

Supplementary Notes

Supplementary Note 1: robot design and fabrication

DNA origami robots were designed using caDNAno (<http://www.cadnano.org>) and fabricated as previously described. The M13mp18 circular ssDNA was used as scaffold strand. Staple strands were ordered from Integrated DNA technologies.

Supplementary Table 1: M13mp18 sequence

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TAGTTGCATATTTAAACATGTTGAGCTACAGCATTATATTAGCAATTAAGCTCTAAGCCATCCGCAAAAAAGACCTTTATCAAAG
GAGCAATTAAGGTACTCTCTAATCTGACCTGTTGGAGTTGCTTCCGGTCTGGTTCGCTTTGAAGCTCGAATTAACCGCATATTT
GAAGTCTTTCCGGCTTCCTCTTAATCTTTTGTGCAATCCGCTTTGCTTCTGACTATAATAGTCAGGGTAAAGACCTGATTTTGATT
TATGGTCATTCGTTTTCTGAACTGTTTAAAGCATTGAGGGGGATTCAATGAATATTTATGACGATTCGCGAGTATGGACGCTATC
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CGAGGGTATGATAGTGTGCTTACTATGCCTCGTAATCCTTTTGGCGTTATGTATCTGCATTAGTTGAATGTGGTATTCCTAAAT
CTCAACTGATGAATCTTTCTACTGTAATAATGTTGTTCCGTTAGTTCGTTTTATTAACGTAGATTTTTCTTCCCAACGCTCGACTGG
TATAATGAGCCAGTCTTAAAATCGCATAAGGTAATCACAATGATTAAGTTGAAATTAACCATCTCAAGCCCAATTTACTACTCGT
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TTATGATTGACCGTCTGCGCTCGTTCGGCTAAGTAACATGGAGCAGGTCGCGGATTCGACACAATTTATCAGGCGATGATACAAT
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TTGGTGCCTTCGTAGTGGCATTACGTATTTTACCCGTTTAAAGTAACTTCTCATGAAAAGTCTTTAGTCTCAAAGCCTCTGTAGC
CGTTGCTACCCCTGTTCCGATGCTGTCTTTCGCTGCTGAGGGTACGATCCCGCAAAAGCGGCTTTAACTCCCTGCAAGCCTCAGCGA
CCGAATATATCGGTTATGCGTGGGCGATGGTGTGTCATTGTGCGGCAACTATCGGATCAAGCTGTTTAAAGAAATTCACCTCGAAA
GCAAGTGATAAACCGATAACAATTAAGGCTCCTTTGGAGCCTTTTTTGGAGATTTTCAACGTGAAAAAATATATTTCGCAATTC
CTTTAGTTGTTCTTTCTATTCTCACTCCGCTGAAACTGTTGAAAGTTGTTAGCAAAATCCCATACAGAAAATTCATTACTAACGTC
TGAAAGACGACAAAATTTAGATCGTTACGCTAACATGAGGGTGTCTGTGGAAATGCTACAGGCGTGTAGTTTGTACTGGTGACGA
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TATCCGCTGGTACTGAGCAAAACCCGCTAATCCTAATCCTTCTCTGAGGAGTCTCAGCCTCTTAATACTTTTATGTTTCCAGAAATA
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CTCCTGTATCATCAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTCGCCTTTCCATCTGGCTTAAATGAGGATTTA
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ACGGCTCAATCTATTAGTTGTTAGTGTCTTAAAGATATTTAGATAACCTTCTCAATTCCTTTCAACTGTGATTTGCCAACTGAC
CAGATATTGATTGAGGGTTGATATTTGAGGTTGAGCAAGGTGATGCTTATGATTTTCTTGTGCTGGCTCTCAGCGTGGCACTGT
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 TATCAGTTCGCGCATTAAAGACTAATAGCATTCAAAAAATGTCTGTGCCAGTATTCTTACGCTTTCAGGTCAGAAGGGTTCTATC
 TCTGTTGGCCAGAAATGTCCTTTTATTACTGGTCGTGTGACTGGTGAATCTGCCAATGTAATAATCCATTTACAGCATTGAGCGTCA
 AAATGTAGGTATTTCCATGAGCGTTTTTCTGTTGCAATGGCTGGCGGTAATATTGTTCTGGATATTACCAGCAAGGCCGATAGTTTGA
 GTTCTTCTACTCAGCAAGTGATGTTATTACTAATCAAAGAAGTATTGCTACAACGGTTAATTTGCGTGATGGACAGACTCTTTTACTC
 GGTGGCCTCACTGATTATAAAAACTTCTCAGGATTCTGGCGTACCGTTCTGTCTAAAATCCCTTAAATCGGCCTCTGTTTAGCTC
 CCGCTCTGATTCTAACGAGGAAAGCACGTTATACGTGCTCGTCAAAGCAACCATAGTACGCGCCCTGTAGCGGCGCATTAAAGCGCGCG
 GGTGTGGTGGTACGCGCAGCGTGACCGCTACACTTGCAGCGCCCTAGCGCCGCTCCTTTCGCTTTCTCCCTTCTTCTCGCCAC
 GTTCGCGCGCTTTCCTCGTCAAGCTCTAAATCGGGGGCTCCCTTAGGGTTCCGATTAGTGCTTACGGCACCTCGACCCCAAAAAAC
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 GGACTCTTGTTCCAAAGTCAACCACTCAACCTATCTCGGGCTATTCTTTGATTATAAGGGATTTTCGCCGATTTTCGGAACACC
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 TTTACACTTTATGCTTCCGGCTCGTATGTTGTGGAAATGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGACCTGACCG
 AATTCGAGCTCGGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTGGCACGGCCGCTGTTTACAACGTCGTGACTG
 GGAAACCTGGCGTTACCCAATTAATCGCCTTGCAGCACATCCCTTTTCGCCAGCTGGCGTAAATAGCGAAGAGGCCCGCACCCGATC
 GCCCTTCCCAACAGTTGCGCAGCTGAATGGCGAATGGCGCTTTCGCTGGTTCCGGCACCAGAAGCGGTGCCGAAAGCTGGCTGGAG
 TGCGATCTTCTGAGGCGGATGCTGCTGCTCCCTCAAACCTGGCAGATGCACGGTTACGATGCGCCCATCTACACCAACGTAACCTG
 TCCATTACGGTCAATCCGCCGTTTGTTCACGGAAGAACCCGACGGTGTACTCGCTCACATTTAATGTTGATGAAAGCTGGCTAC
 AGGAAGGCCAGACGCAATTTTTGATGGCGTTCCTATTGGTTAAAAATGAGCTGATTTAAACAAAAATTAATGCGAATTTAACA
 AAATATTAACGTTTACAATTTAAATATTTGCTTATACAATCTTCTGTTTTTGGGGCTTTTCTGATTATCAACCGGGGTACATATGATT
 GACATGCTAGTTTTACGATTACCGTTCATCGATTCTCTGTTTGGTCCAGACTCTCAGGCAATGACCTGATAGCCTTTGTAGATCTCTC
 AAAAAAGCTACCCTCTCCGGCATTAAATTTATCAGCTAGAACGGTTGAATATCATATTGATGGTATTGACTGTCTCCGGCCTTTCTC
 ACCCTTTTGAATCTTTACCTACACATTACTCAGGCATTGCATTTAAATATATGAGGGTTCTAAAAATTTTATCCTTGGCGTTGAAATA
 AAGGCTTCTCCGCAAAGTATTACAGGTCATAATGTTTTTGGTACAACCGATTAGCTTTATGCTCTGAGGCTTTATTGCTTAATTT
 TGCTAATCTTTGCCCTGCTGATGATTTATTGGATGTT

