

Supplementary Information 2

Addressable DNA nanotubes with repetitive components

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Sequences for structures from different addressable rows of U-SSTs are given in work sheets named U-SSTs-24H, -12H, -6H, etc.

Sequences for structures from different addressable rows of U2-SSTs are given in work sheets named U2-SSTs-12H, -8H, -6H, etc.

A similar denotation is adapted from the previous study¹ and applicable for all the structures. The location of a strand denotes the row and column numbers in the structure. For example, a location named x-y indicates that it is in row x and column y.

For gold nanoparticle decoration, two strands with 3' thiol modification are named U-SSTs-2H-100Column-100 and U-SSTs-2H-100Column-101 respectively in the work sheet U-SSTs-2Hx100C.

1 Wei, B. *et al.* Design Space for Complex DNA Structures. *J. Am. Chem. Soc.* **135**, 18080 (2013).

U-SSTs-24H

Seq_ID	Location	Sequence
U-SSTs-24H-1	1-1	TGGGCTCGTGATGACACCGCCGATCCGCTGGGCTTGTCACC
U-SSTs-24H-2	1-2	AGTTATGCGGGCTTAATGACAGGTCTAAACTTGCCAATTTCA
U-SSTs-24H-3	1-3	GGCCTGACCGCCCTACGTTTGGGGAGGTCATTCCTTCATCCC
U-SSTs-24H-4	1-4	TGCTCGAGGTCACCTTCTCAATTGACCACGATCGGCAGAGTC
U-SSTs-24H-5	1-5	CTGATTCTCCAAGCGAATAACCATCTGGCCAATCTAGCCAA
U-SSTs-24H-6	1-6	CGACTCTAACTACATCTCAGATAGGTAGAGAAAGGGCTCAGA
U-SSTs-24H-7	1-7	GACCCGCTCCCCAGAGTCGTTAACATGATACCATGGGGTCC
U-SSTs-24H-8	1-8	TCAAAAATTTCTATCTACAATGGATGGAGCAGCCGGCCAGCC
U-SSTs-24H-9	1-9	TCAAGCATAGACTGAAGCCCTTCTGTGCGCGCCGGTGCGCA
U-SSTs-24H-10	1-10	CATGACCAAGAAGAGCCCAGTCACACACAGTGCCCATTTACC
U-SSTs-24H-11	1-11	TGGGCGGTGCTTGTCTATGCATACGGCCCGATGGTTAGAGAT
U-SSTs-24H-12	1-12	TTTATTGCTCCTCACGACACAATTAATCGGTTTCATCGTTAA
U-SSTs-24H-13	1-13	CGCCTTGGGAAACATCAGGGATCAGTAAAAGCACAAAATCC
U-SSTs-24H-14	1-14	GGATTTGGAGTACTTCTTCAGTACGGTTTTCGCCAGTAACTA
U-SSTs-24H-15	2-1	TTTTTTTTTTTGCACATAGCATCACGAGGCCATTTTTTTTTT
U-SSTs-24H-16	2-2	TTCAAAGACCATTTTCGTGTGACCCGCATAACTGCGGTGTCAT
U-SSTs-24H-17	2-3	GCCACCACTCTGAACCTCGTATGCGGTCAGGCCTGTCATTAAG
U-SSTs-24H-18	2-4	GGACTCGTGTCAAACTCGAGGACCTCGAGCACAAACGTAGG
U-SSTs-24H-19	2-5	TAAGTCGCGTCTGACAGACACGGAGGAATCAGTTGAGAAGGT
U-SSTs-24H-20	2-6	TGATCATCGGTAACACGAACTAGTTAGAGTCGTTATTCGCTT
U-SSTs-24H-21	2-7	GTATCTAGACGTCCGCAACCAGGGAGCGGGTCTCTGAGATGT
U-SSTs-24H-22	2-8	CGGAGGTAGCGTACTATCAGAGAATTTTTGAACGACTCTGG
U-SSTs-24H-23	2-9	TCGTTCTGTGCCGCACGTTGTTCTATGCTTGACATTGTAGAT
U-SSTs-24H-24	2-10	CCGCTAATGTTGAGACTGCTCTCTTGGTCATGAGGGCTTCAG
U-SSTs-24H-25	2-11	AAAGGATGGGGATAAGCCAGAAGCACCGCCCAACTGGGCTCT
U-SSTs-24H-26	2-12	CGACCCATTCCGCGGTCCGCGGAGCAATAAATGCATAGACA
U-SSTs-24H-27	2-13	CAGGCTCCTAGGTCCGCTTCTTTCCCAAGGCGTGTGTCGTGA
U-SSTs-24H-28	2-14	TCCGAAAGTGGAATGGGTAGAACTCCAAATCCTCCCTGATGT
U-SSTs-24H-29	2-15	CATGGATATTTTTTTTTTTTTTTTTTTTTTTTTTCTGAAGAAGT
U-SSTs-24H-30	3-1	TAGGCTTCTCGACCTCAGCCTGGTCTTTGAAATGCTATGTGC
U-SSTs-24H-31	3-2	CCTTTTGGTGAAGTCTCACCTGAGTGGTGGCTCACACGAAAT
U-SSTs-24H-32	3-3	CAGTAAATTTAGGCCTAATGTACACGAGTCCATACGAGTTCA
U-SSTs-24H-33	3-4	ATGTCGCGACACAAAAGACCGACGCGACTTACTCGAGTTTTG
U-SSTs-24H-34	3-5	AGGGGTATGGCGCACTTGTGCCGATGATCAGTGTCTGTCAG
U-SSTs-24H-35	3-6	CAAAGAACTACGCCCTAAGCAGTCTAGATACAGTTCGTGTTA
U-SSTs-24H-36	3-7	AAGGATTGAAACAGCACCAAGTGCTACCTCCGTGGTTGCGGAC
U-SSTs-24H-37	3-8	CGCGGTCCGCCGCATCCAAACCACAGAACGACTGATAGTAGC
U-SSTs-24H-38	3-9	AAATATATTTTAAGTGGTAGGACATTAGCGGACAACGTGCGG
U-SSTs-24H-39	3-10	AAACCCAGGAATACTGCACACCCCATCCTTTGAGCAGTCTCA
U-SSTs-24H-40	3-11	ACCATCGCTAAGGGGATCGCCGAATGGGTGCTCTGGCTTATC
U-SSTs-24H-41	3-12	TCCATCGAAAATATCCTAATCTAGGAGCCTGGCGCGACCGCG
U-SSTs-24H-42	3-13	CGTCCCGAACAGAATACAAATCACTTTCGGAAGAAGCGGACC
U-SSTs-24H-43	3-14	CTCCCCTTCCAGTGCGCGATGAATATCCATGTCTACCCATTC
U-SSTs-24H-44	4-1	TTTTTTTTTTTGGCCGATTAGCCGAGAAGCCTATTTTTTTTTT
U-SSTs-24H-45	4-2	TCCCCTTCCACCCGACGTGCCTCACCAAAGGGAGGCTGAGGT
U-SSTs-24H-46	4-3	ACCTTGGTGAAGGCGCGGTATAAATTTACTGAGGTGAGACT

Seq_ID	Location	Sequence
U-SSTs-24H-47	4-4	CGGGAAGTACGCTGACCCCTTTTGTGCGGACATACATTAGGCC
U-SSTs-24H-48	4-5	GATAGGGCAATGAGCTGGGAACCATAACCCCTCGGTCTTTTG
U-SSTs-24H-49	4-6	ATCCTATACTTACGCCAATGAGTAGTTCTTTGCACAAGTGCG
U-SSTs-24H-50	4-7	GCTGGCAATGGGGATTGCCAATTTCAATCCTTTGCTTAGGGC
U-SSTs-24H-51	4-8	GACCTTATATAGATTAACCGGGGCGGACCGCGACTGGTGCTG
U-SSTs-24H-52	4-9	CTCATAATTTTCAAGCCCAAGAAAATATATTTGTTGGATGC
U-SSTs-24H-53	4-10	CAGGCAGTACAAATCGGGGCATTCTGGGTTTCTTACCCTT
U-SSTs-24H-54	4-11	AGAATAAATTGATATGACTCGTTAGCGATGGTGTGTGCAGTA
U-SSTs-24H-55	4-12	GTTAATGCACTGTAGATTTTTTTTTTTCGATGGAGGCGATCCCC
U-SSTs-24H-56	4-13	CGTGCAGAAATGCGCCTCCCCCTGTTTCGGGACGGATTAGGATA
U-SSTs-24H-57	4-14	GCTGGGGGTGTCAGAGGGCCCTGGAAGGGGAGATTTGTATTC
U-SSTs-24H-58	4-15	GAGTAAACTATTTTTTTTTTTTTTTTTTTTTTTCATCGCGCAC
U-SSTs-24H-59	5-1	TTATCGTTGAGGATACCTCTTTGGAAGGGGAGCTAATCGGCC
U-SSTs-24H-60	5-2	ATTCCGGCCGACCCGTACAGCCACCAAGGTGGCACGTCGGG
U-SSTs-24H-61	5-3	CAAGCCCAGCGGTAAGACAACCTAGTTCCCGTACGCCGCCTT
U-SSTs-24H-62	5-4	CCTACCCTATTTTTTAGACTATTGCCCTATCAAAGGGTCACG
U-SSTs-24H-63	5-5	TCGGCGCGGACCTCGAGTCAAGTATAGGATTTCCAGCTCA
U-SSTs-24H-64	5-6	AGAACTCTGGCCCAAACAGTACATTGCCAGCTCATTGGCGTA
U-SSTs-24H-65	5-7	TCTATCAGTCTTCCGCGATCCATATAAGGTCTTGGCAATCCC
U-SSTs-24H-66	5-8	ATAGGACAGCATCAGTCTCCTAAATTATGAGCCGGTTAATCT
U-SSTs-24H-67	5-9	ACTAGTGCGGGCTTGCCGACGTTACTGCCTGCTTGGGCTTGA
U-SSTs-24H-68	5-10	ATCGCGATGAAGTCCCCGATAATTTATTTCTTGCCCCGATTT
U-SSTs-24H-69	5-11	ACTTGGCCATATTAACGCTTGTGCATTAACCGAGTCATATC
U-SSTs-24H-70	5-12	CACACGTCCGGCACGAGGAGTATTCTGCACGAAAAATCTACA
U-SSTs-24H-71	5-13	CTGCAGGACATTGCCGGCCGGAACCCCCAGCGGGGGAGGCGC
U-SSTs-24H-72	5-14	GCGTCGTGGTGGGAAGTATTGTAGTTTACTCGGGCCCTCTGC
U-SSTs-24H-73	6-1	TTTTTTTTTTTATAGTACACCCTCAACGATAATTTTTTTTTTT
U-SSTs-24H-74	6-2	TTTAGGTTTCCCTGTTGTGTCGACGCGCCGGAATAAGAGGTATC
U-SSTs-24H-75	6-3	CTAGTCTCGAAATCTGGCGGACGCTGGGCTTGTGTACGGCT
U-SSTs-24H-76	6-4	TTGGGTAGTTACGGATAATGGAATAGGGTAGGGTTGTCTTAC
U-SSTs-24H-77	6-5	ACACGGCCGCGAGAATACGCCTCGCGCGCCGATAGTCTAAAA
U-SSTs-24H-78	6-6	GAACTCTTACTGGGAATCAACGCCAGAGTTCTTGACTCGAGG
U-SSTs-24H-79	6-7	TGACATCTGGTGTTCGGAAGCAGACTGATAGATACTGTTTGG
U-SSTs-24H-80	6-8	TCGGGATGGTTTCCATTCTCATGCTGTCTATGGATCGCGGA
U-SSTs-24H-81	6-9	CTATTAGTTTTGAGTGACCGTCCCGCACTAGTAGGAGACTGA
U-SSTs-24H-82	6-10	CTTCCGCCGTTCTCGCAGTGCTTCATCGCGATCTGCGGCAAG
U-SSTs-24H-83	6-11	TTAGCAGGTATCTCCTACCTTTATGGCCAAGTATCGGGGGAC
U-SSTs-24H-84	6-12	GGACGGATGGTTAGGTACTGGCCCCGACGTGTGAAGCGTTTAA
U-SSTs-24H-85	6-13	CGAGCGATCTAGAGAATGATCATGTCTGCAGACTCCTCGTG
U-SSTs-24H-86	6-14	AGTGACGGTGAATTTATTTGCTCACCACGACGCCCGGGCA
U-SSTs-24H-87	6-15	ACCCGAGAGCTTTTTTTTTTTTTTTTTTTTTTTTCAATACTTCC
U-SSTs-24H-88	7-1	GCAGTGTATGGACGCTGGAAGGAAACCTAAAGGTGTACTATA
U-SSTs-24H-89	7-2	ACCTTAACTGTAAGTAATATGTGAGACTAGGTCGACAACAG
U-SSTs-24H-90	7-3	ATATCTTACCGGACGACGCTAAACTACCCAATCCGCCAGATT
U-SSTs-24H-91	7-4	CATCCTTTGCTCACTACAAGTGCGGCCGTGTCCATTATCCGT
U-SSTs-24H-92	7-5	ATCTGTTCTTCCCTCAAGGTTGTAAGAGTTCGGCGTATTCTC
U-SSTs-24H-93	7-6	CGTGGGATTACAGCCGGTTTGCCAGATGTCAGTTGATTCCCA

Seq_ID	Location	Sequence
U-SSTs-24H-94	7-7	ACCGTCCTCTCGACCTTCCCAACCATCCCGAGCTTCCGAACA
U-SSTs-24H-95	7-8	GTGGTACCTCCGCAGGTTGTCAAATAATAGTGAGAAATGGAA
U-SSTs-24H-96	7-9	AGTGATTGACTGAGTGGCCTCACGGCGGAAGACGGTCACTCA
U-SSTs-24H-97	7-10	CGTGCTAAAAATGCCTTGAGGTACCTGCTAAGCACTGCGAGA
U-SSTs-24H-98	7-11	TAAGTGGTTTTAAAACGCCGTCCCATCCGTCCAAGGTAGGAGA
U-SSTs-24H-99	7-12	ACAATACTTAGTTCGAATCAGAAGATCGCTCGCCAGTACCTAA
U-SSTs-24H-100	7-13	CATATGCCCAAACATTCTACCCACCGTCACTGATCATTTCTCT
U-SSTs-24H-101	7-14	GCTGATCATAATCATCGTTCGGCTCTCGGGTAGCAATAAATT
U-SSTs-24H-102	8-1	TTTTTTTTTTTGTGAGGTTAGTCCATACTGCTTTTTTTTTTT
U-SSTs-24H-103	8-2	GACAGGAAGGGCCTAACAGTCACAGTTAAGGTCTTCCAGCGT
U-SSTs-24H-104	8-3	TCGCGAGTAATCTACCTCCTACGGTAAGATATCATATTACTT
U-SSTs-24H-105	8-4	ACGAGCGGCCAGTGTACCTTTAGCAAAGGATGTAGCGTCGTC
U-SSTs-24H-106	8-5	CGGAGCTTTTGCCCTACATATGAAGAACAGATACTTGTAGTG
U-SSTs-24H-107	8-6	CGAGAAAATGGCCACGACACTGTAATCCACGAACCTTGAGG
U-SSTs-24H-108	8-7	AGCAGTCACTCGCAGTATCGCGAGAGGACGGTCAAACCGGCT
U-SSTs-24H-109	8-8	GCGACCGAAAATCCCGGTGCTGGAGGTACCACTGGGAAGGTC
U-SSTs-24H-110	8-9	ACGCCTGCGCGGTGAGGGTCAATCACTGACAACCTGC
U-SSTs-24H-111	8-10	TCGCGACTTTAGAAGGTATCGTTTTTTAGCACGGAGGCCACTC
U-SSTs-24H-112	8-11	GAACGAAGATAGTGCTATGTTTAAACCACTTACCTCAAGGCA
U-SSTs-24H-113	8-12	GGCTCTCGCGGTACAGCCACTCTAAGTATTGTGACGGCGTTT
U-SSTs-24H-114	8-13	TGAATCTAAGGGCCCTGCGGGTTGGGCATATGTCTGATTCTGA
U-SSTs-24H-115	8-14	CACGCGGGCATGGGTGTTTTATTATGATCAGCGGTAGAATGT
U-SSTs-24H-116	8-15	TTGGCGGATTTTTTTTTTTTTTTTTTTTTTTTTCGAACGATGA
U-SSTs-24H-117	9-1	TCATTACAGGGTTTTGTCTAATCCTTCCGTGCTACTAACCTCAC
U-SSTs-24H-118	9-2	GATTACATGCCAGAAAATAGTTTACTCGCGAGACTGTTAGGC
U-SSTs-24H-119	9-3	AGGCTCTAACGCCGTGCTCCCGGCCGCTCGTTAGGAGGTAGA
U-SSTs-24H-120	9-4	GTTAACTGGCAATCTACTGACAAAAGCTCCGAAAGGTACTACT
U-SSTs-24H-121	9-5	CGCATGTGCTCGCGGCCCATCCATTTTCTCGATATGTAGGGC
U-SSTs-24H-122	9-6	GGAACAAATTCACATACTCGCAGTACTGCTAGTGTCTGTTGGC
U-SSTs-24H-123	9-7	ACCGCCGAGTCCAAGCCGTGCTTTCGGTTCGCGCGATACTGCG
U-SSTs-24H-124	9-8	TCGATTTGTCAGCAGAACTCTGCGCAGGCGTAGCACCGGGGA
U-SSTs-24H-125	9-9	CGATCGCAAGACTTATCCGGCAAAGTCGCGAGACCCCTGACC
U-SSTs-24H-126	9-10	CGACAGTGACCAACGCCTCCCATCTTCGTTCCGATACCTTCT
U-SSTs-24H-127	9-11	ATTTTCTCTGTAACACGCGCTGCGCGAGAGCCAACATAGCACT
U-SSTs-24H-128	9-12	GTCTCGATAAGATCAGGCCGTCTTAGATTCAAGTGGCTGTAC
U-SSTs-24H-129	9-13	GTGGCCAACACATCGTGAAATTGCCCGCGTGCCCGCAGGCC
U-SSTs-24H-130	9-14	TTCGAGCTCGACAGTGAGCTAATCGCGCCAATAAAAACACCCA
U-SSTs-24H-131	10-1	TTTTTTTTTTTTCGCCATCGCGCCCTGTAATGATTTTTTTTTTT
U-SSTs-24H-132	10-2	ATTCTCATTATGGGACGGGGGGCATGTAATCATTAGACAAA
U-SSTs-24H-133	10-3	GCATGATGTACAGGAAGGGAGCGTTAGAGCCTACTATTTTCT
U-SSTs-24H-134	10-4	CGGAGAAGAGGAATATGTGCGTGCCAGTTAACGGGACGACGG
U-SSTs-24H-135	10-5	GAACAGTCTTTCCAAAGCGTCGACGACATGCGGTGAGTAGAT
U-SSTs-24H-136	10-6	GTCTAACGCAAGTAAGGTAATGAATTTGTTCCGATGGGCCGC
U-SSTs-24H-137	10-7	TTATAGCTATGGGGGAGAACAGACTCGGCGGTGCGAGTATGT
U-SSTs-24H-138	10-8	TCATTTGATTCTGCTTAGGTTTGACAAAATCGAGCACGGCTTG
U-SSTs-24H-139	10-9	GTTGGGGCATCTTTCGTACGGTCTTTCGATCGAGAGTTCTGC
U-SSTs-24H-140	10-10	TGCGGACCTCTTACAAATCCCGGTCACTGTTCGGCCGGATAAG

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U-SSTs-24H-141	10-11	GCGTCCTCTTTTCAGGGTCATTACAGGAAAATGGGAGGCGTT
U-SSTs-24H-142	10-12	AGACTCCTTATCCTCGCGAGTCTTATCGAGACCAGCGCGTGT
U-SSTs-24H-143	10-13	CAACCAAGGCGACGTGAGAGTGTGTTGGCCACACGGCCTGAT
U-SSTs-24H-144	10-14	TAAATAGTTTCCCAGTGCAGTCGAGCTCGAAATTTACGAT
U-SSTs-24H-145	10-15	CCAAAGCTCATTTTTTTTTTTTTTTTTTTTTTTTAGCTCACTG
U-SSTs-24H-146	11-1	TTCATCTGAGCGTGCGATACTTAATGAGAATCGCGATGGCGC
U-SSTs-24H-147	11-2	TGGATTTCATCGGATATTCCGCTACATCATGCCCCCGTCCCA
U-SSTs-24H-148	11-3	TGCTTCCTGAAACGACCTTACCTCTTCTCCGCTCCCTTCCCTG
U-SSTs-24H-149	11-4	GCAGGTATCTATCGTAGTCGGAAGACTGTTCCGCACATATTC
U-SSTs-24H-150	11-5	CGCTAACATGTACAAGCATTTTGCCTTAGACGACGCTTTGGA
U-SSTs-24H-151	11-6	ATCGCCGGCCGCCGTTTCGGCATAGCTATAAATTACCTTACT
U-SSTs-24H-152	11-7	TGATCGAGTGAAACTGGAGCCAATCAAAATGATGTTCTCCCCC
U-SSTs-24H-153	11-8	CCTTTCCGTCAGCTTCAAATCATGCCCAACAACCTAAGCAG
U-SSTs-24H-154	11-9	CTTGCGCTTTGGATTGATCGCGAGGTCCGCACCGTACGAAAG
U-SSTs-24H-155	11-10	ACACTATAGCTAGACGTGGGGAAGAGGACGCGGGATTGTAA
U-SSTs-24H-156	11-11	GGACGAGGCCAAACCCCGGAATAAGGAGTCTATGACCCTGAA
U-SSTs-24H-157	11-12	CCCACCATTGGGGCTACACTGCCTTGGTTGACTCGCGAGGA
U-SSTs-24H-158	11-13	TGAAGTTGGTTTCTTATCGAGAAACTATTTAACTCTCACGTC
U-SSTs-24H-159	11-14	GATCTTGGTTGTGTGTGTATCTGAGCTTGGCTGCACGCGGG
U-SSTs-24H-160	12-1	TTTTTTTTTTGAGGTTTGAAGGCTCAGATGAATTTTTTTTTT
U-SSTs-24H-161	12-2	CATAATATGTTTCTCTCCGCTCGATGAATCCAAGTATCGCAC
U-SSTs-24H-162	12-3	TATGCGTCCGACCTCGTGGTTTTTCAGGAAGCAGCGGAATATC
U-SSTs-24H-163	12-4	ATACTATGTTCCGTGTGGGACTAGATACCTGCGTAAGGTCGT
U-SSTs-24H-164	12-5	GAACCCTAATTCCTTAATACGACATGTTAGCGCCGACTACGA
U-SSTs-24H-165	12-6	ACAGTCGAGCGAGTGAGTGACCGGCCGCGATAAATGCTTGT
U-SSTs-24H-166	12-7	TAGGCTGGCCGGTCAAGACCGTCACTCGATCAGCCGAACGGG
U-SSTs-24H-167	12-8	GAAACATGCATGAGGCCATCGTGACGGAAAGGGCTCCAGTT
U-SSTs-24H-168	12-9	TATACCTCAATTTCTATAAACCAAAGCGCAAGGATTTGAAGC
U-SSTs-24H-169	12-10	ATAAAAAGAGCTCTTAAGTGAAGCTATAGTGTGCGATCAATC
U-SSTs-24H-170	12-11	TAGAATCTCATGGGCAACACCTGGCCTCGTCCCCCACGTCT
U-SSTs-24H-171	12-12	AGTCAACAGCATTAGGGTATGCAATGGTGGGGTTCCGGGGTT
U-SSTs-24H-172	12-13	AACTTAATTGGACACTCATTTGAACCAACTTCAAGTGTAGCCC
U-SSTs-24H-173	12-14	CGGGTCGTATTTTCATGTATTTCCAACCAAGATCCTCGATAAGA
U-SSTs-24H-174	12-15	TGTTGCCATATTTTTTTTTTTTTTTTTTTTTTTTGGATACACACA
U-SSTs-24H-175	13-1	CGACCCTACTTTCCCGAGAACACATATTATGCTTCGAACCTC
U-SSTs-24H-176	13-2	CGGCTCCGCGCGCTTTAATGCCGGACGCATAAGCGGAGAGAA
U-SSTs-24H-177	13-3	TTAAATCCAAGCAGACTCCAAAACATAGTATAACCACGAGGT
U-SSTs-24H-178	13-4	ATTTCCCCACGTTAGAGTGACATTAGGGTTCGTCCCCACAGG
U-SSTs-24H-179	13-5	AAGAGAACCTCGATATAATACGCTCGACTGTCGTATTAAGGA
U-SSTs-24H-180	13-6	ACAGGCATTCGAAAACGTTGAGGCCAGCCTAGTCACTCACTC
U-SSTs-24H-181	13-7	CGTGCGTTTTATGCGAATCACTGCATGTTTCCGGTCTTGACC
U-SSTs-24H-182	13-8	ACTCATAACCAAGGAACTATCATTGAGGTATACGATGGCCTCA
U-SSTs-24H-183	13-9	TACACCGGAACTTGATACTCTCTTTTTTATGTTTATAGAAA
U-SSTs-24H-184	13-10	TACGGAGTGTACTAACGCGCTGAGATTCATCACTTAAGAG
U-SSTs-24H-185	13-11	AGATTTCCGACCTGGCTTATGGCTGTTGACTGGTGTGCCCCA
U-SSTs-24H-186	13-12	TTGAGACCCTGTCTAGTAGAACAATTAAGTTCATACCCTAAT
U-SSTs-24H-187	13-13	CCTCGTCTTGCGTGCCGCCAGATACGACCCGCAATGAGTGTC

