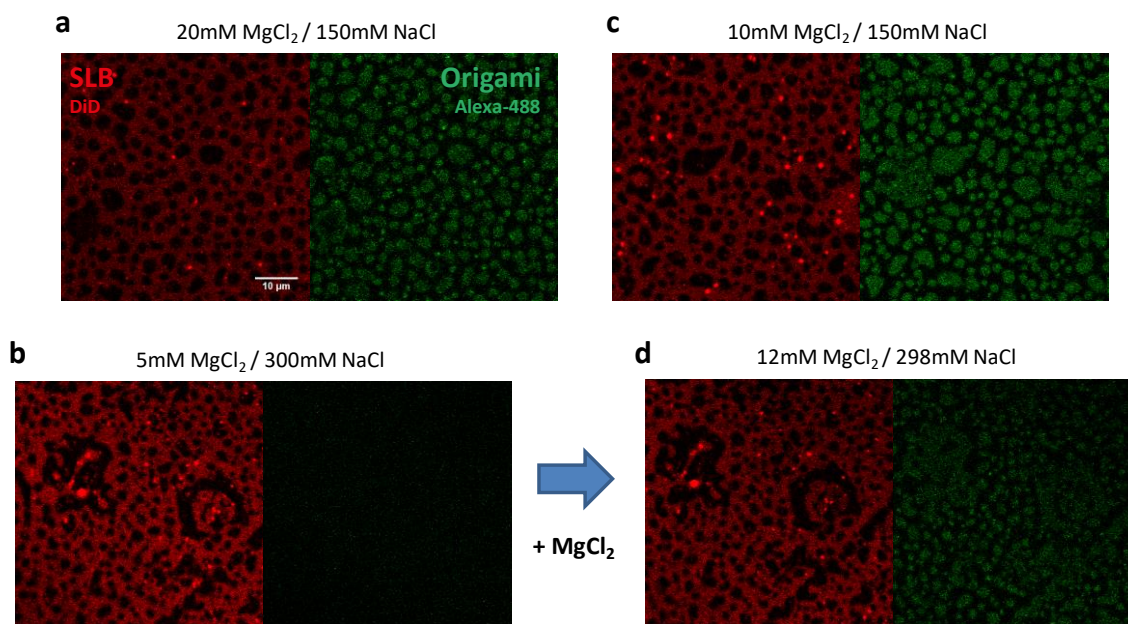
Supplementary Figure 5

Characterization of folded DNA origami nanoscaffolds. (a) Assembly of the folded bare origami structures L, Q, H was initially assessed via agarose gel (2%) electrophoresis analysis. Lanes containing marker DNA ladder (1kb) and M13 single-stranded p7249 scaffold (Sc) were also included. (b) Structure of folded bare origami L, Q and H was further validated using negative-stain transmission electron microscopy (TEM; scale bars: 100 nm) and atomic force microscopy (AFM; scale bars: 200nm).



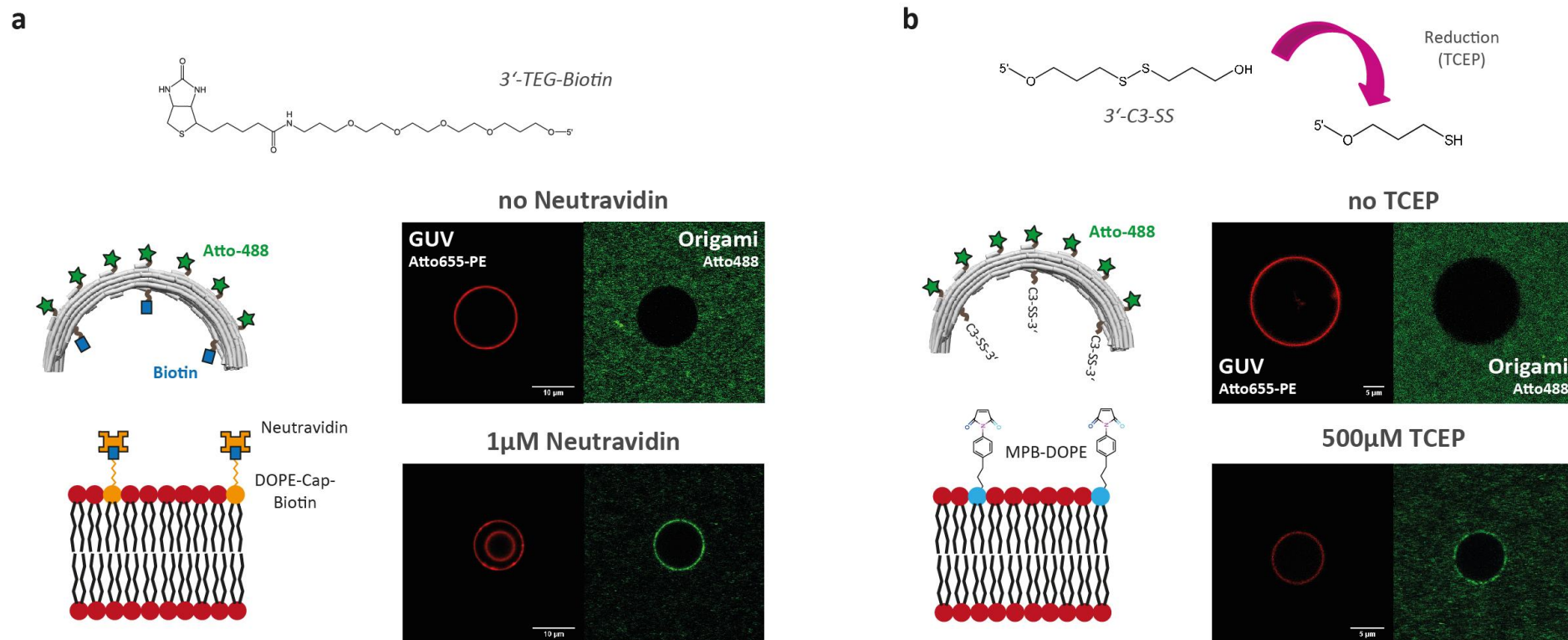
Supplementary Figure 6

Unspecific interaction of curved DNA origami with model lipid membranes, mediated by Mg^{2+} . Binding of bare origami H (labeled with Alexa488, green) to the surface of DOPC GUVs and DOPC:DSPC:Chol (2:2:1 mol ratio) supported lipid bilayers (SLBs) in a 5 mM Tris-HCl, 1 mM EDTA, pH 8.0 buffer containing (a) 20mM MgCl_2 and no NaCl or (b) a buffer with no MgCl_2 and 150mM NaCl. DOPC GUVs were electroformed in sucrose solutions iso-osmolar to the buffers utilized ((a) 70 mOsm kg^{-1} and (b) 300 mOsm kg^{-1}). For fluorescence detection, membranes were labeled with 0.1 % DiD (far-red fluorescent dye). As seen in panel (a), presence of a buffer containing 20 mM MgCl_2 and no NaCl led to extensive binding of DNA origami (labeled with green fluorescent dye Alexa488) to DOPC GUVs and to the liquid-ordered phase of DOPC:DSPC:Chol SLBs (dark regions). On the other hand as seen in panel (b), in the presence of a buffer containing no MgCl_2 and 150 mM NaCl, binding of DNA origami to the surface of membranes was not observed, as green fluorescence can be only found in solution and not at the membrane level. Scale bars:10 μm .



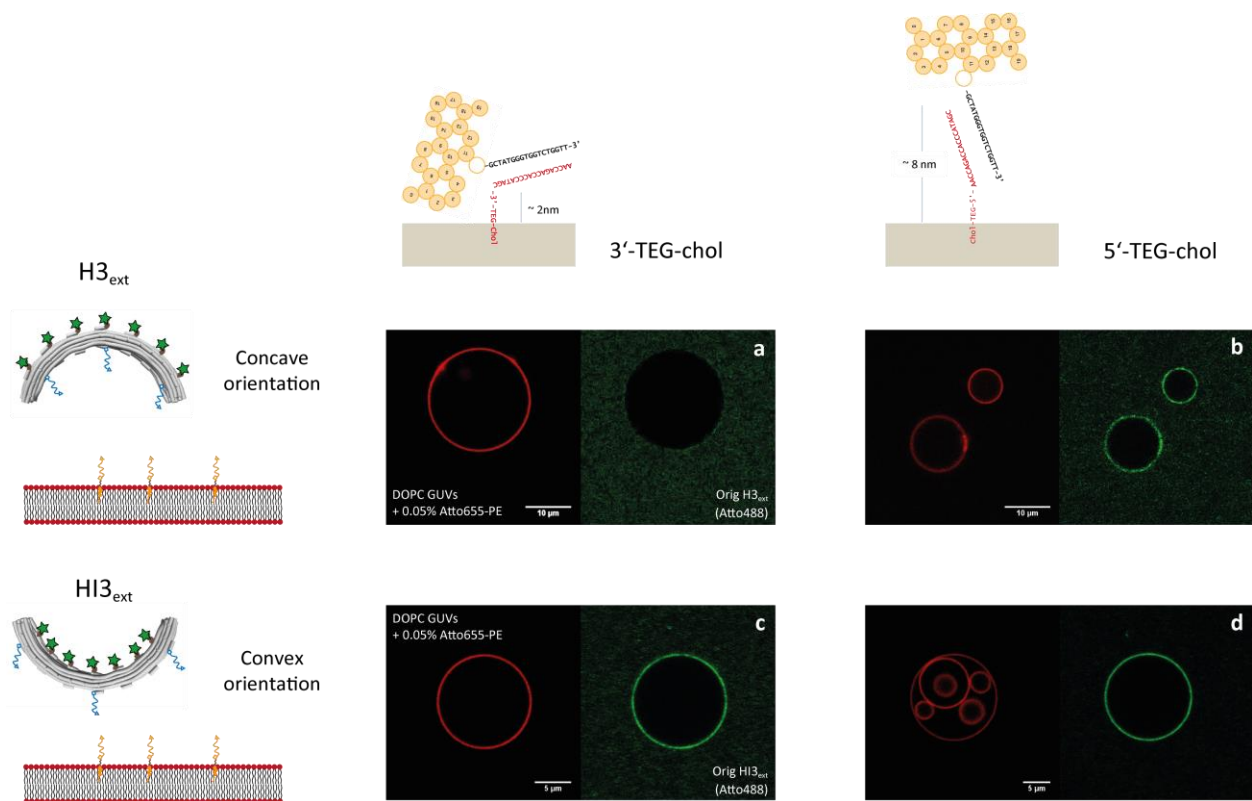
Supplementary Figure 7

Distinct amounts of MgCl₂ and NaCl in solution modulate the attachment of bare DNA origami to membranes. Varying amounts of MgCl₂ and NaCl in solution allowed (a-b) or prevented (c) unspecific attachment of bare DNA origami H (labeled with Alexa488, green) to lipid bilayers (DOPC:DSPC:Chol (2:2:1) SLBs; labeled with DiD, red). Upon addition of MgCl₂ to the lipid bilayer displayed in panel (c), binding of bare origami H to the membrane could be triggered (d). Scale bar: 10 μm.



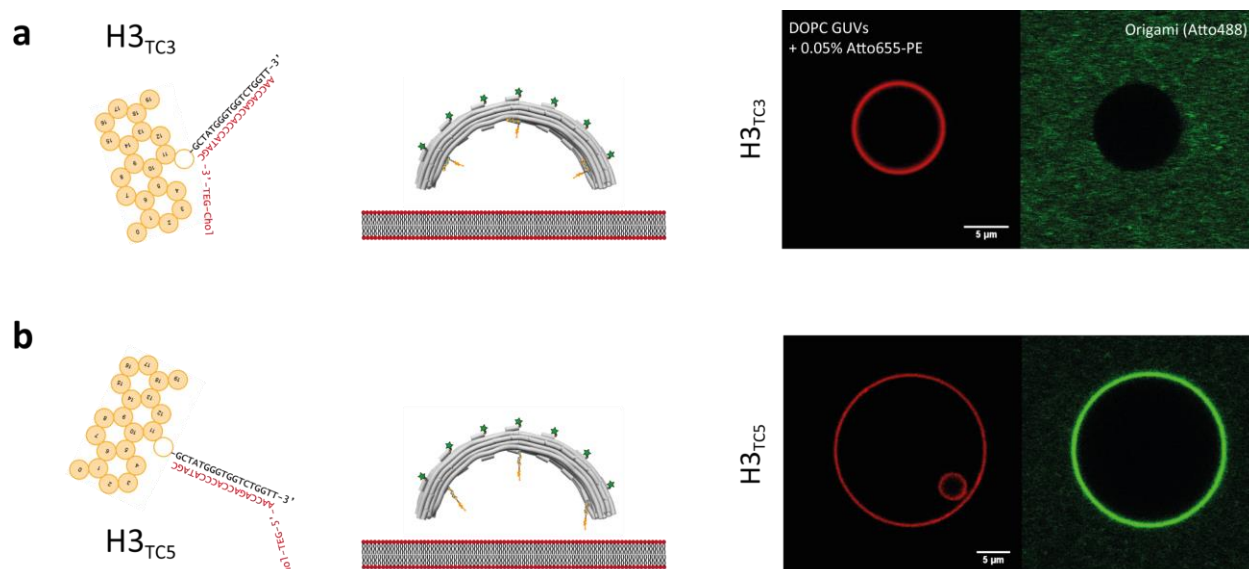
Supplementary Figure 8

Specific attachment of curved origami H to lipid membranes via (a) high affinity polyvalent neutravidin-biotin interaction and (b) covalent attachment. **(a)** DOPC GUVs containing 2 mol% of biotin-modified DOPE molecules (DOPE-Cap-Biotin) were incubated with DNA nanostructures H containing 3'-TEG-biotin functionalized oligonucleotide staples at origami positions B0, B3 and B6. Upon addition of neutravidin (1 μ M) and after less than 1h incubation, extensive binding of the curved nanostructure to the surface of GUVs was observed. **(b)** DOPC GUVs containing 10 mol% of maleimide-modified DOPE lipid molecules (MPB-DOPE) were incubated with DNA origami nanostructure H containing protected 3'-thiol-modified strands (3'-C3-SS at positions B0, B3 and B6). Upon addition of excess concentration of reducing agent (TCEP), which would cleave the protecting disulfide bonds, and after overnight incubation, the thiolated DNA origami nanostructure H was able to be crosslinked to GUVs, although not as efficiently as with the biotin-neutravidin strategy. For these experiments, GUVs were fluorescently-labeled with 0.05 mol% Atto655-DOPE (red) and the DNA origami nanostructures with Atto488-modified strands (green). Moreover, while for strategy **(a)** standard imaging buffer (5 mM Tris-HCl, 1 mM EDTA, 5 mM MgCl₂, 300 mM NaCl, pH 8.0) was utilized, in case of strategy **(b)** we utilized a 10 mM Hepes, 5 mM MgCl₂, 300 mM NaCl, pH 7.4 buffer, as the thiol-maleimide crosslinking requires a lower pH and a non-amine buffer. Scale bars: **(a)** 10 μ m; **(b)** 5 μ m.



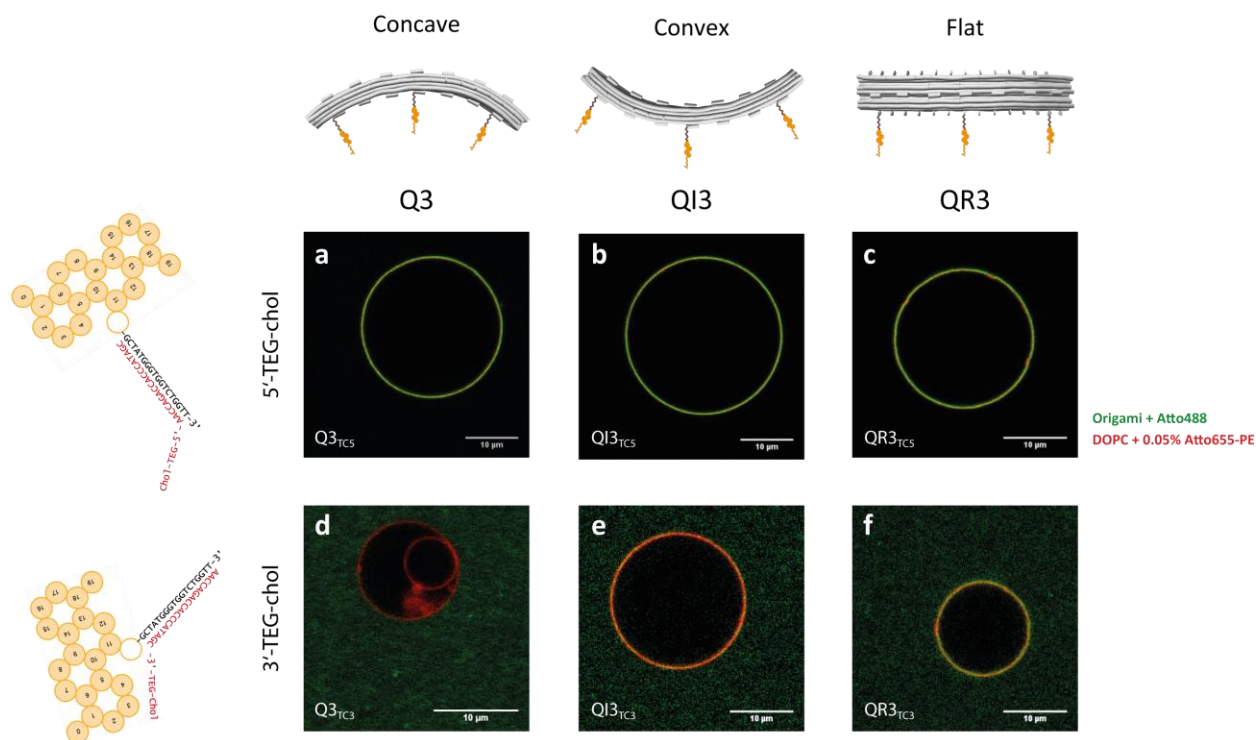
Supplementary Figure 9

Side-specific attachment of origami H to GUVs through hybridization with TEG-chol modified oligonucleotides. Origami H nanostructures (labeled with Atto488, green) presenting 18 nucleotide-long single-stranded overhangs (**a-b**) on the concave surface – origami H3_{ext} (overhangs extending from the 3'-end of bottom positions B0, B3 and B6) or (**c-d**) on the convex surface – origami HI3_{ext} (overhangs extending from the 3'-end of top positions T0, T3 and T6), were added to DOPC GUVs (labeled with Atto655-DOPE, red) previously pre-incubated with 2 μ M of 3'/5'-modified TEG-chol modified complementary oligonucleotide strands. **Panels (a,c):** when 3'-end TEG-chol functionalized oligonucleotides were used (proximal orientation), hybridization between the DNA overhangs on origami H and membrane-bound complementary strands will occur in tight proximity to lipid bilayer surface. Due to the bulkiness and curvature of this nanostructure, membrane attachment of structure H3_{ext} via its concave surface, will be hindered (**a**). On the other hand, significant binding of structure HI3_{ext} to membranes via its more accessible convex surface was still observed (**c**). **Panels (b,d):** when 5'-end TEG-chol functionalized oligonucleotides are used (distal orientation), hybridization between the DNA overhangs on origami H and membrane-bound complementary strands will be more accessible. Independently of the concave (H3_{ext}; **(b)**) or convex (HI3_{ext}; **(d)**) binding orientation, strong attachment of the curved origami H could be achieved. Scale bars: **(a, b)** 10 μ m; **(c, d)** 5 μ m.