Supplementary Table 2: Staple sequences

ID	Description	Sequence
1	Core	AAAAACCAAACCCTCGTTGTGAATATGGTTTGGTC
2	Core	GGAAGAAGTGTAGCGGTCACGTTATAATCAGCAGACTGATAG
3	Core	TACGATATAGATAATCGAACACA
4	Core	CTTTTGCTTAAGCAATAAAGCGAGTAGA
5	Core	GTCTGAAATAACATCGGTACGGCCGCGCACGG
6	Core	GGAAGAGCCAAACAGCTTGCAGGGAACCTAA
7	Core	AAAAATCACCGGAAGCAAACCTCTGTAGCT
8	Core	CCTACATGAAGAACTAAAGGGCAGGGCGGAGCCCGGGC
9	Core	CATGTA AAAAGGTAAAGTAATAAGAACG
10	Core	ATTAATCAGGTCATTGCCTGTCTAGCTGATAAATTGTAATA
11	Core	ATAGTCGCTTTTTCGGGTAATGCC
12	Core	AGTCATGGTCATAGCTGAACCTCACTGCCAGT
13	Core	AACTATTGACGGAAATTTGAGGGAATATAAA
14	Core	ATCGCGTCTGGAAGTTTCATTCCATATAGAAGACCATC
15	Core	AAATATTGAACGGTAATCGTAGCCGGAGACAGTCATAAAAAAT
16	Core	GTCTTTACAGGATTAGTATTCTAACGAGCATAGAACGC
17	Core	GCACCGCAGCAGCTAATGAACAGCTG
18	Core	AACTCATTTTGAATCGAAATC
19	Core	CGTAGAGTCTTTGTTAAGGCCTTCGTTTTCTACCGAG
20	Core	CCAATCAAAGGCTTATCCGGTTGCTATT
21	Core	AGAGGCGATATAATCCTGATTATCATA
22	Core	CCGTAATCCCTGAATAATAACGGAATACTACG
23	Core	AAATGGTATACAGGGCAAGGAAATC
24	Core	TCCTCATCGTAACCAAGACCGACA
25	Core	CATTATCTGGCTTTAGGGAATTATGTTTGGATTAC