Seq_ID	Location	Sequence
U-SSTs-24H-188	13-14	TATTACTTTCTCCTACCAGGTTATGGCAACAGAATACATGAA
U-SSTs-24H-189	14-1	TTTTTTTTTTTGATCAAGGTCAAAGTAGGGTCGTTTTTTTTTTT
U-SSTs-24H-190	14-2	GAGGAACTTGAGTTAGACTTTGCGCGGAGCCGGTTCTCGGGA
U-SSTs-24H-191	14-3	CCAGCAGGACTTTGCCATACCCTTGGATTTAAGCATTAAGC
U-SSTs-24H-192	14-4	TAGTGCCAAGAAAACAATAGACGTGGGGAAATTTGGAGTCTG
U-SSTs-24H-193	14-5	AGGTGAATACTACCCCTATGTGAGGTTCTCTTGTCACTCTAA
U-SSTs-24H-194	14-6	TTGATTGAAGGAAGGAGTGTCCGAATGCCTGTGTATTATATC
U-SSTs-24H-195	14-7	GGCCAATCTGCACGAGCCCGGTAAAACGCACGTCACGTTTTT
U-SSTs-24H-196	14-8	GGCACCTTGCAGATAGTAGGTTTGGTATGAGTGTGATTCGCA
U-SSTs-24H-197	14-9	CGGACAGTTAGAATACCCAGAGTTCCGGTGTATGATAGTTCC
U-SSTs-24H-198	14-10	CCCGACTTGAGTGAGTCCCTCAACACTCCGTAAGAGTATCAA
U-SSTs-24H-199	14-11	TTGGTATAGCATCTAACCCGGGTCCGAAATCTGCGCGTTAGT
U-SSTs-24H-200	14-12	TCACGGAACCTCGCTATCACACAGGGTCTCAACATAAGCCAG
U-SSTs-24H-201	14-13	TCACCAATGGTGAGAAAACAGCGCAAGACGAGGTTCTACTAGA
U-SSTs-24H-202	14-14	CGACCGGACCCTGTTCTCGCTAGAAAAGTAATACTGGCGGCAC
U-SSTs-24H-203	14-15	TAGATGTTCTTTTTTTTTTTTTTTTTTTTTTTTACCTGGTAGG
U-SSTs-24H-204	15-1	GAATGAACCCGGGGTTTTTCATCAAGTTCCTCTGACCTTGATC
U-SSTs-24H-205	15-2	GAATTACGAGAGTCGACTGAGGTCCTGCTGGAAAGTCTAACT
U-SSTs-24H-206	15-3	CAGATTTCCGCTAATTCCTTCCTTGGCACTAGGTATGGCAA
U-SSTs-24H-207	15-4	GTGTATGCCTCCGCGGTATGCGTATTCACCTTCTATTGTTTT
U-SSTs-24H-208	15-5	TAATCCGTAGTTTCCGCGAAACTTCAATCAAACATAGGGGTA
U-SSTs-24H-209	15-6	GATCGACGGTGAACCTTAGTGCAGATTGGCCGACACTCCTTC
U-SSTs-24H-210	15-7	CGGGGCCCTCCCAACCGCGAGCAAGGTGCCCCGGGCTCGTG
U-SSTs-24H-211	15-8	CCATCTTCAGAAATGGCTCTCTTAACTGTCCGACCTACTATCT
U-SSTs-24H-212	15-9	GAACCCTGTACACCTCTAGGTTCAAGTCGGGTCTGGGTATTC
U-SSTs-24H-213	15-10	AGTGTATCTCGAGTGTGATTCGCTATAACCAAGAGGGACTCAC
U-SSTs-24H-214	15-11	ATTGGGCGTTTGATGCGTCTTGGTTCCGTGACCGGGTTAGAT
U-SSTs-24H-215	15-12	GAGCCTGTACGGTTTGCCCCGCCATTGGTGATGTGATAGCGA
U-SSTs-24H-216	15-13	GGACTTCCTCCTCTCGCTGGAGGTCCGGTCCGGCTGTTTCTCA
U-SSTs-24H-217	15-14	AGGCATTACAATACGTATCGAAGAACATCTAAGCGAGAACAG
U-SSTs-24H-218	16-1	TTTTTTTTTTTTTGGCATGTACGCGGGTTCATTCTTTTTTTTTT
U-SSTs-24H-219	16-2	AGAACGGCCACTGTTGTATTCCTCTCGTAATTCATGAAAACCC
U-SSTs-24H-220	16-3	TTCGGAGGCACTCGCTGATCCGCGGAAATCTGCTCAGTCGAC
U-SSTs-24H-221	16-4	GTATACTCAGGTCTAAGGCGGAGGCATACACGAAGGAATTA
U-SSTs-24H-222	16-5	ACTGGGTATAGAGTTGATGAACTACGGATTAGCATAACCGCG
U-SSTs-24H-223	16-6	GAGCTATCCATGATTTACTTTCACCGTCGATCTTTCGCGGAA
U-SSTs-24H-224	16-7	TCTTTGTAATTCATCGAACGGAGGGGCCCGCACTAAGGTT
U-SSTs-24H-225	16-8	GTCTCAGGTGTTGCAACGCGTTCGAAAGATGGTCGCGGTTGG
U-SSTs-24H-226	16-9	TAGGACTGCATAGTCAATGGCGTACAGGTTTCAGAGAGCCAT
U-SSTs-24H-227	16-10	TGTGGTCAAAGAAGCTAAGGGCGAGATACACTACCTAGAGGT
U-SSTs-24H-228	16-11	CATGAGAAGGTGACATCTTGCAAACGCCAATGAATCACACT
U-SSTs-24H-229	16-12	ACTGCATCTCGGTCTCTCTACGTACAGGCTCAAGACGCATC
U-SSTs-24H-230	16-13	TCCAGCGTGGTTGGACAGCGTGGAGGAAGTCCCAGGGCAAAC
U-SSTs-24H-231	16-14	CTCTCTCCCGCGGGGGGCTTGTGTAATGCCTTCCAGCGAGA
U-SSTs-24H-232	16-15	AAGGTCACTATTTTTTTTTTTTTTTTTTTTTTTTCGATACGTA
U-SSTs-24H-233	17-1	ACACCATATTAACCCCGGCTGGCCGTTCTCGTACATGCCA
U-SSTs-24H-234	17-2	CGATTTTCCTTATTAGGGGATGCCTCCGAAGAATACAACAG

Seq_ID	Location	Sequence
U-SSTs-24H-235	17-3	GCGGTGTACCTATTTGAGTGTCTGAGTATACGGATCAGCGAG
U-SSTs-24H-236	17-4	CGAGTGTGTCGTCGGGCACGGTATAACCCAGTGCGCCTTAGAC
U-SSTs-24H-237	17-5	CAATCCGGCACGGTCACGTAATGGATAGCTCTCATCAACCTC
U-SSTs-24H-238	17-6	TGCACATGAGATACGTATAACATTACAAAGAAAAGTAAATCA
U-SSTs-24H-239	17-7	AGCAGGCTGCCCATGCCGGTCCACCTGAGACCGTTTCGATGGA
U-SSTs-24H-240	17-8	CCCGCGGTCAGAGATAATGTATGCAGTCCTAACGCGTTCGAA
U-SSTs-24H-241	17-9	GACATTAACTGTTTCGTATGCATTTGACCACAGCCATTGACTA
U-SSTs-24H-242	17-10	GGTGAGACCGGGGTCCCAACACCTTCTCATGCCCTTAGCTTC
U-SSTs-24H-243	17-11	GATCTGAGCATAACCTAGCTAGAGATGCAGTGCAAGATGTCA
U-SSTs-24H-244	17-12	GTTACGACGGCGGCTACTAACCACGCTGGATAGAGATGACC
U-SSTs-24H-245	17-13	GACAACAAATTTCTTTGACGTCGGGAGAGAGACGCTGTCCAA
U-SSTs-24H-246	17-14	AAGGCGGCTTCCGACATGAATAGTGACCTTCAAGCCCCCG
U-SSTs-24H-247	18-1	TTTTTTTTTTTAGTCTATGCCCTAATATGGTGTTTTTTTTTTT
U-SSTs-24H-248	18-2	TCGGTCATCCTGTCAATTGGCGAAGGAAAATCGGCCGGGGTTT
U-SSTs-24H-249	18-3	GGACACAGGGTTCCTCGTGAGTAGGTACACCGCTCCCCCTAAT
U-SSTs-24H-250	18-4	CACAGTACTTTACCGTGATGACGACACACTCGACACTCAAAT
U-SSTs-24H-251	18-5	TCCCCATTCCGTACTAACGACGTGCCGGATTGCCGTGCCCGA
U-SSTs-24H-252	18-6	TCGGACTTTCATTTCAAAGAGTCTCATGTGCATTACGTGACC
U-SSTs-24H-253	18-7	ACTTTTTCCGAGAACGGAAGTGGCAGCCTGCTGTTATACGTA
U-SSTs-24H-254	18-8	GTCAACAGACATAAATTTAGACTGACCGCGGGGACCGGCATG
U-SSTs-24H-255	18-9	TCATAGATGTTTAAAGATTAGCAGTTAATGTCTACATTATCT
U-SSTs-24H-256	18-10	TACACCGGGCAGCATCAATACCCGGTCTCACCTGCATACGAA
U-SSTs-24H-257	18-11	CAATGTGGGCAATTCTCGTGAATGCTCAGATCTGTTGGGACC
U-SSTs-24H-258	18-12	ACATTCCGCTCCAGTGAATTATGCCGTCGTAAGTAGCTAGGTT
U-SSTs-24H-259	18-13	TCCAAGCGACCGGATGTATAAAATTTGTTGTCTGTTAGTAGCC
U-SSTs-24H-260	18-14	CTAGTTTTCTGGATACGAGAGAAAGCCGCCTTACGTCAAAGA
U-SSTs-24H-261	18-15	ATTCTAAGAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATGTCGG
U-SSTs-24H-262	19-1	AATTAACGCTACTTACCTACCGGATGACCGAGGGCATAGACT
U-SSTs-24H-263	19-2	ACGCACTCGACCACTAGCACCCCTGTGTCCCGCCAATGACA
U-SSTs-24H-264	19-3	CCGCTGAGGATTGTGGACACCAAGTACTGTGACTCACGGGAA
U-SSTs-24H-265	19-4	GAAGACACTGGAGGCGCCGATCGAATGGGGATCATCACGGTA
U-SSTs-24H-266	19-5	GTGCCGTTAGGAAACGTAAAAGAAAAGTCCGAGTCGTTAGTAC
U-SSTs-24H-267	19-6	GCACTGTAATATATCAATGCTCGGAAAAGTCTCTTTGAAAT
U-SSTs-24H-268	19-7	TTCGAATCGGTGGGCTATCAAGTCTGTTGACAGTTCGGTTCT
U-SSTs-24H-269	19-8	TCTATCATATTAGATTAGCACACATCTATGATCTAAATTTAT
U-SSTs-24H-270	19-9	TCTGGAAATAACGGCAGTCCTGCCCGGTGACTAATCTTTAA
U-SSTs-24H-271	19-10	CAAACGGATGGGTTCTCGACTGCCACATTTGGTATTGATGCT
U-SSTs-24H-272	19-11	CCACTACTAGTACATCAATGAGAGCGAATGTTACAGAGAATT
U-SSTs-24H-273	19-12	TACCAGTATGCCCGGGGTGTAGTCGCTTGAATAATTTACTG
U-SSTs-24H-274	19-13	GGTTATTAGCTATTGGTTTAAAGAAAAGTATTATACATCCG
U-SSTs-24H-275	19-14	GGGCGACGGCGTGGTATAAATTTCTTAGAATCTCTCGTATCC
U-SSTs-24H-276	20-1	TTTTTTTTTTTTTAAACATCATAGCGTTAATTTTTTTTTTTTT
U-SSTs-24H-277	20-2	CAGCAAGAAAGACAAGAATGCGTCGAGTCCGTGGTAGGTAAG
U-SSTs-24H-278	20-3	TAAGGCCGCGGTTACTGACGAATCCTCAGCGGGGTGCTAGTG
U-SSTs-24H-279	20-4	CGGCTATTTTTAATTAAGGTCCAGTGTCTTCGGTGTCCACA
U-SSTs-24H-280	20-5	GCGCCTGTTTCGTACGTTCTTGCCTAACGGCACATCGGCGCCT
U-SSTs-24H-281	20-6	TAAGTAATGACCGTGAGATAATATTACAGTGCTTTTACGTTT

Seq_ID	Location	Sequence
U-SSTs-24H-282	20-7	GCTGACTCTCTGCGCCGGAATACCGATTCGAAAGCATTGATA
U-SSTs-24H-283	20-8	ACCTCTCCCTAGATTTTCGGGCAATATGATAGATTGATAGCCC
U-SSTs-24H-284	20-9	TGTCATATCAGGGCACCATTATTATTTCCAGAGTGCTAATCT
U-SSTs-24H-285	20-10	CTTGAAAATTGGAACGGGTATCCATCCGTTTGAGGACTGCCG
U-SSTs-24H-286	20-11	CAGATGTCCGAGCACCCATAAACTAGTAGTGGAGTCGAGAAC
U-SSTs-24H-287	20-12	AAAACTTAAGCCTATGGGGAGCATACTGGTATCATTGATGT
U-SSTs-24H-288	20-13	ACCCGAATTTACCTAGTTGTTAGCTAATAACCTACACCCCGG
U-SSTs-24H-289	20-14	AGGTTGTATGGGGCCACATATCGCCGTCGCCCTTAAACCAAT
U-SSTs-24H-290	20-15	GTAAGTACCGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATACCAA
U-SSTs-24H-291	21-1	AAAGTCATTGCATGTCTTTCGTTTTCTTGCTGTGATGTTAAA
U-SSTs-24H-292	21-2	CCTTCTGATTAAGCAGCACATCGCGGCCTTAGCATTCTTGTC
U-SSTs-24H-293	21-3	AAAAGCGGCAGTGCACCTATCAAATAGCCGTCGTCAGTAAC
U-SSTs-24H-294	21-4	ACCTCAGACCTATTTTGCCTTGAACAGGCGCACCTTTAATTA
U-SSTs-24H-295	21-5	CAACACTTAGTCGTTAAAAGCTCATTACTTACAAGAACGTAC
U-SSTs-24H-296	21-6	CTCAATAGTTCCTTTCGGTTCGGAGAGTCAGCTTATCTCACGG
U-SSTs-24H-297	21-7	ACATCAATGTATCGCCCCGGCGAGGGAGAGGTATTCCGGCGCA
U-SSTs-24H-298	21-8	CTGCGAAGGTGTCCATACTAATGATATGACAGCCCCGAAATCT
U-SSTs-24H-299	21-9	CCCTATGGCTAAACCTAGGGGAATTTTCAAGTAATGGTGCCC
U-SSTs-24H-300	21-10	TATAAACACATCGAATGTCCCCGGACATCTGATAACCGTTCC
U-SSTs-24H-301	21-11	TACGTTTTAAAGCTGTTGCCCTCTTAAGTTTTTTTTTAGGGTGCT
U-SSTs-24H-302	21-12	CGCCAGGCATTGCGTGGTCACAAATTCGGGTTCCCCATAGGC
U-SSTs-24H-303	21-13	GCATTGCTTATTTCCAAGGGACATAACAACCTAACAACTAGGT
U-SSTs-24H-304	21-14	CCACGGCTCACGTTCCAAGCTCGGTACTTACATATGTGGCCC
U-SSTs-24H-305	22-1	TTTTTTTTTTTAGGTTTCCACAGCAATGACTTTTTTTTTTTTTT
U-SSTs-24H-306	22-2	ATACTGTTCCCCAGACCAACCTAATCAGAAGGCGAAAGACAT
U-SSTs-24H-307	22-3	GAGGTATTCTACCCTACGGTCCTGCCGCTTTTATGTGCTGCT
U-SSTs-24H-308	22-4	AGTATTCAAGTTGCTTAACGAAGGTCTGAGGTGATAGGTGCA
U-SSTs-24H-309	22-5	ATCGACTACCGATGGCCACGAACCTAAGTGTGAAGGCAAAAT
U-SSTs-24H-310	22-6	GCATATGTGACACGGGCACTCGAACTATTGAGGCTTTTAACG
U-SSTs-24H-311	22-7	TCGCCTATTTTCGATGGTCTGTACATTGATGTGCAACCGAAA
U-SSTs-24H-312	22-8	CCCAAGCTAGCTGCGGGTGTACACCTTCGCAGCGCCGGGCGA
U-SSTs-24H-313	22-9	GACCAATCGCTAGCGTTTATATAGCCATAGGGTTAGTATGGA
U-SSTs-24H-314	22-10	CGATTTTACACGGCCTGAATTATGTGTTTATAACCCCTAGGTT
U-SSTs-24H-315	22-11	TCCATGGGGGACTATGGAATGCTTTAAACGTAGGGACATTCG
U-SSTs-24H-316	22-12	ACATTAGTTAAACCGACATCAAATGCCTGGCGGAGGCAACAG
U-SSTs-24H-317	22-13	ACACCAGTGCAGTCGGTCCATAAGCAATGCGTGACCACGC
U-SSTs-24H-318	22-14	TATGTCAAGGAATAAACATCGGTGAGCCGTGGTCCCTTGGA
U-SSTs-24H-319	22-15	CGATGCTCGTTTTTTTTTTTTTTTTTTTTTTTTTTTAGCTTGGAAC
U-SSTs-24H-320	23-1	GTATCAATGCAGACAGTCTAAGGAACAGTATTGTGGAAACCT
U-SSTs-24H-321	23-2	CTTGAGGTTGAGACGTTTTTTTAGAATACCTCGGTTGGTCTGG
U-SSTs-24H-322	23-3	GCCGATCCTTTCAGCTACCACCTTGAATACTGACCGTAGGGT
U-SSTs-24H-323	23-4	TCTTTACTGGCGCCACTGAGGGGTAGTCGATTTCGTTAAGCAA
U-SSTs-24H-324	23-5	ATAATGTGCTTCGCCTGAAAATCACATATGCTCGTGGCCATC
U-SSTs-24H-325	23-6	CATCATCAATAACCACGCTTTAAATAGGCGAGAGTGCCCGTG
U-SSTs-24H-326	23-7	TCAATCGACGCTGGGGCAGGGCTAGCTTGGGCAGACCATCGA
U-SSTs-24H-327	23-8	GTACATTTCATGGGATCTGGCCGCGATTGGTCTACACCCGCAG
U-SSTs-24H-328	23-9	TGGTCCGCACCTGTAGCGCCCTGTAAAATCGTATAAACGCTA

U-SSTs-12H

Seq_ID	Location	Sequence
U-SSTs-12H-1	1-1	TGGGCTCGTGATGACACCGCACATATTATGCTTCGAACCTC
U-SSTs-12H-2	1-2	AGTTATGCGGGCTTAATGACACGGACGCATAAGCGGAGAGAA
U-SSTs-12H-3	1-3	GGCCTGACCGCCCTACGTTTGAACATAGTATAACCACGAGGT
U-SSTs-12H-4	1-4	TGCTCGAGGTCACCTTCTCAAATTAGGGTTCGTCCCCACAGG
U-SSTs-12H-5	1-5	CTGATTCCCTCCAAGCGAATAAGCTCGACTGTCGTATTAAGGA
U-SSTs-12H-6	1-6	CGACTCTAACTACATCTCAGAGGCCAGCCTAGTCACTCACTC
U-SSTs-12H-7	1-7	GACCCGCTCCCCCAGAGTCGTTGCATGTTTCCGGTCTTGACC
U-SSTs-12H-8	1-8	TCAAAAATTCTATCTACAATGTTGAGGTATACGATGGCCTCA
U-SSTs-12H-9	1-9	TCAAGCATAGACTGAAGCCCTCTCTTTTTTATGTTTATAGAAA
U-SSTs-12H-10	1-10	CATGACCAAGAAGAGCCCAGTTGAGATTCTATCACTTAAGAG
U-SSTs-12H-11	1-11	TGGGCGGTGCTTGTCTATGCAGCTGTTGACTGGTGTGCCCCA
U-SSTs-12H-12	1-12	TTTATTGCTCCTCACGACACACAATTAAGTTCATACCCTAAT
U-SSTs-12H-13	1-13	CGCCTTGGGAAACATCAGGGAATACGACCCGCAATGAGTGTC
U-SSTs-12H-14	1-14	GGATTTGGAGTACTTCTTCAGTATGGCAACAGAATACATGAA
U-SSTs-12H-15	2-1	TTTTTTTTTTTGCACATAGCATCACGAGGCCATTTTTTTTTT
U-SSTs-12H-16	2-2	TTCAAAGACCATTTTCGTGTGACCCGCATAACTGCGGTGTCAT
U-SSTs-12H-17	2-3	GCCACCACTCTGAACTCGTATGCGGTCAGGCCTGTCATTAAG
U-SSTs-12H-18	2-4	GGACTCGTGTCAAACTCGAGGACCTCGAGCACAAACGTAGG
U-SSTs-12H-19	2-5	TAAGTCGCGTCTGACAGACACGGAGGAATCAGTTGAGAAGGT
U-SSTs-12H-20	2-6	TGATCATCGGTAACACGAACTAGTTAGAGTCGTTATTCGCTT
U-SSTs-12H-21	2-7	GTATCTAGACGTCCGCAACCAGGGAGCGGGTCTCTGAGATGT
U-SSTs-12H-22	2-8	CGGAGGTAGCGTACTATCAGAGAATTTTTGAACGACTCTGG
U-SSTs-12H-23	2-9	TCGTTCTGTGCCGCACGTTGTTCTATGCTTGACATTGTAGAT
U-SSTs-12H-24	2-10	CCGCTAATGTTGAGACTGCTCTCTTGGTCATGAGGGCTTCAG
U-SSTs-12H-25	2-11	AAAGGATGGGGATAAGCCAGAAGCACCGCCCAACTGGGCTCT
U-SSTs-12H-26	2-12	CGACCCATTCCGCGGTCCGCGGAGCAATAAATGCATAGACA
U-SSTs-12H-27	2-13	CAGGCTCCTAGGTCCGCTTCTTTCCCAAGGCGTGTGTCGTGA
U-SSTs-12H-28	2-14	TCCGAAAGTGGAATGGGTAGAACTCCAAATCCTCCCTGATGT
U-SSTs-12H-29	2-15	CATGGATATTTTTTTTTTTTTTTTTTTTTTTTTTCTGAAGAAGT
U-SSTs-12H-30	3-1	TAGGCTTCTCGACCTCAGCCTGGTCTTTGAAATGCTATGTGC
U-SSTs-12H-31	3-2	CCTTTGGTGAAGTCTCACCTGAGTGGTGGCTCACACGAAAT
U-SSTs-12H-32	3-3	CAGTAAATTTAGGCCTAATGTACACGAGTCCATACGAGTTCA
U-SSTs-12H-33	3-4	ATGTCGCGACACAAAAGACCGACGCGACTTACTCGAGTTTTG
U-SSTs-12H-34	3-5	AGGGGTATGGCGCACTTGTGCCGATGATCAGTGTCTGTGTCAG
U-SSTs-12H-35	3-6	CAAAGAACTACGCCCTAAGCAGTCTAGATACAGTTCGTGTTA
U-SSTs-12H-36	3-7	AAGGATTGAAACAGCACCAAGTGCTACCTCCGTGGTTGCGGAC
U-SSTs-12H-37	3-8	CGCGGTCCGCCGCATCCAAACCACAGAACGACTGATAGTAGC
U-SSTs-12H-38	3-9	AAATATATTTTAAGTGGTAGGACATTAGCGGACAACGTGCGG
U-SSTs-12H-39	3-10	AAACCCAGGAATACTGCACACCCCATCCTTTGAGCAGTCTCA
U-SSTs-12H-40	3-11	ACCATCGCTAAGGGGATCGCCGAATGGGTTCGTCTGGCTTATC
U-SSTs-12H-41	3-12	TCCATCGAAAATATCCTAATCTAGGAGCCTGGCGCGACCGCG
U-SSTs-12H-42	3-13	CGTCCCGAACAGAATACAAATCACTTTCGGAAGAAGCGGACC
U-SSTs-12H-43	3-14	CTCCCCTTCCAGTGCGCGATGAATATCCATGTCTACCCATTC
U-SSTs-12H-44	4-1	TTTTTTTTTTTGGCCGATTAGCCGAGAAGCCTATTTTTTTTTT
U-SSTs-12H-45	4-2	TCCCCTTCCACCCGACGTGCCTACCAAAGGGAGGCTGAGGT
U-SSTs-12H-46	4-3	ACTTGGTGGAAGGCGCGTATAAATTTACTGAGGTGAGACT

