Electronic Supplementary Material (ESI) for Nanoscale.

Support Information

High Precision and High Yield Fabrication of Dense Nanoparticle Arrays onto DNA Origami at Statistically Independent Binding Sites †

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S1 – Sequence of the Staple Strands for Each Design

For the DNA nanostructures described in this research (Figure S1), black sequences represent standard sequences, red sequences represent the α sequence, blue sequences represents the β sequence, green sequences represent the filler sequences, **bold orange** sequences represent the **linker strands**, and the **bold black** represents **biotin functionalization**. The standard DNA nanotube oligos are for synthesizing a DNA nanotube without any binding sites (Table S1). Each design was synthesized by replacing the designated standard DNA nanotube oligos with modified oligos (Table S2). The names of the standard DNA nanotube oligos to be replaced by the modified oligos are listed on the “Replace” column of the table.

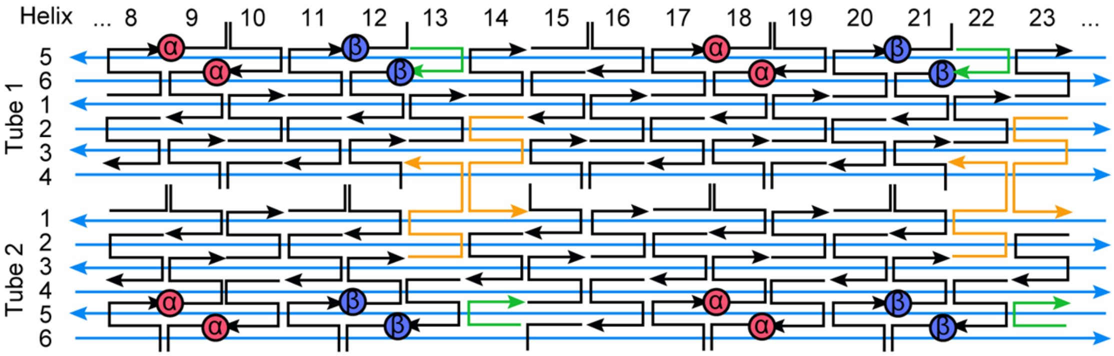

Figure S1: Schematic of a 4x DNA nanostructure. The red and blue circles represent the location of extended α and β tethers, respectively. The orange strands represent the linker strands, which crossover two nanotubes. The green strands represent the filler strands, which fill-in the single stranded DNA regions created by adding the linker strands.

Table S1: List of Standard DNA Nanotube Oligos

Name	Sequence
H1-C2	GCCAGAGGGGGTAAAGACTCCTTATTACAACGCAAAGACACC
H1-C5	CAATACTGCGGAATAACGCAATAATAACATAGAAAATTCATA
H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGA
H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAA
H1-C14	GCGGATTGCATCAACAAGAATTGAGTTAGCCATTTGGGAATT
H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAG
H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTA
H1-C23	TTGCTCCTTTTGATTGAAAATAGCAGCCTTAGCGTCAGACTG
H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATT
H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGA
H1-C32	AACAGTTGATTCCCTTTATCCTGAATCTCCGCCACCCTCAGA
H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGA
H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACT
H1-C41	TCTACTAATAGTAGCAAATCAGATATAGATCCTTTGCCCGAA
H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCG

H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATT
H1-C50	TAATACTTTTGCGGATCAATAATCGGCTAATATAATCCTGAT
H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTA
H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAAT
H1-C59	GACAGTCAAATCACTCTGTCCAGACGACTGAATATACAGTAA
H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTG
H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAAT
H1-C68	AAGAGAATCGATGACCAACGCTCAACAGAGATGATGAAACAA
H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTT
H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATAT
H1-C77	TTTGTTAAAATTCGTAATGGTTTGAAATCGTCGCTATTAATT
H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGA
H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCA
H2-C2	TATCATAACCCTCGCGTCTTTCCAGACGGTACAAACTACAAC
H2-C5	CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCA
H2-C8	TCAGTTGAGATTTAAAGGAACAACTAAACCACCCTCAGAGCC
H2-C11	AACGAACTAACGGATGAAAATCTCCAAAGGTTTAGTACCGCC
H2-C14	TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCC
H2-C17	ATCATTGTGAATTAAGCTTGATACCGATTTTTGCTCAGTACC
H2-C20	CGAGTAGTAAATTGGCCCACGCATAACCAGAGGCTGAGACTC
H2-C23	TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAA
H2-C26	AGAACCGGATATTCAAAGACAGCATCGGGTGCCTTGAGTAAC
H2-C29	GGCGCATAGGCTGGTTGAGGACTAAAGAGATGATACAGGAGT
H2-C32	TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACC
H2-C35	GCCGGAACGAGGCGCGAAAGAGGCAAAACAAACAAATAAATC
H2-C38	GATAAATTGTGTCGCCCAGCGATTATACAGAAGTAGTTGAGG
H2-C41	TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGC
H2-C44	CCAGCTGCATTAATCGCCTGGCCCTGAGTTGAGGAAGGTTAT
H2-C47	GTTGCGCTCACTGCTTGCCCCAGCAGGCAATCAATATCTGGT
H2-C50	AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCAC
H2-C53	CACAATTCCACACAGGGTTGAGTGTTGTGCCTGCAACAGTGC
H2-C56	ATCATGGTCATAGCAAGAACGTGGACTCAGCAGAAGATAAAA
H2-C59	GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACAT
H2-C62	CGTTGTAAAACGACTTTTTGGGGTCGAGCAATATTTTTGAAT
H2-C65	AGGCGATTAAGTTGAAAGGGAGCCCCCGAGAACCCTTCTGAC
H2-C68	TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAA
H2-C71	TTCAGGCTGCGCAAGCTAGGGCGCTGGCAATCGTCTGAAATG
H2-C74	ACCGCTTCTGGTGCACCACACCCGCCGCAACAGGAAAAACGC
H2-C77	GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATAT
H2-C80	GCATCGTAACCGTGAGAATCAGAGCGGGAATAACATCACTTG
H2-C83	GGATTGACCGTAATTTTAGACAGGAACGATCACGCAAATTAA
H3-C1	ATCTAAAGTTTTGTTTTACCAGACGACGGCAAAAGAAGTTTT
H3-C4	TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTC
H3-C7	GGAGTGAGAATAGAGGAATACCACATTCATTGAATCCCCCTC
H3-C10	TAATTTTTTCACGTACAACATTATTACAAATGACCATAAATC
H3-C13	AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAA

H3-C16	TGAATTTCTTAAACCCTTATGCGATTTTAGCCCGAAAGACTT
H3-C19	TGACAACAACCATCGGCTTGAGATGGTTAAGCGAACCAGACC
H3-C22	CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAA
H3-C25	CACCCTCAGCAGCGATTACCCAAATCAAGCGGATGGCTTAGA
H3-C28	CGGCTACAGAGGCTCTGACCTTCATCAATCAACATGTTTTAA
H3-C31	AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATAT
H3-C34	GCACCAACCTAAAACAGACGGTCAATCAGTAGATTTAGTTTG
H3-C37	ACTCATCTTTGACCAAATCCGCGACCTGATAACCTGTTTAGC
H3-C40	AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAAT
H3-C43	TGATTGCCCTTCACGAATCGGCCAACGCAATAAATCATACAG
H3-C46	CGGTCCACGCTGGTCCGCTTTCCAGTCGAATAAAGCCTCAGA
H3-C49	ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTG
H3-C52	AATAGCCCGAGATAACATACGAGCCGGATCAACGCAAGGATA
H3-C55	AGAGTCCACTATTATGTTTCCTGTGTGAAATGCAATGCCTGA
H3-C58	GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGA
H3-C61	CACCCAAATCAAGTGGCCAGTGCCAAGCTCAACCGTTCTAGC
H3-C64	TAAATCGGAACCCTGGTAACGCCAGGGTATTTTTGAGAGATC
H3-C67	GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAAC
H3-C70	CGAAAGGAGCGGGCCTGTTGGGAAGGGCACTAGCATGTCAAT
H3-C73	CGCTGCGCGTAACCCGGAAACCAGGCAAAGCCCCAAAAACAG
H3-C76	TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATAT
H3-C79	GTGCTTTCCTCGTTCATCTGCCAGTTTGTAAATCAGCTCATT
H3-C82	CCGATTAAAGGGATGGGATAGGTCACGTTAATTCGCGTCTGG
H3-C85	TGAGAAGTGTTTTTCGTCGGATTCTCCGTAAATGTGAGCGAG
H4-C1	GCCTGTAGCATTCCCAACATATAAAAGAGCAGTATGTTAGCA
H4-C4	TGTACCGTAACACTTTTTGTCACAATCAGGAATACCCAAAAG
H4-C7	ACCACCCTCATTTTCAAAGACAAAAGGGAACAAAGTTACCAG
H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCC
H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAG
H4-C16	AGGCGGATAAGTGCCACCAGTAGCACCATGAGCGCTAATATC
H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTG
H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAAT
H4-C25	AGTGCCCGTATAAACGGCATTTTCGGTCGAAACGATTTTTTG
H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACA
H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACG
H4-C34	CTCATTAAAGCCAGAGCCACCACCCTCATAGTTGCTATTTTG
H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGC
H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGT
H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCG
H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGA
H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCA
H4-C52	CACGCTGAGAGCCATTCTGAATAATGGAATCCTAATTTACGA
H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGAT
H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACA
H4-C61	GGCTATTAGTCTTTTCGGGAGAAACAATATAAAGTACCGACA
H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGA

H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGA
H4-C70	GATTATTTACATTGAAATTAATTACATTCGTTATACAAATTC
H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTA
H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGAT
H4-C79	CCTGAGTAGAAGAAATCCTTGAAAACATTAGTTAATTTCATC
H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGA
H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAA
H5-C3	ACGGAATAAGTTTAGAGTTTCGTCACCATTAGTAAATGAATT
H5-C6	TGGTTTACCAGCGCCAGGGATAGCAAGCTCAACAGTTTCAGC
H5-C9	TTGAGGGAGGGAAGCACCCTCAGAACCGGGAATTGCGAATAA
H5-C12	AGGTGAATTATCACCACCGTACTCAGGAAAAAAGGCTCCAAA
H5-C15	AGAGCCAGCAAAATCGTCGAGAGGGTTGGCTTGCTTTCGAGG
H5-C18	GCCGGAAACGTCACTAGGATTAGCGGGGAGTTGCGCCGACAA
H5-C21	ATCAGTAGCGACAGACATGAAAGTATTAGATATATTCGGTCG
H5-C24	TAGCGCGTTTTCATCAGTTAATGCCCCCTTTTGCGGGATCGT
H5-C27	AGCGTTTGCCATCTTTTTAACGGGGTCAAACGAGGGTAGCAA
H5-C30	GCCACCACCGGAACCATACATGGCTTTTCTTTTTCATGAGGA
H5-C33	ACCGCCACCCTCAGAATGGAAAGCGCAGATGCCACTACGAAG
H5-C36	ACCACCACCAGAGCGGCCTTGATATTCAGAATACACTAAAAC
H5-C39	TTACAAACAATTCGACATTTGAGGATTTCAAGCGCGAAACAA
H5-C42	CGTTATTAATTTTAGGAGCACTAACAACAGACGGGCAACAGC
H5-C45	GAACAAAGAAACCAACAGTTGAAAGGAAAGAGTTGCAGCAAG
H5-C48	CCTGATTATCAGATAATATCAAACCCTCGAAAATCCTGTTTG
H5-C51	TGTTTGGATTATACGCAGCAAATGAAAATTATAAATCAAAAG
H5-C54	CCATATCAAAATTATCAGTATTAACACCTCCAGTTTGGAACA
H5-C57	TGCGTAGATTTTCACCGAACGAACCACCCAACGTCAAAGGGC
H5-C60	CAGTACCTTTTACAAATGCGCGAACTGAACTACGTGAACCAT
H5-C63	ATTGCTTTGAATACATACGTGGCACAGAGTGCCGTAAAGCAC
H5-C66	TATTCATTTCAATTTGGCCAACAGAGATATTTAGAGCTTGAC
H5-C69	ACATCAAGAAAACAGCAGATTCACCAGTGGAAGGGAAGAAAG
H5-C72	GAATTACCTTTTTTACATTTTGACGCTCAAGTGTAGCGGTCA
H5-C75	GTGAGTGAATAACCCCGCCAGCCATTGCGCTTAATGCGCCGC
H5-C78	AATTTTCCCTTAGACTCAAACTATCGGCCGAGCACGTATAAC
H5-C81	TTAAGACGCTGAGACTTCTTTGATTAGTAGCTAAACAGGAGG
H5-C84	TAGGTCTGAGAGACAAAAGAGTCTGTCCGTACGCCAGAATCC
H6-C3	AACTGGCATGATTATAGTAAAATGTTTAAGTAAGAGCAACAC
H6-C6	AAGGAAACCGAGGACGTCATAAATATTCAACTAATGCAGATA
H6-C9	CTTTTTAAGAAAAGGTTCAGAAAACGAGGGTAGAAAGATTCA
H6-C12	AGCAAGAAACAATGTACCCTGACTATTAATCTACGTTAATAA
H6-C15	AGAGAGATAACCCAAAAGATTAAGAGGAAAGAACTGGCTCAT
H6-C18	AACACCCTGAACAATAATTCGAGCTTCATAATTTCAACTTTA
H6-C21	AACATAAAAACAGGACAGGTCAGGATTAGAGAAACACCAGAA
H6-C24	TTTAACGTCAAAAAAAGAGGTCATTTTTCGTAACAAAGCTGC
H6-C27	GCCATATTATTTATTATAATGCTGTAGCGAGTAATCTTGACA
H6-C30	AGCGTCTTTCCAGATACGGTGTCTGGAACGGTGTACAGACCA
H6-C33	CACCCAGCTACAATAATTCTGCGAACGATAAGGGAACCGAAC