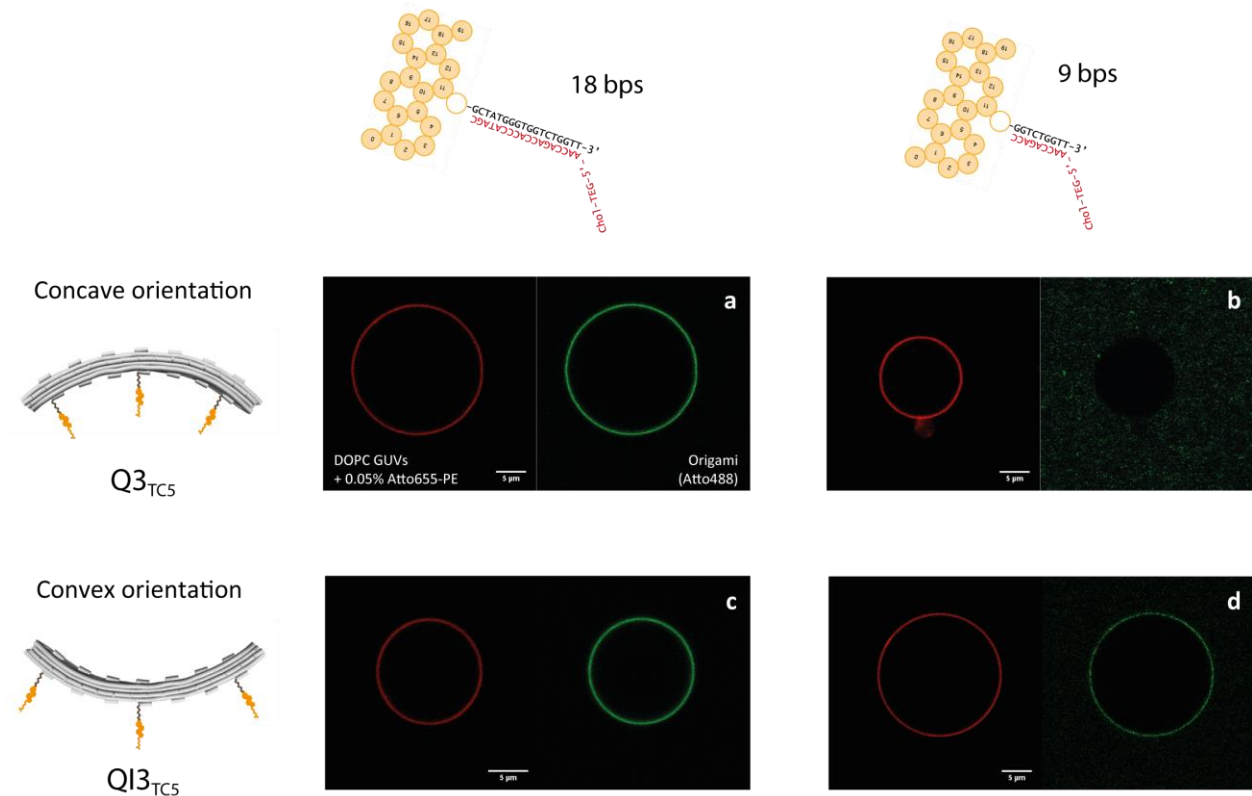
Supplementary Figure 10

Attachment of origami H to GUVs through TEG-chol modified 18bps overhangs. Nanostructures H (labeled with Atto488, green) displaying 3'/5'-TEG-chol modified 18 nucleotide-long DNA strands, now directly hybridized during origami folding with single-stranded overhangs at the bottom positions B0, B3 and B6, were used. **(a)** Proximal positioning of the three TEG-chol modifications on the concave surface ($H3_{TC3}$; TEG-Chol at 3'-end) resulted in virtually no attachment of origami H to DOPC GUVs (labeled with Atto655-DOPE, red), even after longer incubation times (i.e. overnight). **(b)** On the other hand, by placing the three TEG-Chol moieties at the distal end of the 18 bps overhangs ($H3_{TC5}$; TEG-Chol at 5'-end) strong membrane binding of origami H after 1h of incubation was observed. Hence, the increase of the linker length from ~2 nm (length of the TEG moiety) to ~8 nm (combined length of the TEG moiety and the 18 bps overhang) rendered the cholesteryl moieties on the curved and bulky origami H nanostructures less sterically hindered and more accessible for binding macroscopically flat lipid membranes, such as GUVs. Scale bars: 5 μm .



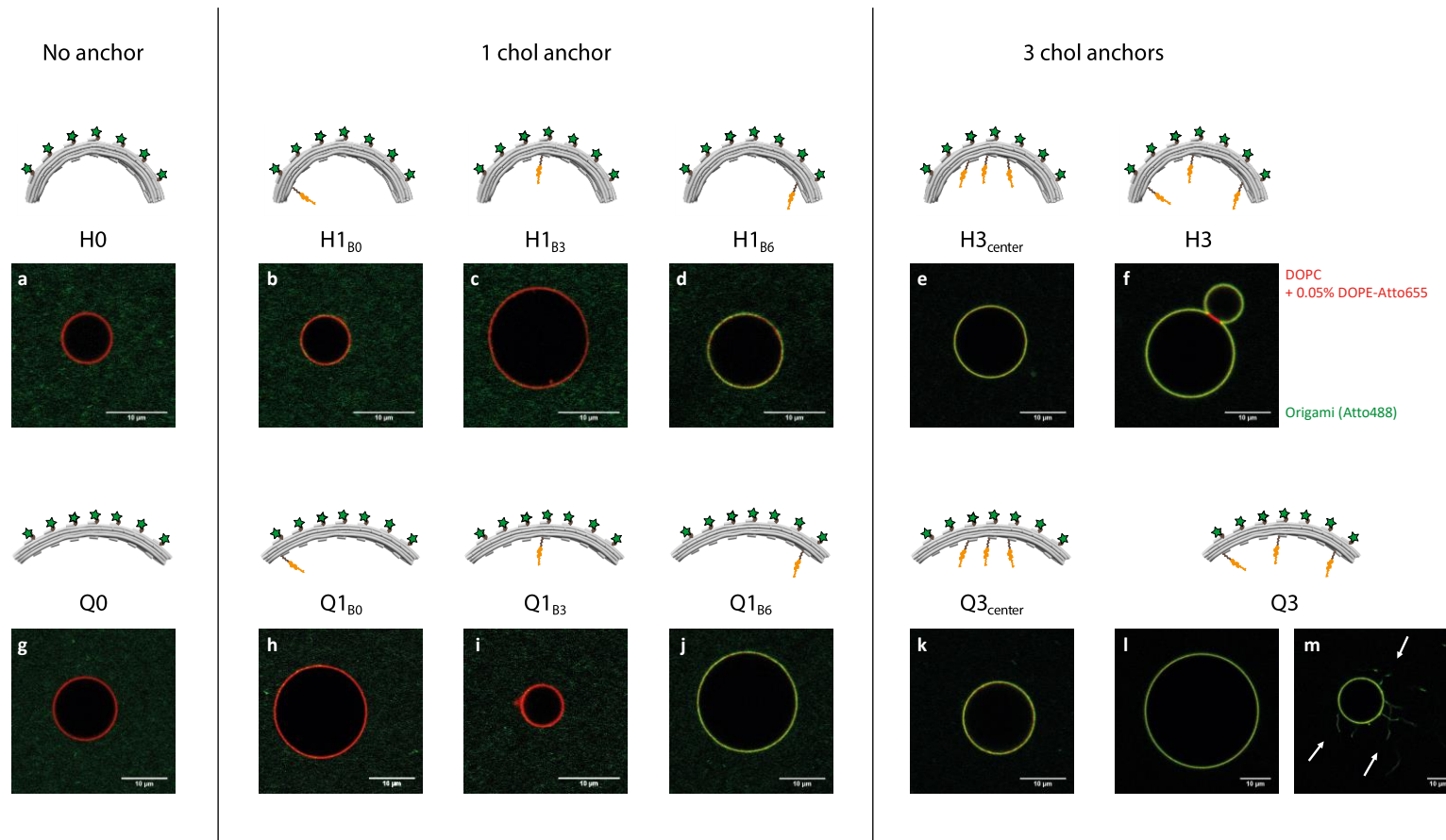
Supplementary Figure 11

Side-specific attachment of origami Q to GUVs through TEG-cholesterol modified 18bps overhangs. We further assessed binding to DOPC GUVs (labeled with Atto655-DOPE, red) of origami Q nanostructures (labeled with Atto488, green), previously functionalized with three TEG-cholesterol moieties at the distal 5' (TC5) and proximal 3' (TC3) ends of 18 bps overhangs at the concave (bottom positions B0, B3 and B6; origami Q3_{TCX}), convex (top positions T0, T3 and T6; origami QI3_{TCX}) or lateral non-curved (right positions R0, R6 and R12; origami QR3_{TCX}) origami surfaces. **(a-c):** Independently of the surface of the nanostructures carrying the modifications, distal positioning of the TEG-cholesterol moieties (TC5) resulted in strong binding of the DNA origami Q nanostructures to GUVs. **(d-f):** When the TEG-cholesterol moieties were positioned in close proximity to the DNA origami core (TC3), membrane binding of those nanostructures depended on which surface was carrying hydrophobic modifications. If the cholesteryl groups are localized on the concave surface of origami Q (origami Q3_{TC3}, **(d)**), no significant binding to GUVs was reported. On the other hand, if the cholesteryl groups were localized on the convex surface of origami Q (QI3_{TC3}, **(e)**) and mainly lateral surface with essentially zero curvature (QR3_{TC3}, **(f)**), significant (yet weaker) membrane binding was observed. Scale bars: 10 μm.



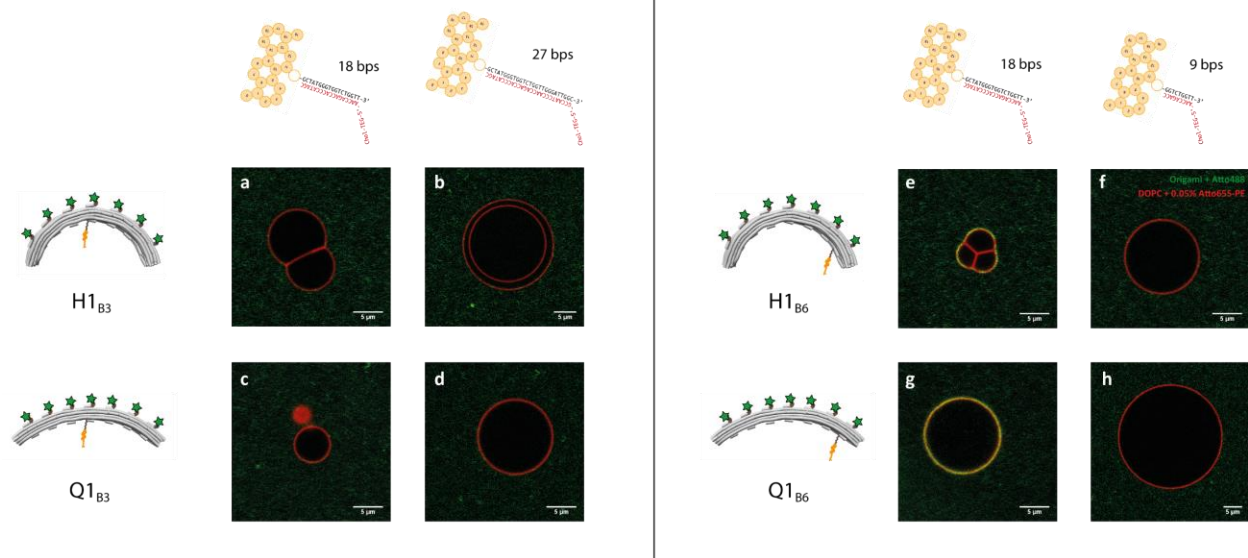
Supplementary Figure 12

Dependence on the length of the TEG-chol modified linkers/overhangs, for attaching origami Q to GUVs. Independently of the origami surface on which the distal 5'-TEG-chol moieties localized, for structure $Q3_{TC5}$ (cholesteryl anchors at the concave facet of origami Q) and $QI3_{TC5}$ (cholesteryl anchors at the convex facet of origami Q) with 18 bps overhangs (linker length ~ 8 nm), a strong attachment to lipid membranes was observed ((a) and (c), respectively). However, shortening those overhangs to 9 bps (linker length ~ 5 nm) resulted in a strong reduction of the binding of curved nanostructures Q to the GUVs. For such linker length, weak binding to lipid membranes was still observed for structure $QI3_{TC5}$ with hydrophobic anchors at the convex origami facet (d); yet no membrane binding of structure $Q3_{TC5}$ with anchors at the concave origami surface (b) was reported. Overall, placing the TEG-chol moieties at the distal end of 18 bps overhangs provided an appropriate linker length for overcoming steric hindrance during the attachment of our nanostructures to GUVs. Scale bars: 5 μ m. Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with Atto655-DOPE.



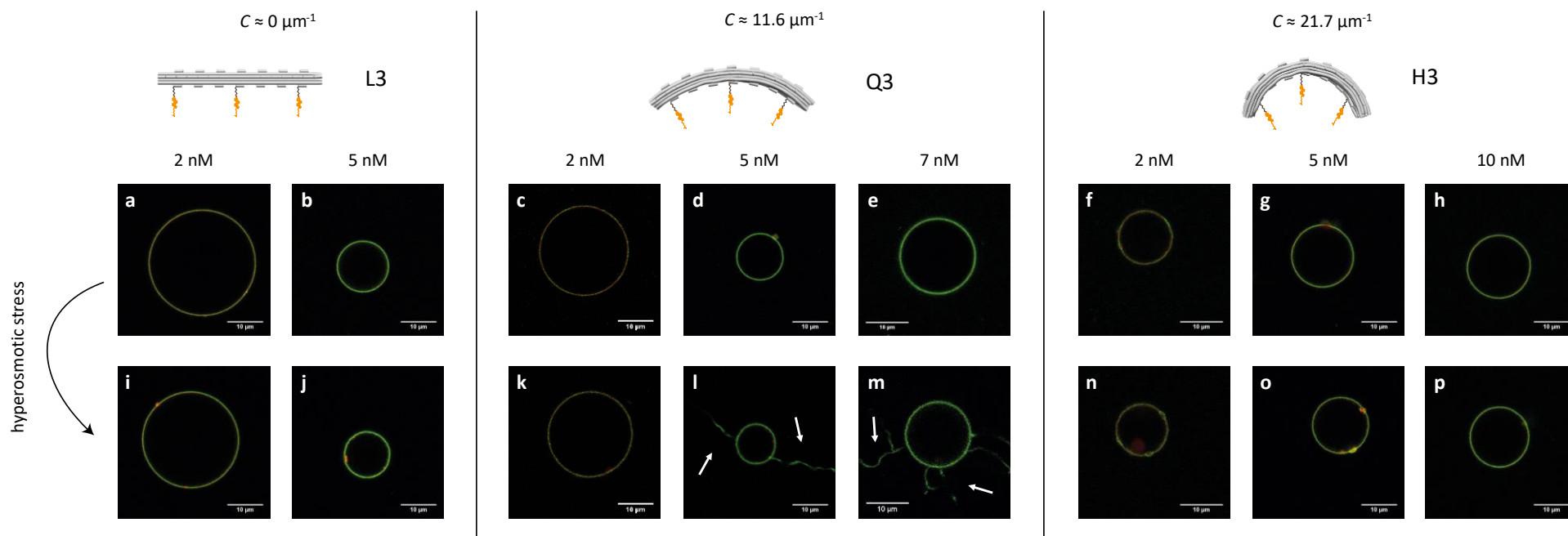
Supplementary Figure 13

Effect of the number and positioning of TC5 anchors on the binding of curved DNA origami nanostructures to freestanding lipid bilayers via their concave surface. TEG-chol moieties placed at the distal 5'-end of 18 bps overhangs (from here on called TC5) were used at the bottom concave origami positions. In the absence of TC5 anchors and using imaging buffer containing 5 mM MgCl₂ and 300 mM NaCl, bare origami structures H0 and Q0 did not attach to GUVs (a, g). Use of single TC5 anchors on structures H1 and Q1 did not promote efficient membrane binding of the nanostructures (b, c, h, i), unless the TC5 anchor was placed at the most accessible edge position B6 (d, j), indicating that steric hindrance clearly affected membrane binding. Strong binding to GUVs was however achieved upon incorporation of 3× TC5 anchors; independently of the anchors being localized at the central positions B2, B3 and B4 (H3_{center}, (e); Q3_{center}, (k)) or distributed across the concave facet at positions B0, B3 and B6 (H3, (f); Q3, (l)). Although membrane attachment did not greatly depend on the degree of curvature of our nanostructures, only in the presence of the moderately-curved structure Q3 a significant amount of GUVs (~ 18%) displayed tubular-like outwards deformations (arrows, (m)). Scale bars: 10 μm. Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with DOPE-Atto655.



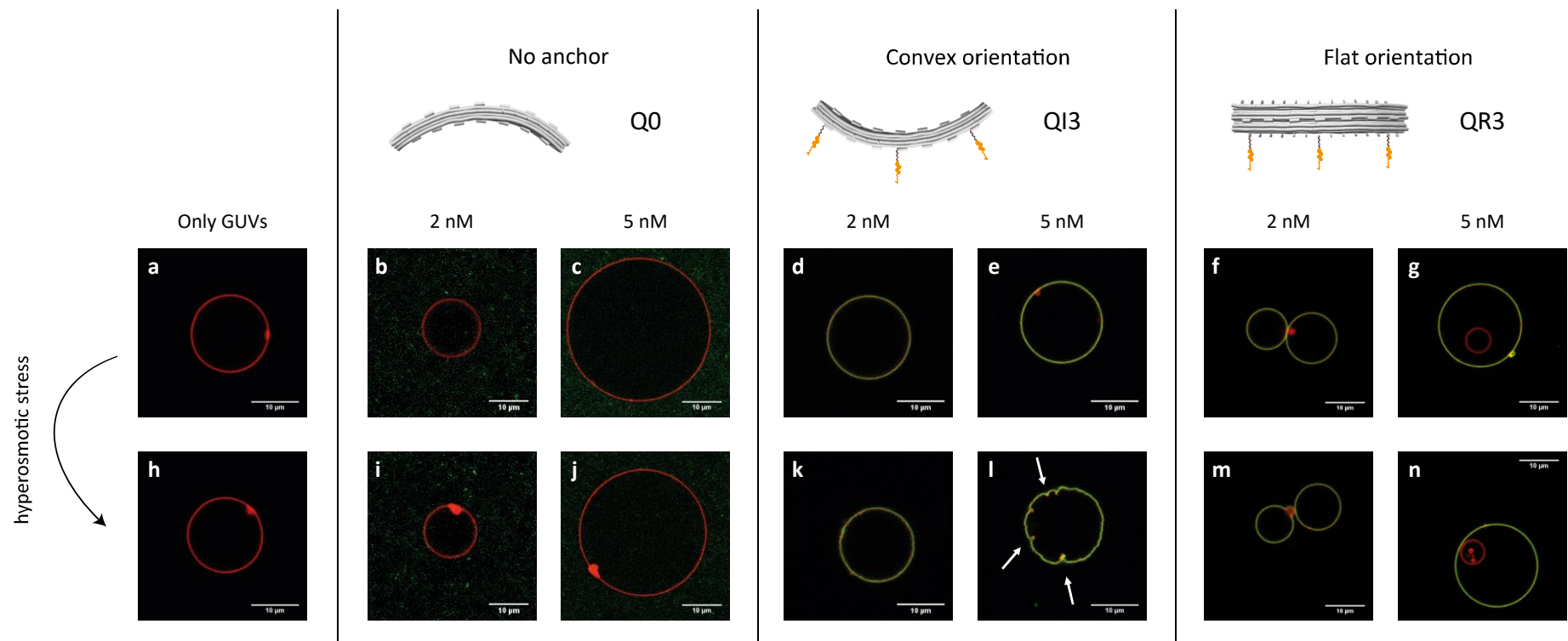
Supplementary Figure 14

Membrane binding of curved DNA nanostructures with single TC5 anchors is dependent on the linker/overhang length. The use of a longer linker/overhang (27 bps, instead of the typical 18 bps) did not improve membrane binding of nanostructures H1_{B3} and Q1_{B3} containing a single TC5 anchor at the central concave position B3 (**a-d**). On the other hand, shortening the linker/overhang from 18 to 9 bps for single TC5 anchors placed at the most accessible edge position B6, fully abolished the weak membrane binding observed for both DNA origami H1_{B6} and Q1_{B6} nanostructures (**e-h**). Scale bars: 5 μm . Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with Atto655-DOPE.



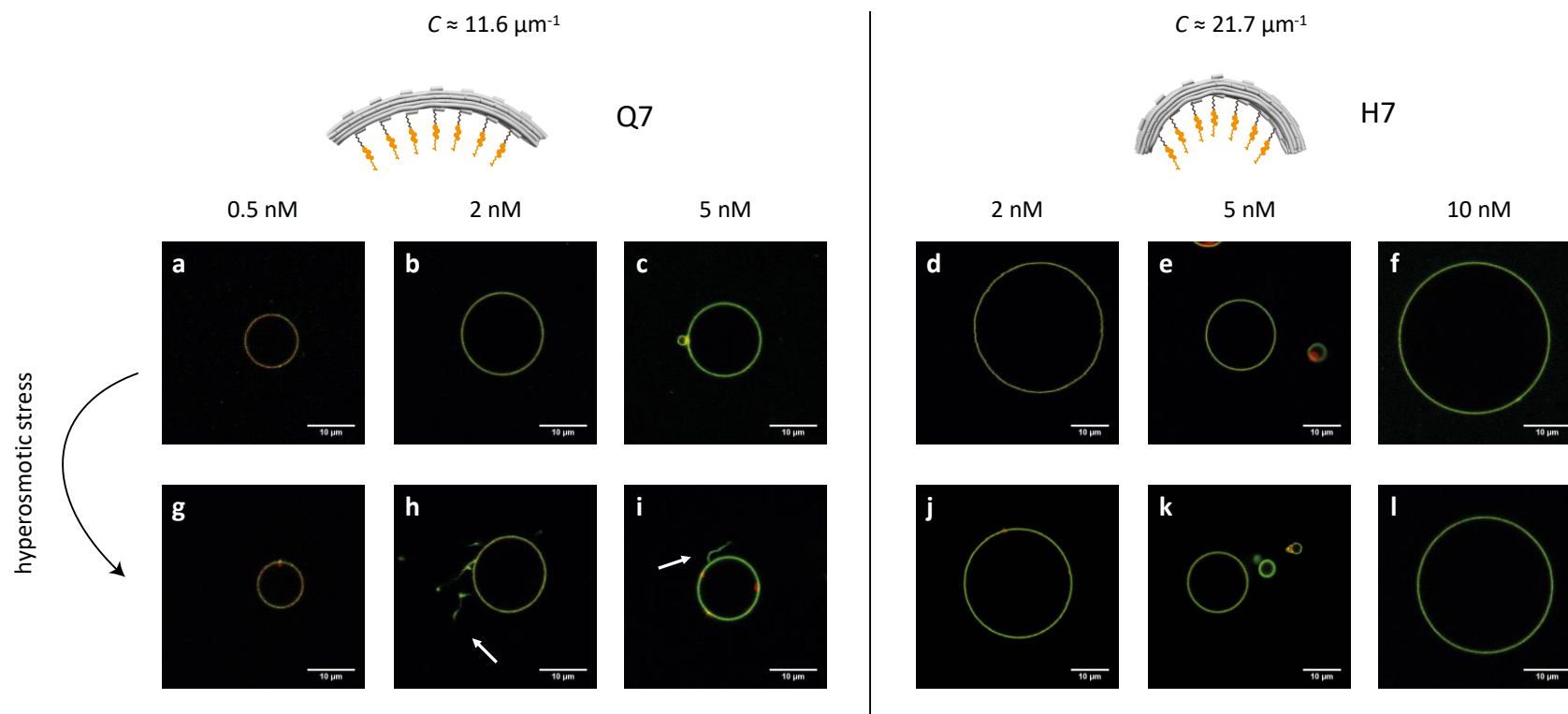
Supplementary Figure 15

Dependence on DNA origami bulk concentration and degree of curvature of DNA nanostructures with concave membrane-binding interface, for triggering membrane tubulation upon hyperosmotic stress. Structures L3, Q3 and H3 (possessing 3× TC5 anchors at positions B0, B3 and B6) bound to DOPC GUVs were imaged after at least 1h incubation period. Osmotic stress was achieved by increasing outer osmolarity in 10%. For origami structure Q3 (moderate curvature; **(c-e, k-m)**), triggering the generation of outwards positively-curved membrane tubules on GUVs upon hyperosmotic stress was dependent on the overall bulk concentration of origami utilized (at least 5 nM bulk concentration was required; deformations marked with arrows). On the other hand, origami structures L3 (no curvature; **(a-b, i-j)**) and H3 (strong curvature; **(f-h, n-p)**) were not able to significantly affect the shape of vesicles upon hyperosmotic stress. Note that even at increased bulk concentrations (10 nM), highly-curved origami H3 was not able to trigger significant membrane deformation on GUVs, e.g. tubulation (panels **(h, p)**). Scale bars: 10 μm . Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with DOPE-Atto655.



