Electronic Supplementary Material (ESI) for Nanoscale. This journal is © The Royal Society of Chemistry 2021

Supplementary material The effects of nanostructure geometry on cell labeling by multivalent DNA origami

Ying Liu,
a‡ Piyumi Wijesekara,
 b‡ Sriram Kumar,
a Weitao Wang,
a Xi Ren, ab* and Rebecca E. Taylor
 abc*

Contents

1	CaDNAno design of the DNA origami nanotile	and nanorod 2
	1.1 CaDNAno design of the nanotile	2
	1.2 CaDNAno design of the nanorod	3
	1.3 Design of the nanosphere .	4
2	2 Sequence list that was used in this paper	4
	2.1 Sequence list of the nanotile .	4
	2.2 Sequence list of the nanorod	7
	2.3 Sequence list of the nanosphere	9
	2.4 Sequence list of the binding overhangs and decor	ations 10
3	3 Agarose gel results for the DNA origami	10
4	4 AFMs for the selected samples	14
5	5 Statistical analysis of the fluorescence data	16

1 CaDNAno design of the DNA origami nanotile and nanorod

1.1 CaDNAno design of the nanotile

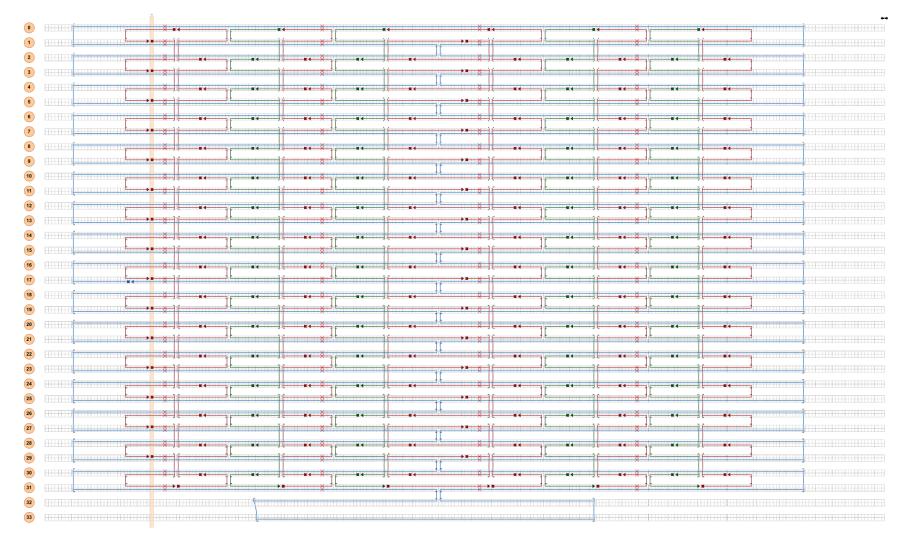


Figure 1: CaDNAno design of the DNA origami nanotile. Blue: M13 scaffold, red: staples with the break points pointing up from the plain, green: staples with the breaks point down from from the plain.

1.2 CaDNAno design of the nanorod

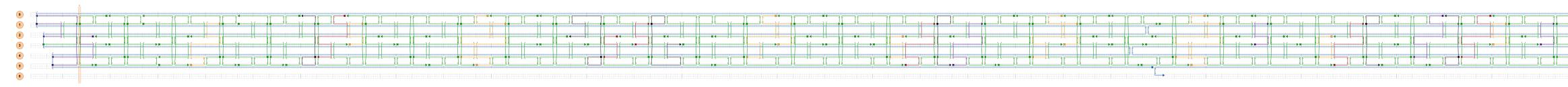
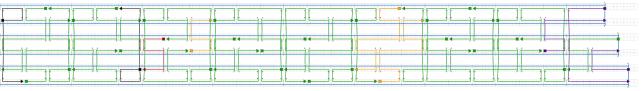
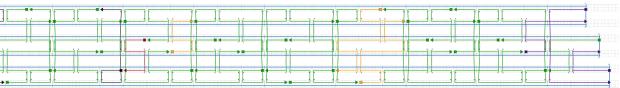


Figure 2: CaDNAno design of the DNA origami nanorod. Blue: M13 scaffold, green: plain staples, purple: edge sequences which are excluded except when we have overhangs on them, red: sequences with biotin tags, yellow: sequences with overhangs.

][][





1.3 Design of the nanosphere

The DNA origami nanosphere was dierctly taken from Benson's work in 2015.¹ The screenshot of the vHelix design is as shown in Figure 3. The numbers next to each helix represents the name of that helix.

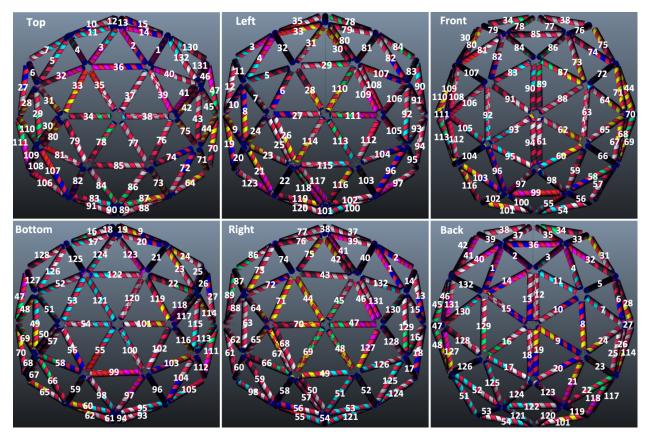


Figure 3: vHelix design of the DNA origami nanosphere. The numbers next to the helixes represent the name of that helix. Each staple would cross two helixes and was named as <starting helix> - <end helix>