26	Core	ACCCGCCAATCATTCTCTGTCC
27	Core	CGACCAGTCACGCAGCCACCGCTGGCAAAGCGAAAGAAC
28	Core	CTAAAGGCGTACTATGGTTGCAACAGGAGAGA
29	Core	TTGGCAGGCAATACAGTGTTTCTGCGCGGGCG
30	Core	TATACAGGAAATAAAGAAATTTTGCCCGAACGTTAAGACTTT
31	Core	AAGTATAGTATAAACAGTTAACTGAATTTACCGTTGAGCCAC
32	Core	ACATTCAGATAGCGTCCAATATTCAGAA
33	Core	AAACATCTTTACCCTCACCAGTAAAGTGCCCGCCC
34	Core	GAGATGACCCTAATGCCAGGCTATTTTT
35	Core	TCCTGAATTTTTTGTTTAACGATCAGAGCGGA
36	Core	GCCGAAAAATCTAAAGCCAATCAAGGAAATA
37	Core	AGCGTAGCGGTTTTCAAAAATCTATGTTAGCAAACGAACGCAACAAA
38	Core	ACCAATCGATTAATTCGCGCCATTATTA
39	Core	ATCTTACTATTTTCAGCGCCGACAGGATTCA
40	Core	CCCTAAAAGAACCCAGTCACA
41	Core	GGAAAGGCGAAAAATCGGGTTTTTCGCGTTGCTCGT
42	Core	CAGACCGGAAGCCGCCATTTTGATGGGGTCAGTAC
43	Core	TAATATTGGAGCAAACAAGAGATCAATATGATATTGCCTTTA
44	Core	TTCTTATAGCAAGCAAATCAAATTTTA
45	Core	ACTACGAGGAGATTTTTTTCACGTTGAAACTTGCTTT
46	Core	AAACAGGCATGTCAATCATATAGATTCAAAAGGGTTATATT
47	Core	AACAGGCACCAAGTTAAAGGCGCTTTGTGAATTTCTTA
48	Core	TTCTGAGTTATCTAAAATATTCAGTTGTTCAAATAGCAG
49	Core	AAAGAAACAAGAGAAGATCCGGCT
50	Core	TTGAGGGTTCTGGTCAGGCTGTATAAGC
51	Core	TTTAACCGTCAATAGTGAATTCAAAAGAAGATGATATCGCGC
52	Core	ACGAGCGCCCAATCCAATAAAATTTGAGCACC
53	Core	AATAAGTCGAAGCCCAATAATTATTATTCTT
54	Core	ACGAAATATCATAGATTAAGAAACAATGGAAGTGA
55	Core	TTTCATAGTTGTACCGTAACACTGGGGTTTT
56	Core	AGGAGCGAGCACTAACAACTAAAACCTATCACCTAACAGTG
57	Core	CAAAGTATTAATTAGCGAGTTTCGCCACAGAACGA
58	Core	TGGGGAGCTATTTGACGACTAAATACCATCAGTTT
59	Core	ATAACGCAATAGTAAAATGTTTAAATCA
60	Core	ACGAATCAACCTTCATCTTATACCGAGG
61	Core	TAATGGTTTTGAAATACGCCAA
62	Core	CGGAACAAGAGCCGTCATAGGCACAGACAATATCCTCAATC
63	Core	ATTAAAGGTGAATTATCAAAGGGCACCACGG
64	Core	GGCAACCCATAGCGTAAGCAGCGACCATTAA
65	Core	AGAAACGTAAGCAGCCACAAGGAAACGATCTT
66	Core	AGAGGTCTTTAGGGGGTCAAAGGCAGT
67	Core	GGGGACTTTTTTCATGAGGACCTGCGAGAATAGAAAGGAGGAT
68	Core	TTTTAGAACATCCAATAAATCCAATAAC
69	Core	AAATGTGGTAGATGGCCCGCTTGGGGCG
70	Core	ACGGATCGTCACCCTCAGATCTAGAATTTT
71	Core	CGCCATAAGACGACGACAATAGTGTCT
72	Core	GCGTATTAGTCTTTAATCGTAAGAATTTACA
73	Core	AGAGAACGTGAATCAAATGCGTATTTCCAGTCCCC
74	Core	AACGAAAAAGCGCGAAAAAAGGCTCCAAAAGG