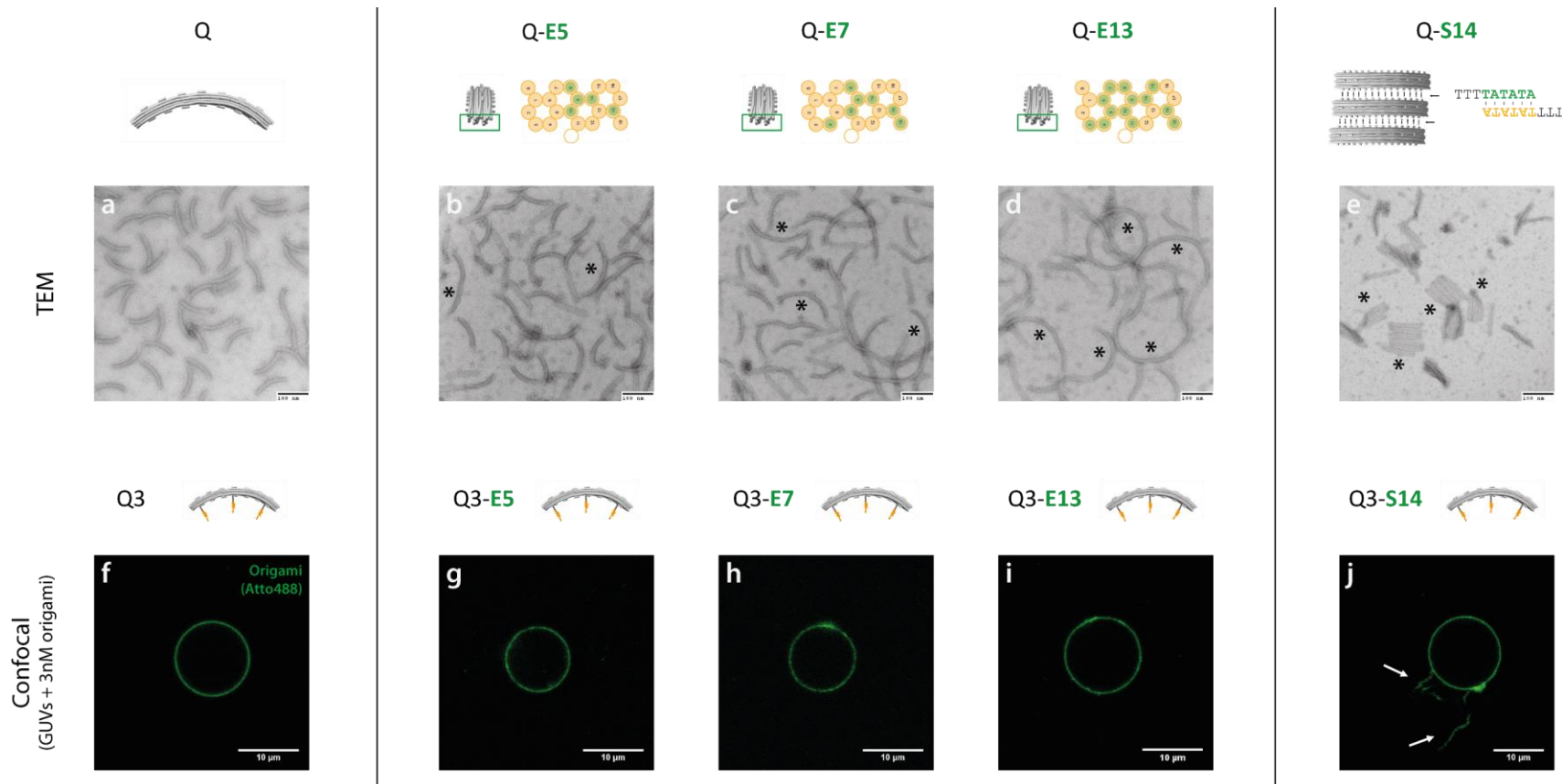
Supplementary Figure 16

Dependence on DNA origami bulk concentration and curvature of membrane anchoring origami facet, for triggering membrane deformations upon hyperosmotic stress with origami Q nanostructures. Data presented in this figure complements the previous data presented in Supplementary Fig. 15, being acquired under the same conditions. When compared with control vesicles in the absence of origami (**a**, **h**), no significant effect on vesicle shape was observed upon hyperosmotic stress when origami Q with no hydrophobic anchor (structure Q0) was present in solution, independently of the bulk concentration assayed (**b-c**, **i-j**). Regarding membrane-bound nanostructure Q variants with three TC5 anchors, for structure QR3 (displaying anchors at the non-curved origami lateral surface) no significant membrane deformations on GUVs were observed even at increased QR3 bulk concentrations (**f-g**, **m-n**). However, evagination/invagination-type of membranes deformations (marked with arrows) were observed for the membrane-bound convex QI3 structure (**d-e**, **k-l**). Similarly to what was reported for the concave Q3 structure (Supplementary Fig. 15), we also observed a dependence on the total bulk concentration of QI3 required for triggering deformations upon vesicle deflation; as shape changes only significantly happened at higher concentrations (5 nM). Scale bars: 10 μm . Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with DOPE-Atto655.



Supplementary Figure 17

Generation of membrane deformations upon hyperosmotic stress by concave nanostructures Q and H bearing increased number of TC5. Data presented in this figure complements previous data presented in Supplementary Fig. 15 and Supplementary Fig. 19, being acquired under the same conditions. The moderately-curved structure Q7 bearing 7 $\times$ TC5 anchors required lower bulk concentrations for triggering membrane tubulation (marked with arrows) on GUVs (**a-c**, **g-i**), when compared with its counterpart bearing only 3 $\times$ TC5 anchors (Supplementary Fig. 15c-e and k-m). For the highly curved DNA origami H7 bearing 7 $\times$ TC5 anchors on their concave surface, on the other hand, despite the increase in the number of hydrophobic anchors resulting in a stronger membrane attachment, we were still not able to observe significant membrane deformations upon hyperosmotic stress (i.e. tubulation) on GUVs (**d-f**, **j-l**). Scale bars: 10 μm . Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with DOPE-Atto655.

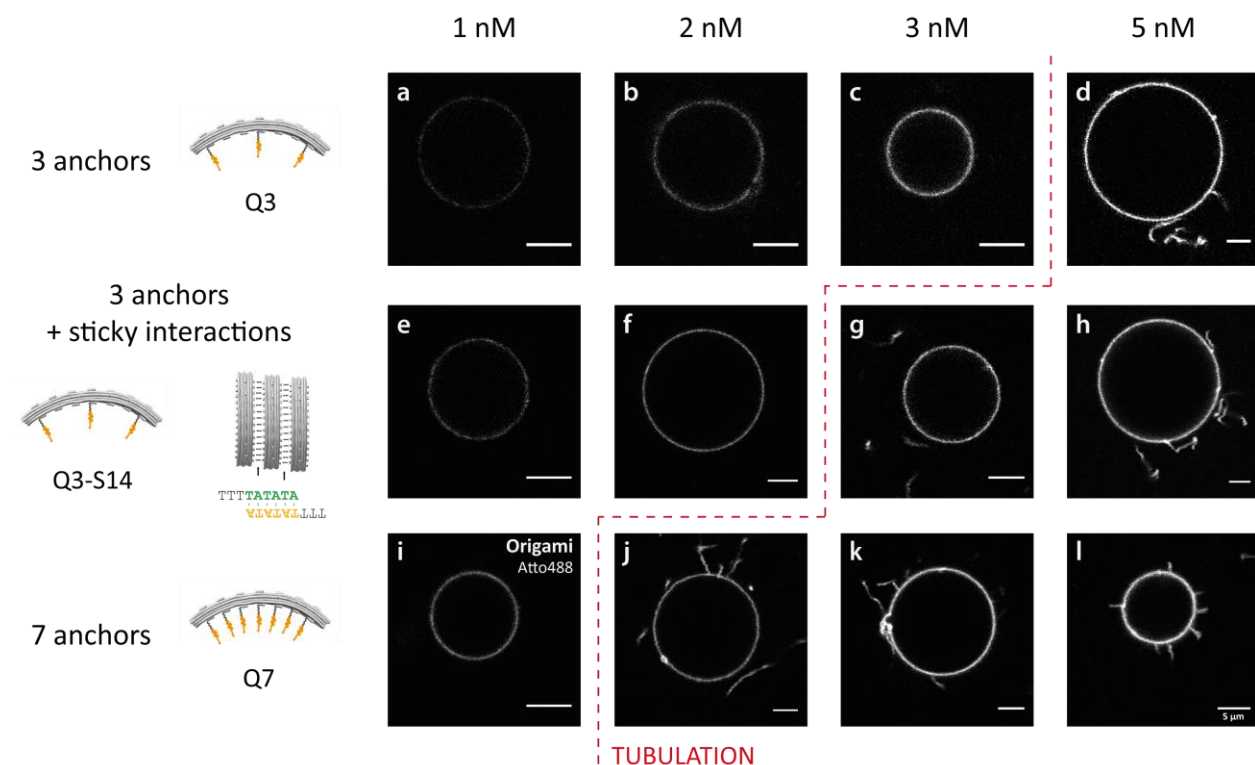


Supplementary Figure 18

Incorporation of polymerizing moieties and its effect on the ability of moderately-curved origami Q nanostructures to deform lipid vesicles.

(a-e): Negative-stain TEM images of bare origami Q structure variants displaying different types and number of polymerizing moieties. Addition of polymerizing staples at the marked ends (in green; upper schemes) of monomeric structure Q **(a)** allowed for tip-to-tip blunt end stacking interactions **(b-d)**. By varying the number of blunt ends from 5 to 7 and 13, it was possible to control the size of the resulting oligomers – dimers, trimers and even tetramers (marked as stars). Polymerization could also be triggered via lateral sticky interactions **(e)**. Incorporation of 14 protrusions capable of hybridizing with their counterparts on each side of the origami Q, resulted in the formation of sheet like polymers of origami Q in solution (marked with asterisks).

(f-j): Variants of structure Q3 (labeled with Atto488, green) with and without corresponding polymerizing moieties were pre-incubated at 3 nM with DOPC GUVs for at least 1h and generation of membrane tubulations was followed after hyperosmotic stress. Altogether, at such intermediate DNA origami bulk concentration, we could only report significant tubulation events (marked with arrows) on GUVs upon osmotic shock were for the membrane-bound variant Q3-S14 bearing lateral polymerization strands **(j)**. Scale bars: **(a-e)** 100 nm; **(f-j)** 10 μ m.

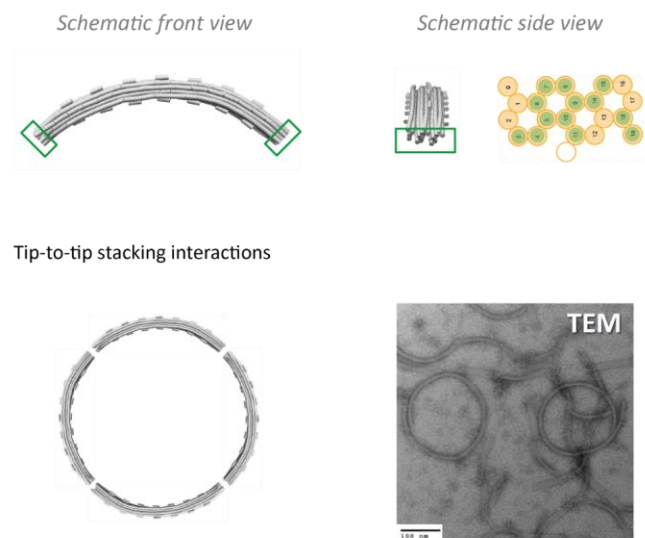


Supplementary Figure 19

Requirements for induction of membrane deformations by BAR-mimicking origami structure Q can be tuned via number of cholesteryl anchors or lateral polymerization. For structure Q3 (a-d), only at high bulk concentrations (5 nM) tubulation of almost all GUVs was triggered. For structure Q7 with additional cholesteryl anchors (i-j), the minimal bulk concentration required to trigger membrane tubulation was shifted to lower values (2 nM). Similarly for structure Q3-S14 displaying lateral sticky overhangs (e-h), lower total bulk concentration were necessary for triggering vesicle tubulation when compared to structure Q3 (a-d). Representative confocal images at the equatorial plane of GUVs incubated for at least 1 h with varying concentrations of Atto488-labeled DNA nanostructures are shown after hyperosmotic stress. The red dotted line indicates the concentration regime (total bulk concentration of origami Q) required for triggering membrane tubulation on freestanding lipid bilayers. Scale bars: 5 μ m.

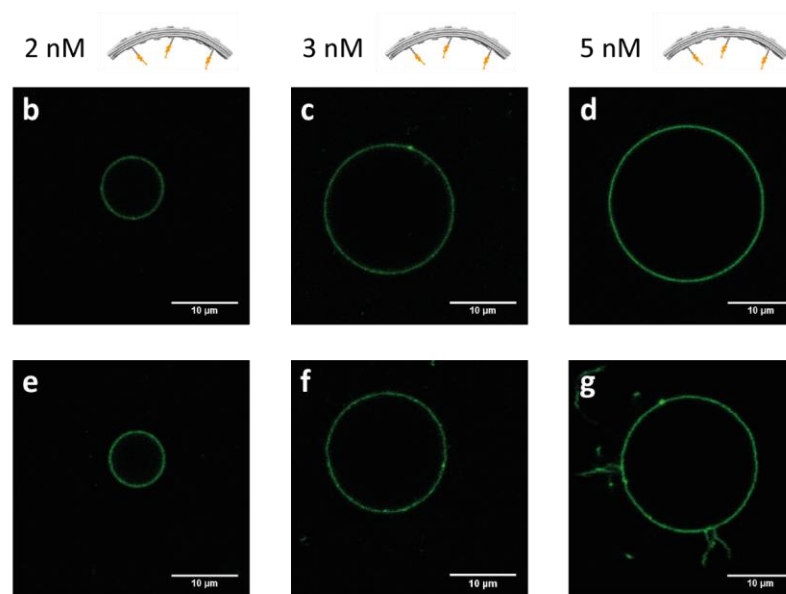
Q-E13

a



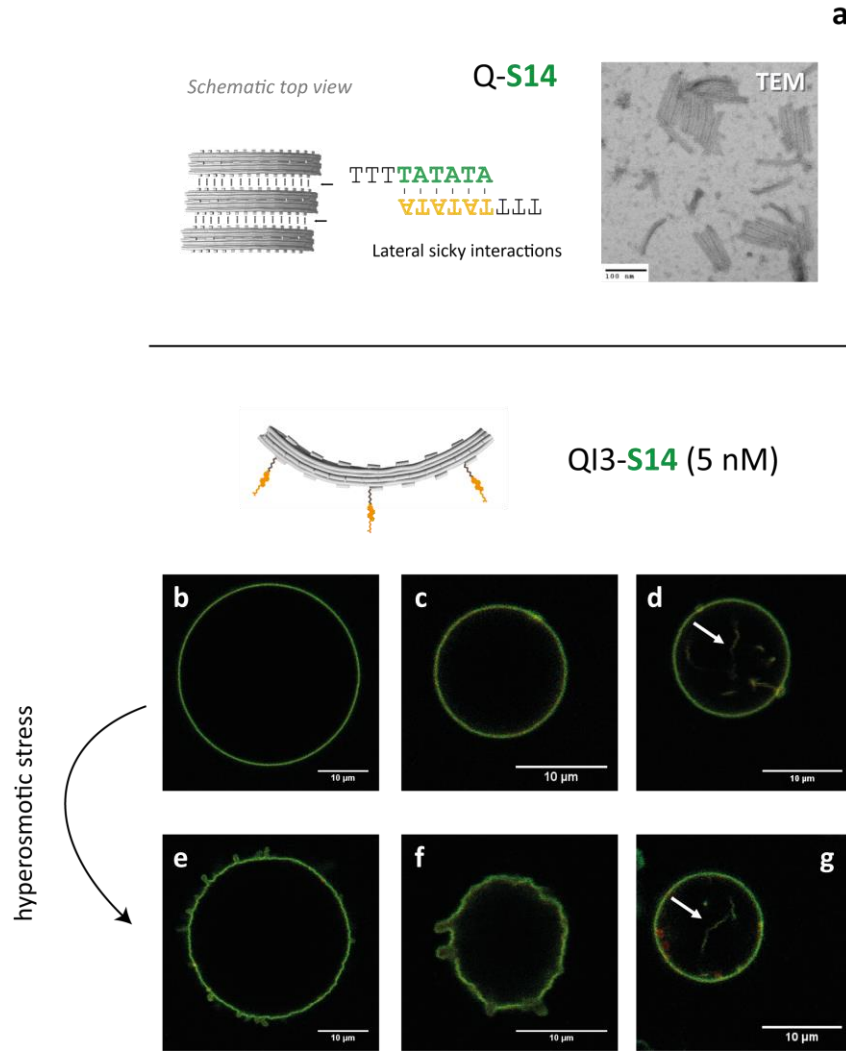
Q3-E13

hyperosmotic stress



Supplementary Figure 20

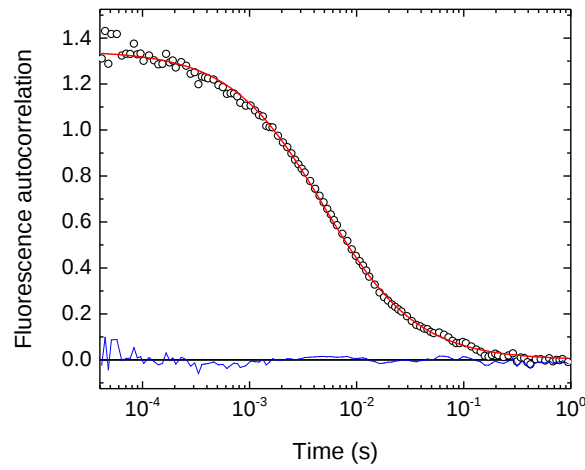
Dependence on the total bulk concentration of linearly-polymerizing concave structure Q3-E13, for triggering membrane shape deformations upon hyperosmotic stress. Data presented in this figure was acquired under the same conditions as the one displayed in Supplementary Fig. 19 and Supplementary Fig. 15. **(a)** Schematic representations of the polymerization strategy based on tip-to-tip stacking interactions via 2×13 blunt ends, based on the polymers observed by negative-stain TEM with bare structure Q-E13. **(b-g)** Similar to what we observed for the monomeric membrane-bound structure Q3 (Supplementary Fig. 19 and Supplementary Fig. 15), membrane-bound structure Q3-E13 (labeled with Atto488, green) only triggered significant membrane deformations (i.e. tubulation) upon hyperosmotic stress at high bulk concentrations (5 nM). Scale bars: **(a)** 100 nm; **(b-g)** 10 μ m.