Seq_ID	Location	Sequence
U-SSTs-12H-47	4-4	CGGGAAGTACGCTGACCCCTTTTGTGCGGACATACATTAGGCC
U-SSTs-12H-48	4-5	GATAGGGCAATGAGCTGGGAACCATAACCCCTCGGTCTTTTG
U-SSTs-12H-49	4-6	ATCCTATACTTACGCCAATGAGTAGTTCTTTGCACAAGTGCG
U-SSTs-12H-50	4-7	GCTGGCAATGGGGATTGCCAATTTCAATCCTTTGCTTAGGGC
U-SSTs-12H-51	4-8	GACCTTATATAGATTAACCGGGCGGACCGCGACTGGTGCTG
U-SSTs-12H-52	4-9	CTCATAATTTTCAAGCCCAAGAAAATATATTTGTTGGATGC
U-SSTs-12H-53	4-10	CAGGCAGTACAAATCGGGGCATTCTGGGTTTCTTACCCTT
U-SSTs-12H-54	4-11	AGAATAAATTGATATGACTCGTTAGCGATGGTGTGTGCAGTA
U-SSTs-12H-55	4-12	GTTAATGCACTGTAGATTTTTTTTTTCGATGGAGGCGATCCCC
U-SSTs-12H-56	4-13	CGTGCAGAAATGCGCCTCCCCCTGTTTCGGGACGGATTAGGATA
U-SSTs-12H-57	4-14	GCTGGGGGTGTCAGAGGGCCCTGGAAGGGGAGATTTGTATTC
U-SSTs-12H-58	4-15	GAGTAAACTATTTTTTTTTTTTTTTTTTTTTTTCATCGCGCAC
U-SSTs-12H-59	5-1	TTATCGTTGAGGATACCTCTTTGGAAGGGGAGCTAATCGGCC
U-SSTs-12H-60	5-2	ATTCCGGCCGACCCGTACAGCCACCAAGGTGGCACGTCGGG
U-SSTs-12H-61	5-3	CAAGCCCAGCGGTAAGACAACCTAGTTCCCGTACGCCGCCTT
U-SSTs-12H-62	5-4	CCTACCCTATTTTTTAGACTATTGCCCTATCAAAGGGTCACG
U-SSTs-12H-63	5-5	TCGGCGCGGACCTCGAGTCAAGTATAGGATTTCCAGCTCA
U-SSTs-12H-64	5-6	AGAACTCTGGCCCAAACAGTACATTGCCAGCTCATTGGCGTA
U-SSTs-12H-65	5-7	TCTATCAGTCTTCCGCGATCCATATAAGGTCTTGGCAATCCC
U-SSTs-12H-66	5-8	ATAGGACAGCATCAGTCTCCTAAATTATGAGCCGGTTAATCT
U-SSTs-12H-67	5-9	ACTAGTGCGGGCTTGCCGAGGTACTGCCTGCTTGGGCTTGA
U-SSTs-12H-68	5-10	ATCGCGATGAAGTCCCCGATAATTTATTTCTTGCCCCGATTT
U-SSTs-12H-69	5-11	ACTTGGCCATATTAACGCTTGTGCATTAACCGAGTCATATC
U-SSTs-12H-70	5-12	CACACGTCCGGCAGGAGGATTTCTGCACGAAAAATCTACA
U-SSTs-12H-71	5-13	CTGCAGGACATTGCCGGCCGGAACCCCCAGCGGGGGAGGCGC
U-SSTs-12H-72	5-14	GCGTCGTGGTGGGAAGTATTGTAGTTTACTCGGGCCCTCTGC
U-SSTs-12H-73	6-1	TTTTTTTTTTTATAGTACACCCTCAACGATAATTTTTTTTTTT
U-SSTs-12H-74	6-2	TTTAGGTTTCCCTGTTGTGCGACGCGCCGGAATAAGAGGTATC
U-SSTs-12H-75	6-3	CTAGTCTCGAAATCTGGCGGACGCTGGGCTTGTGTACGGCT
U-SSTs-12H-76	6-4	TTGGGTAGTTACGGATAATGGAATAGGGTAGGGTTGTCTTAC
U-SSTs-12H-77	6-5	ACACGGCCGCGAGAATACGCCTCGCGCGCCGATAGTCTAAAA
U-SSTs-12H-78	6-6	GAACTCTTACTGGGAATCAACGCCAGAGTTCTTGACTCGAGG
U-SSTs-12H-79	6-7	TGACATCTGGTGTTCGGAAGCAGACTGATAGATACTGTTTGG
U-SSTs-12H-80	6-8	TCGGGATGGTTTCCATTCTCATGCTGTCTTATGGATCGCGGA
U-SSTs-12H-81	6-9	CTATTAGTTTTGAGTGACCGTCCCGCACTAGTAGGAGACTGA
U-SSTs-12H-82	6-10	CTTCCGCCGTTCTCGCAGTGCTTCATCGCGATCTGCGGCAAG
U-SSTs-12H-83	6-11	TTAGCAGGTATCTCCTACCTTTATGGCCAAGTATCGGGGGAC
U-SSTs-12H-84	6-12	GGACGGATGGTTAGGTACTGGCCCGACGTGTGAAGCGTTTAA
U-SSTs-12H-85	6-13	CGAGCGATCTAGAGAATGATCATGTCTTGCAGACTCCTCGTG
U-SSTs-12H-86	6-14	AGTGACGGTGAATTTATTTGCTCACCACGACGCCCGCCGGCA
U-SSTs-12H-87	6-15	ACCCGAGAGCTTTTTTTTTTTTTTTTTTTTTTTTCAATACTTCC
U-SSTs-12H-88	7-1	GCAGTGTATGGACGCTGGAAGGAAACCTAAAGGTGTACTATA
U-SSTs-12H-89	7-2	ACCTTAACTGTAAGTAATATGTGCGAGACTAGGTCGACAACAG
U-SSTs-12H-90	7-3	ATATCTTACCGGACGACGCTAAACTACCCAATCCGCCAGATT
U-SSTs-12H-91	7-4	CATCCTTTGCTCACTACAAGTGCGGCCGTGTCCATTATCCGT
U-SSTs-12H-92	7-5	ATCTGTTCTTCCCTCAAGGTTGTAAGAGTTCGGCGTATTCTC
U-SSTs-12H-93	7-6	CGTGGGATTACAGCCGGTTTGCCAGATGTCAGTTGATTCCCA

Seq_ID	Location	Sequence
U-SSTs-12H-94	7-7	ACCGTCCTCTCGACCTTCCCAACCATCCCGAGCTTCCGAACA
U-SSTs-12H-95	7-8	GTGGTACCTCCGCAGGTTGTCAAATAATAGTGAGAAATGGAA
U-SSTs-12H-96	7-9	AGTGATTGACTGAGTGGCCTCACGGCGGAAGACGGTCACTCA
U-SSTs-12H-97	7-10	CGTGCTAAAAATGCCTTGAGGTACCTGCTAAGCACTGCGAGA
U-SSTs-12H-98	7-11	TAAGTGGTTTTAAAACGCCGTCCCATCCGTCCAAGGTAGGAGA
U-SSTs-12H-99	7-12	ACAATACTTAGTTCGAATCAGAAGATCGCTCGCCAGTACCTAA
U-SSTs-12H-100	7-13	CATATGCCCAAACATTCTACCCACCGTCACTGATCATTTCTCT
U-SSTs-12H-101	7-14	GCTGATCATAATCATCGTTCGGCTCTCGGGTAGCAATAAATT
U-SSTs-12H-102	8-1	TTTTTTTTTTTGTGAGGTTAGTCCATACTGCTTTTTTTTTTT
U-SSTs-12H-103	8-2	GACAGGAAGGGCCTAACAGTCACAGTTAAGGTCTTCCAGCGT
U-SSTs-12H-104	8-3	TCGCGAGTAATCTACCTCCTACGGTAAGATATCATATTACTT
U-SSTs-12H-105	8-4	ACGAGCGGCCAGTGTACCTTTAGCAAAGGATGTAGCGTCGTC
U-SSTs-12H-106	8-5	CGGAGCTTTTGCCCTACATATGAAGAACAGATACTTGTAGTG
U-SSTs-12H-107	8-6	CGAGAAAATGGCCACGACACTGTAATCCACGAACCTTGAGG
U-SSTs-12H-108	8-7	AGCAGTCACTCGCAGTATCGCGAGAGGACGGTCAAACCGGCT
U-SSTs-12H-109	8-8	GCGACCGAAAATCCCGGTGCTGGAGGTACCACTGGGAAGGTC
U-SSTs-12H-110	8-9	ACGCCTGCGCGGTGAGGGTCAATCACTGACAACCTGC
U-SSTs-12H-111	8-10	TCGCGACTTTAGAAGGTATCGTTTTTTAGCACGGAGGCCACTC
U-SSTs-12H-112	8-11	GAACGAAGATAGTGCTATGTTTAAACCACTTACCTCAAGGCA
U-SSTs-12H-113	8-12	GGCTCTCGCGGTACAGCCACTCTAAGTATTGTGACGGCGTTT
U-SSTs-12H-114	8-13	TGAATCTAAGGGCCCTGCGGGTTGGGCATATGTCTGATTCTGA
U-SSTs-12H-115	8-14	CACGCGGGCATGGGTGTTTTATTATGATCAGCGGTAGAATGT
U-SSTs-12H-116	8-15	TTGGCGGATTTTTTTTTTTTTTTTTTTTTTTTCGAACGATGA
U-SSTs-12H-117	9-1	TCATTACAGGGTTTTGTCTAATCCTTCCGTGCTACTAACCTCAC
U-SSTs-12H-118	9-2	GATTACATGCCAGAAAATAGTTTACTCGCGAGACTGTTAGGC
U-SSTs-12H-119	9-3	AGGCTCTAACGCCGTGCTCCCGGCCGCTCGTTAGGAGGTAGA
U-SSTs-12H-120	9-4	GTTAACTGGCAATCTACTGACAAAAGCTCCGAAAGGTACACT
U-SSTs-12H-121	9-5	CGCATGTGCTCGCGGCCCATCCATTTTCTCGATATGTAGGGC
U-SSTs-12H-122	9-6	GGAACAAATTCACATACTCGCAGTACTGCTAGTGTCTGTTGGC
U-SSTs-12H-123	9-7	ACCGCCGAGTCCAAGCCGTGCTTTCGGTTCGCGGATACTGCG
U-SSTs-12H-124	9-8	TCGATTTGTCAGCAGAACTCTGCGCAGGCGTAGCACCGGGGA
U-SSTs-12H-125	9-9	CGATCGCAAGACTTATCCGGCAAAGTCGCGAGACCCCTGACC
U-SSTs-12H-126	9-10	CGACAGTGACCAACGCCTCCCATCTTCGTTCCGATACCTTCT
U-SSTs-12H-127	9-11	ATTTTCTGTAACACGCGCTGCGCGAGAGCCAACATAGCACT
U-SSTs-12H-128	9-12	GTCTCGATAAGATCAGGCCGTCTTAGATTCAAGTGGCTGTAC
U-SSTs-12H-129	9-13	GTGGCCAACACATCGTGAAATTGCCCGCGTGCCCGCAGGCC
U-SSTs-12H-130	9-14	TTCGAGCTCGACAGTGAGCTAATCGCGCCAATAAAAACACCCA
U-SSTs-12H-131	10-1	TTTTTTTTTTTTCGCGCCATCGCGCCCTGTAATGATTTTTTTTTT
U-SSTs-12H-132	10-2	ATTCTCATTATGGGACGGGGGGGCATGTAATCATTAGACAAA
U-SSTs-12H-133	10-3	GCATGATGTACAGGAAGGGAGCGTTAGAGCCTACTATTTTCT
U-SSTs-12H-134	10-4	CGGAGAAGAGGAATATGTGCGTGCCAGTTAACGGGACGACGG
U-SSTs-12H-135	10-5	GAACAGTCTTTCCAAAGCGTCGACGACATGCGGTGAGTAGAT
U-SSTs-12H-136	10-6	GTCTAACGCAAGTAAGGTAATGAATTTGTTCCGATGGGCCGC
U-SSTs-12H-137	10-7	TTATAGCTATGGGGGAGAACAGACTCGGCGGTGCGAGTATGT
U-SSTs-12H-138	10-8	TCATTTGATTCTGCTTAGGTTTGACAAAATCGAGCACGGCTTG
U-SSTs-12H-139	10-9	GTTGGGGCATCTTTCGTACGGTCTTTCGATCGAGAGTTCTGC
U-SSTs-12H-140	10-10	TGCGGACCTTTACAAATCCCGGTCACTGTTCGGCCGGATAAG

U-SSTs-6H

Seq_ID	Location	Sequence
U-SSTs-6H-1	1-1	TGGGCCTCGTGATGACACCGCGAAACCTAAAGGTGTA CTATA
U-SSTs-6H-2	1-2	AGTTATGCGGGCTTAATGACATCGAGACTAGGTCGACAACAG
U-SSTs-6H-3	1-3	GGCCTGACCGCCCTACGTTTGA ACTACCCAATCCGCCAGATT
U-SSTs-6H-4	1-4	TGCTCGAGGTCACCTTCTCAAGCGGCCGTGCCATTATCCGT
U-SSTs-6H-5	1-5	CTGATTCCCTCCAAGCGAATAAGTAAGAGTTCGGCGTATTCTC
U-SSTs-6H-6	1-6	CGACTCTAACTACATCTCAGACCAGATGTCAGTTGATTCCCA
U-SSTs-6H-7	1-7	GACCCGCTCCCCCAGAGTCGTACCATCCCGAGCTTCCGAACA
U-SSTs-6H-8	1-8	TCAAAAATTCTATCTACAATGAAACTAATAGTGAGAATGGAA
U-SSTs-6H-9	1-9	TCAAGCATAGACTGAAGCCCTACGGCGGAAGACGGTCACTCA
U-SSTs-6H-10	1-10	CATGACCAAGAAGAGCCAGTTACCTGCTAAGCACTGCGAGA
U-SSTs-6H-11	1-11	TGGGCGGTGCTTGTCTATGCACCATCCGTCCAAGGTAGGAGA
U-SSTs-6H-12	1-12	TTTATTGCTCCTCACGACACAAGATCGCTCGCCAGTACCTAA
U-SSTs-6H-13	1-13	CGCCTTGGGAAACATCAGGGACACCGTCACTGATCATTCTCT
U-SSTs-6H-14	1-14	GGATTTGGAGTACTTCTTCAGGCTCTCGGGTAGCAATAAATT
U-SSTs-6H-15	2-1	TTTTTTTTTTTGCACATAGCATCACGAGGCCATTTTTTTTTT
U-SSTs-6H-16	2-2	TTCAAAGACCATTTTCGTGTGACCCGCATAACTGCGGTGTCAT
U-SSTs-6H-17	2-3	GCCACCCTCTGAACTCGTATGCGGTCAGGCCTGTCATTAAG
U-SSTs-6H-18	2-4	GGACTCGTGTCAAAACTCGAGGACCTCGAGCACAAACGTAGG
U-SSTs-6H-19	2-5	TAAGTCGCGTCTGACAGACACGGAGGAATCAGTTGAGAAGGT
U-SSTs-6H-20	2-6	TGATCATCGGTAAACACGAACTAGTTAGAGTCGTTATTTCGCTT
U-SSTs-6H-21	2-7	GTATCTAGACGTCCGCAACCAGGGAGCGGGTCTCTGAGATGT
U-SSTs-6H-22	2-8	CGGAGGTAGCGCTACTATCAGAGAATTTTTGAACGACTCTGG
U-SSTs-6H-23	2-9	TCGTTCTGTGCCGCACGTTGTTCTATGCTTGACATTGTAGAT
U-SSTs-6H-24	2-10	CCGCTAATGTTGAGACTGCTCTCTTGGTCATGAGGGCTTCAG
U-SSTs-6H-25	2-11	AAAGGATGGGGATAAGCCAGAAGCACCGCCCAACTGGGCTCT
U-SSTs-6H-26	2-12	CGACCCATTCCGCGGTGCGCGGAGCAATAAATGCATAGACA
U-SSTs-6H-27	2-13	CAGGCTCCTAGGTCGCTTCTTTCCCAAGGCGTGTGTCGTGA
U-SSTs-6H-28	2-14	TCCGAAAGTGGAATGGGTAGAACTCCAAATCCTCCCTGATGT
U-SSTs-6H-29	2-15	CATGGATATTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGAAGAAGT
U-SSTs-6H-30	3-1	TAGGCTTCTCGACCTCAGCCTGGTCTTTGAAATGCTATGTGC
U-SSTs-6H-31	3-2	CCCTTTGGTGAAGTCTCACCTGAGTGGTGGCTCACACGAAAT
U-SSTs-6H-32	3-3	CAGTAAATTTAGGCCTAATGTACACGAGTCATACGAGTTCA
U-SSTs-6H-33	3-4	ATGTCGCGACACAAAAGACCGACGCGACTTACTCGAGTTTTG
U-SSTs-6H-34	3-5	AGGGGGTATGGCGCACTTGTGCCGATGATCAGTGTCTGTCAG
U-SSTs-6H-35	3-6	CAAAGAACTACGCCCTAAGCAGTCTAGATACAGTTCGTGTTA
U-SSTs-6H-36	3-7	AAGGATTGAAACAGCACCCAGTGCTACCTCCGTGGTTGCGGAC
U-SSTs-6H-37	3-8	CGCGGTCCGCCGCATCCAAACCACAGAACGACTGATAGTAGC
U-SSTs-6H-38	3-9	AAATATATTTTAAGTGGTAGGACATTAGCGGACAACGTGCGG
U-SSTs-6H-39	3-10	AAACCCAGGAATACTGCACACCCCATCCTTTGAGCAGTCTCA
U-SSTs-6H-40	3-11	ACCATCGCTAAGGGGATCGCCGAATGGGTGCTCTGGCTTATC
U-SSTs-6H-41	3-12	TCCATCGAAAAATATCCTAATCTAGGAGCCTGGCGCGACCGCG
U-SSTs-6H-42	3-13	CGTCCCGAACAGAATACAAATCACTTTCGGAAGAAGCGGACC
U-SSTs-6H-43	3-14	CTCCCCTTCCAGTGC GCGATGAATATCCATGTCTACCCATTC
U-SSTs-6H-44	4-1	TTTTTTTTTTTGGCCGATTAGCCGAGAAGCCTATTTTTTTTTT
U-SSTs-6H-45	4-2	TCCCCTTCCACCCGACGTGCCTCACCAAAGGGAGGCTGAGGT
U-SSTs-6H-46	4-3	ACCTTGGTGAAGGCGGCGTATAAATTTACTGAGGTGAGACT

U-SSTs-4H

Seq_ID	Location	Sequence
U-SSTs-4H-1	1-1	TGGGCTCGTGATGACACCGCTGGAAGGGGAGCTAATCGGCC
U-SSTs-4H-2	1-2	AGTTATGCGGGCTTAATGACACCACCAAGGTGGCACGTCGGG
U-SSTs-4H-3	1-3	GGCCTGACCGCCCTACGTTTGCTAGTTCCCCTACGCCGCCTT
U-SSTs-4H-4	1-4	TGCTCGAGGTCACCTTCTCAATTGCCCTATCAAAGGGTCACG
U-SSTs-4H-5	1-5	CTGATTCCCTCCAAGCGAATAAAGTATAGGATTTCCAGCTCA
U-SSTs-4H-6	1-6	CGACTCTAACTACATCTCAGACATTGCCAGCTCATTGGCGTA
U-SSTs-4H-7	1-7	GACCCGCTCCCCCAGAGTCGTATATAAGGTCTTGGCAATCCC
U-SSTs-4H-8	1-8	TCAAAAATTCTATCTACAATGAAATTATGAGCCGGTTAATCT
U-SSTs-4H-9	1-9	TCAAGCATAGACTGAAGCCCTGTACTGCCTGCTTGGGCTTGA
U-SSTs-4H-10	1-10	CATGACCAAGAAGAGCCCAGTAATTTATTCTTGCCCCGATTT
U-SSTs-4H-11	1-11	TGGGCGGTGCTTGTCTATGCAGTGCATTAACCGAGTCATATC
U-SSTs-4H-12	1-12	TTTATTGCTCCTCACGACACAATTCTGCACGAAAAATCTACA
U-SSTs-4H-13	1-13	CGCCTTGGGAAACATCAGGGAAACCCCCAGCGGGGGAGGCGC
U-SSTs-4H-14	1-14	GGATTTGGAGTACTTCTTCAGTAGTTTACTCGGGCCCTCTGC
U-SSTs-4H-15	2-1	TTTTTTTTTTTGCACATAGCATCACGAGGCCATTTTTTTTTT
U-SSTs-4H-16	2-2	TTCAAAGACCATTTTCGTGTGACCCGCATAACTGCGGTGTCAT
U-SSTs-4H-17	2-3	GCCACCCTCTGAACTCGTATGCGGTCAGGCCTGTCATTAAG
U-SSTs-4H-18	2-4	GGACTCGTGTCAAACTCGAGGACCTCGAGCACAAACGTAGG
U-SSTs-4H-19	2-5	TAAGTCGCGTCTGACAGACACGGAGGAATCAGTTGAGAAGGT
U-SSTs-4H-20	2-6	TGATCATCGGTAAACACGAACTAGTTAGAGTCGTTATTTCGCTT
U-SSTs-4H-21	2-7	GTATCTAGACGTCCGCAACCAGGGAGCGGGTCTCTGAGATGT
U-SSTs-4H-22	2-8	CGGAGGTAGCGCTACTATCAGAGAATTTTTGAACGACTCTGG
U-SSTs-4H-23	2-9	TCGTTCTGTGCCGCACGTTGTTCTATGCTTGACATTGTAGAT
U-SSTs-4H-24	2-10	CCGCTAATGTTGAGACTGCTCTCTTGGTCATGAGGGCTTCAG
U-SSTs-4H-25	2-11	AAAGGATGGGGATAAGCCAGAAGCACCGCCCAACTGGGCTCT
U-SSTs-4H-26	2-12	CGACCCATTCCGCGGTGCGCGGAGCAATAAATGCATAGACA
U-SSTs-4H-27	2-13	CAGGCTCCTAGGTCGCTTCTTTCCCAAGGCGTGTGTCTGTA
U-SSTs-4H-28	2-14	TCCGAAAGTGGAATGGGTAGAACTCCAAATCCTCCCTGATGT
U-SSTs-4H-29	2-15	CATGGATATTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGAAGAAGT
U-SSTs-4H-30	3-1	TAGGCTTCTCGACCTCAGCCTGGTCTTTGAAATGCTATGTGC
U-SSTs-4H-31	3-2	CCCTTTGGTGAAGTCTCACCTGAGTGGTGGCTCACACGAAAT
U-SSTs-4H-32	3-3	CAGTAAATTTAGGCCTAATGTACACGAGTCCATACGAGTTCA
U-SSTs-4H-33	3-4	ATGTCGCGACACAAAGACCGACGCGACTTACTCGAGTTTTG
U-SSTs-4H-34	3-5	AGGGGGTATGGCGCACTTGTGCCGATGATCAGTGTCTGTCAG
U-SSTs-4H-35	3-6	CAAAGAACTACGCCCTAAGCAGTCTAGATACAGTTCGTGTTA
U-SSTs-4H-36	3-7	AAGGATTGAAACAGCACCAAGTGTACCTCCGTGGTTGCGGAC
U-SSTs-4H-37	3-8	CGCGGTCCGCCGCATCCAAACCACAGAACGACTGATAGTAGC
U-SSTs-4H-38	3-9	AAATATATTTTAAGTGGTAGGACATTAGCGGACAACGTGCGG
U-SSTs-4H-39	3-10	AAACCAGGAATACTGCACACCCCATCCTTTGAGCAGTCTCA
U-SSTs-4H-40	3-11	ACCATCGCTAAGGGGATCGCCGAATGGGTGCTCTGGCTTATC
U-SSTs-4H-41	3-12	TCCATCGAAAAATATCCTAATCTAGGAGCCTGGCGCGACCGCG
U-SSTs-4H-42	3-13	CGTCCCGAACAGAATACAAATCACTTTCGGAAGAAGCGGACC
U-SSTs-4H-43	3-14	CTCCCCTTCCAGTGC GCGATGAATATCCATGTCTACCCATTC
U-SSTs-4H-44	4-1	TTTTTTTTTTTGGCCGATTAGCCGAGAAGCCTATTTTTTTTTT
U-SSTs-4H-45	4-2	TCCCCTTCCACCCGACGTGCCTCACCAAAGGGAGGCTGAGGT
U-SSTs-4H-46	4-3	ACCTTGGTGAAGGCGGCGTATAAATTTACTGAGGTGAGACT