H6-C36	GGGAGGTTTTGAAGTTCGCAAATGGTCACTCCATGTTACTTA
H6-C39	ATTCTAAGAACGCGGGGCGCGAGCTGAATTGTATCATCGCCT
H6-C42	CGCCCAATAGCAAGTAGCATTAACATCCGCGGGGAGAGGCGG
H6-C45	ACAAGCAAGCCGTTTAGCAAAATTAAGCGGAAACCTGTCGTG
H6-C48	TTCCAAGAACGGGTCGGTTGTACCAAAACTCACATTAATTGC
H6-C51	GCATGTAGAAACCAGAGAAGCCTTTATTAGCATAAAGTGTAA
H6-C54	AAGTCCTGAACAAGCCTCATATATTTTAAATTGTTATCCGCT
H6-C57	TGTTCAGCTAATGCAAGATTCAAAAGGGAGCTCGAATTCGTA
H6-C60	AAAGGTAAAGTAATCATCAATATGATATTTGCATGCCTGCAG
H6-C63	GGCATTTTCGAGCCCGGAGAGGGTAGCTTTTCCCAGTCACGA
H6-C66	GAATCGCCATATTTGGTCATTGCCTGAGGGGGATGTGCTGCA
H6-C69	TTACCAGTATAAAGACGGTAATCGTAAAGATCGGTGCGGGCC
H6-C72	CTAGAAAAAGCCTGTTGATAATCAGAAAAGCGCCATTCGCCA
H6-C75	AAATAAGGCGTTAACAAATATTTAAATTGCCAGCTTTCCGGC
H6-C78	TTCTGACCTAAATTCATTAAATTTTTGTAGGGGACGACGACA
H6-C81	ACGCGAGAAAACTTAACGCCATCAAAAATGGTGTAGATGGGC
H6-C84	CTATATGTAAATGCGCTTTCATCAACATTGGGAACAAACGGC

Table S2: List of Replacement Oligos for each Design

$1x9_{\alpha}$ Replacement Oligos

Name	Replace	Sequence
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG

$2x9_{\alpha}$ Replacement Oligos

Name	Replace	Sequence
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG

$4x9_{\alpha}$ Replacement Oligos

A-Tube

Name	Replace	Sequence
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG

H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
A_H3-C4	H3-C4	**TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTCTGTACCGTAACACT**
A_H3-C13	H3-C13	**AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT**
A_H3-C22	H3-C22	**CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA**
A_H3-C31	H3-C31	**AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT**
A_H3-C40	H3-C40	**AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT**
A_H3-C49	H3-C49	**ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA**
A_H3-C58	H3-C58	**GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA**
A_H3-C67	H3-C67	**GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC**
A_H3-C76	H3-C76	**TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA**
A_H6-C5	H1-C5	AACGCAATAATAACATAGAAAATTCATA
A_H6-C14	H1-C14	CAAGAATTGAGTTAGCCATTTGGGAATT
A_H6-C23	H1-C23	TGAAAATAGCAGCCTTAGCGTCAGACTG
A_H6-C32	H1-C32	TTTATCCTGAATCTCCGCCACCCTCAGA
A_H6-C41	H1-C41	CAAATCAGATATAGATCCTTTGCCCGAA
A_H6-C50	H1-C50	ATCAATAATCGGCTAATATAATCCTGAT
A_H6-C59	H1-C59	TCTGTCCAGACGACTGAATATACAGTAA
A_H6-C68	H1-C68	CCAACGCTCAACAGAGATGATGAAACAA
A_H6-C77	H1-C77	TAATGGTTTGAAATCGTCGCTATTAATT

B-Tube

H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG

H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
B_H2-C14	H2-C14	TTTTGTCACAATCAGGAATACCCAAAAG
B_H2-C23	H2-C23	CGTCACCGACTTGAAGCCCAATAATAAG
B_H2-C32	H2-C32	AATCAAGTTTGCCTTTTACAGAGAGAAT
B_H2-C41	H2-C41	CGCCTCCCTCAGAGTACCAACGCTAACG
B_H2-C5	H2-C5	ACAACTCGTATTAAAAGGCTTATCCGGT
B_H2-C50	H2-C50	GATGGCAATTCATCGTCTTTCCTTATCA
B_H2-C59	H2-C59	GGTTTAACGTCAGAGACAATAAACAACA
B_H2-C68	H2-C68	ACCTGAGCAAAAGATAGGGCTTAATTGA
B_H2-C77	H2-C77	TTGCTTCTGTAAATACCGACCGTGTGAT
B_H5-C13	H4-C13	**CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT**
B_H5-C22	H4-C22	**TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA**
B_H5-C31	H4-C31	**TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT**
B_H5-C4	H4-C4	**TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC**
B_H5-C40	H4-C40	**TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG**
B_H5-C49	H4-C49	**AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG**
B_H5-C58	H4-C58	**GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC**
B_H5-C67	H4-C67	**TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA**
B_H5-C76	H4-C76	**GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG**

1x9$_{\beta}$ Replacement Oligos

Name	Replace	Sequence
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG

2x9$_{\beta}$ Replacement Oligos

Name	Replace	Sequence
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG

H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG

4x9$_{\beta}$ Replacement Oligos
A-Tube

Name	Replace	Sequence
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
A_H3-C13	H3-C13	AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT
A_H3-C22	H3-C22	CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA
A_H3-C31	H3-C31	AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT
A_H3-C40	H3-C40	AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT
A_H3-C49	H3-C49	ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA
A_H3-C58	H3-C58	GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA
A_H3-C67	H3-C67	GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC
A_H3-C76	H3-C76	TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA
A_H6-C5	H1-C5	**AACGCAATAATAACATAGAAAATTCATA**
A_H6-C14	H1-C14	**CAAGAATTGAGTTAGCCATTTGGGAATT**
A_H6-C23	H1-C23	**TGAAAATAGCAGCCTTAGCGTCAGACTG**
A_H6-C32	H1-C32	**TTTATCCTGAATCTCCGCCACCCTCAGA**
A_H6-C41	H1-C41	**CAAATCAGATATAGATCCTTTGCCCGAA**
A_H6-C50	H1-C50	**ATCAATAATCGGCTAATATAATCCTGAT**
A_H6-C59	H1-C59	**TCTGTCCAGACGACTGAATATACAGTAA**
A_H6-C68	H1-C68	**CCAACGCTCAACAGAGATGATGAAACAA**
A_H6-C77	H1-C77	**TAATGGTTTGAAATCGTCGCTATTAATT**

B-Tube

H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
B_H2-C14	H2-C14	**CGTCACCGACTTGAAGCCCAATAATAAG**TCTCTACCGCCTACG
B_H2-C23	H2-C23	**AATCAAGTTTGCCTTTTACAGAGAGAAT**TCTCTACCGCCTACG
B_H2-C32	H2-C32	**CGCCTCCCTCAGAGTACCAACGCTAACG**TCTCTACCGCCTACG
B_H2-C41	H2-C41	**ACAACTCGTATTAAAAGGCTTATCCGGT**TCTCTACCGCCTACG
B_H2-C5	H2-C5	**GATGGCAATTCATCGTCTTTCCTTATCA**TCTCTACCGCCTACG
B_H2-C50	H2-C50	**GGTTTAACGTCAGAGACAATAAACAACA**TCTCTACCGCCTACG
B_H2-C59	H2-C59	**ACCTGAGCAAAAGATAGGGCTTAATTGA**TCTCTACCGCCTACG
B_H2-C68	H2-C68	**TTGCTTCTGTAAATACCGACCGTGTGAT**TCTCTACCGCCTACG
B_H2-C77	H2-C77	CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT
B_H5-C13 β	H4-C13	TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA
B_H5-C22 β	H4-C22	TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT
B_H5-C31 β	H4-C31	TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC
B_H5-C40 β	H4-C40	TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG
B_H5-C49 β	H4-C49	AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG
B_H5-C58 β	H4-C58	GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC
B_H5-C67 β	H4-C67	TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA
B_H5-C76 β	H4-C76	GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG

$1x14_{\alpha}$ Replacement Oligos

Name	Replace	Sequence
H4-C7 α	H4-C7	ACCACCCTCATTTTCAAAGACAAAAGGGAACAAAGTTACCAGACCAGTGCTCCTACG
H4-C13 α	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C25 α	H4-C25	AGTGCCCGTATAAACGGCATTTTCGGTCGAAACGATTTTTTGACCAGTGCTCCTACG
H4-C31 α	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C43 α	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCGACCAGTGCTCCTACG
H4-C49 α	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C61 α	H4-C61	GGCTATTAGTCTTTTCGGGAGAAACAATATAAAGTACCGACAACCAGTGCTCCTACG
H4-C67 α	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C79 α	H4-C79	CCTGAGTAGAAGAAATCCTTGAAAACATTAGTTAATTTCATCACCAGTGCTCCTACG
H4-C85 α	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAAACCAGTGCTCCTACG