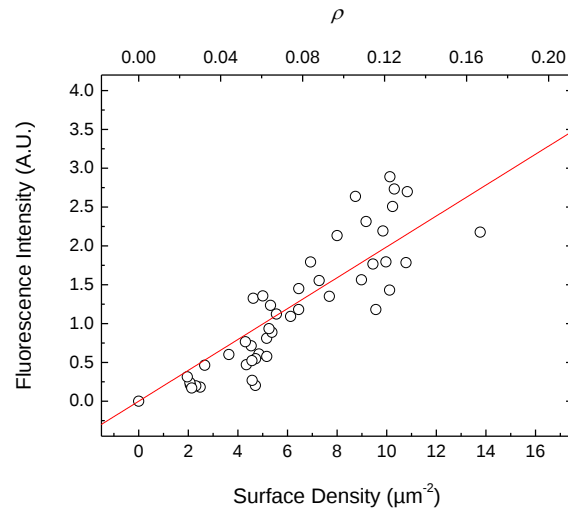
Supplementary Figure 21

GUV shape deformations triggered by membrane-bound convex variants of origami Q with lateral polymerization strands. Data presented in this figure complements previous data presented in Fig. 3 and Supplementary Fig. 16, being acquired under the same conditions. **(a)** Schematic representation of the formation of origami sheets by sticky interactions between neighboring origami structures displaying 2×14 lateral TATATA overhangs, based on the observations by negative-stain TEM imaging of origami Q-S14. **(b-g)** For vesicles incubated with high DNA origami bulk concentrations (i.e. 5 nM) of convex polymerizing structure QI3-S14, stable evagination-like deformations were reported upon hypersosmotic (**e, f**). Additionally, a small percentage of vesicles ($\sim 15\%$) presented inwards tubules decorated with DNA origami (arrows), even in the absence of osmotic shock (**d, g**). Scale bars: **(a)** 100 nm; **(b-g)** 10 μ m. Green fluorescence: origami labeled with Atto488; red fluorescence: membranes labeled with DOPE-Atto655.

a

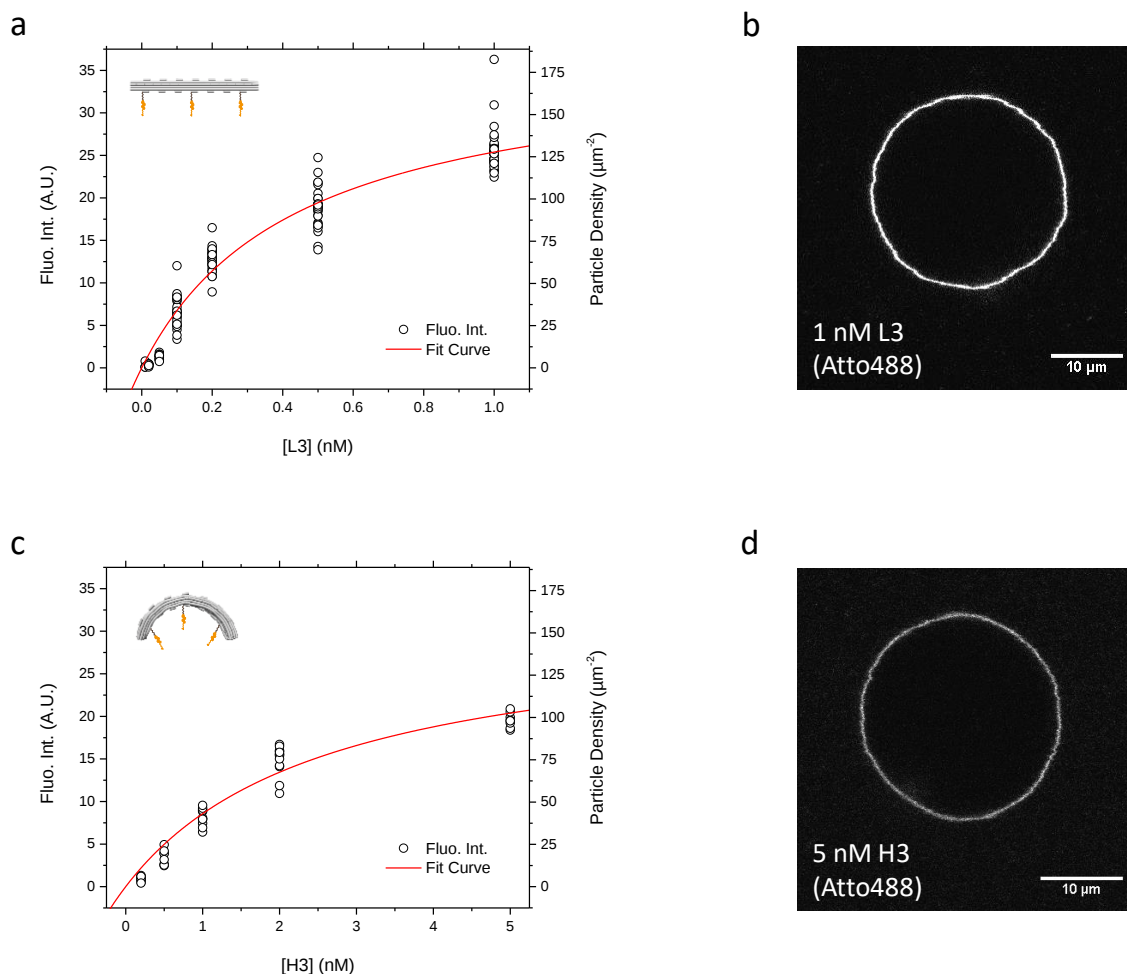


b



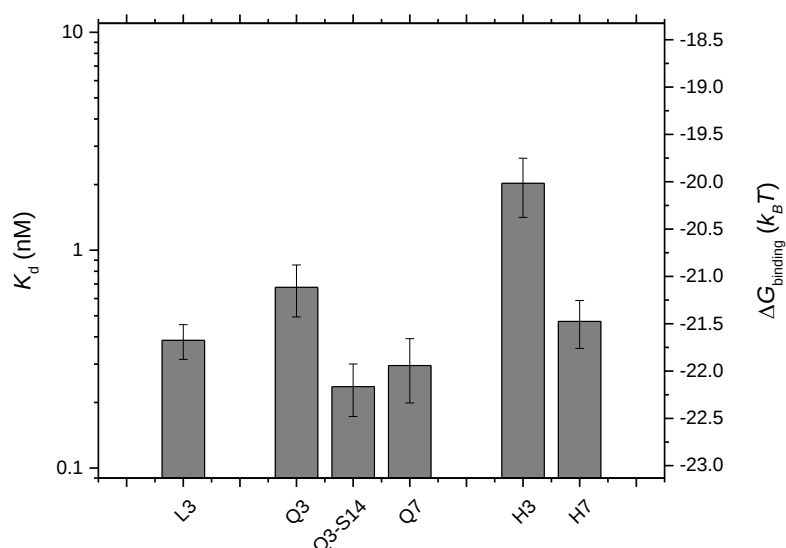
Supplementary Figure 22

Determination of DNA origami particle density at the surface of GUVs by point FCS and fluorescence intensity calibration. (a) Representative auto-correlation curve obtained for structure Q3 on the upper pole of a GUV at low ($\rho = 0.06$) surface densities. **(b)** Linear relationship (calibration curve in red) between fluorescence intensities (obtained via confocal microscopy) and surface densities (determined for $\rho < 0.2$, where the one-component two-dimensional diffusion model (equation 2) is valid) recovered for membrane-bound DNA origami on individual GUVs by FCS (open circles).



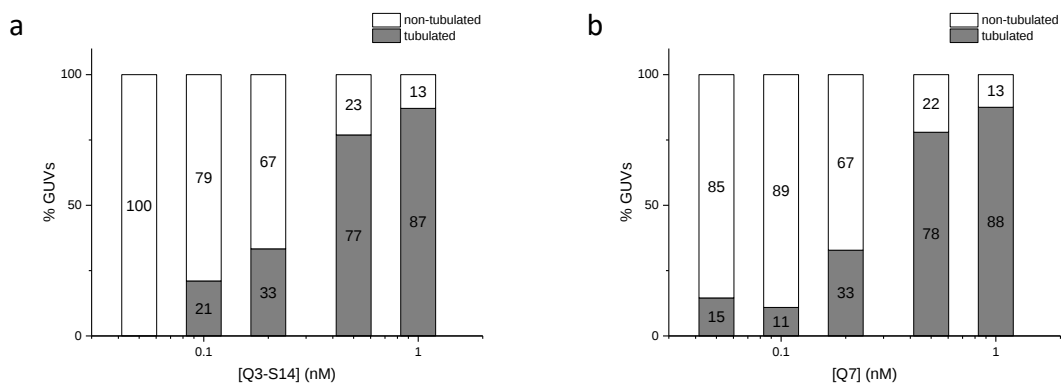
Supplementary Figure 23

Attachment of origami structures L3 and H3 to GUVs upon overnight incubation. (a, c) Representative membrane binding curves obtained using a Langmuir isotherm fit (equation 1) for the flat origami structure L3 (a) and the highly-curved origami structure H3 (c). Each data point corresponds to the fluorescence intensity at the membrane level of DNA origami structures (labeled with $3\times$ Atto-488 dyes) for single GUVs. **(b, d)** Shape variations observed for GUVs incubated overnight with structures L3 and H3. Even at high densities of membrane-bound DNA origami (≥ 100 particles per μm^2 , estimated from the fluorescence brightness via calibration curve of Supplementary Figure 22b), no tubulation events were observed for GUVs incubated with the flat structure L3 (b) or highly-curved structure H3 (d). Unlike the GUVs incubated with moderately-curved structure Q3 (Fig. 4c), GUVs with membrane-bound structures L3 and H3 displayed, at best, increased flaccid membrane deformations. Scale bars: 10 μm .



Supplementary Figure 24

Apparent dissociation constants (K_d) recovered from the analysis of membrane binding of different variants of curved DNA origami scaffolds. Affinity of various cholesteryl-modified BAR-mimicking DNA nanostructures to DOPC GUVs was determined after overnight incubation, from the analysis of the fluorescence intensity of membrane-bound DNA origami as a function of total bulk concentration. Representative binding curves obtained and respective Langmuir isotherm fits (equation 1) are depicted in Fig. 4a and Supplementary Fig. 23. Values correspond to the average K_d ($\pm$ st. dev.): L3 ($n_{\text{total}} = 288$ GUVs; $n = 131$ -157 GUVs per fit, 2 repeats), Q3 ($n_{\text{total}} = 277$ GUVs; $n = 83$ -100 GUVs per fit, 3 repeats), Q3-S14 ($n_{\text{total}} = 84$ GUVs; $n = 36$ -48 GUVs per fit, 2 repeats), Q7 ($n_{\text{total}} = 117$ GUVs; $n = 53$ -64 GUVs per fit, 2 repeats), H3 ($n_{\text{total}} = 106$ GUVs; $n = 48$ -58 GUVs per fit, 2 repeats) and H7 ($n_{\text{total}} = 103$ GUVs; $n = 47$ -56 GUVs per fit, 2 repeats). $\Delta G_{\text{binding}}$ was calculated via $\Delta G = RT \ln K_d$.



Supplementary Figure 25

Efficiencies of vesicle tubulation for origami structure Q3-S14 bearing lateral polymerization overhangs and origami structure Q7 possessing additional cholesteryl anchors. Percentages of GUVs with (closed bars) and without (open bars) outwards tubules observed after overnight incubation at different total bulk concentrations of DNA origami structures Q3-S14 (**a**; $n_{\text{total}} = 118$ GUVs; $n = 13\text{-}31$ GUVs per origami concentration) and Q7 (**b**; $n_{\text{total}} = 297$ GUVs; $n = 55\text{-}64$ GUVs per origami concentration).

Supplementary Table 1
List of DNA staples - Origami L

Start	End	Sequence	Length	Type	Pos.
00[031]	03[027]	CTTAATGCGCCAGCACGTTTCTCGGATTAAA	32	#0_core	
00[053]	06[049]	CGTAACCACCACGAAGTATTAGACTTTTAAAAG	33	#0_core	
00[073]	06[070]	AGTGTAGCGGTTCAATTACCTGAATAATTTCA	32	#0_core	
00[094]	06[091]	GCGGGCGCTAGTTTGAAATACCGTTAGAAAAA	32	#0_core	
00[115]	06[112]	GAAGGGAAGAAATCCAAGAACGAGATCGTAG	32	#0_core	
00[136]	06[133]	CCGGCGAACGTCAATTAGACGGGAGAAAGAGATA	32	#0_core	
00[157]	06[154]	AACCGTCTATCGCGACATTCAACAGATCACCG	32	#0_core	
00[178]	06[175]	CTCCAACGTCAACCAGAGCGCCGTAACAAAT	32	#0_core	
00[199]	06[196]	TCCACTATTAAAGGTTTAGTACCAGATTTTCA	32	#0_core	
00[220]	06[217]	TGTTCCAGTTTTCTTAAACAGCTATTATATTC	32	#0_core	
00[241]	06[238]	GCCCGAGATAGAGCCGGAACGAGTTATGAACG	32	#0_core	
00[262]	06[259]	CCCTTATAAATCCACATTCAACTGCTCATAAC	32	#0_core	
00[283]	06[280]	TGGTTCCGAAAAACAGGTCAAGAAATTAGAGC	32	#0_core	
00[304]	06[301]	GGCGAAAACTGACCTGTAATTTTCATATA	32	#0_core	
00[325]	06[322]	CCACGCTGGTTGCATTAAATTTTTCTGGCC	32	#0_core	
00[346]	01[346]	GAGAGAGTTGCTGAGACGGGCA	22	#0_core	
02[034]	07[048]	TTGTGCTATAACGACGCAAAATAGAAGAACTCAAAC TAGTAAC	42	#0_core	
02[346]	02[329]	GGCGCCAGGGTGGTTTTT	18	#0_core	
03[028]	03[063]	GGGATTTTAGACCCGTCAAACAATTCGACAACTACA	36	#0_core	
03[064]	03[105]	AAATAAGATGATGAAACATAATTTTCGATAAAATAGGCGCTCCA	42	#0_core	
03[106]	03[147]	ATCAAACCAAGTACCGCACAGAGAGCTGAACACCCCTGAAATA	42	#0_core	
03[148]	03[189]	TGGTGGGAGGGAAGGTAAACCACCCCTGACAGGAGGTTGGCC	42	#0_core	
03[190]	03[231]	CGGATCAGAACCGCCACCGGTTTAGATAGTTGCGCCGATCG	42	#0_core	
03[232]	03[273]	AAATCGGTCAATCATAAGGAAAGATATACATAACGCCAATCA	42	#0_core	
03[274]	03[315]	AAGCGTACCTTTAATTGCAAAGCTACGGGAGAAAGCCTTTATT	42	#0_core	
03[316]	03[346]	GTAATCAGCTCATTTTTTAATGAATCGGCC	31	#0_core	
04[048]	10[028]	TTTGCAGAGAGGAACGGTACGTCTGTCCTTGCTCA	35	#0_core	
04[090]	04[049]	AACACTAGTAACATCAAGAAAAACAAAGTTCTGATTAAATCC	42	#0_core	
04[132]	04[091]	GTAATTTTACTCATCGAGAACAAGCAGAAATAAATAAGAATA	42	#0_core	
04[174]	04[133]	CGATTAGCCATATTGACGGAAATTATATTCCAAAGTCAGAGG	42	#0_core	
04[216]	04[175]	CCATCGTATCTCAGAACCGCCACCTTATAAGGCAGGTGAGA	42	#0_core	
04[258]	04[217]	GGCATGGTAGGAACCGAACTGACCAATGTGCAATGACAACAA	42	#0_core	
04[300]	04[259]	GGATAGCATTCTTTTGATAAGAGGTAGCTAAGGAATTACGA	42	#0_core	
04[342]	04[301]	CAGCTGCATAACCAATAGGAACGCCATTAATTTCAACGCAA	42	#0_core	
05[049]	05[048]	CGTTATTGGAGGAGCGAATTGAGGAAGGATATAGATTCCGAA	42	#0_core	
05[070]	05[069]	TTACATTGATGTGAGCCTTTTACATCGAAATACCAATTAA	42	#0_core	
05[091]	05[090]	TCATAATAAAAAGCCATGCAAAATCCAATTATATATTTTCGGAA	42	#0_core	
05[112]	05[111]	TTTTTATAAGCTTATCAGATAAGTCTGTAGCATGTAAGCCG	42	#0_core	
05[133]	05[132]	GCTAATAGAAATGAAAAATCCAAATAAGTTAGCAGCCTGAGC	42	#0_core	
05[154]	05[153]	AAAGGTGGCCAGTAGCAAGAAACGCAAAATCATAGAAATCATT	42	#0_core	
05[175]	05[174]	TGATATTAGTACCGTTACCAACCGGAACCAACCTCAGGGCCT	42	#0_core	
05[196]	05[195]	CCACCACGATTTTCGTGCGGGTTTTGCTCCAATATAAGCAGAG	42	#0_core	
05[217]	05[216]	CGCATAAAATCGTCACCTTTTTTACGTTCTTTAATTGCCCA	42	#0_core	
05[238]	05[237]	AAAGAGGTCTAATCTTATACCAAGCGCGCCGATAAATCTTTG	42	#0_core	
05[259]	05[258]	GAGCAACAGTTTTGTCATGGGAAGAAAAAACTATTACAAGTAA	42	#0_core	
05[280]	05[279]	TTGCGGACATGCAACTTCAAAAAGATTAACTAATTCGCATTT	42	#0_core	
05[301]	05[300]	TTTTAGACAAGGGTGAAAAATCATACAGGTGCCTCAGAAAAAT	42	#0_core	
05[322]	05[321]	AATAATTTCAACCCGCCGGTTGATAATACCAAAATATTCAA	42	#0_core	
06[048]	00[032]	TTTGAACAACTACAGGATTTAACC GCCCGG	31	#0_core	
06[069]	00[054]	TTTGATGCTTTGTTATTCTTACGCTGCG	30	#0_core	
06[090]	00[074]	GCCTGTTTCAAACTTAATGGGGCGCTGGCA	31	#0_core	
06[111]	00[095]	GAATCTTTACGACTCCTTATCAGCGAAAGGA	31	#0_core	
06[132]	00[116]	ACCCATGAAAATTCGGAAGCGGGCGAGAAAG	31	#0_core	
06[153]	00[137]	TCACCACAATCAAGCAAAAGGACGGGGAAAG	31	#0_core	
06[174]	00[158]	AAATCACCGCCATTAACCACCAAGGGCGAAA	31	#0_core	
06[195]	00[179]	GGGATAGGGTTGCAACTCAGGAGAACGTGGA	31	#0_core	
06[216]	00[200]	GGTCGAGGAGCCTCGTGAATTGGAACAAGAG	31	#0_core	

06[237]	00[221]	GTGTAATCGCCTGAGTTACTTGGTTGAGTGT	31	#0_core	
06[258]	00[242]	CCTCGACAACATAGAGGAATACAAAAGAATA	31	#0_core	
06[279]	00[263]	TTAATCGCGTTTTAAACTCCTCGGCAAAAT	31	#0_core	
06[300]	00[284]	TTTTAAATAAAGGCAACATTATGTTTGATGG	31	#0_core	
06[321]	00[305]	TTCTGTATAAGCCAAAATTCTGCCCCAGCA	31	#0_core	
06[342]	00[326]	TCACATTAATTGCGTCAACGAGCAAGCGGT	31	#0_core	
07[021]	04[021]	CCTGAGTTAACCGTAAAAGAGCCAGAAT	28	#0_core	
07[049]	07[090]	ATTATCATTTTGTGATATTACCTTTTTAATGGACTTTTTAG	42	#0_core	
07[091]	07[132]	TATCATATGCGTCTAAATTACCGCGCCCAATAGAAAACAAGA	42	#0_core	
07[133]	07[174]	ATTGAGTTAAGCTGTCGACTTGAGCCATTTGGGCAGACTCAT	42	#0_core	
07[175]	07[216]	TAAAGCCAGAATCGAGAGCAAGCCCAATAGGAACAAACTGAG	42	#0_core	
07[217]	07[258]	GCTTGCAGGGAGTATCCAGACCAGGCGCATAGCGGATTTAC	42	#0_core	
07[259]	07[300]	CAGACGACGATAATATTGCTGAATATAATGCTGAAGCAATGC	42	#0_core	
07[301]	07[342]	AATGCCTGAGTAGATTGTAGCCAGCTTTCATCACATAAAGTG	42	#0_core	
08[048]	08[021]	ACTAGGAGCACTATCGGCCCTTGCTGGTA	28	#0_core	
08[090]	08[070]	TACGAGAAAAACAGTACATA	21	#0_core	
08[132]	08[112]	GCAACGTCAACAGCAAATCAG	21	#0_core	
08[174]	08[153]	CTCCACCCTAATTAGAGCCAGC	22	#0_core	
08[216]	08[196]	TTAAGGCTCCCCATGTACCGT	21	#0_core	
08[258]	08[238]	GCGAACTAACTGGCTGACCTT	21	#0_core	
08[300]	08[280]	AGCAAAATTTAGCTCAACATG	21	#0_core	
08[347]	11[347]	ATACGAGCCGGATCTGTGATTCTGTAATGCCTGCGAGGT	38	#0_core	
09[021]	15[048]	AACAGGAAAAACATAAGAATAATAGCCCTAAAAGGTCGTTTG	42	#0_core	
09[063]	09[062]	AACGGTCAATATCATAGAAATCCTTGAGTCAGATATAACAAT	42	#0_core	
09[105]	09[104]	TAATAATAGAAGACGGAGGTTTTGAACAGAACGGCAGAAAAA	42	#0_core	
09[147]	09[146]	ATAAGAAATCACCTTAGCAGCACCGTCATACATGACCACGGA	42	#0_core	
09[189]	09[188]	GATAAACTGAGAAAGTTAGCGTAACCTCAAGGTCCAGGCG	42	#0_core	
09[231]	09[230]	AACGGTCAAGAGTACATTCACTGAATCACTCATCAAAGTAC	42	#0_core	
09[273]	09[272]	GAAAGTTAATAAGATTCTGCGAACGATAGTCAATGAAGCCC	42	#0_core	
09[315]	09[314]	CAAAACGAGTAAATGTCACGTTGGTGAAGTACGCTAAAGCCC	42	#0_core	
10[027]	11[048]	TGGAAATGATTATTTACATTGGCAGATGAAAGGGA	35	#0_core	
11[070]	11[090]	AATAACCTTGCTATGCTGAAC	21	#0_core	
11[112]	11[132]	GTATTCTAAGAATTATCCCTA	21	#0_core	
11[154]	11[175]	CATTACCATTAGCAGAGCCCCA	22	#0_core	
11[196]	11[216]	CAGTACAACTAATAATAACC	21	#0_core	
11[238]	11[258]	CAAGAACCGGATAGGACGTAA	21	#0_core	
11[280]	11[300]	AGTACGGTGTCTATCCAATGA	21	#0_core	
11[322]	05[342]	GGATTCTCCGTGGCATCATGGCGGTTGCGCTCAC	35	#0_core	
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12[090]	12[049]	AATCGGTAATCTGTAATCGTCGTACAGTTTCTGATTATC	42	#0_core	
12[132]	12[091]	TTTTTTATCGCGAGGCGTTTTAGCGTTATGGCTTAATTGAG	42	#0_core	
12[174]	12[133]	ATGATGAACCAAGGCCGGAACGTGAGCAATTACCGAAGCCC	42	#0_core	
12[216]	12[175]	ACGAGGCGACAACGCCTGTAGCATTCTTAGACATGGCTTTTG	42	#0_core	
12[258]	12[217]	AGTAAAGTCATTATTACCCAAATCACCCGACAGCATCGGA	42	#0_core	
12[300]	12[259]	ATCAATAACGGAAGTTTCATTCCATAAGCGAGAGGGGGTAAT	42	#0_core	
12[335]	12[301]	TTGGAACAACGCGGATTTTCATAGTCAAATCACC	35	#0_core	
13[049]	13[048]	AATTCTAGTACTACCATCTGAACCTCAAAGCAAATCAAATGGC	42	#0_core	
13[091]	13[090]	TTTAACAGAAAAGTACTCTGAGAGACTACCACTATATCCATA	42	#0_core	
13[133]	13[132]	AAGTAAGGCAATACCCTAACGAGCGCTTGTAGCCATAAAGAA	42	#0_core	
13[175]	13[174]	AGTGTACACGTTAATGCGGTCATAGCCCTCATACCGACAGG	42	#0_core	
13[217]	13[216]	CAACGGCCGGTAAAAAATCTTCAACAGTCAGGAATTGGTAG	42	#0_core	
13[259]	13[258]	TTAGACTAAATGCTTCTTTAATCATTGTGTATACCAATGT	42	#0_core	
13[301]	13[300]	TATTCAAAACAAAGGCATTTGGGGCGCGCCGTAGCATTATGA	42	#0_core	
14[048]	14[049]	TGATTAGTTGGCGTCTAAAATATCTTCACCAGAAGATAATCC	42	#0_core	
14[090]	14[091]	TAATTTTATATACTAGACAAAGAACGCGAGTATCACAACATG	42	#0_core	
14[132]	14[133]	ACAAAAATAAACCGGATTTTTGTTTAAAGAAACCATAGCCGA	42	#0_core	
14[174]	14[175]	TTTAAATCAAAGACCCTCAGAGCGCTGAATTTAAATAAGT	42	#0_core	
14[216]	14[217]	TGAGGCAACTAAATATCTCCAAAAAATGCGGGAACGAGGCTT	42	#0_core	
14[258]	14[259]	AATACTGGCTCACTCGTTAATAAAACGAGAGGCAGAGCGTCC	42	#0_core	
14[300]	14[301]	GATAAAATAGTACAGCAAAGAATTAGATTCAAAGATCTAGCT	42	#0_core	
14[342]	08[322]	TAAGTTGGGTAAAGAGCTGTAGACATTAAATGTG	35	#0_core	
15[021]	12[021]	CGAACTGCGTGGCACTTCTGAACGACCA	28	#0_core	
15[049]	15[090]	GATTATACTTCTTAACAAACATAGCGATAGCTTTGGGTAGGC	42	#0_core	
15[091]	15[132]	AGAGGCATTTTCAATGGCCTTAAATCAAGATTAAACAAGTTAC	42	#0_core	