75	Core	TAATTTAGAACGCGAGGCGTTAAGCCTT
76	Core	ACCAGGCGTGCATCATTAATTTTTTAC
77	Core	CAGCCTGACGACAGATGTCGCCTGAAAT
78	Core	ATTAGTCAGATTGCAAAGTAAGAGTTAAGAAGAGT
79	Core	CTCGAATGCTCACTGGCGCAT
80	Core	GGGCAGTCACGACGTTGAATAATTAACAACC
81	Core	TAAAAACAGGGGTTTTGTTAGCGAATAATATAATAGAT
82	Core	TCAACCTCAGCGCCGAATATATTAAGAATA
83	Core	ATTATACGTGATAATACACATTATCATATCAGAGA
84	Core	GCAAATCTGCAACAGGAAAAATTGC
85	Core	ATAATTAAGTAAATTTTAC
86	Core	TATCACCGTCCCTTGGTAAACGCGTCATACATGGCCCTCAG
87	Core	AAGTAGGTTAACGCGCTGCCAGCTGCA
88	Core	CCAGTAGTTAAGCCCTTTTTAAGAAAAGCAA
89	Core	TGGCGAAGTTGGGACTTTCCG
90	Core	CAGTGAGTGATGGTGGTCCGAAAACCGTCTATCACGATTTA
91	Core	AAATCAAAGAGAATAACATAACTGAACACAGT
92	Core	CTGTATGACAACCTAGTGTCTGA
93	Core	ATCATAAATAGCGAGAGGCTTAGCAAAGCGGATTGTTCAAAT
94	Core	TTGAGTAATTTGAGGATTTAGCTGAAAGGCGCGAAAGATAAA
95	Core	ATAAGAATAAACCCGCTCAA
96	Core	CGTTGTAATTCACCTTCTGACAAGTATTTTAA
97	Core	AACCGCTCATAATTCGGCATAGCAGCA
98	Core	AAATAGGTCACGTTGGTAGCGAGTCGCGTCTAATTCGC
99	Core	CAGTATAGCCTGTTTATCAACCCCATCC
100	Core	TTGCACCTGAAAATAGCAGCCAGAGGGTCATCGATTTTCGGT
101	Core	CGTCGGAAATGGGACCTGTGCGGGGAGA
102	Core	AAGAACTAGAAGATTGCGCAACTAGGG
103	Core	CCAGAACCTGGCTCATTATACAATTACG
104	Core	ACGGGTAATAAATTAAGGAATTGCGAATAGTA
105	Core	CCACGCTGGCCGATTCAAATATCGGCCGCT
106	Core	GCCTTACCAGAAAGCCCTCCGCTCACGCCAGC
107	Core	CAGCATTAAAGACAACCGTCAAAAATCA
108	Core	ACATCGGAAATATTTGCACGTAAAGT
109	Core	CAACGGTCGCTGAGGCTTGATACCTATCGGTTTATCAGATCT
110	Core	AAATCGTACAGTACATAAATCAGATGAA
111	Core	TTAACACACAGGAACCTTGCTGAGTATTTG
112	Core	AGGCATAAGAAGTTTTGCCAGACCTGA
113	Core	GACGACATTCACCAGAGATTAAGCCTATTAACCA
114	Core	AGCTGCTCGTTAATAAACGAGAATACC
115	Core	CTTAGAGTACCTTTTAAACAGCTGCGGAGATTTAGACTA
116	Core	CACCCTCTAATTAGCGTTTGCTACATAC
117	Core	GAACCGAAAATTGGGCTTGAGTACCTTATGCGATTCAACACT
118	Core	GCAAGGCAGATAACATAGCCGAACAAAGTGGAACGGGA
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120	Core	GGATGTGAAATTGTTATGGGGTGACAGTAT
121	Core	GGCTTGCACGTTGGGAAGAACAGATAC
122	Core	TAAATGCCTACTAATAGTAGTTTTTCATT
123	Core	TGCCGCTGCTATTTTCGGAACAGAAATGGAAAGCCACCAGAAC