2 Sequence list that was used in this paper

2.1 Sequence list of the nanotile

Name	Sequence	biotin sites	28	3 fac	ebir	ndin	ng si	tes	1	2 e	dge	site	es		geo	met	ry st	udy	
seam02	TCAGGAGGTTTAGTACCGCCACCCTCAGAAC TTTGCTAAGTAAATGAATTTTCTGAGTGCCTT GAGTAACAGTTTTAACGGGGTCTATGGGAT								12	8		+			g1				
seam04	TAACCGATATGACAACAACCATCGCACCACCC TCAGAGCCGCCACCCTCAGAGCCCCACGCA													*		g2			
seam07	CACTAAAATAAAACGAAAGAGGCAACGTCACC AATGAAATTAGCAAGGCCGGAAAAAGAATA TGACCTTCTACAGACCAGGCGCATACCACGGA	\$1										+		*				\dashv	_
seam09	ATAAGTTAAGAAACGCAAAGACAGGCTGGC AAAATCTAATACCAGTCAGGACGTGCAAGAAA													*			g3		
seam12	CAATGAAAGCCCAATAATAAGATGGGAAGA GGGGTAATTTTGCAAAAGAAGTTTAAATAAAC AGCCATAAATTTGCCAGTTACATGCCAGAG	S1									_	+		*				g4	
seam15		S1												*					
seam17	AGTAGATTAGTTGATTCCCAATTCTTCTGTCC AGACGACCAAAAGGTAAAGTAATGCGAACG CCCTGTAATCGGTTGTACCAAAAATAAGGCGT											+		*				\dashv	g5
seam20	TAAATAACGACCGTGTGATAAACATTATGA AGGCTATCTAGCTATTTTGAGAGAAGACGCT	\$1																	
seam22	GAGAAGAGCGATAGCTTAGATTATCTACAA ACGCCATCCAGCTCATTTTTTAACAGGCGAAT TATTCATTACAAAATCGCGCAGCAATAGGA										-	+	+					\dashv	_
seam25	AGCTTTCCCCTCAGGAAGATCGCACATCAATA TAATCCTCAGATGATGGCAATTCTCCAGCC GGTCGACTCAGTGCCAAGCTTGCAGGAGCACT																		
seam27	AACAACTICTAAAATATCTTTATGCCTGCA TTAATGAAGGGAAACCTGTCGTGCATTAAAAA	\$1																	
seam30	TACCGAACCCTAAAACATCGCCCAGCTGCA CCCGAGATATCCCTTATAAATCAAAAACGCTC ATGGAAACCATTGCAACAGGAAAAGAATAG											+						$ \rightarrow$	
seam32	GAGCTTGACGGGGAAAAAAGGGATTTTAGAC TAGGAACCCATGTACACAACGCC								12	8				*					
X01Y03	TGTAGCATAATTTTTTCACGTTCCTTTAAT TGTATCGAGCGAAAGACAGCATTGAGGACT AAAGACTCATCGCCTGATAAATTTAGCCGG										+	+		* * *		g2	g3	\dashv	_
X01Y05 X01Y06	AACGAGGATTCAGTGAATAAGGTAAATTGG GCTTGAGTAGGAATACCACATTTTACGAGG													*				g4	
X01Y08	CATAGTACCCCTCAAATGCTTTCAAAAATC AGGTCTTTCCTTTTGATAAGAGCTGAATAT AATGCTGGGGCGCGAGCTGAAATTAACATC										_	+		* * *					g5
X01Y11	CAATAAATTTAAATGCAATGCCGAGAAAGG CCGGAGAATGTCAATCATATGTCAGGAAGA											+		* *					
X01Y13	TTGTATAACAACCCGTCGGATTTGGGATAG GTCACGTTGGGAAGGGCGATCGGAAAGGGG GATGTGCAATTGTTATCCGCTCAAAGTGTA										+	+		* *				\dashv	
X01Y16	AAGCCTGAGTGAGACGGGCAACGAGTTGCA GCAAGCGCAAAGGGCGAAAAACCATCACCCAAATCAA								12	\rightarrow	-	_		*					
X02Y02	GCGAATAATTCCACAGACAGCCCTGGGATAGCAAGCCCAA CCCTCAGCGTTTATCAGCTTGCTTAAGGAATT ATTTGTATTTTTCATGAGGAAGTTGATCGTCA	\$1							12	8	6	4 2	2 1		g1			\dashv	_
X02Y04 X02Y05	AGCTGCTCCGCAGACGGTCAATCACAACGGAG TTGAGATTATGGTTTAATTTCAACCGTAACAA	S1										+	+	F					
X02Y07	ATTGAATCAGAGCAACACTATCATTTCATCAG TTAATTGCTACCCTGACTATTATAAAATATTC TTCATTTGTAGCTCAACATGTTTTGAGTACCT	\$1 										+		╞				\rightarrow	
X02Y09 X02Y10	TCATATATTCATACAGGCAAGGCAGCTATATT AAACTAGCCAGTCAAATCACCATCTAGAACCC												T	F					
X02Y12	AGCGAGTAAGCAAATATTTAAATTTAATCGTA GCAACTGTTGGTGTAGATGGGCGCCTAAATGTG CTGTGTGATGCAAGGCGATTAAGTCAGGCTGC	\$1	E						E	╞		+		F					
X02Y14 X02Y15	TTTTCACCGGGTGCCTAATGAGTGGCTGTTTC TCCAACGTGTCCACGCTGGTTTGCGGTTTTTC	भ				H						+	F	F					
X03Y01 X03Y02	GTTTTTTGGGGTCGAGACGTGGAC ACCACCCTCATTTTCACATAGTTAGCGTAACGTAGAAAGG AACAACTATCGAGGTGAATTTCTTAAGGCCGC		28	16	10	6	4	2 1	E				ŧ	F		g2			
X03Y03 X03Y04	TTTTGCGGTCCATTAAACGGGTAAAGCGCGAA ACAAAGTATAAGGGAACCGAACTGTCATTACC		28									+	F				g3		
X03Y06 X03Y07	CAAATCAATITAATCATIGIGAATATIACAGG TAGAAAGAAACCCTCGTITACCAGACIGCGGA ATCGTCAIGICAGAAGCAAAGCGGACAGGICA			16					E				+	F				g4	
X03Y09	GGATTAGAAAATATGCAACTAAAGGTCAATAA CCTGTTTAAAGAATTAGCAAAATTCAAGGATA AAAATTTTAATATGATATTCAACCGAGAATCG		28 28	16	10	6	H		\vdash		-	+	╞	F				-	g5
X03Y11 X03Y12	ATGAACGGGTAAACGTTAATATTTCAGCTTTC ATCAACATATCGTAACCGTGCATCAGCGCCAT		28	10		╞			E			+	+	F					
X03Y14	TCGCCATTTGGGTAACGCCAGGGTCGTAATCA TGGTCATAAGCTAACTCACATTAATATTGGGC GCCAGGGTCCCAGCAGGCGAAAATAGTCCACT		28	16	10	6	4				_	+						\square	
X03Y16	ATTAAAGAGTGCCGTAAAGCACTA AGTGAGAAATCTAAAGTTTTGTCGCCACCCTCAGAGCC								12 12						g1				
X04Y03	GGGAGTTAAAACAGCTTGATACCTCAGCGG TTATACCAAATACGTAATGCCACGCTTGCA CCGGATATACCAACTTTGAAAGACCAGCGA	\$1										+						$ \rightarrow$	
X04Y05	ACAACATTTACCTTATGCGATTTACAAGAA CGTCCAATACGACGATAAAAACCTAACGGA	S1																	
X04Y08	AAACTCCAATTGCATCAAAAAGATGGATAG CGCAAATGTACGGTGTCTGGAAGCGGAAGC TTTCAACGAAGCAATAAAGCCTCTACATTT	\$1 									_	+							
X04Y10	GCAAACAAGTTCTAGCTGATAAAGCCTTTA CCTGTAGCTGTTAAAATTCGCATGTCTGGA																		
X04Y13	CCAGGCAATGCCAGTTTGAGGGGTGGCCTT CTCGAATTTTTCCCAGTCACGACCCGGAAA	S1	-			\square		_		$\left \right $	+	+	+	\vdash		\vdash			_
170-1-14	GGTTGCGTTGCGTTGCGCTCACTACCGAG					H	\vdash	-			+	+	-	-			-		
X04Y15	GGTTTGCGTTGCGTTGCGCTCACTACCGAG GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT	S1																	
X04Y15 X04Y16 X05Y01 X05Y02	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG		28	16												g2			
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT		28	16												g2	g3		
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG		28	16	10											g2		g4	
X04Y15 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT		28		10											g2		_	g5
X04Y15 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGAGGCAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTGTTAAATAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC		28 28 28 28 28													g2		_	g5
X04Y15 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGAGGCAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCGAGAGGCTAATAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTGAACGGAAGGCTAATAGC GGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAAATA		28 28 28 28 28 28 28	16												g2		_	g5
X04Y15 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y11 X05Y11 X05Y15 X05Y16 X06Y01	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCGAGAGGCTAATAGCG AACCAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTACATTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTGTTAAATAAAAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGGA TCCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA		28 28 28 28 28 28 28	16							-+					g2		_	g5
X04Y15 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y07 X05Y08 X05Y07 X05Y07 X05Y10 X05Y11 X05Y11 X05Y11 X05Y15 X05Y16 X06Y01 X06Y02 X06Y03 X06Y04	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCGCAGTCAAAGCG AACCAGACTTTACATTCCATATAACTAGTTTGA CCATTAGAAGAGGAAGCCGAGCAAATCTTG CCGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAAAAATAA TTCGCGTCACGACGACAGATGACGGCAAGCCGC TTCTGGTGGTTGTAAAACGACGGCCAGCCAGC CACTGGGTGCCCGCTTTCCAGTCTGGGCCACCGC TTCTGGTGGTTGTAAAACGACGGCCAAGGGCAGGTGAT CCCCGGGTGCCCGCTTTCCAGTCTGGGCCAAC CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCCGATTAACACAGGTGTATCACCGTAC CTCAGAAACGGCCCCCGATTAAACAAGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACCACCGAGTGTAC CCATAACACGCCACCAGAACCACCGACGC CTCAGAACCGCCACCAGAACCACCGACGC ACATATAATATTTTGTCACAATCAAGTAGCAC	S1	28 28 28 28 28 28 28	16							-+					g2		_	g5
X04Y15 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y07 X05Y07 X05Y08 X05Y07 X05Y10 X05Y10 X05Y11 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCGCAGTCAAAGCG AACCAGACTTTACATTCCATATAACTAGTTTGA CCATTAGAAGAGGAAGCCGAGGAGGAGGTCATT GCCTGAGATAAATTCCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCCGAGGAGGGCATT GCCTGAGATAAATTTTTGTTAAATAAAAAATAA TTCGCGTCACGACGACAGATACGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCAAGGGCAGGCA CCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCCGATTAACACAGGGTGATCACCGTAC CCTCAGAACAACGCCCCGATAAAACAAGGGTGAACACCGCCAACCCGCACGC CTCAGAACCGCCCCCGATTAAACAAGGTGTATCACCCGTAC CCTCAGAACCGCCACCAGAACCACCGAGGTGATC	S1	28 28 28 28 28 28 28	16							-+					g2		_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y07 X05Y07 X05Y07 X05Y10 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y09	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCGATCAAAGCG AACCAGACTTACATTACCTATTAACTAGTTTGA CCATTAGAAGAGGAAGCCGATCAAAGCG AACCAGACTTTCATTCCATTATAACAAGTGG CCATTAGAAGAGCATAAAGCCGAGGAGGTCATT GCCTGAGATAAATTTTTGTTAAAACTAGTTTGG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAAGA TCCCCGGGGTCCCGATTTCCAGTCTCGGCCAA CGCCGGGGTCCCGAAATCGGCAAAAGGTGTATCACCGTAC CCTCAGAAACGCCCCCGATTTA TGGTAATAAGTGCCCGATAAAACAAGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACCACCGAGAGTGAAC CCATTACAACGCCCCGATTAAACAAGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACCACCGAGAGTACC CTCAGAACCGCCACCAGAACCACCGAGAGTAC CATTACAACACGCACAATAGCAACAAGGTGTATC CATTACACCACTGGATAGCAGCACCCGC TTGAGTTAATAGCAATAGCTATCAAGAAGACC CATATAATATTTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCTATCAGGAGAA ACAAGCAAACCGCGCCCCAATAGCACGTCTTTC AGTACCAGAATAAACAACAGCAGCACCGCACAGAA CAAGCAAACCGCGCCCCAATAGCACCACCGAGAA CAAGCAAACCGCGCCCCAATAGCACCACCGAAGAA ACAAGCAAACCGCGCCCCAATAGCACCACCGAGA TGAAATAACGAATAAACAACAGCGGAATGAATATAA	S1	28 28 28 28 28 28 28	16							-+				g1	g2		_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y07 X05Y07 X05Y07 X05Y10 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y09 X06Y10 X06Y10 X06Y11	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCGATCAAAGCG AACCAGACTTACATTACCTATTACTAAGAG CCATTAGAAGAGGAAGCCGATCAAAGCG AACCAGACTTTCATTCCATTATAACAAGTGTTGA CCATTAGAAGAGCATAAAGCTGAATAACTTTTG CCGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA CCCCGGGGTCCCGAATCGGCCAAGGGAGGTCATT GGCTGGGTGGTCCGAAATCGGCCAAAGGGTTGA CGCTGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCCGGGGTCCCGAAATCGGCAAAAGGTGTATCACCGTAC CTCAGAAACGCCCCCGATTTA TGGTAATAAGTGCCCGATAAACAAGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACCACCGAGAGTGAC CCTTAGCACCACCAGAACCACCGAGAGTGAAC CATTACAACGACAGCAATAGCAACAAGGTGTATCACCGTAC CATTACACCACTGGATAGCAGCACCGC TTGAGTTAATAGCAATAGCTATCAGGAGA CAGAGCTTTATTATCCCAATCCAAGAGAA ACAAGCAAACCGCGCCCCAATAGCACCTCTTC AGTACCGAGACAATAAACAACATGCATCGAGAA	S1 S1 S1 S1 S1 S1 S1 S1	28 28 28 28 28 28 28	16							-+							_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y06 X05Y07 X05Y08 X05Y07 X05Y10 X05Y10 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y07 X06Y08 X06Y09 X06Y00 X06Y01 X06Y10 X06Y11 X06Y12 X06Y11 X06Y12 X06Y13 X06Y14	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGGATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA CCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCCGGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGATTAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGATTAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGATTAA CGCACGACCACCAGAACCACCGACGTGTAC CTCAGAACCGCCACCAGAACCACCGACGTGTAC CTCAGAACCGCCACCAGAACCACCGACGTGTAC CATTACACCACCATGATAGCAACCACCGACTTC CCCAGAGCCTTTATTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCTATCTAGGTGGCA CAGAATAAGCAATAAGCAATAGCAATCAAGTAGCAC TTGAGGAGACTATAAACAACAGCGCCTTTC AGTACCGAGACAATAAACAACAGCACCGCAA ACAAGCAAACCGCGCCCAATAGCACCGTCTTC AGTACCGAGACAATAAACAACAGGAGCACCTGGAA ACAAGCAAAACCAGCGCCCAATAGCACCATTCACGAGA ACAAGCAAAACAGCGCCCAATAGCACCACCGAGA CAGAGCCTTTATTATTATCCCAATCCAACAAGAACACCGCGAC CAGAATACGAATAAACAACACGGAATGAATATAA AAAACATAGTCAATAAGTAAGAATTAAACAACATGCATTGAGA CTGATTATGATTAGTTGTGGAGTTATAACCAAGCACCTTG CTGATTATGATTAGTTAGGAATTAAGCTTTGAA GAAGGTTAAATAGATTAGAGTAGAG	S1	28 28 28 28 28 28 28	16							-+				g1			_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y10 X05Y10 X05Y11 X05Y12 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y05 X06Y06 X06Y07 X06Y06 X06Y07 X06Y07 X06Y08 X06Y07 X06Y10 X06Y11 X06Y12 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y14 X06Y15 X06Y16	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGGATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA TCCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCCGGGGTCCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGATTAA TGGCTAATAAGTGCCCGTATAAACAAGGGTGAAC CCTCAGAACCGCCCCGATTAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGATTAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA CTCAGAACCGCCACCAGAACCACCGACGC CTCAGAACCGCCACCAGAACCACCGACGC CTCAGAACCGCCACCAGAACCACCGACGTGTAC CATTAATAAGTGCCCGTATAAACAAGGTGTACCCCGAA CAGAGCATTAATAGCAATAGCAATCAGGAGCACCCGCAA CAGAGCAAACCGCCCCAATAGCACCGCCACC ACATATAATATTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCAATCAGCACGTCTTC AGTACCGAGACAATAAACAACATGCATCGAGAA ACAAGCAAACCGCGCCCAATAGCACCGTCTTC AGTACCGAGACAATAAACAACAGCGACTGCACC CAGAAGCCAATAAACAACACGCGAATGAATATAA AAAACATAGTCAATAAGAACAACAGACATCCACGGA CGGAGAATAACAACACCGGAATGAATATAA AAAACATAGTCAATAGGAATTAAACAACGACGTTTT TACCAAGTTCAATAGGAATAACAACAACGACCATTGAGAA CAAGGAATAACAACACCGGAATGAATATAA AAAACATAGTCAATAGGAATAACAACAACGACATTGAA CTGGATATAATAGATAAGAACACCGGAATGAATATAA AAAACATAGTCAATAGGAATTAAAGATTAAGGTT TACCAAGTTCAATAGGAATAACAACCGGAATGAATATAA GAAGGTTAAATAGATTAGAGTTAGGACCGTTCATATTC	S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1 S1	28 28 28 28 28 28 28	16							-+							_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y10 X05Y10 X05Y11 X05Y12 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y11 X06Y12 X06Y10 X06Y11 X06Y12 X06Y03 X06Y04 X06Y11 X06Y12 X06Y03 X06Y04 X06Y11 X06Y12 X06Y03 X06Y04 X06Y07 X06Y03 X06Y04 X06Y11 X06Y12 X06Y03 X06Y04 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y13 X06Y11 X06Y12 X06Y13 X06Y11 X06Y12 X06Y13 X06Y11 X06Y12 X06Y13 X06Y11 X06Y12 X06Y13 X06Y14 X06Y12 X06Y13 X06Y14 X06Y12 X06Y13 X06Y14 X06Y12 X06Y13 X06Y14 X06Y12 X06Y13 X06Y14 X06Y12 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X06Y13 X06Y14 X07Y13	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTGTTAAATAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA CCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCCGGGGTCCCGACGACGCACTAGAGGA TCCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGATTAA TGGTAATAAGTGCCCGTATAAACAAGGGTGACCCC CTCAGAACCGCCACCAGAACCACCGAGTGTAC CTTAGCACCACCAGAACCACCGAGTGTAC CATTACACCACCACCAGAACCACCGAGTGTAC CATTACACCACCACCAGAACCACCGACGTGTAC CTCAGAACCGCCACCAGAACCACCGACGC TTGGGTATAATAGTCCCAATAGCAGCACCC ACATATAATATTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCTATCAGGTGGCA CAGAGCCTTTATTTACCCAATCCACACAGAAA ACAAGCAAACCGCGCCCCAATAGCACGTCTTC AGTACCGAGAATAAACAACATGCATCGAGAA ACAAGCAAACCGCGCCCCAATAGCACGTCTTC AGTACCGAGAATAAACAACAGCAGCACTCGAGA TGAAATACGAATAAACAACAACGACGTCTTC AGTACCGAGACAATAAACAACATGCATCGAGA TGAAATACGAATAAACAACAGCAGCACTCGAGA TGAATACGAATAAACAACAGCAGCACTTGAGAA AAAACATAGTCAATAGTAATAGAATTAAA AAAACATAGTCAATAGTAATAGAAATCGGAATTAAA AAAACATAGTCAATAGTAATAGAAACACGCGTTCATATTC ACTGATTAGCGAACCACCAGCAGAAAACCCCCTG CTGAGTAACGGAACCACCAGAAGAATTGAG ACCGCCAGTACCACCAGACACAATATT AAGGAAACGGTACGCCACAGAACACATTGAGAAACTGGCGA AGGAACGGTACGCCAGACACACACACGCCTC CCTCAGAGCGAACCACCAGAGACAATATT AAGTATAGCCCGGAATGTTAATGCTTGAACGCCCTTG CTGATACGGAACCACCAGAGCCGCCCCCACCCGCCTC CCTCAGAGCGTAATCAGTAGTGAGGGACAGCCAGCAGCAGCACACCCCCCCC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16							-+					g2		_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y10 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y05 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y07 X06Y10 X06Y11 X06Y12 X06Y11 X06Y12 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X06Y11 X06Y15 X06Y16 X07Y01 X07Y02 X07Y03 X07Y06	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGATTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGAGGCAGTCATT GCCTGAGATAAATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGGCACTT GCCTGAGATAAATTTTTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA TCCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCCGATTTA TGGTAATAAGTGCCCGCTATAAACAAGGGTGTACACCGTAC CTCAGAACCGCCACCAGAACCACCGAGTGTAC CATTACCACCATCGATAGCAGCACCCGCACC ACATATAATATTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCAACACCGGCACC CAGAGCCTTTATTATCCCAATCCAGCAGCACC CAGAGCCTTTATTATCCCAATCCAGCAGCAC CAGAGCCTTTATTATCCCAATCCACAGAA ACAAGCAAACCGCGCCCAATAGCACGCTCTTC AGTACCAGAATAAACACCGGAATGAGCAC CTGAATAAGTCAATAAGCAACATGCACCTTG CTGATTAATAGCAATAACACCGGAATGAATATAA AAAACATAGTCAATAAGTAAACACATGCATCAGAGA TGAAATACGAATAAACACCGGAATGAATATAA AAAACATAGTCAATAAGAATAGCAATCCTTG CTGATTAAGCAATAAACACCGGAATGAATATAA AAAACATAGTCAATAAGAATTAAACACATGCATCAGGA ACGGCAGGACCACCAGCAGCAGAATATAA AAAACATAGTCAATAAGTAAACACCGGCATCATATGA GAAGGTTAAATAGATTAAGATTAAGCATTGAG ACCGCCAGTACCTACACTGAGCAGAATGCATCTTG CTGATTAAGCAATAAACACCCGGAATGAATATAA AAAACATAGTCAATAAGAACACCGGCAATCCTTG CTGATTAAGCGAACCACCCAGCAGAAGAATTGAG ACCGCCAGTACCTACATTTGAAGCGATCAGCGCGA AAGGAACGGTACCCCAGCAGAAGAATTGAG ACCGCCAGTACCCACAGAAGAATATT AAGTATAGCCCGGAATGATATAAGCATTGAGGAAAATAC ATACATCAATAAGAAACCACACTTTTTATGAGGAACCGCCTC CCTCAGAGCGTAACCAGAGACCCCTTTTTATGAGGAAAATAC ATACATAACCAAATAAGAAAATCCATTTTAACCAAGG AGGATAACCAAATAAGAAACGATTTTAACGAAGCAGCCTTC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2								-+							_	g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y09 X06Y10 X06Y11 X06Y12 X06Y13 X06Y10 X06Y11 X06Y12 X06Y13 X06Y11 X06Y12 X06Y13 X06Y14 X07Y03 X07Y03 X07Y04 X07Y05 X07Y08	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGCAGGTCATT GCCTGAGATAAATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGCCATT GCCTGAGATAAATTTTCCATATAACAAGTTAACAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA TCCCCGGGTGCCCGCTTTCCAGTCTCGGCCAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCCGATTTA TGGTAATAAGTGCCCGTATAAACCAAGGGTGTATCACCGTAC CTCAGAACCGCCCCCGATTAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTATCACCGTAC CTAGAACCGCCACCAGAACCACCGGCACC ACATTAATAATGTGCCCATATAAACAAGGTGTATCACCGTAC CTTAGCACCATCGATAGCAGCACCCCGCCACC ACATTAATAATTTTTGTCACAATCAAGTAGCAC TTGAGTAATAAGTGCCCAATAGCACCACCGCAAC CAGGACCTTTATTTTGCCAATCAAGTAGCAC TTGAGAACCGCGCCCCAATAGCACCGCCACC ACATATAATAGTCAATAAGCAATACCAAGGAGCACCCGGCA CAGAGCCTTTATTTTTCCCAATCCACAGAA ACAAGCAAACCGCGCCCCAATAGCACGGCACCCGAA CAGGAACCAGCAGCACCCGGAATGAATATAA AAAACATAGTCAATAAACACGGGAATGCACTTG GTGAATAAGTCAATAAACACCGGAATGAATATAA AAAACATAGTCAATAAGAACACGGAATGCACTTG CTGATTATGATCACATAAGTGAATTAA AAAACATAGTCAATAAGATAACACGGAATGAATATAA AAAACATAGTCAATAAGAACACGGGAATGAATATAA AAAACATAGTCAATAAGAACACCGGAATGAATATAA AAAACATAGTCAATAAGAACACCGGAATGAATATAA AAAGGTTAAATAGGAATAACACCGGAATGAAATGGA ACCGCCAGTACCTACATTTGAACGAAGAATTGAG ACCGCCAGTACCTACATTTGAACGAAGCCGTCCCTC CCTCAGAGGTAACCCACAGAAGCAGCCAGCAGCAAGCAATAC AAATACCAAATAAGAAACGATTTTAATGGAAATAC ATACATAATAAGAAACGAGCCTTTTTAATGGAAAATAC ATACATAACAAAATACAAATCCAATTAGGAAAAATAC ATACATAACAAAATACAATAGAAATCAATTAGGAAACCAAGG CTAACGAGGTAATCAGAAACGATTTTACAAGG AGGAACCGAAATAAGAAACGATTTTACCAACG CTAACGAAGGACAAATCAGAATAGGAATTAGAAACCAAGT	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2								-+								g5
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y09 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y01 X07Y02 X07Y03 X07Y04 X07Y05 X07Y06 X07Y010 X07Y10 X07Y10 X07Y11	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCCGATCAAAGCG AACCAGACTTTCATGACGAGAGGCCGATCAAAGCG AACCAGACTTTCATTCATTCATTAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG GCGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTGTTAAACTAGTTTGG CCGGGAGAATTAATGCCGGAGAGGGAGGCATT GCCTGAGATAAATTGTTAAACGACGGCCAGCGC TTCTGGTGGTGTAAAACGACGCCTAGAGGGA CCCCCGGGTCCCGAATCGGCCAACGCCCC TTCTGGTGGTGTAAAACGACGCCTAGAGGGA GCCCCGGGTTCCGAATCGGCAAAGGGCTGAT GCCTGGGGCCCCCGCTTTCCAGTCTCGGCCAA CGCGCGGGTTCCGAATCGGCAAAAGGGTGAA GTGTTGTTGGGAGCCCCCGATTA TGGTAATAAGTGCCCCCGATTAA TGGTAATAAGTGCCCCCGATTA TGGTAATAAGTGCCCCCAATACGACAAGGTGTATCACCGTAC CTCAGAACCGCCCCAATAGCACCGCACC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2								-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y10 X05Y10 X05Y11 X05Y12 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X05Y11 X05Y15 X05Y16 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y07 X06Y10 X06Y10 X06Y11 X06Y12 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X06Y16 X07Y07 X07Y03 X07Y04 X07Y07 X07Y08 X07Y07 X07Y08 X07Y01 X07Y10 X07Y10 X07Y10 X07Y10 X07Y10 X07Y11 X07Y12 X07Y11 X07Y12 X07Y13	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACGACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCCTAGTAAAAT GTTTAGACTTAAGAGGAGAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGGATAAAGCTAAATACTTTTG GCCTGAGAATTAATGCCGGAGAGGCCAGTTAAAAAT TTGGCGTCACGACGACAGTATCAGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGGCCAGGCACTT GCCTGAGATAAATTTTTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA CCCCGGGTGCCCGCTTTCCAGTCTCGGGCCAA CGCGCGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGCATTTA TGGTAATAAGTGCCCGTATAAACAAGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACCACCGAGTGTAC CTTAGCACCACGCACAGTATCAGGTGACC CTCAGAACCGCCACCAGAACCACCGAGTGTAC CATTACCACCATCGATAGCAGCACCCGCACC ACATATAATAGTGCCCGTATAAACAAGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACCACCGACGCAC CAGAGCCTTTATTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCAACTCCGAGCACCC ACATATAATAGCAATAGCAACTACCAGCAGCCTTTC AGTACCGAGACAATAAACAACAGGCGTCTTC AGTACCGAGACAATAAACAACAGGACCTCGAGA CAAGGATAAACCGGCGCCCAATAGCACGGCACCC CAGAGCCTTTATTTATCCCAATCCAACAGGACTCTG CTGATAATAGCAATAACACGGGAATGAATATAA AAAACATAGTCAATAACACCGGAATGACACCTTG CTGATTAGGAACAACACGGCGCCAACACGAAATGC ACAGGTTAAATAAGATTAAGCAACATGCATCTTG AGAATACGAACCACCACCACAGAATATAA AAAACATAGTCAATAAGACACGGACACCCTGCCAC CCCCAGAACCACCACCACACAATATT AAGAATAAGCATAAACACCGGAAAGAATTGAA AACCGCCAGAACCACCACACAATATT AAGTATAGCCAAACCACACGCGCCAACCGCCTC CCCCAGAGCCAAATAAGAAATCCAATATTA AAACCATAGCCAAACAACAATTGAAATAC AAATCACCAATAAAGAAACGATTTTAATGGAGAAATAC AAATCACCAATAAAGAAACGATTTTAATGGAAACCAAGG CTAACGAACCACAAATAAGAAATCCAATATGGAAAATAC ATACATAATAACCAAAATCAAGAATCAAGAAATAC AAACCAAACC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2								-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y01 X07Y02 X07Y03 X07Y04 X07Y05 X07Y06 X07Y11 X07Y12 X07Y13 X07Y14 X07Y15 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACCGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCGATCAAGCG AAACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CCGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCGGGAGAATTAATGCCGGAGAGGGCACCGC TTCGGGTGGTTGTAAACGACGGCCAAGGCCACGC TTCGGGTGGCCCCGCTTTCCAGCCCGGCCAA CCCCGGGTGCCGAAATCGGCAAAAGGGTGAAC CGCGCGGGTTCCGAATCGGCAAACGGCCACGCAA CCCCGGGTTCCGAATCGGCAAACCACCGGCCAA CCCCGGGTTCCGAATGCCCGAATACCACCGGCCAC CATTACAACGCCCCCCATAACCACCGAGTGTAC CTCAGAACCGCCCCAATAGCACCGCCCACC ACATAAGTAATTTTGTCACAATCAAGGTGTATCACCGTAC CTCAGAAACCGCCCCAATAGCACCGCCCACC ACATAAGCAATAGCAATAGCAATCCACCGGCAA CCAGAACCGCCCCCAATAGCACCGCCCACCACCACCACCACCACCACCACCACCACC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2								-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y010 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y03 X07Y04 X07Y05 X07Y07 X07Y08 X07Y07 X07Y08 X07Y01 X07Y10 X07Y11 X07Y05 X	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCAACCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAACGGCCGATCAAGAGG AACCAGACATTCATGCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTITTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGCCACCGC TTCTGGTGGTTGTAAAACGACGGCCAAGGCAGGAG GCCTGAGATAAATTTTTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGCCACGCC GCCTGGGGTGCCGAAATCGGCAAAGGGTGAT CCCCGGGTTCCGAAATCGGCAAAGGGTGAAC CCCGGGGTTCCGAAATCGGCAAAAGGTTATCACCGTAC CTCAGAACCGCCACCAGACCCGCCACGC CTCAGAACCGCCACCAGAACCACCGGCATAC CCCGGGGTTCCGAATGCGCAAACGGTTACACCGTAC CTCAGAACCGCCACCAGAACCACCGAGTGTAC CTTAGAATAAGTGCCCCGATTACAGGTGGCA CATTACACCACTGATAGCAGCACCGCCACC CATTACAACGCCCCCAATAGCACGGCACG	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y010 X06Y11 X06Y02 X06Y03 X06Y04 X06Y05 X06Y01 X06Y10 X06Y11 X06Y12 X06Y13 X07Y01 X07Y03 X07Y04 X07Y05 X07Y07 X07Y08 X07Y11 X07Y11 X	