15[133]	15[174]	CAGAAGGAAACCAATAATCAGTAGCGACAGAATCATCGGGG	42	#0_core	
15[175]	15[216]	TCAGTGCCTTGAGACTGATCTAAAGTTTTGTCGGGAACTAA	42	#0_core	
15[217]	15[258]	AGACTTTTTCATAAAAAGGCTTGCCCTGACGAGAAGTGC	42	#0_core	
15[259]	15[300]	AATCGTCATAAATATTAGTAGATTAGTTTGACTACTATTAA	42	#0_core	
15[301]	15[342]	TGCCGGAGAGGGGTAATAGATGGGCGCATCGTAATTACGCCA	42	#0_core	
16[062]	16[021]	TTGAATAATGGAAGGGAATATCTCATCGCCATTAATAATACC	42	#0_core	
16[104]	16[063]	CTGAGCCAGTAATAAGCTTAGGTAGATTAAGACGCTGTCAGG	42	#0_core	
16[147]	16[105]	GAAGAGGAAACGCAATAGCCAGTTGTTGCTATTTTGCATTACG	43	#0_core	
16[189]	16[148]	TGAGTAACAGTGCCCGTCATCTTTCAAGTTTGCCTTTCGTA	42	#0_core	
16[231]	16[190]	ACTGAGGAAGTTTCCATATAGAAATCTTCCAGACGTTAGGC	42	#0_core	
16[273]	16[232]	GACTATTCAATGAATCCATTTAAGAAACACCGAAGACGATAC	42	#0_core	
16[315]	16[274]	ATCTAGCTATTTTGTAGTCAATTCATTAGATACATTTCCCT	42	#0_core	
16[347]	19[347]	CGGGCCTCTTCGGCCATTCGGAACAGGAAGATCGC	38	#0_core	
17[021]	17[034]	TGAGGCGGTCAATC	14	#0_core	
17[329]	16[316]	GCCATTCTACCGTGCATCTGCCGGTA	27	#0_core	
18[027]	19[062]	ACACCGCAATGAAAAATCTAAAGCATCCTTGATCAAAATTATTGCA	49	#0_core	
18[062]	18[063]	AAATAAACAGAAATATATTAATTAATTTCTCAATAGAACAG	42	#0_core	
18[104]	18[105]	AGACGACACCGCTGTAACTCCCGACTTTACAATTTGTCC	42	#0_core	
18[146]	18[147]	TTATTACCAAAAGGTGCCAATGAAACACCGACTGTAACCTC	42	#0_core	
18[188]	18[189]	TTCTGAATGAGAAGGACACAGACAGCCCTTGAATTTTATTA	42	#0_core	
18[230]	18[231]	CCTAAATACTTTGACACGTAACAAAGCTGAATTTGGGACCAA	42	#0_core	
18[272]	18[273]	ATAAATCGGGAAGCAATAACAGTTGATTAGGGTCAATTGACC	42	#0_core	
18[314]	18[315]	AGCAAACCATGTCAAGACCGTAATGGGAAGGGGACGCTGG	42	#0_core	
19[063]	19[104]	CGTAATGAATTTATCAAAATCATAGGCGACAAAGGTAAAGT	42	#0_core	
19[105]	19[146]	AATTCTATCCTGAATCTTACCAACGCAAAAGAACTGGCATGA	42	#0_core	
19[147]	19[188]	TTAAGGCGCGTTTTCATCGGCATTTTCCCTGCCTATTTG	42	#0_core	
19[189]	19[230]	GAACCCTGTATGGGATTTTGTAAACAGTAATGCCACTACG	42	#0_core	
19[231]	19[272]	AAGGCCTTGAGATGGTTAATTTCAAAACAGTTCAGAAAAAC	42	#0_core	
19[273]	19[314]	GAGAAAACCTGTTTAGCTATATTTTCTATCAGGTCAATTGCCT	42	#0_core	
19[315]	12[336]	GAGAGACGACAGTATCGGCCTCCAGGCAATCGCCAGGGTTTTGCCAAGC	49	#0_core	
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11[091]	11[111]	GCTCAACAGTAGCAACAATCG	21	#1_bottom	B1
11[133]	11[153]	GCAATAGCTATCCATATAAAC	21	#1_bottom	B2
11[176]	11[195]	GTAAGCGTCATGATTAGCAC	20	#1_bottom	B3
11[217]	11[237]	TCAGCAGCGAAAAGCGATTGA	21	#1_bottom	B4
11[259]	11[279]	AGAAGTTTTGCCGATTGCAAA	21	#1_bottom	B5
11[301]	11[321]	AAGGCCGGAGACATGTACCTC	21	#1_bottom	B6
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08[111]	08[091]	ATTCCCATCTATACAAATTCT	21	#2_top	T1
08[152]	08[133]	ATTTATTTCCAATAATAAGA	20	#2_top	T2
08[195]	08[175]	AAGTGCCGTGGAAAGCGCAGT	21	#2_top	T3
08[237]	08[217]	CAAGATTTGTTAAAGCGCGCT	21	#2_top	T4
08[279]	08[259]	TTACTTCAAAAAACCAAAATA	21	#2_top	T5
08[321]	08[301]	AGACAGGAAATGTGTAGGTAA	21	#2_top	T6
02[055]	02[035]	AATTTACAATAGATAATACAT	21	#3_left	L0
02[076]	02[056]	AAGCAAAAGCGCGCAGAGCGC	21	#3_left	L1
02[097]	02[077]	CTACCGTGTATCTTCTGACCT	21	#3_left	L2
02[118]	02[098]	ACGGTATTAATAATCGGCTGT	21	#3_left	L3
02[139]	02[119]	AAGAATTAATAAACATAAAAA	21	#3_left	L4
02[160]	02[140]	CCCGATTGATTACGAGCGCCA	21	#3_left	L5
02[181]	02[161]	CCGCCAGCATCAGAGCGCCA	21	#3_left	L6
02[202]	02[182]	CGGCCACCCATAGGTGTATCA	21	#3_left	L7
02[223]	02[203]	CCTGATACCTCAGCTTGCTTT	21	#3_left	L8
02[244]	02[224]	ATGCGCAGACCGCGACCTGCT	21	#3_left	L9
02[265]	02[245]	AAAATGCAGTCATCAGTTGAG	21	#3_left	L10
02[286]	02[266]	CATTAGAGAGAACCGACCGG	21	#3_left	L11
02[307]	02[287]	TGACTTTTGAATCGGTTGTAC	21	#3_left	L12
02[328]	02[308]	CTTGTTAAACGTTAATATTT	21	#3_left	L13
17[035]	17[055]	AAACCTCAATCTAGAACAA	21	#4_right	R0
17[056]	17[076]	TTGCGTAGATTTAGAAGAGTT	21	#4_right	R1
17[077]	17[097]	TTTAACCTCCGGAGAATATCA	21	#4_right	R2
17[098]	17[118]	ATAAACAACATGCCAGCTCC	21	#4_right	R3
17[119]	17[139]	AGAGCCTAATTTATAACGGAG	21	#4_right	R4
17[140]	17[160]	TATGTTAGCAAAAGCGTCATT	21	#4_right	R5

17[161]	17[181]	ATTAGCGTTTGCATAAACAAT	21	#4_right	R6
17[182]	17[202]	GAAAGTATTAAGAGTAAATTC	21	#4_right	R7
17[203]	17[223]	AGCGGAGTGAGATAAACGGAA	21	#4_right	R8
17[224]	17[244]	AGAGGCAAAAGAAGTAGTAAA	21	#4_right	R9
17[245]	17[265]	TTACCTTATGCGCCCTCAAAA	21	#4_right	R10
17[266]	17[286]	ATCAGGTCTTTACGCAAATCT	21	#4_right	R11
17[287]	17[307]	GAAAAGGTGGCAAGATCTAGA	21	#4_right	R12
17[308]	17[328]	GAATCGATGAACAGTTTGAGC	21	#4_right	R13
00[020]	00[005]	GCTACAGGGCGCGTAC	16	#5_ends	E0
00[361]	00[347]	TCACCGCCTGGCCCT	15	#5_ends	F0
01[005]	01[020]	TATGGTTGCTTTGACG	16	#5_ends	E1
01[347]	01[361]	ACAGCTGATTGCCCT	15	#5_ends	F1
02[020]	02[005]	TTAGAATCAGAGCGGG	16	#5_ends	E2
02[361]	02[347]	GCGGTTTGCGTATTG	15	#5_ends	F2
03[005]	03[020]	AGCTAAACAGGAGGCC	16	#5_ends	E3
03[347]	03[361]	AACGCGCGGGGAGAG	15	#5_ends	F3
04[020]	04[002]	CCTGAGAAGTGTTTTATA	19	#5_ends	E4
04[358]	04[343]	GGGAAACCTGTCGTGC	16	#5_ends	F4
05[002]	05[020]	ATCAGTGAGGCCACCGAGT	19	#5_ends	E5
05[343]	05[358]	TGCCCGCTTTCCAGTC	16	#5_ends	F5
06[020]	06[002]	TGTAGCAATACTTCTTTGA	19	#5_ends	E6
06[358]	06[343]	TAATGAGTGAGCTAAC	16	#5_ends	F6
07[002]	07[020]	TTAGTAATAACATCACTTG	19	#5_ends	E7
07[343]	07[358]	TAAAGCCTGGGTGCC	16	#5_ends	F7
08[020]	08[005]	ATATCCAGAACAATAT	16	#5_ends	E8
08[361]	08[348]	CAATTCCACACAAC	14	#5_ends	F8
09[005]	09[020]	TACCGCCAGCCATTGC	16	#5_ends	E9
09[343]	09[361]	TGAAATTGTTATCCGCTCA	19	#5_ends	F9
10[020]	10[005]	ACCTACATTTTGACGC	16	#5_ends	E10
10[361]	10[343]	CCCCGGGTACCGAGCTCGA	19	#5_ends	F10
11[005]	11[020]	TCAATCGTCTGAAATG	16	#5_ends	E11
11[348]	11[361]	CGACTCTAGAGGAT	14	#5_ends	F11
12[020]	12[002]	GTAATAAAAGGGACATTCT	19	#5_ends	E12
12[358]	12[343]	TAAAACGACGGCCAGT	16	#5_ends	F12
13[002]	13[020]	GGCCAACAGAGATAGAACC	19	#5_ends	E13
13[343]	13[358]	CCCAGTCACGACGTTG	16	#5_ends	F13
14[020]	14[002]	CAGACAATATTTTGAATG	19	#5_ends	E14
14[358]	14[343]	TGTGCTGCAAGGCGAT	16	#5_ends	F14
15[002]	15[020]	GCTATTAGTCTTTAATGCG	19	#5_ends	E15
15[343]	15[358]	GCTGGCGAAAGGGGGA	16	#5_ends	F15
16[020]	16[005]	GAACGAACCACCAGCA	16	#5_ends	E16
16[361]	16[348]	AAGGGCGATCGGTG	14	#5_ends	F16
17[005]	17[020]	GAAGATAAACAGAGG	16	#5_ends	E17
17[343]	17[361]	AGGCTGCGCAACTGTTGGG	19	#5_ends	F17
18[020]	18[005]	CTGCAACAGTGCCACG	16	#5_ends	E18
18[361]	18[343]	TCCGGCACCGCTTCTGGTG	19	#5_ends	F18
19[005]	19[020]	CTGAGAGCCAGCAGCA	16	#5_ends	E19
19[348]	19[361]	ACTCCAGCCAGCTT	14	#5_ends	F19

Supplementary Table 2
List of DNA staples - Origami Q

Start	End	Sequence	Length	Type	Pos.
00[031]	03[027]	ACAGGGCGCGTACTTTCCTCGAGCGGAGACAG	32	#_core	
00[053]	06[049]	CCCGCCGCGCTTATTACAAACAATTTTGAGTAAC	34	#_core	
00[073]	06[070]	CGCTGCGCTACTGAGCAAAAGAGGATTTGAA	32	#_core	
00[094]	06[091]	GCGCTGGCAAGTACCGACCGTGTATGCCTGTT	32	#_core	
00[115]	06[112]	AGCGAAAGGAGCAGAACGGGTATTAAGGAATC	33	#_core	
00[136]	06[133]	TGGCGAGAAAGGAGACGGGAGAATTAAGATAACC	34	#_core	
00[157]	06[154]	AACCGTCTATCATTCAACCGATTACACCGTCA	32	#_core	
00[178]	06[175]	ACTCCAACGTCGAGCCGCCGCACTAATAAAT	32	#_core	
00[199]	06[196]	AGTCCACTATTATTAGTACCGCCGATTTTCA	33	#_core	
00[220]	06[217]	GTTGTTCCAGTTTTCTTAACAGCTGATATAT	32	#_core	
00[241]	06[238]	ATAGCCCGAGATACTTAGCCGGAACGAGACAGAT	34	#_core	
00[262]	06[259]	AAATCCCTTATAAATACCACATTCCCAACCTA	33	#_core	
00[283]	06[280]	GATGGTGGTTCACTCCAACAGGTGTGGATGGC	32	#_core	
00[304]	06[301]	CCAGCAGGCGAACATTATGACCTAGAACCTT	32	#_core	
00[325]	06[322]	AAGCGGTCCACGAAAATTCGATTGGAATTCGC	33	#_core	
00[346]	01[346]	CTGGCCCTGAGATTTACCAAGTGA	24	#_core	
02[034]	07[048]	AGAATCAGTTAGTAGTTGTAGTATCGGCTTGCGATTATTTT	43	#_core	
02[346]	02[329]	GCGTATTGGGCGCCAGG	17	#_core	
03[028]	03[063]	GAACGGTACGCTACATTTTCGTATTAAATCCGCG	34	#_core	
03[064]	03[105]	CAGAGAAACAAACATCAATCTTCTAAGGCGTTAAATAAATA	41	#_core	
03[106]	03[147]	ATCGTACCGCACTCATCGAATAACACCTGAACAAAGGTT	40	#_core	
03[148]	03[189]	TACCGGAAGGTAATATCCCTCAGCAGGAGGTTGAGGCGGA	41	#_core	
03[190]	03[231]	ATAGAACC GCCACCTATCGGTTCCGATAGTTGCGCCTGT	40	#_core	
03[232]	03[273]	CGAAGACGGTCAATCATGTAGAAGCAGATACATAACGAG	39	#_core	
03[274]	03[315]	CTTCAGAGAGTACCTTTGAGCATACTTTTGCGGGAGAAATT	41	#_core	
03[316]	03[346]	TAATGTTAAATCAGCTCGCTGCATTAATG	29	#_core	
04[048]	10[028]	GTTAATAAAGAATCCTGAGAGCAAATTCACATT	34	#_core	
04[090]	04[049]	GAATCTTTCAGAAAACAAATTAATAATCTTTGCCGGAAC	40	#_core	
04[132]	04[091]	TGAGGAGAGAGAACAAGCAAGCCGATCAGAATAAACACCG	40	#_core	
04[174]	04[133]	TGGCCACCATGACGGAATTTATCATATGTCAGAGGGTAAT	41	#_core	
04[216]	04[175]	AACCATTGTCAGAACCGCCACCCTGCCAGGTGACACGAT	40	#_core	
04[258]	04[217]	TTACACAGAAGGGAACCGAACTGAATTGGACAATGACAAC	40	#_core	
04[300]	04[259]	ACGCACTCAAATGCTCCTTTTGATATTCGCCAAAAGGAA	40	#_core	
04[342]	04[301]	TCGTGCAATTTTTTAACCAATAGAAATGCCTTTATTTCA	40	#_core	
05[049]	05[048]	TTTAAAAAATATCATCTATCTAAAATATAATCAATAGTTAAT	42	#_core	
05[070]	05[069]	TTAACAACAGAATAACATCGGGAGAAACGTGTACAATACAT	42	#_core	
05[091]	05[090]	TACTAGAAAACGCTCACCAATCGCAAGATTTAGTTAAATAAT	42	#_core	
05[112]	05[111]	ATTTTCAGACCGGTATGTCCTGAACAAGAAGAAACCATTTTT	42	#_core	
05[133]	05[132]	AATATCACAAATAGCAAATAAGAAACTCCTTTACACGCT	40	#_core	
05[154]	05[153]	GGTGAATTGCGACCATACGCAAAGACACGAAAATTCATTAA	42	#_core	
05[175]	05[174]	ATTCACAACGTTCCAGCCGGAACCGCCTAAGAGCCTTGAT	40	#_core	
05[196]	05[195]	CCACCATTTCGTCAGTTTGTCTAGTAAAGATATACAGAG	42	#_core	
05[217]	05[216]	CACGCATCGGATCGTCAATTTTTTACGCGCCTTTAATCGCC	42	#_core	
05[238]	05[237]	CTTGAAAAGAGTAATATTATACCAAGAACTGATAACCAA	40	#_core	
05[259]	05[258]	ATAGTAAAGAGGCTTACGTTGGGAAGAAGCATTATTGAGGC	42	#_core	
05[280]	05[279]	GTCATTTTAAATATGTTGCATCAAAAGAGTTTAAAGAG	40	#_core	
05[301]	05[300]	AAAAATTTGTTCAAATCCAATAAATCATTATAAAGCAGGAT	42	#_core	
05[322]	05[321]	CCATCAATACGAGTAAATGTACCCCGTTTATAAGCGAACG	42	#_core	
06[048]	00[032]	ATTATAGAGCCGCTTAGACTATGCGCCGCT	31	#_core	
06[069]	00[054]	TTACCATAACCAATTCAATTACACCACACA	30	#_core	
06[090]	00[074]	TAGTATATATTTCTTTGAAATGTAGCGGTCA	32	#_core	
06[111]	00[095]	ATTACGCATGTAACATTCCAGGGCGCTAGG	31	#_core	
06[132]	00[116]	CACAAGTAGCAGCGTGCAGATTAAAGGGAAGAA	32	#_core	
06[153]	00[137]	CCGACCAATAGAGAGGGCGACACGGCGAACG	31	#_core	
06[174]	00[158]	CCTCACCACCTCTCCACCACCAAAAGGGCGAAA	34	#_core	
06[195]	00[179]	GGGATTTGATATCACAGGAGGAAGAAGCTGG	31	#_core	
06[216]	00[200]	TCGGTAAAGGAGTCAGGTGAATTGGAACAAG	31	#_core	