2x14$_\alpha$ Replacement Oligos

Name	Replace	Sequence
H4-C7 α	H4-C7	ACCACCCTCATTTTCAAAGACAAAAGGGAACAAAGTTACCAGACCAGTGCTCCTACG
H4-C13 α	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C25 α	H4-C25	AGTGCCCGTATAAACGGCATTTTCGGTCGAAACGATTTTTTGACCAGTGCTCCTACG
H4-C31 α	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C43 α	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCGACCAGTGCTCCTACG
H4-C49 α	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C61 α	H4-C61	GGCTATTAGTCTTTTCGGGAGAAACAATATAAAGTACCGACAACCAGTGCTCCTACG
H4-C67 α	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C79 α	H4-C79	CCTGAGTAGAAGAAATCCTTGAAAACATTAGTTAATTTCATCACCAGTGCTCCTACG
H4-C85 α	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAAACCAGTGCTCCTACG
H1-C11 α	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C29 α	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGAACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C47 α	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C65 α	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C83 α	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCAACCAGTGCTCCTACG
H1-C5 α	H1-C5	CAATACTGCGGAATAACGCAATAATAACATAGAAAATTCATAACCAGTGCTCCTACG
H1-C23 α	H1-C23	TTGCTCCTTTTGATTGAAAATAGCAGCCTTAGCGTCAGACTGACCAGTGCTCCTACG
H1-C41 α	H1-C41	TCTACTAATAGTAGCAAATCAGATATAGATCCTTTGCCCGAAACCAGTGCTCCTACG
H1-C59 α	H1-C59	GACAGTCAAATCACTCTGTCCAGACGACTGAATATACAGTAAACCAGTGCTCCTACG
H1-C77 α	H1-C77	TTTGTTAAAATTCGTAATGGTTTGAAATCGTCGCTATTAATTACCAGTGCTCCTACG

4x14$_\alpha$ Replacement Oligos

A-Tube

Name	Replace	Sequence
H4-C7 α	H4-C7	ACCACCCTCATTTTCAAAGACAAAAGGGAACAAAGTTACCAGACCAGTGCTCCTACG
H4-C13 α	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C25 α	H4-C25	AGTGCCCGTATAAACGGCATTTTCGGTCGAAACGATTTTTTGACCAGTGCTCCTACG
H4-C31 α	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C43 α	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCGACCAGTGCTCCTACG
H4-C49 α	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C61 α	H4-C61	GGCTATTAGTCTTTTCGGGAGAAACAATATAAAGTACCGACAACCAGTGCTCCTACG
H4-C67 α	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG

H4-C79 α	H4-C79	CCTGAGTAGAAGAAATCCTTGAAAACATTAGTTAATTTCATCACCAGTGCTCCTACG
H4-C85 α	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAAACCAGTGCTCCTACG
H1-C11 α	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C29 α	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGAACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C47 α	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C65 α	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C83 α	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCAACCAGTGCTCCTACG
A_H6-C5 α	H1-C5	AACGCAATAATAACATAGAAAATTCATAACCAGTGCTCCTACG
A_H6-C23 α	H1-C23	TGAAAATAGCAGCCTTAGCGTCAGACTGACCAGTGCTCCTACG
A_H6-C41 α	H1-C41	CAAATCAGATATAGATCCTTTGCCCGAAACCAGTGCTCCTACG
A_H6-C59 α	H1-C59	TCTGTCCAGACGACTGAATATACAGTAAACCAGTGCTCCTACG
A_H6-C77 α	H1-C77	TAATGGTTTGAAATCGTCGCTATTAATTACCAGTGCTCCTACG
A_H3-C4	H3-C4	**TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTCTGTACCGTAACACT**
A_H3-C13	H3-C13	**AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT**
A_H3-C22	H3-C22	**CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA**
A_H3-C31	H3-C31	**AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT**
A_H3-C40	H3-C40	**AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT**
A_H3-C49	H3-C49	**ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA**
A_H3-C58	H3-C58	**GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA**
A_H3-C67	H3-C67	**GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC**
A_H3-C76	H3-C76	**TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA**
A_H6-C14	H1-C14	CAAGAATTGAGTTAGCCATTTGGGAATT
A_H6-C32	H1-C32	TTTATCCTGAATCTCCGCCACCCTCAGA
A_H6-C50	H1-C50	ATCAATAATCGGCTAATATAATCCTGAT
A_H6-C68	H1-C68	CCAACGCTCAACAGAGATGATGAAACAA

B-Tube

H4-C7 α	H4-C7	ACCACCCTCATTTTCAAAGACAAAAGGGAACAAAGTTACCAGACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C25 α	H4-C25	AGTGCCCGTATAAACGGCATTTTCGGTCGAAACGATTTTTTGACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C43 α	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCGACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C61 α	H4-C61	GGCTATTAGTCTTTTCGGGAGAAACAATATAAAGTACCGACAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C79 α	H4-C79	CCTGAGTAGAAGAAATCCTTGAAAACATTAGTTAATTTCATCACCAGTGCTCCTACG
H4-C85 α	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAAACCAGTGCTCCTACG
H1-C11 α	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C29 α	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGAACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C47 α	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTACCAGTGCTCCTACG

H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C65 α	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C83 α	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCAACCAGTGCTCCTACG
H1-C5 α	H1-C5	CAATACTGCGGAATAACGCAATAATAACATAGAAAATTCATAACCAGTGCTCCTACG
H1-C23 α	H1-C23	TTGCTCCTTTTGATTGAAAATAGCAGCCTTAGCGTCAGACTGACCAGTGCTCCTACG
H1-C41 α	H1-C41	TCTACTAATAGTAGCAAATCAGATATAGATCCTTTGCCCGAAACCAGTGCTCCTACG
H1-C59 α	H1-C59	GACAGTCAAATCACTCTGTCCAGACGACTGAATATACAGTAAACCAGTGCTCCTACG
H1-C77 α	H1-C77	TTTGTTAAAATTCGTAATGGTTTGAAATCGTCGCTATTAATTACCAGTGCTCCTACG
H4-C13 α	H4-C13	CGTCACCGACTTGAAGCCCAATAATAAGACCAGTGCTCCTACG
H4-C31 α	H4-C31	CGCCTCCCTCAGAGTACCAACGCTAACGACCAGTGCTCCTACG
H4-C49 α	H4-C49	GATGGCAATTCATCGTCTTTCCTTATCAACCAGTGCTCCTACG
H4-C67 α	H4-C67	ACCTGAGCAAAAGATAGGGCTTAATTGAACCAGTGCTCCTACG
B_H2-C14	H2-C14	TTTTGTCACAATCAGGAATACCCAAAAG
B_H2-C23	H2-C23	AATCAAGTTTGCCTTTTACAGAGAGAAT
B_H2-C32	H2-C32	ACAACTCGTATTAAAAGGCTTATCCGGT
B_H2-C41	H2-C41	GGTTTAACGTCAGAGACAATAAACAACA
B_H2-C5	H2-C5	TTGCTTCTGTAAATACCGACCGTGTGAT
B_H2-C50	H2-C50	**CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT**
B_H2-C59	H2-C59	**TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA**
B_H2-C68	H2-C68	**TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT**
B_H2-C77	H2-C77	**TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC**
B_H5-C22	H4-C22	**TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG**
B_H5-C4	H4-C4	**AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG**
B_H5-C40	H4-C40	**GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC**
B_H5-C58	H4-C48	**TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA**
B_H5-C76	H4-C76	**GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG**

2x18$_{\alpha/\beta}$ Replacement Oligos

Name	**Replace**	**Sequence**
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG

H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG

4x18$_{\alpha/\beta}$ Replacement Oligos

A-Tube

Name	**Replace**	**Sequence**
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG

H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
A_H3-C4	H3-C4	**TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTCTGTACCGTAACACT**
A_H3-C13	H3-C13	**AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT**
A_H3-C22	H3-C22	**CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA**
A_H3-C31	H3-C31	**AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT**
A_H3-C40	H3-C40	**AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT**
A_H3-C49	H3-C49	**ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA**
A_H3-C58	H3-C58	**GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA**
A_H3-C67	H3-C67	**GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC**
A_H3-C76	H3-C76	**TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA**
A_H6-C5	H1-C5	AACGCAATAATAACATAGAAAATTCATA
A_H6-C14	H1-C14	CAAGAATTGAGTTAGCCATTTGGGAATT
A_H6-C23	H1-C23	TGAAAATAGCAGCCTTAGCGTCAGACTG
A_H6-C32	H1-C32	TTTATCCTGAATCTCCGCCACCCTCAGA
A_H6-C41	H1-C41	CAAATCAGATATAGATCCTTTGCCCGAA
A_H6-C50	H1-C50	ATCAATAATCGGCTAATATAATCCTGAT
A_H6-C59	H1-C59	TCTGTCCAGACGACTGAATATACAGTAA
A_H6-C68	H1-C68	CCAACGCTCAACAGAGATGATGAAACAA
A_H6-C77	H1-C77	TAATGGTTTGAAATCGTCGCTATTAATT

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H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG

H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
B_H2-C5	H2-C5	**TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA**
B_H2-C14	H2-C14	**TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT**
B_H2-C23	H2-C23	**TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC**
B_H2-C32	H2-C32	**TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG**
B_H2-C41	H2-C41	**CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT**
B_H2-C50	H2-C50	**AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG**
B_H2-C59	H2-C59	**GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC**
B_H2-C68	H2-C68	**TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA**
B_H2-C77	H2-C77	**GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG**
B_H5-C4	H4-C4	TTTTGTCACAATCAGGAATACCCAAAAG
B_H5-C13 β	H4-C13	CGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
B_H5-C22 β	H4-C22	AATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
B_H5-C31 β	H4-C31	CGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
B_H5-C40 β	H4-C40	ACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
B_H5-C49 β	H4-C49	GATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
B_H5-C58 β	H4-C58	GGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
B_H5-C67 β	H4-C67	ACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
B_H5-C76 β	H4-C76	TTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG

H1 Replacement Oligos

A-Tube

Name	Replace	Sequence
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG

H4-C43 Bio	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCG**TTTTTTTTTT/3Bio/**
A_H3-C4	H3-C4	**TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTCTGTACCGTAACACT**
A_H3-C13	H3-C13	**AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT**
A_H3-C22	H3-C22	**CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA**
A_H3-C31	H3-C31	**AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT**
A_H3-C40	H3-C40	**AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT**
A_H3-C49	H3-C49	**ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA**
A_H3-C58	H3-C58	**GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA**
A_H3-C67	H3-C67	**GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC**
A_H3-C76	H3-C76	**TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA**
A_H6-C5	H1-C5	AACGCAATAATAACATAGAAAATTCATA
A_H6-C14	H1-C14	CAAGAATTGAGTTAGCCATTTGGGAATT
A_H6-C23	H1-C23	TGAAAATAGCAGCCTTAGCGTCAGACTG
A_H6-C32	H1-C32	TTTATCCTGAATCTCCGCCACCCTCAGA
A_H6-C41	H1-C41	CAAATCAGATATAGATCCTTTGCCCGAA
A_H6-C50	H1-C50	ATCAATAATCGGCTAATATAATCCTGAT
A_H6-C59	H1-C59	TCTGTCCAGACGACTGAATATACAGTAA
A_H6-C68	H1-C68	CCAACGCTCAACAGAGATGATGAAACAA
A_H6-C77	H1-C77	TAATGGTTTGAAATCGTCGCTATTAATT

B-Tube

H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H4-C43 Bio	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCG**TTTTTTTTTT/3Bio/**
B_H2-C5	H2-C5	**CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT**
B_H2-C14	H2-C14	**TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA**
B_H2-C23	H2-C23	**TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT**
B_H2-C32	H2-C32	**TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC**
B_H2-C41	H2-C41	**TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG**
B_H2-C50	H2-C50	**AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG**
B_H2-C59	H2-C59	**GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC**
B_H2-C68	H2-C68	**TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA**
B_H2-C77	H2-C77	**GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG**
B_H5-C40 β	H4-C40	ACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
B_H5-C49 β	H4-C49	GATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
B_H5-C4	H4-C4	TTTTGTCACAATCAGGAATACCCAAAAG
B_H5-C13	H4-C13	CGTCACCGACTTGAAGCCCAATAATAAG
B_H5-C22	H4-C22	AATCAAGTTTGCCTTTTACAGAGAGAAT
B_H5-C31	H4-C31	CGCCTCCCTCAGAGTACCAACGCTAACG
B_H5-C58	H4-C58	GGTTTAACGTCAGAGACAATAAACAACA
B_H5-C67	H4-C67	ACCTGAGCAAAAGATAGGGCTTAATTGA
B_H5-C76	H4-C76	TTGCTTCTGTAAATACCGACCGTGTGAT