U-SSTs-2Hx10C

Seq_ID	Location	Sequence
U-SSTs-2H-10Column-1	1-1	TGGTGGGACGTCTGTCTTCGTGACATGCATAACCTCAGTCGC
U-SSTs-2H-10Column-2	1-2	CGAACGGTTTGTCTGTACGCGAGTCAGTATACTACTAATGT
U-SSTs-2H-10Column-3	1-3	TGATTCCTCATCGTGGTGTCCGTTATGCGTAAGACCGGTACA
U-SSTs-2H-10Column-4	1-4	AGCAGATTGCCTGGCATGGCGAGCTTACCTCGTGGTCCGGTA
U-SSTs-2H-10Column-5	1-5	TCTGCAGGTGAGCCGCCCGGTGGGCATGGTTCGCAGAGAC
U-SSTs-2H-10Column-6	1-6	ATTTAGGCGTGCGCGAACTCGGCCAGCCCTTGATCGTCCGC
U-SSTs-2H-10Column-7	1-7	CTCGTTCTGCACATGTTGCCCTGCCTGGGCACACCTTTACAA
U-SSTs-2H-10Column-8	1-8	TAGTTCCTACTCCACACTGCTATGTCCTGAGAAATGATACCC
U-SSTs-2H-10Column-9	1-9	TATGCTCCTATAGAAAGACTTGTAGATGGTCTATTTACTGAA
U-SSTs-2H-10Column-10	1-10	GTGTAAGAGATttttttttttttttttttttttttttttttTGGCTGAGTGC
U-SSTs-2H-10Column-11	2-1	tttttttttttGCGACTGAGGTACGTCCCACCAttttttttttt
U-SSTs-2H-10Column-12	2-2	TATGCATGTCACATTAGTAGTCAAACCGTTCGACGAAGACAG
U-SSTs-2H-10Column-13	2-3	ATACTGACTCTGTACCGGTCTATGAGGAATCAGCGTGACAGA
U-SSTs-2H-10Column-14	2-4	TACGCATAACTACCCGACCACGGCAATCTGCTGGACACCACG
U-SSTs-2H-10Column-15	2-5	GAGGTAAGCTGTCTCTGCGAATCACCTGCAGACGCCATGCCA
U-SSTs-2H-10Column-16	2-6	CCATGCCACGCGGACGATCACACGCCTAAATCGGCGGCGGC
U-SSTs-2H-10Column-17	2-7	AGGGCTGGGCTTGTAAGGTGTGCAGAACGAGCGAGTTCGCG
U-SSTs-2H-10Column-18	2-8	TGCCCAGGCAGGGTATCATTTAGTAGGAACTAGGGCAACATG
U-SSTs-2H-10Column-19	2-9	CTCAGGACATTTTCAGTAAATAATAGGAGCATAAGCAGTGTGG
U-SSTs-2H-10Column-20	2-10	GACCATCTACGCACTCAGCCAATCTCTTACACAAGTCTTTCT

U-SSTs-2Hx30C

Seq_ID	Location	Sequence
U-SSTs-2H-30Column-1	1-1	TGGTGGGACGTCTGTCTTCGTGACATGCATAACCTCAGTCGC
U-SSTs-2H-30Column-2	1-2	CGAACGGTTTTGTCTGTACGCGAGTCAGTATACTACTAATGT
U-SSTs-2H-30Column-3	1-3	TGATTCCCTCATCGTGGTGTCCGTTATGCGTAAGACCGGTACA
U-SSTs-2H-30Column-4	1-4	AGCAGATTGCCTGGCATGGCGAGCTTACCTCGTGGTCCGGTA
U-SSTs-2H-30Column-5	1-5	TCTGCAGGTGAGCCGCCCGGTGGGCATGGTTCGCAGAGAC
U-SSTs-2H-30Column-6	1-6	ATTTAGGCGTGCGCGAACTCGGCCAGCCCTTGATCGTCCGC
U-SSTs-2H-30Column-7	1-7	CTCGTTCTGCACATGTTGCCCTGCCTGGGCACACCTTTACAA
U-SSTs-2H-30Column-8	1-8	TAGTTCCTACTCCACACTGCTATGTCCTGAGAAATGATACC
U-SSTs-2H-30Column-9	1-9	TATGCTCCTATAGAAAGACTTGTAGATGGTCTATTTACTGAA
U-SSTs-2H-30Column-10	1-10	GTGTAAGAGATACAGATATCAGAGATTAAAGTGGCTGAGTGC
U-SSTs-2H-30Column-11	1-11	CGCGTCCCTGGGATGGAAATCTCATGCGGTCCAAAGCAGGCT
U-SSTs-2H-30Column-12	1-12	GGTTTGGATTCCGAAACAACCGAAATCGCGAGCGCCACGAGC
U-SSTs-2H-30Column-13	1-13	CTTTACGGCAGTAAACGGAAACTAATGGATCCTCATATCCGT
U-SSTs-2H-30Column-14	1-14	CATAATTAGTACTGCCGGCCTGGCCTACGTCCGCTATTACGA
U-SSTs-2H-30Column-15	1-15	TATATAGACACAAGGTGCCACTAGGACTTCCGCCTCCGGTAA
U-SSTs-2H-30Column-16	1-16	GTCCACTTATGACGAAAGTGAATCGGCCAATAGTGCTGGTG
U-SSTs-2H-30Column-17	1-17	CCGTAAATGGGCATTAACTCGCCTTTCCGTAAACTGACTGCC
U-SSTs-2H-30Column-18	1-18	GACGGGCATGAGGCTGACTCCGCCCGTACCCGTTTGACAAC
U-SSTs-2H-30Column-19	1-19	GATTATTTGATACTGCTCGTGCCACATTCAACTCTTGAGGAA
U-SSTs-2H-30Column-20	1-20	ACCTCTCGGGCCGAGCCTCTTCACCTAAAGTGTCCCTTCTC
U-SSTs-2H-30Column-21	1-21	GCTATGGTTTTAGACCTTGCCCTGCGTGAGAGAGCGGATTTGGT
U-SSTs-2H-30Column-22	1-22	GGCCCGCACCCCTTACGTGACACGCAACAGAGTCGAATAGAAT
U-SSTs-2H-30Column-23	1-23	CTAACTGCTCACAGACATCGTAGCGGGACGGGCTCCTTGCTT
U-SSTs-2H-30Column-24	1-24	GCCTGTGAGAAGTACGTTACATCAACCTAACATCTTCAGGAT
U-SSTs-2H-30Column-25	1-25	AAGCAAATTCACGGGCCTCAACTGATTTAGCGGCTATGGCCC
U-SSTs-2H-30Column-26	1-26	AGTTGTGGGACTGGGCTCTCGCGGCGACGAACGTTAGAACTC
U-SSTs-2H-30Column-27	1-27	CAAAGACATATGGGACAACACTGAGTCCCGGATATCCCTGAC
U-SSTs-2H-30Column-28	1-28	CATCTCCGCTGAGTTATTGTACCGAACATGTGGTTGGTTACA
U-SSTs-2H-30Column-29	1-29	TGTTACCTGCCTAAGCCATCATTTGGGCTCACCGTGCCGCGTG
U-SSTs-2H-30Column-30	1-30	CGGGTCACCACttttttttttttttttttttttttttttttGCTTGAACAAG
U-SSTs-2H-30Column-31	2-1	ttttttttttttGCGACTGAGGTACGTCCCACCAttttttttttt
U-SSTs-2H-30Column-32	2-2	TATGCATGTCACATTAGTAGTCAAACCGTTCGACGAAGACAG
U-SSTs-2H-30Column-33	2-3	ATACTGACTCTGTACCGGTCTATGAGGAATCAGCGTGACAGA
U-SSTs-2H-30Column-34	2-4	TACGCATAACTACCCGACCACGGCAATCTGCTGGACACCACG
U-SSTs-2H-30Column-35	2-5	GAGGTAAGCTGTCCTGCGAATCACCTGCAGACGCCATGCCA
U-SSTs-2H-30Column-36	2-6	CCATGCCACGCGGACGATCACACGCCTAAATCGGCGGGCGGC
U-SSTs-2H-30Column-37	2-7	AGGGCTGGGCTTGTAAGGTGTGCAGAACGAGCGAGTTCGCG
U-SSTs-2H-30Column-38	2-8	TGCCAGGCAGGGTATCATTTAGTAGGAACTAGGGCAACATG
U-SSTs-2H-30Column-39	2-9	CTCAGGACATTTTCAGTAAATAATAGGAGCATAAGCAGTGTGG
U-SSTs-2H-30Column-40	2-10	GACCATCTACGCACTCAGCCAATCTCTTACACAAGTCTTTCT
U-SSTs-2H-30Column-41	2-11	CTTTAATCTCAGCCTGCTTTGCCAGGGACGCGTGATATCTGT
U-SSTs-2H-30Column-42	2-12	GACCGCATGAGCTCGTGGCGGAATCCAAACCGATTTCCATC
U-SSTs-2H-30Column-43	2-13	TCGCGATTTACGGATATGAGCTGCCGTAAAGGGTTGTTTCG
U-SSTs-2H-30Column-44	2-14	GATCCATTAGTCGTAATAGCGTACTAATTATGTTTTCCGTTTA
U-SSTs-2H-30Column-45	2-15	GACGTAGGCCTTACCGGAGGCGTGTCTATATAAGGCCGGCAG
U-SSTs-2H-30Column-46	2-16	GGAAGTCCTACACCAGCACTACATAAGTGGACGTGGCACCTT

Seq_ID	Location	Sequence
U-SSTs-2H-30Column-47	2-17	TTGGCCGATTGGCAGTCAGTTCCCATTTACGGACACTTTCGT
U-SSTs-2H-30Column-48	2-18	TACGGAAAGGAGTTGTCAAATCATGCCCGTCCGAGTTAATG
U-SSTs-2H-30Column-49	2-19	GGGTACGGGCTTCCTCAAGAGATCAAATAATCGGAGTCAGCC
U-SSTs-2H-30Column-50	2-20	TTGAATGTGGGAGAAGGGACAGCCCGAGAGGTCACGAGCAGT
U-SSTs-2H-30Column-51	2-21	CTTTAGGTGAACCAAATCCGCTAAACCATAGCAGAGGCTGCG
U-SSTs-2H-30Column-52	2-22	TCTCTCACGCATTCTATTTCGAGGGTGCGGGCCAGGCAAGGTC
U-SSTs-2H-30Column-53	2-23	CTCTGTTGCGAAGCAAGGAGCTGAGCAGTTAGTGTCACGTAA
U-SSTs-2H-30Column-54	2-24	CCGTCCCCTATCCTGAAGATTTCTGACAGGCACGATGTCTG
U-SSTs-2H-30Column-55	2-25	GTTAGGTTGAGGGCCATAGCCTGAATTTGCTTTGTAACGTAC
U-SSTs-2H-30Column-56	2-26	GCTAAATCAGGAGTTCTAACGGTCCCACAACCTTTGAGGCCCG
U-SSTs-2H-30Column-57	2-27	TTCGTCGCCGGTCAGGGATATATATGTCTTTGCGAGAGCCCA
U-SSTs-2H-30Column-58	2-28	CCGGGACTCATGTAACCAACCCAGCGGAGATGGTGTTGTCCC
U-SSTs-2H-30Column-59	2-29	ACATGTTTCGGCACGGGCACGGGCAGGTAACATAACAATAACT
U-SSTs-2H-30Column-60	2-30	GTGAGCCCAACTTGTTCAAGCGTGGTGACCCGTGATGGCTTA

U-SSTs-2Hx70C

Seq_ID	Location	Sequence
U-SSTs-2H-70Column-1	1-1	TGGTGGGACGTCTGTCTTCGTGACATGCATAACCTCAGTCGC
U-SSTs-2H-70Column-2	1-2	CGAACGGTTTGTCTGTACGCGAGTCAGTATACTACTAATGT
U-SSTs-2H-70Column-3	1-3	TGATTCCCTCATCGTGGTGTCCGTTATGCGTAAGACCGGTACA
U-SSTs-2H-70Column-4	1-4	AGCAGATTGCCTGGCATGGCGAGCTTACCTCGTGGTCCGGTA
U-SSTs-2H-70Column-5	1-5	TCTGCAGGTGAGCCGCCGCCGTGGGCATGGTTCGCAGAGAC
U-SSTs-2H-70Column-6	1-6	ATTTAGGCGTGCGCGAACTCGGCCAGCCCTTGATCGTCCGC
U-SSTs-2H-70Column-7	1-7	CTCGTTCTGCACATGTTGCCCTGCCTGGGCACACCTTTACAA
U-SSTs-2H-70Column-8	1-8	TAGTTCCTACTCCACACTGCTATGTCCCTGAGAAATGATACCC
U-SSTs-2H-70Column-9	1-9	TATGCTCCTATAGAAAGACTTGTAGATGGTCTATTTACTGAA
U-SSTs-2H-70Column-10	1-10	GTGTAAGAGATACAGATATCAGAGATTAAGTGGCTGAGTGC
U-SSTs-2H-70Column-11	1-11	CGCGTCCCTGGGATGGAAATCTCATGCGGTCCAAAGCAGGCT
U-SSTs-2H-70Column-12	1-12	GGTTTGGATTCCGAAACAACCGAAATCGCGAGCGCCACGAGC
U-SSTs-2H-70Column-13	1-13	CTTTACGGCAGTAAACGGAAACTAATGGATCCTCATATCCGT
U-SSTs-2H-70Column-14	1-14	CATAATTAGTACTGCCGGCCTGGCCTACGTCCGCTATTACGA
U-SSTs-2H-70Column-15	1-15	TATATAGACACAAGGTGCCACTAGGACTTCCGCCTCCGGTAA
U-SSTs-2H-70Column-16	1-16	GTCCACTTATGACGAAAGTGTAAATCGGCCAATAGTGTGGTG
U-SSTs-2H-70Column-17	1-17	CCGTAAATGGGCATTAACCTCGCCTTTCCGTAAACTGACTGCC
U-SSTs-2H-70Column-18	1-18	GACGGGCATGAGGCTGACTCCGCCGTACCCGTTTGACAACCT
U-SSTs-2H-70Column-19	1-19	GATTATTTGATACTGCTCGTGCCACATTCAACTCTTGAGGAA
U-SSTs-2H-70Column-20	1-20	ACCTCTCGGGCCGAGCCTCTTCACCTAAAGTGTCCCTTCTC
U-SSTs-2H-70Column-21	1-21	GCTATGGTTTACACCTTGCCTGCGTGAGAGAGCGGATTTGGT
U-SSTs-2H-70Column-22	1-22	GGCCCGCACCCCTTACGTGACACGCAACAGAGTCGAATAGAAT
U-SSTs-2H-70Column-23	1-23	CTAACTGCTCACAGACATCGTAGCGGGACGGGCTCCTTGCTT
U-SSTs-2H-70Column-24	1-24	GCCTGTGAGAAGTACGTTACATCAACCTAACATCTTCAGGAT
U-SSTs-2H-70Column-25	1-25	AAGCAAATTCACGGGCCCTCAACTGATTTAGCGGCTATGGCCC
U-SSTs-2H-70Column-26	1-26	AGTTGTGGGACTGGGCTCTCGCGGCGACGAACGTTAGAATC
U-SSTs-2H-70Column-27	1-27	CAAAGACATATGGGACAACACTGAGTCCCGGATATCCCTGAC
U-SSTs-2H-70Column-28	1-28	CATCTCCGCTGAGTTATTGTACCGAACATGTGGTTGGTTACA
U-SSTs-2H-70Column-29	1-29	TGTTACCTGCCTAAGCCATCATTGGGCTCACCGTGCCGCGTG
U-SSTs-2H-70Column-30	1-30	CGGGTCACCACCAACCAGCCACACGTGAAGGCTTGAACAAG
U-SSTs-2H-70Column-31	1-31	GGGAATATAACACACGATCGGAATACGTTATCGAGCATCCTC
U-SSTs-2H-70Column-32	1-32	AACAAGAGCTTCCCAGGTTTCGCGCAGAGTCCCTCCGAAACG
U-SSTs-2H-70Column-33	1-33	TACTCGCACTATAAATACATCTTTCAAATAGCCTCTCCAGCA
U-SSTs-2H-70Column-34	1-34	CATTCAGCTCTTTATCATAAAGAAATCAGCTAAATTGCTCCA
U-SSTs-2H-70Column-35	1-35	CTAGACACCTCTAGCGTTCGTGATACTCTCGTGGACTTTAGC
U-SSTs-2H-70Column-36	1-36	GTGGTGCGGCCCTTGGGCCGTGGAGAAATTTAGCTCTGGTACC
U-SSTs-2H-70Column-37	1-37	AAGCAATTAGTTACGCTGAAGAGAGAGAATAGATGTTCGAAGT
U-SSTs-2H-70Column-38	1-38	CTATAACTTCCGGTCCATAAGGTATGGCTCGAGCTCAGGTCC
U-SSTs-2H-70Column-39	1-39	CAGGGCCGAAGTACCCGCGGCTCCAGCCGAGGCAAATAGAA
U-SSTs-2H-70Column-40	1-40	TCGTATGAACAAAGACCCACTACAATCGCCGACCTTAACGAT
U-SSTs-2H-70Column-41	1-41	TGCTCATGACATAGGGTGTACGCACCCAGCCAACTCATCGAT
U-SSTs-2H-70Column-42	1-42	TACACGGTACCGATCTGAGGCGAAGGCAGAGATAACGCAGAC
U-SSTs-2H-70Column-43	1-43	TACTACCTTTGACCGGAAAGAGGCAGAAGTACGCATCGCAC
U-SSTs-2H-70Column-44	1-44	CGCATTCAGAATAGTGGGAAGCAACTCTGGATATGTAGGTAT
U-SSTs-2H-70Column-45	1-45	ACGGGAGGCTTTGACATGGATACTAGAGTGGCGCTACGGCCG
U-SSTs-2H-70Column-46	1-46	GGGCTGATCGTATCTTTACTCGCGATAAGACGGTTATGTTGT
U-SSTs-2H-70Column-47	1-47	TATTGTCAACGTGTCCCAAGCTGACGCCACCCGCGTCAACA

Seq_ID	Location	Sequence
U-SSTs-2H-70Column-48	1-48	CAGTAACAAGTAATAGTTAGAAAGCGTTCCTTTATGCACCCAAA
U-SSTs-2H-70Column-49	1-49	TAATTACAATATTTAATCCACCCTACTCAAGTCGTTGGGCAG
U-SSTs-2H-70Column-50	1-50	CATTTGCCGAGGGCTACCATATGACACAGGTTCTCCTCCGGG
U-SSTs-2H-70Column-51	1-51	CGACTGCTTGCAGGGCCTTTGAGCGGAATAGCCACTCTGTGA
U-SSTs-2H-70Column-52	1-52	ATCGGATCCAAAGTGTGGTTCGACAGCAGGAGGCTAAGACA
U-SSTs-2H-70Column-53	1-53	TGTACCAGGTGTAGATCGCCTTACGAGTCGTAGCTAAGGCAT
U-SSTs-2H-70Column-54	1-54	GCGAGTGCCGTTGATACGCTGGGTCGCCGTGACCTTTCGCGT
U-SSTs-2H-70Column-55	1-55	TCCTAAAGACGCAGAACAGCGTCCCATCCCTGCTGTTTCGTCC
U-SSTs-2H-70Column-56	1-56	GGCCCTGTGTATAGGGCCAGACTAGCTAACGGGTTGCCTGT
U-SSTs-2H-70Column-57	1-57	AGCATCTTGC GCGAGCACACCGACCGACGATCGAGTTGGTTG
U-SSTs-2H-70Column-58	1-58	AGCCTAGTTACCCTCTCAACTCAAGATTCCCTTAGGCCTGAG
U-SSTs-2H-70Column-59	1-59	CTATGGCTTGATTTAATAAGCGAGGGTCAATAGGGTCCAATC
U-SSTs-2H-70Column-60	1-60	CAAAGCATTGATTGACATCTGGCGGTTCTGTAGAGAACACGC
U-SSTs-2H-70Column-61	1-61	ACCATAGACGGATACCAACCTTAGTCTTCCATAACGCCATCC
U-SSTs-2H-70Column-62	1-62	GCTAGTACCAGCAAGGTACTGAACGCCGGCCTAGGGATAAA
U-SSTs-2H-70Column-63	1-63	TCTCATCTGTGCCGGGCTCTACGGAATTAGGAAAGACCTATT
U-SSTs-2H-70Column-64	1-64	GTCAATACCAGACCCAAGTCTGGATCTAAGAATTCCAGGGAA
U-SSTs-2H-70Column-65	1-65	CGGAAGCTTAACCCTAGAGATATGCTCTCGGCGTAACTCGTC
U-SSTs-2H-70Column-66	1-66	GCGTAGGTGGGAGCTCCTAGTAACAGTAACGATTGGTAAAGA
U-SSTs-2H-70Column-67	1-67	AGCGGTCCGTAGCCCAGCTACTTCCCATACTGGTCTCAGATA
U-SSTs-2H-70Column-68	1-68	GCTGGAGCCATTCCCTCGTCAACCTCACAGCAGTGCCGCTTCC
U-SSTs-2H-70Column-69	1-69	GGTAACGTGGGAACGGTGTAGTGTGCGGGTGATAGGGCTGTG
U-SSTs-2H-70Column-70	1-70	CAAACCTGAATGttttttttttttttttttttttttttTCCCTCCCTGT
U-SSTs-2H-70Column-71	2-1	tttttttttttGCGACTGAGGTACGTCCCACCAttttttttttt
U-SSTs-2H-70Column-72	2-2	TATGCATGTCACATTAGTAGTCAAACCGTTCGACGAAGACAG
U-SSTs-2H-70Column-73	2-3	ATACTGACTCTGTACCGGTCTATGAGGAATCAGCGTGACAGA
U-SSTs-2H-70Column-74	2-4	TACGCATAACTACCCGACCACGGCAATCTGCTGGACACCACG
U-SSTs-2H-70Column-75	2-5	GAGGTAAGCTGTCTCTGCGAATCACCTGCAGACGCCATGCCA
U-SSTs-2H-70Column-76	2-6	CCATGCCACGCGGACGATCACACGCCATAATCGGCGGGCGGC
U-SSTs-2H-70Column-77	2-7	AGGGCTGGGCTTGTAAGGTGTGCAGAACGAGCGAGTTCGCG
U-SSTs-2H-70Column-78	2-8	TGCCCAGGCAGGGTATCATTTAGTAGGAACTAGGGCAACATG
U-SSTs-2H-70Column-79	2-9	CTCAGGACATTTTCAAGTAAATAATAGGAGCATAAGCAGTGTGG
U-SSTs-2H-70Column-80	2-10	GACCATCTACGCACTCAGCCAATCTCTTACACAAGTCTTTCT
U-SSTs-2H-70Column-81	2-11	CTTTAATCTCAGCCTGCTTTGCCAGGGACGCGTGATATCTGT
U-SSTs-2H-70Column-82	2-12	GACCGCATGAGCTCGTGGCGGAATCCAAACCGATTTCCATC
U-SSTs-2H-70Column-83	2-13	TCGCGATTTTACGGATATGAGCTGCCGTAAAGGGTTGTTTCG
U-SSTs-2H-70Column-84	2-14	GATCCATTAGTCGTAATAGCGTACTAATTATGTTTCCGTTTA
U-SSTs-2H-70Column-85	2-15	GACGTAGGCCTTACCGGAGGCGTGTCTATATAAGGCCGGCAG
U-SSTs-2H-70Column-86	2-16	GGAAGTCTTACACCAGCACTACATAAGTGGACGTGGCACCTT
U-SSTs-2H-70Column-87	2-17	TTGGCCGATTGGCAGTCAGTTCCCATTTACGGACACTTTCGT
U-SSTs-2H-70Column-88	2-18	TACGGAAAGGAGTTGTCAAACCTCATGCCCGTCCGAGTTAATG
U-SSTs-2H-70Column-89	2-19	GGGTACGGGCTTCCCTCAAGAGATCAAATAATCGGAGTCAGCC
U-SSTs-2H-70Column-90	2-20	TTGAATGTGGGAGAAGGGACAGCCGAGAGGTACACGAGCAGT
U-SSTs-2H-70Column-91	2-21	CTTTAGGTGAACCAAATCCGCTAAACCATAGCAGAGGCTGCG
U-SSTs-2H-70Column-92	2-22	TCTCTCACGCATTCTATTCGAGGGTGCGGGCCAGGCAAGGTC
U-SSTs-2H-70Column-93	2-23	CTCTGTTGCGAAGCAAGGAGCTGAGCAGTTAGTGTACGTAA
U-SSTs-2H-70Column-94	2-24	CCGTCCCGCTATCCTGAAGATTTCTGACAGGCACGATGTCTG
U-SSTs-2H-70Column-95	2-25	GTTAGGTTGAGGGCCATAGCCTGAATTTGCTTTGTAACGTAC