06[237]	00[221]	GAACGGTCATCGCCCCATGTTAGGGTTGAGT	32	#0_core	
06[258]	00[242]	TCATAGGAACAAAGATTAGGAATCAAAAGA	31	#0_core	
06[279]	00[263]	TTAGAAATATCGCGCGGAAGCAACGAAATCGGCA	34	#0_core	
06[300]	00[284]	CATATTTAAGCAGCACCAAAAAATCCTGTTT	32	#0_core	
06[321]	00[305]	GTCTGAAGATTGTATTTTGTCTGGTTTGCC	31	#0_core	
06[342]	00[326]	GCTAACTCACATTATTTTCTGAGTTGCAGC	32	#0_core	
07[021]	04[021]	ACTCAAACCAATACTTCATCACAGTGTT	28	#0_core	
07[049]	07[090]	GCGGAACAAAGATTGATTTTTTAATGGAACAGTCAAATCATA	43	#0_core	
07[091]	07[132]	TGCGTTATACAAACGACGCGCCCAATAGCAAGCAAAAAAATTGA	44	#0_core	
07[133]	07[174]	GTTAAGCCCAATCAATTTGAGCCATTTGGGAATTACCGTTAAA	43	#0_core	
07[175]	07[216]	GCCAGAATGGAAAGGGAGCAAGCCCAATAGGAACTCCACGCTG	43	#0_core	
07[217]	07[258]	AGGCTTGCGGGGTGTATGTACAGACCAGGCGCATTAAACCCCTC	44	#0_core	
07[259]	07[300]	GTTTACCAGACGATTGAGCTTAATTGCTGAATATAAAAAATTTT	44	#0_core	
07[301]	07[342]	AAATGCAATGCCAGGGCCTTCTGTAGCCAGCTCCGGAAGCAT	44	#0_core	
08[048]	08[021]	GAACTAATATGGTAATATCCAGAACAATA	30	#0_core	
08[090]	08[070]	ATACTTTTACATAAATCAATA	22	#0_core	
08[132]	08[112]	AACAAAAATGAATCAGATATAG	22	#0_core	
08[174]	08[153]	GACCTCAGAAGAGCCAGCAAAAT	23	#0_core	
08[216]	08[196]	CTAAAAGGCCCATGTACCGTA	21	#0_core	
08[258]	08[238]	AAAAACGAACAGGCTGGCTGAC	22	#0_core	
08[300]	08[280]	AGAATTAGCATGCTGTAGCTCA	22	#0_core	
08[347]	11[347]	CACACAACATACGATAGCTGTGAGCTCAGCTTGCATGC	38	#0_core	
09[021]	15[048]	CATGGAAATACCTTTCACAGACTCGCCATTAATCAATATACT	44	#0_core	
09[063]	09[062]	CGCCTTGAGTAACCTTGAAACATAATATACCTACGGATT	42	#0_core	
09[105]	09[104]	CCCATGGCTTATTTTTTGAAGCCTTCGCTGTGATAATAT	42	#0_core	
09[147]	09[146]	TTTATACCAGTACCCAGCACCGTAATATAAAGGAGGAATAAG	42	#0_core	
09[189]	09[188]	AAGTGACTGAGTGAATAGTTAGCGTAAAGAGAATAGCGGGAT	42	#0_core	
09[231]	09[230]	GTACAATCATCAAACTGCTCATTCAGTAACACTCTAAAACAAA	44	#0_core	
09[273]	09[272]	AGCCCATGTTTTCAATCCCAATTCTCTATTATAAGTAAGAGGA	44	#0_core	
09[315]	09[314]	AAAGCATGTGAGATTGGGATAGGTCATCGTAAATCAATCAGA	42	#0_core	
10[027]	11[048]	TTGACGCAGATTCACCAGTCACACGAAGGTAT	32	#0_core	
11[070]	11[090]	TGCTTCTGTAATGCAAAATAC	20	#0_core	
11[112]	11[132]	TAAGAACGCGAGCAATCCAT	20	#0_core	
11[154]	11[175]	CCATTAGCAAGGCCACCATAA	21	#0_core	
11[196]	11[216]	AGTACAACTAGAATAATAC	20	#0_core	
11[238]	11[258]	TGACAAGAACCGGTCAGGTG	20	#0_core	
11[280]	11[300]	ACTAAAGTACGATTAACAGG	20	#0_core	
11[322]	05[342]	ACCCGTCGGATTGAGAAATTCGAAATTCGCTTGC	34	#0_core	
12[048]	18[028]	CAATTGAGGACCAAGTAATAAGAAATACATAACAG	34	#0_core	
12[090]	12[049]	ATATTCTGAATCGTCGTATTAATTGTAAGTATGATGG	40	#0_core	
12[132]	12[091]	AAGAATCCGCGTTTTAGCGAACCTCAATTTGAGAATCGCC	40	#0_core	
12[174]	12[133]	TACAGCAGAGCCGGAACGTCACCAATATGAAGCCCTTTT	41	#0_core	
12[216]	12[175]	GAACGTTGCAACGCCTGTAGCATGATTGGCTTTTGATGA	40	#0_core	
12[258]	12[217]	GGTAACCAGATATTCATTACCCAAACCAAGACAGCATCG	40	#0_core	
12[300]	12[259]	ATCACTAGCGTGTCTGGAAGTTTCAAGCATTGCCAGAGGG	40	#0_core	
12[335]	12[301]	GCCTCCGTGGGAACAACTGTGGGAGACAGTCAA	34	#0_core	
13[049]	13[048]	AATATAAGTCAAAATTATCAAACCTCAGTAAGGAATTCATC	42	#0_core	
13[091]	13[090]	ACGCCAAAACGACAAAGACTACCTTTTGAGTAAATGTAACA	42	#0_core	
13[133]	13[132]	TAAGCAGATCCAAAAGAGCGTCTTCCGAATTATTTAAAG	40	#0_core	
13[175]	13[174]	TACTGGTTGATGCCCCATAGCCCCCTATCGGAACGAGTG	40	#0_core	
13[217]	13[216]	AGCAACGAAGGGTAAAAACAACCTTCAACCCAAAGGAAAGGGT	42	#0_core	
13[259]	13[258]	AAAATGTTATCAATGTCAACTTTAATCAATCATTATATAGT	42	#0_core	
13[301]	13[300]	ATATGATAGGATCTACATTTTCATTTGGGTATAGTAGCATCA	42	#0_core	
14[048]	14[049]	TGGATCAGTTGAGGAGGAGCACTAACGCGGAATTAGATTGTT	42	#0_core	
14[090]	14[091]	GGCAGACTATATGAACGCGAGAAAAAGCCAAATAATTTA	42	#0_core	
14[132]	14[133]	AAGTTACAGCCATGGTTTTGTTAACGTACAATGACGCCGAACA	44	#0_core	
14[174]	14[175]	ACGGGAAAATCACAGTCAGAGCCGCCACATTTACCAAGTTTTA	44	#0_core	
14[216]	14[217]	TTTGAAACAACCTCAAATCTCCAAATTTGCGGCGCAGAGGC	42	#0_core	
14[258]	14[259]	AGCGTAACTGGCAGTCTACGTTAATATAGCGAGATACTGGAT	42	#0_core	
14[300]	14[301]	CTAGCTCTACTATGGGCAAGGCAAGGTAAAGAATAACCGTT	42	#0_core	
14[342]	08[322]	GGCGATTAAAGTTGAACATGGTCAGTTTCATCAACATT	36	#0_core	
15[021]	12[021]	CTAAACAATAATTTTAGCGTAAAGGGA	28	#0_core	
15[049]	15[090]	TCTGAATAATGGGATGAGCGATAGCTTAGATTAATATAAGGCA	43	#0_core	
15[091]	15[132]	TTTTGAGCCAGAACGAAATCAAGATTAGTTGCTTAACCGAGAA	44	#0_core	

15[133]	15[174]	GGAAACCGAGGAATACCACTAGCGACAGAATCAAATCGTCAG	43	#0_core	
15[175]	15[216]	TGCCTTGAGTAACCTCACGATCTAAAGTTTTGTCAAGGGGACT	43	#0_core	
15[217]	15[258]	AAAGACTTTTTCTAAGAATAAGGCTTGCCTGATAAGCCAATA	44	#0_core	
15[259]	15[300]	CTGCGGAATCGTCCTGAGCGAACGAGTAGATTAGCAATTGATA	44	#0_core	
15[301]	15[342]	AATTAATGCCGGGTAACTGTGGTGATAGTGGCGCTTCGCTATT	44	#0_core	
16[062]	16[021]	CAAAGGGTTAGAACCTTTGGCAAAATACCGAACGAACCACCAGC	44	#0_core	
16[104]	16[063]	AGTAATAAGAGAATATTGGGTTAGACGCTGAGAAGAGTAACGT	43	#0_core	
16[147]	16[105]	TACAACGCAATAATAACTTACAAAAATTTTGACCCAGCTAATGC	45	#0_core	
16[189]	16[148]	ACTCAGTGCCCGTATAATTTTCATGTTTGCCTTTAGCGTAAAA	43	#0_core	
16[231]	16[190]	ACAATGAGGAAGTTCCGAATAGAGTCTTTCCAGACGTCTGAG	43	#0_core	
16[273]	16[232]	ACCATAAATATTCTTATGATGCGATTTCGAGAAACACCAGAAGAAT	45	#0_core	
16[315]	16[274]	ACGAGAGGGTAGCTATTGTGGCATTTTGACCATTAGATACTTT	43	#0_core	
16[347]	19[347]	GATCGGTGCGGGCGCGCATTTTCTGGTCGGCTCAGG	38	#0_core	
17[021]	17[034]	TAACACCGCCTGCCA	15	#0_core	
17[329]	16[316]	AGGCAAACCTCATCGTAACCGTGCGATGA	28	#0_core	
18[027]	19[062]	TGCCACGCATCACCTTGCTGAACCTCAAATATTGCACGTAAAC	45	#0_core	
18[062]	18[063]	AAATTGCTCAGTAACAAATTTCCCTTAAAGAATTTATAAAG	42	#0_core	
18[104]	18[105]	CGACAATCATTATCAACCCGACTTGCGGAGTTATCCTGACGA	42	#0_core	
18[146]	18[147]	ACGCAGTATTGGCAACATGAACCATCGTATAGCGCGTTATT	42	#0_core	
18[188]	18[189]	TGAAACAAAGGATTAGTCCACAGACAGCAGTGAATTTTATTC	42	#0_core	
18[230]	18[231]	CCAACCTGCATCTTGATCAACGTAACATGTAAATTGGCA	40	#0_core	
18[272]	18[273]	TGACCATTGTGAGATTCCATATAACAGGCAAAATGGGAGAA	40	#0_core	
18[314]	18[315]	AGTCTGGATACTAGCAGGCGGATTGACCAAAGTTTGACTGAG	42	#0_core	
19[063]	19[104]	AGAAATCAAATCATAGGTCTGAGAAGGTAAGTAATTCTG	41	#0_core	
19[105]	19[146]	TCCAGAATCTTACCAACGCTAACGAACCTGGCATGATTAAG	40	#0_core	
19[147]	19[188]	ACTCCTTTTCATCGGCATTTTCGGTCTGCCTATTTTCGGAAC	41	#0_core	
19[189]	19[230]	CTATTCTGTATGGGATTTTGCTAAATACGTAATGCCACTA	40	#0_core	
19[231]	19[272]	CGAAGGGCTTGAGATGGTTTAATTCTTTAAACAGTTCAG	39	#0_core	
19[273]	19[314]	AAAACCTCAATAACCTGTTTAGCTATAAAGGCTATCAGGTCA	41	#0_core	
19[315]	12[336]	TTGCGGGGACGACGACAGTATGCCGGAGTGGTAACGCCAGGCCAGT	46	#0_core	
11[049]	11[069]	ATTCTGTATTACTTTTACCT	20	#1_bottom	B0
11[091]	11[111]	AGTAGGGCTTAAAGATAATC	20	#1_bottom	B1
11[133]	11[153]	AGCTATCTTACCAAAAGAATA	21	#1_bottom	B2
11[176]	11[195]	GCGTCATACATAGCGGGCC	19	#1_bottom	B3
11[217]	11[237]	CCTCAGCAGCGACCGCGCT	20	#1_bottom	B4
11[259]	11[279]	CAAAGAAGTTAAGCGGACA	20	#1_bottom	B5
11[301]	11[321]	GTGAGAAAGGCCAATCATCA	20	#1_bottom	B6
08[069]	08[049]	TAGATTGCTAACCAACAGAAG	21	#2_top	T0
08[111]	08[091]	AACCTAATTTATTCTTACCAGT	22	#2_top	T1
08[152]	08[133]	CTTTGTCAAATAAGAGCAAG	20	#2_top	T2
08[195]	08[175]	ACCCGTGAGAGCGCAGTCTCT	22	#2_top	T3
08[237]	08[217]	CTCGGAGATTAGTTAAAGCCCG	22	#2_top	T4
08[279]	08[259]	ACGAAAGACCGATAAAACCAA	22	#2_top	T5
08[321]	08[301]	AACCCAAAAATGAGTAATGTGT	22	#2_top	T6
02[055]	02[035]	ATCGACAACCTGAGGATTTAGA	21	#3_left	L0
02[076]	02[056]	ATAGATGATGGCGAATTATTC	21	#3_left	L1
02[097]	02[077]	TTGATAAATGACCTAAATTTA	21	#3_left	L2
02[118]	02[098]	GGAACCAAGGCTGTCTTCC	21	#3_left	L3
02[139]	02[119]	AAAACCTGAACATAAAACAG	20	#3_left	L4
02[160]	02[140]	GAGAGGGAGAGCGCCAAAGAC	21	#3_left	L5
02[181]	02[161]	TAGCATTGAAGCCGCCACCA	20	#3_left	L6
02[202]	02[182]	TTACCCTCAGGTGTATCACCG	21	#3_left	L7
02[223]	02[203]	TGCTTGATATATCAGCTTGCT	21	#3_left	L8
02[244]	02[224]	TGGAGGCGCAATCCGCGACC	20	#3_left	L9
02[265]	02[245]	GAAACTAATAGATTTCATCAGT	21	#3_left	L10
02[286]	02[266]	TTCAGGATTAAGCGAACCA	20	#3_left	L11
02[307]	02[287]	AATGTAATAAAGCTAAATCGG	21	#3_left	L12
02[328]	02[308]	GTAATTTTATTGTAAACGTT	21	#3_left	L13
17[035]	17[055]	ATATCTGGTCAGACCATATAG	21	#4_right	R0
17[056]	17[076]	ATTTTCAGGTTTCAATAGTCC	21	#4_right	R1
17[077]	17[097]	TCCGGCTTAGGTAAAGTACAC	21	#4_right	R2
17[098]	17[118]	AACATGTTTCAGCTACAATTAG	21	#4_right	R3
17[119]	17[139]	CCTAATTTGCCAGGGAATACGT	22	#4_right	R4
17[140]	17[160]	TAGCAAACGTAGCAGACTGTT	21	#4_right	R5

17[161]	17[181]	AGCGTTTGCCATCACAGTTAA	22	#4_right	R6
17[182]	17[202]	AGTATTAAGAGGTAGTAAATT	21	#4_right	R7
17[203]	17[223]	TCAGCGGAGTGAATTAACAA	21	#4_right	R8
17[224]	17[244]	CGAAAGAGGCAAAACGAGTATG	22	#4_right	R9
17[245]	17[265]	TGAATTACCTTAATCCCCAA	21	#4_right	R10
17[266]	17[286]	TCAAAAATCAGGTCATTTGCGG	22	#4_right	R11
17[287]	17[307]	CGAGCTGAAAAGTTTGAGACA	21	#4_right	R12
17[308]	17[328]	AACAAGAGAATCATCTGCCCC	21	#4_right	R13
00[020]	00[005]	CTATGGTTGCTTTGAC	16	#5_ends	E0
00[361]	00[347]	ATTGCCCTTCACCGC	15	#5_ends	F0
01[005]	01[020]	GAGCACGTATAACGTG	16	#5_ends	E1
01[347]	01[361]	GACGGGCAACAGCTG	15	#5_ends	F1
02[020]	02[005]	GAGCTAAACAGGAGGC	16	#5_ends	E2
02[361]	02[347]	GGGGAGAGGCGGTTT	15	#5_ends	F2
03[005]	03[020]	CGATTAAAGGGATTTT	16	#5_ends	E3
03[347]	03[361]	AATCGGCCAACGCGC	15	#5_ends	F3
04[020]	04[002]	TTTATAATCAGTGAGGCCA	19	#5_ends	E4
04[358]	04[343]	CCAGTCGGGAAACCTG	16	#5_ends	F4
05[002]	05[020]	CCGAGTAAAAGAGTCTGTC	19	#5_ends	E5
05[343]	05[358]	GCTCACTGCCGCTTT	16	#5_ends	F5
06[020]	06[002]	CTTGATTAGTAATAACAT	19	#5_ends	E6
06[358]	06[343]	GGTGCCTAATGAGTGA	16	#5_ends	F6
07[002]	07[020]	CACCTGCCTGAGTAGAAGA	19	#5_ends	E7
07[343]	07[358]	AAAGTGTAAGCCTGG	16	#5_ends	F7
08[020]	08[005]	TTACCGCCAGCCATTG	16	#5_ends	E8
08[361]	08[348]	TCCGCTCACAATTC	14	#5_ends	F8
09[005]	09[020]	CAACAGGAAAAACGCT	16	#5_ends	E9
09[343]	09[361]	TTCCTGTGTGAAATTGTTA	19	#5_ends	F9
10[020]	10[005]	CTCAATCGTCTGAAAT	16	#5_ends	E10
10[361]	10[343]	TAGAGGATCCCCGGGTACC	19	#5_ends	F10
11[005]	11[020]	GGATTATTTACATTGG	16	#5_ends	E11
11[348]	11[361]	CTGCAGGTCGACTC	14	#5_ends	F11
12[020]	12[002]	CATTCTGGCCAACAGAGAT	19	#5_ends	E12
12[358]	12[343]	ACGTTGTAAAACGACG	16	#5_ends	F12
13[002]	13[020]	AGAACCTTCTGACCTGAA	19	#5_ends	E13
13[343]	13[358]	GGTTTTCCAGTCACG	16	#5_ends	F13
14[020]	14[002]	TGAATGGCTATTAGTCTTT	19	#5_ends	E14
14[358]	14[343]	GGGGGATGTGCTGCAA	16	#5_ends	F14
15[002]	15[020]	AATGCGCGAACTGATAGCC	19	#5_ends	E15
15[343]	15[358]	ACGCCAGCTGGCGAAA	16	#5_ends	F15
16[020]	16[005]	AGAAGATAAACAGAG	16	#5_ends	E16
16[361]	16[348]	CTGTTGGGAAGGGC	14	#5_ends	F16
17[005]	17[020]	GTGAGGCGTCAGTAT	16	#5_ends	E17
17[343]	17[361]	CGCCATTGAGGCTGCGCAA	19	#5_ends	F17
18[020]	18[005]	GCTGAGAGCCAGCAGC	16	#5_ends	E18
18[361]	18[343]	GCCAGCTTTCCGGCACCGC	19	#5_ends	F18
19[005]	19[020]	AAATGAAAAATCTAAA	16	#5_ends	E19
19[348]	19[361]	AAGATCGCACTCCA	14	#5_ends	F19