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCGTCATTAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CACACGTAGTAACGAAGCGCCGACAATATTCGG TCGCTGAGTAACGAAGGACGCCCATCGGG TAGCTGAGTAACGAAGGAGCCCATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCCAGTCAAAGCG AACCAGAACTTTAATAGCGAGAGGCCGATCAAAGCG AACCAGACCTTTCATTCCATATAACTAGTTTGA CCATAGAAGAGCATAAAGCTAAATACTTG CGGGAGAATTAATGCCGGAGAGGGCACAGTATT GCCTGAGGATAAATTCGGGGCACCGC TTCTGGTGGTTGTAAAACGAAGCGGCCAAGTCG GCCGAGGAATTAATGCCGGAGAGGGGCCACGC TTCGGTGGTTGTAAAACGAACGGCCTAGGAGA GCCCGGGTGCCGGCTTTCCAGTCCGGCCAA CGCCGGGTGCCGGCTTTCCAGTCCGGCCAA CGCCGGGTGCCGGCTTTCCAGTCCGGCCAA CGCCGGGTGCCGGATTAAACAAAGGTGTATCACCGTAC CTCAGAACGCCCCCGATTTA TGGTTATTAGGGAGCCCCCGATTA CGCTGAGGAGCCCCCGAATCGGCAAACGGTGAT CCCCGGGTGCCGGTATAAACAAGGTGTATCACCGTAC CATATAATATTTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAGCTATCTAGGTGGCA CATATAATATTTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGCAATAAGCAACGCGCCCAAC CAAGCCTTCATTTATCCCAATGCACGCACC CAGAACCGCCCAATAGCACCGCGCACC ACATATAATATTTTTGTCCACAATGCATCCAGGAA CAAGCAAACCGGCCCAATAGCACCGCCGCACC ACAAGCAAACCGCGCCCAATAGCACGCCTGGAGA TGAAATACGAATAAACAACCGGACTGCAC CGGAGCTTTATTATCCCAATGCATGCAGGA TGAAATACGAATAAACAACCGGACTGCAGCA CAAGGCTTAATTAACTAGCAAGCATGCATCGAGA TGAAATACGAATAAACAACCGGACTGCAGA ACAAGCAAACCGCGCAAATGCATTGAA GAAGGTTAAATAGCAATAGGAACCTTGG CTGATTAGAGTAAAACACCGGAATGAATATAA AAAACATAGTCAATAGGAAGCCGCTCATATTC ACTGATAGCGAAACCACCAGCAGAAGAATTGAA GAAGGTTAAATAGAATAG	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y010 X06Y11 X06Y02 X06Y03 X06Y04 X06Y05 X06Y01 X06Y10 X06Y11 X06Y12 X06Y13 X07Y01 X07Y03 X07Y04 X07Y05 X07Y01 X07Y11 X07Y12 X07Y13 X	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTAACGAAGGCACCAACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCCAGTAAAAAT GTTTAGACTTTAAGAAGGAAGCCCGATCAAAGCG AACCAGACAAAATAGCGAGAGGCCAGTAAAAAT GTTTAGACTTAAGAAGGAAGCCCGATCAAAGCG AACCAGACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGAACTTAAGAGGAAGCCGGAGTCATT GCCGGAGAATTAATGCCGGAGAGGCAGCACTGT GCCTGAGATAAATTTTGAAATAAATAAA TTGGCGTGGGTTGTAAAACGACGGCCTAGTAGAGA TCCCCGGGTGCCGGCTTCCAGTCTGGGCCAA CGCGGGGTGCCGGCTTCCAGTCTGGGCCAA CGCGGGGGTTCCGAAATCGGCAAAAGGGTTGA GTGTTGTTGGGAGCCCCGGATTTA TGGTGATTAAGTGCCGTATAAACAAGGGTGTATCACCGTAC CTCAGAACCGCCACCAGAACACCGGAGGTGAC CATTAATAATTTTTGTCACAATCAGTAGGAGA CATATAATATTTTGTCACAATCAGTAGCAGCA CAGAGCCTTTATTATCCCAATCCAGTGGGCA CAGAGCCTTTATTTATCCCAATCCAGTGGGCA CAGAGCCTTTATTTATCCCAATCCAGTGGGCA CAGAGCCTTTATTTATCCCAATCCAGTGGGCA CAGAGCCTTTATTTATCCCAATCCAGTGGGCA CAGAGCCTTTATTTATCCCAATCCAGTGGGCA CAGAGCCTTTATTTATCCCAATCCAGCGCACCGC CACATTAATACTGGAATTAACACCGGCAATGGTGT CTGATTAGATTA	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y010 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X07Y03 X07Y04 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCCACCCTCAGAACCGTCTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGAGGCACCAACCCACTCATC TTTGACCCGGACAAGATGGCCCGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCCGGTACAAGCG AACCAGACTTAAGAGGAAGCCCGATCAAAGCG CATTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATATAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGGCACTG CCCTGGGGTGTGTAAAACGACGGCAACAGCG TCTGGGGTGTGTAAAACGACGGCCAACAGCG TCTGGGGGTGTGTAAAACGACGGCCAACAGCG CCTGAGATAAATTTTTGTTAATAAAAATAA TTCGCGCCACGACAGTTTCGGGCCAACGC TTCGGGGGTGTGAAAACGACGGCAACAGC GCGCGGGTTCCGAAATCGGCAAAAGGGTTAC CCCCGGGGTCCCGAATCGGCAAAAGGGTTACACCGTAC CTCAGAACGCCCCGCAATAGCCAGCACCGC CTTAGAACGGCCCCGAATAGCAGCAGCGCCACC CATTACACCATCGCAGAAGCGACCACCGCCACC CATTACACCATCGCAGAAGCAGCACCGCCACC CATTACACCATCGCAGAAGCACCCGCCACC CATTACACCACTCGCATAGCACACGGCGCAC CCCGGGGCCCAATAGCACCGCGCACC CATTACACCACCACGAAACCAGGAGTGAC CTGAGACGCCCCAATAGCACCGGCACC CACATATAATATTTGCACAATCAGCAGCACTTTC CTGAGTTAATAGCAATAACAACAGGAGTGTAT CAGAGCAAACAGCGGCCAATAGCACGCTTTC CGGTAGCGAACAACAACCGGAATGAATAA ACAAGCAAACCGGGAATGAACATGCAC CTGAGATCACAATAAACAACCGGAATGAATATAA AAAACATAGTCAATAACACCGGAATGAATATAA AAAACATAGTCAATAACACCGGAATGAATATAA AAAACATAGTCAATAACACCGGAATGAATATAA AAAACATAGTAAACAACCGGAAATGACACTGGCGA CCGCCAGTACCCACCAGCAGAAATGCG CTCAAGGTAACACAGGACACCGCCAACCGCCCA CACGCCAGTACCCACCAGCAGAAATGCA CAGGAACGGTAACCCAGCAGCAACCAGCAGCA CCCCAGGACCACCAGCAGCAGCAGCCAGC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X07Y05 X07Y01 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCCACCCTCASAACCGTCTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TTGACCCGGACAAGATGGCCCAATCATCAG TTGACCCGGACAGATGGCCCAATCACAGAG TATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGAGGCTAGTAAAAT GTTTAGACTTAAGAGGAAGCCCAATCAAGCG AACCAGACTTTCATTACGTAAACTAGTTTGA CCATTAGAAGGACTAAAGCTAAATACTTTG CCGGAGAATTAATGCCGGAGAGGCCAATCAAGCG AACCAGACTTTCATGCGGAGAGGCCAAGGAGGCCATT GCCTGAGATAAATTTGTTAAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGGCACCGC TTCTGGGGGGTGTGTAAAACGACGGCCTAGAGGA CCCGGGGGGTCCGAAATCGGCAAAGGGGTGAT GCCCGGGGGTCCGAAATCGGCAAAGGGTGAC CCCGGGGGTTCCGAAATCGGCAAAGGGTTACACCGTAC CCCGGGGGTTCCGAAATCGGCAAAGGGTGTACACCGTAC CCCGGGGGTCCGAAATCGGCAACAGGGGTGAC GTGTTGTTGGGAGCCCCCGATTAAACAAGGGTGTACACCGTAC CCCAGAACCGCCACCAGAACCACCGACGCTAC CCCAGAACCGCCACCAGAACCACCGACGC CATATAATATTTTTGCACAATCAGTAGCAC CACTATAATATTTTTGCACAATCAGCAGCACCGCCCA CAAGGCCTTTATTACCCCAATGCACCACCGACAC CAGAGCCTTTATTACCCCAATGCACCGCCCC ACAAGCCAACACGCGCCCAATAGCACGGCTTTC AGTACAACACGGCGCCCAATAGCACGGCTTTC AGTACGAAACAGCGGCCCAATAGCACGGCTTTC AGTACGAAACCGCGCCCAATAGCACGGCTTTC AGTACGAAACCGCGCCCAATAGCACGGCTTTC AGTACGAAACAGCGGACCGCCAATGGATGAATAA AAAACATAGCAATAAGCAGATGCATGCATGAG CTGAATTAGAATAGGAATTAGGAATTAAA AAAACATAGTCAATAGGAATTAAA AAAACATAGCAATAAGCAGATGCATGCAGA CCGCCAGTACCTACACCAGCAGAAGAATTGAG ACCGCCAGTACCTCACGACAGCAGTCGCGCA AAGGTTAATAGATTAGGACAATTGAG CTGAATTAGAATAGGAAATTCAATGGAAAATTC ACGAAGGTAAATAGAAATTGAAGGCGTTTGAA GAAGGTTAATAGAATCAGATGAGGCGCCCCCCCCCC	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X07Y01 X0	GGAACAAGCCTGTTIGATGGTGGGAGAGGC AATCGGAACCCTTAAACCAGTTT CGCCACCCTCAGAACCGTCTTTCCAGACGTTAACAACTTT CGCTGAGTACGAAGGCACCAACCCACTCATC TITGACCCGGACAGATGAACGGTGATCAAGAG TAATCTTGTAAGAAGCGGCCACACCCACTCATC TITGACCCGGACAGATGAACGGTCATTAATA AAACGAACAAATAGCGAGAGCCCAATCAGAGG AAACGAACAAATAGCGAGAGAGCCAATAAGCG AAACGAACAAATAGCAAGAGCCGAACAAAGCG AACCAAGACTTTCATTCCATTAAACAAGGGGAACCTTGG CCATTAGAAGAGACCAAGTATCGGGGACGCGAC CGCGGAGATTAAGCCGACAAATGCGGCAAAGGGTCATT GGCCGAGAAATTAATGCGGGAAACGGGCCTAGAGGA TCCCCGGGTTCCCAGCACACGGCCAAAAGGGTGTATCACCCGTAC CTGGGTGGTCCGAAATCGGCAAAAGGGTGTATCACCGTAC CTCAGAACCGCCCCCGATTTAA TGGTAATAAGTGCCCCGTATAAACAAGGTGTATCACCGTAC CTCAGAACCGCCCCCAATAGCACCGCCCCAC ACATATAATATTTTTGTCACAATCACGGAGTGTAC CAGAGCCTTTAATTACTCAGAACCGGACTGACAC CAGAGCCTTAATAACAACACGGAATGAATATAA AAAACAATAGCAATAAACAACAACAGGACTCTGGCA CAGAGCCTTAATAACAACACGGAATGAATATAA AAAACAATAGCAATAAACAACAACAGGAATGAAATCGAA CAAAGCGAAATAAACAACAGCGAAATGAAATCCAACACGGAAATGAAATAC ACAAGCAAAATAAACAACAGGAATGAAATAC ACAAGGCTTAATAACAAGGAGAATGAAATAC ACAAGAGCTAAATAAACAAGGAGCAAGCAAAAAC CG	S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X05Y16 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X07Y05 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCCACCTCACAACCAGTTT CGCCTAGATGTAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAGGCACCAACCCACTCATC TTTGACCGGACAGATGCAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGAGGAGCCCAGTCAAAGCG ACCAGACTTTCATTCCATTAACTAGTTTGA CGTTAGACTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATTCCATTAAACTAGTTTGA CCATTAGAAGAGCATAAAGCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGCAGTCAAT CCCTGAGATAAATTTGTTAAATAAATAA TTCGCGTCACGACGACGACGTATCGGGGCACCGC TTCTGGTGGTTGTAAACGACGGCCTAGAGGA TCCCCGGGTTCCGAAATGCGGGCAACGGC TTCTGGTGGTTGTAAAACGACGGCCTAGAGGA TCCCCGGGTCCCGACATTCGGGCCAACGGC TTCTGGTGGTGTAAAACGACGGCCTAGAGGA CCCCGGGTCCCGACATGACGCGC TTCTGGTGGTGGAGCCCCGATTTA CGGTGATAAGTGCCCCGTATAACAAGGTGTATCACCGTAC CTCAGAACCGCCCCGATTAA CGGCGGGTCCCGAATGCCACCGCGCACC ACAATAAGTAATTTTTGTCACAATCAAGTAGCAC TTGAGTTAAAGCAATAGCAACGACGCGCCTTC CAGAACCGCCCCCAATAGCACCGCGCACC ACAATAAGCAATAGCAATGCAACCACGAGAA ACAAGCAAACGGCGCCCAATAGCACCGCGCACC ACAATACGATAAACAACAGGCGTCTTC AGTACCGAGCAATAAACAACATGCATCGAGA CAAGGCAAACGGCGCCCAATAGCACGGCTTTC AGTACCGAGACAATAAACACCGGATGAATATAA AAAACATAGTCAATAGGAATTATAA CAAGCAAACCGCGCCCAATAGCACGGCTCTTC AGTACCGAGCAACAACACCGGAATGAATATAA AAAACATAGTCAATAGGAATTATAA CAAGCAAACCGCGCCCAATAGCACGTCTGGA CTGATTAGGAATCACACCGAGAAGAATTGAG CTGATTAGGAATCACACCGGAAGAATGAGG CTGACGGAACCACCACCAGCAGAAGAATTGAG ACCGGCCAGTAACCACCACGAGAAGAATTGAG ACCGGCCAGTACCCACCACGACGAAGAATTGAG ACCGCCAGTAACCACCACCAGCAGAAGAATTGAG ACCGCCAGTAACCACCACCAGCAGCAGCAGCA AATCACAAATAGGAAGCAGCCTTTTTAACGGCAGCA AATCACAAATAGGAAGCAGCCGCCCCCCCCCC	S1 S1	28 28 28 28 28 28 28 3 3 3 4 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X07Y05 X07Y06 X07Y07 X07Y08 X07Y01 X07Y12 X07Y14 X08Y05 X08Y06 X08Y07 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGGTCTTCCAGACGTTAACAACTTT CGCCGAGATAGATGGCCCGACCAATTGCGG TTGGCTGAGTACGAAGGCACGATGACCGATCAACGG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACACAAATTAGCGAGAGGCTGATAAAAT GTTTAGACTTAGAGGGAGAGCCCGATCAAAGCG AACCAACAAATTAGCGAGAGGCTGATAAAT GTTTAGACTTAGAGGAGAGCCCGATCAAAGCG AACCAACAAATTAGCGGGAGAGGCTGATAAAT GCCTTAGAGAGAATAGTTTCCATATAACTAAGTTGG GGGGAGATAAATTTTGTTAAATAAACAATGATTG GCCCGGGGTCCCGAAAACGGCACAAGCGCCACCCG TTTGTGTGTGTTAAAACAAGGGCTAAAGCGTGAC CCCCGGGGTCCCGAAATCGGCAAAAGGGTTACACCGGACA CCCCGGGGTCCCGAATAGCCTACCGGACAAGGGTATCCACCGTAC CCCCGGGGTCCCGAATAGCCACCCGACCCAA CCCCCGGGGTCCCGAATAGCCACCCGCACCC CATTACCACCACTGAATAGCTATCCACACGGAAT CCCCGGGGTCCGCAATAGCACTACCACGGCAC CATTACCACCACTGAATAGCTATCCCCAATGGCCA CAAGCAAACCGCGCCCCACCAAAGAATTGAA AAACCAAGCAAACCGGCCCACCAAAACGCCCCCCCCCC	S1 S1	28 28 28 28 28 28 28 3 3 3 4 3 3 4 3 4 3 4 3 4 3 4 3 4 3 4	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X07Y05 X07Y06 X07Y07 X07Y08 X07Y01 X07Y12 X07Y13 X08Y04 X08Y05 X08Y07 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCGAAACCCTGATGCGCCGTCATTCCGG TCGCTGAGTACGAAGCGCACCAACCCACTCATC TTTGACCCCGGACAGATGAACGGTGATCAAGAG TTAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGACAGGCTGATCAAGAG TTAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACAAAATAGCGCAGAGGCTAGTAAAAT GTTTAGAACTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTAGTCCATATAACTAGTTTGA CCGTTAGAAGAGCATAAAGCTGAATACTTTTG CCGGGAGAATTAATGCCGGAGAGGGGCAATT GCCGGAGAATAATTGTCTGTAATAAAAATAA TTCGCGTCACGACGACAGTATCGGGGAGGCCATG CCCGGGGGTTCGAAATCGGCAAAAGGGTGAA CCCTGGGATGATTGTAAACGACGGCCTGCGGCA CCCCGGGGTCCCGAATTCGGCAAAAGGGTGTATCACCGTAC CCCGCGGGGTCCCGAATTCGGCAAAAGGGTGTATCACCGTAC CTCAGAACCGCCCCCGATTTA TGGTATAATAGTGCCCGCAACAAGGTGGCA CCTCAGAACGCCCCCGATTAA CGCGCGGGGCCCCGATTAA CAAGCAAACCGCGCCCCAATGCACGCCAC CATATAATATTTTGTCACAATCAAGTAGCAC TTGAGTTAATAGGCAATAGCTATCTAGGTGGCA CAGAGCAAACCGCGCCCAATGCACGCGAGTGTAC CCGGGGGTCCGAATGACGCGGCACGC CATTACCACATCGAAAGGCAGCGCGCCAC CAGAACCAACCCGGCCCAATGACACGCGCAC CAGAACCAATAAACACACGGCATGCAGGA TGAATTACGAATAAACACCGGGATGAATAAA AAAACAAGTGCAATAAACACACGGCATCGAGG TGAATTACGAATAAACACCGGGAATGAATAAA AAAACAAGTGCAATAAACACCGGGATGAATTAA AAAACAAGTGCAATAAACACCGGGAATGCATG GGAATGCGCAACACCACGGCACGCGCA CAGAGCGTACGCCAACACACAGCGCCGCCAC CCCGCCGAGACCAATTAACACACGCGGCCACCGGA ACGGACCGGTACGCCCACACACACATTT AAGTATAGGCCGCACACACACATTT AAGTATAGCCAACACACGGCCGCCCCCCCCCC	S1 S1	28 28 28 28 28 28 28 3 3 3 4 3 4 4 5 4 5 4 5 4 5 4 5 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	16 16 16 16 16 16 16 16 16 16							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y01 X06Y01 X06Y12 X06Y13 X06Y14 X07Y05 X07Y01 X07Y01 X07Y01 X07Y01 X07Y12 X07Y14 X08Y05 X08Y07 X08Y08 X0	GGAACAAGCCTGTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCCCGACAACCCCACCCACTCATC TTTGACCCGGACAAGTGACCGGTGATCAAGAG TAACGTTACGAAGGCACGATCAACGGTGATCAAGAG TAATCTTGTAAGAACTGGCTCATTCGTTAATA AAACGAACACAAATTACGGCGACAGCTAGAAGCG CAACAGATTAAGAGGAGAGCCCGATCAAAGCG AAACGAACACAAATTACCATTATAACTAGTTTGA CCCATTGAGAGGCACAGAATCGGGGCACGCTATG