Supporting Information 2

Design space for complex DNA structures

Bryan Wei[1,2] Mingjie Dai[1,3] Cameron Myhrvold[1,2] Yonggang Ke[1,4] Ralf Jungmann[1,2] Peng Yin[1,2*]

Wyss Institute for Biologically Inspired Engineering, Harvard University, Boston, MA 02115[1],
Department of Systems Biology, Harvard Medical School, Boston, MA 02115[2],
Program in Biophysics, Harvard University, Boston, MA 02115[3],
Dana Farber Cancer Institute, Boston, MA 02215[4]
E-mail address[*]: py@hms.harvard.edu

Sequences for the 10H×11T structures are given in work sheets named Motif 0 (10H×11T), Motif 1 (10H×11T), etc.

Sequences for the 24H×29T structures are given in work sheets named Motif 0 (24H×28T), Motif 1 (24H×29T), etc.

Sequences for the twist study are given in work sheets named Motif 4.1X and Motif 4.2X.

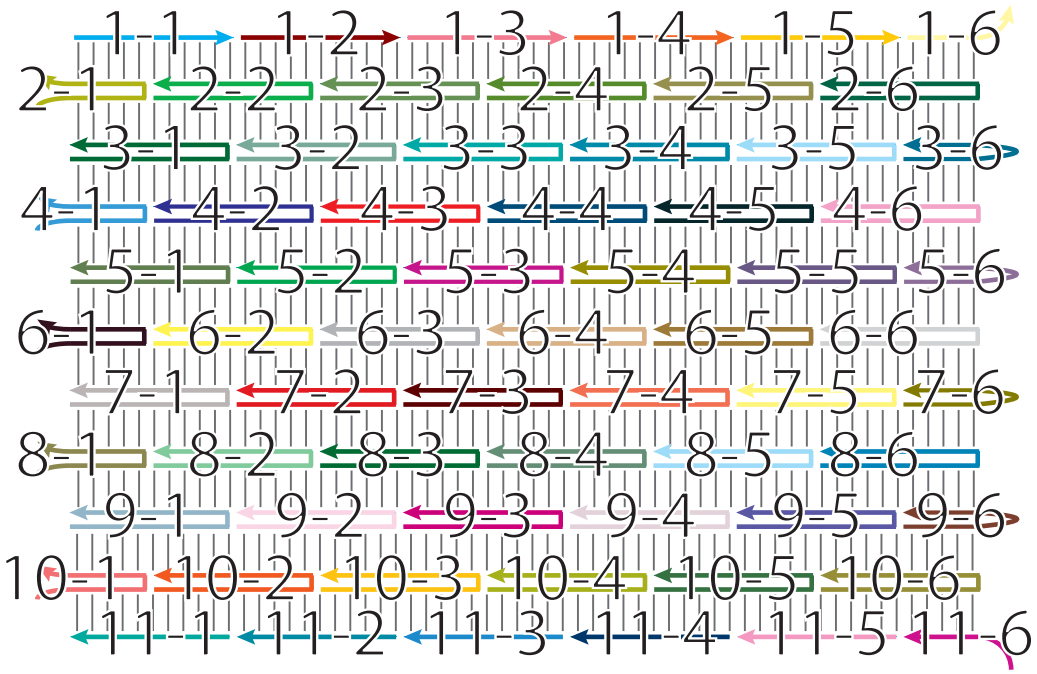

Fig. SS1. Strand denotation for for the 10H×11T structure of motif 0.

The name of a strand denotes the row and column numbers in the structure. For example, a strand named x-y indicates that it is in row x and column y. The full denotation of strands for the 10H×11T structure of motif 0 is shown as an example in Fig. SS1. The similar denotation is applicable for all other structures of different motifs.

For landing assay, the strands left out to form the hole are: 6-5, 6-6, 7-5, 7-6, 8-5, 8-6.

For super-resolution assay, four strands are modified with a handle at 3' end (TTGGAAGGGATGGAGGA) to be complementary to a biotinated strand TCCTCCATCCCTTCC-biotin and the modified strands substitute strands 2-1, 2-15, 24-1 and 24-15 of the original mixture for the rectangle structures of respective motifs; 12 strands are modified with a handle at 3’ end (TTATCTACATA) to be complementary to the PAINT strand (TATGTAGATC) and the modified strands substitute strands 1-1, 1-2, 1-3, 1-13, 1-14, 1-15, 25-1, 25-2, 25-3, 25-14 and 25-15 (or 1-1, 1-2, 1-3, 1-12, 1-13, 1-14, 25-1, 25-2, 25-3, 25-12, 25-13, 25-14 for motif 0) of the original mixture for the rectangle structures of respective motifs.

Motif 0 (10H×11T)

Name	Sequence
1-1	TCCGCCGTCGGCGTCTCGGGA
1-2	ACTTGTACCAAGAGGCCAGTG
1-3	GTCTGTGCCCTAGCTGCATCG
1-4	CGTAGACGTTAAGACCTCGGA
1-5	AGGTGGTTTATACGGACTGTA
1-6	GGACTATGCGTTTTTTTTTTT
2-1	TTTTTTTTTTGCCCAATGCGTCCGACGGCGGATTTTTTTTTT
2-2	GTGCAGCAAGTCCGTTAACCATTGGTACAAGTTCCCGAGACG
2-3	GAATGAACTAGGGATAATAAGAGGGCACAGACCACTGGCCTC
2-4	ACCGACTAAATGATTGAGTCCTAACGTCTACGCGATGCAGCT
2-5	TACAAAGTTCAACCATAGACGATAAACCACCTTCCGAGGTCT
2-6	TGGGATAGTAGACACCTGCCCACGCATAGTCCTACAGTCCGT
3-1	AGTTATCCCTCATCGGTTACTCTTGCTGCACACGCATTGGGC
3-2	TAGAAGGGCCCTCAAGATGCATAGTTCATTCTGGTTAACGGA
3-3	ATGCGGGCCTAGCATGTAAGCTTTAGTCGGTCTTATTATCCC
3-4	TCCGTAAATTTAGTTTAGGACGAACTTTGTAGGACTCAATCA
3-5	GTTTACTGCACCAACTTGAAGTACTATCCCACGTCTATGGTT
3-6	ACTCGCAGCACTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC
4-1	TTTTTTTTTTCACGTGGGCATGAGGGATAACTTTTTTTTTTT
4-2	CGAGTCCGCGAGGTCCGAATCGGGCCCTTCTAAGTAACCGAT
4-3	CGCGCCAACGGGTGGAGCTGTTAGGCCCGCATTGCATCTTGA
4-4	CCATCGCGCCCTAAGTGTATGAAATTTACGGAGCTTACATGC
4-5	GGTACCGGACCGTGGTCACCGGTGCAGTAAACGTCCTAAACT
4-6	AGGTAATCTAATAGCAGCAGTGTGCTGCGAGTCTTCAAGTTG
5-1	ACATAGCGAGTCAAACGGTGACGCGGACTCGATGCCCACGTG
5-2	ATGGGCGGGCCGGTCACAAGTCGTTGGCGCGGATTCGGACCT
5-3	CCGGAGCCCTAAGTCCGAGGTGGCGCGATGGACAGCTCCACC
5-4	AAGGATCTGGAGGAAGTTCCAGTCCGGTACCCATACACTTAG
5-5	TTAGGGAAATAAAGGATTGACTAGATTACCTCGGTGACCACG
5-6	TCAGCGCTTCATTTTTTTTTTTTTTTTTTTTACTGCTGCTAT
6-1	TTTTTTTTTTGTATCTGCACAACTCGCTATGTTTTTTTTTTT
6-2	CCGCATGATCCGCAAGAGCTTGGCCCGCCCATTCACCGTTTG
6-3	AGTGCTTATGACCCTAAATTGTAGGGCTCCGGACTTGTGACC
6-4	CGTCAGAAAGATAAAGAGGGCTCCAGATCCTTACCTCGGACT
6-5	CATACGCTGTCCCTAACGTTATATTTCCCTAATGGAACTTCC
6-6	GCCAATCCAGGTTTAAAGAGATGAAGCGCTGAGTCAATCCTT
7-1	TATTTGGCATCTGACTATAGGGATCATGCGGTGTGCAGATAC
7-2	GTACGCCCTGACCCACCGATGCATAAGCACTAAGCTCTTGCG
7-3	GTTAAAGGCGTTCGCGAAATTCTTTCTGACGCAATTTAGGGT

7-4	CCTTTGACTTTCACTGAACAGACAGCGTATGGCCCTCTTTAT
7-5	GCCCTGACGGGAGCTGCGGGCCTGGATTGGCTAACGTTAGGG
7-6	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC
8-1	TTTTTTTTTTACAGAAAGGTCGATGCCAAATATTTTTTTTTT
8-2	TGGCGGTTGGATTAATTAGGCTCAGGGCGTACCCTATAGTCA
8-3	AATCCCTGTGGCTACCGAGGCACGCCTTTAACCATCGGTGGG
8-4	AACTGAAGCGGCTTGGCCACTAAAGTCAAAGGAATTTCGCGA
8-5	ACCGTGACGCAACTAAACAATCCCGTCAGGGCCTGTTCAGTG
8-6	GGACTCTATCCCTACGGAACCAATTCAACGTCGCCCGCAGCT
9-1	GGGACCCTTCACTAACGACCACCAACCGCCAGACCTTTCTGT
9-2	GCCTGATATTGCAATCACTCCCACAGGGATTGCCTAATTAAT
9-3	GGGTACCGACTCCCTTTACGGCGCTTCAGTTGCCTCGGTAGC
9-4	CTTCCGAGAAGTCATTTGGAAGCGTCACGGTAGTGGCCAAGC
9-5	GTCTCAGGCGCTTGAGAATGAGATAGAGTCCATTGTTTAGTT
9-6	TCGAACACTTCTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
10-1	TTTTTTTTTTCACATAGGCCGTGAAGGGTCCCTTTTTTTTTT
10-2	CCCACCTAGAAGAAGAAAGGGCAATATCAGGCTGGTCGTTAG
10-3	TAGAACTGAGAGACAGGGCTAAGTCGGTACCCGGAGTGATTG
10-4	TATAGCGCGTCTGTGGCGCGACTTCTCGGAAGCCGTAAAGGG
10-5	CTGGCGGTACCATAAACTCGCGCGCCTGAGACTTCCAAATGA
10-6	ATTTCCCTGACCTTGAGGGAGGAAGTGTTCGATCATTCTCAA
11-1	TCTAGGTGGGCGGCCTATGTG
11-2	CTCAGTTCTACCCTTTCTTCT
11-3	ACGCGCTATATAGCCCTGTCT
11-4	GTACCGCCAGTCGCGCCACAG
11-5	TCAGGGAAATGCGAGTTTATG
11-6	TTTTTTTTTTCTCCCTCAAGG

Motif 1 (10H×11T)