Seq_ID	Location	Sequence
U-SSTs-2H-70Column-96	2-26	GCTAAATCAGGAGTTCTAACGGTCCCACAACTTTGAGGCCCG
U-SSTs-2H-70Column-97	2-27	TTCGTCGCCGGTCAGGGATATATATATGTC'TTTGCGAGAGCCCA
U-SSTs-2H-70Column-98	2-28	CCGGGACTCATGTAACCAACCCAGCGGAGATGGTGTGTGCC
U-SSTs-2H-70Column-99	2-29	ACATG'TTCGGCACGCGGCACGGGCAGGTAACATAACAATAACT
U-SSTs-2H-70Column-100	2-30	GTGAGCCCAACTTGT'TCAAGCGTGGTGACCCGTGATGGCTTA
U-SSTs-2H-70Column-101	2-31	CTTCACGTGTGAGGATGCTCGGTTATAT'TCCCGGCGTGGTTG
U-SSTs-2H-70Column-102	2-32	ATAACGTAT'TCGTTTCCGGAGAAGCTCTTGT'TCCGATCGTGT
U-SSTs-2H-70Column-103	2-33	GGACTCTGCGTGCTGGAGAGGTAGTGCGAGTACGAACCTGGG
U-SSTs-2H-70Column-104	2-34	CTATTTGAAATGGAGCAATTTAGAGCTGAATGGATGTATTTA
U-SSTs-2H-70Column-105	2-35	AGCTGATTTTCGCTAAAGTCCAGAGGTGTCTAGTTTATGATAA
U-SSTs-2H-70Column-106	2-36	CGAGAGTATCGGTACCAGAGCGGCCGCACCACACGAACGCTA
U-SSTs-2H-70Column-107	2-37	TAAATTTCTCACTTCGACATCACTAAT'TGCTTACGGCCCAA
U-SSTs-2H-70Column-108	2-38	TAT'TCTCTCTGGACCTGAGCTGGAAGTTATAGCTTCAGCGTA
U-SSTs-2H-70Column-109	2-39	CGAGCCATACTTCTATTTGCCC'TTCGGCCCTGCTTATGGACC
U-SSTs-2H-70Column-110	2-40	TCCGCTGGGAATCGTTAAGGTTGTT'CATACGAGCCGCGGGTA
U-SSTs-2H-70Column-111	2-41	CGGCGATTGTATCGATGAGTTTGT'CATGAGCAAGTGGTCTT
U-SSTs-2H-70Column-112	2-42	GGCTGGGTGCGTCTGCGTTATGGTACCGTGTAGTACACCCTA
U-SSTs-2H-70Column-113	2-43	CTCTGCCTTCGTGCGATGCGCAAAGGTAGTAGCCTCAGATC
U-SSTs-2H-70Column-114	2-44	TAGTTCTGCCATACTACATATTCTGAATGCGTCTTTCCGGT
U-SSTs-2H-70Column-115	2-45	TCCAGAGTTGCGGCCGTAGCGAAGCCTCCCGTCTTCCCCTA
U-SSTs-2H-70Column-116	2-46	CCACTCTAGTACAACATAACCACGATCAGCCCATCCATGTCA
U-SSTs-2H-70Column-117	2-47	GTCTTATCGCTGTTGACGCGCGTTGACAATAGAGTAAAGAT
U-SSTs-2H-70Column-118	2-48	GTGGGCGTCATTTGGGTGCATACTTGT'TACTGGCTTGGGACA
U-SSTs-2H-70Column-119	2-49	AAAGAACGCTCTGCCCAACGATATTGTAATTATCTAACTATT
U-SSTs-2H-70Column-120	2-50	CTTGAGTAGGCCCGGAGGAGACTCGGCAAATGGTGGATTAAA
U-SSTs-2H-70Column-121	2-51	ACCTGTGT'CATCACAGAGTGGGCAAGCAGT'CGTATGGTAGCC
U-SSTs-2H-70Column-122	2-52	CTAT'TCCGCTTGTCTTAGCCTTTGGATCCGATCAAAGGCCTC
U-SSTs-2H-70Column-123	2-53	CGT'CGTCTGCATGCCTTAGCTCACCTGGTACAGACCAACT
U-SSTs-2H-70Column-124	2-54	ACGACTCGTAACGCGAAAGGTACGGCACTCGCAGGCGATCTA
U-SSTs-2H-70Column-125	2-55	CACGGCGACCGGACGAACAGCCGCTCTTTAGGACAGCGTATCA
U-SSTs-2H-70Column-126	2-56	AGGGATGGGAACAGGCAACCCTACACAGGGCCCGCTGTTCTG
U-SSTs-2H-70Column-127	2-57	GTTAGCTAGTCAACCAACTCGCGCAAGATGCTCTGGGCCCTA
U-SSTs-2H-70Column-128	2-58	ATCGTCGGTCC'CTCAGGCCTAAGTAACTAGGCTGGTGTGCTCG
U-SSTs-2H-70Column-129	2-59	AGGAATCTTGGATTGGACCCTTCAAGCCATAGAGTTGAGAGG
U-SSTs-2H-70Column-130	2-60	ATTGACCCTCGCGTGT'TCTTCAATGCTTTGGCTTATTTAA
U-SSTs-2H-70Column-131	2-61	ACAGAACC'CGGATGGCGTTACCGTCTATGGTCAGATGTCAA
U-SSTs-2H-70Column-132	2-62	TGGAAGACTATTTATCCCTAGCTGGTACTAGCAGGTTGGTAT
U-SSTs-2H-70Column-133	2-63	TGCCGGCGTTAATAGGTCTTTACAGATGAGACAGTACCTTG
U-SSTs-2H-70Column-134	2-64	CCTAAT'TCCGTTCCCTGGAATCTGGTATTGACTAGAGCCCGG
U-SSTs-2H-70Column-135	2-65	TCTTAGATCCGACGAGTTACGTTAAGCTTCCGAGACTTGGGT
U-SSTs-2H-70Column-136	2-66	CCGAGAGCAT'TCTTTACCAATCCCACCTACGCATCTCTAGGG
U-SSTs-2H-70Column-137	2-67	CGTTACTGTTTATCTGAGACCTACGGACCGCTACTAGGAGCT
U-SSTs-2H-70Column-138	2-68	AGTATGGGAAGGAAGCGGCACATGGCTCCAGCGTAGCTGGGC
U-SSTs-2H-70Column-139	2-69	TGCTGTGAGGCACAGCCCTATCCCACGTTACCTTGACGAGGA
U-SSTs-2H-70Column-140	2-70	CACCCGCACAACAGGGAGGGACATTCAGTTTGCTACACCGTT

U-SSTs-2Hx100C

Seq_ID	Location	Sequence
U-SSTs-2H-100Column-1	1-1	TGGTGGGACGTCTGTCTTCGTGACATGCATAACCTCAGTCGC
U-SSTs-2H-100Column-2	1-2	CGAACGGTTTGTCTGTACGCGAGTCAGTATACTACTAATGT
U-SSTs-2H-100Column-3	1-3	TGATTCCCTCATCGTGGTGTCCGTTATGCGTAAGACCGGTACA
U-SSTs-2H-100Column-4	1-4	AGCAGATTGCCTGGCATGGCGAGCTTACCTCGTGGTCGGGTA
U-SSTs-2H-100Column-5	1-5	TCTGCAGGTGAGCCGCCCGGTGGGCATGGTTCGCAGAGAC
U-SSTs-2H-100Column-6	1-6	ATTTAGGCGTGCGCGAACTCGGCCAGCCCTTGATCGTCCGC
U-SSTs-2H-100Column-7	1-7	CTCGTTCTGCACATGTTGCCCTGCCTGGGCACACCTTTACAA
U-SSTs-2H-100Column-8	1-8	TAGTTCCTACTCCACACTGCTATGTCTGAGAAATGATACCC
U-SSTs-2H-100Column-9	1-9	TATGCTCCTATAGAAAGACTTGTAGATGGTCTATTTACTGAA
U-SSTs-2H-100Column-10	1-10	GTGTAAGAGATACAGATATCAGAGATTAAGTGGCTGAGTGC
U-SSTs-2H-100Column-11	1-11	CGCGTCCCTGGGATGGAAATCTCATGCGGTCCAAAGCAGGCT
U-SSTs-2H-100Column-12	1-12	GGTTTGGATTCCGAAACAACCGAAATCGCGAGCGCCACGAGC
U-SSTs-2H-100Column-13	1-13	CTTTACGGCAGTAAACGGAACTAATGGATCCTCATATCCGT
U-SSTs-2H-100Column-14	1-14	CATAATTAGTACTGCCGGCTGGCCTACGTCCGCTATTACGA
U-SSTs-2H-100Column-15	1-15	TATATAGACACAAGGTGCCACTAGGACTTCCGCCTCCGGTAA
U-SSTs-2H-100Column-16	1-16	GTCCACTTATGACGAAAGTGTAATCGGCCAATAGTGCTGGTG
U-SSTs-2H-100Column-17	1-17	CCGTAAATGGGCATTAACCTCGCCTTTCCGTAAACTGACTGCC
U-SSTs-2H-100Column-18	1-18	GACGGGCATGAGGCTGACTCCGCCCGTACCCGTTTGACAACCT
U-SSTs-2H-100Column-19	1-19	GATTATTTGATACTGCTCGTGCCACATTCAACTCTTGAGGAA
U-SSTs-2H-100Column-20	1-20	ACCTCTCGGGCCGCAGCCTCTTCACCTAAAGTGTCCTTCTC
U-SSTs-2H-100Column-21	1-21	GCTATGGTTTAGACCTTGCCGTGAGAGAGCGGATTTGGT
U-SSTs-2H-100Column-22	1-22	GGCCCGCACCCCTTACGTGACACGCAACAGAGTCGAATAGAAT
U-SSTs-2H-100Column-23	1-23	CTAACTGCTCACAGACATCGTAGCGGGACGGGCTCCTTGCTT
U-SSTs-2H-100Column-24	1-24	GCCTGTGAGAAGTACGTTACATCAACCTAACATCTTCAGGAT
U-SSTs-2H-100Column-25	1-25	AAGCAAATTCACGGGCCTCAACTGATTTAGCGGCTATGGCCC
U-SSTs-2H-100Column-26	1-26	AGTTGTGGGACTGGGCTCTCGCGGCGACGAACGTTAGAATC
U-SSTs-2H-100Column-27	1-27	CAAAGACATATGGGACAACACTGAGTCCCAGGATATCCCTGAC
U-SSTs-2H-100Column-28	1-28	CATCTCCGCTGAGTTATTGTACCGAACATGTGGTTGGTTACA
U-SSTs-2H-100Column-29	1-29	TGTTACCTGCCTAAGCCATCATTTGGGCTCACCGTGCCGCGTG
U-SSTs-2H-100Column-30	1-30	CGGGTCAACCACCAACCACGCCACACGTGAAGGCTTGAACAAG
U-SSTs-2H-100Column-31	1-31	GGGAATATAACACACGATCGGAATACGTTATCGAGCATCCTC
U-SSTs-2H-100Column-32	1-32	AACAAGAGCTTCCCAGGTTTCGCGCAGAGTCCCTCCGGAAACG
U-SSTs-2H-100Column-33	1-33	TACTCGCACTATAAATACATCTTTCAAATAGCCTCTCCAGCA
U-SSTs-2H-100Column-34	1-34	CATTACGCTCTTTATCATAAAGAAATCAGCTAAATTGCTCCA
U-SSTs-2H-100Column-35	1-35	CTAGACACCTCTAGCGTTTCGTGATACTCTCGTGGACTTTAGC
U-SSTs-2H-100Column-36	1-36	GTGGTTCGGCCTTGGGCCGTGGAGAAATTTAGTCTGTTGTTACC
U-SSTs-2H-100Column-37	1-37	AAGCAATTAGTTACGCTGAAGAGAGAGAATAGATGTCGAAGT
U-SSTs-2H-100Column-38	1-38	CTATAACTTCCGGTCCATAAGGTATGGCTCGAGCTCAGGTCC
U-SSTs-2H-100Column-39	1-39	CAGGGCCGAAGTACCCGCGGCTCCCAGCCGAGGCAAATAGAA
U-SSTs-2H-100Column-40	1-40	TCGTATGAACAAAGACCCACTACAATCGCCGACCTTAACGAT
U-SSTs-2H-100Column-41	1-41	TGCTCATGACATAGGGTGTACGCACCCAGCCAACCTCATCGAT
U-SSTs-2H-100Column-42	1-42	TACACGGTACCGATCTGAGGCGAAGGCAGAGATAACGCAGAC
U-SSTs-2H-100Column-43	1-43	TACTACCTTTGACCGAAAGAGGCAGAAGTACGCGATCGCAC
U-SSTs-2H-100Column-44	1-44	CGCATTGAGAAATAGTGGGAAGCAACTCTGGATATGTAGGTAT
U-SSTs-2H-100Column-45	1-45	ACGGGAGGCTTTGACATGGATACTAGAGTGGCGCTACGGCCG
U-SSTs-2H-100Column-46	1-46	GGGCTGATCGTATCTTTACTCGCGATAAGACGGTTATGTTGT
U-SSTs-2H-100Column-47	1-47	TATTGTCAACGTGTCCAAGCTGACGCCACCCGCGTCAACA

Seq_ID	Location	Sequence
U-SSTs-2H-100Column-48	1-48	CAGTAACAAGTAATAGTTAGAAGCGTTCTTTATGCACCCAAA
U-SSTs-2H-100Column-49	1-49	TAATTACAATATTTAATCCACCCTACTCAAGTCGTTGGGCAG
U-SSTs-2H-100Column-50	1-50	CATTTGCCGAGGGCTACCATATGACACAGGTTCTCCTCCGGG
U-SSTs-2H-100Column-51	1-51	CGACTGCTTGCGAGGCCTTTGAGCGGAATAGCCACTCTGTGA
U-SSTs-2H-100Column-52	1-52	ATCGGATCCAAAGTGTTGGTTCGCAGACGACGAGGCTAAGACA
U-SSTs-2H-100Column-53	1-53	TGTACCAGGTGTAGATCGCCTTACGAGTCGTAGCTAAGGCAT
U-SSTs-2H-100Column-54	1-54	GCGAGTGCCGTTGATACGCTGGGTGCGCCGTGACCTTTCGCGT
U-SSTs-2H-100Column-55	1-55	TCCTAAAGACGCAGAACAGCGTCCCATCCCTGCTGTTTCGTCC
U-SSTs-2H-100Column-56	1-56	GGCCCTGTGTATAGGGCCAGACTAGCTAACGGGTTGCCTGT
U-SSTs-2H-100Column-57	1-57	AGCATCTTGC GCGAGCACACCGACCGACGATCGAGTTGGTTG
U-SSTs-2H-100Column-58	1-58	AGCCTAGTTACCCTCTCAACTCAAGATTCCTTTAGGCCTGAG
U-SSTs-2H-100Column-59	1-59	CTATGGCTTGATTTAATAAGCGAGGGTCAATAGGGTCCAATC
U-SSTs-2H-100Column-60	1-60	CAAAGCATTGATTGACATCTGGCGGTTCTGTAGAGAACACGC
U-SSTs-2H-100Column-61	1-61	ACCATAGACGGATACCAACCTTAGTCTTCCATAACGCCATCC
U-SSTs-2H-100Column-62	1-62	GCTAGTACCAGCAAGGTACTGAACGCCGGCACTAGGGATAAA
U-SSTs-2H-100Column-63	1-63	TCTCATCTGTGCCGGGCTCTACGGAATTAGGAAAGACCTATT
U-SSTs-2H-100Column-64	1-64	GTCAATACCAGACCCAAGTCTGGATCTAAGAATTCAGGGAA
U-SSTs-2H-100Column-65	1-65	CGGAAGCTTAACCCTAGAGATATGCTCTCGGCGTAACTCGTC
U-SSTs-2H-100Column-66	1-66	GCGTAGGTGGGAGCTCCTAGTAACAGTAACGATTGGTAAAGA
U-SSTs-2H-100Column-67	1-67	AGCGGTCCGTAGCCAGCTACTTCCATACTGGTCTCAGATA
U-SSTs-2H-100Column-68	1-68	GCTGGAGCCATTCCTCGTCAACCTCACAGCAGTGCCGCTTCC
U-SSTs-2H-100Column-69	1-69	GGTAACGTGGGAACGGTGTAGTGTGCGGGTGATAGGGCTGTG
U-SSTs-2H-100Column-70	1-70	CAAAGTGAATGATGTGGGCGATCGACTTCATTCCCTCCCTGT
U-SSTs-2H-100Column-71	1-71	TCAATAGTACTCCATATTTTCAGACGAGAGAAGCAGAGCCAAA
U-SSTs-2H-100Column-72	1-72	TATGCAATACGCTCGGGTGAGTGTATTTGAGCTTCATCCACG
U-SSTs-2H-100Column-73	1-73	ACTGTGAGTTAGGCTTCGAGCTTCTTTAAGGGCTTAGCCAGG
U-SSTs-2H-100Column-74	1-74	CGCCAAGAAAGAAAGGGTGTGGCGAAGAACC CGCTAAGTAGA
U-SSTs-2H-100Column-75	1-75	TAGCGACCACCAGAAGACTGATGTACCCTTTAGCGCACTCTT
U-SSTs-2H-100Column-76	1-76	CTTTGTAGAGTCTTACGGCGAGTTGCTGCACCTATGATGCAA
U-SSTs-2H-100Column-77	1-77	AGGTCTGGAACCGTACGATATACAGCCCAAGTGGCACTTTAC
U-SSTs-2H-100Column-78	1-78	TGATGTCTTACGGCTGGATGGAGCCTCTAACTTCGCAGCGTT
U-SSTs-2H-100Column-79	1-79	CTAGATTTTATTGAAGTCTATCAGTCTAGAATGAGTACATTTA
U-SSTs-2H-100Column-80	1-80	AGCCGGCATGGATCTGAACTTCAGCGAGACACTGTTATCTT
U-SSTs-2H-100Column-81	1-81	AGTATATCTATCTCACC GAAGGTATGCCCGCCAGTATAGGC
U-SSTs-2H-100Column-82	1-82	TCGTATGTCCGGCCACGGCGGAAACAGGTTTCCCTGATGATG
U-SSTs-2H-100Column-83	1-83	CACACGGGTTTATAGCATTTCGATGATGGTCCACCCATTCCGC
U-SSTs-2H-100Column-84	1-84	ATCGATGGGATAGTTTAATTAGCCTGCGGAGGGCATGCGGAC
U-SSTs-2H-100Column-85	1-85	ATCGTCCACCTCGAGGCTTGT CATCTAAAGATGACCCAGTCT
U-SSTs-2H-100Column-86	1-86	TATTCGAACGTCTCTGTGCGCAAGTTTATTCTTGCCGTATTA
U-SSTs-2H-100Column-87	1-87	GAATGTACGACCAAAGTACGGTACAACGTTACGTAGCTTCTG
U-SSTs-2H-100Column-88	1-88	GATGATATGGCGTAATAAACACTTAAACAATGAGAGACGGCA
U-SSTs-2H-100Column-89	1-89	ACGAGGAGATATCTAAGTCGCTGAGTGGCATTTCTGTGCTA
U-SSTs-2H-100Column-90	1-90	GCCGAAAGGCCGTAATTTCCCGAGACCATTAGAGACGCTAATC
U-SSTs-2H-100Column-91	1-91	CGGACCGTATTGTTTGACCCGATCAGTTCTTTGGAAGCCAAG
U-SSTs-2H-100Column-92	1-92	CTAAGGTCCCTCTGGTGTCTGGGCGACTGGACTCTCGCTCCG
U-SSTs-2H-100Column-93	1-93	CGGCGGGACTTACACTTAGGTACAAGCGTTT TAGGAAGCAGGT
U-SSTs-2H-100Column-94	1-94	AACCCGCAGATCACTACCGCGTCGCTAGTCGGCGGTTAGCTC
U-SSTs-2H-100Column-95	1-95	CGTTTAAATAAGCTCAGTGGTCGAGACGATGTTGATGAACTT

Seq_ID	Location	Sequence
U-SSTs-2H-100Column-96	1-96	AGGACCAGGATAACTTTCTTCTCCTACGCTCAATTGCCTCAA
U-SSTs-2H-100Column-97	1-97	AGAGCTGGGTAGGTACGCAGCATCCAGATAAGGGTAGAACCC
U-SSTs-2H-100Column-98	1-98	ATTGCGCCACATACGTTTCCAGGTCGGGAAGTTGTCGTCTAA
U-SSTs-2H-100Column-99	1-99	GCGACCGCGGCATTGACTGTTGCCGGTCGGGCTATCCCCACA
U-SSTs-2H-100Column-100	1-100	GAATTTCCGCTttttttttttttttttttttttttttttTTGTAAATTGT
U-SSTs-2H-100Column-101	2-1	tttttttttttGCGACTGAGGTACGTCCCACCAttttttttttt
U-SSTs-2H-100Column-102	2-2	TATGCATGTCACATTAGTAGTCAAACCGTTTCGACGAAGACAG
U-SSTs-2H-100Column-103	2-3	ATACTGACTCTGTACCGGTCTATGAGGAATCAGCGTGACAGA
U-SSTs-2H-100Column-104	2-4	TACGCATAACTACCCGACCACGGCAATCTGCTGGACACCACG
U-SSTs-2H-100Column-105	2-5	GAGGTAAGCTGTCTCTGCGAATCACCTGCAGACGCCATGCCA
U-SSTs-2H-100Column-106	2-6	CCATGCCACGCGGACGATCACACGCCTAAATCGGCGGCGGC
U-SSTs-2H-100Column-107	2-7	AGGGCTGGGCTTGTAAAGGTGTGCAGAACGAGCGAGTTCGCG
U-SSTs-2H-100Column-108	2-8	TGCCCAGGCAGGGTATCATTTAGTAGGAAGTACGGCAACATG
U-SSTs-2H-100Column-109	2-9	CTCAGGACATTTTCAGTAAATAATAGGAGCATAAGCAGTGTGG
U-SSTs-2H-100Column-110	2-10	GACCATCTACGCACTCAGCCAATCTCTTACACAAGTCTTTCT
U-SSTs-2H-100Column-111	2-11	CTTTAATCTCAGCCTGCTTTGCCAGGGACGCGTGATATCTGT
U-SSTs-2H-100Column-112	2-12	GACCGCATGAGCTCGTGGCGGAATCCAAACCGATTTCCATC
U-SSTs-2H-100Column-113	2-13	TCGCGATTTACGGATATGAGCTGCCGTAAAGGGTTGTTTCG
U-SSTs-2H-100Column-114	2-14	GATCCATTAGTCGTAATAGCGTACTAATTATGTTTCCGTTTA
U-SSTs-2H-100Column-115	2-15	GACGTAGGCCTTACCGGAGGCGTGTCTATATAAGGCCGGCAG
U-SSTs-2H-100Column-116	2-16	GGAAGTCCTACACCAGCACTACATAAGTGGACGTGGCACCTT
U-SSTs-2H-100Column-117	2-17	TTGGCCGATTTGGCAGTCAGTCCCATTTACGGACACTTTTCGT
U-SSTs-2H-100Column-118	2-18	TACGGAAAGGAGTTGTCAAACCTCATGCCCGTCCGAGTTAATG
U-SSTs-2H-100Column-119	2-19	GGGTACGGGCTTCCTCAAGAGATCAAATAATCGGAGTCAGCC
U-SSTs-2H-100Column-120	2-20	TTGAATGTGGGAGAAGGGACAGCCCAGAGGTCACGAGCAGT
U-SSTs-2H-100Column-121	2-21	CTTTAGGTGAACCAAATCCGCTAAACCATAGCAGAGGCTGCG
U-SSTs-2H-100Column-122	2-22	TCTCTCACGCATTTCTATTCGAGGGTGCGGGCCAGGCAAGGTC
U-SSTs-2H-100Column-123	2-23	CTCTGTTGCGAAGCAAGGAGCTGAGCAGTTAGTGTACAGTAA
U-SSTs-2H-100Column-124	2-24	CCGTCCCCTATCCTGAAGATTTCTGACAGGCACGATGTCTG
U-SSTs-2H-100Column-125	2-25	GTTAGGTTGAGGGCCATAGCCTGAATTTGCTTTGTAACGTAC
U-SSTs-2H-100Column-126	2-26	GCTAAATCAGGAGTTCTAACGGTCCCACAACCTTTGAGGCCCG
U-SSTs-2H-100Column-127	2-27	TTCTGTCGCCGTCAGGGATATATATGTCTTTGCGAGAGCCCA
U-SSTs-2H-100Column-128	2-28	CCGGGACTCATGTAACCAACCAGCGGAGATGGTGTGTTGCC
U-SSTs-2H-100Column-129	2-29	ACATGTTCCGGCACGCGGCACGGGCAGGTAACATACAATAACT
U-SSTs-2H-100Column-130	2-30	GTGAGCCCAACTTGTTC AAGCGTGGTGACCCGTGATGGCTTA
U-SSTs-2H-100Column-131	2-31	CTTCACGTGTGAGGATGCTCGGTTATATTTCCCGCGTGTTG
U-SSTs-2H-100Column-132	2-32	ATAACGTATTCGTTTCCGGAGAAGCTCTTGTTCGGATCGTGT
U-SSTs-2H-100Column-133	2-33	GGACTCTGCGTGCTGGAGAGGTAGTGCGAGTACGAACCTGGG
U-SSTs-2H-100Column-134	2-34	CTATTTGAAATGGAGCAATTTAGAGCTGAATGGATGTATTTA
U-SSTs-2H-100Column-135	2-35	AGCTGATTTTCGCTAAAGTCCAGAGGTGTCTAGTTTATGATAA
U-SSTs-2H-100Column-136	2-36	CGAGAGTATCGGTACCAGAGCGGCCACCACACGAACGCTA
U-SSTs-2H-100Column-137	2-37	TAAATTTCTCACTTCGACATCACTAATTGCTTCACGGCCCAA
U-SSTs-2H-100Column-138	2-38	TATTCTCTCTGGACCTGAGCTGGAAGTTATAGCTTCAGCGTA
U-SSTs-2H-100Column-139	2-39	CGAGCCATACTTCTATTTGCCCTTCGGCCCTGCTTATGGACC
U-SSTs-2H-100Column-140	2-40	TCGGCTGGGAATCGTTAAGGTTGTTTCATACGAGCCGCGGGTA
U-SSTs-2H-100Column-141	2-41	CGGCGATTGTATCGATGAGTTTGTTCATGAGCAAGTGGGTCTT
U-SSTs-2H-100Column-142	2-42	GGCTGGGTGCGTCTGCGTTATGGTACCGTGTAGTACACCCTA
U-SSTs-2H-100Column-143	2-43	CTCTGCCTTCGTGCGATGCGCCAAAGGTAGTAGCCTCAGATC