124	Core	TGACCATAGCAAAGGGAGACAAC
125	Core	CGAGCCAGACGTTAATAATTTGTATCA
126	Core	GCTCAGTTTCTGAAACATGAAACAAATAAATCCTCCCGCCGC
127	Core	AGACGCTACATCAAGAAAACACTTTGAA
128	Core	AGTACTGACCAATCCGCGAAGTTAAGACAG
129	Core	GATTCCTGTTACGGGCAGTGAGCTTTTCTGTGTGCTG
130	Core	GGTATTAAGGAATCATTACCGAACGCTA
131	Core	GTTTCATCAAATAAAACGCGACTCTAGAGGATCGGG
132	Core	AGCCTTTAATTGGATAGTTGAACCGCCACCCTCATAGGTG
133	Core	ACAGAGGCTGAGATTCTTTGATTAGTAATGG
134	Core	AACGAGATCAGGATTAGAGAGCTTAATT
135	Core	TACCAAGTTATACTTCTGAATCACCAGA
136	Core	CAGTAGGTTCAGCTAATGCGTAGAAA
137	Core	AGGATGACCATAGACTGACTAATGAAATCTACATTCAGCAGGCGGTAC
138	Core	TTTCAACCAAGGCAAAGAATTTAGATAC
139	Core	TTGAAATTAAGATAGCTTAACTAT
140	Core	CTATTATCGAGCTTCAAAGCGTATGCAA
141	Core	CAGGGTGCAAAATCCCTTATAGACTCCAACGTCAAAAGCCGG
142	Core	GAGCTTGTTAATGCGCCGCTAATTTTAGCGCTGCTGCTGAA
143	Core	CGAACGTTAACCACCACACCCCAAGAATTGAG
144	Core	GTGTGATAAATAAGTGAGAAT
145	Core	GCTATATAGCATTAAACCTCAGAGA
146	Core	AGGAGAGCCGGCAGTCTTGCCCGGAGAGGGAGGG
147	Core	CGGCCTCCAGCCAGAGGGCGAGCCCAA
148	Core	CCAAAACAAAATAGGCTGGCTGACGTAACAA
149	Core	GGCGTTAGAATAGCCCGAGAAGTCCACTATTA AAAAGGAAG
150	Core	ATAAAGGTTACCAGCGCTAATTCAAAACAGC
151	Core	ATTGCCCCAGCAGGCGAAAAGGCCACTACGTGACGGAACC
152	Core	TTTTAAAACATAACAGTAATGGAACGCTATTAGAACGC
153	Core	AATTGGGTAACGCCAGGCTGTAGCCAGCTAGTAAACGT
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155	Edge	TTTTTTTTTTTTTTTTAATAAGAGAATA
156	Edge	TTTTTTTTTTTTTTTTCCAGTTTGGGAGCGGGCTTTTTTTTTTTTT
157	Edge	GGTTGAGGCAGGTCAGTTTTTTTTTTTTTTTT
158	Edge	TTTTTTTTTTTTTTTTGATTAAAGACTCCTTATCCAAAAGGAAT
159	Edge	TTTTTTTTTTTTTTTTCTTCGCTATTACAATT
160	Edge	TTTTTTTTTTTTTTTTCTTGCGGGAGAAGCGCATTTTTTTTTTTTTTT
161	Edge	TTTTTTTTTTTTTTTTGGGAATTAGAGAAACAATGAATTTTTTTTTTTTT
162	Edge	TCAGACTGACAGAATCAAGTTTGTTTTTTTTTTTTTTT
163	Edge	TTTTTTTTTTTTTTTTGGTCGAGGTGCCGTAAGCAGCACGT
164	Edge	TTTTTTTTTTTTTTTTAATCATTTACCAGACTTTTTTTTTTTTTTT
165	Edge	TTTTTTTTTTTTTTTCATCTGGCCAAATTCGACAACTCTTTTTTTTTTTTT
166	Edge	TTTTTTTTTTTTTTTTTACCGGATATTCA
167	Edge	TTTTTTTTTTTTTTTTAGACGGGAAACTGGCATTTTTTTTTTTTTTT
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169	Edge	CTGAGAGAGTTGTTTTTTTTTTTTTTTT
170	Edge	CAATGACAACAACCATTTTTTTTTTTTTTTTT
171	Edge	TTTTTTTTTTTTTTTTTGAGAGATCTACAAGGAGAGG
172	Edge	TCACCAGTACAACTATTTTTTTTTTTTTTTTT