Name	Sequence
1-1	GCCGGTGTCATAGGACCAGAG
1-2	GCCTCAACGGCTTTAGCACGT
1-3	AACAGAGAGGTACTCCAAAGA
1-4	ACTTAGTTACCGGCTCGTTGA
1-5	GTGTAAAGCTGGCGGTGACGC
1-6	GGTTACAGATACTTTTTTTTT
2-1	TTTTTTTTTTTGCCATTGAGCTATGACACCGGCTTTTTTTTT
2-2	GAGACGGCGTCGTCGGCGAACAGCCGTTGAGGCCTCTGGTCC
2-3	CTGGGCGGATGTTACAGTGCGTACCTCTCTGTTACGTGCTAA
2-4	TCCGATTGCTAGACGCATTGTCGGTAACTAAGTTCTTTGGAG
2-5	CAACATCTGCAGCAGCTGTAGCCAGCTTTACACTCAACGAGC
2-6	ATCTGCCGCGGTAGTTGCTGCGTATCTGTAACCGCGTCACCG
3-1	CACGGAACGGCATCGAACGTGGACGCCGTCTCGCTCAATGGC
3-2	TCGTCCTAGGCCCTGGACTTCCATCCGCCCAGGTTCGCCGAC
3-3	TTCCGGATCGACCCTCGCCATTAGCAATCGGACGCACTGTAA
3-4	TTACCTAGAAATACCCGATGATGCAGATGTTGACAATGCGTC
3-5	GAAGCTGGCAAGGTTGCTATACCGCGGCAGATCTACAGCTGC
3-6	CGGGAAGATGGATTTTTTTTTTTTTTTTTTTTGCAGCAACTA
4-1	TTTTTTTTTTTGGTTTCGAGATGCCGTTCCGTGTTTTTTTTT
4-2	GATTAGAGCATAATCTCTTTCGGCCTAGGACGACACGTTCGA
4-3	GCTGAGGTGTGCCGAGAAACAGTCGATCCGGAAGAAGTCCAG
4-4	TCTAGGAAACCCGGATATGTGATTTCTAGGTAAATGGCGAGG
4-5	CGGCAGTTTAAGACCTGCTCTCTTGCCAGCTTCTCATCGGGT
4-6	GAACAAATATCTACACCCTATTCCATCTTCCCGTATAGCAAC
5-1	GGTCGGATCACTCCCGCCAACATGCTCTAATCTCTCGAAACC
5-2	GAACTCGTCTCCGCTCAGGGTCACACCTCAGCGAAAGAGATT
5-3	CTAATAATAAGCGTGCCTAGCGGTTTCCTAGATGTTTCTCGG
5-4	TGAGCAAAGCAGACACAAAGGTTAAACTGCCGCACATATCCG
5-5	ACCATCACCCTACGATTCTCAGATATTTGTTCAGAGCAGGTC
5-6	TAGCAAACTCAGTTTTTTTTTTTTTTTTTTTTATAGGGTGTA
6-1	TTTTTTTTTTTCTAGCTCACCAGTGATCCGACCTTTTTTTTT
6-2	ACTTCACTATTTAAGGTGTTGGGAGACGAGTTCGTTGGCGGG
6-3	ATTTAGACTAGTCGCCTGGATGCTTATTATTAGACCCTGAGC
6-4	CAGAAAGTGAGGGCCTCAGGTCTGCTTTGCTCAGCTAGGCAC
6-5	GGTCAGGTCAACGGTCATCTCTAGGGTGATGGTCCTTTGTGT
6-6	AAAGCTCGGATTAGCGCCCGGCTGAGTTTGCTATGAGAATCG
7-1	TTGCACGACCGTATCGTCTCTAATAGTGAAGTGGTGAGCTAG
7-2	ACTTACAACGCCTGAAATAAGCTAGTCTAAATCAACACCTTA
7-3	AATAATTACCTCACATACGCTCTCACTTTCTGATCCAGGCGA

7-4	CTGGTCATCTCAGAATGAGAATTGACCTGACCACCTGAGGCC
7-5	TAGCGTGAATGGATGAGACGCATCCGAGCTTTGAGATGACCG
7-6	GTCACTCAAGTCTTTTTTTTTTTTTTTTTTCCGGGCGCTA
8-1	TTTTTTTTTTTGGACATTCCTACGGTCGTGCAATTTTTTTTT
8-2	TGCGAAGGCCGAAGCTGGCAGGGCGTTGTAAGTAGAGACGAT
8-3	TGCAGGCGGGCCAAAGGATAAGAGGTAATTATTCTTATTTCA
8-4	GCTTCCGTTGCTGATGCCATTTGAGATGACCAGAGCGTATGT
8-5	CAGGCGAAATCAGCGTTGGCTCCATTCACGCTATTCTCATTC
8-6	AGCGCTGGAGGGCTCAATGTTGACTTGAGTGACGCGTCTCAT
9-1	AATCTCCCACGCATTGGACCTCGGCCTTCGCAAGGAATGTCC
9-2	TCAGTGTATACCGACTGTAAAGCCCGCCTGCACTGCCAGCTT
9-3	GCCTTCGCACAGTGGTCTGACGCAACGGAAGCTTATCCTTTG
9-4	GTCTAGGTATCCCTGCTGGGAGATTTCGCCTGAATGGCATCA
9-5	GCCGGAATTTGCTAGCATTTACCTCCAGCGCTAGCCAACGCT
9-6	ATTACCTTTATTTTTTTTTTTTTTTTTTTTAACATTGAGC
10-1	TTTTTTTTTTTCTGTCTCGTAGCGTGGGAGATTTTTTTTTTT
10-2	TAGTAAACTCCAAGGCTACCCGGTATACACTGAAGGTCCAAT
10-3	TGTAAGTCGATTAAACCACTGCTGTGCGAAGGCTTTACAGTC
10-4	CAGAAATATTGAACTGTGATTGGATACCTAGACGTCAGACCA
10-5	TGAGAGCTCTGATGAATTCGCGCAAATTCCGGCTCCCAGCAG
10-6	TTTCCTAGTTGAATATCCACGAATAAAGGTAATTAAATGCTA
11-1	GGAGTTTACTATACGAGACAG
11-2	ATCGACTTACAGGGTAGCCTT
11-3	CAATATTTCTGCAGTGGTTTA
11-4	CAGAGCTCTCAAATCACAGTT
11-5	CAACTAGGAAAGCGAATTCAT
11-6	TTTTTTTTTTTCGTGGATATT

Motif 2 (10H×11T)

Name	Sequence
1-1	TGATTTAGGCGTCCTCCGTCT
1-2	GCCCGGTTTATATATCCTCGT
1-3	TGTATCCCTCATATTCGGCCG
1-4	TGCTCGTGTGGGCCTCTATGA
1-5	AGCCCACAAGCCTGGTGCGAG
1-6	GCTAATGACGGTTTTTTTTTT
2-1	TTTTTTTTTTTCGCAGTACGTACGCCTAAATCATTTTTTTTT
2-2	TCGGTGAGCAAGCTGGAGGGTTATAAACCGGGCAGACGGAGG
2-3	GCTTGGGATGAGTTATCGGATATGAGGGATACAACGAGGATA
2-4	ACCGCTATGGAATCCCTAAGACCCACACGAGCACGGCCGAAT
2-5	TCCATTGAATGAATTGATGCCGGCTTGTGGGCTTCATAGAGG
2-6	AGTCCTGTAATCAGCCGCCAGACCGTCATTAGCCTCGCACCA
3-1	TTGCTCACCGAACGTACTGCGTTAAAGCGTAAGCCAAAGCAG
3-2	TCATCCCAAGCACCCTCCAGCGCTATCGCGAGTACTTGCTCT
3-3	TCCATAGCGGTATCCGATAACTTCGTAGACTACGCATATAAT
3-4	CATTCAATGGATCTTAGGGATCAGCGAATTCATGCTTAAATC
3-5	ATTACAGGACTGGCATCAATTCACTGCCCTACAGCAGAGATA
3-6	TTTTTTTTTTTCTGGCGGCTGACAAACCGCGTTTTTTTTTTT
4-1	TTTTTTTTTTTCTCCCGCGAACTTACGCTTTAATTTTTTTTT
4-2	GTAACCACTGCGCGTTACAAGACTCGCGATAGCCTGCTTTGG
4-3	GTACACCCGACTGGGACCCGAGTAGTCTACGAAAGAGCAAGT
4-4	TGTATACCGTAATATGGTTACATGAATTCGCTGATTATATGC
4-5	AACCCACCTAGGGCCCTGAGGTGTAGGGCAGTGGATTTAAGC
4-6	CACACAAATAGGCCGCGTCAGAACGCGGTTTGTTATCTCTGC
5-1	GCAGTGGTTACTTCGCGGGAGTCCCGCTGGCTGCGGATACGG
5-2	GTCGGGTGTACCTTGTAACGCCTGCGTCTGCACGCGGGTAAG
5-3	TACGGTATACATCGGGTCCCAAATGCGAGCGGGTGTAATGGC
5-4	CTAGGTGGGTTGTAACCATATGAGGTTCGAGGGTTCACAGCC
5-5	CTATTTGTGTGCCTCAGGGCCGGCCAGGGTCCAGTGCCCGTC
5-6	TTTTTTTTTTTCTGACGCGGCAAACTGCGAGCTTTTTTTTTT
6-1	TTTTTTTTTTTCGTCTCGCTTCAGCCAGCGGGATTTTTTTTT
6-2	GATTAGAGACCTTATCACCCAGTGCAGACGCAGCCGTATCCG
6-3	GCCGCATAAAGTATGATCCCACCCGCTCGCATTCTTACCCGC
6-4	CCAGCACGGAAAGCCTCCTAACCCTCGAACCTCGCCATTACA
6-5	ATTTCCTTTCGGTTAAACTAGTGGACCCTGGCCGGCTGTGAA
6-6	CTTGACAGTAAAGATCCGCCGAGCTCGCAGTTTGACGGGCAC
7-1	GGTCTCTAATCAAGCGAGACGGCGCAGCGATGGAGTTGCCGC
7-2	CTTTATGCGGCTGGGTGATAACGTTCCCAACGGGAACTCGAT
7-3	TTCCGTGCTGGTGGGATCATAGACGCTCTGGTTGCTAGACGG

7-4	CGAAAGGAAATTTAGGAGGCTATTCCTATGCGTGAATAAGTT
7-5	TTACTGTCAAGCTAGTTTAACGGCGTAGACCATGACCTGGTC
7-6	TTTTTTTTTTTCGGCGGATCTGAGCCAGTTCCGTTTTTTTTT
8-1	TTTTTTTTTTTTCTAATGTTCCCATCGCTGCGCTTTTTTTTT
8-2	CTCGGCATGGGCGCCAAGATCCCGTTGGGAACGGCGGCAACT
8-3	GAGAACATAGATGAATTCACGAACCAGAGCGTCATCGAGTTC
8-4	TCATTTCTTTCTAATCCCTGCACGCATAGGAATCCGTCTAGC
8-5	TTCAGCGGGCGGGACCAGCATATGGTCTACGCCAACTTATTC
8-6	CCTACAGCATTAAAGGATTCACGGAACTGGCTCGACCAGGTC
9-1	CCCATGCCGAGGAACATTAGATCACGTGAGCCACGTCATTAA
9-2	TCTATGTTCTCGATCTTGGCGTTGTGGTGTCATCAGCTGGGA
9-3	GAAAGAAATGACGTGAATTCATGCGTTACAGCACTGCAAGCG
9-4	CGCCCGCTGAAGCAGGGATTACGATCACGCTCCGTCCGATCT
9-5	AATGCTGTAGGATGCTGGTCCTTAATTGGTGTTGGTAAACGA
9-6	TTTTTTTTTTTTGAATCCTTTGTTCGTGCAAGTTTTTTTTTT
10-1	TTTTTTTTTTTGGGATGCGCCTGGCTCACGTGATTTTTTTTT
10-2	CGAGTCCCAAGGCTACTTCTAATGACACCACAATTAATGACG
10-3	GAGACACCCGTACTATTGACGTGCTGTAACGCATCCCAGCTG
10-4	AGACACCGGATCGTGATTTATGGAGCGTGATCGCGCTTGCAG
10-5	AACTTCGGCGAGCCCGTACTCAACACCAATTAAAGATCGGAC
10-6	CGTAGCAGTCACCTGCGCTTGACTTGCACGAACTCGTTTACC
11-1	CTTGGGACTCGGGCGCATCCC
11-2	ACGGGTGTCTCTAGAAGTAGC
11-3	ATCCGGTGTCTCGTCAATAGT
11-4	TCGCCGAAGTTATAAATCACG
11-5	TGACTGCTACGGAGTACGGGC
11-6	TTTTTTTTTTTCAAGCGCAGG

Motif 3.1 (10H×11T)