Seq_ID	Location	Sequence
U-SSTs-2H-100Column-144	2-44	TAGTTCTGCCATACCTACATATTCTGAATGCGTCTTTCCGGT
U-SSTs-2H-100Column-145	2-45	TCCAGAGTTGCGGCCGTAGCGAAGCCTCCCGTCTTCCCCTA
U-SSTs-2H-100Column-146	2-46	CCACTCTAGTACAACATAACCACGATCAGCCCATCCATGTCA
U-SSTs-2H-100Column-147	2-47	GTCTTATCGCTGTTGACGCGGCGTTGACAATAGAGTAAAGAT
U-SSTs-2H-100Column-148	2-48	GTGGGCGTCATTTGGGTGCATACTTGTTACTGGCTTGGGACA
U-SSTs-2H-100Column-149	2-49	AAAGAACGCTCTGCCCAACGATATTGTAATTATCTAACTATT
U-SSTs-2H-100Column-150	2-50	CTTGAGTAGGCCCGGAGGAGACTCGGCCAAATGGTGGATTAAA
U-SSTs-2H-100Column-151	2-51	ACCTGTGTCATCACAGAGTGGGCAAGCAGTCGTATGGTAGCC
U-SSTs-2H-100Column-152	2-52	CTATTCGCTTGTCTTAGCCTTTGGATCCGATCAAAGGCCCTC
U-SSTs-2H-100Column-153	2-53	CGTCGTCTGCATGCCTTAGCTCACCTGGTACAGACCAACACT
U-SSTs-2H-100Column-154	2-54	ACGACTCGTAACGCGAAAGGTACGGCACTCGCAGGCGATCTA
U-SSTs-2H-100Column-155	2-55	CACGGCGACCGGACGAACAGCCGTCTTTAGGACAGCGTATCA
U-SSTs-2H-100Column-156	2-56	AGGGATGGGAACAGGCAACCCTACACAGGGCCCCGCTGTTCTG
U-SSTs-2H-100Column-157	2-57	GTTAGCTAGTCAACCAACTCGCGCAAGATGCTCTGGGCCCTA
U-SSTs-2H-100Column-158	2-58	ATCGTCGGTCCCTCAGGCCTAAGTAACTAGGCTGGTGTGCTCG
U-SSTs-2H-100Column-159	2-59	AGGAATCTTGATTGGACCCCTCAAGCCATAGAGTTGAGAGG
U-SSTs-2H-100Column-160	2-60	ATTGACCCCTCGCGTGTCTCTTCAATGCTTTGGCTTATTAAA
U-SSTs-2H-100Column-161	2-61	ACAGAACC GCGGATGGCGTTACCGTCTATGGTCAGATGTCAA
U-SSTs-2H-100Column-162	2-62	TGGAAGACTATTTATCCCTAGCTGGTACTAGCAGTTGGTAT
U-SSTs-2H-100Column-163	2-63	TGCCGGCGTTAATAGGTCTTTCACAGATGAGACAGTACCTTG
U-SSTs-2H-100Column-164	2-64	CCTAATTCCGTTCCCTGGAATCTGGTATTGACTAGAGCCCCGG
U-SSTs-2H-100Column-165	2-65	TCTTAGATCCGACGAGTTACGTTAAGCTTCCGAGACTTGGGT
U-SSTs-2H-100Column-166	2-66	CCGAGAGCATTTCTTTACCAATCCCACCTACGCATCTCTAGGG
U-SSTs-2H-100Column-167	2-67	CGTTACTGTTTATCTGAGACCTACGGACCGCTACTAGGAGCT
U-SSTs-2H-100Column-168	2-68	AGTATGGGAAGGAAGCGGCACATGGCTCCAGCGTAGCTGGGC
U-SSTs-2H-100Column-169	2-69	TGCTGTGAGGCACAGCCCTATCCCACGTTACCTTGACGAGGA
U-SSTs-2H-100Column-170	2-70	CACCCGCACAACAGGGAGGGACATTCAGTTTGCTACACCGTT
U-SSTs-2H-100Column-171	2-71	ATGAAGTCGATTTGGCTCTGCAGTACTATTGATCGCCCACAT
U-SSTs-2H-100Column-172	2-72	TTCTCTCGTCCGTGGATGAAGCGTATTGCATATGAAATATGG
U-SSTs-2H-100Column-173	2-73	CTCAAATACACCTGGCTAAGCTAACTCACAGTCTCACCCGAG
U-SSTs-2H-100Column-174	2-74	CCTTAAAGAACTACTTAGCGCTTTCTTGGCGGCTCGAAGCC
U-SSTs-2H-100Column-175	2-75	GGTTCTTCGCAAGAGTGCGCTGGTGGTTCGCTACACACCCTTT
U-SSTs-2H-100Column-176	2-76	AAAGGGTACATTGCATCATAGACTCTACAAAGTCAGTCTTCT
U-SSTs-2H-100Column-177	2-77	GTGCAGCAACGTAAGTGCCAGTTCCAGACCTTCGCCGTAAG
U-SSTs-2H-100Column-178	2-78	CTTGGGCTGTAACGCTGCGAAGTAGGACATCAATATCGTACG
U-SSTs-2H-100Column-179	2-79	GTTAGAGGCTTAAATGTACTCAATAAATCTAGCCATCCAGCC
U-SSTs-2H-100Column-180	2-80	ATTCTAGACTAAGATAACAGTCCATGCCGGCTGATAGACTTC
U-SSTs-2H-100Column-181	2-81	GTCTCGCTGGGCCTATACTGGATAGATATACTAAGTTCAGAT
U-SSTs-2H-100Column-182	2-82	CGGGCATACCCATCATCAGGGCGGACATACGACTTCGGTGAG
U-SSTs-2H-100Column-183	2-83	AAACCTGTTTGC GGAATGGGTAAACCCGTGTGCCGCCGTGGC
U-SSTs-2H-100Column-184	2-84	GGACCATCATGTCCGCATGCCATCCCATCGATCGAATGCTAT
U-SSTs-2H-100Column-185	2-85	CTCCGCAGGCAGACTGGGTCAAGGTGGACGATTAATTAAACT
U-SSTs-2H-100Column-186	2-86	TCTTTAGATGTAATACGGCAAACGTTTCAATAACAAGCCTCG
U-SSTs-2H-100Column-187	2-87	GAATAAACTTCAGAAGCTACGGTCGTACATTCGGCGACAGAG
U-SSTs-2H-100Column-188	2-88	TAACGTTGTATGCCGTCTCTCGCCATATCATCCCGTACTTTG
U-SSTs-2H-100Column-189	2-89	ATTGTTTTAAGTAGCACAGAAATATCTCCTCGTTGTTTATTAC
U-SSTs-2H-100Column-190	2-90	TGCCACTCAGGATTAGCGTCTGGCCTTTCCGGCGGACTTAGA
U-SSTs-2H-100Column-191	2-91	CTAATGGTCTCTTGGCTTCCAAATACGGTCCGCGGGAATTAC

Seq_ID	Location	Sequence
U-SSTs-2H-100Column-192	2-92	AAGAACTGATCGGAGCGAGAGAGGGACCTTAGCGGGTCAAAC
U-SSTs-2H-100Column-193	2-93	TCCAGTCGCCACCTGCTTCCTAAGTCCCGCCGAGACACCAG
U-SSTs-2H-100Column-194	2-94	AAACGCTTGTGAGCTAACCGCATCTGCGGGTTACCTAAGTGT
U-SSTs-2H-100Column-195	2-95	CGACTAGCGAAAGTTCATCAATTATTTAAACGCGCGGTAGTG
U-SSTs-2H-100Column-196	2-96	CATCGTCTCGTTGAGGCAATTATCCTGGTCCCTACCACTGAGC
U-SSTs-2H-100Column-197	2-97	GAGCGTAGGAGGGTTCTACCCTACCCAGCTCTGAAGAAAGTT
U-SSTs-2H-100Column-198	2-98	TTATCTGGATTTAGACGACAATGTGGCGCAATGCTGCGTACC
U-SSTs-2H-100Column-199	2-99	CTTCCCGACCTGTCGGGATAGGCCGCGGTGCTGGAAACGTA
U-SSTs-2H-100Column-200	2-100	CCCACCGGCACAATTAACAAAGCGAAATTC AACAGTCAAT

U2-SSTs-12H

Seq_ID	Location	Sequence
U2-SSTs-12H-1	1-1	CATGACACTTAAACATCTAATACACGTTTGTACTGCCTACCT
U2-SSTs-12H-2	1-2	TCCGAAAGGTCGGTGGCCTCTGCTCCAGGGACAAGGACAAGG
U2-SSTs-12H-3	1-3	TTCAATATGGGCTGGGACGCCTGTGTCGTACCATTTTCGGAAC
U2-SSTs-12H-4	1-4	CTGGACATGTGGGCATCAAGATAGACCTGGACCAGGACACGC
U2-SSTs-12H-5	1-5	TCATCCTACATCCCTAAAGGTCGTACCACGCCGACAATTTAG
U2-SSTs-12H-6	1-6	GGGTCCGTTCAACGAAAGACTGCTTTGCCCTTTGGTGATGCA
U2-SSTs-12H-7	1-7	CAGGGCGTAGCAAATATTTACGTACCCGTTGTGTCGTCAATG
U2-SSTs-12H-8	1-8	TCTAATGTTATTACCTTGCACGGGCTTCCACCGATACTATA
U2-SSTs-12H-9	1-9	ATCAAGCCGCCTGTGATTATCGGTTTCCAGGTAGACACCGAA
U2-SSTs-12H-10	1-10	GCTGCAGAGCCCTCTTGCACATGGTACCGTGACCTATCGGGC
U2-SSTs-12H-11	1-11	AATTGGTTATCTAAGGACTGGGCACGGAAAGACATCTCCGAC
U2-SSTs-12H-12	1-12	GAAAGGATTATAGAGGACTATATGCGTGCCCTCCGGACGACC
U2-SSTs-12H-13	1-13	GAAAGCAGAATGATTTACTAATTGCTTTGCTGGCTGGCAGCT
U2-SSTs-12H-14	1-14	GCATGCGTGATACTAACTACATAGTAGAGCAAATTTTCAGCCA
U2-SSTs-12H-15	1-15	AACTATCGATGGTTTTTTTTTTTTTTTTTTTTTTTATGCACATAA
U2-SSTs-12H-16	2-1	TTTTTTTTTTTTGCGCTAAGCATTAAAGTGTCATGTTTTTTTTTT
U2-SSTs-12H-17	2-2	ACGATTTAGGCCACTACTAATCGACCTTTCGGAATTAGATGT
U2-SSTs-12H-18	2-3	CACGGGCTCGAATCGTTAACTGCCCATATTGAAAGAGGCCAC
U2-SSTs-12H-19	2-4	AAACAGGAGAACCCTGAGTCGCCACATGTCCAGGGCGTCCCA
U2-SSTs-12H-20	2-5	CTCATCCCGGGCGTTTGGACCGATGTAGGATGATCTTGATGC
U2-SSTs-12H-21	2-6	GAGCTTGCAGAGTCCCAATGGTTGAACCGACCCACCTTTAGG
U2-SSTs-12H-22	2-7	GAAATTCGATAGCCGTGCGATGCTACGCCCTGAGTCTTTTCG
U2-SSTs-12H-23	2-8	GACTCATGGTCTGTGTCGTCGCAAATAACATTAGAGTAAATATT
U2-SSTs-12H-24	2-9	GCGAGATACACGGTTCAGGATAGGCGCTTGATTTCGCAAGGT
U2-SSTs-12H-25	2-10	CTTAGAACTATCGGAGCGCTCGGGCTCTGCAGCGATAATCAC
U2-SSTs-12H-26	2-11	GGACGATCCTTGTGTCTCCAAGATAACCAATTTGTGCAAGA
U2-SSTs-12H-27	2-12	CTTAGTGGGCAAATAAACGTGTATAATCCTTTCCAGTCCTT
U2-SSTs-12H-28	2-13	GGTAAGTGACGTGTTTAGAATCATTCTGCTTTCATAGTCCTC
U2-SSTs-12H-29	2-14	TAGTATAACCGTCACAGAGGTTATCACGCATGCTTAGTAAAT
U2-SSTs-12H-30	2-15	TTGCAAACCTCAGAATGGCACTCCATCGATAGTTTGTAGTTAG
U2-SSTs-12H-31	3-1	ACGCATATTGCCGGCACCTAAGCCTAAATCGTTGCTTAGCGC
U2-SSTs-12H-32	3-2	GCAGCGGTCCCTGCCAGAACCGTCGAGCCCGTGATTAGTAGTG
U2-SSTs-12H-33	3-3	GGACATTATATGCTGCCATGGTTCTCCTGTTTAGTTAACGAT
U2-SSTs-12H-34	3-4	CACGTGACTCAGTCCTATTATCCCGGATGAGCGACTCAGGG
U2-SSTs-12H-35	3-5	TACACTAATCTTCGAGGCTGCCTCGCAAGCTCGGTCCAAACG
U2-SSTs-12H-36	3-6	TTGAGGTTGGAGGACATATCCATCGGAATTTCCCATTTGGGAC
U2-SSTs-12H-37	3-7	GAGCTCGGACGCGTCCGCGTGGACCATGAGTCTCGCACGGCT
U2-SSTs-12H-38	3-8	GCTTAGTCGCCGAGAAAGATAGTGTATCTCGCTGGCACGACA
U2-SSTs-12H-39	3-9	ACGGTAGACTCTCGTGCTTGGATAGTTCTAAGATCCTGAACC
U2-SSTs-12H-40	3-10	TCGCCCTACTGTTTACAGTTGAAGGATCGTCCGAGCGCTCCG
U2-SSTs-12H-41	3-11	CTTTCGTAACAGTCCTCGTTCTGCCACTAAGTGGGAGACAC
U2-SSTs-12H-42	3-12	TGGAAACGGTGTGGCGCCCATCGTCACTTACCCACGTTTATT
U2-SSTs-12H-43	3-13	TATGCGAGTTTAAATGGGCTCTCGGTTATACTAATTTCTAAACA
U2-SSTs-12H-44	3-14	AGGACACACAGCTTTCCTGCTGAGTTTGCAAACCTCTGTGA
U2-SSTs-12H-45	3-15	CAGTCCAAGGCGTTTTTTTTTTTTTTTTTTTTTTTAGTGCCATTC
U2-SSTs-12H-46	4-1	TTTTTTTTTTTTCTTCATTCTCGGCAATATGCGTTTTTTTTTTT

Seq_ID	Location	Sequence
U2-SSTs-12H-47	4-2	GACGGGCGGGACTGTTGGAGTCAGGACCGCTGCTTAGGTGCC
U2-SSTs-12H-48	4-3	GTAAGATCGTTTACCCTAGTTCATATAATGTCCCGTTCTGG
U2-SSTs-12H-49	4-4	CCCATAGTTTGAGGGTTCCTACTGAGTCACGTGCCATGGCAG
U2-SSTs-12H-50	4-5	AGATGCGCTCATAACATCTCAAAGATTAGTGTAATAATAGGA
U2-SSTs-12H-51	4-6	TACGGTTCGAGATTAATTCTACTCCAACCTCAAGCAGCCTCG
U2-SSTs-12H-52	4-7	GACTCTGAACCCTACCTAAGTGCGTCCGAGCTCGGATATGTC
U2-SSTs-12H-53	4-8	ACGTGACATAAGCATCAACCTCGGGACTAAGCCACGCGGAC
U2-SSTs-12H-54	4-9	TCTTTAGCATGCATCGTGTAGAGAGTCTACCGTTATCTTTCT
U2-SSTs-12H-55	4-10	GGCGTTATCATTAGATTTACCACAGTAGGGCGACCAAGCAGG
U2-SSTs-12H-56	4-11	CTGTGCGGGCGAACGACTTAGGCTGTTACGAAAGCAACTGTAA
U2-SSTs-12H-57	4-12	TTTCTTTATGCCGCGTATTTACACCGTTTCCAGAACGAGGA
U2-SSTs-12H-58	4-13	GACTTTGGCTTCCTTGACGCTTAAACTCGCATAATGGGCGCC
U2-SSTs-12H-59	4-14	GCAGATCCAATCGTTATTCAGCTGTGTGTCTAGAGCCCAT
U2-SSTs-12H-60	4-15	CACCCTTAGACGAGAGTTGTACGCCCTTGACTGGCAGGGAAA
U2-SSTs-12H-61	5-1	CTTAGTATAGGCCTTCTCGCTTCCCGCCGTCGAGAATGAAG
U2-SSTs-12H-62	5-2	CTTAGGTTGCGAGGTGTTCTTAACGATCTTACACTCCAACAG
U2-SSTs-12H-63	5-3	TCTCTTATGAGTGCAGTCTGCAAACCTATGGGAACCTAGGGTA
U2-SSTs-12H-64	5-4	TCTTCTAAATGCGACCGGTACTGAGCGCATCTTGGGAACCCT
U2-SSTs-12H-65	5-5	CCTTAAGCTGGGCCAAGGTATCTGCGACCGTATGAGATGTTA
U2-SSTs-12H-66	5-6	AAATGATGCTCTATACAAAGCGGTTTACAGAGTCTAGAATTAAT
U2-SSTs-12H-67	5-7	CGTCGCCCTTGAGGGTCTGCCTTATGTCACGTACTTAGGTAG
U2-SSTs-12H-68	5-8	AACAATATTGGCGACTGTCGTCATGCTAAAGAAGGTTGATGC
U2-SSTs-12H-69	5-9	TTACCGAGGTAGACTTTCATATGATAACGCCCTACACGATG
U2-SSTs-12H-70	5-10	TTAATCATGTTGGTACTACGTTTCGCCCACAGGGTAAATCTA
U2-SSTs-12H-71	5-11	TACGTGGAGGTGCGTAAGGCAGCATAAAGAAACCTAAGTCGT
U2-SSTs-12H-72	5-12	GTCGCGCATCGTTAAGCCCGTAAGCCAAAGTCGAAATACGCG
U2-SSTs-12H-73	5-13	CCATGCATCGGCTGTAGTCCAATTGGATCTGCAGCGTCAAGG
U2-SSTs-12H-74	5-14	GGGCCTATTCATGGTCTACTGTCTAAGGGTGTGGAATAACG
U2-SSTs-12H-75	5-15	GTATTATCGATATTTTTTTTTTTTTTTTTTTTACAACCTCTC
U2-SSTs-12H-76	6-1	TTTTTTTTTTTTTACTACTCCCGCCTATACTAAGTTTTTTTTTT
U2-SSTs-12H-77	6-2	GCTTCCATATTGTATACTGTATCGCAACCTAAGAGCGAGAAG
U2-SSTs-12H-78	6-3	GCAGAGTAGTAGACCATCGAAACTCATAAGAGAAGGAACACC
U2-SSTs-12H-79	6-4	GCTACTTTCACCCTTTAGCGAGCATTTAGAAGACAGGACTGC
U2-SSTs-12H-80	6-5	AAGCGCAAAGAACGGCCCATGCCAGCTTAAGGGTACCGGTC
U2-SSTs-12H-81	6-6	CGTCTCATGTCGCCCTCGCTAAGAGCATCATTTATACCTTGG
U2-SSTs-12H-82	6-7	CTCTATCCACCCTTCGTAGGACTCAAGGCGACGGCTTTGTAT
U2-SSTs-12H-83	6-8	TTTAGTTGAACTCGAGTGAAGCCAATATTGTTGGCAGGACC
U2-SSTs-12H-84	6-9	AGCCAGGATCAACCAACTCTGCTACCTCGGTAAACGACAGTC
U2-SSTs-12H-85	6-10	CAAGGAAAGCATTTCCTGCTCAACATGATTAAGTGAAAGT
U2-SSTs-12H-86	6-11	GGCTAAGCGTTGCGAACTCCGCACCTCCACGTAACGTAGTAC
U2-SSTs-12H-87	6-12	ATGACTGTTTCACACTGGAGCACGATGCGCGACTGCCTTACG
U2-SSTs-12H-88	6-13	TTCCAAATCCACAAGTGAAGGGCCGATGCATGGACGGGCTTA
U2-SSTs-12H-89	6-14	AACCTACGGTCTGTACCCTATATGAATAGGCCCTGGACTACA
U2-SSTs-12H-90	6-15	TTGCTCAATTTACACGCAGATTATCGATAATACAGTAGGACC
U2-SSTs-12H-91	7-1	GGACTCGGTAGCGTTTAATTGAATATGGAAGCCGGGAGTATG
U2-SSTs-12H-92	7-2	AGCTTTATCGACTCGAGTCTCTACTACTCTGCTACAGTATAC
U2-SSTs-12H-93	7-3	ACAGATCGACGTTTAGGGTATGTGAAAGTAGCTTCGATGGTC