H2 Replacement Oligos

A-Tube

Name	Replace	Sequence
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
H4-C43 Bio	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCG**TTTTTTTTTT/3Bio/**
A_H3-C4	H3-C4	**TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTCTGTACCGTAACACT**
A_H3-C13	H3-C13	**AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT**
A_H3-C22	H3-C22	**CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA**
A_H3-C31	H3-C31	**AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT**
A_H3-C40	H3-C40	**AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT**

A_H3-C49	H3-C49	**ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA**
A_H3-C58	H3-C58	**GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA**
A_H3-C67	H3-C67	**GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC**
A_H3-C76	H3-C76	**TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA**
A_H6-C5	H1-C5	AACGCAATAATAACATAGAAAATTCATA
A_H6-C14	H1-C14	CAAGAATTGAGTTAGCCATTTGGGAATT
A_H6-C23	H1-C23	TGAAAATAGCAGCCTTAGCGTCAGACTG
A_H6-C32	H1-C32	TTTATCCTGAATCTCCGCCACCCTCAGA
A_H6-C41	H1-C41	CAAATCAGATATAGATCCTTTGCCCGAA
A_H6-C50	H1-C50	ATCAATAATCGGCTAATATAATCCTGAT
A_H6-C59	H1-C59	TCTGTCCAGACGACTGAATATACAGTAA
A_H6-C68	H1-C68	CCAACGCTCAACAGAGATGATGAAACAA
A_H6-C77	H1-C77	TAATGGTTTGAAATCGTCGCTATTAATT

B-Tube

H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
H4-C43 Bio	H4-C43	CTAAAATATCTTTAAAAGTTTGAGTAACAGGAATCATTACCG**TTTTTTTTTT/3Bio/**
B_H2-C5	H2-C5	**CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT**
B_H2-C14	H2-C14	**TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA**

B_H2-C23	H2-C23	**TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT**
B_H2-C32	H2-C32	**TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC**
B_H2-C41	H2-C41	**TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG**
B_H2-C50	H2-C50	**AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG**
B_H2-C59	H2-C59	**GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC**
B_H2-C68	H2-C68	**TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA**
B_H2-C77	H2-C77	**GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG**
B_H5-C4	H4-C4	TTTTGTCACAATCAGGAATACCCAAAAG
B_H5-C13 β	H4-C13	CGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
B_H5-C22 β	H4-C22	AATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
B_H5-C31 β	H4-C31	CGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
B_H5-C40 β	H4-C40	ACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
B_H5-C49 β	H4-C49	GATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
B_H5-C58 β	H4-C58	GGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
B_H5-C67 β	H4-C67	ACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
B_H5-C76 β	H4-C76	TTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG

H3 Replacement Oligos

A-Tube

Name	Replace	Sequence
H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG
H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG

H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C13 β	H4-C13	CGGAATAGGTGTATCGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
H4-C22 β	H4-C22	CCTATTATTCTGAAAATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
H4-C31 β	H4-C31	GTTCCAGTAAGCGTCGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
H4-C40 β	H4-C40	CGTCAATAGATAATACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
H4-C49 β	H4-C49	CTTGCTGAACCTCAGATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
H4-C58 β	H4-C58	CGCCATTAAAAATAGGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
H4-C67 β	H4-C67	TAAAAGGGACATTCACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
H4-C76 β	H4-C76	CCAGAACAATATTATTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
H4-C16 Bio	H4-C16	AGGCGGATAAGTGCCACCAGTAGCACCATGAGCGCTAATATC**TTTTTTTTTT/3Bio/**
H4-C34 Bio	H4-C34	CTCATTAAAGCCAGAGCCACCACCCTCATAGTTGCTATTTTG**TTTTTTTTTT/3Bio/**
H4-C52 Bio	H4-C52	CACGCTGAGAGCCATTCTGAATAATGGAATCCTAATTTACGA**TTTTTTTTTT/3Bio/**
H4-C70 Bio	H4-C70	GATTATTTACATTGAAATTAATTACATTCGTTATACAAATTC**TTTTTTTTTT/3Bio/**
A_H3-C4	H3-C4	**TTCTGTATGGGATTGAATTACGAGGCATGACTGGATAGCGTCTGTACCGTAACACT**
A_H3-C13	H3-C13	**AGGAGCCTTTAATTCGTTGGGAAGAAAATAGTCAGAAGCAAACGGAATAGGTGTAT**
A_H3-C22	H3-C22	**CTGAGGCTTGCAGGAGGCTTGCCCTGACGAGAGTACCTTTAACCTATTATTCTGAA**
A_H3-C31	H3-C31	**AGTTTCCATTAAACAGAGGACAGATGAAGTTTCATTCCATATGTTCCAGTAAGCGT**
A_H3-C40	H3-C40	**AGTACAATGGTTTTGCCAGGGCGGAGATAAGGTGGCATCAATCGTCAATAGATAAT**
A_H3-C49	H3-C49	**ATGGTGGTTCCGAAAATGAGTGAGCTAAACATTATGACCCTGCTTGCTGAACCTCA**
A_H3-C58	H3-C58	**GAAAAACCGTCTATATCCCCGGGTACCGTGAGAAAGGCCGGACGCCATTAAAAATA**
A_H3-C67	H3-C67	**GGGGAAAGCCGGCGCCAGCTGGCGAAAGAGTCTGGAGCAAACTAAAAGGGACATTC**
A_H3-C76	H3-C76	**TACAGGGCGCGTACAAGATCGCACTCCAGTAAACGTTAATATCCAGAACAATATTA**
A_H6-C5	H1-C5	AACGCAATAATAACATAGAAAATTCATA
A_H6-C14	H1-C14	CAAGAATTGAGTTAGCCATTTGGGAATT
A_H6-C23	H1-C23	TGAAAATAGCAGCCTTAGCGTCAGACTG
A_H6-C32	H1-C32	TTTATCCTGAATCTCCGCCACCCTCAGA
A_H6-C41	H1-C41	CAAATCAGATATAGATCCTTTGCCCGAA
A_H6-C50	H1-C50	ATCAATAATCGGCTAATATAATCCTGAT
A_H6-C59	H1-C59	TCTGTCCAGACGACTGAATATACAGTAA
A_H6-C68	H1-C68	CCAACGCTCAACAGAGATGATGAAACAA
A_H6-C77	H1-C77	TAATGGTTTGAAATCGTCGCTATTAATT

B-Tube

H1-C17 α	H1-C17	CAAATATCGCGTTTAGTCAGAGGGTAATTTACCATTAGCAAGACCAGTGCTCCTACG
H1-C26 α	H1-C26	GCTTAATTGCTGAACCCAATCCAAATAAATAGCCCCCTTATTACCAGTGCTCCTACG
H1-C35 α	H1-C35	ACCATTAGATACATCCTTAAATCAAGATGAGCCGCCACCAGAACCAGTGCTCCTACG
H1-C44 α	H1-C44	GCAAGGCAAAGAATTTTATTTTCATCGTATTATCATTTTGCGACCAGTGCTCCTACG
H1-C53 α	H1-C53	AAAATTTTTAGAACAAAAATAATATCCCAGGGTTAGAACCTAACCAGTGCTCCTACG
H1-C62 α	H1-C62	TGATAAATTAATGCAGTAATAAGAGAATAACGGATTCGCCTGACCAGTGCTCCTACG
H1-C71 α	H1-C71	CATATGTACCCCGGTTTAGTATCATATGTAACAATTTCATTTACCAGTGCTCCTACG
H1-C8 α	H1-C8	AAATGCTTTAAACATAAGCAGATAGCCGCGACATTCAACCGAACCAGTGCTCCTACG
H1-C80 α	H1-C80	TTTTAACCAATAGGTTTCAAATATATTTAGCGATAGCTTAGAACCAGTGCTCCTACG
H4-C10 α	H4-C10	ACCCTCAGAACCGCGTAAATATTGACGGATCTTACCGAAGCCACCAGTGCTCCTACG
H4-C19 α	H4-C19	CTCAAGAGAAGGATCAATGAAACCATCGGGGAGAATTAACTGACCAGTGCTCCTACG
H4-C28 α	H4-C28	GTACTGGTAATAAGTTTCATAATCAAAATTACAAAATAAACAACCAGTGCTCCTACG

H4-C37 α	H4-C37	CAGGTCAGACGATTCGCCGCCAGCATTGACCTCCCGACTTGCACCAGTGCTCCTACG
H4-C46 α	H4-C46	CAGTTGGCAAATCACCAGAAGGAGCGGACGCACTCATCGAGAACCAGTGCTCCTACG
H4-C55 α	H4-C55	CAGAGGTGAGGCGGTTTGCACGTAAAACTATCAACAATAGATACCAGTGCTCCTACG
H4-C64 α	H4-C64	CTGAAAGCGTAAGACAAGTTACAAAATCGTAATTTAGGCAGAACCAGTGCTCCTACG
H4-C73 α	H4-C73	TCATGGAAATACCTAATGGAAACAGTACCGGAATCATAATTAACCAGTGCTCCTACG
H4-C82 α	H4-C82	CCGTTGTAGCAATAAGAGTCAATAGTGATCGCAAGACAAAGAACCAGTGCTCCTACG
H1-C20 β	H1-C20	GGAAGCAAACTCCAGAAGCGCATTAGACATAGCAGCACCGTATCTCTACCGCCTACG
H1-C29 β	H1-C29	ATATGCAACTAAAGGCCTAATTTGCCAGTCACCGGAACCAGATCTCTACCGCCTACG
H1-C38 β	H1-C38	TATATTTTCATTTGAGGCGTTTTAGCGAACAGGAGTTAGACTTCTCTACCGCCTACG
H1-C56 β	H1-C56	GTAATGTGTAGGTAAGAACGCGCCTGTTAGAAATAAAGAAATTCTCTACCGCCTACG
H1-C65 β	H1-C65	TACAAAGGCTATCAAACAACGCCAACATGCGCAGAGGCGAATTCTCTACCGCCTACG
H1-C74 β	H1-C74	GAAGATTGTATAAGATAAGAATAAACACATAAATCAATATATTCTCTACCGCCTACG
H1-C11 β	H1-C11	AAAAATCAGGTCTTAAATAGCAATAGCTAAATTATTCATTAATCTCTACCGCCTACG
H1-C47 β	H1-C47	GCATAAAGCTAAATATTAAACCAAGTACATTATCATCATATTTCTCTACCGCCTACG
H1-C83 β	H1-C83	CCTTCCTGTAGCCATGATGCAAATCCAAATTTATCAAAATCATCTCTACCGCCTACG
H4-C85 β	H4-C85	TGAGGCCACCGAGTTACCTTTTTAACCTGTTGGGTTATATAATCTCTACCGCCTACG
H4-C16 Bio	H4-C16	AGGCGGATAAGTGCCACCAGTAGCACCATGAGCGCTAATATC**TTTTTTTTTT/3Bio/**
H4-C34 Bio	H4-C34	CTCATTAAAGCCAGAGCCACCACCCTCATAGTTGCTATTTTG**TTTTTTTTTT/3Bio/**
H4-C52 Bio	H4-C52	CACGCTGAGAGCCATTCTGAATAATGGAATCCTAATTTACGA**TTTTTTTTTT/3Bio/**
H4-C70 Bio	H4-C70	GATTATTTACATTGAAATTAATTACATTCGTTATACAAATTC**TTTTTTTTTT/3Bio/**
B_H2-C5	H2-C5	**CATAACGCCAAAAGTTGCTAAACAACTTCCAATAGGAACCCACAATACTGCGGAAT**
B_H2-C14	H2-C14	**TATACCAGTCAGGAGTATCGGTTTATCAATATAAGTATAGCCGCGGATTGCATCAA**
B_H2-C23	H2-C23	**TCATTCAGTGAATAGAGTTAAAGGCCGCTGCCTATTTCGGAATTGCTCCTTTTGAT**
B_H2-C32	H2-C32	**TGACCAACTTTGAAGGGTAAAATACGTATCTCTGAATTTACCAACAGTTGATTCCC**
B_H2-C41	H2-C41	**TTTGCGTATTGGGCTCTTTTCACCAGTGTAATAGATTAGAGCTCTACTAATAGTAG**
B_H2-C50	H2-C50	**AGCCTGGGGTGCCTATCGGCAAAATCCCATCTAAAGCATCACTAATACTTTTGCGG**
B_H2-C59	H2-C59	**GTCGACTCTAGAGGCAGGGCGATGGCCCTAGCCCTAAAACATGACAGTCAAATCAC**
B_H2-C68	H2-C68	**TCTTCGCTATTACGAACGTGGCGAGAAACACACGACCAGTAAAAGAGAATCGATGA**
B_H2-C77	H2-C77	**GTATCGGCCTCAGGTATGGTTGCTTTGACTTGCTGGTAATATTTTGTTAAAATTCG**
B_H5-C4	H4-C4	TTTTGTCACAATCAGGAATACCCAAAAG
B_H5-C13 β	H4-C13	CGTCACCGACTTGAAGCCCAATAATAAGTCTCTACCGCCTACG
B_H5-C22 β	H4-C22	AATCAAGTTTGCCTTTTACAGAGAGAATTCTCTACCGCCTACG
B_H5-C31 β	H4-C31	CGCCTCCCTCAGAGTACCAACGCTAACGTCTCTACCGCCTACG
B_H5-C40 β	H4-C40	ACAACTCGTATTAAAAGGCTTATCCGGTTCTCTACCGCCTACG
B_H5-C49 β	H4-C49	GATGGCAATTCATCGTCTTTCCTTATCATCTCTACCGCCTACG
B_H5-C58 β	H4-C58	GGTTTAACGTCAGAGACAATAAACAACATCTCTACCGCCTACG
B_H5-C67 β	H4-C67	ACCTGAGCAAAAGATAGGGCTTAATTGATCTCTACCGCCTACG
B_H5-C76 β	H4-C76	TTGCTTCTGTAAATACCGACCGTGTGATTCTCTACCGCCTACG