Name	Sequence
1-1	ATTGTTTAGTAGAAGTAGCGA
1-2	CTTTATTTACGGACCGGCCTG
1-3	AGAAAGGAGTAAATGTCGGAC
1-4	GACCCTACATACCGAATTGGA
1-5	ACGAGTATGTGGACGGGCAGC
1-6	TTTTTTTTTGGCTTTAGTTCT
2-1	TTTTTTTTTTCGCTACTTCTATTCCGTTGCCTTGAGTATAAA
2-2	CTAAACAATCAGGCCGGTCCGCGATTTGTTCGGCCTTCTTTA
2-3	TAAATAAAGGTCCGACATTTACACAACCGATCAGAACTGCGC
2-4	CTCCTTTCTTCCAATTCGGTAAGTGCTGGGCGTAACCCGGGT
2-5	TGTAGGGTCGCTGCCCGTCCAAACGGTTACGACTTTATCGGT
2-6	CATACTCGTAGAACTAAAGCCAAAGGGCAATGTTTTTTTTTT
3-1	AAGATTAACTCTACCTAGCTAAGGCAACGGAATTTTTTTTTT
3-2	TCAGATCAGCCCTCTGGTTACCGAACAAATCGTTTATACTCA
3-3	CGTTTCGAAAGCCCGCGATGTGATCGGTTGTGTAAAGAAGGC
3-4	TGACCCTAAGGAAACGGGAATCGCCCAGCACTGCGCAGTTCT
3-5	CACGGAAAGATTTACATAGTGTCGTAACCGTTACCCGGGTTA
3-6	TTTTTTTTTGTACGGTGCATGCATTGCCCTTTACCGATAAAG
4-1	TTTTTTTTTTAGCTAGGTAGAATGGACGCGGTCCGAGGGCCC
4-2	GTTAATCTTGTAACCAGAGGGTGAGACGTTGCTGGTTCCGAA
4-3	CTGATCTGAACATCGCGGGCTACATGTTATAGACGCGGCCCA
4-4	TTCGAAACGATTCCCGTTTCCATTGATGGGTTCACCCGTCTG
4-5	TTAGGGTCACACTATGTAAATAGTCAGACGAAGGAGTTAGAT
4-6	CTTTCCGTGCATGCACCGTACTCTTCCGGCGCTTTTTTTTTT
5-1	CCATTACGACAAGATTGGTGAACCGCGTCCATTTTTTTTTTT
5-2	AAAGCGCCAGACCCTCGTTGGGCAACGTCTCAGGGCCCTCGG
5-3	CTTAGACCAGTCGCGATATACCTATAACATGTTTCGGAACCA
5-4	ACGCGATGCGTCTCTAGGGTTAACCCATCAATTGGGCCGCGT
5-5	CCCATTATTACGAATAACGGCTTCGTCTGACTCAGACGGGTG
5-6	TTTTTTTTTATAGAGAGGTGGGCGCCGGAAGAATCTAACTCC
6-1	TTTTTTTTTTCACCAATCTTGCCGACCAAGATCTTGATATTA
6-2	TCGTAATGGCCAACGAGGGTCACGTCGCCATCTCATACTCCA
6-3	TGGCGCTTTGTATATCGCGACAGCTCAAAGCCCACGGAAATC
6-4	TGGTCTAAGAACCCTAGAGACGGGACGCTCATTGGTTCATTA
6-5	GCATCGCGTGCCGTTATTCGTGTTTAGACAACACGATGCATG
6-6	AATAATGGGCCACCTCTCTATGTATGCCTTTGTTTTTTTTTT
7-1	CGCGGGCGCTCCCGTATTTATATCTTGGTCGGTTTTTTTTTT
7-2	CGGGCTTGGACGTGTGCCCTGGATGGCGACGTTAATATCAAG
7-3	CCACCGCAGATCGGGCAGATGGGCTTTGAGCTTGGAGTATGA

7-4	CTGGTATGAGCCGACGAGGGAATGAGCGTCCCGATTTCCGTG
7-5	GCGTTGCCGGAACAGGACGGCGTTGTCTAAACTAATGAACCA
7-6	TTTTTTTTTCCGATATCATCACAAAGGCATACCATGCATCGT
8-1	TTTTTTTTTATAAATACGGGAAGAGACAGTATGTTTATACCA
8-2	GCGCCCGCGCAGGGCACACGTACGGCAATTCGAAGAGGAACA
8-3	CCAAGCCCGCATCTGCCCGATCGATAACGGGCCCAATAATGC
8-4	CTGCGGTGGTCCCTCGTCGGCATGTCCACAAACCCATCATTG
8-5	TCATACCAGGCCGTCCTGTTCACGCTGACGAACCCGCTGGTT
8-6	CGGCAACGCTGATGATATCGGTGCGAAAGTTCTTTTTTTTTT
9-1	AGATGGCTAAGCAATAAGCGTATACTGTCTCTTTTTTTTTT
9-2	GGCCTTAAAGACCGTGTCTGCCGAATTGCCGTTGGTATAAAC
9-3	GTCTACGGGCTCGTATGCAGCGCCCGTTATCGTGTTCCTCTT
9-4	GAAACTGTTACTGCGCAGCCCTTTGTGGACATGCATTATTGG
9-5	CTAGGTCTCCACCGAGGGTCGTTCGTCAGCGTCAATGATGGG
9-6	TTTTTTTTTAAGTGAGGGATTGAACTTTCGCAAACCAGCGGG
10-1	TTTTTTTTTACGCTTATTGCTGTACGCCTCCATAATTGCGAC
10-2	TAGCCATCTGCAGACACGGTCTGAAGCCGAGCATGGATGCTA
10-3	TTTAAGGCCGCTGCATACGAGCAGTGCGGCTTTGCGATCATT
10-4	CCCGTAGACGGGCTGCGCAGTTATAATGTTGACCACTGCTCA
10-5	AACAGTTTCCGACCCTCGGTGTTGCTTAAGCGTGTGGCGTGC
10-6	GAGACCTAGAATCCCTCACTTTCTGCTTGGTTTTTTTTTTTT
11-1	TGGAGGCGTACTTTTTTTTTT
11-2	GCTCGGCTTCAGTCGCAATTA
11-3	AAGCCGCACTGTAGCATCCAT
11-4	TCAACATTATAAATGATCGCA
11-5	CGCTTAAGCAATGAGCAGTGG
11-6	AACCAAGCAGAGCACGCCACA

Motif 3.2 (10H×11T)

Name	Sequence
1-1	ATACAACACCGCCAAACACGC
1-2	GGGCGACCGCATACTGTGTAT
1-3	CCAGGTACGATGAGTAGTTGT
1-4	TAATTTGGTACGCGCATTCAA
1-5	GTCCACGGCGGCTAATAAGTT
1-6	TTTTTTTTTTGTTCTCGTCAT
2-1	TTTTTTTTTTGCGTGTTTGGCGATTTGACTAACCTGTGTGAG
2-2	GGTGTTGTATATACACAGTATTCATGATATCTCATAGGGCCT
2-3	GCGGTCGCCCACAACTACTCAGCATTGGGCGGTTGGGCTACC
2-4	TCGTACCTGGTTGAATGCGCGAGGCCTCCGCCTAAGTAGATT
2-5	TACCAAATTAAACTTATTAGCGTGGTTGACGCAATTTCGAGA
2-6	CGCCGTGGACATGACGAGAACATGGGAATGGCTTTTTTTTTT
3-1	GCTGCTATATCCCTGCTTCTCTTAGTCAAATCTTTTTTTTTT
3-2	ACCTTTCTGCAGAAAGTGATCAGATATCATGACTCACACAGG
3-3	CAGGTGGAAGGGCCAAAGAATCCGCCCAATGCAGGCCCTATG
3-4	AGCCAAACTGCTTGCATGATGGGCGGAGGCCTGGTAGCCCAA
3-5	ATACTGGTTTGTTCAGCCGTGGCGTCAACCACAATCTACTTA
3-6	TTTTTTTTTTCGAGTAGTCTGGCCATTCCCATTCTCGAAATT
4-1	TTTTTTTTTTGAGAAGCAGGGACTCACGGATGCTTAGGACCC
4-2	ATATAGCAGCGATCACTTTCTAAGCTCATCCTCATTATCAAT
4-3	GCAGAAAGGTATTCTTTGGCCTTACATGAGCGTGGACCAACT
4-4	CTTCCACCTGCATCATGCAAGGCAAACGCTCGCGTACGACAC
4-5	CAGTTTGGCTCACGGCTGAACAGTTATTTGTACTCGGTATAG
4-6	AAACCAGTATCAGACTACTCGAGCTCCAACCCTTTTTTTTTT
5-1	ACGGCAGGATGATCTGTGATTCATCCGTGAGTTTTTTTTTTT
5-2	TGGCGCCAGCACGCGGTACTTAGGATGAGCTTGGGTCCTAAG
5-3	ACCGACGTTCTTCGACTGCTACGCTCATGTAAATTGATAATG
5-4	AGACAGTGTGCTGACATAATTCGAGCGTTTGCAGTTGGTCCA
5-5	TATCACGTGATGATGTAAACGTACAAATAACTGTGTCGTACG
5-6	TTTTTTTTTTAGCTAGATCACGGGTTGGAGCTCTATACCGAG
6-1	TTTTTTTTTTAATCACAGATCAGTTCCTACTAGGGCACCAGT
6-2	ATCCTGCCGTAAGTACCGCGTGAGCGTGCCAGTCGGACTGGG
6-3	GCTGGCGCCATAGCAGTCGAAAGACAGTATCTCTACCCGTAG
6-4	GAACGTCGGTAATTATGTCAGCGCCCGTGGAGGATGATTCAT
6-5	CACACTGTCTCGTTTACATCAGAATTCCCGGCAAGCGGGCCG
6-6	TCACGTGATAGTGATCTAGCTACAAGCGCTGATTTTTTTTTT
7-1	TTGAACGATAATCAATGGAAGTAGTAGGAACTTTTTTTTTTT
7-2	CCGTTCTGCTGCAACCGCCGGCTGGCACGCTCACTGGTGCCC
7-3	ACTCCGCGTAGATCCAAAGATAGATACTGTCTCCCAGTCCGA

7-4	AATGACCGCTCCACACGCTCACTCCACGGGCGCTACGGGTAG
7-5	CTTCAAGGATCCTATTTCTCCGCCGGGAATTCATGAATCATC
7-6	TTTTTTTTTTCGACTCTCGGATCAGCGCTTGTCGGCCCGCTT
8-1	TTTTTTTTTTCTTCCATTGATATATGCCTAATACTGAACGTT
8-2	TATCGTTCAACCGGCGGTTGCGTGGTACTCTTATACCCTCGC
8-3	AGCAGAACGGATCTTTGGATCAAACGACTCGAATCAAAGGCT
8-4	TACGCGGAGTTGAGCGTGTGGGTCTTGTGTCCTGCTAATATG
8-5	AGCGGTCATTGGAGAAATAGGGTCTATTCTGAACTCTAGTAG
8-6	ATCCTTGAAGTCCGAGAGTCGCGCCGAGCGATTTTTTTTTTT
9-1	CTCATTTACCTACCATAATATATTAGGCATATTTTTTTTTTT
9-2	AATAGTGAGGCACGCTTCATTAAGAGTACCACAACGTTCAGT
9-3	GATATTTAAACGTCCGCTCCCTCGAGTCGTTTGCGAGGGTAT
9-4	CATCCCGGCAGCATAAGAGGAGGACACAAGACAGCCTTTGAT
9-5	ACGCCTACAGGCGCCTTACTGTCAGAATAGACCATATTAGCA
9-6	TTTTTTTTTTAATGCACAACGATCGCTCGGCGCTACTAGAGT
10-1	TTTTTTTTTTATATTATGGTAGGACCGCTGTAACTTTACTAA
10-2	GGTAAATGAGAATGAAGCGTGAGCAGGATGAATTCAAAGTCG
10-3	CCTCACTATTGGGAGCGGACGTCTTCTCATGTTGCTTGTGGG
10-4	TTTAAATATCTCCTCTTATGCCGGCAAACTGAACTGGGCTGC
10-5	TGCCGGGATGCAGTAAGGCGCCGTCCTCCGGTTCACTTACGT
10-6	CTGTAGGCGTCGTTGTGCATTCCTCTAGCATATTTTTTTTTT
11-1	TACAGCGGTCCTTTTTTTTTT
11-2	TTCATCCTGCTTTAGTAAAGT
11-3	ACATGAGAAGACGACTTTGAA
11-4	TCAGTTTGCCGCCCACAAGCA
11-5	ACCGGAGGACGGCAGCCCAGT
11-6	TATGCTAGAGGACGTAAGTGA

Motif 4.1 (10H×11T)