173	Edge	TTTTTTTTTTTTGGCAATTCATCAAATTATTCATTTTTTTTTTTTTTTTT
174	Edge	TAAAGTTACCGCACTCATCGAGAAGCTTTTTTTTTTTTTTTTT
175	Edge	TTTTTTTTTTTTTTCCACCCTCAGAACCGCC
176	Edge	TTTTTTTTTTTTTAGGTTAACGTCAATATATGTGAGTTTTTTTTTTTTTT
177	Edge	CCACACAACATACGTTTTTTTTTTTTTT
178	Edge	TTTTTTTTTTTTTTTGCTAGGGCAGTAAAAGATTTTTTTTTTTTTTTTT
179	Edge	TTTTTTTTTTTTTTTAGTTGATCCCAATTCTGCGAACCTCA
180	Edge	TTATTTAGAGCCTAATTTGCCAGTTTTTTTTTTTTTTTTTT
181	Edge	TTTTTTTTTTTTTTTACGGCGGAT
182	Edge	TTTTTTTTTTTTTTTATATGCGTTAAGTCCTGATTTTTTTTTTTTTTTTT
183	Edge	TTTTTTTTTTTTTTTACGATTGGCCTTGATA
184	Edge	TTTTTTTTTTTTTTTCAACGCCTGTAGCATT
185	Edge	TTTTTTTTTTTTTTTGCCTTGAGCCGGAACGATTTTTTTTTTTTTTTTT
186	Edge	TTTTTTTTTTTTTTTAAGCAAGCCGTTT
187	Edge	TTTTTTTTTTTTTTATGTGTAGGTAAGTACCCCGTTGTTTTTTTTTTTTTT
188	Edge	ATCGTCATAAATATTCATTTTTTTTTTTTTTTTTTT
189	Edge	TTTTTTTTTTTTTTTGTTAATTCATCT
190	Edge	TTTTTTTTTTTTTTTGATTAATAACCTGCGTAGATTTCTTTTTTTTTTTTTTT
191	Edge	GCCATATAAGAGCAAGCCAGCCCGACTTGAGCCATGGTT
192	Edge	GTAGCTAGTACCAAAAACATTCATAAAGCTAAATCGGTTTTTTTTTTTTTTTT
193	Edge	ATAACGTGCTTTTTTTTTTTTTTTTTTT
194	Edge	TTTTTTTTTTTTTTTAAAATACCGAACGAACCACCGTGAAGTAAAC
195	Edge	TTTTTTTTTTTTTTTACAAAATAACA
196	Edge	TTTTTTTTTTTTTTTACAAGAAAACCTCCCGATTTTTTTTTTTTTTTTTTT
197	Edge	TTTTTTTTTTTTTTTGACGATAAAAAGATTAAGTTTTTTTTTTTTTTTTTT
198	Edge	TTTTTTTTTTTTTTTCAATTACCTGAGTATCAAAATCATTTTTTTTTTTTTTTTT
199	Edge	GGTACGCCAGTGCCAAGCTTTTTTTTTTTTTTTTTTT
200	Edge	TTTTTTTTTTTTTTTGAATAACCTTGAATATATTTTATTTTTTTTTTTTTTTTT
201	Edge	CACTAAAACACTTTTTTTTTTTTTTTTTTT
202	Edge	TTTTTTTTTTTTTTTAAACCAATATGGGAACAATTTTTTTTTTTTTTTTTTT
203	Edge	TACGTCACAATCAATAGAATTTTTTTTTTTTTTTTTTT
204	Edge	TTTTTTTTTTTTTTTAGAAAGATTCATCAGTTGA
205	Edge	TTTTTTTTTTTTTTGTGGCATCAATTAATGCCTGAGATTTTTTTTTTTTTTTTTTT
206	Edge	TTTTTTTTTTTTTTTTCATGCCTGCATTAATTTTTTTTTTTTTTTTTTTTTTT
207	Edge	CCAGCGAAAGAGTAATCTTGACAAGATTTTTTTTTTTTTTTTTTTTTTT
208	Edge	TTTTTTTTTTTTTTTGAATCCCCCTCAAATGCTT
209	Edge	AGAGGCTGAGACTCCTTTTTTTTTTTTTTTTTTT
210	Edge	ACAAACACAGAGATACATCGCATTATTTTTTTTTTTTTTTTTTT
211	Edge	TTTTTTTTTTTTTTTCAAGAGAAGGATTAGG
212	Edge	TTTTTTTTTTTTTTTGAATTGAGGAAGTTATCAGATGATTTTTTTTTTTTTTTTTTT
213	Edge	CAGAACAATATTTTTTTTTTTTTTTTTTT
214	Edge	TTTTTTTTTTTTTTTAGCCGGAAGCATAAAGTGTCTGGCC
215	Edge	TGACCGTTCTCCGGGAACGCAATCAGCTCATTTTTTTTTTTTTTTTTTTTTTT
216	Edge	TTTTTTTTTTTTTTTGGTAATAAGTTTAAC
217	Edge	TTTTTTTTTTTTTTGTCTGTCCATAATAAAGGGATTTTTTTTTTTTTTTTTTTTTTT
218	Edge	TTTTTTTTTTTTTTTTCCTCGTTAGAATCAGAGCGTAATATC
219	Edge	AATTGCTCCTTTTGATAAGTTTTTTTTTTTTTTTTTT
220	Edge	CATCGGACAGCCCTGCTAAACAACCTTCAACAGTTTTTTTTTTTTTTTTTTTTTT
221	Edge	TTTTTTTTTTTTTTTAAACCGCCTCCCTCAGACCAGAGC