CGGGAGAATTAATGCCGGAGAGGCCTAAGAGCA TTCGGCTGCAGACGACGATTCGGGGCACCGCG TTCGGTGTGCAAGACGCCCGAATTGAGGGCCACGAGA TCCCCGGGTCCCGAATTCGGCGCAAAGGGGTGAC TCGCGGTGCCCGCGCTTTCCAGTCCGGCCAA CGCCGCGGTTCCGAAATCGGCCACGGGGCTCCGAACC GTGTTGTTGGAGAGCCCCCGATTAACACGGGGGCACCGGAC TTCGGTGTACGAGAACCACCGGCAATCAACGGGCCACC ACAAGCAAACCGCGCCCCCGCCACCGCCACC CACATATAATTTTTGTCAATCAGGTGGCA CTCAGAACCGCGCCCCCAATAGCACCGCCCCCCCCCCC CACAAGCAATAACCACCGGACATGCACTGGCA CGGCAGATAAACACACTGCACTGCACTG CTGATTATAGCCGAACACACGGCAATAGCCACTGGCA CGGAACTAAATAGCTAAGCACAGTGCTGCGAA CCCCGGGTTCCAAATAACCCGGAACACCGCCTC CCCCGGGTTCCGAAATAACACACGGCACTCACCGCCTC CCCCGCAATACACACACGCGCCAACCGCCTC CCTGAAACGAAACCACAGAGTCTAAGCCGCTAGAGAA CAAACGAAACACAACACACGCCCACC	S1 S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 1 16 1							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y01 X06Y01 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X07Y05 X07Y07 X07Y08 X07Y07 X07Y10 X07Y11 X07Y12 X07Y13 X0	GGAACAAGCCTGTTTGATGGTGGGAGGGC AATCGGAACCCTAAACCAGTTT CGCCACCCCCAGAACCGTTTCCGTGACGAACAGTTTCGGG CGCCACCCCCAGAACATATTCGGG TTGATGATAGTGCCCCGACAATATTCGGG TTGATGACTGAAGGCCCCATCCATCC TTTGACCTGAGAAGGCACAACCCAACCAATCA CAACAGTTAAGAGGGAGCCCGATCAAAGCG AAACCAGACTTAAGAGGGAAGCCCGATCAAAGCG AACCAGACTTAAGAGGCAAAACCTAAATACTTTTG CGGGAGAATTAATGCCGGAGAGGGAGGTCATT GCCTGAGATAAATTTTTTGTTAAATAAAAATAA TTCGCGTCACGACGACGCGCTTCGAGCCACCGC TTCGCGTCCGACACGACGCCTAGAGGAG TCCCGGGGTGCCGGCTTTCCAGTCTGGGCCAACCCGGACTGTAC CGGCGGGGTTCCGAATAGCACTACCAGGAGTGTAC CATTACCACACCGAATAGCCTATCTAGGTGGCA CACAGCAACCGGCCCCAATAGCACTGCCCCACC ACACACCACCCCAATAGCACTGCACGCCACC ACACACGGACAATAGCCTATCTAGGTGGCA CAAGGACAACCGGCGCCCAATAGCACTGGCCACC CACAGCAAACCGGCGCCCAATAGCACTGGCAA CGGAACATTAAACAGTGAATAGCATATATAA AAAACCATGGAATAGACTATTATAATGGTT AAACCATGATAGATAGAATATATAA AAACCAGTAACACGGGCCCAATAGCTTTC CCTAAAGCAAACCGGCGCCCAATAGCTTTC CTAACGGAACACTACAGTATATAGCAACTGGGAA CTAACCGAAACAGCGCGCCCCAACAACTTC CTAAACGAAACAGCGCGCCCCCCCGCAACCAGCA AAACTAGAATACAAATAGAATAA	S1 S1	28 28 28 28 28 28 28 28 28 28 28 28 28 2	16 1 <							-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y01 X06Y12 X06Y13 X06Y14 X07Y05 X07Y06 X07Y07 X07Y08 X07Y07 X07Y14 X08Y11 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTTATGCAGATCGTTACCAGACTTAT CGCCACCCTCAGAACCGTCTTCGG TTGACTGAGTAGCGAGAGCGGCACCACCCACTCATC TTTGACCCGGACAGATGAACGGTGATCAAGAG TTGGAGTAAGAAGTGGCCCATTCGTTAATA AAACGAACAAAATAGCGGAGAGGCTGATAATA AAACGAACTAAAATAGCGGAGAGGCCAGTCAATAT GTTTAGACTTAAGAAGGAGACCCGATCAAAGCG AACCAGACTTTCATTCATTATACATGTTTGA CCCTGAGATACATGTCCTCTATACATGTTTGA CGCGGAGATTAATACCGCGGAGAGGGAGGTCAT TCGCGTCACGACAGACGCCGGACCGAC CCCCGGGTTCGAAATCGGCCAAAGGGGTCAT CCCCGGGTGCCGAAATCGGCCAAAGGGGTGAT CCCCGGGTTCGAAATCGGCCAAAGGGTGATCACCGTCA CGCGGGGGTTCGAAATCGGCCAAAGGGTGATCACCGTCA CGCGCGGGTTCCGAATCGGCAAAAGGGTGATCACCGTAC CCCGGGGGGCCCGATATAAACAAGGTGTATCACCGTAC CCCGCGGGGTCCGAATGCGGCAAAGGGGTGA CGCGGGGGGTCCGAAAGGGCACCGC CCAGAACCACCCCCGATTAAACAAGGTGTATCACCGTAC CTCAGAACCGCCCCCCCATTAA CATACCACCATCGATAGACAACGGCGTGAC CCGCGGGGGTCCGAATGACACACGGGCAAGGCA CAGAATAACCACCGCCCCCACGAA CAGAACAACCGCCCCCCCATCAACGGGCA CAGAATACCACCGCCCCCACAGAAAGGGTGATCACCGTAC CTGAATATCGCCCGAATGCCGGCAA CAGAACAACCGCCCCCCAATGCCACAGAA CAGACAACCGCCCCCCAATGCCACAGAA CAGACAACCGCGCCCCCAATGCCCACGGAA CAGAATAGCAATAACACCGGGACTGAATTAA AAAACATAGTCATAGGTATAACACAAGGCGTTCT CCTCAGAAGCCACCCCGCAACGCGAACACACTGAG CAGACTACCCCAGACAACACATGCAGCGGA CAGAGGTAACTACCACCGGAATGCAATTAA AAAACATAGTCCAGAATGAATATAA AAAACGGTAACCACCACCAGCAAAATTGA CAGGCAGTACCCCAGCACACACACAACAGCGCG CCCCAGAACCACCCAC	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6					-+								
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y07 X07Y08 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X07Y01 X0	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCACCCTCAGAACCGGTTTTCCAGACCGTTAACAACTTTT CGCCTGAGTACGAAGAGGCCCAACCCACCTCATC TTTGACCCCGGACAGATGAACGGGTCAATAAA AAACGAACAAAATAGCGAGAGGCTCATTCGTTAATA AAACGAACATTAACTGGTCTCGTTAATA AAACGAACATTCATTCCATTAACAAGTGTGA AACCAGACTTTCATTCCATTAACATAGTTTGA CCATTAGAAGAGGCCCCGGCGAAGGGAGGCTATT GCGCGGAGTTCATCCGGGAGAGGCGCCATTG GCCTGAGATAAATTTATGCCGGGACACGGCCTAGAGGA TTCCCGGTGCCGCATTTCAGGTGCGGCAA CCGCCGGGTCCCGATTTAACGAGGGGCTAGA GGGCGGCTCCGATTAACACGGCCAAAAGGGGTTGA GGGCGGGTCCGATTAACACGGCGCCAAAAGGGGTGAC CTCAGAACCGGCCCCGATAGACACCCGGCACC CCTCAGAACCGGCCCCAATAGCACGTGGCA CCCCGGGGCCCATAGGACGTGGGCA CGGAGGACTAAAGCACGGGCCCAATAGCACGTCGGCA CGGCGGGCTTATTTTATTCCCAATCACAGGAGCACTCGAGA CACAGCCACACCAGCAGAGAGGTTAATAA AAACAGACACCACACCAGCAGAGAGGATTAA ACAAGCAATAACACCCGGAGAGAGACTATAA ACAGGTAAGCCACACCAGCAGAAGAGTTAA CACAGTAGCACACAGCAGCAGAAATTAA AAACATAGCCGAACACACAGCAGAGAGCAGAAATAC CTCAGAGAGCAAAAGATAAGCCCGCCACACAGAAAAGTAAGCCGTTATAA AAACATAGCAGAAAAGTAAGCCGCGCAAAAGGGTAGAGGG AATTAGCAATAAGACCGGACGACACAGAGGAGGCAA </td <td>S1 S1 </td> <td>28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7</td> <td>16 1 16 1</td> <td></td> <td>6</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>-</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X06Y01 X06Y01 X06Y01 X06Y01 X06Y03 X06Y04 X06Y05 X06Y06 X06Y01 X06Y01 X06Y01 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y03 X07Y04 X07Y05 X07Y01 X07Y05 X07Y06 X07Y07 X07Y08 X07Y07 X07Y08 X07Y07 X08Y01 X08Y01 X08Y01	GGAACAAGCCTGTITGATGGTGGGAGAGGC AATCGGAACCCGTATACACGTTT CGCCACCCTCAGAACCGCTCTTCCAGACGTTAACAACTTT CAACAGTTGATAGTIGCGCCGACAATATTCGG TCGCTGAGTACGAAGAGTGAACGGTGATCAAGAG TTAGCCCGGACAGATGAACGGGTGATCAAGAG TTAGCCCGGACAGATGAACGGGCAATCATA AAACCAAACTTTAAGAGGAAGCCCGATCAAAGCG AACCAGACTTTCATCCATATACTAGTTTGA CCGTAGAGACAAATAGCGGAGAGGGGAGTCATT GCCCTGAGATAATGCCGGAGAGGGGGAGCACTG CCGTGAGATAATTCTTCAATAAAAAATAA TCCCCGGGGTCCCGACAGTATCGGGCCACCGC TCCCGGGGTCCCGAATTCGGCGCCAAGGGCA CCGCGGGGTCCCGAATTCGGCGCCAAGGGCCA CCGCGGGGTCCCGAATTCGGCCCAAGGGGTGAT CCCCGGGGTCCCGAATTCAGCCGCAA GGGCGGGTCCCGAATTCAGCCGCAA CGCGCGGGTCCCGAATTCAAGCAGGGTGATAC CTCCGGGGTCCCGAATTCAACCAGGGTGATAC CCCGGGGTCCCGAATTCAACCAGGGGTGATCACCGTAC CTCAGAACGCCCCCCGATTTA TGGTAATAAGGCACGCCGCACACGCCCCAC CTCAGAACGCCCCCCGATTAACAAGGGTGTATCACCGTAC CTCAGAACGCCCCCAGATCAACAGGGGTGAA CGGCCCGCCCATAGATAACAAGGGTGTATCACCGTAC CTCAGAACGCCCCCAGATCAACAGGAGTGAAC CTGAATAAGGACAATAACAAGCGGTGAACCCCGCAC CACAGCAACACCAGGAAGAATTAA ACAACCAAGCAACCGCGCCAATAGCAC CGGCCCGAATAAACAACCGGAATATAA AAACATAGCAATAACACCGGAAGAATTACA AAACATACGAATAACACCGGAAGAATTACA AAACATACGAATAACACCGGGAAGAATTACA AAACATAGGAACAACCGGGCCAATATTAC CGGAATTAGGAACAACCGGGCCAATATTAC CGGAAGGTAACGCCAGGACAACCCGGCA AAACCACAGCAACCACGAGAAAATTAC AGGAACGGTAACCCCAGGAGAAAATTAC AAGGAACGGAAC	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y03 X07Y04 X07Y05 X07Y07 X07Y08 X07Y07 X07Y01 X07Y11 X07Y12 X08Y01 X08Y01	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCTATTGCAGACCGTTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGCGCCGACAATATTCGG TCGCTGAGTACGAAACGGCCACCCCACC	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X05Y16 X06Y01 X05Y15 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y09 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y01 X07Y01 X07Y03 X07Y04 X07Y05 X07Y07 X07Y01 X07Y03 X07Y04 X07Y05 X07Y06 X07Y01 X07Y11	GGAACAAGCCTGTTGATGGTGGGAGAGGC AATCGGAACCCGTATGACAGGTT CGCTGAGTACGAAACCGTCTTCCAGACGTTAACAACTTT CAACAGTTGATAGTGGCGCGACAACCACCCACTCA TTGAACCTGGAACAGAGTGAACGGGTGATAAGAG TAATCTTGTAAGAGCAGCGACGGCTGATAAAT AAACGAACAAATAGCGCAGCGAGCGAGTAAAAT GTTGAACCTGAGAACAAATAGCGCGAGCAGGG AACCAGACATTAATGCGGGAGAGGCGATATAA GCGGAGAATTAATGCGGAGAGGGCATATTG GGGGAGAATTATTGTGTAAAAGCTAAGGGCTGAT GGGGGAGAATTATAGCGGGAGAGGCCTATAGAG TTGGTGGTGTGTGTGGGGCCAAGGGCTGAT GGGGAGAATTATAGCGGGAGAGGCCTGAG GGGGGGGTCCGAAATCGGGCGCAAGGG TCCCGGGGTGCCGGCTTCAAGTGCGGGCCAA CGCGCGGGTTCCGAAATCGGCACAGGG TCGCGGGGTCCGAAATCGGCAAAGGGTGAG GGTGGTGGGGGGCCCCGATTAACAAGGGTGTAG GTGTGTTGGGGGGCCCCGATTAACAAGGGTGTAG CTCGGGGGTTCCGAAATCGCCAAGGGGTGA CGCGCGGGTTCCGAAATCGCACAGGGGTGA CTTGGTGGGGGGCCCCGATTAACAAGGGTGTAG CTGTGTGTGGGGGCCCCGCATTAACCAAGGTGTGC CTCAGAACGCCCCCGACGACCCGCACC ACATATAATTATTTGCCACAAGGGTGGGC CATTACCACACGCGACGCCGCACCG CATATACCGACGCCCGCAATGAATGAA ACAGGCAAACCGCGGCCCAATGGCATGCGGA CGCGCGGATTGATTAGCGGGAAGAGGTGTAT GGAATTAGGAATAACCGCGGGATGAATTAA AAACATAGCCAATGACGGGAAGAATTAA AAACATTAGCGAATGGATGAATTAA AAACATAGCCAAGCCGGCCGCCACCGGCA CAGGGCTTACTAGTGGATATAGGGACCGGCA CAAGGGTAACTACACGGGAACGAGTGAATTAA AAACATAGGCAACCACCGGGAACGAGTGATTAA AAACATAGGCAACCACCAGGAAGAATTG GGGATTAAAGGCACGACCAGCCGGCAACCGGCA AAGGATAACGAAACCGGCGCCCACCCGCCC CTCCAGAGCGTAATCAGTGAGAAATTG AGGATAACGAAAACCGGGAACAATTT AAGTATAGCGAAAGCGAACAGATTTAA AAGTATAGCGAAAGCGGACAGCCGGCA AAACGAGGAACGCACACCACCGGCCACCGGCCA CAACGGTAATAACGAGAAGTGAAAACGGGATTC CCCTGAAATAGAAAATCATAGGAGAAGGGGT AATAACGAAAATAGAAGAGGGAAGGGGAACGAGG AATTACCAAATAGAAAGAGAGGAGTTAGCCAGGCAA CAACGTATATACGAAAGAGAGGGTAAGGCGA CAACGGTATAAGGAAGAGTAGCAGAGGGCAA CAACGGTAAGGAAGAGAGGAGGAGGGGAAACCAGCGCAAATAC CTTTAACTCAAGGAGAGTAGCAGAGGGCAAACCGGCAAATCA CCGCCATTAGGCTAAGCGAGAGGGAAAACCGGGAAATTG CGGGATAAAGGAGAAGAGAGAGAGAGAAAACCGCCACA CTTACAATACAA	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y08 X06Y01 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y01 X07Y03 X07Y04 X07Y05 X07Y07 X07Y08 X07Y01 X07Y11 X07Y12 X08Y01 X08Y01	GGAACAAGCCTGTTTGATGGTGGGAGAGGC AATCGGAACCCGTATTGCAGACCGTTTCCAGACGTTAACAACTTT CAACAGTTGATAGTTGGCGCCGACAATATTCGG TCGCTGAGTACGAAAGGGACGGCACCTAACAG TTGACCCGGACAGACGACGGGTGATAAAT TTGACCCCGGACAGAGAGGCGGTGATTAATA AAACGAACAAATAGCGAGGGGAGGG	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y09 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y14 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y01 X07Y03 X07Y04 X07Y01 X07Y11 X07Y12 X07Y13 X07Y14 X07Y15 X08Y06 X08Y07	GAACAAGCCTGITTGAATGGTGGGAGAGGC AATCGGAACCCTAAACCAGTTT CGCCAACCTCAAACCAGACCGACTATCGG TIGGCTGGACAACCAAGCCAATCGGG TIGGCTGGACAACAGACGCACAATCAGG TIGACCCGGACAAGACGGCCAATATCGG TITAACCTGGACAAGACGGCACAATCACGG AACCAACAATAAGCGAGGCCCAATCAATAG GITTAACACTGACAATAAGCGACGCCCCATCAAAGCG AACCAACATTAAGCGACGCCCCATCAAAGCG CCATTAGAAGAGAATAATGCCGGAACAGTATACCTTTGG GGGGAGAATTAATGCCGGACAGTATCACGGACGC TICCGGGCGCGCTTCCCAGTCTGGGGCACCGC TICCGGGGCGCCCCGATTTA GGCGGGGGTTCCCAATCGGCGCCACCC CACAGACGCCCCCAAAGAGGGTGAACCCGGCACC CACAGCACCCACGAACACCACCGCACCCC CACAGCACCCACGAACACCACCGACGCACCC CACAGCACTCAAACACGCACTCGGCAACAGGAATTAA AACAAGCACCCCACCACACACCCCACACACCACCCACCAC	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							
X04Y15 X04Y16 X05Y01 X05Y02 X05Y03 X05Y04 X05Y05 X05Y05 X05Y06 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y07 X05Y08 X05Y10 X05Y11 X05Y12 X05Y13 X05Y14 X05Y15 X06Y01 X06Y01 X06Y02 X06Y03 X06Y04 X06Y05 X06Y06 X06Y07 X06Y10 X06Y11 X06Y12 X06Y13 X06Y14 X06Y15 X06Y16 X07Y01 X07Y03 X07Y04 X07Y05 X07Y07 X07Y11 X07Y12 X07Y13 X08Y01 X0	GAACAAGCCTGITTIGATGGGGAGGGC AATCGGAACCCTAAACCAGTTT CGCCAACCCTAAACCAGTTTICCGAACGTTAACAACTT TITGACCCGGACAAGACGCCGACCAACCATCG TITGACCCGGACAGACGACCAACCCATCAT TITGACCCGGACAGATGAACGGTGATCAGGA AATGAACAAAATAGCGAGGCTATTGATAATA AAACGAACAATAGCGAGGCAATAATCGTTTGA CCATTAGAAGACATAAGCGAAGGCAGGCACAATTCGGGGCACCGC TITGACCTGCGACGACATTATGCGGGGCACCGG TITGACCTGCGGACGACGATTGCGGGCACCGG TICGCGTGCACGACGACATTGCGGGCACCGGC TICGCGTGCACGACGACATTGCGGGGCACCGGC TICGGGTGCGCCTCCATTCCAGTCGGGGCACCGC CCCGGGGGTCCCCCAATTGCACGCGGAGTGA GGGGGGGTGTATAACCAACAGGAGTGATACCCGTAC CGCGGGGGCTCCCCCAATAGCACCGGCCAA CGCGGGGGCTCCCCCAATAGCACCGGCCAACCGGCA CATATAGCAATAGCCGAATAGCAGGTGATTCC CTCAGAACCGGCCCCCACAGAGCACCGCCACCCGC CATATAGCAATAGCACGGAAGAATAGAGA CAGAGCAAACGGCGCCCCACCGGCCACCGCCACCGCCACCGCGCAAGAGATGAGA CAGAGCAATAACAACCGGAATATAA AAACATAGCAATAGCAGCGCGAACAATATAA AAACATAGTAATACCGGAAGCAATATAA CAGAGCAAATAATACCGGAAGCAATATAA CAGAGCAAATAACACCGGCCGCCAACCAGCCAGACACACAGAGCAGACACACACAGAGCCGCAGACACACAGAGCCGCACACACAGACACACACAGAGCAGACACACAGAGCCGCAAAATATAA	S1 S1	28 28 28 28 28 28 28 28 3 28 3 3 3 4 3 4 3 4 4 5 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7	16 1 16 1		6						-							