Name	Sequence
1-1	ACTAAGCACTTTTTTTTTTT
1-2	TGTATAGTATCCAGCAGCTTA
1-3	CATCGTTACCGAGATTGATGG
1-4	GGACTAGACCGTTAACCAGTT
1-5	AATTCAAGCGTAGCCATCCTC
1-6	TGGAGTTTCACCTGATGTTCG
2-1	AGTGCTTAGTTAAGCTGCTGGGCCTGCTGGATCGGCATGTAG
2-2	ATACTATACACCATCAATCTCAGAAAGACTTTGACGATACTC
2-3	GGTAACGATGAACTGGTTAACTCGCGCGAGCGACCCTCAGTG
2-4	GGTCTAGTCCGAGGATGGCTAACTATTATTTATGGACCGAAA
2-5	CGCTTGAATTCGAACATCAGGGTATGCTCCCTACTGAAATAG
2-6	TGAAACTCCATTTTTTTTTTTCCTCAGCTTTTTTTTTTTTTT
3-1	TCCAGCAGGCTTTTTTTTTTTTACCGTTTGTTTTTTTTTTTT
3-2	AAGTCTTTCTCTACATGCCGACTTTAACCTAGATGCTCATTC
3-3	GCTCGCGCGAGAGTATCGTCATGCTTAATACGAATCCTGACT
3-4	AAATAATAGTCACTGAGGGTCTTCCCATCAAGTGGTTTGCCA
3-5	GGGAGCATACTTTCGGTCCATTCCCGTACAGAGGTACGAGGT
3-6	AAAGCTGAGGCTATTTCAGTATAGCCATACTCGAAGGTCTTA
4-1	ACAAACGGTAGAATGAGCATCCAGGGCGTGAGCCCTTGAGTT
4-2	TAGGTTAAAGAGTCAGGATTCAGACATAGCGTCCGCGATCAG
4-3	GTATTAAGCATGGCAAACCACGCCAGTATGTAAATCCCGGGC
4-4	TTGATGGGAAACCTCGTACCTCGGCTCGGCCCAGTGGTCAAG
4-5	CTGTACGGGATAAGACCTTCGGTGGTAGCCCACCACTCGCCT
4-6	AGTATGGCTATTTTTTTTTTTCCCGACCACTTTTTTTTTTTT
5-1	TCACGCCCTGTTTTTTTTTTTCCTACACTCATTTTTTTTTTT
5-2	CGCTATGTCTAACTCAAGGGCCAGTTACGTAAATCCGCGCAA
5-3	ACATACTGGCCTGATCGCGGACCATAGACCATCGGACCCGCA
5-4	GGCCGAGCCGGCCCGGGATTTATTCCTGCTGCTCAGATCAGA
5-5	GGGCTACCACCTTGACCACTGCTTAGATTTATGTGTTCGTAC
5-6	AGTGGTCGGGAGGCGAGTGGTATGAGTGGCACATCGCATTTA
6-1	TGAGTGTAGGTTGCGCGGATTGACCCATGTGCGCACGACTCC
6-2	TACGTAACTGTGCGGGTCCGATCCCGTCTGAGTCTATTCATC
6-3	TGGTCTATGGTCTGATCTGAGAGTGCACTTCAAGCAAAGTTG
6-4	CAGCAGGAATGTACGAACACATAGTGACACGGTGCGGAGCGT
6-5	TAAATCTAAGTAAATGCGATGGGCACAACCCTCCACAATGAA
6-6	TGCCACTCATTTTTTTTTTTTTATTGCACTTTTTTTTTTTTTT
7-1	CACATGGGTCTTTTTTTTTTTCCTCCGATAGTTTTTTTTTTT
7-2	TCAGACGGGAGGAGTCGTGCGGTTCGCATTACGAGGTAAGTA
7-3	GAAGTGCACTGATGAATAGACAAACTGTTTAGGCTAGGATAT

7-4	CGTGTCACTACAACTTTGCTTATAGGTCCTGGGCCGCCTCCT
7-5	GGGTTGTGCCACGCTCCGCACGATACTTATTCTAGAACTAGC
7-6	AAAGTGCAATTTCATTGTGGAATCCGGTTTCCATTTGTTCTA
8-1	CTATCGGAGGTACTTACCTCGAGAAAGGGCGATTCCGATCGC
8-2	TAATGCGAACATATCCTAGCCACCTTTCAGCATGCAAAGTTC
8-3	TAAACAGTTTAGGAGGCGGCCAGAACTCCACCTGCCACGTGA
8-4	CAGGACCTATGCTAGTTCTAGTAGCTAGTCGTAGAATCTACT
8-5	AATAAGTATCTAGAACAAATGGTGGCTTGTACCCGGAATGTG
8-6	GAAACCGGATTTTTTTTTTTTTCGACCGTGTTTTTTTTTTTT
9-1	CGCCCTTTCTTTTTTTTTTTTATAGAATTCATTTTTTTTTTT
9-2	GCTGAAAGGTGCGATCGGAATGACGTAAACGACAAAGTAAGG
9-3	GTGGAGTTCTGAACTTTGCATAGTGAAATGTTGGAACATTGG
9-4	CGACTAGCTATCACGTGGCAGGTGCACAGAATGAGCGGAAAT
9-5	TACAAGCCACAGTAGATTCTATTTGATCATCGATGCCCGCAG
9-6	ACACGGTCGACACATTCCGGGAACCAAGTCTGTTTAAAGTAC
10-1	TGAATTCTATCCTTACTTTGTTTCGAAAGTAATCCCATTGTC
10-2	CGTTTACGTCCCAATGTTCCACGACTGTGACGACAATTGTCG
10-3	ACATTTCACTATTTCCGCTCAGGCTATGGCATGCAACGATAC
10-4	TTCTGTGCACCTGCGGGCATCCATCCAGTGCCGTATGATACT
10-5	GATGATCAAAGTACTTTAAACTCATCCCTGTTCAACTCTGCA
10-6	AGACTTGGTTTTTTTTTTTTTGCAAGACATCTTTTTTTTTTT
11-1	TACTTTCGAATTTTTTTTTT
11-2	GTCACAGTCGGACAATGGGAT
11-3	TGCCATAGCCCGACAATTGTC
11-4	GCACTGGATGGTATCGTTGCA
11-5	ACAGGGATGAAGTATCATACG
11-6	GATGTCTTGCTGCAGAGTTGA

Motif 4.2 (10H×11T)

Name	Sequence
1-1	TTCAGCCTTCTTTTTTTTTT
1-2	AAACACGGCAAAGGTCGAAG
1-3	CCATGTACCAACCTGACAAG
1-4	GTCTCCTGGCCCAGACGAAT
1-5	CATTTGGTCTCCGGATAAGG
1-6	ACGAACTTCGGGATTGACTA
2-1	GAAGGCTGAACTTCGACCTTCTTGTTCAGCACGGGACAGG
2-2	TGCCGTGTTTCTTGTCAGGTTCAGACGACGGTCCAAAGCA
2-3	TGGTACATGGATTCGTCTGGTGGCCTTCTGTCCGAGATCA
2-4	GCCAGGAGACCCTTATCCGGGCAACCCGATGCGGGCGGAA
2-5	AGACCAAATGTAGTCAATCCCAATCGGCCCTCGGAACGAC
2-6	CGAAGTTCGTTTTTTTTTTTGCGTCGTCTTTTTTTTTTTT
3-1	GCTGAACAAGTTTTTTTTTTGCTTAAGACATTTTTTTTTT
3-2	CGTCGTCTGACCTGTCCCGTCGCCACTTGTCTTCTAACGA
3-3	CAGAAGGCCATGCTTTGGACTGGTTAATGGATCATACGTC
3-4	ATCGGGTTGCTGATCTCGGAGGTACCGCACCCAGCGAGCA
3-5	GGGCCGATTGTTCCGCCCGCTCAACAGGCCGTAAACGCAA
3-6	AAGACGACGCGTCGTTCCGACATGTACTCCAATCATCCGC
4-1	TGTCTTAAGCTCGTTAGAAGTATGAGAGAGTATCCTTATG
4-2	ACAAGTGGCGGACGTATGATAGCATCTGAGGACGCCACCA
4-3	CCATTAACCATGCTCGCTGGGAGTCCCTCGAACAAAGAGA
4-4	GTGCGGTACCTTGCGTTTACGTGCGGTGATGCAGGACACA
4-5	GGCCTGTTGAGCGGATGATTACATGCACTCTCGGTCATGT
4-6	GGAGTACATGTTTTTTTTTTTCCCAACCGCTTTTTTTTTT
5-1	CTCTCTCATATTTTTTTTTTTCTCTAGGCGTTTTTTTTTT
5-2	CTCAGATGCTCATAAGGATAGGTCCGTGTAAAGCATGAAG
5-3	CGAGGGACTCTGGTGGCGTCGTTCTCCAGTCTGGCACACA
5-4	ATCACCGCACTCTCTTTGTTCTCGACCGGCTTTCTTTGTA
5-5	GAGTGCATGTTGTGTCCTGCTCTTGTCGTCCTTGGGACGT
5-6	GCGGTTGGGAACATGACCGAGAAGATTCGGGTCCCTGTAT
6-1	CGCCTAGAGACTTCATGCTTTAGGAGCGTTTCTAAAGGAG
6-2	TACACGGACCTGTGTGCCAGCAGTAATACGTTATGGCGGT
6-3	ACTGGAGAACTACAAAGAAATCTAAGGCAGTTACAGTGCA
6-4	GCCGGTCGAGACGTCCCAAGAGGGAAAGGCAAACCACCCT
6-5	GACGACAAGAATACAGGGACCCTCAACCCTTCACAAGTGT
6-6	CCGAATCTTCTTTTTTTTTTTGCTTTATCTTTTTTTTTTT
7-1	AACGCTCCTATTTTTTTTTTCCTAATTCTCTTTTTTTTTT
7-2	CGTATTACTGCTCCTTTAGACCTCCCTTTAATGTGGATTT
7-3	CTGCCTTAGAACCGCCATAAAGCTTATTCCTTGCGAAGGC

7-4	GCCTTTCCCTTGCACTGTAAGACCCACTTCGCCAAAGTAG
7-5	AGGGTTGAGGAGGGTGGTTTAAATACAGATCTCAGACTGG
7-6	AAGATAAAGCACACTTGTGAACTCCGATCTTCTTGAAGGG
8-1	GAGAATTAGGAAATCCACATCTAGTGCTAAGTTAAACAGT
8-2	TAAAGGGAGGGCCTTCGCAACGGCCATCCCGGAGGTCCAC
8-3	GGAATAAGCTCTACTTTGGCTACCGCAATCTCATGAGCCG
8-4	GAAGTGGGTCCCAGTCTGAGCTGTGAACATATAGTCCTCG
8-5	ATCTGTATTTCCCTTCAAGAGGAAGGTTTGTTCGCTCCTA
8-6	AGATCGGAGTTTTTTTTTTTCGGGCTGAATTTTTTTTTTT
9-1	TTAGCACTAGTTTTTTTTTTGCGTCGTTGTTTTTTTTTT
9-2	GGGATGGCCGACTGTTTAACCAGGGCAGTTAGAAGCCAGC
9-3	GATTGCGGTAGTGGACCTCCTCTAGGGCGTTTAACAAGCG
9-4	ATGTTCACAGCGGCTCATGACTGTGACCACTGGACAGTAT
9-5	CAAACCTTCCCGAGGACTATTAAGGAGTGCAGGCTGCCTT
9-6	ATTCAGCCCGTAGGAGCGAACCTTGGATCCCACACCAAAT
10-1	ACAACGACGCGCTGGCTTCTTTGTGAGCGATGCAGCGATC
10-2	AACTGCCCTGCGCTTGTTAATCGCAATTGGCAGTCCCATA
10-3	ACGCCCTAGAATACTGTCCAATGGGATGAAGCGTCCCATT
10-4	GTGGTCACAGAAGGCAGCCTGCCTACTCGCACGACAAAGT
10-5	GCACTCCTTAATTTGGTGTGCATCGTCTGCAGACGAAGCG
10-6	GGATCCAAGGTTTTTTTTTTTCGCTCACTTTTTTTTTTT
11-1	TCGCTCACAATTTTTTTTT
11-2	CCAATTGCGAGATCGCTGCA
11-3	TTCATCCCATTATGGGACTG
11-4	GCGAGTAGGCAATGGGACGC
11-5	GCAGACGATGACTTTGTCGT
11-6	AGTGAGCGAACGCTTCGTCT

Motif 4.3 (10H×11T)