222	Edge	TCTGACAGAGGCATTTTCGAGCCAGTTTTTTTTTTTTTTTT
223	Edge	TTTTTTTTTTTTTTTTTTCAGCGGAGTCCATGTCATAAAGG
224	Edge	TTTTTTTTTTTTTTTTTCGCCACGCATAACCG
225	Edge	AATTACTTAGGACTAAATAGCAACGGCTACAGATTTTTTTTTTTTTTT
226	Edge	CAAGTTTTTGGTTTTTTTTTTTTTTTT
227	Edge	TTTTTTTTTTTTTTTTTCCTTTAGCGCACCCAGTTTTTTTTTTTTTTTT
228	Edge	TTTTTTTTTTTTTTTTTGAATCGGCCGAGTGTGTTTTTTTTTTTTTTTT
229	Edge	TTTTTTTTTTTTTTCATCTTTGACCC
230	Edge	TTTTTTTTTTTTTTATAATCAGAAAATCGGTGCGGGCCTTTTTTTTTTTTTT
231	Edge	GATACAGGAGTGTACTTTTTTTTTTTTTTTTT
232	Edge	TTTTTTTTTTTTTTTTTGGCGCAGACAATTTCAACTTTTTTTTTTTTTTTTT
233	Edge	GGAGTTTAGTACCGCTTTTTTTTTTTTTTTTT
234	Edge	TTTTTTTTTTTTTACC GCCAGCCATAACAGTTGAAAGTTTTTTTTTTTTTTTT
235	Edge	TTTTTTTTTTTTTTTTATAGCAATAGCT
236	Handles	AATAAGTTTTGCAAGCCCAATAGGGGATAAGTTGTGCTACTCCAGTTC
237	Handles	ACATAGCTTACATTTAACAATAATAACGTTGTGCTACTCCAGTTC
238	Handles	CCTTTTTGAATGGCGTCAGTATTGTGCTACTCCAGTTC
239	Handles	CGTAACCAATTCATCAACATTTGTGCTACTCCAGTTC
240	Handles	CACCAACCGATATTCATTACCATTATTGTGCTACTCCAGTTC
241	Handles	CCACCCTCATTTTCTTGATATTTGTGCTACTCCAGTTC
242	Handles	AACTTTGAAAGAGGAGAAACATTGTGCTACTCCAGTTC
243	Handles	CAAGGCGCGCCATTGCCGGAATTGTGCTACTCCAGTTC
244	Handles	CATAGCCCCCTTAAGTACCATTGTGCTACTCCAGTTC
245	Handles	TTCCCTGAATTACCTTTTTTACCTTTTTTGTGCTACTCCAGTTC
246	Handles	AACGGTGTACAGACTGAATAATTGTGCTACTCCAGTTC
247	Handles	GATTCGCGGGTTAGAACCTACCATTTTGTGCTACTCCAGTTC
248	Guides	AGAGTAGGATTTCCGCAACATGTTTTAAAAACC
249	Guides	ACGGTGACCTGTTTAGCTGAATATAATGCCAAC
250	Guides	CGTAGCAATTTAGTTC TAAAGTACGGTGTTTTA
251	Guides	GCTTAATGCGTTAAATGTAATGCTGATCTTGAAATGAGCGTT
252	Guides	AAGCCAACGGAATCTAGGTTGGGTTATATAGATTAAGCAACTG
253	Guides	TTTAACAACCGACCAATCGCAAGACAAAATTAATCTCACTGC
254	Guides	TTTAGGCCTAAATTGAGAAAACCTTTTTCTCTGTTCCTAGAT
255	Guides Removal	GGTTTTTAAACATGTTGGCGAAATCCTACTCT
256	Guides Removal	GTTGGCATTATATTCAGCTAACAGGTCACCGT
257	Guides Removal	TAAAACACCGTACTTTAGAACTAAATTGCTACG
258	Guides Removal	AACGCTCATTTCAAGATCAGCATTACATTTAACGCATTAAGC
259	Guides Removal	CAGTTGCTTAATCTATATAACCCAACCTAGATTCGGTTGGCTT
260	Guides Removal	GCAGTGAGATTAATTTTGCTTTGCGATTGGGTCGGTTGTTAAA
261	Guides Removal	ATCTAGGAACAGAAGGAAAAGTTTTCTCAATTTAGGCCTAAA

To fold the robots, scaffold and staple DNA were mixed at a ratio of 1:10, respectively, in Tris-Acetate-EDTA buffer supplemented with 10 mM MgCl₂. The mixture was subjected to a temperature-annealing ramp in the following sequence: 1) from 85°C to 60° C, 5 min/°C; 2) from 60 °C to 25 °C, 75 min/°C. Subsequently, excess staples were

removed by centrifugal filtration using Amicon Ultra-0.5mL 100K MWCO centrifugal filters (Millipore).

Payload synthesis

GFP was fused to loading-sequence DNA (5AmMC6/GAACTGGAGTAGCAC Integrated DNA Technologies) by EDC conjugation according to the manufacturer's instructions. Anti-human p75/AIRM Fab' fragments were obtained by digesting whole IgG using a Fab' generation kit (Pierce) according to the manufacturer's instructions. After purification, Fab' fragments were fused to loading sequence DNA by EDC conjugation.

Robot loading and purification

100 pmol folded robots were loaded with autoinducer and payload (at a 3:1 ratio) by incubation at a 5-fold molar excess of mixture to loading sites. Loading was performed for 2 hours on a rotary shaker at room temperature in folding buffer (10 mM MgCl₂ in 1X TAE). Finally, loaded robots were cleaned by centrifugal filtration with a 100K MWCO Amicon column (Millipore) as described above.

Loading in this design was done stochastically. However, by redesigning the loading site sequences and autoinducer/payload specificities, loading can be directed to specific sites. However, stochastic loading was effective (albeit potentially less optimal than directed loading), for the following reasons: a) robots containing only autoinducer can serve as autoinducer sources indicating population size; b) robots containing only payload (GFP/Fab') respond to external autoinducer and contribute to the readout; and c) robots containing both serve both functions.