S2 – AFM HEIGHT IMAGES OF FIGURE 3

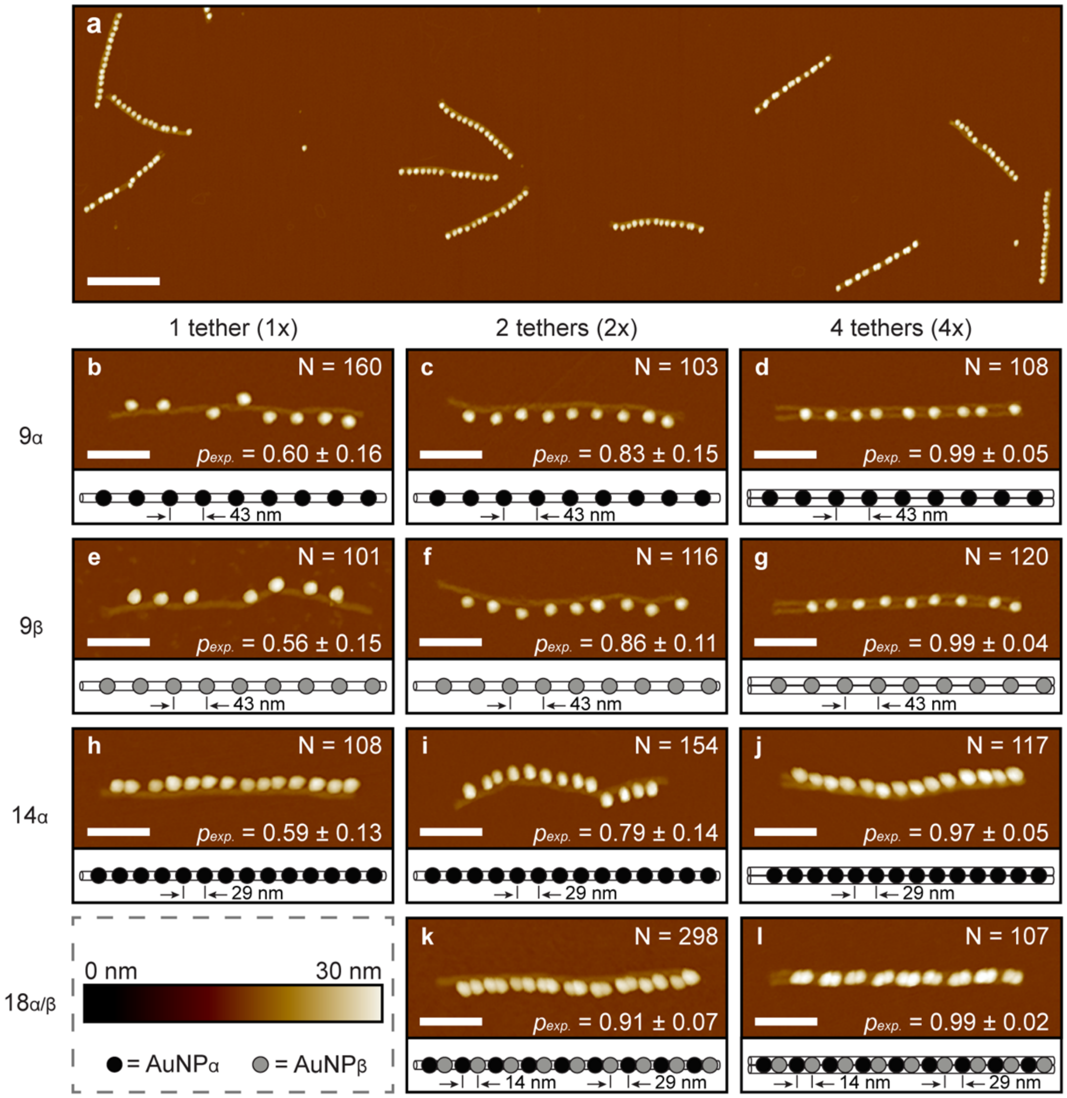

Figure S2: AFM height images of DNA nanostructures functionalized with gold nanoparticles (AuNPs). The scale bars are 300 nm for (a) and 100 nm for (b - l). (a) Low-resolution AFM height image of $4x14_{\alpha}$ nanostructures. (b-l) High-resolution AFM height images of DNA nanostructures with corresponding nanoparticle schematics. DNA nanostructure designs included: (b) $1x9_{\alpha}$, (c) $2x9_{\alpha}$, (d) $4x9_{\alpha}$, (e) $1x9_{\beta}$, (f) $2x9_{\beta}$, (g) $4x9_{\beta}$, (h) $1x14_{\alpha}$, (i) $2x14_{\alpha}$, (j) $4x14_{\alpha}$, (k) $2x18_{\alpha/\beta}$, and (l) $4x18_{\alpha/\beta}$. The columns from left to right represent increasing numbers of tethers per binding site including one tether (1x), two tethers (2x), and four tethers (4x). The rows from top to bottom represent increasing numbers of binding sites including 9 sites, 14 sites, and 18 sites for α (5'-ACCAGTGCTCCTACG-3') and/or β (5'-TCTCTACCGCCTACG-3') tethers. N is the total number of nanostructures counted to determine the average probability of AuNP site-occupation, p_{exp}. The designed diameter and length of the 1x and 2x nanostructures was 6 nm and 412 nm, respectively. The designed width, height, and length of the cross-linked, 4x nanostructure were 12 nm, 6 nm, and 412 nm, respectively.

S2 – AFM HEIGHT IMAGES OF FIGURE 7

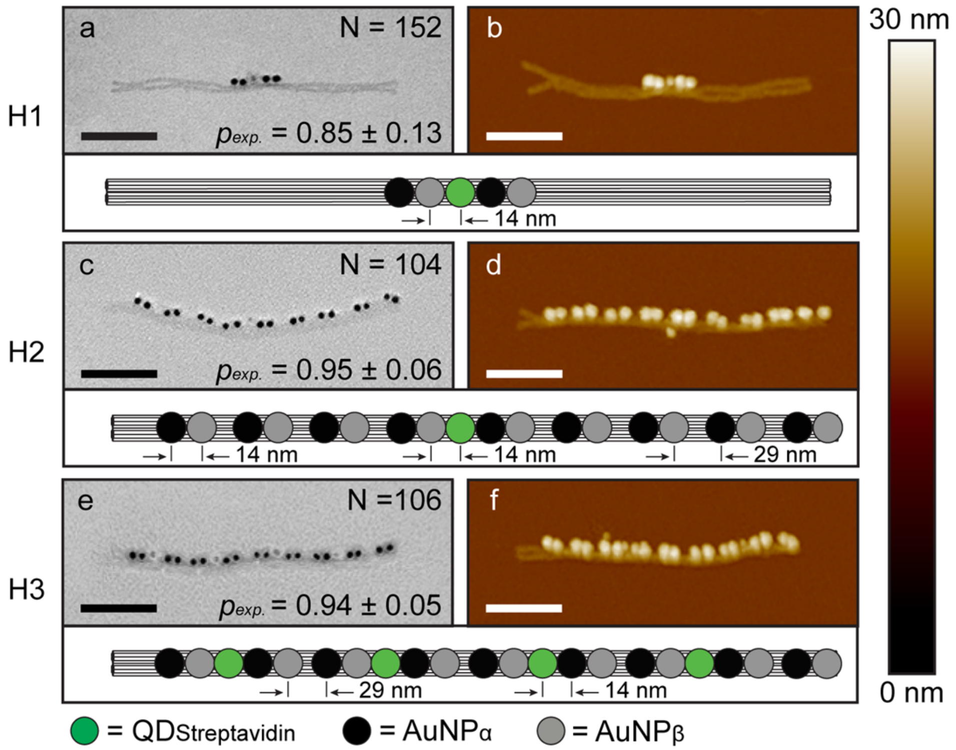

Figure S3: TEM (a, c, e) and AFM (b, d, f) height images of H1, H2, and H3 heterostructures, including schematics for each design. The images show successful site-specific attachment of AuNPs and QDs. The number of samples evaluated, N, and the experimentally measured average probability of overall site-occupation, p_{exp}, are shown in the upper and lower right-hand corners for the TEM images, respectively. The EDS analysis of the QD and the AuNP for H1, shown in Support Information S3, confirmed that the nanoparticle attached in the middle of H1 is a QD and the two nanoparticles on either side of the QD are AuNPs. Based on the QD and AuNP mass contrast difference in TEM, successful synthesis of H2 and H3 is also implied. The scale bars are 100 nm.

S3 – EDS LINE-SCAN OF H1

Due to the small interparticle distance, an extremely small probe size was required for EDS analysis. A TEM with a field emission gun (Tecnai TF30-FEG STwin STEM) was utilized at the Center for Advanced Energy Studies (CAES) in Idaho. Images of the sample were taken in scanning transmission electron microscopy (STEM) mode at 300 kV and the EDS line-scan across the AuNPs and the QDs were performed (Figure S4). The EDS spectra of AuNPs and QDs clearly showed the elemental difference between two nanoparticles. Although the QDs consisted of CdSe cores and ZnS shells, the EDS spectrum only showed the distinct sulfur peak. The peaks of the other elements did not appear in the spectrum because of the low concentration of the elements. In addition, some of their peaks overlapped with the background signals. An EDS line-scan of H1 with a missing QD was also performed for comparison. The EDS spectrum of the empty QD site showed only the background signal, which confirms that the sulfur peak was generated by the QD. In addition, uranium was detected because of the staining.