Supplementary Table 3

List of DNA staples - Origami H

Start	End	Sequence	Length	Type	Pos.
00[031]	03[027]	GTAATATGTTGTTAGAATCCTAAACCGGTAC	32	#_core	
00[053]	06[049]	GCTTAATGCGCCGAATTCGACAACCTATTATCAT	34	#_core	
00[073]	06[070]	CGTAACCACCACAAAGAAGATGATAAATTACCT	33	#_core	
00[094]	06[091]	CAAGTGTAGCGCGTGTGATAAATACAGTTTAGTA	34	#_core	
00[115]	06[112]	AGGAGCGGGCGCGTATTAAACCAAATTCATTAC	33	#_core	
00[136]	06[133]	AGAAAGGAAGGGGAGAATTAACGACGACCCACA	34	#_core	
00[157]	06[154]	AACCGTCTATCACCGATTGAGGGCACACCGAC	32	#_core	
00[178]	06[175]	ACTCCAACGTGCGCGCCGACGACAAATAAA	32	#_core	
00[199]	06[196]	GAGTCCACTATTGTTTAGTACCGCGGTCAATTTTC	35	#_core	
00[220]	06[217]	GTGTTGTTCCACTTAAACAGCTTCCATATATT	32	#_core	
00[241]	06[238]	AGAATAGCCCGATTAGCCGGAACGAGAGACAGAT	34	#_core	
00[262]	06[259]	GGCAAAATCCCTATACCACATTACGACACTAT	33	#_core	
00[283]	06[280]	GTTTGATGGTGCTCCAACAGGTCTTGATGGCT	32	#_core	
00[304]	06[301]	TGCCCCAGCAGAAACATTATGACCGTTTTTTAGA	34	#_core	
00[325]	06[322]	GCAGCAAGCGGTTTGTTAAATTTCCCAAAAT	33	#_core	
00[346]	01[346]	CACCGCTGGCCTTTTCTTTTCA	24	#_core	
02[034]	07[048]	ACGGGAGAGAGCTTCAATACTCTGCTGGTAACCGTGAACA	44	#_core	
02[346]	02[329]	GCGGTTTGCCTATTGGG	17	#_core	
03[028]	03[063]	GCCAGAATCCTAGGATTAATCCTTTGCCGCGG	33	#_core	
03[064]	03[105]	AATACATCAAGAAAACGACCTAATAAATAAGAAATAGCT	39	#_core	
03[106]	03[147]	GTCACCTATCGAGAACCATAAAGAACAAAGTCAGACCA	38	#_core	
03[148]	03[189]	GCGCGTAAATATTGACGTCAGAGGGAGGTTGAGGCACGG	39	#_core	
03[190]	03[231]	AATAGAACCGCCACCGGTTTATATAGTTGCGCGGATCG	39	#_core	
03[232]	03[273]	AAAACGGTCAATCATATAGAAACAGATACATAACGAGC	38	#_core	
03[274]	03[315]	TTCAGAGAGTACCTTTAAGAGCATACTTTTGCGGGACAA	39	#_core	
03[316]	03[346]	ATAATTTTGTAAATGTGCCAGCTGCA	28	#_core	
04[048]	10[028]	TTTTTTGGAGAAGTGTTAACGTTGCGGCTC	33	#_core	
04[090]	04[049]	ATAATTTCTAAAATTAATTACATTAGAGAACGTTATTAA	39	#_core	
04[132]	04[091]	CGCTATAAAGCAAGCCGTTTTTTCGACACCGGAATC	38	#_core	
04[174]	04[133]	TGGCACCCGAAATTATTCATTAATTTAGGGTAATTGAG	39	#_core	
04[216]	04[175]	ACCATTATCTCAGAACCGCCACCCAGCCGTCAGACGAT	39	#_core	
04[258]	04[217]	TACGCAGGAGGGAAACCGAATGATGTGCAATGACAACA	38	#_core	
04[300]	04[259]	TTCACTCTATTGCTCTTTTGATATTGCGCAAAAGGAAT	39	#_core	
04[342]	04[301]	AACCTGTCCAGCTCATTTTAAATAAGGAAGCCTTTAT	38	#_core	
05[049]	05[048]	TTTGAGTGGTATTCTATATCTTAGGAGTTAATACAAAAAG	42	#_core	
05[070]	05[069]	ATTTATCGCTTGCTTGAAACAATAACAATCGCGCTAACA	40	#_core	
05[091]	05[090]	GAAAAAATCAGTAGCAAGACAAAGAATTTTCATCTACTA	40	#_core	
05[112]	05[111]	CATCGTATTTCTAAGAACAGAAAAATAGCATCAATAATTT	42	#_core	
05[133]	05[132]	TCAGAGAAAAATAGCTGAACGATTTTGAGAGAGAGAAATA	40	#_core	
05[154]	05[153]	ATTATCACTATTACCAAAGACACCACGGGACATATGGGGTGA	42	#_core	
05[175]	05[174]	TATTCATATTCCAGTGAACCGCTCCCGCCACCCCTTGA	40	#_core	
05[196]	05[195]	GCCACCAACGTCACGGTTTTGCTCAGAATAAGTATTCAGA	40	#_core	
05[217]	05[216]	ACGCATACGCGTCACCTTTTTCACGTTGACTTAATTGCGCCC	42	#_core	
05[238]	05[237]	CTTTGAAAAGTAATCTTATACCAAGCGACGATAAATCCAA	40	#_core	
05[259]	05[258]	TAGTAAGGAGGCTTTTCGTTGGGAAGAAAGATTATTAAGGCA	42	#_core	
05[280]	05[279]	TCATTTTATAATATGCTGCATCAAAAAAGTTTAAAGAGG	40	#_core	
05[301]	05[300]	AGGATACCGATTCAATCCAATAAATCTGAATAAAGACGCA	40	#_core	
05[322]	05[321]	AGGAACGGAGTGAGCGATCATATGTACCAAGATTGTACCAAT	42	#_core	
06[048]	00[032]	TTTGCCAATAGAAGTACAAACCTACAGGGCGC	32	#_core	
06[069]	00[054]	TTTTTTTACAAAACACCTGAGCAACCCGCGC	32	#_core	
06[090]	00[074]	TCATATAGTTAAGATACCGACGTACGCTGCG	32	#_core	
06[111]	00[095]	CGCGCGAAACCACTAGAACGGTAGGGCGCTGG	32	#_core	
06[132]	00[116]	AGAATTCCTTTACAATAGACGGAAGAAAGCGAA	33	#_core	
06[153]	00[137]	TTGAGGAAAATTAACATTCAAGAACGTGGCG	32	#_core	
06[174]	00[158]	TCCTCCCCCTCAGAGTCCACGAGAAAGGGCGAAA	34	#_core	
06[195]	00[179]	AGGGAGTTGATAACTCAGGAGAAAGAACGTGG	32	#_core	
06[216]	00[200]	CGGTCGGAGCCTCCTGAATTTGTTTGGAAACAA	32	#_core	

06[237]	00[221]	GAACGGATCGCTCGATGTTACGATAGGTTGA	33	#0_core	
06[258]	00[242]	CATAAGAACAAACAGTTTAGGATATAAATCAAA	32	#0_core	
06[279]	00[263]	TAGAGATATCGCGCAGAAGCAAAGTTCCGAAATC	34	#0_core	
06[300]	00[284]	ACCCTATTAAGCCGGTACCAAGCGAAATCCT	32	#0_core	
06[321]	00[305]	AATTACAGGAAAATAATATTCCACGCTGGTT	32	#0_core	
06[342]	00[326]	AGTGAGCTAACTCATAGGGTGGCTGAGAGAGTT	33	#0_core	
07[021]	04[021]	CTATCGGCTCTTTGATCAAATTTTATAA	28	#0_core	
07[049]	07[090]	AAGAAACCAACCACAAGAATGGAACAGTACATAAAATTTGCGT	44	#0_core	
07[091]	07[132]	TATACAAATCTTTGTACCAATAGCAAGCAAATCAGGCAGGAGTTA	46	#0_core	
07[133]	07[174]	AGCCCAATAATAAAATACCATTTGGGAATTAGAGCGCCAATTAA	44	#0_core	
07[175]	07[216]	AGCCAGAATGGAAGAGGTAGCAAGCCCAATAGGAACAAAAGCTGA	45	#0_core	
07[217]	07[258]	GGCTTGCAGGGAGTATCTGTACAGACCAGGCGATAAACGCCCTCG	46	#0_core	
07[259]	07[300]	TTTACCAGACGACTCAACTTAATTGCTGAATATAACAAACATAT	44	#0_core	
07[301]	07[342]	ATTTTAAATGCAAAAAGCGTCTGGCCTTCTGTAGTACGAGCCGG	46	#0_core	
08[048]	08[021]	TTGATTAGAGTCCAGAACAATATTACCGCCA	31	#0_core	
08[090]	08[070]	CACAAATATTCAATATATGTGA	22	#0_core	
08[132]	08[112]	TGTGAAAATAATATAGAAGGCTT	23	#0_core	
08[174]	08[153]	AACAGAACCCAGCAAAATCACCA	23	#0_core	
08[216]	08[196]	TTAGGCTCCCATGTACCGTAA	22	#0_core	
08[258]	08[238]	ATAACGAACTGGCTGGCTGACCT	23	#0_core	
08[300]	08[280]	TGGAATTAGTGCTGTAGCTCAA	22	#0_core	
08[347]	11[347]	CAATTCCACACAACATGGTCAGGGTACGTGCCAAGCTT	38	#0_core	
09[021]	15[048]	ACCTACATTTTGAACAATATTTAAAAATACCGAATGAATGAATA	45	#0_core	
09[063]	09[062]	TTGCTGAATAACCGAAACATAGCGATGTAACAGTTTTTCGCTGA	44	#0_core	
09[105]	09[104]	TAATTCCGGTATGTAAGCCTTAAATCTTATCAAATCCCATCC	42	#0_core	
09[147]	09[146]	TTTGTAGCACCCACCGTAATCAGTAGGTGGCAGAAGTTTAT	42	#0_core	
09[189]	09[188]	TAAGTCTGAGTTTAAATAGTTAGCGTAACAAGAGAAAAGGCGGA	44	#0_core	
09[231]	09[230]	ACAACGATCAAGAATCTGCTCATTCACTCATACACAAAAGT	44	#0_core	
09[273]	09[272]	GCCCGTGTTTTAACTTCCCAATTTCTGTATTATAGGAAAGAGGAA	44	#0_core	
09[315]	09[314]	TCAGAATTAATATACCGTAATGGGAGGTAATCATTTGATAA	42	#0_core	
10[027]	11[048]	AATCGTCAGTCACACGACCAAGTCTCTAAGA	31	#0_core	
11[070]	11[090]	GTAATTCGTCGCAATCGGG	20	#0_core	
11[112]	11[132]	GCGAGGCGTTTAAATAAAT	19	#0_core	
11[154]	11[175]	AGCAAGGCCGGCCACCGAAG	20	#0_core	
11[196]	11[216]	GTACAACTACTAATAATCT	20	#0_core	
11[238]	11[258]	ACAAGAACCGGTGAGGAGC	19	#0_core	
11[280]	11[300]	CTAAAGTACGGATTAAACA	19	#0_core	
11[322]	05[342]	TAACAACCCGTACGAGCTCCACATTAATTGC	33	#0_core	
12[048]	18[028]	CAATGTTAATAAAAGGGACGTGGCACCTACGCT	33	#0_core	
12[090]	12[049]	TAACAAATCTATTAATTAATTTTACATGGCAATTCAT	39	#0_core	
12[132]	12[091]	AAAGATCCTAGCGAACCTCCCGATAAGATCGCCATATT	38	#0_core	
12[174]	12[133]	ATACGCCAAAACGTACCAATGAAAAGCCTTTTAAAGA	39	#0_core	
12[216]	12[175]	AACGACGAAAACGCCTGTAGCATTGGATGGCTTTTGATG	39	#0_core	
12[258]	12[217]	GTAACCAGATATTATTACCAACCCCGACAGCATCGG	38	#0_core	
12[300]	12[259]	GTCATAGCTGTCTGGAAGTTTCATGCAATGCCAGAGGGG	39	#0_core	
12[335]	12[301]	GCCGGATTCTCCGTGGGTAGCGGCCGGAGACA	32	#0_core	
13[049]	13[048]	CCTGATTTTTTGCACCTCAATCAATATAGGAGGAAGATAAT	42	#0_core	
13[091]	13[090]	AACATGATGTAAGCTTTTTAACCTCTTCTGATGCACGCC	40	#0_core	
13[133]	13[132]	CAGATAGAGGAAGTGTTCAGAGCCTTTATCCATAAG	40	#0_core	
13[175]	13[174]	TGTAAGTATATGCCCCGCCCTTATTAGACCAGAAGGAG	40	#0_core	
13[217]	13[216]	GCAACGGAATAAAATAACTTTCAACAGTCCGGAATTGGGGTA	42	#0_core	
13[259]	13[258]	AAATGTTAACAAATGCCAATTTAATCAAACATTATATAGTA	42	#0_core	
13[301]	13[300]	CCATCATCAGAGATATTTTCAATTTGTTATAGTAGAATCA	40	#0_core	
14[048]	14[049]	ACTTCAGGAATTACTAACAACTAATAATCATCAATGGATTAT	42	#0_core	
14[090]	14[091]	AGGCAGTAAATGGAAGAAAACCTTTTACGCTCAAATTTAGGCAG	44	#0_core	
14[132]	14[133]	TACCAGTATTATTGTTAACGTCAAAAAAATAGCTAACAAAGT	44	#0_core	
14[174]	14[175]	TAACGTACCGGACAGAGCGCCACCTTTTACCGCTAAGTTT	44	#0_core	
14[216]	14[217]	TTGAGAACTAAATCTCTCAAAAAAAGCGGGAATAAGAGGCT	42	#0_core	
14[258]	14[259]	GCGTCACTGGGTAGCTACGTTAATAAAGCGAGATTCTGGATA	42	#0_core	
14[300]	14[301]	ACCGTTCTACTAGAAGGCAAGGCAATAGGTAAGGGATATTCA	44	#0_core	
14[342]	08[322]	TGCAAGGCGATTATGTCGAATCACCAGCTTTCATCA	37	#0_core	
15[021]	12[021]	ATCGCCATTTGAATGGGAATACATTCTG	28	#0_core	
15[049]	15[090]	ATGGAAGGGTTATACAAGCTTAGATTAAGACGCTGATATTTTCG	45	#0_core	
15[091]	15[132]	AGCCAGTAATAAGCTGTAAGATTAGTTGCTATTTTGCCAAAGGAA	46	#0_core	

15[133]	15[174]	ACCGAGGAAACGCTAAAGCGACAGAATCAAGTTTGAAAAGGGTC	44	#0_core	
15[175]	15[216]	AGTGCCCTTGAGTATCCTCGATCTAAAGTTTTGTCGTGAACGACTA	45	#0_core	
15[217]	15[258]	AAGACTTTTTCATAAAAGAATAAGGCTTGCCCTGACAAGACAATAC	46	#0_core	
15[259]	15[300]	TGCGGAATCGTCATGACCGAACGAGTAGATTTAGTCAATTCTAG	44	#0_core	
15[301]	15[342]	CTGATAAAATTAATGAACTAGGTCACGTTGGTGTAGAGGGCCTCTTC	46	#0_core	
16[062]	16[021]	TAGAACCTACCATATCTCAACAGTCGAACCAACAGCAGAAGATAA	45	#0_core	
16[104]	16[063]	GCAGAATATAAAGTACCATATAACTAGAAGAGTCAATAGTGATGAA	46	#0_core	
16[147]	16[105]	ACAAATAATAACGGAATAAATAAACACACCCAGCTACAATTGAACGC	47	#0_core	
16[189]	16[148]	GACACAGTGCCGTATAACATAATCCCTTTAGCGTCAGACACAT	44	#0_core	
16[231]	16[190]	ACTGAGGAAGTTTCCATTAGAAAAGCTTTCAGACGTTAGGCTGA	45	#0_core	
16[273]	16[232]	CCCTAAATATTCATTGAAGCGATTTTGAGAAACACCAACAATAC	46	#0_core	
16[315]	16[274]	GATGCCGGAGAGGGTAGCGTGGCATTTGACCATTAGATACTTTA	44	#0_core	
16[347]	19[347]	AAGGGCGATCGGTAGGCAAAGGCACCCAGACATATCGGC	38	#0_core	
17[021]	17[034]	CTGCAACAGTGCCGG	15	#0_core	
17[329]	16[316]	GGAACCGCTGGGCGCATCGTAACGAATC	29	#0_core	
18[027]	19[062]	GAGAGCTGCTGAACCTCAAATATCAAACGCTAAAACAGAAATAA	44	#0_core	
18[062]	18[063]	GTAGATGTACCTTCCCTTAGAATCCCGTCAAATATTGC	40	#0_core	
18[104]	18[105]	AAACAACACAATAGACTTGCGGGAGGTTAGAATCTTACAAT	42	#0_core	
18[146]	18[147]	GTATGTTCCACATATAACCATCGATAGCAGCGTTTTACGCA	42	#0_core	
18[188]	18[189]	CTGAAACGTAGGATTACCACAGACAGCTTTTTCTTTATT	40	#0_core	
18[230]	18[231]	AACCTAACTCTTTGACATCAACGTAACCTTAAATTTGGCACC	40	#0_core	
18[272]	18[273]	GACCATTATCAGAATCCATATAACAGGGAAATGGTAGAAT	40	#0_core	
18[314]	18[315]	CTGAGAGATGTAAACAACAAACGGCGGTCTGCCAGATTGC	42	#0_core	
19[063]	19[104]	AGAACATAGGTCTGAGAGACTACTAATTCTGTCCAGAC	38	#0_core	
19[105]	19[146]	GACGACCAACGCTAACGAGCGTCCATGATTAGACTCC	38	#0_core	
19[147]	19[188]	TTATTATCGGCATTTTCGGTCATACTGCCTATTTTCGGAA	39	#0_core	
19[189]	19[230]	CCTAGTATGGGATTTTGCTAACACGTAATGCCACTACG	39	#0_core	
19[231]	19[272]	AAGGGCTTGAGATGGTTTAAATTTTTTAAACAGTTTCAGA	38	#0_core	
19[273]	19[314]	AAACGCAATAACCTGTTTAGCTATCTACAAAGGCTATCA	39	#0_core	
19[315]	12[336]	GGTCTTTGAGGGGACGACGCTCTGGATAGTTGGGTAAACGACG	45	#0_core	
11[049]	11[069]	TTATCAGATGATCGGGACT	19	#1_bottom	B0
11[091]	11[111]	CTTAATTGAGATCCTGAAC	19	#1_bottom	B1
11[133]	11[153]	CTTACCGAAGCAAACGCATT	20	#1_bottom	B2
11[176]	11[195]	CGTCATACATTAGCGGCA	18	#1_bottom	B3
11[217]	11[237]	CAGCAGCGAAAAGCGATTG	19	#1_bottom	B4
11[259]	11[279]	AAAAGAAGTTTAGCGGATAA	20	#1_bottom	B5
11[301]	11[321]	AGGGTGAGAAAATGTCAAG	19	#1_bottom	B6
08[069]	08[049]	GTTTGAATACGAAGGAGCGGAA	22	#2_top	T0
08[111]	08[091]	ATTACGAGCAACCAAGTATAAAGC	23	#2_top	T1
08[152]	08[133]	GCACAATCGAGCAAGAAACAA	21	#2_top	T2
08[195]	08[175]	CAGCCGTCGAAGCGCAGTCTCTG	23	#2_top	T3
08[237]	08[217]	TCGAGATTTGTTAAAGGCGCTT	23	#2_top	T4
08[279]	08[259]	CAAAAGACTGATAAAACCAA	22	#2_top	T5
08[321]	08[301]	ACAAAGCCCTGCCTGAGTAATG	23	#2_top	T6
02[055]	02[035]	ATCGTATTATAGAAGTATTAG	21	#3_left	L0
02[076]	02[056]	GAGAAACAATATTCATTCA	20	#3_left	L1
02[097]	02[077]	TCAGGCGTATTTAATGTTT	20	#3_left	L2
02[118]	02[098]	GCGTACCGCTTTCCTTATCAT	21	#3_left	L3
02[139]	02[119]	GGACACCCTAACAGGGAAGC	20	#3_left	L4
02[160]	02[140]	ACAGGGAAGCAAAGACAAAAG	21	#3_left	L5
02[181]	02[161]	GTATTGACACCGCCACCAGA	20	#3_left	L6
02[202]	02[182]	GAACCTCAGGTGTATCACC	20	#3_left	L7
02[223]	02[203]	CTGATACCGCAGCTTGCTTTC	21	#3_left	L8
02[244]	02[224]	GAGGCGCAGTCCGCGACCTG	20	#3_left	L9
02[265]	02[245]	ACACTAATGGATTATCAGTT	21	#3_left	L10
02[286]	02[266]	GGAGGATTAAAGCGAACCAG	20	#3_left	L11
02[307]	02[287]	ACCTGTAATAAAGCTAAATC	20	#3_left	L12
02[328]	02[308]	CGGCATTAAATTTAAATTGTAA	21	#3_left	L13
17[035]	17[055]	TCAGTTGGCAAAAAATTATC	21	#4_right	R0
17[056]	17[076]	AGGTTTAAACGTAGAATTTAGC	22	#4_right	R1
17[077]	17[097]	TTAGGTTGGGTTGACAAAAGGT	22	#4_right	R2
17[098]	17[118]	TCAGCTAATGCATTATCCTAT	21	#4_right	R3
17[119]	17[139]	TTGCCAGTTACAACCCAAAACA	22	#4_right	R4
17[140]	17[160]	AACGTAGAAAAATTGTAGCGCG	21	#4_right	R5