Supplementary Note 2: QS system design

5'-amine-modified linker oligonucleotide (5AmMC6/TTTTTGAAGTGGAGTAGCAC, Integrated DNA Technologies) was conjugated using the heterobifunctional crosslinker SMCC to the C-terminal thiol group in Lys-Pro-Leu-Gly-Met-Trp-Ser-Arg-Cys (custom ordered from American Peptide Company), containing the cleavage site of MMP-2, according to the manufacturer instruction, at a DNA:peptide ratio of 1:2. After quenching with 2-mercaptoethanol and purification, the oligonucleotide-peptide hybrid was further conjugated with PDGF using EDC crosslinking, purified and verified with spectrophotometry to yield to complete autoinducer. The cleaved autoinducer maintained its ability to bind to anti-PDGF antibodies as well as to the PDGF aptamer.

Kinetics of peptide cleavage by MMP-2 was measured by fluorometry using a fluorogenic MMP-2/MMP-2 substrate (5 μ M) and human recombinant MMP-2 in assay buffer (Tris-EDTA containing 150 mM NaCl, 10 mM MgCl₂ and 1 μ M ZnSO₄, pH 7.5) at room temperature. The desired concentration of MMP-2 for this study was fixed at 5 μ g/mL (**Fig. S1**).

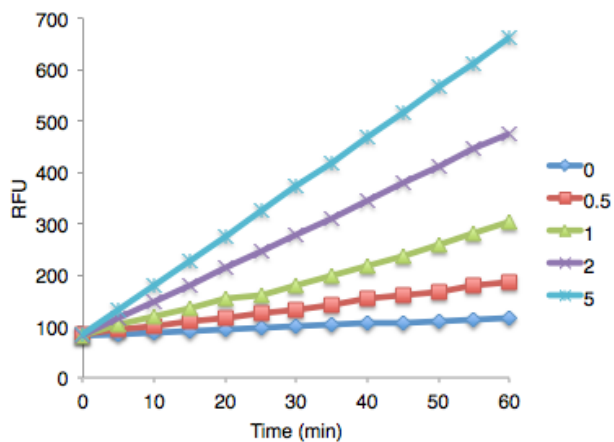


Fig. S1: MMP-2 calibration assay, used to determine desired MMP-2 concentration for the purpose of activating QS in robots for this study (see above for detail).

To evaluate the kinetics of autoinducer release from robots, autoinducer-loaded robots were exposed to MMP-2 (5 μ g/mL) for 1 h at room temperature, after which the samples were measured directly in a PDGF ELISA (**Fig. S2**).

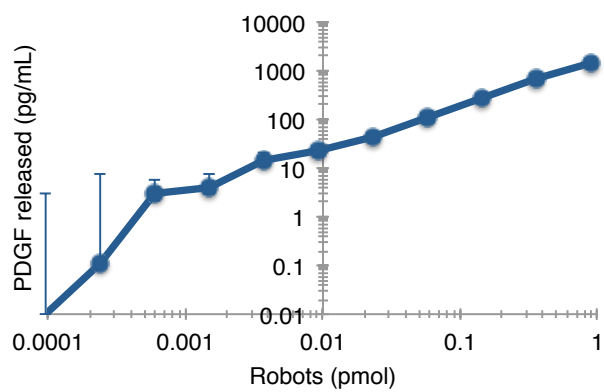


Fig. S2: Autoinducer release from MMP-2 treated robots.

Supplementary Note 3: Cell culture

Jurkat cells were obtained from American Type Culture Collection (ATCC) and maintained at 37 deg. and 5% CO₂ in RPMI 1640 containing 10% fetal calf serum. Prior to incubation with robots, cells were diluted to a density of 100,000 cells/mL in 96 well plates and activated with 200 ng/mL of recombinant human IL-6 (Peprotech) overnight. Following activation, the cells were treated with varying concentrations of either free anti-p75/AIRM Fab' fragments (cross-linked by 25 ug/mL secondary anti-mouse IgM), or the equivalent amount of Fab' fragments loaded into QS-regulated robots, for 24 hours. Following this period, the cells were analyzed for cell cycle distribution using propidium iodide as previously described.

Supplementary Note 4: Dynamic light scattering and flow cytometry

Dynamic light scattering was performed using a Malvern Zetasizer Nano instrument using various concentrations of robots in Tris-EDTA buffer supplemented with 10 mM MgCl₂. The minimal robot concentration that enabled reliable detection (based on good correlation function) was 29 pM, and the results obtained were good as a qualitative confirmation of QS-driven switch from closed to open state.

The advantage of flow cytometry is the use of target-coated microspheres, which isolate from any population only the robots that open and directly bind them, allowing much more reliable measurements and at lower population densities. Flow cytometry was performed using an Accuri C6 flow cytometer equipped with 488 nm and 640 nm lasers, and analyzed with FlowPlus software. Cell cycle analysis was done using propidium iodide as previously described.