Name	Sequence
1-1	CGGACTGTGCTTTTTTTTTTTTT
1-2	CGGCTAACCATCTCCTCTCGAGGG
1-3	GTGAGTCAAGCCCTTTAATGAGCG
1-4	TTTACGGACCTGGGCCAGGCGTCT
1-5	CCTCTGCCACTGTGATCCGAGCAA
1-6	GTCCCAGCATCCGCGCGTCACTGC
2-1	AAGCACAGTCCGCCCTCGAGAGGACACTTTAAGATGCGTTTAGGGCAT
2-2	GATGGTTAGCCGCGCTCATTAAAGCCACCATGGGAATTAGTAAACCCA
2-3	GGCTTGACTCACAGACGCCTGGCCCAGAACCTCGCGGATGATCTCTTT
2-4	CAGGTCCGTAAATTGCTCGGATCAGGTGCAGGACCATGTACAGGCAGC
2-5	CAGTGGCAGAGGGCAGTGACGCGCCATGGATTGTCAGTGCATCAACCG
2-6	GGATGCTGGGACTTTTTTTTTTTTGTGTCCTCTTTGTTTTTTTTTTTT
3-1	CATCTTAAAGTGTTTTTTTTTTTTATGTCGGGCGGCTTTTTTTTTTTT
3-2	TTCCCATGGTGGATGCCCTAAACGGAGGTCTATATGCTCTTCCCTGGG
3-3	CGCGAGGTTCTGTGGGTTTACTAATGGGCCGGATAACTACGCCCAAGG
3-4	TGGTCCTGCACCAAAGAGATCATCGTTGCTAGAGTGTAAGGCAAAGAC
3-5	TGACAATCCATGGCTGCCTGTACATGCCCAAGAGCTTGGAGCGAACGT
3-6	CAAAGAGGACACCGGTTGATGCACGAACACTTCGCAAGGTGAGAAAGA
4-1	GCCGCCCGACATCCCAGGGAAGAGCCTGTATTTACGGTACCCTCGTAT
4-2	CATATAGACCTCCCTTGGGCGTAGTCGCGAGGGTCAAAGGCCGCATTG
4-3	TTATCCGGCCCAGTCTTTGCCTTAACATGCGGACAATCTTCCCTGAGC
4-4	CACTCTAGCAACACGTTCGCTCCATAAATTGCCCTGGCGCTTAAAGCA
4-5	AGCTCTTGGGCATCTTTCTCACCTCATCGTGTAATACGGGTGGCGAAC
4-6	TGCGAAGTGTTCTTTTTTTTTTTTTCAGGTAGTGGATTTTTTTTTTT
5-1	CGTAAATACAGGTTTTTTTTTTTTACAACGGGCACTTTTTTTTTTTT
5-2	TGACCCTCGCGAATACGAGGGTACGGACCTCGCTGCGAGAAGAAACCG
5-3	TTGTCCGCATGTCAATGCGGCCTTCGATGCAGTCGTACTGGCGATGCG
5-4	CAGGGCAATTTAGCTCAGGGAAGAATGGTCGTAAGCAGCAGGCCAGTG
5-5	TATTACACGATGTGCTTTAAGCGCTATACTTCATTAGATGGAAAGAGC
5-6	TCCACTACCTGAGTTCGCCACCCGCTTTATAGCTAGTTCCATAGTCTC
6-1	AGTGCCCGTTGTCGGTTTCTTCTCGGGACTCTCGAAGCGACAAGCGTC
6-2	GCAGCGAGGTCCCGCATCGCCAGTGTTAACCGCTTCGTCTAAGATCAA
6-3	ACGACTGCATCGCACTGGCCTGCTAGTCGGGTTGCTGAAGCTGCACGA
6-4	GCTTACGACCATGCTCTTTCCATCTTGGCCCATACTTAACCTGAATCC
6-5	TAATGAAGTATAGAGACTATGGAAGGCGTGTTTATTGCTTGATGATCG
6-6	CTAGCTATAAAGTTTTTTTTTTTTTATCTTGAGTGTGTTTTTTTTTTT
7-1	TTCGAGAGTCCCTTTTTTTTTTTTTAGAGTCGGGCAGTTTTTTTTTTT
7-2	GAAGCGGTTAACGACGCTTGTCGCACTTGTCATTGATTGCGGCTTACA
7-3	AGCAACCCGACTTTGATCTTAGACCTTAGTTCCAAGTTTGACAATTTA

7-4	AGTATGGGCCAATCGTGCAGCTTCAAACGTCTTCACGTTCGACAACCT
7-5	AATAAACACGCCGGATTCAGGTTAAACGTATGTAGCATACTTACTAAC
7-6	CACACTCAAGATCGATCATCAAGCTCGACTTACGTGAGCTGGGAGTGA
8-1	CTGCCCGACTCTTGTAAGCCGCAATGCGCTCACGATAGGGCGTGGAGT
8-2	TCAATGACAAGTTAAATTGTCAAAGACGGATTACTGAGCAGACTCCCA
8-3	CTTGGAACTAAGAGGTTGTCGAACTGGTAGTCTCTGTGATTTAGCCCT
8-4	GTGAAGACGTTTGTTAGTAAGTATCGACTAGGGAAAGTGGGACATAGA
8-5	GCTACATACGTTTCACTCCCAGCTGACGTTAGGTGCGCCTCTTTCGCA
8-6	CACGTAAGTCGATTTTTTTTTTTTACTCGAGTAGGTTTTTTTTTTTT
9-1	ATCGTGAGCGCATTTTTTTTTTTTCTGAATCCGGGCTTTTTTTTTTT
9-2	CAGTAATCCGTCACTCCACGCCCTTTAAACACCAGGATTATACAAACT
9-3	CAGAGACTACCATGGGAGTCTGCTTTATCATCAGTCCGCGGCCATCAG
9-4	TTTCCCTAGTCGAGGGCTAAATCAATGTGGTAAAGGAAACTGCTCTTA
9-5	GCACCTAACGTCTCTATGTCCCACCTGCGTTCAGCATGAGTGGCATCC
9-6	ACCTACTCGAGTTGCGAAAGAGGCTCCGCTTGGTCCCGCACGAGTTGG
10-1	GCCCGGATTCAGAGTTTGTATAATGCAGTCGGTCCTTCGTTTGATTAC
10-2	CCTGGTGTTTAACTGATGGCCGCGAAATTAGCCGTGCGGGCTCATCTA
10-3	GACTGATGATAATAAGAGCAGTTTACTCTTCAGTTCGGGCGGGAGAAA
10-4	CCTTTACCACATGGATGCCACTCACAACATCCTTTAAATGATCGGAGT
10-5	TGCTGAACGCAGCCAACTCGTGCGAACAGTTGAACACAGATAGGAAGC
10-6	GGACCAAGCGGATTTTTTTTTTTTTGGACCAGGCAATTTTTTTTTTT
11-1	AGGACCGACTGCTTTTTTTTTTT
11-2	CACGGCTAATTTGTAATCAAACGA
11-3	GAACTGAAGAGTTAGATGAGCCCG
11-4	TAAAGGATGTTGTTTCTCCCGCCC
11-5	TGTTCAACTGTTACTCCGATCATT
11-6	TTGCCTGGTCCAGCTTCCTATCTG

Motif 4.4 (10H×11T)

Name	Sequence
1-1	CAACCTCTGCGTTTTTTTTTT
1-2	TTAACGGACGTAGGTACCTCCG
1-3	CGTAGGCACTGTCGCAGCTAGT
1-4	CAGAACCATCCATCCTCTTGAA
1-5	CATTTCGTGCACAGAAGGGTCC
1-6	ATTTATACCGCTAACATCGGCC
2-1	CGCAGAGGTTGCGGAGGTACCTATGCTGAGCTAATCGTATCCAA
2-2	ACGTCCGTTAAACTAGCTGCGAATATAGTCAGCCGTGAACAAGC
2-3	CAGTGCCTACGTTCAAGAGGATAAAGGAACACCCTATTATTGGC
2-4	GGATGGTTCTGGGACCCTTCTGAACGACGGCCCTTGCTGGAGGA
2-5	TGCACGAAATGGGCCGATGTTATATTACAGATTGCGGTAGGTTG
2-6	GCGGTATAAATTTTTTTTTTTTAGTCAGATAGTTTTTTTTTTT
3-1	TAGCTCAGCATTTTTTTTTTTTTTACACGGACTTTTTTTTTTT
3-2	GCTGACTATATTTGGATACGATTTGGATGCTATGAGGGCTACCC
3-3	GGTGTTCCTTTGCTTGTTCACGGTCTATCTTCAAGTCGCCAGGC
3-4	GGGCCGTCGTTGCCAATAATAGCCTGGTCCGTCTGACTAAGAGG
3-5	AATCTGTAATATCCTCCAGCAAGAGGCTTCCATAGGGCGGACCG
3-6	ACTATCTGACTCAACCTACCGCACGCAAGACTTCCGGCCTGCTG
4-1	AGTCCGTGTAAGGGTAGCCCTCGCGGCAAAGGTCGTTAATACGA
4-2	ATAGCATCCAAGCCTGGCGACTCGAAGATCGCACGTACAACAGG
4-3	TGAAGATAGACCCTCTTAGTCATCAGTAAGCAAGTGATGTCGCA
4-4	GACGGACCAGGCGGTCCGCCCTGGTTGGGTAGCACACTTGTAGA
4-5	ATGGAAGCCTCCAGCAGGCCGGACGGCTTACGCCGTGATCTTCC
4-6	AAGTCTTGCGTTTTTTTTTTTCTATGTGATGATTTTTTTTTT
5-1	ACCTTTGCCGCTTTTTTTTTTTTACGTGACAGTTTTTTTTTTT
5-2	TGCGATCTTCGTCGTATTAACGCTTATTACATTTGTTGTAGATT
5-3	TTGCTTACTGACCTGTTGTACGTCCCATTCATACGTGGCCGAGT
5-4	GCTACCCAACCTGCGACATCACATCGCGATGCAAACATAAGGCC
5-5	GCGTAAGCCGTTCTACAAGTGTCGCGATGCTTAAAGACTATCTT
5-6	TCATCACATAGGGAAGATCACGATGAGGCTACCGCAAATCTCCA
6-1	ACTGTCACGTAAATCTACAACAGACAAAGATCCCTACGAGAAAG
6-2	AATGTAATAAGACTCGGCCACGGGCTGAAGCCAGTGAGTTGCGC
6-3	TATGAATGGGAGGCCTTATGTTGCAGAGCCAAAGAGGCGGTCTA
6-4	TGCATCGCGATAAGATAGTCTTCCTTCGCAGCAGTAACGATGAT
6-5	TAAGCATCGCGTGGAGATTTGCTCGTTATACGGGCCAGTTGGTC
6-6	GGTAGCCTCATTTTTTTTTTTTTATAACCCTCTATTTTTTTTTT
7-1	GGATCTTTGTCTTTTTTTTTTTTTCTAGCTAGTGTTTTTTTTTT
7-2	TGGCTTCAGCCCTTTCTCGTAGTAATAACCTACTATCCACCGCT
7-3	TTTGGCTCTGCGCGCAACTCACCCTCGAGACGGCGATGGTCATG

7-4	TGCTGCGAAGGTAGACCGCCTCTGGACTCACCGAATGCCGACGG
7-5	CCGTATAACGAATCATCGTTACAAACTAACAAGCTGCATGACTT
7-6	TAGAGGGTTATGACCAACTGGCACAGTCTATAACTGTATATGGC
8-1	CACTAGCTAGAAGCGGTGGATAGCCACACTTCGGTGGGCAGCTC
8-2	GTAGGTTATTACATGACCATCGTGAACGTATTGCTACTGCTGTC
8-3	CCGTCTCGAGGCCGTCGGCATTAAATGCCACCCTTGTACTATAC
8-4	CGGTGAGTCCAAAGTCATGCAGCGGGCCGATTTACACACTCCGC
8-5	CTTGTTAGTTTGCCATATACAGAGGCAACACCATCCGAAACCGC
8-6	TTATAGACTGTTTTTTTTTTTTCAGGCAAGGCGTTTTTTTTTTT
9-1	CGAAGTGTGGCTTTTTTTTTTTAAAGGTCGTGTTTTTTTTTTT
9-2	CAATACGTTCAGAGCTGCCCACTGCCAGGTTAATTATAGAGTTC
9-3	GGGTGGCATTTGACAGCAGTAGCGCTTGGCTGATTACTTCCAGA
9-4	AAATCGGCCCGGTATAGTACAACCGAGAAATCACAGTCTGTAAA
9-5	TGGTGTTGCCTGCGGAGTGTGTCGTGCTTTCGATCTTTAATGTA
9-6	CGCCTTGCCTGGCGGTTTCGGAAGCTACGCATCAGCCCGGCAGA
10-1	ACACGACCTTTGAACTCTATAATTCCATATCTATGGCCTTTGCG
10-2	TTAACCTGGCATCTGGAAGTAACTCGTAGTTTGCACCTATCCAT
10-3	TCAGCCAAGCGTTTACAGACTGTGCTACTCCGCGAATGTACGTG
10-4	TGATTTCTCGGTACATTAAAGAACCTCCTCTCTCCTGCCCTATT
10-5	TCGAAAGCACGTCTGCCGGGCTAGATCAAATAGATCTGTATGCG
10-6	GATGCGTAGCTTTTTTTTTTTTCTTTATGGTTCTTTTTTTTTTT
11-1	TAGATATGGAATTTTTTTTTT
11-2	CAAACTACGAGCGCAAAGGCCA
11-3	GCGGAGTAGCAATGGATAGGTG
11-4	AGAGAGGAGGTCACGTACATTC
11-5	CTATTTGATCTAATAGGGCAGG
11-6	GAACCATAAAGCGCATACAGAT