Figure 4: The staple list of the nanotile. The notes next to each staples represent the location of the binding overhangs in each condition, including the biotin, binding overhangs without the bridge, and binding overhangs with the bridge.

2.2 Sequence list of the nanorod

[2] [27]	Sequece CTCAAATGCTTTCCCCTTATTAGCGTTTGCC	biotin sites	*	28	28 k 16	indi 10				1		Geo	met	ry la	you 	ť
[27] [28] [33]	CACCGGATCATAGCAAACAGT TTTCGGACCAGAGCGCCGAC TCAGAAATCGTCATGAGGCT							-	-	-						
.[41]	TGCGGAAACGAGAAATCGGCAT TGCAGGGAATAGTTGCCACCAC		F													
[42] 0[49] 6[55]	GCCTCCCACAGCTTGATACCGGTTAAAGCCAATAC AAATCAGGTCAGACTGTAGCG CGGAACCCGTTTTCTGACCATAAATCAAATAGCGTGCCGCTT			28												
[56] [69] [70]	GGTGAATATCGTCAAATGTTTAGACTGG TTGCGGGTTCTTAATCAGAGCCGCCACCCTTTAGCGTCTTTA GGGGGTATATTATAAGAATCAAGTTTGCCTCAGAACTTTCGA															
.[70] .[83] .[84]	CCCTGACATAGTAACCCTCAGCAGCGAACAGCTTGCCGCCAC GCCACCATTGTATCGGTTTATAGACAGCTGCCAGA	S1														
[90] [91]	CCTCAGATAGCGACGTCAGAA TGCAAAAGGATTGCAGCACCGTAATCAG		$\left \right $	28	16											
[104] [105] [111]	GCAAAGCGAAGTTTATCGGAACGAGGGTCCTTTAACCCTCAG AAACCATACCAGAAGGCTCCAAAAGGAGAGCAACGAGGCTTT AGCCGCCCGATAGCATCAAAA															
[119] [125]	ACCAAAAGAGGAAGACCAATG AGATTAATAGCGAGGCTACAGAGGCTTTAAAAAAACCACCAC	C1														
[126] [139] [139]	GGCCGGGGCCGCCAGTTGAAAATCTCCAGAGGACTGATAAAA AATAATTGAGGAAGAACCCTCGTTTACCAATATCGATTAGCAA CAGAGCCAAACGTCCCCGAAAGACTTCAAGACGACAAAGACT	S1	╞	28		10					_					╞
[146] [154]	TTTTCATTTTTCACGCATTGA AGCAACACTTCAAAATCACCAGTAGCACTTGAGGCTGCGAAT	S1	F													
[160] [168] [174]	CAGGAGGCATTACCCGTTTTAATTCGAGCTATCATTTTCCAT ACAACTAGTAAAATTAGTAAG TAAACGGAAGGAATAGGTCAGACGATTGCAGCAAAGCGAACC		╞													
[175] [188]	GGAATTAAAGCAAATTGGGAATTAGAGCGCCTTGAGAAAGGA AGACCGGCGAGGCAACGTAATGCCACTAGAGAATATATTCAC		E	28	16											
[189] [195] [202]	CGACTITAAATCCAGTITCAGCGGAGTCGAAGGCGCCAAAA AAACAAAGAGCCATCTCCAAC TGCAGATGATTAGAACCGTCAC	S1	╞													╞
[209] [210]	AGGTCAGACATAACACCAACCTAAAACGTTTCAACTCATTAA AAAGGTGATGGAAATTTTGCTAAACAACAAAGAGGGCAACTAA	S1	Ē													
[223] [224] .[230]	AGCCAGAAATTATCGAGTACCTTTAATTCCACATTCAAAAGA TTTCTGAAAACACGAGATTTAGGAATAGCTCCTTATTCATT ATACACTTATGGGAGCGCAGT		╞	28			6	_	_							
[237] [244]			F													
[251] [252] [259]	TGACCCCCGTTAGTTTCCAGT TTCCAGACAGCGATAGGTAGA AACAACATTAATTGTTCAACCGATTGAGATACATGGTCGTCT	S1	╞								_					╞
[265] [272]	AAGCGTCGGAGGGAGGATGGCTTAGAGCTTATTACTATACCA AGCGCGAAAGTTTTGCTTTTG	S1	F													
[273] [280] [286]	CGATCTAAACAAAGCTAACGG GTTAATAGTAGCTCGCCAAAGACAAAAGAGGAGTGAGCGTAA ATGATACGGCGACACTGAATATAATGCTAAACGAATACAACG		╞	28	16	10					_					╞
[294] [300]	CAGCCCTGTATCATAATCTAC GAGATTTCATAGTTTACTGGTAATAAGTTACCAGCAACATGT		F													
[301] .[314] .[315]	ACGTTGGATGCAACAAATTCATATGGTTTTTAACGCCACAGA TTTAAATGAAGAAACGCCTGATAAATTGTAGCATTGGGTCAG TCACAATAGTAACAAACTACAACGCCTGTGTCGAAAGTCAGG	S1	╞	28	16			_								
[328] [329]	TGCCTTGCAATAGATAAAAGTACGGTGTCTTATACCATCCGCG TCGTCACCCATGTTTAAGAACTGGCTCATGGAAGTTATTTTG		Ē													
.[335] [343]	ACCTGCTCAGTACAGTGCCCG 7 CCACGGAAGTTAATCTGAGTT	S1	╞													
[349] [350] [356]	TATAAACATAAGTTTTCATTCCATATAAGCGATTTACTTAGC CATGTACAGGCGCAGTGAATTACCTTATCAGTTGAAAAGACA CGGAACGCGTAACAGCCCCCT		ŧ	28							F					F
[364] [370]	CAACTITAACGAGTGGCAACATATAAAATCGGAACAGGAACC GCCTATTGAAACGCTTCCCAATTCTGCGAATCATTGACGGTC	C1	F								F					F
[378] [384] [385]	ATAGCAAAGGGAACTTAATTT AATCATAGCCCAATCTATTATTCTGAAATAAAGGTAGATTTA GGGCTTGCATTAGAAGAAAATACATACACATGAAATTCAGGG	S1	ŧ													╞
[398] [399]	GTTTGACAGATGGTCGAACTGACCAACTCCTCATTGTATTAA CCACCACTTGAAAGGTAAATT	S1	F													F
[405] [406] [419]	GAGGCTGCAAACGTTACATTT CACCAGAGGTCAATACGCAGTATGTTAGAGACTCCCTCAGAG CGCAAATACGAGTAAGGACAGATGAACGCGCCACCTCAAGAG		╞	28	16	10		4								╞
[420] [425]	TAAGACTAGGATTAGCCACCCTCAGAACGTGTACACGAGAAA AAGGATTCCTTATTAACCTG		F													F
[434] .[440] [441]	AAGGCTTTATTTTCGCATGAT TTTAGCTAGCCCTGAGACCAGGCGCATAGCAGAACCGCGGGGT ACCCAAAAGTACCAAGTACCGCCACCCTGCTGGCTAGTGAAT	S1	╞													╞
[454] [455]	TTTGCTCAGAACTGATTTGGGGGCGCGAGCTCATTCGACCTTC TACTCAGGTAATCTACGTAACAAAGCTGCTGAAAAAACGGAAT		F	28							E					F
[461] [469] [475]	ATCAAGAGAGGTTTGGCGGAT GAAACGCGTCGAGAATCACCG AAGTGCCAATAATAGGTGGCATCAATTCCAAATCATGACAAG	S1	╞													╞
[476] [488]	AGCATTCCCAGTTTGGAACATTCATTACCTACTAATAACCGAG AACCGGATAGGTGTGGGTTGATATAAGTAGAAGGAAGTAGT		E													
[490] [495] [496]	CCTAGCCCGGAATAAGAGTC CACTATTAAAGAAACGGATTCG GTTGTTCAATAAATCGAACAAAGTTACCATGATTG		╞	28	16		6									
[504] [510]	AGTAAGCTTACAAACGGGAGAAACAATACGTGGACGTTGAGT CTTTGAATACCAAGAGATAGCCATACAG	S1	E													
[518] .[524] :[532]	AGTACCTGCGAAAAAAAAAGAATAGCCCGAAAGAATTAAGAAA GCAAGGCAGATAGGTCCAACGTCAAAGGTTTACATATCGCGC ACCGAAGAATTATTCAGTAAC	S1	╞													
[538] [539]	AGAGGCGCCCTTTTTAGCAAAATTAAGCATAAATCACCGTCT GTCAGATCGATGGCCGGCAAAATCCCCTTAATAAAGCATCATCTT		F								_					
[545] [553] [558]	ATCAGGGGAATATACATTTCA GGTGGTTGCTAAATGAAACAATGAAATAGAGCAAAGTTTAAC ATTACCTGCAATAGCCTCAGAGCATAAACCGAAATCCACTA		╞	28		10										
[567] [573]	GCGTAGAATCACCCGTTTGAT CGTGAACCTTTTCAGAGAAGATGATGAAAAGAGCAACGGTTGT	S1	╞													
[574] [587]	CAGGCGAACATTATTAAGCCCAATAATACAAACATAGAAATT ACCAAAAAAATCCTAAATCAAGTTTTTTGAAATAACAAGAAA	S1														
[588] [594] [601]	CACAAGATAATTACTTGCACGTAAAACAGGGGTCGGCCCCAG ACAAAATATTGAGTGACCCTG TAATACTCTGGTTTAGGTGCC		╞	28	16											╞
[602] [609]	GTCCACGTTTGCGGGATAACC GCTAATATTTGAATAACCTACCATATCAACTAAATGCAAGCG		F													
[615] [623] .[629]	GTAAAGCAAATTATATTTAACAATTTCATCAGAGAGAGAAGC CTGAGAGTCAACGCATTGAGC CTTTATTAGTTGCACGGAACCCTAAAGGGGGGTTAGTACCTTT		╞	28	16											
[630] [643]	AAAGTCAGAAACAGTCTGAATAATGGAAGAGCCCCCCTGGCC TTTAATGGAGGGTAAAGGATAAAAATTTTTCACCGCGATTTA	S1									g6					
[644] .[650] .[658]	GTTTGGAACGGGGAACAGCTGATTGCCCTTAGAACCCTGAAC GAGCTTGTTATACTTACATAA CAGTGAGAATGCAAACGGGAGAATTAACTATGTGACCTGATT	S1	╞													╞
[664] [671]	ATCAATATGAACACCCTCATATATTTTAACGGGCAAAGCCGG CGAACGTATATAATGTGAATA			28		10					g6					
[672] [679] [685]	TTCATCAGGCGAGATTTTCAC CAGGGTGGTAGGTAAAAAACAGGGAAGCTTCTGTAATGGCAA ACCTTGCGCATTAGTGCCTGAGTAATGTGTTTTTCAAGGAAG		F								g6					
[693] [699]	AGAGAGAATTAATTCATATTCCTGATTAAGCGAAATGGGCGC GGAAGAATCAGATGAATCGTCGCTATTAATAACATAAGATTC	S1														
0[707] .[713] .[714]	GGCGGTTTGAGAAACCTTTAC AAAAGGGTGCGTATGGAGCGGGCGCTAGTTATCATTTCCCTT AATGAAATTGAAAACAGAAGGAGCGGAAGGCGCTGGGGGAGA	S1	╞													
[720] [728]	AGAATCCATAGCAGGGCCGGA AACAAAGCACGCTGTTAATGAATCGGCCAAATCACCGTCAAA			28	16		6									
[734] [742] [748]	GACAGTCAACGCGCGCAAGTGTAGCGGTAAACCACCATAGCG TCGTGCCTCAACCGAAGAAACGATTTTTAGATTAATTTGCGG ATAGCTTTGTTTAACATCAATATGATATAGCTGCACGCGTAA		╞													╞
[755] [756]	CCACCACTTATCATGACGCTG AGTAACAACCCGCCAAACCTG	S1	Ē													
[763] [769] [776]	GCTTTCCTTAATGCATTATTTATCCCAATCAATAGAAGTTTG AGAAGAGTCCAAATTTCTAGCTGATAAAAGTCGGGGGCGCTTA ATGCGCCATTTTAATGAATTT	S1	╞	28								g5				
[777] [784]	GTTATTAGCTACAGACTGCCC ATTGCGTATTTTTGAGTTACAAAATAAATCATAGGCCCGAAC															
[790] [798] [804]	ATCAAAACAGCCATCGGAGAGGGTAGCTTGCGCTCGGCGCGT TATTAAATTGCTTTCACATTA ACTATGGTCCTTTGTCTGAGAGACTACCATTTGCCAGAGATC		╞								F	g5				╞
[804] [805] [811]	ACTAIGGICCTTIGICIGAGAGAGCIACCATTIGCCAGAGAIC TGAGTGAGCTATCACTTICCAGAGCCTATTITTAACAACTCG TACAAAGGCTAACTGACGAGC		ŧ	28	16	10		4			E	g5				ŧ
[819] [825] [833]	ACGCTAATGGGTTATAGACTITACAAACACGTGCTTGCCTAA ACGTATAAATTCGACCTCCGGCTTAGGTCGAGCGTGGTCATT GGATTTACAGAGCGCATAAAGTGTAAAGAGTCTGGCTTACCA	S1	F								F					╞
[833] .[839] [846]	GGATTTACAGAGCGCATAAAGTGTAAAGAGTCTGGCTTACCA GCCTGAGCCTGGGGTTCCTCGTTAGAATGAAGTATTATAACT ATATGTACCTGAATAGCAAAC	S1	ŧ	E							E			E		F
[847] [854] [860]	ATTTTATAATGCTGCATTTGA GTCAATAGGCCGATACACAACATACGAGTCGATGAAGCTACA AAGAGAACCGGAAGGGAGCTAAACAGGAGATAATGCAAA		╞	28							F					╞
.[860] :[868] :[874]	AAGAGAACCGGAAGGGAGCTAAACAGGAGATAATAATGCAAA CCGCTCAACTAGCAATTAGTTGCTATTTGCAAGACTAGAGCC TCCAATCTGCACCCACGGTAATCGTAAACAATTCCTAAAGGG		ŧ	28 	F						E		g4			F
[881] [882]	ATTITAGAATAGATAAAGAAC AACAACTACAGGAATTGTTAT TITCCTGACCCCGGGTTTTGAAGCCTTAAACTTTTGAGCACT	S1	╞													╞
[889] [895] [902]	TTTCCTGACCCCGGGTTTTGAAGCCTTAAACTTTTGAGCACT GCGAGAAAATCAAGTGTCAATCATATGTTGTGAAACGGTACG CCAGAATTCTTTAGTCAAATA	S1	ŧ								F		g4			ŧ
[903] [910]	TAAAATACCTGAGAATAGCTG TCGTAATAGCCCCAGAACCTCCCGACTTGTTAATTGGTTATC		F	28	16						F		-			╞
[916] [924] [930]	TATTTTAGCGGGAGTTGATAATCAGAAACATGGTCAGTGTTT CGAGGCGAAATTTACAGTTGAAAGGAATCAGTGAGCTCGAAT TTATAATTGAGGAATCATCTTCTGACCTTTTTAGCAAAACAG		ŧ										g4			╞
[938] .[944]	CCCCGGGGTATAAGAAGAACG GAAGATTTACCGAGGCCACCGAGTAAAAAAATCAAATGGTTT	64	F	28	16	10										F
[945] [958] [959]	TTATCCGCGACCGTTCTGGTCAGTTGGCGAGTCTGAGAGGAT GAAATACGTATTCTCAAATATTTAAATTCGACTCTTCCATCA ACCCTCATAACCGTGCATGCCTGCAGGTGTAAACGAGAAGGC	S1	ŧ											g3		╞
[965] [973]	CGCAAATATCAATAGTGATAA CCAGTGCAAATTCGAATAGCAAGCAAATGTTAAATATATCAA	S1	F													F
[979] [986] [987]	ATAAGGCCAGATATITTAATATTITGTTACAAGCTTTGTAGCA ATACTTCACCTCAAAAGAATA TTGCTGATTTGATT		╞	28			6				F			g3		ŀ
[994] [1000]	CACGACGTAAATCAGTAGGAATCATTACGAATCATCATCACC AACACCGCGCGCCCCATTAAATTTTTGTTTGTAAAAGTAATA	C1	F					-			F			g3		F
[1008] [1014] [1022]	TTTTTATGCCTGTTCAGCAAATGAAAAATTGCCTGTCCCAGT ACATCACTCTAAAGAATTACTAGAAAAATTTCATCGCTCATT TAACGCCCAATAGGCAAGCCG	S1	F													F
[1028] [1029]	TTTTAACAGGGTTTAGTAGAAGAACTCAGAGCCAGTAGTATC TCATCGATTATACACAGTGCCACGCTGAAACTATCAGTTGGG	S1	F	-												F
[1035] [1043] [1049]	ATATGCGGAACAAGAACGCCA CTGCAAGTAATTCGACCGCAC TCAAAAAGCGATTAGGCCTTGCTGGTAACCTGCAAAATTCTT		Ħ	28	16						F					F
[1050] [1063]	GTATTAATAAAGCCCAGTATTAACACCGTATCCAGGGATGTG ACCAGTAACCAAGTCGTCTGGCCTTCCTGAAAGGGAACAATA		F												g2	F
[1064] [1070] [1071]	AGCTGGCGTAGCCAAGAACGG TTACCGCAGGCGGTAACGCTC AGAGGTGCAGCCATTTACGCC	S1	╞													╞
[1078] [1084]	GGGCCTCTAAATGTCTGTCTTTCCTTATGGGCTTAATAAAAC AACAGTACATTCCAGCTTTCATCAACATTTCGCTATGCAACA		F	28	F	10									g2	F
[1091] [1092] [1099]	GGAAAAAGCAGAAGATTGAGA ACCACCACGCTCATTCGGTGC GTTGGGACCGTCGGTAGAAACCAATCAATATTTAACGAACG	S1	╞													╞
[1105] [1113]	ATCGCCATAATCGGGAGCGAGTAACAACAGGGCGAGGAAATA GCCATTATTTGACGCGCAACT		F												g2	F
[1119] [1120] .[1133]	CCTACATAAAATACCAACGCCAACATGTGAGCATGATTCTCC CGCCATTCAAACGGCCATCCTAATTTACAATTTAGAAACATC GTGGGAACAGGCTGCTCAATCGTCTGAAAGCCCTAGCAGAGG		╞	28	16											╞
[1134] [1140]	AGAAAAAGAGCCAGATGCGCGAACTGATATGGATTCGCCATT CATTTTCTAATATCCGGATTG	S1	F													F
[1148] [1154] [1162]	GCTATTAATTCACCGGTGCCGGAAACCATGGGATACTGAACA ACCGTAAGGCAAAGATTTACATTGGCAGGTCTTTATAATAAG ACAATAGAAAGTACTTGAATG	S1	╞													╞
[1168] [1169]	AGAATATATAAGTCGGTCACGTTGGTGTCGCTTCTAGTCACA CACAGACTAATAAACAGCTTTCCGGCACAGATGGGTTTATCA		F	28												Į
[1183]	CGACCAGAATATTTCGACAAA GATCGCAGCATCTGAGCTAATGCAGAACGTAATTCTACGTGG AGGTAAAGCGCCTGCGCATCGTAACCGTCTCCAGCAGGGACA		╞								╞					E
2[1162] 2[1168] 2[1169] 2[1175] 2[1183] 2[1189]	AGAATATATAAGTCGGTCACGTTGGTGTCGCTTCTAGTCACA CACAGACTAATAAACAGCTTTCCGGCACAGATGGGTTTATCA CGACCAGAATATTTCGACAAA		*		16	10	6	4	2					-		