Seq_ID	Location	Sequence
U2-SSTs-12H-94	7-4	ATTAGCGATTGAGAAGCTGTTTCTTTGCGCTTTCGCTAAAGG
U2-SSTs-12H-95	7-5	GTCTAAGCCGATAGTAGATAGGACATGAGACGCATGGGCCGT
U2-SSTs-12H-96	7-6	GGCTGTAAAGAACAAATGTTGGTGGATAGAGTAGCGAGGGC
U2-SSTs-12H-97	7-7	GACATGCGCCAGGTGGTAGGAGTTCAACTAAATCCTACGAAG
U2-SSTs-12H-98	7-8	ATTGAAGTGCCTCCCTGCGTGTGATCCTGGCTCTTCACTCGA
U2-SSTs-12H-99	7-9	AAAGCGACCTAATTCTAATAGTGCTTTCCTTGCAAGTTGGT
U2-SSTs-12H-100	7-10	CGGACACCAGATGCTGATCTCAACGCTTAGCCAGCAGGGAAA
U2-SSTs-12H-101	7-11	GCGCTATCTGCTCAGTATCTAGAAACAGTCATCGGAGTTCGC
U2-SSTs-12H-102	7-12	GGCCGCGTTCGACTAGACCCGTGGATTTGGAAGCTCCAGTGT
U2-SSTs-12H-103	7-13	CTAAGGACGTACTATAACCCTCGACCGTAGGTTCTTCACTTG
U2-SSTs-12H-104	7-14	CTGGAAGTCCGCTATCCCGCAAATTGAGCAAATAGGGTACA
U2-SSTs-12H-105	7-15	CTGTATCATATCTTTTTTTTTTTTTTTTTTTTTATCTGCGTGT
U2-SSTs-12H-106	8-1	TTTTTTTTTTTTAATGCCCATCGCTACCGAGTCCTTTTTTTTT
U2-SSTs-12H-107	8-2	AGCAATACTTTCTGTGGGAGGGTCGATAAAGCTCAATTAAC
U2-SSTs-12H-108	8-3	AGAGCTGAGTGTTTACACGGCACGTCGATCTGTGAGACTCGA
U2-SSTs-12H-109	8-4	TGCCAAGAGTCCATAACCGTGCTCAATCGCTAATATACCCTAA
U2-SSTs-12H-110	8-5	CATAACCAACAATTTAGTTGTATCGGCTTAGACAACAGCTTC
U2-SSTs-12H-111	8-6	GAATTATCAATGCAACGAGCTTCTTTACAGCCCTATCTACT
U2-SSTs-12H-112	8-7	ACGCGCGGGCCTGTCCGAGCCCTGGCGCATGTCAACAATTTG
U2-SSTs-12H-113	8-8	TCTAGTGCATACAAATTCGGTACGCACTTCAATTCCTACCAC
U2-SSTs-12H-114	8-9	TAATTGCATTGCAGTAGGCTCTTAGGTCGCTTTCACGCAGGG
U2-SSTs-12H-115	8-10	GTTTCTGTTCGATACCGATGGATCTGGTGTCCGCTATTAGAA
U2-SSTs-12H-116	8-11	GACGCGGGCGTACAAATTCGCAGCAGATAGCGCGAGATCAGC
U2-SSTs-12H-117	8-12	GTAGGAAACTAACGCTCTTGATCGAACGCGGCCTAGATACTG
U2-SSTs-12H-118	8-13	TTTAAGAAGCTGAGCGTAGCTGTACGTCCTTAGCGGGTCTAG
U2-SSTs-12H-119	8-14	CAATTATAGTAATGGTAACCACGGAACCTCCAGGAGGGTATA
U2-SSTs-12H-120	8-15	CTTTCAGTGATAGATGAAAGAGATATGATACAGGCGGGATAG
U2-SSTs-12H-121	9-1	CTGCTTATCCAGACCATTTCCAAAGTATTGCTGATGGGCATT
U2-SSTs-12H-122	9-2	ACAGTCCCGTCTACGGGCCAGCACTCAGCTCTCCTCCACAG
U2-SSTs-12H-123	9-3	GCGTGGTACGTAGCCGGAGCAGACTCTTGGCAGCCGTGTAAA
U2-SSTs-12H-124	9-4	TGTATTTCTACAACCTGTACGTGTTGGTTATGGCACGGTATG
U2-SSTs-12H-125	9-5	CATGCATGTCTAACGTCGCGATTGAATAATTCACAATAAAT
U2-SSTs-12H-126	9-6	GGTCTTCTACTGTAGGAGGACGGCCCGCGCGTGCTCGTTGCA
U2-SSTs-12H-127	9-7	GCATCTTTCAGCGCTCAATCATATGCACTAGAGGCTCCGACA
U2-SSTs-12H-128	9-8	CCCTGAAACTCTACAGAGGGCCAATGCAATTAACCGAATTTG
U2-SSTs-12H-129	9-9	CATCTAGAAAGGGCGTTGGGTGGAACAGAAACGAGCCTACTG
U2-SSTs-12H-130	9-10	ATCTTTGATCTGCGGGACATAACGCCCGCGTCCCATCGGTAC
U2-SSTs-12H-131	9-11	TGGTAGTTCCCTTCTTTTCGGCGTAGTTTCCTACGCGAATTTGT
U2-SSTs-12H-132	9-12	GAACGAAGGTTTACTGTGACTAGCTTCTTAAATCAAGAGCGT
U2-SSTs-12H-133	9-13	TGGGACAAGACATATACACCTTACTATAATTGAGCTACGCTC
U2-SSTs-12H-134	9-14	GTTGCGACCACGCAAGATAGCATCACTGAAAGTGGTTACCAT
U2-SSTs-12H-135	9-15	CTTTAAGCCGGATTTTTTTTTTTTTTTTTTTTTTCTTTCATCT
U2-SSTs-12H-136	10-1	TTTTTTTTTTTTGCGGGCGAAACTGGATAAGCAGTTTTTTTTTT
U2-SSTs-12H-137	10-2	GTACCAGCTGGTGTGATAGAGACGGGACTGTGGAAATGGT
U2-SSTs-12H-138	10-3	TAGAGGGCTATTGGAGGGAGTTACGTACCACGCCTGGCCCGT
U2-SSTs-12H-139	10-4	TGGATGTTTAGGGCGGACAGTTGTAGAAATACATGCTCCGGC
U2-SSTs-12H-140	10-5	TCTGTATTGGACCCTATGAAATAGACATGCATGCGTACAAGT

Seq_ID	Location	Sequence
U2-SSTs-12H-141	10-6	GGCCCTTTAATAAACCTAGGCCAGTAGAAGACCTCGCGACGT
U2-SSTs-12H-142	10-7	TTGGTCCTCATCAGAGATGCGGCTGAAAGATGCGTCCTCCTA
U2-SSTs-12H-143	10-8	CGAGCGGGCATTATAGCGACAGAGTTTCAGGGTGATTGAGC
U2-SSTs-12H-144	10-9	AGCATGTAGTGGGCCGTGGAGCCTTCTAGATGGCCCTCTGT
U2-SSTs-12H-145	10-10	GAAGTCGTTTATTATTAGTCCACAGATCAAAGATACCCAACGC
U2-SSTs-12H-146	10-11	GGTGCAGGAGGAGCAGACTCAAAGGAACTACCATATGTCCCG
U2-SSTs-12H-147	10-12	TTACTTGCTTCATTTAGCGATAAACCTTCGTTCCGCCGAAAG
U2-SSTs-12H-148	10-13	GGCAATTAGAGAATTGTATCCTGTCTTGTCCCAAGTCACAGT
U2-SSTs-12H-149	10-14	CTTACGCTGAAGCGCCTTTAGCGTGGTTCGCAACAGGTGTATA
U2-SSTs-12H-150	10-15	CCAAAGACGAAAGACCGTTTATCCGGCTTAAAGGCTATCTTG
U2-SSTs-12H-151	11-1	TTCTAAAGTGGCTCTAATCGACCAGCTGGTACTTTCGCCCCGC
U2-SSTs-12H-152	11-2	CAGAAGGTGATAACTTCCAAGATAGCCCTCTACTATCAAGCA
U2-SSTs-12H-153	11-3	GCCTCGCCCTGTCTGACTCGTCTAAACATCCAACCTCCCTCCA
U2-SSTs-12H-154	11-4	CTGAAGCTCCCTCGACACGTGTCCAATACAGAAGTGTCCGCC
U2-SSTs-12H-155	11-5	CAGCGGAGTCTATATCTACGTATTAAAGGGCCTTTCATAGGG
U2-SSTs-12H-156	11-6	GACCCACTAAGTGGTTTCCGCATGAGGACCAAGCCTAGGTTT
U2-SSTs-12H-157	11-7	GACTGTGCTCCCTGGACCCGAATGCCCGCTCGCGCATCTCTG
U2-SSTs-12H-158	11-8	TGAGGTACAGCGTTTCGTGTCACTACATGCTGTGCTGCTATAA
U2-SSTs-12H-159	11-9	GAGTAGCATTAGGCACAGCAGTAAACGACTTCCTCCACGGCC
U2-SSTs-12H-160	11-10	TGCTGCGTCGTGCGTGCTTCTCCTCCTGCACCTGACTAATAA
U2-SSTs-12H-161	11-11	CGTTGGCAGCACTTCTACCTAGAAGCAAGTAATGAGTCTGCT
U2-SSTs-12H-162	11-12	AATTCTCGTGC GCGGGTGAGTCTCTAATTGCCATCGCTAAAT
U2-SSTs-12H-163	11-13	TGGTAGAAAGAAGGGAGGCTCTTCAGCGTAAGGGATACAATT
U2-SSTs-12H-164	11-14	GACCCAGGGTTAGTTCCGGAGTTCGTCTTTGGCTAAAGGCGC
U2-SSTs-12H-165	11-15	ACTTCGTGCTTGT TTTTTTTTTTTTTTTTTTTTTTTTAAACGGTCT
U2-SSTs-12H-166	12-1	TTTTTTTTTTTTTAGGTAGGCAGGCCACTTTAGAATTTTTTTTTT
U2-SSTs-12H-167	12-2	TACAAACGTGTCCTTGTCTTTATCACCTTCTGTGCTGATTAGA
U2-SSTs-12H-168	12-3	GTCCCTGGAGCGTTCGAAATACAGGGCGAGGCCCTTGGAAGT
U2-SSTs-12H-169	12-4	GGTACGACACAGCGTGTCTGAGGGAGCTTCAGACGAGTCAG
U2-SSTs-12H-170	12-5	GTCCAGGTCTACTAAATTGTCTAGACTCCGCTGCACGTGTGCG
U2-SSTs-12H-171	12-6	GGCGTGGTACGTGCATCACC AACTTAGTGGGTCACGTAGATA
U2-SSTs-12H-172	12-7	AAGGGCAAAGCCATTGACGACGGGAGCACAGTCGCGGAAACC
U2-SSTs-12H-173	12-8	ACAACGGGTACTATAGTATCGCGCTGTACCTCATCGGGTCCA
U2-SSTs-12H-174	12-9	GTGGAAGCCCGTTCCGGTGTCTCTAATGCTACTCTGACACGAA
U2-SSTs-12H-175	12-10	ACCTGGA AACC GCCCGATAGGCACGACGCAGCACTGCTGTGC
U2-SSTs-12H-176	12-11	TCACGGTACCAGTCCGAGATGGTGTGCTGCCAACGAGAAGCACG
U2-SSTs-12H-177	12-12	TCTTTCCGTGCGGTCCGTCGGGCGCACGAGAATTTAGGTAGAA
U2-SSTs-12H-178	12-13	AGGGCACGCATAGCTGCCAGCTTCTTTCTACCAACTCACCCG
U2-SSTs-12H-179	12-14	CAGCAAAGCAATGGCTGAAATTAACCCTGGGTCGAGCCTCCC
U2-SSTs-12H-180	12-15	TTGCTCTACTATTATGTGCATCAAGCACGAAGTCTCCGGAAC

U2-SSTs-8H

Seq_ID	Location	Sequence
U2-SSTs-8H-1	1-1	CTTAGTATAGGCCTTCTCGCTACACGTTTGTACTGCCTACCT
U2-SSTs-8H-2	1-2	CTTAGGTTGCGAGGTGTTCC TGCTCCAGGGACAAGGACAAGG
U2-SSTs-8H-3	1-3	TCTCTTATGAGTGCAGTCC TGTGTGTCGTACCATTTTCGGAAC
U2-SSTs-8H-4	1-4	TCTTCTAAATGCGACCGGTACTAGACCTGGACCAGGACACGC
U2-SSTs-8H-5	1-5	CCTTAAGCTGGGCCAAGGTATCGTACCACGCCGACAATTTAG
U2-SSTs-8H-6	1-6	AAATGATGCTCTATACAAAGCGCTTTGCCCTTTGGTGATGCA
U2-SSTs-8H-7	1-7	CGTCGCCTTGAGGGTCC TGCCGTACCCGTTGTGTGTCGCAATG
U2-SSTs-8H-8	1-8	AACAATATTGGCGACTGTCGTCGGGCTTCCACC GATACTATA
U2-SSTs-8H-9	1-9	TTACCGAGGTAGACTTTTCACTGGTTTCCAGGTAGACACCGAA
U2-SSTs-8H-10	1-10	TTAATCATGTTGGTACTACGTTGGTACCGTGACCTATCGGGC
U2-SSTs-8H-11	1-11	TACGTGGAGGTGCGTAAGGCAGCACGGAAAGACATCTCCGAC
U2-SSTs-8H-12	1-12	GTCGCGCATCGTTAAGCCCGTATGCGTGCCCTCCGGACGACC
U2-SSTs-8H-13	1-13	CCATGCATCGGCTGTAGTCCATTGCTTTGCTGGCTGGCAGCT
U2-SSTs-8H-14	1-14	GGGCCTATTCATGGTCC TACTTAGTAGAGCAAATTT CAGCCA
U2-SSTs-8H-15	1-15	GTATTATCGATATTTTTTTTTTTTTTTTTTTTTTTTATGCACATAA
U2-SSTs-8H-16	2-1	TTTTTTTTTTTTTTCATACTCCCGGCCTATACTAAGTTTTTTTTTTT
U2-SSTs-8H-17	2-2	GCTTCCATATTGTATACTGTATCGCAACCTAAGAGCGAGAAG
U2-SSTs-8H-18	2-3	GCAGAGTAGTAGACCATCGAAACTCATAAGAGAAGGAACACC
U2-SSTs-8H-19	2-4	GCTACTTTTACCCTTTAGCGAGCATTTAGAAGACAGGACTGC
U2-SSTs-8H-20	2-5	AAGCGCAAAGAACGGCCCATGCCCAGCTTAAGGGTACCGGTC
U2-SSTs-8H-21	2-6	CGTCTCATGTGCGCCCTCGCTAAGAGCATATTTATACTTTGG
U2-SSTs-8H-22	2-7	CTCTATCCACCCTTCGTAGGACTCAAGGCGACGGCTTTGTAT
U2-SSTs-8H-23	2-8	TTTAGTTGAACTCGAGTGAAGGCCAATATTGTTGGCAGGACC
U2-SSTs-8H-24	2-9	AGCCAGGATCAACCAACTCTGCTACCTCGGTAAACGCAGTC
U2-SSTs-8H-25	2-10	CAAGGAAAGCATTTCCCTGCTCAACATGATTAAAGTGAAAGT
U2-SSTs-8H-26	2-11	GGCTAAGCGTTGCGAACTCCGCACCTCCACGTAACGTAGTAC
U2-SSTs-8H-27	2-12	ATGACTGTTT CACTGGAGCACGATGCGCGACTGCC TTACG
U2-SSTs-8H-28	2-13	TTCCAAATCCACAAGTGAAGGGCCGATGCATGGACGGGCTTA
U2-SSTs-8H-29	2-14	AACCTACGGTCTGTACCCTATATGAATAGGCCCTGGACTACA
U2-SSTs-8H-30	2-15	TTGCTCAATTTACACGCAGATTATCGATAATACAGTAGGACC
U2-SSTs-8H-31	3-1	GGACTCGGTAGCGTTTAAATTGAATATGGAAGCCGGGAGTATG
U2-SSTs-8H-32	3-2	AGCTTTTATCGACTCGAGTCTCTACTACTCTGCTACAGTATAC
U2-SSTs-8H-33	3-3	ACAGATCGACGTTT AGGGTATGTGAAAGTAGCTTCGATGGTC
U2-SSTs-8H-34	3-4	ATTAGCGATTGAGAAGCTGTTTCTTTGCGCTTTTCGCTAAAGG
U2-SSTs-8H-35	3-5	GTCTAAGCCGATAGTAGATAGGACATGAGACGCATGGGCCGT
U2-SSTs-8H-36	3-6	GGCTGTAAAGAACA AATTGTTGGTGGATAGAGTAGCGAGGGC
U2-SSTs-8H-37	3-7	GACATGCGCCAGGTGGTAGGAGTTCAACTAAATCCTACGAAG
U2-SSTs-8H-38	3-8	ATTGAAGTGCGTCCCTGCGTGTGATCCTGGCTCTTCACTCGA
U2-SSTs-8H-39	3-9	AAAGCGACCTAATTCTAATAGTGCTTTTCCTTGCAGAGTTGGT
U2-SSTs-8H-40	3-10	CGGACACCAGATGCTGATCTCAACGCTTAGCCAGCAGGGAAA
U2-SSTs-8H-41	3-11	GCGCTATCTGCTCAGTATCTAGAAACAGTCATCGGAGTTTCG
U2-SSTs-8H-42	3-12	GGCCGCGTTCGACTAGACCCGTGGATTTGGAAGCTCCAGTGT
U2-SSTs-8H-43	3-13	CTAAGGACGTACTATACCCTCGACCGTAGGTTCCCTTCACTTG
U2-SSTs-8H-44	3-14	CTGGAAGTTCGCTATCCCGCAAATTGAGCAAATAGGGTACA
U2-SSTs-8H-45	3-15	CTGTATCATATCTTTTTTTTTTTTTTTTTTTTTTTTATCTGCGTGT
U2-SSTs-8H-46	4-1	TTTTTTTTTTTTTAAATGCCCATCGCTACCGAGTCCTTTTTTTTTT

Seq_ID	Location	Sequence
U2-SSTs-8H-47	4-2	AGCAATACTTTCTGTGGGAGGGTCGATAAAGCTCAATTA AAC
U2-SSTs-8H-48	4-3	AGAGCTGAGTGTTTACACGGCACGTCGATCTGTGAGACTCGA
U2-SSTs-8H-49	4-4	TGCCAAGAGTCCATAACCGTGCTCAATCGCTAATATAACCCTAA
U2-SSTs-8H-50	4-5	CATAACCAACAATTTAGTTGTATCGGCTTAGACAACAGCTTC
U2-SSTs-8H-51	4-6	GAATTATTCAATGCAACGAGCTTCTTTACAGCCCTATCTACT
U2-SSTs-8H-52	4-7	ACGCGCGGGCCTGTGCGGAGCCCTGGCGCATGTCAACAATTTG
U2-SSTs-8H-53	4-8	TCTAGTGCATACAAATTCGGTACGCACTTCAATTCCTACCAC
U2-SSTs-8H-54	4-9	TAATTGCATTGCAGTAGGCTCTTAGGTCGTTTTACAGCAGGG
U2-SSTs-8H-55	4-10	GTTTCTGTTCCGTACCGATGGATCTGGTGTCCGCTATTAGAA
U2-SSTs-8H-56	4-11	GACGCGGGCGTACAAATTCGCAGCAGATAGCGCGAGATCAGC
U2-SSTs-8H-57	4-12	GTAGGAAACTAACGCTCTTGATCGAACGCGGCCCTAGATACTG
U2-SSTs-8H-58	4-13	TTTAAGAAGCTGAGCGTAGCTGTACGTCCTTAGCGGGTCTAG
U2-SSTs-8H-59	4-14	CAATTATAGTAATGGTAACCACGGA ACTTCCAGGAGGGTATA
U2-SSTs-8H-60	4-15	CTTTCAGTGATAGATGAAAAGAGATATGATACAGGCGGGATAG
U2-SSTs-8H-61	5-1	CTGCTTATCCAGACCATTTCCAAAGTATTGCTGATGGGCATT
U2-SSTs-8H-62	5-2	ACAGTCCCCTACGCGCCAGCACTCAGCTCTCCTCCCACAG
U2-SSTs-8H-63	5-3	GCGTGGTACGTAGCCGGAGCAGACTCTTGGCAGCCGTGTA AA
U2-SSTs-8H-64	5-4	TGTATTTCTACA ACTTGTACGTGTTGGTTATGGCACGGTATG
U2-SSTs-8H-65	5-5	CATGCATGTCTAACGTCGCGATTGAATAATTCACA ACTAAAT
U2-SSTs-8H-66	5-6	GGTCTTCTACTGTAGGAGGACGGCCCCGCGCGTGTCTCGTTGCA
U2-SSTs-8H-67	5-7	GCATCTTTCAGCGCTCAATCATATGCACTAGAGGCTCCGACA
U2-SSTs-8H-68	5-8	CCCTGAAACTCTACAGAGGGCCAATGCAATTAACCGAATTTG
U2-SSTs-8H-69	5-9	CATCTAGAAAGGGCGTTGGGTGGAACAGAAACGAGCCTACTG
U2-SSTs-8H-70	5-10	ATCTTTGATCTGCGGGACATAACGCCCGCGTCCCATCGGTAC
U2-SSTs-8H-71	5-11	TGGTAGTTCCTTCTTTTCGGCGTAGTTTCTTACGCGAATTTGT
U2-SSTs-8H-72	5-12	GAACGAAGGTTTACTGTGACTAGCTTCTTAAATCAAGAGCGT
U2-SSTs-8H-73	5-13	TGGGACAAGACATATAACCTTACTATAATTGAGCTACGCTC
U2-SSTs-8H-74	5-14	GTTGCGACCACGCAAGATAGCATCACTGAAAGTGGTTACCAT
U2-SSTs-8H-75	5-15	CTTTAAGCCGATTTTTTTTTTTTTTTTTTTTTTTCTTTCATCT
U2-SSTs-8H-76	6-1	TTTTTTTTTTTTGCGGGCGAAACTGGATAAGCAGTTTTTTTTTT
U2-SSTs-8H-77	6-2	GTACCAGCTGGTGCTTGATAGAGACGGGACTGTGGAAATGGT
U2-SSTs-8H-78	6-3	TAGAGGGCTATTGGAGGGAGTTACGTACCACGCCTGGCCCCGT
U2-SSTs-8H-79	6-4	TGGATGTTTAGGGCGGACAGTTGTAGAAATACATGCTCCGGC
U2-SSTs-8H-80	6-5	TCTGTATTGGACCCTATGAAATAGACATGCATGCGTACAAGT
U2-SSTs-8H-81	6-6	GGCCCTTTAATAAACCTAGGCCAGTAGAAGACCTCGCGACGT
U2-SSTs-8H-82	6-7	TTGGTCCCTCATCAGAGATGCGGCTGAAAGATGCGTCCCTCCTA
U2-SSTs-8H-83	6-8	CGAGCGGGCATTTATAGCGACAGAGTTTCAGGGTGATTGAGC
U2-SSTs-8H-84	6-9	AGCATGTAGTGGGCCGTGGAGCCTTCTTAGATGGCCCTCTGT
U2-SSTs-8H-85	6-10	GAAGTCGTTTATTATTAGTCACAGATCAAAGATACCCAACGC
U2-SSTs-8H-86	6-11	GGTGCAGGAGGAGCAGACTCAAAGGA ACTACCATATGTCCCG
U2-SSTs-8H-87	6-12	TTACTTGCTTCATTTAGCGATAAACCTTCGTTCCGCCGAAAG
U2-SSTs-8H-88	6-13	GGCAATTAGAGAATTGTATCCTGTCTTGTCCCAAGTCACAGT
U2-SSTs-8H-89	6-14	CTTACGCTGAAGCGCCTTTAGCGTGGTCGCAACAGGTGTATA
U2-SSTs-8H-90	6-15	CCAAAGACGAAAGACCGTTTATCCGGCTTAAAGGCTATCTTG
U2-SSTs-8H-91	7-1	TTCTAAAGTGGCTCTAATCGACCAGCTGGTACTTTCGCCCGC
U2-SSTs-8H-92	7-2	CAGAAGGTGATAACTTCCAAGATAGCCCTCTACTATCAAGCA
U2-SSTs-8H-93	7-3	GCCTCGCCCTGTCTGACTCGTCTAAACATCCA ACTCCCTCCA

Seq_ID	Location	Sequence
U2-SSTs-8H-94	7-4	CTGAAGCTCCCTCGACACGTGTCCAATACAGAACTGTCCGCC
U2-SSTs-8H-95	7-5	CAGCGGAGTCTATATCTACGTATTAAAGGGCCTTTCATAGGG
U2-SSTs-8H-96	7-6	GACCCACTAAGTGGTTTCCGCATGAGGACCAAGCCTAGGTTT
U2-SSTs-8H-97	7-7	GACTGTGCTCCCTGGACCCGAATGCCCGCTCGCGCATCTCTG
U2-SSTs-8H-98	7-8	TGAGGTACAGCGTTCGTGTCACACTACATGCTGTGCTATAA
U2-SSTs-8H-99	7-9	GAGTAGCATTAGGCACAGCAGTAAACGACTTCCTCCACGGCC
U2-SSTs-8H-100	7-10	TGCTGCGTCGTGCGTGCTTCTCCTCCTGCACCTGACTAATAA
U2-SSTs-8H-101	7-11	CGTTGGCAGCACTTCTACCTAGAAGCAAGTAATGAGTCTGCT
U2-SSTs-8H-102	7-12	AATTCTCGTGCGCGGGTGAGTCTCTAATTGCCATCGCTAAAT
U2-SSTs-8H-103	7-13	TGGTAGAAAAGAAGGGAGGCTCTTCAGCGTAAGGGATACAATT
U2-SSTs-8H-104	7-14	GACCCAGGGTTAGTTCCGGAGTTCGTCTTTGGCTAAAGGCGC
U2-SSTs-8H-105	7-15	ACTTCGTGCTTGTTTTTTTTTTTTTTTTTTTTTAAACGGTCT
U2-SSTs-8H-106	8-1	TTTTTTTTTTTAGGTAGGCAGGCCACTTTAGAATTTTTTTTTT
U2-SSTs-8H-107	8-2	TACAAACGTGTCCTTGTCCTTTATCACCTTCTGTGATTAGA
U2-SSTs-8H-108	8-3	GTCCCTGGAGCGTTCGAAATACAGGGCGAGGCCTTGGAAGT
U2-SSTs-8H-109	8-4	GGTACGACACAGCGTGTCTGAGGGAGCTTCAGACGAGTCAG
U2-SSTs-8H-110	8-5	GTCCAGGTCTACTAAATTGTCTAGACTCCGCTGCACGTGTCG
U2-SSTs-8H-111	8-6	GGCGTGGTACGTGCATCACCACTTAGTGGGTACGCTAGATA
U2-SSTs-8H-112	8-7	AAGGGCAAAGCCATTGACGACGGGAGCACAGTCGCGGAAACC
U2-SSTs-8H-113	8-8	ACAACGGGTACTATAGTATCGCGCTGTACCTCATCGGGTCCA
U2-SSTs-8H-114	8-9	GTGGAAGCCCCTTCGGTGTCTCTAATGCTACTCTGACACGAA
U2-SSTs-8H-115	8-10	ACCTGGAAACCGCCCGATAGGCACGACGCAGCACTGCTGTGC
U2-SSTs-8H-116	8-11	TCACGGTACCAGTCGGAGATGGTGCTGCCAACGAGAAGCACG
U2-SSTs-8H-117	8-12	TCTTTCCGTGCGGTGCTCCGGCGCACGAGAATTTAGGTAGAA
U2-SSTs-8H-118	8-13	AGGGCACGCATAGCTGCCAGTTCCTTTCTACCAACTCACCCG
U2-SSTs-8H-119	8-14	CAGCAAAGCAATGGCTGAAATTAACCCTGGGTGAGCCTCCC
U2-SSTs-8H-120	8-15	TTGCTCTACTATTATGTGCATCAAGCACGAAGTCTCCGGAAC