Motif 4.5 (10H×11T)

Name	Sequence
1-1	TTGCATTGGCTCGTTTTTTTTTTTT
1-2	AATAGGCAATACACCACGCGCTGCTC
1-3	ACACACTAACCACTGACATGGCACCC
1-4	AATCAACATTAGCGACCGTTTCAGTA
1-5	GTTAGCCGCCGTTAGGGCCCATCGGG
1-6	GACCCTTTATGGATGTGGAGTCTAAG
2-1	CGAGCCAATGCAAGAGCAGCGCGTGGTTGATCGTTAGGTATCGTGAAACTGC
2-2	TGTATTGCCTATTGGGTGCCATGTCAGACGAAGATCGATATGGTTTACAGCT
2-3	GTGGTTAGTGTGTTACTGAAACGGTCTCACGTTGAGGAGCTAATAATTCGTA
2-4	GCTAATGTTGATTCCCGATGGGCCCTGGTCCCAGGAAATGATCTGTATAAAC
2-5	AACGGCGGCTAACCTTAGACTCCACAAGATTGTCTAAGGGCGGTCGTACCCT
2-6	TCCATAAAGGGTCTTTTTTTTTTTTTTCGTTACTGCCAGCTTTTTTTTTTTT
3-1	ACCTAACGATCAATTTTTTTTTTTTTTGCTATTTGACTCGTTTTTTTTTTTT
3-2	ATCGATCTTCGTCGCAGTTTCACGATCAAGTCAGCCGGTTTCGGCCAAGGCA
3-3	CTCCTCAACGTGAAGCTGTAAACCATGCTCCAAGGCGCCTCTTCGAAAGAAG
3-4	ATTTCCTGGGACCTACGAATTATTAGACCATCAGGTACCTGACTCGCGACTG
3-5	CCTTAGACAATCTGTTTATACAGATCAATTTGAGACGGACTCGCGTACAACA
3-6	GCTGGCAGTAACGAGGGTACGACCGCAGGCTGGAATCGAACACATATAATAC
4-1	CGAGTCAAATAGCTGCCTTGGCCGAATTTGCGAGTCTGAGGATGGTCTTGAC
4-2	ACCGGCTGACTTGCTTCTTTCGAAGAGACCCTAGCTACACGATGCAAATAGA
4-3	GGCGCCTTGGAGCCAGTCGCGAGTCAAGAACACACGGGTCCTAGATGGATAG
4-4	GGTACCTGATGGTTGTTGTACGCGAGCGCCCTTAGTTGCATGGACGCTCCTT
4-5	TCCGTCTCAAATTGTATTATATGTGTAGTCACCGCTCCTGCGAAATAGGATC
4-6	TCGATTCCAGCCTTTTTTTTTTTTTTAAAGTTGAGTGGCTTTTTTTTTTTT
5-1	TCAGACTCGCAAATTTTTTTTTTTTTTATGGAGGCTTCATTTTTTTTTTTT
5-2	TGTAGCTAGGGTCGTCAAGACCATCCTGCTAATCGAGGCTATACCCTTTCCC
5-3	ACCCGTGTGTTCTTCTATTTGCATCGAGACATACTCACACATGTCCAAGACT
5-4	GCAACTAAGGGCGCTATCCATCTAGGGCGATTCTGCCACGCCTGTGTTGGAA
5-5	AGGAGCGGTGACTAAGGAGCGTCCATAGGCAGAGGGACCCTAACAAGGAGTA
5-6	GCCACTCAACTTTGATCCTATTTCGCCCTTAGGGCCGTCAGTTTCTTTCAAG
6-1	TGAAGCCTCCATAGGGAAAGGGTATACCAGGGCCAGGTGTCGATGCATGAGA
6-2	GCCTCGATTAGCAAGTCTTGGACATGTCTATTGTAGTAGAGACGCGCGTAGA
6-3	TGTGAGTATGTCTTTCCAACACAGGCTATTGCAGTAGACCAGAGCTATCCCT
6-4	GTGGCAGAATCGCTACTCCTTGTTAGCCTGCTACCAATCATACCCTGTATAG
6-5	GGTCCCTCTGCCTCTTGAAAGAAACTTTAGATCACCCTCCGTTTGCATAAGG
6-6	GACGGCCCTAAGGTTTTTTTTTTTTTTATTACAACCCTTCTTTTTTTTTTTT
7-1	CACCTGGCCCTGGTTTTTTTTTTTTTCAAGAGCTCCTGCTTTTTTTTTTTT
7-2	CTACTACAATAGATCTCATGCATCGAATTACCCTCAACGTAGTGGTAGGCTT
7-3	GTCTACTGCAATATCTACGCGCGTCTGGGTCCTAAGGCGGGAAGTAGATTAA

7-4	GATTGGTAGCAGGAGGGATAGCTCTGCATAGCGTACGCCCGGGCGCCAGACC
7-5	GAGGGTGATCTAACTATACAGGGTATTTCTGCTAGGACGTCGAGCATGGGAT
7-6	GAAGGGTTGTAATCCTTATGCAAACGCCGCTGCCTGGCAGATCAATCGGACC
8-1	GCAGGAGCTCTTGAAGCCTACCACTAGACACTAACGTATTTCAGAGTTACGA
8-2	CGTTGAGGGTAATTTAATCTACTTCCCTTCTACGGGTGTTCAACGGATTGCT
8-3	CGCCTTAGGACCCGGTCTGGCGCCCGTAGTCCGACCGACTGCTAAGTGATTG
8-4	GGCGTACGCTATGATCCCATGCTCGACATCAGTGCTAAATGAAAGCCCTCTG
8-5	CGTCCTAGCAGAAGGTCCGATTGATCTAGCCGTCCAATGGTCCCATAGACCG
8-6	TGCCAGGCAGCGGTTTTTTTTTTTTTAAAGACGGCTCGGTTTTTTTTTTTT
9-1	ATACGTTAGTGTCTTTTTTTTTTTTTGTTGTGAGAAAGATTTTTTTTTTTT
9-2	ACACCCGTAGAAGTCGTAACTCTGAACAAGTCTGTTTCGACCGCTTGTCACG
9-3	GTCGGTCGGACTAAGCAATCCGTTGAAACGATTGCCACCTCACTCGGCGCGA
9-4	TTTAGCACTGATGCAATCACTTAGCACGTCAGGCCTTCAAACCTTGCGTGGC
9-5	CATTGGACGGCTACAGAGGGCTTTCAGCATTTAGTGGGAATGCTCGTCGGTG
9-6	CCGAGCCGTCTTTCGGTCTATGGGACCACTGATTGGGTCTACACGTGGAAGT
10-1	TCTTTCTCACAACCGTGACAAGCGGTATGGGATCGTGATCTCTTCGTCATTT
10-2	CGAAACAGACTTGTCGCGCCGAGTGAATATGGTCATACGCTCGAATAGATTC
10-3	GGTGGCAATCGTTGCCACGCAAGGTTCGTAAACTTGTTAGTAATCCGAGCCT
10-4	TGAAGGCCTGACGCACCGACGAGCATCACCCTACCCTCTACACCATGGGATA
10-5	TCCCACTAAATGCACTTCCACGTGTAGATAAATTGGGCCATAGATTCGAGTC
10-6	GACCCAATCAGTGTTTTTTTTTTTTTCCAAATGTGAGGCTTTTTTTTTTTT
11-1	ATCACGATCCCATTTTTTTTTTTTT
11-2	CGTATGACCATATAAATGACGAAGAG
11-3	TAACAAGTTTACGGAATCTATTCGAG
11-4	AGAGGGTAGGGTGAGGCTCGGATTAC
11-5	GGCCCAATTTATCTATCCCATGGTGT
11-6	GCCTCACATTTGGGACTCGAATCTAT

Motif 4.6 (10H×11T)

Name	Sequence
1-1	GAGCCCAAATTTTTTTT
1-2	CCCGTTAGCGCGAAGCGC
1-3	TCCCATTCGGAATCATCG
1-4	CCTATCGCAACCAGTGTA
1-5	CTTTACCTTTGTTTAGTG
1-6	GGCACCTAGGTTGTATCG
2-1	TTTGGGCTCGCGCTTCGCCTGAGCTAGGCGCCATTT
2-2	GCTAACGGGCGATGATTCGAATTGTCGGGTAGAAGC
2-3	CGAATGGGATACACTGGTTTAACTGCCGTCGTCTTT
2-4	TGCGATAGGCACTAAACAAATTTGGCGTTAAGCGTT
2-5	AAGGTAAAGCGATACAACAACCAAACATGAATCTTA
2-6	CTAGGTGCCTTTTTTTTTGCTCTCTCCTTTTTTTTT
3-1	CTAGCTCAGTTTTTTTTTTATCAGCGCTTTTTTTTT
3-2	CGACAATTCAAATGGCGCGAAGATGTGTGAAATGTA
3-3	GGCAGTTAAGCTTCTACCTATCGAGTCTCATGTCAT
3-4	CGCCAAATTAAAGACGACATACGTAACCCAGAGGAG
3-5	TGTTTGGTTAACGCTTAAGATACCACCAGTGTCCGC
3-6	GGAGAGAGCTAAGATTCATTGTTGCAATCGCGCCCT
4-1	GCGCTGATATACATTTCAGGCGATCTTCGCTTGACC
4-2	CACATCTTCATGACATGACTAGTTGAGGTATTAGGA
4-3	GACTCGATACTCCTCTGGCCTGCCACCTCTGAGTGG
4-4	GTTACGTATGCGGACACTTGAGGTACCTTACTCTGG
4-5	GGTGGTATCAGGGCGCGACGAGCGATGCTACCGAGA
4-6	TTGCAACAATTTTTTTTTCAAGTTGTTTTTTTTTTT
5-1	AAGATCGCCTTTTTTTTTCCAGTACGATTTTTTTTT
5-2	CTCAACTAGGGTCAAGCGTGCCGCGTTATCGTGTGA
5-3	GGTGGCAGGTCCTAATACCTGCTTGACACGCCGTAG
5-4	GGTACCTCACCACTCAGAAATACACTTCCTGCGCGA
5-5	CATCGCTCGCCAGAGTAACACCCTAATCTGACTCGT
5-6	AACAACTTGTCTCGGTAGACGATTGCAGGCGCTACA
6-1	TCGTACTGGTCACACGATTGCGGCCGAACGTCGAAC
6-2	AACGCGGCACTACGGCGTATATATGCCGTCTAGGGC
6-3	GTCAAGCAGTCGCGCAGGGCTCCGCGTGCTAGCGAG
6-4	AAGTGTATTACGAGTCAGTCAGTGGAAGTGAGGCTG
6-5	ATTAGGGTGTGTAGCGCCGTAAGTCTCGACTTTGGC
6-6	TGCAATCGTTTTTTTTTTTGCGTTCAGATTTTTTTTT
7-1	TCGGCCGCATTTTTTTTTTCTCCTAGTCTTTTTTTTT
7-2	GGCATATATGTTCGACGTAGCCGTTACTCAGTCAGT
7-3	ACGCGGAGCGCCCTAGACCCTCGACCAGGCTAATGG

7-4	TTCCACTGACTCGCTAGCACTTTGCCAGTTTAACTA
7-5	GAGACTTACCAGCCTCACTCTTAGAGTATTCCCTCC
7-6	TCTGAACGCGCCAAAGTCGACTTAATGCCCATAGCA
8-1	GACTAGGAGACTGACTGATATTGCGAGGCTATACCA
8-2	GTAACGGCTCCATTAGCCGCTACAATTCTTGCTGTG
8-3	TGGTCGAGGTAGTTAAACGGTTAGACGTGTCTCGGA
8-4	TGGCAAAGTGGAGGGAATCTACTGAAACTTTGCCCT
8-5	ACTCTAAGATGCTATGGGCCTCCAGCCCAGCCACAG
8-6	CATTAAGTCTTTTTTTTTATGCAGGGATTTTTTTTT
9-1	CTCGCAATATTTTTTTTTCACGTAAGTTTTTTTTTT
9-2	AATTGTAGCTGGTATAGCGTATTCGTTGGAGTGATA
9-3	CGTCTAACCCACAGCAAGGCTCTAGTCACGCCTCAG
9-4	TTTCAGTAGTCCGAGACACTGCCTGGGCGTCCCGTT
9-5	GGCTGGAGGAGGGCAAAGTTAGGGCCCTCATGGTTA
9-6	TCCCTGCATCTGTGGCTGAACGTTCATTTATGCGTA
10-1	ACTTACGTGTATCACTCCCAATTCCTTATTTCCTCC
10-2	AACGAATACCTGAGGCGTTTGAATAATAAGGAGCGG
10-3	GACTAGAGCAACGGGACGGAGCGACACCGACGCCGC
10-4	CCCAGGCAGTAACCATGATAGCCCACCACACCTGAA
10-5	GGGCCCTAATACGCATAATAATGGACACGTTTCGGA
10-6	ATGAACGTTTTTTTTTTTTCAACTACATTTTTTTTT
11-1	AAGGAATTGTTTTTTTTT
11-2	ATTATTCAAGGAGGAAAT
11-3	GTGTCGCTCCCGCTCCTT
11-4	GGTGGGCTAGCGGCGTCG
11-5	TGTCCATTATTCAGGTGT
11-6	TGTAGTTGATCCGAAACG