Figure 5: The staple list of the nanorod. The notes next to each staples represent the location of the binding overhangs in each condition, including the biotin and the binding overhangs to target to cells. The stars represent the sequences at the end. And we generally exclude those sequences to prevent DNA origami stacking except when we need to add the binding overhangs to that location.

2.3 Sequence list of the nanosphere

name(5'-3') helix1-helix14	sequence CCACCCTCAGAGCCACCACCCTCATAGCTATCTTACCGAAGCCCT	biotin sites S1		28 b	indi	ng	site	s
helix2-helix36 helix3-helix11	AGCCACCACCGGAACCGCCTCCCACTATATGTAAATGCTGATGCAAATCC TTATTAGCGTTTGCCATCTTTTCATGTTAGCAAACGTAGAAAAT		28					+
helix4-helix32 helix5-helix7 helix6-helix28	CGTCAGACTGTAGCGCGTTTTCAATCATATGCGTTATACAAATTCTTACC GATAGCAGCACCGTAATCAGTAGAAAGGTGAATTATCACCGTCACCG ACCATTACCATTAGCAAGGCCATGTTCAGCTAATGCAGAACGCGC	\$1	28	16				+
helix7-helix24 helix8-helix10	ACTTGAGCCATTTGGGAATTAGATTTCATCGTAGGAATCATTAC AATATTGACGGAAATTATTCATTTATAAAAGAAAACGCAAAGACACCA		28 28	16	10	6	4	2 1
helix9-helix20 helix10-helix12 helix11-helix4	AGCGCCAAAGACAAAAGGGCGACATTCGAGCGTCTTTCCAGAGCCTAATT CGGAATAAGTTTATTTTGTCACAGGAATACCCAAAAGAACTGGCATG ACATACATAAAGGTGGCAACACGACAGAATCAAGTTTGCCTTTAG	S1	28	16	10			+
helix12-helix13 helix13-helix15	ATTAAGACTCCTTATTACGCAGTAGCCGAACAAAGTTACCAGAAGGA AACCGAGGAAACGCAATAATAACAATTGAGTTAAGCCCAATAATAAG		28	16	10			\pm
helix14-helix2 helix15-helix129 helix16-helix18	TTTTAAGAAAAGTAAGCAGATATAATCAAAATCACCGGAACCAG AGCAAGAAACAATGAAATAGCAATACCGTTCCAGTAAGCGTCATACATGG ATATCAGAGAGATAACCCACAAGCAAAAATGAAAATAGCAGCCTTTA		28	16	10			+
helix17-helix125 helix18-helix19	ATTAACTGAACACCCTGAACAGATTAGCGGGGTTTTGCTCAGTAC CAGAGAGAATAACATAAAAACAGATATTATTTATCCCAATCCAAATA	S1						+
helix19-helix9 helix20-helix123	AGAAACGATTTTTTGTTTAACGTATCAATAGAAAATTCATATGGTTTACC TGCCAGTTACAAAATAAACAGCCAGGTTTAGTACCGCCACCCTC		28					+
helix21-helix23 helix22-helix119 helix23-helix25	ATCCTGAATCTTACCAACGCTAACAGATATAGAAGGCTTATCCGGTA TGAAGCCTTAAATCAAGATTAGTTGCAGTTTTGTCGTCTTTCCAGACGTT TTCTAAGAACGCGAGGCGTTTTAATTAAACCAAGTACCGCACTCATC		28				_	+
helix24-helix8 helix25-helix26	CGCGCCCAATAGCAAGCAAATCAACCGATTGAGGGAGGGA	\$1 \$1						\pm
helix26-helix114 helix27-helix6 helix28-helix110	TCCTTATCATTCCAAGAACGGGTATAGTTGCGCCGACAATGACAACAACC ATCCTAATTTACGAGCATGTAGAGCCAGCAAAATCACCAGTAGC CTGTTTATCAACAATAGATAAGTCCATTAAACGGGTAAAATACGTAATGC	\$1						+
helix29-helix31 helix30-helix80	TCCAGACGACGACAATAAACAACGGCTTAATTGAGAATCGCCATATT GTAATAAGAGAATATAAAGTAACCTGTCGTGCCAGCTGCATT							\pm
helix31-helix33 helix32-helix5	TAACAACGCCAACATGTAATTTATAAGAATAAACACCGGAATCATAA AGTATAAAGCCAACGCTCAACAGTAGGGAAACGTCACCAATGAAACCATC	64						+
helix33-helix35 helix34-helix79 helix35-helix37	TTACTAGAAAAAGCCTGTTTAGTACTTTTTCAAATATATTTTAGTTA TGTGATAAATAAGGCGTTAAAGGAGAGGCGGTTTGCGTATTGGGC ATTTCATCTTCTGACCTAAATTTGTCTGAGAGAGACTACCTTTTTAACC	<u>\$1</u>	28					+
helix36-helix3 helix37-helix39	AATCGCAAGACAAAGAACGCGAGAAATCGGCATTTTCGGTCATAGCCCCC TCCGGCTTAGGTTGGGTTATATATTAATTTTCCCTTAGAATCCTTGA	S1						\pm
helix38-helix77 helix39-helix41 helix40-helix1	GTGAATTTATCAAAATCATAGAGAGTTGCAGCAAGCGGTCCACGC AAACATAGCGATAGCTTAGATTACATTTAACAATTTCATTTGAATTA TTGCTTCTGTAAATCGTCGCTATTAATCAGAGCCGCCACCCTCAGAACCG							+
helix40-helix1 helix41-helix42 helix42-helix75	CCTTTTTTAATGGAAACAGTACAAGCAAAAGAAGAAGATGATGAAACAAA CATCAAGAAAACAAAATTAATTAAAAGAATAGCCCGAGATAGGG	S1	28					+
helix43-helix45 helix44-helix71 helix45 helix77	GAATTATTCATTTCAATTACCTGATTGCGTAGATTTTCAGGTTTAAC CGGATTCGCCTGATTGCTTTGAATACGGGAGCCCCCGATTTAGAGCTTGA							+
helix45-helix47 helix46-helix131 helix47-helix127	GTCAGATGAATATACAGTAACAGTCCTGATTGTTTGGATTATACTTC ACGTAAAACAGAAATAAAGAAAGGTTGAGGCAGGTCAGACGA TGAATAATGGAAGGGTTAGAACCAACAGTTAATGCCCCCTGCCT	S1						+
helix48-helix69 helix49-helix51	ATGATGGCAATTCATCAATATAACAAGTGTAGCGGTCACGCTGCGCGTAA GAAACCACCAGAAGGAGCGGAATGAGGATTTAGAAGTATTAGACTTT	\$1	28	16	10	6	4	\pm
helix50-helix57 helix51-helix53 helix52-helix126	ATTAATTTTAAAAGTTTGAGTTGATAGCCCTAAAACATCGCC ACAAACAATTCGACAACTCGTATTGGCAAATCAACAGTTGAAAGGAA TAGAGCCGTCAATAGATAATACATTTAAACATGAAAGTATTAAGAGGCTG	\$1						+
helix52-helix126 helix53-helix121 helix54-helix56	TTGAGGAAGGTTATCTAAAAATATTAGGAACCCATGTACCGTAACACTGAG CCCTCAATCAATATCTGGTCAGTACCAGCAGAAGATAAAACAGAGGT							+
helix55-helix100 helix56-helix58	CAGCAAATGAAAAATCTAAAGCATCATGGCTCATTATACCAGTCAGGACG GAGGCGGTCAGTATTAACACCGCGGCACAGACAATATTTTTGAATGG		28	16				\mp
helix57-helix50 helix58-helix66 helix59-helix98	ATTAAAAATACCGAACGAACCTAAATCCTTTGCCCGAACGTT CTATTAGTCTTTAATGCGCGAACAAAGGGATTTTAGACAGGAACGGTACG GACCTGAAAGCGTAAGAATACGTAGTTGAGATTTAGGAATACCA						_	+
helix60-helix62 helix61-helix94	ACCAGTAATAAAAGGGACATTCTACAATATTACCGCCAGCCA	\$1						\pm
helix62-helix88 helix63-helix65	ACAGGAAAAACGCTCATGGAAATTTGCGGATGGCTTAGAGCTTAATTGCT CGGCCTTGCTGGTAATATCCAGAATCAGTGAGGCCACCGAGTAAAAG	<u>\$1</u>						+
helix64-helix72 helix65-helix67 helix66-helix59	GATTAGTAATAACATCACTTGGTTTTTTGGGGTCGAGGTGCCGTA AGTCTGTCCATCACGCAAATTAATGCTTTCCTCGTTAGAATCAGAGC CCAGAATCCTGAGAAGTGTTTTTATAGGCCAACAGAGATAGAACCCTTCT	\$1 						+
helix67-helix68 helix68-helix70	GGGAGCTAAACAGGAGGCCGATTCCGCTACAGGGCGCGTACTATGGT TGCTTTGACGAGCACGTATAACGGAGAAAGGAAGGGAAG		28					\mp
helix69-helix49 helix70-helix44 helix71-helix64	CCACCACACCCGCCGCGCGCTTAATGCGAACATTATCATTTTGCGGAACAAA AGGAGCGGGCGCTAGGGCGCTGGTACCTTTTACATCGGGAGAAACAATAA CGGGGAAAGCCGGCGAACGTGGCCCGTTGTAGCAATACTTCTTT	\$1	28	16	10	6	4	2
helix72-helix74 helix73-helix87	AAGCACTAAATCGGAACCCTAAAAACAAGAGTCCACTATTAAAGAAC ACTACGTGAACCATCACCCAAATCAATTTAAATATGCAACTAAAGTACGG	S1		16	10		-	
helix74-helix76 helix75-helix43	GTGGACTCCAACGTCAAAGGGCGTCCTGTTTGATGGTGGTTCCGAAA TTGAGTGTTGTTCCAGTTTGGCAAGTTACAAAATCGCGCAGAGGC	64						+
helix76-helix38 helix77-helix85 helix78-helix34	TCGGCAAAATCCCTTATAAATCAAGACGCTGAGAAGAGTCAATA TGGTTTGCCCCAGCAGGCGAAAATAGATACATTTCGCAAATGGTCAATAA GCCCTTCACCGCCTGGCCCTGAGAATGGTTTGAAATACCGACCG	S1						+
helix79-helix81 helix80-helix30	GCCAGGGTGGTTTTTCTTTTCACACTCACATTAATTGCGTTGCGCTC AATGAATCGGCCAACGCGCGGGGCAGAGGCATTTTCGAGCCA	S1	28	16	10	6	4	\pm
helix81-helix107 helix82-helix84 helix83-helix91	ACTGCCCGCTTTCCAGTCGGGAACTGATAAATTGTGTCGAAATCCGCGAC TGGGGTGCCTAATGAGTGAGCTAGCGCGAGCTGAAAAGGTGGCATCA ACAATTCCACACAACATACGACAAAAAGATTAAGAGGAAGCCCGA	\$1	28	16	10			+
helix84-helix86 helix85-helix78	ACTATICCACACAACATACGACAAAAAGATTAAGAGGGAGCCCGA ATTCTACTAATAGTAGTAGCATTAACAGTTGATTCCCAATTCTGCGA CCTGTTTAGCTATATTTTCATTTGGGCAGTGAGACGGGCAACAGCTGATT		28	10	10			+
helix86-helix73 helix87-helix89	ACGAGTAGATTTAGTTTGACCATAAAAACCGTCTATCAGGGCGATGGCCC TGTCTGGAAGTTTCATTCCATATAGGATTAGAGAGTACCTTTAATTG							+
helix88-helix63 helix89-helix90 helix90-helix83	GAATATAATGCTGTAGCTCAACATGTCCTGAGTAGAAGAACTCAAACTAT CTCCTTTTGATAAGAGGTCATTTATTCGAGCTTCAAAGCGAACCAGA CCGGAAGCAAACTCCAACAGGTCGTGTGAAATTGTTATCCGCTC							+
helix91-helix93 helix92-helix106	AAGACTTCAAATATCGCGTTTTACCCTCAAATGCTTTAAACAGTTCA ATAGTCAGAAGCAAAGCGGATTGCATAGGCGCAGACGGTCAATCATAAGG	\$1						\pm
helix93-helix95 helix94-helix61 helix95-helix97	GAAAACGAGAATGACCATAAATCAAGAAGTTTTGCCAGAGGGGGGTAA TCATAAATATTCATTGAATCCACCTACATTTTGACGCTCAAT TAGTAAAATGTTTAGACTGGATATAACGCCAAAAGGAATTACGAGGC							+
helix96-helix104 helix97-helix99	ACCAAAATAGCGAGAGGCTTTTGCAACTTCATCAAGAGTAATCTTGACAA ATAGTAAGAGCGAACACTATCATCATAAAACGAACTAACGGAACAACAT	S1	28	16	10	6		\pm
helix98-helix60 helix99-helix55	CATTCAACTAATGCAGATACAATTGGCAGATTCACCAGTCACACG TATTACAGGTAGAAAGATTCATCCTGCAACAGTGCCACGCTGAGAGCCAG		28	16				+
	TTGGGAAGAAAAATCTACGTTAAAGAAACACCAGAACGAGTAGTAAA ACCTTATGCGATTTTAAGAACCCTGTAGCATTCCACAGACAG							+
helix103-helix96 helix104-helix112	AGTGAATAAGGCTTGCCCTGACGACCCTCGTTTACCAGACGACGATAAAA	\$1	28					\pm
helix105-helix92 helix106-helix108 helix107-helix82	ACCAGGCGCATAGGCTGGCTGACAAAAATCAGGTCTTTACCCTGACTATT GAACCGAACTGACCAACTTTGAAATTATACCAAGCGCGAAACAAAGT CTGCTCCATGTTACTTAGCCGGAACGGCCGGAAGCATAAAGTGTAAAGCC							+
helix108-helix109	ACAACGGAGATTTGTATCATCGCAAAGAGGCAAAAGAATACACTAAA ACACTCATCTTTGACCCCCAGCGCGGCTACAGAGGCTTTGAGGACTA	S1						+
helix110-helix29 helix111-helix113	CACTACGAAGGCACCAACCTAAAACGCCGACAAAAGGTAAAGTAATTCTG AAGACTTTTTCATGAGGAAGTTTGGTCGCTGAGGCTTGCAGGGAGTT CCATCCGAACCACCGCTACAACACCACCACACACCACCACGCGTGTACAC	\$1	28	16				$\overline{+}$
helix112-helix105 helix113-helix115 helix114-helix27		\$1						+
helix115-helix117 helix116-helix103	ATTTCTTAAACAGCTTGATACCGGGAACAACTAAAGGAATTGCGAAT AGGAGCCTTTAATTGTATCGGTCAACGTAACAAAGCTGCTCATTC	S1						+
helix117-helix118 helix118-helix22 helix119-helix101	TTTCAGCGGAGTGAGAATAGAAAGCGAACCTCCCGACTTGCGGGAGGTTT	<u>S1</u>						+
helix119-helix101 helix120-helix122 helix121-helix54	AGTAAATGAATTTTCTGTATGGGCAACTTTAATCATTGTGAATT TCATAGTTAGCGTAACGATCTAAGCCACCCTCAGAGCCACCACCCTC TTTCGTCACCAGTACAAACTACAACGCCTTGCTGAACCTCAAATATCAAA	\$1 \$1	28					+
helix122-helix124 helix123-helix21	ATTTTCAGGGATAGCAAGCCCAAGGGTTGATATAAGTATAGCCCGGA AGAACCGCCACCCTCAGAACCTATTTTGCACCCAGCTACAATTTT		28					+
helix124-helix17 helix125-helix52 helix126-helix128	ATAGGTGTATCACCGTACTCAGGGGAAGCGCATTAGACGGGAGA CAGGCGGATAAGTGCCGTCGAGACTTTAGGAGCACTAACAACTAATAGAT AGACTCCTCAAGAGAAGGATTAGTAATAAGTTTTAACGGGGTCAGTG							+
helix127-helix48 helix128-helix130	ATTTCGGAACCTATTATTCTGTATCATCATATTCCTGATTATCAG CCTTGAGTAACAGTGCCCGTATAAAATAAA		28	16	10			+
helix129-helix16 helix130-helix132 helix131-helix46								+
helix131-helix46 helix132-helix40	TTGGCCTTGATATTCACAAACTACCATATCAAAATTATTTGC GAGCCGCCGCCAGCATTGACAGGTAAATCAATATATGTGAGTGA		28	16	10	6		\pm