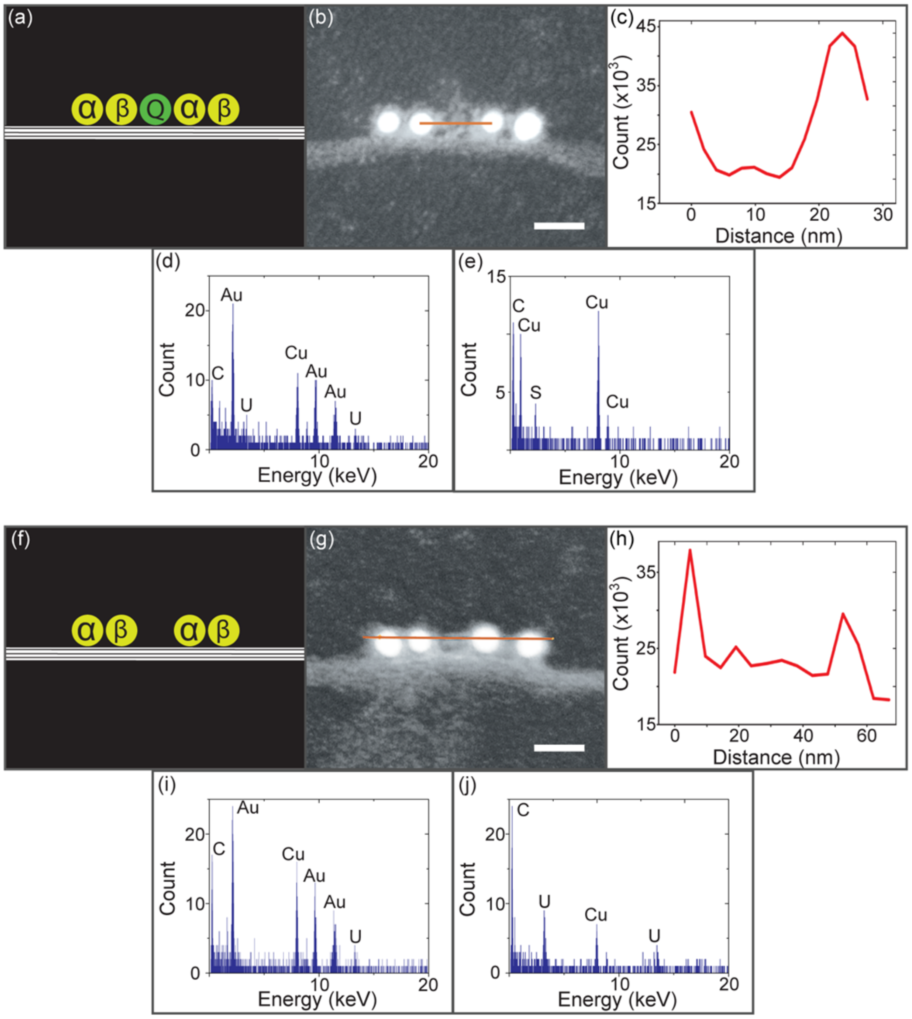

Figure S4 (a) A schematic of H1 with complete nanoparticle attachment, (b) STEM image of the H1 nanostructure with complete nanoparticle attachment, (c) counts vs. distance plot along the EDS line scan shown as orange line in (b), (d) EDS spectrum of the AuNP attached to the nanostructure, (e) EDS spectrum of QD attached to the nanostructure, (f) schematic of H1 nanostructure with a missing QD, (g) STEM image of the H1 nanostructure with a missing QD, (h) counts vs. distance plot along the EDS line scan shown as orange line in (g), (i) EDS spectrum of the AuNP attached to the nanostructure, (j) EDS spectrum at the empty QD binding site. The EDS spectrums of the nanoparticles, (d), (e), and (i), clearly show that they are indeed AuNP and QD. Although the QD consists of CdSe core and ZnS shell, the spectrum only shows the distinct sulfur peak because of the low concentration of the other elements. Also, some of their peaks overlap with the background signal. The EDS spectrum of the empty QD binding site did not show the sulfur peak seen in (e), which confirms that the sulfur peak came from the attached QD. In addition, uranium peaks were observed because of the staining of the sample. The scale bars are 20 nm.

S4 – ADDITIONAL AFM IMAGES OF THE H2 NANOSTRUCTURE

Several AFM images of the H2 heterostructure were acquired using a Bruker MultiMode 8 with a Nanoscope V controller. High-resolution AFM images clearly show QD attachment between the fourth and the fifth AuNP pairs, which agree with the H2 heterostructure design (Figure S5). The QDs for select heterostructures were offset toward either side of the nanostructure axis because of steric hindrance between the QD and neighboring AuNPs. Because there were 10-thymine spacers on the biotin tethers, the QDs were anticipated to have a high degree of freedom after attaching to the nanostructure.

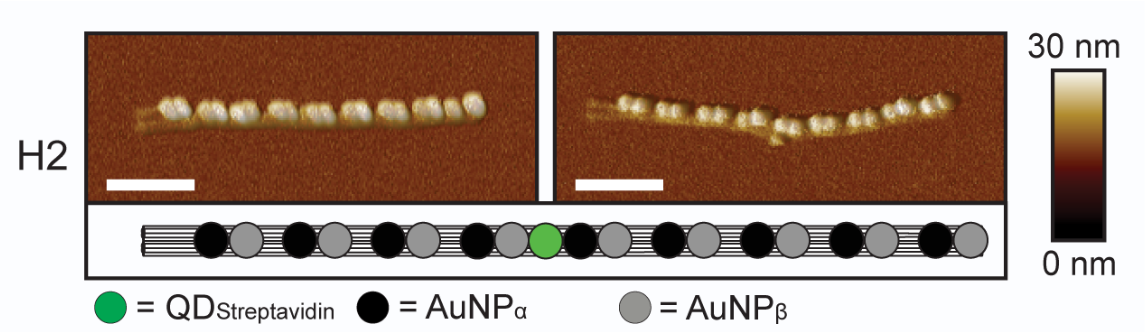

Figure S5: High-resolution AFM images and the schematic of the H2 heterostructure. Both images clearly show QD placement between the fourth and the fifth AuNP pairs, which is consistent with the heterostructure design shown as the schematic. The size of the scale bars is 100 nm.

S5 – DNA NANOSTRUCTURE SYNTHESIS

1X & 2X NANOSTRUCTURES: The 1x and 2x nanostructures were synthesized by mixing 10 nM of DNA from the M13mp18 bacteriophage (New England Biolabs) with 100 µM of staple strands (IDT) in a 1:10 molar ratio. 10x TAE (40 mM tris, 20 mM acetic acid, 2 mM ethylenediaminetetraacetic acid (EDTA); pH 8.0), and 1 M $MgCl_2$ were added to the mixture to bring the final buffer concentration to 1x TAE, 14mM $MgCl_2$. The solution was heated at 90 ˚C for 20 min and then cooled to 20 ˚C at 0.6 ˚C/min via a thermocycler (Eppendorf Mastercycler Nexus Gradient). DNA nanotubes were purified using gel electrophoresis (0.7% agarose gel, 40 V, 35 mA, 180 min). The buffer used for casting and running gels was 0.5x TBE, 12 mM $MgCl_2$ (89 mM tris-borate, 2 mM EDTA, and 12 mM $MgCl_2$; pH 8.3). Gels were stained with 1x SYBR Gold (Life Technologies) / 0.5x TBE, 12 mM $MgCl_2$ solution for 30 min and then placed on a UV light table (Hoefer MACROVUE UVIS-20) to extract bands using a razor blade. Bands were cut into sub millimeter pieces and then loaded into Freeze N' Squeeze microcentrifuge filters (Bio-Rad). Filters were spun at 4800 rcf at 4 ˚C for 10 min using a centrifuge (Eppendorf 5430R).

4X NANOSTRUCTURES: 4x nanostructures were cross-linked in a parallel orientation by hybridizing two 2x nanostructures. Individual 2x nanostructures were synthesized and purified using the procedure described above and mixed in an equal molar volume. 0.5x TBE 200 mM $MgCl_2$ buffer was added to the solution to increase the magnesium ion concentration to 40 mM. The mixture was heated to 45 ˚C for 2 hrs and then cooled to 20 ˚C at 0.6 ˚C/min. The yield was approximately 83%, and no purification was required.

S6 – AuNP and DNA Nanostructure Functionalization

AUNP FUNCTIONALIZATION: A colloidal solution of 10 nm gold (Ted Pella) was mixed with bis(*p* sulfonatophenyl)phenylphosphine dihydrate dispotassium salt (BSPP) from Sigma Aldrich in 1:748,000 molar ratio. The solution was wrapped with tin foil and shaken for 48 hours to saturate the surface with BSPP. A 5 M NaCl solution was titrated into the colloidal mixture, in 0.2 mL increments, until the gold colloids began to precipitate out of the solution. The mixture was then centrifuged at 3200 rcf for 30 min to acquire a gold colloidal pellet at the bottom of the container. The transparent supernatant was discarded. 400 µL of 2.5 mM BSPP and 400 µL of methanol were added to the gold colloidal pellet. The mixture was spun at 1,600 rcf for 30 min, and the supernatant was discarded. Then 200 µL of 2.5 mM BSPP was added to the remaining solution. The concentration of the gold colloidal solution was calculated using Beer-Lambert law based on the absorbance measured at 490 nm via Eppendorf BioPhotometer Plus.

Tris(2-carboxyethyl) phosphine hydrochloride (TCEP) from Sigma Aldrich was then mixed with thiolated single stranded DNA (T-ssDNA) in a 99:1 ratio in a 0.5x TBE buffer solution. The mixture was agitated for 30 min. Both the concentrated gold colloidal solution and the T-ssDNA solution were mixed in 1:300 molar ratio (later this ratio was cut down to 1:150 molar ratio). The mixture was agitated for 3 days at room temperature. The excess T-ssDNA in the mixture was removed using 100 kDal Amicon Ultra microcentrifuge filter (Millipore). 100 µL of AuNP solution and 400 µL of 0.5x TBE buffer were mixed in the filter, and it was spun at 13,000 rcf for 6 min. After the initial spin, 480 µL of 0.5x TBE buffer were added to the filter, and it was re-spun at 13,000 rcf for 6 min for rinsing. After repeating two additional rinsing processes, the functionalized AuNP solution was transferred into a new filter using a pipette. Four additional rinsing steps were done to assure excess oligos were removed from the solution. Inverting the Amicon filter and then spinning it at 1,000 rcf for 3 min recovered the AuNPs. The absorbance of the AuNP solution was then measured at 521 nm via an Agilent Cary 5000 UV-Vis-NIR to calculate the concentration.

1X & 2X DNA NANOSTRUCTURE FUNCTIONALIZATION: The functionalized AuNPs and the 1x and 2x nanostructures were mixed in a 1:5 binding site to AuNP ratio. The mixture was heated at 45 ˚C for 41 min then cooled to 20 ˚C at 0.6 ˚C/min. The functionalized 1x and 2x nanostructures were then purified by agarose gel electrophoresis (0.7% Agarose Gel, 40 V, 35 mA, and 180 min). The buffer used for casting and running the gels was 0.5x TBE, 12 mM $MgCl_2$. The band of interest was extracted visually using a razor blade. The extracted bands were chopped into sub millimeter sized pieces. The pieces were then loaded in a Freeze N' Squeeze microcentrifuge filter and spun at 4800 rcf at 4 ˚C for 10 min for recovery.

4X DNA NANOSTRUCTURE FUNCTIONALIZATION: The $MgCl_2$ concentration of the 4x nanostructure solution was adjusted to 12 mM by adding 0.5x TBE buffer prior to mixing the AuNPs. This prevents the AuNPs from precipitating out of the solution prematurely. The AuNPs and 4x nanostructures were then mixed in a 1:5 binding site to AuNP ratio. The mixture was heated to 45 ˚C for 41 min then cooled to 20 ˚C at 0.6 ˚C/min.