Motif 5.1 (10H×11T)

Name	Sequence
1-1	GCCAATCACAGTTTTTTTTTTTTTTTTTTTTTTTGCCTCAAC
1-2	AGAATTGTCGGTTTTTTTTTTTTTTTTTTTTTCAAGAGTTCG
1-3	TTCCGCTCTTATTTTTTTTTTTTTTTTTTTTTGACGACCGTC
1-4	GCGAGCACCTTTTTTTTTTTTTTTTTTTTTTTGCTGAAGAAA
1-5	TCTTTATACGTTTTTTTTTTTTTTTTTTTTTTTAAAGTACAT
1-6	GATCCTGTGGGTTTTTTTTTT
2-1	AGAATGGAAGACGTTGAGGCAATTTTTTTTTTTTTTTTTTTT
2-2	GACAATATTCATCGAACTCTTGCTGTGATTGGTAAAGTCGTA
2-3	CCGTAGGCACCAGACGGTCGTCCCGACAATTCCGGTGCGACC
2-4	AGAGACGTGCTCTTTCTTCAGCTAAGAGCGGATTGTGGAGCT
2-5	GACTTGGATTTAATGTACTTTAAAGGTGCTCGCGTGACGTGA
2-6	CTAGCAGGGATCCCACAGGATCACGTATAAAGGTGTCTGGCA
3-1	GACGCTCAGTTACGACTTTATCTTCCATTCTGAACTACCGAC
3-2	ATGGACCAACGGTCGCACCGTGAATATTGTCTCTTCCGAAAG
3-3	AGTGAGGGTGAGCTCCACAAGGTGCCTACGGTTCTATGCTTA
3-4	CCGCTGCCTATCACGTCACGAGCACGTCTCTTCCCTTGTTGA
3-5	AAGGTGAAAGTGCCAGACACAAATCCAAGTCGTAGATGGTAC
3-6	TTTTTTTTTTTTTTTTTTTTTATCCCTGCTAGGACCTGAGTCA
4-1	GCCAAAGAGCAGTCGGTAGTTCTTTTTTTTTTTTTTTTTTTT
4-2	CAGATGCTGGTCTTTCGGAAGAACTGAGCGTCAGGTCGTTCG
4-3	CTGTTGTAAATTAAGCATAGAAGTTGGTCCATATGCAAATAG
4-4	GTTAGAGTATGTCAACAAGGGACACCCTCACTTTGTGTAGCA
4-5	TAGGGTCGATCGTACCATCTACTAGGCAGCGGGTCATGCCTG
4-6	AGACGCAATTATGACTCAGGTCCTTTCACCTTGAACAGCGTC
5-1	CGGTGTTTCACGAACGACCTTGCTCTTTGGCACACCTAAAGT
5-2	GGGAAATTCCCTATTTGCATACCAGCATCTGTAATCGTATGC
5-3	TATAATGAAATGCTACACAAATTTACAACAGCTCCGGCATAA
5-4	CGAAACAAATCAGGCATGACCATACTCTAACTCGTTGGCAAT
5-5	GCGGAGCCTGGACGCTGTTCGATCGACCCTACGCTGATAATA
5-6	TTTTTTTTTTTTTTTTTTTTTTAATTGCGTCTCTCTGCTATAA
6-1	AAGGTAGCTGCACTTTAGGTGTTTTTTTTTTTTTTTTTTTTT
6-2	GCACAAGGATCGCATACGATTATGAAACACCGCGCCTTATGA
6-3	ACAGAAGGTCCTTATGCCGGAGGGAATTTCCCTATTCTCGAG
6-4	CCCTTTAATGAATTGCCAACGATTTCATTATATACCCTGTAG
6-5	CATAGTAGGTATATTATCAGCGATTTGTTTCGTGGATCGTTG
6-6	CTTCCTTTAGCTTATAGCAGAGCAGGCTCCGCTGAACACGTA
7-1	TGCAGTCGAGTCATAAGGCGGCAGCTACCTTTAAGGAACCGA
7-2	CAGGCACTGCCTCGAGAATAGATCCTTGTGCGATTCGTCATA
7-3	TTGTGACCATCTACAGGGTAGGACCTTCTGTACACACGGCGC

7-4	CGTTGTGAAACAACGATCCATCATTAAAGGGCCAAGTTTATG
7-5	ACGGGATACCTACGTGTTCATACCTACTATGTTTACCATGCC
7-6	TTTTTTTTTTTTTTTTTTTTGCTAAAGGAAGCACGGCCAAGA
8-1	TTTGAATGTTATCGGTTCCTTATTTTTTTTTTTTTTTTTTTT
8-2	AATTAGCGCGGTATGACGAATCCTCGACTGCAAACGTCCTTT
8-3	TAACCGCTGTAGCGCCGTGTGTGCAGTGCCTGAAGGTCGTTT
8-4	AAGCTGATCTCCATAAACTTGGATGGTCACAACTTCCACTCG
8-5	GAGCAACGATCGGCATGGTAAATTTCACAACGCCACTCGCAC
8-6	TACTTACTAGTTCTTGGCCGTGGGTATCCCGTAAGAGTCGTG
9-1	AAGTGGTTTGAAAGGACGTTTAACATTCAAACATGCCTGAAG
9-2	GTAGGTATGTAAACGACCTTCCGCGCTAATTATATTGTATTG
9-3	TCAACAATTCCGAGTGGAAGTACAGCGGTTAGAGATTGTAAT
9-4	CCATGTAGACGTGCGAGTGGGAGATCAGCTTGCGATTTCACG
9-5	AACTTCGTTTCACGACTCTTGATCGTTGCTCCCTTTGGTCCT
9-6	TTTTTTTTTTTTTTTTTTTTTACTAGTAAGTAAGTGCAACAAG
10-1	CAGAAATCCGCCTTCAGGCATGTTTTTTTTTTTTTTTTTTTT
10-2	GCTCATCTTGTCAATACAATATCAAACCACTTCGGTACTCAT
10-3	ATTCACTAGTTATTACAATCTCACATACCTACGCGTCCACTC
10-4	CCGAATCGGCGCGTGAAATCGCGAATTGTTGAGGGCTCTGAG
10-5	AGTCCAGAACCAGGACCAAAGGGTCTACATGGTAGAAACCGC
10-6	TTTCTGGAACTCTTGTTGCACTAAACGAAGTTGAGCTGCGCA
11-1	TTTTTTTTTTTATGAGTACCGGCGGATTTCTGTTTTTTTTTT
11-2	TTTTTTTTTTTGAGTGGACGCACAAGATGAGCTTTTTTTTTT
11-3	TTTTTTTTTTTCTCAGAGCCCAACTAGTGAATTTTTTTTTTT
11-4	TTTTTTTTTTTGCGGTTTCTACGCCGATTCGGTTTTTTTTTT
11-5	TTTTTTTTTTTTGCGCAGCTCGGTTCTGGACTTTTTTTTTTT
11-6	TTTTTTTTTTAGTTCCAGAAA

Motif 5.2 (10H×11T)

Name	Sequence
1-1	GAAGAAGCAGATTTTTTTTTTTTTTTTTTTTTGTCAACTCTT
1-2	TTTTTTTTTTGACACAAAGCGTGGCAGTATATTTTTTTTTTT
1-3	ACTGCCCGCCTTTTTTTTTTTTTTTTTTTTTTAATGACGCTC
1-4	TTTTTTTTTTCAATTGTAAAGATCGGCCCTCTTTTTTTTTTT
1-5	CCACTGCAAGCTTTTTTTTTTTTTTTTTTTTTTTTCGATTGT
1-6	GCTTGCTATGATTTTTTTTTT
2-1	GTACCAGGTAACAAGAGTTGACTTTTTTTTTTTTTTTTTTT
2-2	TCTGCTTCTTACATGTCCGATCACTCATAATCGCTTTGTGTC
2-3	AAGAGTGGCACTGAGCGTCATTTATACTGCCAACGCCCTTGC
2-4	AGGCGGGCAGCGGGCTTCGAGAGACAGTTTCCTTTACAATTG
2-5	CGTTGTCGGCCGACAATCGAAAGAGGGCCGATGTCAAGCATT
2-6	GCTTGCAGTGACTTATATATACCAGAACGGATCATAGCAAGC
3-1	CCAAGGCGCCTCGGACATGTTTACCTGGTACCTGTCGTTTAC
3-2	ATTATGAGTGAACGTGCTCTATGCGTCGCGCAGCAAGGGCGT
3-3	GCCGGCACTATCGAAGCCCGGTGCCACTCTTCCAGAATGTGG
3-4	GAAACTGTCTCACACGTTTAGTGGATACTATTAATGCTTGAC
3-5	GTAAAGGCAAATATATAAGTGGCCGACAACGGCAATCACCTT
3-6	TCCGTTCTGGTTACCACACCCATTTTTTTTTTTTTTTTTTT
4-1	CGTGCGAGGATGTAAACGACAGTTTTTTTTTTTTTTTTTTT
4-2	GGCGCCTTGGCGAAAGGACCGGTGCATGTATATAGAGCACGT
4-3	TATTTCAAACTCCACATTCTGGTGCGCGACGCGCACCGGTAG
4-4	TAGTGCCGGCGAAACTATAGTTGTCAGGGAGACTAAACGTGT
4-5	AGGTATGTTCAAAGGTGATTGCAATAGTATCCGAGTCATGTT
4-6	TTGCCTTTACGGTAACCGTCGCTTTCCACTATGGGTGTGGTA
5-1	AGCTGTTGTGGGTCCTTTCGATCCTCGCACGCTGCATTAAAG
5-2	ATACATGCACCGCTGCCTCGCGTACGTCATTTCTACCGGTGC
5-3	GGGCTTCGCCCTATAGTTTCAGTTTGAAATACATCAGAGTGG
5-4	CTCCCTGACAAGTTGGCACCCTACGGCGTTATAACATGACTC
5-5	TCCAGATCGGGACGGTTACCTGAACATACCTGCTTAGCCCTC
5-6	TAGTGGAAAGCTCAGTGCGCTCTTTTTTTTTTTTTTTTTTT
6-1	ACGAACAAGGACTTTAATGCAGTTTTTTTTTTTTTTTTTTT
6-2	CACAACAGCTATATGGTCCCATATCGCCAGACGCGAGGCAGC
6-3	CGGTAACTTAACCACTCTGATGAAATGACGTAAAGTTATGCT
6-4	GGCGAAGCCCGGGAACTAGACAAATATAGTCAGGGTGCCAAC
6-5	GCCGTACACACGAGGGCTAAGCATAACGCCGTCCTTAACGCT
6-6	CCGATCTGGATCGTTGACTTCGCCATAAGAGGAGCGCACTGA
7-1	CACACGGTTTGGGACCATATTCCTTGTTCGTGCAGAGGAATA
7-2	TCTGGCGATATCGTTTGAGTGGTCTCCTCCATAGCATAACTT
7-3	AGAACAACACTCTAGTTCCCTTAAGTTACCGAGGTCTATAAG