Figure 6: The staple list of the nanosphere. The notes next to each staples represent the location of the binding overhangs in each condition, including the biotin and the binding overhangs to target to cells.

2.4 Sequence list of the binding overhangs and decorations

name	sequence	Note
S1	staples - TT GAGAGCAGACCTGGAACTCG	stalks on the origami
S1'	biotin - CGAGTTCCAGGTCTGCTCTC	sequence with biotin
S2	staples - TT CAGTCAGTCAGTCAGTCAGT	binding sites to target to cells
S2'	Chol-TEG - ACTGACTGACTGACTGACTG	cholesterol-ssDNA initiator
S3	staples - TT GTCTCGTCGTCTACCGCAAT	stalks to attach the bridge sequences
bridge 1	CAGTGATATTCGTTCACCTCAGGCAGGTTGTACTAGCACCAGTTCGGAGACACATTCCTGCAGTCAGT	dsDNA bridge part1
bridge 2	CAGGAATGTGTCTCCGAACTGGTGCTAGTACAACCTGCCTG	dsDNA bridge part2

Figure 7: The sequences of the binding overhangs and decorations used in this paper.

3 Agarose gel results for the DNA origami

All the gels shown below was 2% agarose gel with 1x TBE and 12.5 mM MgCl₂ pre-stained with 1x SYBR Safe dye. We loaded 15 μ l of 15 nM purified DNA origami to each well and run under 100 V voltage for 1.5 - 2 hours in a cold room. The gel was imaged under the SYBR Safe channel with a Bio-rad ChemiDoc Imaging System.

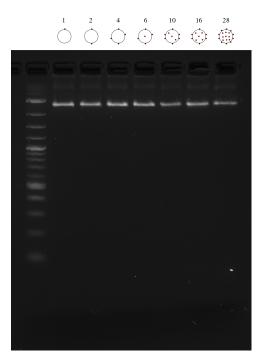


Figure 8: The agarose gel result of the nanosphere shape with different number of binding overhangs. From left to right: Ladder, nanosphere with 1, 2, 4, 6, 10, 16, 28 binding overhangs.

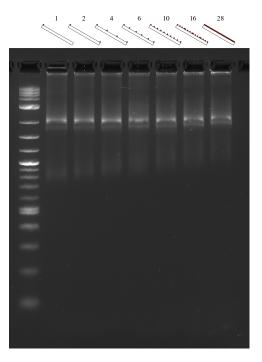


Figure 9: The agarose gel result of the nanorod shape with different number of binding overhangs. The gel image implies that there are some impurities and aggregations other than the brightest band. But further AFM images (Figure SI 15) show that the nanorods are intact. From left to right: Ladder, nanorod with 1, 2, 4, 6, 10, 16, 28 binding overhangs.

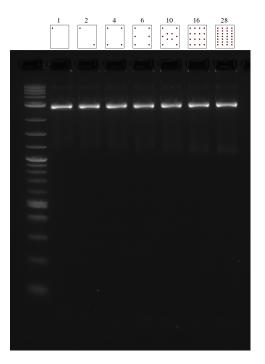


Figure 10: The agarose gel result of the nanotile shape with different number of binding overhangs on the face. From left to right: Ladder, nanotile with 1, 2, 4, 6, 10, 16, 28 binding overhangs on the face.

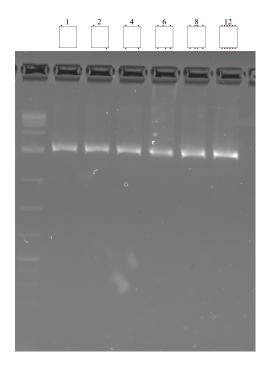


Figure 11: The agarose gel result of the nanotile shape with different number of binding overhangs on the edge. From left to right: Ladder, nanotile with 1, 2, 4, 6, 8, 12 binding overhangs on the edge.

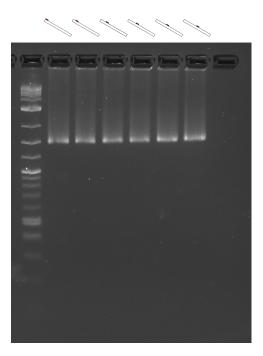


Figure 12: The agarose gel result of the nanorod shape with 3 binding overhangs at different location of the nanorod. From left to right: Ladder, nanorod with binding overhangs at position 1, 2, 3, 4, 5, 6.

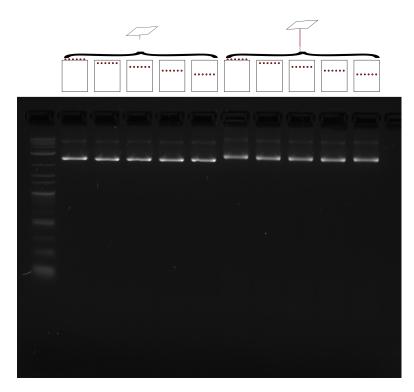


Figure 13: The agarose gel result of the nanotile shape with 6 binding overhangs at different location of the nanotile and with/without the dsDNA bridge sequences. From left to right: Ladder, nanotile with 6 binding overhangs without bridge at position 1, 2, 3, 4, 5, nanotile with 6 binding overhangs with bridge at position 1, 2, 3, 4, 5.

We then mixed the 15 μ l DNA origami with 6FAM conjugated initiator ssDNA that was complementary to the overhangs. The final concentration of the 6FAM-ssDNA was 1.25 μ M. The mixture was incubated at room temperature for one hour to allow hybridization. The samples was run through a non-stained agarose gel at 100 V for 1.5 - 2 hours and observed the bands under the Cy2 channel. And the total intensities of each band was analyzed by ImageJ. The result in Fig. S14 shows that the linear relationship of the 6FAM band intensity versus the number of binding overhangs in each shape, which indicates that the number of binding overhangs corresponds to the design.

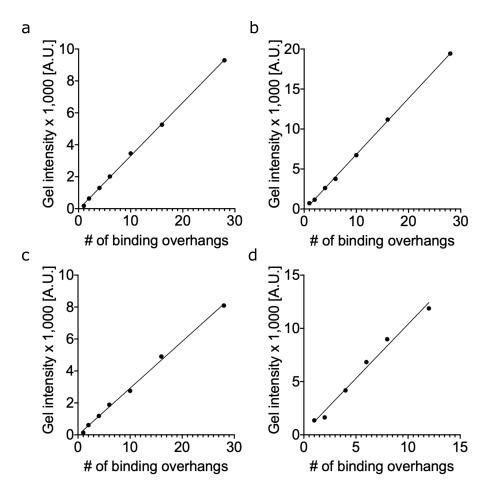


Figure 14: The 6FAM labeled DNA origami running through agarose gels. The linear relationship of the 6FAM band intensity versus the number of binding overhangs in each shape indicates that the binding overhangs are successfully assembled. (a) The DNA origami nanosphere with different number of binding overhangs. (b) The DNA origami nanorod. (c) The DNA origami nanotile with the binding overhangs located on the face. (d) The DNA origami nanotile with the binding overhangs on the edge.

4 AFMs for the selected samples

To further prove that the DNA origami was intact after purification, we selectively imaged some conditions used in the cell experiment.

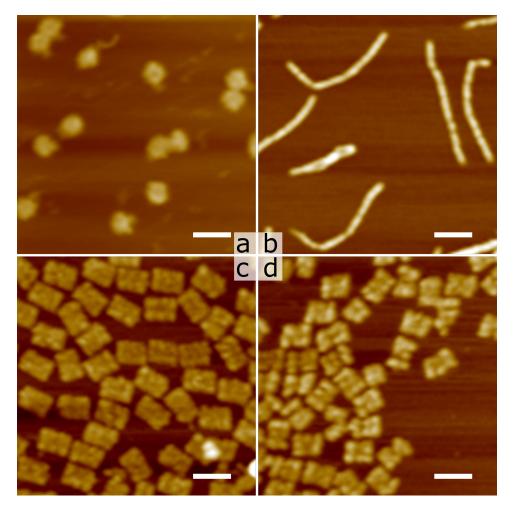


Figure 15: The AFM of the purified samples. (a) The nanosphere with 6 binding overhangs. (b) The nanorod with 28 binding overhangs. (c) The nanotile with 28 binding overhangs on the face. (d) The nanotile with 12 binding overhangs at the edge. Scale bars: 100 nm.

The dimension of DNA origami was determined by the measuring the profile of AFM images in 1 with FIJI ImageJ, as shown in 16. The measured dimension suggested that the distance of neighboring double-stranded helices is around 2.8 nm, instead of 2 nm, the diameter of a single dsDNA helix. This agrees with previous literature report.²

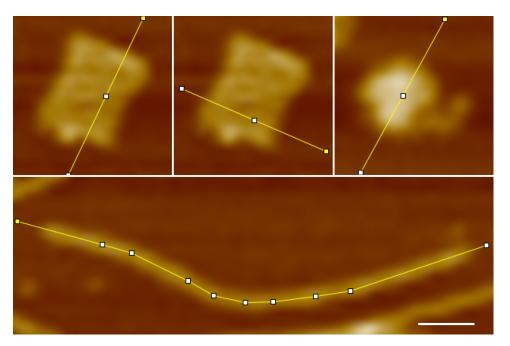


Figure 16: Using ImageJ to measure the dimension of the three DNA origami nanostructures. The AFM image showed the approximate dimension of a nanotile is around 66 by 88 nm. The lenth of a nanorod is around 398 nm. And the diameter of a nanosphere is around 68 nm. Scale bar: 50 nm.

5 Statistical analysis of the fluorescence data

We ran an one-way ANOVA analysis with post hoc Tukey's test between the targeted and non-targeted condition to show the significance of the labeling. The results are shown below.

а

С

е

9					
	0 nm	35 nm	70 nm	98 nm	133 nm
35 nm	***				
70 nm	***	ns			
98 nm	***	ns	ns		
133 nm	***	ns	ns	ns	
175 nm	***	ns	ns	ns	ns

Proximity of nanorod: P values among different test conditions

ns

ns

ns

Proximity of nanotile without

ns

٠

ns

Proximity of nanotile with

spacers: P values among

different test conditions

0 nm 10 nm 20 nm 30 nm

spacers: P values among

different test conditions

10 nm 20 nm 30 nm

ns

ns

ns

ns

ns

ns

0 nm

ns

ns

٠

ns

10 nm

20 nm

30 nm

40 nm

10 nm

20 nm

30 nm

40 nm

0 nm	35 nm	70 nm	98 nm	133 nm	175 nm
***	ns	ns	ns	ns	ns

Proximity of nanorod: P values between with and without initiator conditions

d

b

0 nm	10 nm	20 nm	30 nm	40 nm
***	*	ns	ns	ns

Proximity of nanotile without spacers: P values between with and without initiator conditions

f

0 nm	10 nm	20 nm	30 nm	40 nm
***	***	***	***	***

Proximity of nanotile with spacers: P values between with and without initiator conditions

Figure 17: The P value of each conditions in the proximity dependent experiment. Oneway ANOVA test was done with the proximity dependent experiment data including the proximity study with the nanorod ((a), (b)), and nanotiles with ((c), (d)) and without ((e), (f)) the bridge tethers. ns P > 0.05, * $P \le 0.05$, ** $P \le 0.01$, *** $P \le 0.001$

E. Benson, A. Mohammed, J. Gardell, S. Masich, E. Czeizler, P. Orponen and B. Högberg, *Nature*, 2015, **523**, 441–444.

D. Schiffels, T. Liedl and D. K. Fygenson, ACS nano, 2013, 7, 6700–6710.