17[161]	17[181]	TTTGCCATCTTTACAGTTAGA	22	#4_right	R6
17[182]	17[202]	AAGTATTAAGAGTAAATGAACA	22	#4_right	R7
17[203]	17[223]	GCGGAGTGAGAAAAACGGGCG	21	#4_right	R8
17[224]	17[244]	AAAGAGGCAAAAGGAGTAGTGT	22	#4_right	R9
17[245]	17[265]	GAATTACCTTATCCCTAT	21	#4_right	R10
17[266]	17[286]	CAAAAATCAGGTCATTCGCCG	22	#4_right	R11
17[287]	17[307]	CGAGCTGAAAAGTATTTTGTG	22	#4_right	R12
17[308]	17[328]	GAGCAAACAAGACGTGCATCC	21	#4_right	R13
00[020]	00[005]	CTTTGACGAGCACGTA	16	#5_ends	E0
00[361]	00[347]	ACAGCTGATTGCCCTT	16	#5_ends	F0
01[005]	01[020]	TAACGTGCTTTCCTCG	16	#5_ends	E1
01[347]	01[361]	CCAGTGAGACGGGCA	15	#5_ends	F1
02[020]	02[005]	AGGAGGCCGATTAAAG	16	#5_ends	E2
02[361]	02[347]	AACGCGCGGGGAGAG	15	#5_ends	F2
03[005]	03[020]	GGATTTTAGACAGGAA	16	#5_ends	E3
03[347]	03[361]	TTAATGAATCGGCC	14	#5_ends	F3
04[020]	04[002]	TCAGTGAGGCCACCGAGTA	19	#5_ends	E4
04[358]	04[343]	GCTTCCAGTCGGGA	15	#5_ends	F4
05[002]	05[020]	AAAGAGTCTGTCCATCACG	19	#5_ends	E5
05[343]	05[358]	GTTGCGCTCACTGCC	16	#5_ends	F5
06[020]	06[002]	TAGTAATAACATCACTTGC	19	#5_ends	E6
06[358]	06[343]	CCTGGGGTGCCTAATG	16	#5_ends	F6
07[002]	07[020]	CTGAGTAGAAGAAGTCAAA	19	#5_ends	E7
07[343]	07[358]	AAGCATAAAGTGTAAG	17	#5_ends	F7
08[020]	08[005]	GCCATTGCAACAGGAA	16	#5_ends	E8
08[361]	08[348]	ATTGTTATCCGCTCA	15	#5_ends	F8
09[005]	09[020]	AAACGCTCATGGAAAT	16	#5_ends	E9
09[343]	09[361]	TAGCTGTTTCTGTGTGAA	19	#5_ends	F9
10[020]	10[005]	CTGAAATGGATTATTT	16	#5_ends	E10
10[361]	10[343]	TCGACTCTAGAGGATCCCC	19	#5_ends	F10
11[005]	11[020]	ACATTGGCAGATTAC	16	#5_ends	E11
11[348]	11[361]	GATGCCTGCAGG	13	#5_ends	F11
12[020]	12[002]	GCCAACAGAGATAGAACCC	19	#5_ends	E12
12[358]	12[343]	TCACGACGTTGTAAA	15	#5_ends	F12
13[002]	13[020]	TTCTGACCTGAAAGCGTAA	19	#5_ends	E13
13[343]	13[358]	GCCAGGGTTTTCCAG	16	#5_ends	F13
14[020]	14[002]	CTATTAGTCTTTAATGCGC	19	#5_ends	E14
14[358]	14[343]	CGAAAGGGGGATGTGC	16	#5_ends	F14
15[002]	15[020]	GAACTGATAGCCCTAAAAC	19	#5_ends	E15
15[343]	15[358]	GCTATTACGCCAGCTGG	17	#5_ends	F15
16[020]	16[005]	AACAGAGGTGAGGCGG	16	#5_ends	E16
16[361]	16[348]	TGCGCAACTGTTGGG	15	#5_ends	F16
17[005]	17[020]	TCAGTATTAACACCGC	16	#5_ends	E17
17[343]	17[361]	CGCCATTCGCCATTACGGC	19	#5_ends	F17
18[020]	18[005]	CAGCAGCAAATGAAAA	16	#5_ends	E18
18[361]	18[343]	CACTCCAGCCAGCTTTCCG	19	#5_ends	F18
19[005]	19[020]	ATCTAAAGCATCACCT	16	#5_ends	E19
19[348]	19[361]	CTCAGGAAGATCG	13	#5_ends	F19

Supplementary Notes – List of functional DNA staples

1. Functional staples for Origami H

Bottom positions

oligoname	Sequence	Description	Partner staples	
B_00	TTATCAGATGATCGGGACT	unmodified staples	Partner staples	
B_01	CTTAATTGAGATCCTGAAC			
B_02	CTTACCGAAGCAAACGCATT			
B_03	CGTCATACATTAGCGGCA			
B_04	CAGCAGCGAAAAGCGATTG			
B_05	AAAAGAAGTTTAGCGGATAA			
B_06	AGGGTGAGAAAATGTCAAG			
B18_00	TTATCAGATGATCGGGACTGCTATGGGTGGTCTGGTT	staples with extension for TEG-Chol(18)	5'-Chol-TEG-AACCAGACCACCCATAGC	
B18_01	CTTAATTGAGATCCTGAACGCTATGGGTGGTCTGGTT			
B18_02	CTTACCGAAGCAAACGCATTGCTATGGGTGGTCTGGTT			
B18_03	CGTCATACATTAGCGGCAGCTATGGGTGGTCTGGTT			AACCAGACCACCCATAGC-TEG-Chol-3'
B18_04	CAGCAGCGAAAAGCGATTGGCTATGGGTGGTCTGGTT			
B18_05	AAAAGAAGTTTAGCGGATAAGCTATGGGTGGTCTGGTT			
B18_06	AGGGTGAGAAAATGTCAAGGCTATGGGTGGTCTGGTT			
B09_06	AGGGTGAGAAAATGTCAAGGGTCTGGTT	staples with extension for TEG-Chol(9)	5'-Chol-TEG-AACCAGACC	
B27_03	CGTCATACATTAGCGGCAGCTATGGGTGGTCTGGTTGGGATTGGC	staple with extension for TEG-Chol(27)	5'-Chol-TEG-GCCAATCCCAACCAGACCACCCATAGC	
BD_00	TTATCAGATGATCGGGACTAAAAACACCAAACCC	staples with extension for Atto488 dye	5'-Atto488-GGGTTTGGTGTTTTT	
BD_01	CTTAATTGAGATCCTGAACAAAAACACCAAACCC			
BD_02	CTTACCGAAGCAAACGCATTAAAAACACCAAACCC			
BD_03	CGTCATACATTAGCGGCAAAAAACACCAAACCC			
BD_04	CAGCAGCGAAAAGCGATTGAAAAACACCAAACCC			
BD_05	AAAAGAAGTTTAGCGGATAAAAAACACCAAACCC			
BD_06	AGGGTGAGAAAATGTCAAGAAAAACACCAAACCC			
B_00_Biot	TTATCAGATGATCGGGACT-TEG-Biotin-3'	biotinylated staples		
B_03_Biot	CGTCATACATTAGCGGCA-TEG-Biotin-3'			
B_06_Biot	AGGGTGAGAAAATGTCAAG-TEG-Biotin-3'			
B_00_Thio	TTATCAGATGATCGGGACT-C3-SS-3'	thiolated staples		
B_03_Thio	CGTCATACATTAGCGGCA-C3-SS-3'			
B_06_Thio	AGGGTGAGAAAATGTCAAG-C3-SS-3'			

Top positions

oligoname	Sequence	Description	Partner staples
T_00	GTTTGAATACGAAGGAGCGGAA	unmodified staples	
T_01	ATTACGAGCAACCAAGTATAAAGC		
T_02	GCACAATCGAGCAAGAAACAA		
T_03	CAGCCGTCGAAGCGCAGTCTCTG		
T_04	TCGAGATTGTAAAGGCCGCTT		
T_05	CAAAAGACTGATAAAACCAA		
T_06	ACAAAGCCCCTGCCTGAGTAATG		
TD_00	GTTTGAATACGAAGGAGCGGAA AAAAACACCAAACCC	staples with extension for At488 dye	<i>5'-Atto488-GGGTTTGGTGT</i> TTTTT
TD_01	ATTACGAGCAACCAAGTATAAAGC AAAAACACCAAACCC		
TD_02	GCACAATCGAGCAAGAAACAA AAAAACACCAAACCC		
TD_03	CAGCCGTCGAAGCGCAGTCTCTG AAAAACACCAAACCC		
TD_04	TCGAGATTGTAAAGGCCGCTT AAAAACACCAAACCC		
TD_05	CAAAAGACTGATAAAACCAA AAAAACACCAAACCC		
TD_06	ACAAAGCCCCTGCCTGAGTAATG AAAAACACCAAACCC		
T18_00	GTTTGAATACGAAGGAGCGGAAGCTATGGGTGGTCTGGTT	staples with extension for TEG-Chol(18)	<i>5'-Chol-TEG-AACCAGACCACCCATAGC</i> AACCAGACCACCCATAGC-TEG-Chol-3'
T18_03	CAGCCGTCGAAGCGCAGTCTCTGGCTATGGGTGGTCTGGTT		
T18_06	ACAAAGCCCCTGCCTGAGTAATGGCTATGGGTGGTCTGGTT		

Edge positions

oligoname	Sequence	Description	Partner staples
E_06	TAGTAATAACATCACTTGCA AAAAACACCAAACCC	staples with extension for A1488 dye	<i>5'-Alexa488-GGGTTTGGTGT</i> TTTTT TTTTTTGTGGTTTGGG-Alexa488-3'
E_13	CCCAAACCAAAAAA TTCTGACCTGAAAGCGTAA		
F_06	CCCAAACCAAAAAA ACCTGGGGTGCCTAATG		
F_13	GCCAGGGTTTCCCA AAAAACACCAAACCC		

2. Functional staples for Origami Q

Bottom positions

oligoname	Sequence	Description	Partner staples
B_00	ATTCCTGATTACTTTTACCT	unmodified staples	
B_01	AGTAGGGCTTAAAGATAATC		
B_02	AGCTATCTTACCAAAGAATA		
B_03	GCGTCATACATAGCGGGCC		
B_04	CCTCAGCAGCGACCAGCGCT		
B_05	CAAAAGAAGTTAAGCGGACA		
B_06	GTGAGAAAGCCAATCATCA		
B18_00	ATTCCTGATTACTTTTACCTGCTATGGGTGGTCTGGTT	staples with extension for TEG-Chol(18)	5'-Chol-TEG-AACCAGACCACCCATAGC
B18_01	AGTAGGGCTTAAAGATAATCGCTATGGGTGGTCTGGTT		AACCAGACCACCCATAGC-TEG-Chol-3'
B18_02	AGCTATCTTACCAAAGAATAGCTATGGGTGGTCTGGTT		
B18_03	GCGTCATACATAGCGGGCCGCTATGGGTGGTCTGGTT		
B18_04	CCTCAGCAGCGACCAGCGCTGCTATGGGTGGTCTGGTT		
B18_05	CAAAAGAAGTTAAGCGGACAGCTATGGGTGGTCTGGTT		
B18_06	GTGAGAAAGCCAATCATCAGCTATGGGTGGTCTGGTT		
B09_00	ATTCCTGATTACTTTTACCTGGTCTGGTT	staples with extension for TEG-Chol(9)	5'-Chol-TEG-AACCAGACC
B09_03	GCGTCATACATAGCGGGCCGGTCTGGTT		
B09_06	GTGAGAAAGCCAATCATCAGGTCTGGTT		
B27_03	GCGTCATACATAGCGGGCCGCTATGGGTGGTCTGGTTGGGATTGGC	staple with extension for TEG-Chol(27)	5'-Chol-TEG-GCCAATCCCAACCAGACCACCCATAGC
BD_00	ATTCCTGATTACTTTTACCTAAAAACACCAAAACCC	staples with extension for Atto488 dye	5'-Atto488-GGGTTTGGTGTTTTTT
BD_01	AGTAGGGCTTAAAGATAATCAAAAAACACCAAAACCC		
BD_02	AGCTATCTTACCAAAGAATAAAAAACACCAAAACCC		
BD_03	GCGTCATACATAGCGGGCCAAAAACACCAAAACCC		
BD_04	CCTCAGCAGCGACCAGCGCTAAAAACACCAAAACCC		
BD_05	CAAAAGAAGTTAAGCGGACAAAAAACACCAAAACCC		
BD_06	GTGAGAAAGCCAATCATCAAAAAACACCAAAACCC		

Top positions

oligoname	Sequence	Description	Partner staples
T_00	TAGATTGCTAACCACCAGAAG	unmodified staples	
T_01	AACCTAATTTATTCTTACCAGT		
T_02	CTTTGTCAAATAAGAGCAAG		
T_03	ACCCGTCGAGAGCGCAGTCTCT		
T_04	CTCGGAGATTAGTTAAAGGCCG		
T_05	ACGAAAGACCGATAAAAACCAA		
T_06	AACCCAAAAATGAGTAATGTGT		
TD_00	TAGATTGCTAACCACCAGAAG AAAAAACACCAAAACCC	staples with extension for At488 dye	<i>5'-Atto488-GGGTTTGGTGTTTTTT</i>
TD_01	AACCTAATTTATTCTTACCAGT AAAAAACACCAAAACCC		
TD_02	CTTTGTCAAATAAGAGCAAG AAAAAACACCAAAACCC		
TD_03	ACCCGTCGAGAGCGCAGTCTCT AAAAAACACCAAAACCC		
TD_04	CTCGGAGATTAGTTAAAGGCCG AAAAAACACCAAAACCC		
TD_05	ACGAAAGACCGATAAAAACCAA AAAAAACACCAAAACCC		
TD_06	AACCCAAAAATGAGTAATGTGT AAAAAACACCAAAACCC		
T18_00	TAGATTGCTAACCACCAGAAG GCTATGGGTGGTCTGGTT	staples with extension for TEG-Chol(18)	<i>5'-Chol-TEG-AACCAGACCACCCATAGC</i> <i>AACCAGACCACCCATAGC-TEG-Chol-3'</i>
T18_03	ACCCGTCGAGAGCGCAGTCTCT GCTATGGGTGGTCTGGTT		
T18_06	AACCCAAAAATGAGTAATGTGT GCTATGGGTGGTCTGGTT		
T09_00	TAGATTGCTAACCACCAGAAG GGTCTGGTT	staples with extension for TEG-Chol(9)	<i>5'-Chol-TEG-AACCAGACC</i>
T09_03	ACCCGTCGAGAGCGCAGTCTCT GGTCTGGTT		
T09_06	AACCCAAAAATGAGTAATGTGT GGTCTGGTT		

Lateral positions (left side)

oligoname	Sequence	Description	Partner staples
L_00	ATCGACAACTGAGGATTTAGA	unmodified staples	
L_01	ATAGATGATGGCGAATTATTC		
L_02	TTGATAAATGACCTAAATTTA		
L_03	GGAAACCAAGGCTGTCTTTCC		
L_04	AAAACTGAACATAAAAAACAG		
L_05	GAGAGGGAGAGCGCCAAAGAC		
L_06	TAGCATTGAAGCCGCCACCA		
L_07	TTACCCTCAGGTGTATCACCG		
L_08	TGCTTGATATATCAGCTTGCT		
L_09	TGGAGGCGCAATCCGCGACC		
L_10	GAAACTAATAGATTCATCAGT		
L_11	TTCAGGATTAAAGCGAACCA		
L_12	AATGTAATAAAGCTAAATCGG		
L_13	GTAAATTTTATTGTAAACGTT		
LS_00	TATATATTT ATCGACAACTGAGGATTTAGA	staples for lateral oligomerization	
LS_01	TATATATTT ATAGATGATGGCGAATTATTC		
LS_02	TATATATTTT GATAAATGACCTAAATTTA		
LS_03	TATATATTTT GGAAACCAAGGCTGTCTTTCC		
LS_04	TATATATTTT AAAACTGAACATAAAAAACAG		
LS_05	TATATATTTT GAGAGGGAGAGCGCCAAAGAC		
LS_06	TATATATTTT TAGCATTGAAGCCGCCACCA		
LS_07	TATATATTTT TACCCTCAGGTGTATCACCG		
LS_08	TATATATTTT TGCTTGATATATCAGCTTGCT		
LS_09	TATATATTTT TGGAGGCGCAATCCGCGACC		
LS_10	TATATATTTT GAAACTAATAGATTCATCAGT		
LS_11	TATATATTTT TTCAGGATTAAAGCGAACCA		
LS_12	TATATATTTT AATGTAATAAAGCTAAATCGG		
LS_13	TATATATTTT GTAAATTTTATTGTAAACGTT		

Lateral positions (right side)

oligoname	Sequence	Description	Partner staples
R_00	ATATCTGGTCAGACCATATAG	unmodified staples	
R_01	ATTTTCAGGTTTCAATAGTCC		
R_02	TCCGGCTTAGGTAAAGTACAC		
R_03	AACATGTTCAAGTACAATTAG		
R_04	CCTAATTTGCCAGGGAATACGT		
R_05	TAGCAAACGTAGCAGACTGTT		
R_06	AGCGTTTGCCATCACAGTTAAA		
R_07	AGTATTAAGAGGTAGTAAATT		
R_08	TCAGCGGAGTGAATTAACAA		
R_09	CGAAAGAGGCAAAACGAGTATG		
R_10	TGAATTACCTTAATCCCCAA		
R_11	TCAAAAATCAGGTCATTTGCGG		
R_12	CGAGCTGAAAAGTTTGAGACA		
R_13	AACAAGAGAATCATCTGCCCC		
RS_00	TATATATTT ATATCTGGTCAGACCATATAG	staples for lateral oligomerization	
RS_01	TATATATTT ATTTTCAGGTTTCAATAGTCC		
RS_02	TATATATTT TCCGGCTTAGGTAAAGTACAC		
RS_03	TATATATTT AACATGTTCAAGTACAATTAG		
RS_04	TATATATTT CCTAATTTGCCAGGGAATACGT		
RS_05	TATATATTT TAGCAAACGTAGCAGACTGTT		
RS_06	TATATATTT AGCGTTTGCCATCACAGTTAAA		
RS_07	TATATATTT AGTATTAAGAGGTAGTAAATT		
RS_08	TATATATTT TCAGCGGAGTGAATTAACAA		
RS_09	TATATATTT CGAAAGAGGCAAAACGAGTATG		
RS_10	TATATATTT TGAATTACCTTAATCCCCAA		
RS_11	TATATATTT TCAAAAATCAGGTCATTTGCGG		
RS_12	TATATATTT CGAGCTGAAAAGTTTGAGACA		
RS_13	TATATATTT AACAAGAGAATCATCTGCCCC		
R18_00	ATATCTGGTCAGACCATATAG GCTATGGGTGGTCTGGTT	staples with extension for TEG-Chol(18)	<i>5'-Chol-TEG-AACCAGACCACCCATAGC</i> <i>AACCAGACCACCCATAGC-TEG-Chol-3'</i>
R18_06	AGCGTTTGCCATCACAGTTAAAG GCTATGGGTGGTCTGGTT		
R18_12	CGAGCTGAAAAGTTTGAGACA GCTATGGGTGGTCTGGTT		

Edge positions

oligoname	Sequence	Description	Partner staples
E_08	TTACCGCCAGCCATTG	staples for tip-to-tip interactions: - Q-E5 structures (10 of 10) - Q-E7 structures (10 of 14) - Q-E13 structures (10 of 26)	
E_09	CAACAGGAAAAACGCT		
E_10	CTCAATCGTCTGAAAT		
E_14	TGAATGGCTATTAGTCTTT		
E_18	GCTGAGAGCCAGCAGC		
F_08	TCCGCTCACAAATTC		
F_09	TTCCTGTGTGAAATTGTTA	additional staples: - Q-E7 structures (4 of 14) - Q-E13 structures (4 of 26)	
F_10	TAGAGGATCCCCGGGTACC		
F_14	GGGGGATGTGCTGCAA		
F_18	GCCAGCTTTCGGCACC GC		
E_04	TTTATAATCAGTGAGGCCA		
E_19	AAATGAAAAATCTAAA		
F_04	CCAGTCGGGAAACCTG	additional staples: - Q-E13 structures (12 of 26)	
F_19	AAGATCGCACTCCA		
E_03	CGATTAAAGGGATTTT		
E_05	CCGAGTAAAAGAGTCTGTC		
E_06	CTTTGATTAGTAATAACAT		
E_07	CACTTGCCTGAGTAGAAGA		
E_11	GGATTATTTACATTGG		
E_15	AATGCGCGAACTGATAGCC		
F_03	AATCGGCCAACGCGC		
F_05	GCTCACTGCCC GCTTT		
F_06	GGTGCCTAATGAGTGA		
F_07	AAAGTGTAAGCCTGG		
F_11	CTGCAGGTCGACTC		
F_15	ACGCCAGCTGGCGAAA		

3. Functional staples for Origami L

Bottom positions

oligoname	Sequence	Description	Partner staples
B_00	ATTATCATCATAAACAGTATG	unmodified staples	
B_01	GCTCAACAGTAGCAACAATCG		
B_02	GCAATAGCTATCCATATAAAC		
B_03	GTAAGCGTCATGATTAGCAC		
B_04	TCAGCAGCGAAAAGCGATTGA		
B_05	AGAAGTTTGGCCGATTGCAA		
B_06	AAGGCCGGAGACATGTACCTC		
B18_00	ATTATCATCATAAACAGTATGGCTATGGGTGGTCTGGTT	staples with extension for TEG-Chol(18)	5'-Chol-TEG-AACCAGACCACCCATAGC
B18_03	GTAAGCGTCATGATTAGCACGCTATGGGTGGTCTGGTT		
B18_06	AAGGCCGGAGACATGTACCTCGCTATGGGTGGTCTGGTT		

Top positions

oligoname	Sequence	Description	Partner staples
T_00	AAATTCGCCCCGAACAAAGAA	unmodified staples	
T_01	ATTCCCATCTATACAAATTCT		
T_02	ATTTATTTCCAATAATAAGA		
T_03	AAGTGCCGTGGAAAGCGCAGT		
T_04	CAAGATTTGTAAAGGCCGCT		
T_05	TTACTTCAAAAAACCAAATA		
T_06	AGACAGGAAATGTGTAGGTAA		
TD_00	AAATTCGCCCCGAACAAAGAAAAAAACACCAAACCC	staples with extension for At488 dye	5'-Atto488-GGGTTTGGTGTTTTTT
TD_01	ATTCCCATCTATACAAATTCTAAAAACACCAAACCC		
TD_02	ATTTATTTCCAATAATAAGAAAAACACCAAACCC		
TD_03	AAGTGCCGTGGAAAGCGCAGTAAAAACACCAAACCC		
TD_04	CAAGATTTGTAAAGGCCGCTAAAAACACCAAACCC		
TD_05	TTACTTCAAAAAACCAAATAAAAAACACCAAACCC		
TD_06	AGACAGGAAATGTGTAGGTAAAAAACACCAAACCC		