U2-SSTs-6H

Seq_ID	Location	Sequence
U2-SSTs-6H-1	1-1	GGACTCGGTAGCGTTTAAATTGACACGTTTGTACTGCCTACCT
U2-SSTs-6H-2	1-2	AGCTTTATCGACTCGAGTCTCGCTCCAGGGACAAGGACAAGG
U2-SSTs-6H-3	1-3	ACAGATCGACGTTTAGGGTATTGTGTGCTACCATTTTCGGAAC
U2-SSTs-6H-4	1-4	ATTAGCGATTGAGAAGCTGTTTAGACCTGGACCAGGACACGC
U2-SSTs-6H-5	1-5	GTCTAAGCCGATAGTAGATAGCGTACCACGCCGACAATTTAG
U2-SSTs-6H-6	1-6	GGCTGTAAAGAACAAATTGTTGCTTTGCCCTTTGGTGATGCA
U2-SSTs-6H-7	1-7	GACATGCGCCAGGTGGTAGGAGTACCCGTTGTGTGCTCAATG
U2-SSTs-6H-8	1-8	ATTGAAGTGCCTCCCTGCGTGCGGGCTTCCACCGATACTATA
U2-SSTs-6H-9	1-9	AAAGCGACCTAATTCTAATAGGGTTTCCAGGTAGACACCGAA
U2-SSTs-6H-10	1-10	CGGACACCAGATGCTGATCTCTGGTACCGTGACCTATCGGGC
U2-SSTs-6H-11	1-11	GCGCTATCTGCTCAGTATCTAGCACGGAAAGACATCTCCGAC
U2-SSTs-6H-12	1-12	GGCCGCGTTCGACTAGACCCGATGCGTGCCCTCCGGACGACC
U2-SSTs-6H-13	1-13	CTAAGGACGTACTATACCCTCTTGCTTTGCTGGCTGGCAGCT
U2-SSTs-6H-14	1-14	CTGGAAGTTCCGCTATCCCGCTAGTAGAGCAAATTTTCAGCCA
U2-SSTs-6H-15	1-15	CTGTATCATATCTTTTTTTTTTTTTTTTTTTTTTTTATGCACATAA
U2-SSTs-6H-16	2-1	TTTTTTTTTTTTAATGCCCATCGCTACCGAGTCCTTTTTTTTTT
U2-SSTs-6H-17	2-2	AGCAATACTTTCTGTGGGAGGGTCGATAAAGCTCAATTAAAC
U2-SSTs-6H-18	2-3	AGAGCTGAGTGTTTACACGGCACGTCGATCTGTGAGACTCGA
U2-SSTs-6H-19	2-4	TGCCAAGAGTCCATAACCGTGCTCAATCGCTAATATACCCTAA
U2-SSTs-6H-20	2-5	CATAACCAACAATTTAGTTGTATCGGCTTAGACAACAGCTTC
U2-SSTs-6H-21	2-6	GAATTATTCAATGCAACGAGCTTCTTTACAGCCCTATCTACT
U2-SSTs-6H-22	2-7	ACGCGCGGGCCTGTCGGAGCCCTGGCGCATGTCAACAATTTG
U2-SSTs-6H-23	2-8	TCTAGTGCATACAAATTCGGTACGCACTTCAATTCCTACCAC
U2-SSTs-6H-24	2-9	TAATTGCATTGCAGTAGGCTCTTAGGTGCTTTTCACGCAGGG
U2-SSTs-6H-25	2-10	GTTTCTGTTCCGTACCGATGGATCTGGTGTCCGCTATTAGAA
U2-SSTs-6H-26	2-11	GACGCGGGCGTACAAATTCGCAGCAGATAGCGCGAGATCAGC
U2-SSTs-6H-27	2-12	GTAGGAAACTAACGCTCTTGATCGAACGCGGCCTAGATACTG
U2-SSTs-6H-28	2-13	TTTAAGAAGCTGAGCGTAGCTGTACGTCCCTTAGCGGGTCTAG
U2-SSTs-6H-29	2-14	CAATTATAGTAATGGTAACCACGGAACCTCCAGGAGGGTATA
U2-SSTs-6H-30	2-15	CTTTCAGTGATAGATGAAAGAGATATGATACAGGCGGGATAG
U2-SSTs-6H-31	3-1	CTGCTTATCCAGACCATTTCCAAAGTATTGCTGATGGGCATT
U2-SSTs-6H-32	3-2	ACAGTCCCGTCTACGGGCCAGCACTCAGCTCTCCTCCCACAG
U2-SSTs-6H-33	3-3	GCGTGGTACGTAGCCGGAGCAGACTCTTGGCAGCCGTGTAAA
U2-SSTs-6H-34	3-4	TGTATTTCTACAACCTTGTACGTGTTGGTTATGGCACGGTATG
U2-SSTs-6H-35	3-5	CATGCATGTCTAACGTGCGGATTGAATAATTCACAATAAAT
U2-SSTs-6H-36	3-6	GGTCTTCTACTGTAGGAGGACGGCCCGCGGTGCTCGTTGCA
U2-SSTs-6H-37	3-7	GCATCTTTCAGCGCTCAATCATATGCACTAGAGGCTCCGACA
U2-SSTs-6H-38	3-8	CCCTGAAACTCTACAGAGGGCCAATGCAATTAACCGAATTTG
U2-SSTs-6H-39	3-9	CATCTAGAAAGGGCGTTGGGTGGAACAGAAACGAGCCTACTG
U2-SSTs-6H-40	3-10	ATCTTTGATCTGCGGGACATAACGCCCGCGTCCCATCGGTAC
U2-SSTs-6H-41	3-11	TGGTAGTTCCCTTCTTTTCGGCGTAGTTTCTTACGCGAATTTGT
U2-SSTs-6H-42	3-12	GAACGAAGGTTTACTGTGACTAGCTTCTTAAATCAAGAGCGT
U2-SSTs-6H-43	3-13	TGGGACAAGACATATACACCTTACTATAAATTGAGCTACGCTC
U2-SSTs-6H-44	3-14	GTTGCGACCACGCAAGATAGCATCACTGAAAGTGGTTACCAT
U2-SSTs-6H-45	3-15	CTTTAAGCCGATTTTTTTTTTTTTTTTTTTTTTTTCTTTCATCT
U2-SSTs-6H-46	4-1	TTTTTTTTTTTTGCGGGCGAAACTGGATAAGCAGTTTTTTTTTT

Seq_ID	Location	Sequence
U2-SSTs-6H-47	4-2	GTACCAGCTGGTGCTTGATAGAGACGGGACTGTGGAAATGGT
U2-SSTs-6H-48	4-3	TAGAGGGCTATTGGAGGGAGTTACGTACCACGCCTGGCCCGT
U2-SSTs-6H-49	4-4	TGGATGTTTAGGGCGGACAGTTGTAGAAATACATGCTCCGGC
U2-SSTs-6H-50	4-5	TCTGTATTGGACCCTATGAAATAGACATGCATGCGTACAAGT
U2-SSTs-6H-51	4-6	GGCCCTTTAATAAACCTAGGCCAGTAGAAGACCTCGCGACGT
U2-SSTs-6H-52	4-7	TTGGTCCTCATCAGAGATGCGGGCTGAAAGATGCGTCTCCTA
U2-SSTs-6H-53	4-8	CGAGCGGGCATTATATAGCGACAGAGTTTCAGGGTGATTGAGC
U2-SSTs-6H-54	4-9	AGCATGTAGTGGGCCGTGGAGCCTTTCTAGATGGCCCTCTGT
U2-SSTs-6H-55	4-10	GAAGTCGTTTATTATTAGTCACAGATCAAAGATACCCAACGC
U2-SSTs-6H-56	4-11	GGTGCAGGAGGAGCAGACTCAAAGGAACTACCATATGTCCCG
U2-SSTs-6H-57	4-12	TTACTTGCTTCATTTAGCGATAAACCTTCGTTCCGCCGAAAG
U2-SSTs-6H-58	4-13	GGCAATTAGAGAATTGTATCCTGTCTTGTCCCAAGTCACAGT
U2-SSTs-6H-59	4-14	CTTACGCTGAAGCGCCTTTAGCGTGGTCGCAACAGGTGTATA
U2-SSTs-6H-60	4-15	CCAAAGACGAAAGACCGTTTATCCGGCTTAAAGGCTATCTTG
U2-SSTs-6H-61	5-1	TTCTAAAGTGGCTCTAATCGACCAGCTGGTACTTTCCGCCGC
U2-SSTs-6H-62	5-2	CAGAAGGTGATAACTTCCAAGATAGCCCTCTACTATCAAGCA
U2-SSTs-6H-63	5-3	GCCTCGCCCTGTCTGACTCGTCTAAACATCCAACCTCCCTCCA
U2-SSTs-6H-64	5-4	CTGAAGCTCCCTCGACACGTGTCCAATACAGAAGTGTCCGCC
U2-SSTs-6H-65	5-5	CAGCGGAGTCTATATCTACGTATTAAAGGGCCTTTCATAGGG
U2-SSTs-6H-66	5-6	GACCCACTAAGTGGTTTCCGCATGAGGACCAAGCCTAGGTTT
U2-SSTs-6H-67	5-7	GACTGTGCTCCCTGGACCCGAATGCCCGCTCGCGCATCTCTG
U2-SSTs-6H-68	5-8	TGAGGTACAGCGTTCGTGTCACTACATGCTGTGCTGCTATAA
U2-SSTs-6H-69	5-9	GAGTAGCATTAGGCACAGCAGTAAACGACTTCCTCCACGGCC
U2-SSTs-6H-70	5-10	TGCTGCGTGCCTGCGTGTCTCTCCTCCTGCACCTGACTAATAA
U2-SSTs-6H-71	5-11	CGTTGGCAGCACTTCTACCTAGAAGCAAGTAATGAGTCTGCT
U2-SSTs-6H-72	5-12	AATTCTCGTGC GCGGGTGAGTCTCTAATTGCCATCGCTAAAT
U2-SSTs-6H-73	5-13	TGGTAGAAAGAAGGGAGGCTCTTCAGCGTAAGGGATACAATT
U2-SSTs-6H-74	5-14	GACCCAGGGTTAGTTCCGGAGTTCGTCTTTGGCTAAAGGCGC
U2-SSTs-6H-75	5-15	ACTTCGTGCTTGTTTTTTTTTTTTTTTTTTTTTTTTAAACGGTCT
U2-SSTs-6H-76	6-1	TTTTTTTTTTTTTAGGTAGGCAGGCCACTTTAGAATTTTTTTTTT
U2-SSTs-6H-77	6-2	TACAAACGTGTCCTTGTCTTTATCACCTTCTGTGATTAGA
U2-SSTs-6H-78	6-3	GTCCCTGGAGCGTTCGGAAAACAGGGCGAGGCCTTGGAAAGT
U2-SSTs-6H-79	6-4	GGTACGACACAGCGTGTCTGAGGGAGCTTCAGACGAGTCAG
U2-SSTs-6H-80	6-5	GTCCAGGTCTACTAAATTGTCTAGACTCCGCTGCACGTGTCTG
U2-SSTs-6H-81	6-6	GGCGTGGTACGTGCATCACCAACTTAGTGGGTCACGTAGATA
U2-SSTs-6H-82	6-7	AAGGGCAAAGCCATTGACGACGGGAGCACAGTCGCGGAAACC
U2-SSTs-6H-83	6-8	ACAACGGGTACTATAGTATCGCGCTGTACCTCATCGGGTCCA
U2-SSTs-6H-84	6-9	GTGGAAGCCCGTTCGGTGTCTCTAATGCTACTCTGACACGAA
U2-SSTs-6H-85	6-10	ACCTGGAACCGCCCGATAGGCACGACGCAGCACTGCTGTGC
U2-SSTs-6H-86	6-11	TCACGGTACCAGTCCGAGATGGTGCTGCCAACGAGAAGCACG
U2-SSTs-6H-87	6-12	TCTTTCGGTGC GGTCTCCGGCGCACGAGAATTTAGGTAGAA
U2-SSTs-6H-88	6-13	AGGGCACGCATAGCTGCCAGCTTCTTTCTACCAACTCACCCG
U2-SSTs-6H-89	6-14	CAGCAAAGCAATGGCTGAAATTAACCCTGGGTCGAGCCTCCC
U2-SSTs-6H-90	6-15	TTGCTCTACTATTATGTGCATCAAGCACGAAGTCTCCGGAAC

U2-SSTs-4H

Seq_ID	Location	Sequence
U2-SSTs-4H-1	1-1	CTGCTTATCCAGACCATTTCCACACGTTTGTACTGCCTACCT
U2-SSTs-4H-2	1-2	ACAGTCCCGTCTACGGGCCAGGCTCCAGGGACAAGGACAAGG
U2-SSTs-4H-3	1-3	GCGTGGTACGTAGCCGGAGCATGTGTGCTACCATTTTCGGAAC
U2-SSTs-4H-4	1-4	TGTATTTCTACAAC TTGTACGTAGACCTGGACCAGGACACGC
U2-SSTs-4H-5	1-5	CATGCATGTCTAACGTCGCGACGTACCACGCCGACAATTTAG
U2-SSTs-4H-6	1-6	GGTCTTCTACTGTAGGAGGACGCTTTGCCCTTTGGTGATGCA
U2-SSTs-4H-7	1-7	GCATCTTTCAGCGCTCAATCAGTACCCGTTGTGTGCTCAATG
U2-SSTs-4H-8	1-8	CCCTGAAACTCTACAGAGGGCCGGGCTTCCACCGATACTATA
U2-SSTs-4H-9	1-9	CATCTAGAAAAGGGCGTTGGGTGGTTTTCCAGGTAGACACCGAA
U2-SSTs-4H-10	1-10	ATCTTTGATCTGCGGGACATATGGTACCGTGACCTATCGGGC
U2-SSTs-4H-11	1-11	TGGTAGTTCCCTTCTTTTCGGCGGCACGGAAAGACATCTCCGAC
U2-SSTs-4H-12	1-12	GAACGAAGGTTTACTGTGACTATGCGTGCCCTCCGGACGACC
U2-SSTs-4H-13	1-13	TGGGACAAGACATATACACCTTTGCTTTGCTGGCTGGCAGCT
U2-SSTs-4H-14	1-14	GTTGCGACCACGCAAGATAGCTAGTAGAGCAAATTTTCAGCCA
U2-SSTs-4H-15	1-15	CTTTAAGCCGGATTTTTTTTTTTTTTTTTTTTTTTTATGCACATAA
U2-SSTs-4H-16	2-1	TTTTTTTTTTTTTGCGGGCGAAACTGGATAAGCAGTTTTTTTTTTT
U2-SSTs-4H-17	2-2	GTACCAGCTGGTGCTTGATAGAGACGGGACTGTGGAAATGGT
U2-SSTs-4H-18	2-3	TAGAGGGCTATTGGAGGGAGTTACGTACCACGCCTGGCCCGT
U2-SSTs-4H-19	2-4	TGGATGTTTTAGGGCGGACAGTTGTAGAAAATACATGCTCCGGC
U2-SSTs-4H-20	2-5	TCTGTATTGGACCCTATGAAATAGACATGCATGCGTACAAGT
U2-SSTs-4H-21	2-6	GGCCCTTTAATAAACCTAGGCCAGTAGAAGACCTCGCGACGT
U2-SSTs-4H-22	2-7	TTGGTCCTCATCAGAGATGCGGCTGAAAGATGCGTCCTCCTA
U2-SSTs-4H-23	2-8	CGAGCGGGCATTTATAGCGACAGAGTTTCAGGGTGATTGAGC
U2-SSTs-4H-24	2-9	AGCATGTAGTGGGCCGTGGAGCCTTTCTAGATGGCCCTCTGT
U2-SSTs-4H-25	2-10	GAAGTCGTTTTATTATTAGTCACAGATCAAAGATACCCAACGC
U2-SSTs-4H-26	2-11	GGTGCAGGAGGAGCAGACTCAAAGGAACTACCATATGTCCCG
U2-SSTs-4H-27	2-12	TTACTTGCTTCATTTAGCGATAAACCTTCGTTCCGCCGAAAG
U2-SSTs-4H-28	2-13	GGCAATTAGAGAATTTGTATCCTGTCTTGTCCCAAGTCACAGT
U2-SSTs-4H-29	2-14	CTTACGCTGAAGCGCCTTTAGCGTGGTCGCAACAGGTGTATA
U2-SSTs-4H-30	2-15	CCAAAGACGAAAGACCGTTTATCCGGCTTAAAGGCTATCTTG
U2-SSTs-4H-31	3-1	TTCTAAAGTGGCTCTAATCGACCAGCTGGTACTTTTCGCCC GC
U2-SSTs-4H-32	3-2	CAGAAGGTGATAACTTCCAAGATAGCCCTCTACTATCAAGCA
U2-SSTs-4H-33	3-3	GCCTCGCCCTGTCTGACTCGTCTAAACATCCAACCTCCCTCCA
U2-SSTs-4H-34	3-4	CTGAAGCTCCCTCGACACGTGTCCAATACAGA ACTGTCCGCC
U2-SSTs-4H-35	3-5	CAGCGGAGTCTATATCTACGTATTAAGGGCCTTTCATAGGG
U2-SSTs-4H-36	3-6	GACCCACTAAGTGGTTTTCCGCATGAGGACCAAGCCTAGGTTT
U2-SSTs-4H-37	3-7	GACTGTGCTCCCTGGACCCGAATGCCCGCTCGCGCATCTCTG
U2-SSTs-4H-38	3-8	TGAGGTACAGCGTTCGTGTCACACTACATGCTGTGCTATAAA
U2-SSTs-4H-39	3-9	GAGTAGCATTAGGCACAGCAGTAAACGACTTCCTCCACGGCC
U2-SSTs-4H-40	3-10	TGCTGCGTTCGTGCGTCTTCTCCTCCTGCACCTGACTAATAA
U2-SSTs-4H-41	3-11	CGTTGGCAGCACTTCTACCTAGAAGCAAGTAATGAGTCTGCT
U2-SSTs-4H-42	3-12	AATTCTCGTGC GCGGGTGAGTCTCTAATTGCCATCGCTAAAT
U2-SSTs-4H-43	3-13	TGGTAGAAAAGAAGGGAGGCTTTCAGCGTAAGGGATACAATT
U2-SSTs-4H-44	3-14	GACCCAGGGTTAGTTCCGGAGTTCGTCTTTGGCTAAAGGCGC
U2-SSTs-4H-45	3-15	ACTTCGTGCTTGTTTTTTTTTTTTTTTTTTTTTTTTAAACGGTCT
U2-SSTs-4H-46	4-1	TTTTTTTTTTTTTAGGTAGGCAGGCCACTTTAGAATTTTTTTTTT

Seq_ID	Location	Sequence
U2-SSTs-4H-47	4-2	TACAAACGTGTCCTTGTCCCTTATCACCTTCTGTCGATTAGA
U2-SSTs-4H-48	4-3	GTCCCTGGAGCGTTCCGAAATACAGGGCGAGGCCTTGGAAGT
U2-SSTs-4H-49	4-4	GGTACGACACAGCGTGTCCCTGAGGGAGCTTCAGACGAGTCAG
U2-SSTs-4H-50	4-5	GTCCAGGTCTACTAAATTGTCTAGACTCCGCTGCACGTGTCG
U2-SSTs-4H-51	4-6	GGCGTGGTACGTGCATCACCAACTTAGTGGGTCACGTAGATA
U2-SSTs-4H-52	4-7	AAGGGCAAAGCCATTGACGACGGGAGCACAGTCGCGGAAACC
U2-SSTs-4H-53	4-8	ACAACGGGTACTATAGTATCGCGCTGTACCTCATCGGGTCCA
U2-SSTs-4H-54	4-9	GTGGAAGCCCGTTCGGTGTCTCTAATGCTACTCTGACACGAA
U2-SSTs-4H-55	4-10	ACCTGGAAACCGCCCGATAGGCACGACGCAGCACTGCTGTGC
U2-SSTs-4H-56	4-11	TCACGGTACCAGTCGGAGATGGTGCTGCCAACGAGAAGCACG
U2-SSTs-4H-57	4-12	TCTTTCCGTGCGGTCGTCCGGCGCACGAGAATTTAGGTAGAA
U2-SSTs-4H-58	4-13	AGGGCACGCATAGCTGCCAGCTTCTTTCTACCAACTCACCCG
U2-SSTs-4H-59	4-14	CAGCAAAGCAATGGCTGAAATTAACCCTGGGTCGAGCCTCCC
U2-SSTs-4H-60	4-15	TTGCTCTACTATTATGTGCATCAAGCACGAAGTCTCCGGAAC

U2-SSTs-2H

Seq_ID	Location	Sequence
U1-SSTs-2H-1	1-1	TTCTAAAGTGGCTCTAATCGAACACGTTTGTACTGCCTACCT
U1-SSTs-2H-2	1-2	CAGAAGGTGATAACTTCCAAGGCTCCAGGGACAAGGACAAGG
U1-SSTs-2H-3	1-3	GCCTCGCCCTGTCTGACTCGTTGTGTGCGTACCATTTCCGGAAC
U1-SSTs-2H-4	1-4	CTGAAGCTCCCTCGACACGTGTAGACCTGGACCAGGACACGC
U1-SSTs-2H-5	1-5	CAGCGGAGTCTATATCTACGTCGTACCACGCCGACAATTTAG
U1-SSTs-2H-6	1-6	GACCCACTAAGTGGTTTCCGCGCTTTGCCCTTTGGTGATGCA
U1-SSTs-2H-7	1-7	GACTGTGCTCCCTGGACCCGAGTACCCGTTGTGTGCGTCAATG
U1-SSTs-2H-8	1-8	TGAGGTACAGCGTTCGTGTCACGGGCTTCCACCGATACTATA
U1-SSTs-2H-9	1-9	GAGTAGCATTAGGCACAGCAGGGTTTCCAGGTAGACACCGAA
U1-SSTs-2H-10	1-10	TGCTGCGTTCGTGCGTGCTTCTTGGTACCGTGACCTATCGGGC
U1-SSTs-2H-11	1-11	CGTTGGCAGCAGCTTCTACCTAGCACGGAAAGACATCTCCGAC
U1-SSTs-2H-12	1-12	AATTCTCGTGC GCGGGTGAGTATGCGTGCCCTCCGGACGACC
U1-SSTs-2H-13	1-13	TGGTAGAAAGAAGGGAGGCTCTTGCTTTGCTGGCTGGCAGCT
U1-SSTs-2H-14	1-14	GACCCAGGGTTAGTTCCGGAGTAGTAGAGCAAATTTTCAGCCA
U1-SSTs-2H-15	1-15	ACTTCGTGCTTGTTTTTTTTTTTTTTTTTTTTTTTTATGCACATAA
U1-SSTs-2H-16	2-1	TTTTTTTTTTTTTAGGTAGGCAGGCCACTTTAGAATTTTTTTTTTT
U1-SSTs-2H-17	2-2	TACAAACGTGTCCTTGTCTTTATCACCTTCTGTGCGATTAGA
U1-SSTs-2H-18	2-3	GTCCCTGGAGCGTTCGGAAATACAGGGCGAGGCCTTGGAAGT
U1-SSTs-2H-19	2-4	GGTACGACACAGCGTGTCTGAGGGAGCTTCAGACGAGTCAG
U1-SSTs-2H-20	2-5	GTCCAGGTCTACTAAATTGTCTAGACTCCGCTGCACGTGTTCG
U1-SSTs-2H-21	2-6	GGCGTGGTACGTGCATCACCAACTTAGTGGGTACGTCAGATA
U1-SSTs-2H-22	2-7	AAGGGCAAAGCCATTGACGACGGGAGCACAGTCGCGGAAACC
U1-SSTs-2H-23	2-8	ACAACGGGTACTATAGTATCGCGCTGTACCTCATCGGGTCCA
U1-SSTs-2H-24	2-9	GTGGAAGCCCGTTCGGTGTCTCTAATGCTACTCTGACACGAA
U1-SSTs-2H-25	2-10	ACCTGGAAACCGCCCGATAGGCACGACGCAGCACTGCTGTGC
U1-SSTs-2H-26	2-11	TCACGGTACCAGTCGGAGATGGTGCTGCCAACGAGAAGCACG
U1-SSTs-2H-27	2-12	TCTTTCCGTGCGGTTCGTCGCGGCACGAGAATTTAGGTAGAA
U1-SSTs-2H-28	2-13	AGGGCACGCATAGCTGCCAGCTTCTTTCTACCAACTCACCCG
U1-SSTs-2H-29	2-14	CAGCAAAGCAATGGCTGAAATTAACCCTGGGTGAGCCTCCC
U1-SSTs-2H-30	2-15	TTGCTCTACTATTATGTGCATCAAGCACGAAGTCTCCGGAAC