The functionalized 4x nanostructures were purified using agarose gel electrophoresis (1.4% Agarose Gel, 70 V, 66 mA, and 180 min). The buffer used for casting and running the gel was 0.5x TBE, 12 mM $MgCl_2$. The bands were extracted visually using a razor blade. The extracted bands were then chopped in sub-millimeter pieces that were loaded into Freeze N' Squeeze microcentrifuge filter and spun at 4800 rcf at 4 ˚C for 10 min for recovery.

S7 – HETEROSTRUCTURE FUNCTIONALIZATION

The magnesium concentration of the heterostructure solution was adjusted to 12 mM by adding 0.5x TBE buffer before mixing it with the AuNPs and QDs. The nanoparticles and heterostructures were mixed in a 1:5 binding site to nanoparticle ratio. The mixture was heated to 45 ˚C for 41 min then cooled to 20 ˚C at 0.6 ˚C/min for AuNP and QD attachment.

The functionalized heterostructures were then purified using agarose gel electrophoresis (0.7% Agarose Gel, 60 V, 65 mA, and 90 min). The buffer used for casting and running the gels was 0.5x TBE 12 mM $MgCl_2$. The bands were extracted visually using a razor blade. Extracted bands were chopped into sub-millimeter pieces which were loaded into a Freeze N' Squeeze microcentrifuge filter and spun at 4800 rcf at 4 ˚C for 10 min for recovery.

S8 – AFM AND TEM SPECIMEN PREPARATION

AFM SPECIMEN PREPARATION: Substrates for AFM were prepared by adhering a sheet of mica (V4 grade, SPI Supplies) onto an AFM puck (TED PELLA) using superglue. Five micro-liters of the sample solution was deposited onto the mica substrate and incubated for 2 min. Then 20 µL of 1x TAE, 12 mM nickel-acetate was dispensed onto the mica surface for 5 min. The mica surface was rinsed with 1 mL of NANOpure water (Thermo Scientific) three times and dried with high purity nitrogen gas.

TEM SPECIMEN PREPARATION: TEM grids with ultrathin carbon films (TED PELLA) were plasma treated using an in-house glow discharge unit for 5 sec to induce hydrophilicity of the carbon surface. Three micro-liters of the sample solution was dispensed onto the grid for 5 min and then the excess solution was extracted using a piece of filter paper. Ten micro-litters of 2% uranyl acetate staining solution was dispensed onto the grids and removed immediately to pre-wet the surface, and another 10 µL of the staining solution was deposited for 12 sec to stain the samples. The 2% uranyl acetate staining solution was prepared by mixing 15 mg of uranyl acetate dihydrate (bis(aceto-O)dioxouranium) (SPI Supplies) with 1.1 mL of 95 ˚C NANOpure water. The solution was agitated until all of the uranyl acetate was dissolved, and roughly 1.1 mL of 5 M NaOH solution was added to the uranyl acetate solution.

S9 – NANOPARTICLE ATTACHMENT COUNTING

The nanoparticle attachment counting for the AuNP arrays, except for $2x14_{\alpha}$ were done based on the AFM images, and the nanoparticle counting for $2x14_{\alpha}$ and the three heterostructures were done based on the TEM images. AFM images were acquired using a Bruker MultiMode 8 with a Nanoscope V controller. Nanoscope Analysis software from Bruker was utilized to flatten the images, as well as change the color settings and the height scale to enhance the contrast between the nanostructures and their background. A visual grid was placed on top of the images using Adobe Illustrator to prevent counting the same nanostructure multiple times. Images with the grid were opened in Adobe Reader and the number of AuNPs attached to individual nanostructures was manually counted. For statistical purposes, more than 100 nanostructures were analyzed for each design. The histograms for each design shown in Figure 4 are numerically expressed in Table S3. The analysis was performed objectively by rejecting nanostructures that satisfy any of the following criterion:

- A nanostructure partially overlapping with another nanostructure(s)
- A malformed nanostructure
- A nanostructure with indistinguishable AuNP(s) under AFM analysis
- A nanostructure sharing AuNP(s) with other nanostructure(s)
- A nanostructure extended beyond the image boundary
- A nanostructure with binding sites(s) that have more attached AuNP(s) than available tether(s)

In addition to the criteria above, the criterion below was added to reject inappropriate nanostructures when calculating the average probability of AuNP site-occupation, p_{exp}.

- A nanostructure having more AuNP(s) attached than available binding site(s) on the nanostructure

Below is a representative AFM image for the $4x14_{\alpha}$ design (Figure S6). The nanostructures pointed to with a red arrow were rejected, the nanostructure pointed to with a blue arrow was included in the histogram, shown in Figure 4, but was rejected for calculating the average probability of AuNP site-occupation, p_{exp}, and the nanostructures pointed to with a green arrow were valid for analysis.

Hundreds of TEM micrographs of $2x14_{\alpha}$ and the three heterostructures were acquired using a JEOL JEM-2100 HR analytical transmission electron microscope with the beam voltage of 120 kV. Instead of taking large low-magnification images containing many nanostructures, high-magnification images of individual nanostructures were taken to carefully inspect individual nanostructures for counting. In addition to the nanostructures satisfying the above criterion for the counting using AFM, the structures with insufficient staining were eliminated from counting for maintaining the quality of the analysis.

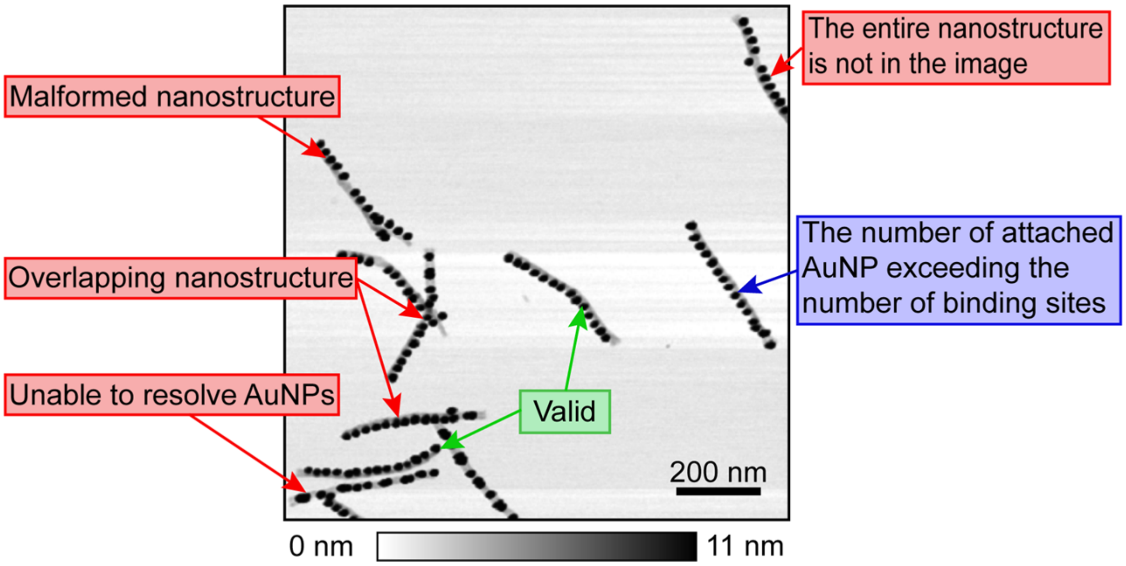

Figure S6: Representative AFM image for the 4x14$_\alpha$ design. The nanostructures pointed to with a red arrow were rejected, the nanostructure pointed to with a blue arrow was included in the histogram, shown in Figure 4, but was rejected for calculating the average probability of AuNP site-occupation, p_{exp}, and the nanostructures pointed to with a green arrow were valid for both analyses.

Table S3: Numerical Values of the Histogram Shown in Figure 4

Design		**1x9$_{\alpha}$**	**1x 9$_{\beta}$**	**2x 9$_{\alpha}$**	**2x 9$_{\beta}$**	**4x 9$_{\alpha}$**	**4x 9$_{\beta}$**	**1x 14$_{\alpha}$**	**2x 14$_{\alpha}$**	**4x 14$_{\alpha}$**	**2x 18$_{\alpha/\beta}$**	**4x 18$_{\alpha/\beta}$**
Number of Structures (N)		160	101	104	116	137	134	108	154	133	306	121
Number of Attached AuNPs	**0**	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00
	2	0.01	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	3	0.07	0.07	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	4	0.17	0.24	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	5	0.31	0.25	0.06	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.00
	6	0.23	0.28	0.13	0.10	0.01	0.01	0.17	0.01	0.00	0.00	0.00
	7	0.13	0.10	0.23	0.21	0.00	0.00	0.18	0.03	0.00	0.00	0.00
	8	0.07	0.02	0.32	0.41	0.08	0.04	0.19	0.02	0.00	0.00	0.00
	9	0.01	0.01	0.23	0.25	0.70	0.85	0.19	0.12	0.00	0.00	0.00
	10		0.00	0.01	0.00	0.20	0.10	0.09	0.17	0.00	0.00	0.00
	11		0.00	0.00	0.00	0.01	0.00	0.11	0.19	0.02	0.00	0.00
	12							0.03	0.26	0.05	0.00	0.00
	13							0.01	0.11	0.27	0.02	0.00
	14							0.00	0.08	0.54	0.04	0.00
	15									0.11	0.14	0.00
	16									0.02	0.28	0.01
	17										0.31	0.18
	18										0.17	0.69
	19										0.03	0.11
	20											0.01

S10 – NEAREST NEIGHBOR AUNP SEPARATION MEASUREMENT

The nearest neighbor AuNP separation distance was measured via AFM images acquired for the AuNP attachment counting in S4. Images were acquired using a Bruker MultiMode 8 with a Nanoscope V controller. All measurements were done using Windows Scanning X Microscope (WSxM™) from Nanotec.[1] The zoomed-in images of individual nanostructures were acquired with a multiple dynamic zoom tool. Profile lines were carefully drawn along the axis of the nanostructure using the profile tool. The process also generated the height profile window. The profile line was slid on top of the AuNP array to acquire the height profile of the AuNP array (Figure S7a). In the height profile window, the nearest neighbor AuNP separation was measured by moving the sliders to the center of the two adjacent AuNPs (Figure S7b). The center position of the AuNPs were determined based on the AFM image.

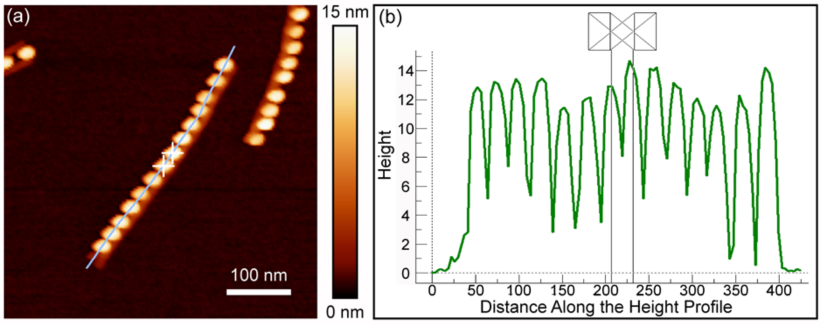

Figure S7: (a) AFM micrograph of 4x14$_{\alpha}$ design with a profile line along the axis of the nanostructure. (b) Height profile along the profile line. Both the micrograph and the height profile were generated using WSxM. The peaks of the height profile often did not match with the exact center of the AuNP.

The 4x nanostructures laid on the mica substrate in two orientations: upright and sideways. The upright orientation refers to AuNPs on top of the nanostructure, whereas the sideways orientation refers to AuNPs on the side of the nanostructure (Figure S8). The ratio of the upright oriented nanostructures decreased between 9-site and 14-site designs even though it increased between the 14-site and 18-site designs; 85%, 48%, and 52% for 4x9$_{\alpha}$, 4x14$_{\alpha}$, and 4x18$_{\alpha/\beta}$, respectively. For the 4x9$_{\alpha}$ design, there was not a noticeable deviation in the AuNP separation between the two orientations; however, a large deviation was observed for the 4x14$_{\alpha}$. When the nanostructures adsorbed onto the mica surface in the upright orientation, the AuNPs formed dimers. Dimer formation is attributed to the capillary force during drying. In comparison, sideways oriented AuNPs on the 4x14$_{\alpha}$ design were equally distributed. Unlike the upright oriented samples, the AuNPs on the sideways oriented nanostructures were in contact with the mica. The charge attraction and secondary forces between the AuNPs and the mica surface likely overcame the capillary force between the water and the AuNPs. As a consequence, AuNP separation measurements were taken from sideways oriented nanostructures for the 4x14$_\alpha$ design.

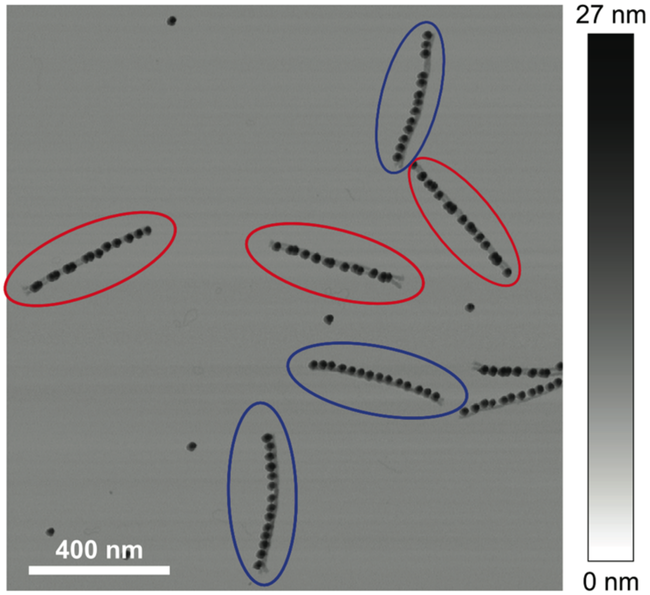

Figure S8: AFM micrograph of a 4x14$_\alpha$ design showing that the nanostructures lie on a mica surface in two orientations: upright and sideways. The upright oriented nanostructures are highlighted in red ovals and the sideways oriented nanostructures are highlighted in blue ovals. While the AuNPs attached on sideways oriented nanostructures had equal AuNP separation, the AuNPs attached to the upright oriented nanostructures formed dimers. Dimer formation was anticipated to be caused by capillary action when drying the sample.

S11 – TRINOMIAL DISTRIBUTION EQUATION

The distribution of nanoparticles on arrays having events where more than one nanoparticle binds to one site may be analyzed using a trinomial distribution. If the probability of binding two or more nanoparticles per site is low, then a good approximation is acquired by assuming that no more than two nanoparticles bind per site. Analogous to the binomial distribution, a trinomial distribution, *P(m)*, for the probability that *m* nanoparticles bind to an array with *n* binding sites can be written in terms of *Prob(0* Bound*)*, *Prob(1* Bound*)*, and *Prob(2* Bound*)* – the site-binding probabilities for zero, one, or two nanoparticles, respectively. All possible ways to attach *m* particles to *n* sites are summed over the possible numbers of double-occupancy sites, indexed by *j*, where for a given *j*, the variables u_j, v_j, and w_j are the number of zero-, single-, and double-occupancy sites respectively, yielding the trinomial distribution:

$$P_{tri}(m) = \sum_{j = \max(0, m-n)}^{\lfloor m/2 \rfloor} \frac{n!}{u_j! v_j! w_j!} Prob(0\ Bound)^{u_j} Prob(1\ Bound)^{v_j} Prob(2\ Bound)^{w_j} \tag{S5}$$

The trinomial distribution may be reduced to a single unknown parameter by conditioning the probability that one or two particles are bound on the probability that a site is occupied, *Prob(*Occupied*)* = p_{fit}, a value which is estimated by fitting to the data. The unknown conditional probability, *Prob(*1 Bound|Occupied*)* = *c*, is a parameter that can also be estimated by fitting to the data. Combining the law of total probability and the assumption that a maximum of two particles bind per site yields the following:

$$Prob(0\ Bound) = 1 - p_{fit} \tag{S6}$$

$$Prob(1\ Bound) = Prob(1\ Bound \mid Occupied) Prob(Occupied) = c p_{fit} \tag{S7}$$

$$Prob(2\ Bound) = Prob(2\ Bound \mid Occupied) Prob(Occupied) = (1 - c) p_{fit} \tag{S8}$$

Substituting the above equations for the site-binding probabilities and writing u_j,v_j, and w_j in terms of *j*, *n*, and *t* yields the following form of the trinomial distribution:

$$P_{tri}(m) = \sum_{j = \max(0, m-n)}^{\lfloor m/2 \rfloor} \frac{n!}{(n - m + j)!(m - 2j)!j!} (1 - p_{fit})^{(n - m + j)} (c p_{fit})^{(m - 2j)} \{(1 - c) p_{fit}\}^{j} \tag{S9}$$

The data was fit to this equation to estimate the parameter *c*, yielding an estimate of how often single occupancy of binding sites can be expected and p_{fit}, the fitted average probability of site-occupation. To validate the fit parameters *c* and p_{fit}, we compared the expected value of the average site-occupancy based on these parameters, y_{th}:

$$y_{th} = 1 \cdot c \cdot p_{fit} + 2 \cdot (1 - c) p_{fit} \tag{S10}$$

to the measured value of average site-occupancy over all nanostructures, y_{exp}, including those with more nanoparticles than binding sites (Table S4).

Table S4: Comparison of calculated and observed average site-occupancy

	2x9$_{\alpha}$	**2x 9$_{\beta}$**	**4x 9$_{\alpha}$**	**4x 9$_{\beta}$**	**2x 14$_{\alpha}$**	**4x 14$_{\alpha}$**	**2x 18$_{\alpha/\beta}$**	**4x 18$_{\alpha/\beta}$**
p_{fit}	0.83	0.87	0.99	1.00	0.77	0.96	0.91	0.99
c	0.98	1.00	0.97	0.99	0.96	0.99	0.99	0.99
y_{th}	0.85	0.86	1.02	1.01	0.80	0.98	0.91	0.99
y_{exp}	0.83	0.86	1.01	1.01	0.79	0.98	0.91	1.00

S12 – EXPERIMENTAL BINDING SITE PERIODICITY DETERMINATION

Assuming that the difference between the experimental and the theoretical binding site periodicity is equal to the difference between the experimental and the theoretical nanostructure length, the experimental binding site periodicity was calculated by:

$$d_{\mathrm{exp}} = \left(\frac{l_{\mathrm{exp}}}{l_{\mathrm{th}}} \right) \times d_{\mathrm{th}} \qquad \text{(S1)}$$

where d_{exp} is the experimental binding site periodicity, d_{th} is the theoretical binding site periodicity, l_{exp} is the experimental nanostructure length, and l_{th} is the theoretical nanostructure length. The theoretical binding site periodicity and the nanostructure length were calculated by multiplying the number of base-pairs with the unit length of the base-pair (0.34 nm). The experimental nanostructure length was determined by measuring the end-to-end nanostructure length under AFM using WSxM. The zoomed-in images of individual nanostructures were then acquired via a multiple dynamic zoom tool. The profile line was carefully drawn along the axis of the nanostructure using the profile tool (Figure S9a). In the height profile window, the nanostructure length was then measured by moving the sliders to the ends of the nanostructure (Figure S9b). To account for the width of the probe, the ends of the nanostructure were estimated at the mid points of the slopes at the ends of the nanostructure. Twenty experimental nanostructure lengths were acquired from each design.

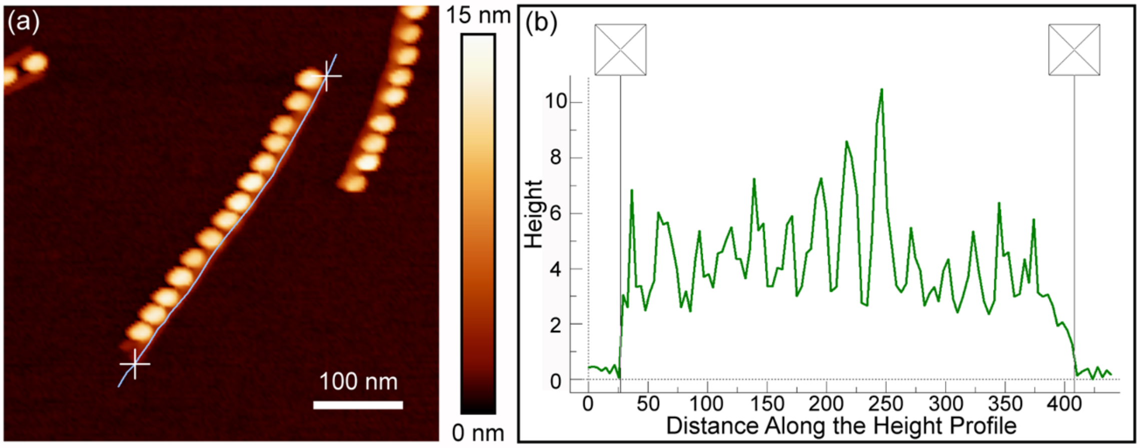

Figure S9: (a) AFM image of 4x14$_{\alpha}$ with a height profile line. (b) Height profile of the nanostructure. To account for the width of the AFM probe, the ends of the nanostructure were estimated to be at the midpoints of the slopes at the ends of the nanostructure.

S13 – MODIFIED GEOMETRIC DISTRIBUTION EQUATION

In a previous study, steric hinderance and site-bridging were examined by comparing the nearest neighbor QD separation histogram with the geometric distribution plot.[2] In the absence of steric hinderance or site-bridging, the histogram expected to follow a geometric distribution, *P(k)*, given by:

$$P(k) = p_{exp}\left(1 - p_{exp}\right)^{(k-1)} \tag{S2}$$

where p_{exp} is the average probability of AuNP site-occupation, and k is the integer number of periods between nearest neighbors. The standard deviation of the AuNP separation was determined by decreasing the bin size of the histogram from 1 to 0.25. When considering a separation between two adjacent AuNPs, the separation, x, should follow the normal distribution because of the random motion of the AuNPs. The normal distribution, *f(x)*, is given by:

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} exp\left[-\frac{(x-\mu)^2}{2\sigma^2}\right] \tag{S3}$$

where μ is the mean nearest neighbor separation and σ is the standard deviation of the separation. Therefore, with a smaller bin size, the resulting nearest neighbor separation histogram is expected to follow the distribution that combined both the geometric and normal distributions. In this paper, this is referred to as a "modified geometric distribution", *P(x)*, and is given by:

$$P_{geo}(x) = \sum_{k=1}^{\infty} \frac{1}{\sigma\sqrt{2\pi}} exp\left[-\frac{(x-k)^2}{2\sigma^2}\right] p_{exp}\left(1 - p_{exp}\right)^{(k-1)} \tag{S4}$$

The mean separation, μ, in the Eqn. 3 has become the integer number of periods between nearest neighbors, k, because the x-axis of the histogram was normalized by the experimental binding site periodicity. Likewise, the separation and standard deviations are fractional.

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2. H. Bui, C. Onodera, C. Kidwell, Y. Tan, E. Graugnard, W. Kuang, J. Lee, W. B. Knowlton, B. Yurke, and W. L. Hughes, *Nano Lett*, 2010, **10**, 3367–72.