7-4	GACTATATTTGGAAACTACAGACGTGTTGGGCAGCGTTAAGG
7-5	GTAGAATACTAAGTCAACGAGTGTGTACGGCGAAAGACAAGG
7-6	CTCTTATGGCGGTAGTATTCCCTTTTTTTTTTTTTTTTTTT
8-1	TTTATGTCAGATATTCCTCTGCTTTTTTTTTTTTTTTTTTT
8-2	AAACCGTGTGCCATATATATTCAGGGCTTGACCACTCAAACG
8-3	CTGGGTGCCTGCTTATAGACCTATGGAGGAGATATGACCAAC
8-4	GTGTTGTTCTTGTTCCCGAGCATCTGTTCCGTCTGTAGTTTC
8-5	TCTTTCGTGAGCCTTGTCTTTCGCCCAACACGGAACACCCTT
8-6	AGTATTCTACGGCACGGGCGGTTTGATATTAGGGAATACTAC
9-1	CTTGCAGCTAATATATATGGTCTGACATAAAGTCAGTCGATC
9-2	TCAAGCCCTGACGTTTAACTGCATTACATAAAGTTGGTCATA
9-3	GTAAGATCTACTCGGGAACACAGGCACCCAGCTGCTGGTGCG
9-4	CGGAACAGATGAGGTTAACACAGCCTTATTTCAAGGGTGTTC
9-5	AGAGAGACTACGCCCGTGCCCTCACGAAAGAGTGTCCGAGAG
9-6	TAATATCAAACGATTTCACCTATTTTTTTTTTTTTTTTTTT
10-1	GGGTATATAACGATCGACTGACTTTTTTTTTTTTTTTTTTT
10-2	TAGCTGCAAGAGAGTGTCCAATCTCCTCGCAGCAGTTAAACG
10-3	GATTTGTGCTCCGCACCAGCAGTTTATGTAATCCGACTTACG
10-4	TAGATCTTACTGCAGCGGAAACACAACGTACTGTGTTAACCT
10-5	AATACGGGCAACTCTCGGACACGAAATAAGGCCCATAGGTCT
10-6	TAGTCTCTCTGGTAGTATTCATCTCTTTCAATAGGTGAAATC
11-1	GTTATATACCCTTTTTTTTTTTTTTTTTTTTTGGACACTCT
11-2	TTTTTTTTTTCGTAAGTCGGTGCGAGGAGATTTTTTTTTTTT
11-3	GAGCACAAATCTTTTTTTTTTTTTTTTTTTTTTTCCGCTGCA
11-4	TTTTTTTTTTAGACCTATGGGTACGTTGTGTTTTTTTTTTTT
11-5	TTGCCCGTATTTTTTTTTTTTTTTTTTTTTTTGAATACTACC
11-6	TTGAAAGAGATTTTTTTTTT

Motif 5.3 (10H×11T)

Name	Sequence
1-1	TGCAGTTTTTTTTTTTTTTTTTTTTTTTCCTCCTATGCCAAT
1-2	TAGGCATTTTTTTTTTTTTTTTTTTTTCTACTGGAACAACCA
1-3	CTATTGTTTTTTTTTTTTTTTTTTTTTTAATCCGGAGTGCAGC
1-4	CACTTATTTTTTTTTTTTTTTTTTTTGTGAATCGGCGCTTA
1-5	CCTAGGTTTTTTTTTTTTTTTTTTTTTTTCAAGGGCGCGGA
1-6	AACATTGGAGGTTTTTTTTT
2-1	AGCCTGGCATAGGAGGATTTTTTTTTTTTTTTTTTTGTAAG
2-2	CATGAGTGTTCCAGTAGACTGCAATTGAAGAGTTTGTCACCT
2-3	CAGATACACTCCGGATTTGCCTATGGTGGCTACCAGATCCTT
2-4	CTCAGACGCCGATTCACCAATAGGCTGTGCACGCTGGCGTCA
2-5	TCATACCGCCCTTGAAATAAGTGTAAGAGATCAATAATATGA
2-6	TTCGGTCCTCCAATGTTCCTAGGTCCGGTGCGGCCGATGAGG
3-1	CGGTGGACAAACTCTTCAGGCTCTTACGTTGAGAGCGAGTTA
3-2	CAGCCATCTGGTAGCCCTCATGAGGTGCCGTACGGCGCAGAT
3-3	AAACGACCAGCGTGCATATCTGAAGGATGGAAAGCAAACCGG
3-4	TAAGGATTATTGATCTTCTGAGTGACGCGAGTAACCCGGAGA
3-5	CCCTGCTCGGCCGCACGTATGATCATATGTACCCTCTAAACG
3-6	TTTTTTTTTTTTTTTTACCGAACCTCAATCCGGAACTTTTTT
4-1	ACTAATTCGCTCTCAACTTTTTTTTTTTTTTTTTTTTAAGG
4-2	TCCCGAGCGCCGTACGGCCACCGTAACGCAACGACGGTCTTC
4-3	TTCACGTTTGCTTTCCATGGCTGATCTAGTAGTACGTACCTC
4-4	CACTCTCGGGTTACTCGTCGTTTCCGGTGCCGGGCTCGAAAG
4-5	CGAAGTTAGAGGGTACATCCTTATCTCGGCATAAAGAAATTA
4-6	CGCCAGAAGTTCCGGATGCAGGGCGTTTAAGCATGACGGGTG
5-1	CATTACCCGTCGTTGCATTAGTCCTTATAAATGCTGGTAGAA
5-2	GGGATAACGTACTACTTCGGGAGAAGACCTTCAGTGACTGCC
5-3	TTACACGAGCCCGGCACGTGAAGAGGTGCCCTAGCTCGCGGC
5-4	AAGGCGTCTTTATGCCAGAGTGCTTTCGCGGCTGGACATCCT
5-5	TGAAATGTCATGCTTAACTTCGTAATTACCTCCGAGCAGAAG
5-6	TTTTTTTTTTTTTTTTCTGGCGCACCCTTACTGCAATGTTTT
6-1	CAGTGAACCAGCATTTATTTTTTTTTTTTTTTTTTTCCACA
6-2	CGCTCTGTCACTGAAGGGTAATGTTCTGCCGCCTTAAGCTAT
6-3	TGGTCACGAGCTAGGGCTATCCCGGCAATGTCACCCAGGACT
6-4	ATGTGTTGTCCAGCCGCGTGTAAGCCGCTCTCTCCGGAAAGA
6-5	TGTAACTGCTCGGAGGTCGCCTTAGGATGCACCTTATCCCTT
6-6	CGCCACCATTGCAGTAAATTTCACTTCAGGTAAACACAAAGA
7-1	AGGGCGTTAAGGCGGCTCACTGTGTGGGCATTGCAATTCATC
7-2	AACGGTTGGGTGACATAGAGCGATAGCCTAGACATGCTACGG
7-3	TTGAACCCGGAGAGAGTGACCAAGTCCCTATGACCTCTCACT

7-4	CATGACATAAGGTGCAACACATTCTTTCGCAATCCGTTGAGA
7-5	TATACGGTGTTTACCTGTTACAAAGGGCCGACTCGGTACGAG
7-6	TTTTTTTTTTTTTTTTGTGGCGTCTTTCATTCACGCCTTTTT
8-1	AGATACAATTGCAATGCTTTTTTTTTTTTTTTTTTTTTAGCA
8-2	GCGCACAGCATGTCTAGCGCCCTGATGCTCAAACGATGCTAC
8-3	TAGCTCAGAGGTCATAGACCGTTCCGTCGTGCGGCCCGGGAG
8-4	TAAAGTAACGGATTGCGGTTCAAAGTGCGCTCCGTCCGCTTG
8-5	GTCGCTTACCGAGTCGGGTCATGTCTCCTGTACAATAGAGGC
8-6	GAGCCTAGGCGTGAATGCGTATACTCGGAATAGGCCACAAGT
9-1	TCACAGATCGTTTGAGGTATCTTGCTAAAGAGAGCGTTACTG
9-2	GTTATCGGGCCGCACGGTGCGCGTAGCTACAGGCAAGCGGTA
9-3	GTCGCGGGACGGAGCGGAGCTACTCCCTTTACCTGGGTTCCA
9-4	ATCCCTTATTGTACAGACTTTACAAGCATGCTGCCCTGGCCA
9-5	TCCCTCTGGCCTATTCAGCGACGCCTCGCAGCTCAAGAATGG
9-6	TTTTTTTTTTTTTTTTTAGGCTCACTTGCTAGCTGACATTTTT
10-1	ACCGTGAACGCTCTCTTTTTTTTTTTTTTTTTTTTTTTGTAAT
10-2	GTGAAAGCTTGCCTGTACTGTGACAGTCAACCGCGCTCCTAC
10-3	ACCAGGACCCAGGTAAAGATAACTACCTGGGCGCGCTGGTAT
10-4	ACAATGCAGGGCAGCATCGCGACTGGAAGCTCATGGGTTCAA
10-5	TGTACTTCTTGAGCTGCAGGGATTGGCCTTAAAGGCCTTGCT
10-6	GGGTAGATGTCAGCTAGGAGGGACCATGGGCCCTTGATTTCC
11-1	TTTTTTAGCGCGGTTGCACGGTATTACTTTTTTTTTTTTTTT
11-2	TTTTTTAGCGCGCCCATTTCACGTAGGTTTTTTTTTTTTTTT
11-3	TTTTTTCCCATGAGCTCCTGGTATACCTTTTTTTTTTTTTTT
11-4	TTTTTTGGCCTTTAAGCATTGTTTGAATTTTTTTTTTTTTTT
11-5	TTTTTTTCAAGGGCCCAGTACAAGCAATTTTTTTTTTTTTTT
11-6	TTTTTTTTTTCTACCCGGAAA

Motif 6.0 (10H×11T)

Name	Sequence
1-1	AGTTGTGTGTCTGCACTAATA
1-2	CTATAGGTAACGAGACCGGAA
1-3	AGGCAGTCCGTAACGCCTACC
1-4	CACTGAAGGGTTTGCGTTCGT
1-5	TGCATCTCTCCGTGTCGTATA
1-6	TACGTATAGGCTTTTTTTTTT
2-1	TTTTTTTTTTCAAGCACACGTGACACACAACTTTTTTTTTTT
2-2	GTTACCTATAGTATTAGTGCAGCAGTGAATAAGAAATATCCT
2-3	GCCTCACATTCGGCCCGAGCCACGGACTGCCTTTCCGGTCTC
2-4	ACCCTTCAGTGGGTAGGCGTTCAATAAGCATTTGAAGGGCCC
2-5	TCACTTTAGAACAGCCCATTCGGAGAGATGCAACGAACGCAA
2-6	GCCTATACGTATATACGACACGCCTGATTAGTCCGATATTTA
3-1	AGTAGGATAGCGTCAAAGACGTATTCACTGCACGTGTGCTTG
3-2	AATGTGAGGCAGGATATTTCTACTTTCAGCCTCGCACTTTGT
3-3	CACGAAGGGCAACCTCGATAAATGCTTATTGGGCTCGGGCCG
3-4	TCTAAAGTGAGGGCCCTTCAACAGAGTCTCGGAAAGCAACCT
3-5	CGACTTGCGTAGTTCCGTTATCTAATCAGGCGAATGGGCTGT
3-6	TTTTTTTTTTTAAATATCGGAAAGGCTCCCTCTTTTTTTTTT
4-1	TTTTTTTTTTCGCTCCCTACTGCTATCCTACTTTTTTTTTTT
4-2	AGGCTGAAAGTCGTCTTTGACTAGATAGAGGTAGAGCATGGA
4-3	TGGCGTATATCTACTTTGCGATGCCCTTCGTGACAAAGTGCG
4-4	CCGAGACTCTGTTATCGAGGTTACCCGCCGTTTCCCTCATAC
4-5	GTCCTAGAGAGCATATTGAAGTACGCAAGTCGAGGTTGCTTT
4-6	GAGGGAGCCTTATAACGGAACTGAGAAAGTTCATCGGATTCA
5-1	TCTGGACGGGCTTTACTTAGACCTCTATCTAAGTAGGGAGCG
5-2	ATATACGCCATCCATGCTCTATCGGATATCGAATCTTTAAGC
5-3	CGACTCGAGGGCAGTTAGTGTACGGCGGGTATCGCAAAGTAG
5-4	TCTCTAGGACGTATGAGGGAAATATTCGAACTTGCTCTTGGT
5-5	CAAGGACTGCTGGAGGAACTAAACTTTCTCACTTCAATATGC
5-6	TTTTTTTTTTTGAATCCGATGAATGGGCAGCATTTTTTTTTT
6-1	TTTTTTTTTTGTCTTATTTAGGCCCGTCCAGATTTTTTTTTT
6-2	TCGATATCCGATCTAAGTAAACCAGGTATGTGCATAGAACAT
6-3	CGTAATGTTTAAGGCGGTCGGCCCTCGAGTCGGCTTAAAGAT
6-4	AGTTCGAATATACACTAACTGTTGCTTTACAGGCTCATCATC
6-5	GGTGTGCAATGGAACCTGCCCAGCAGTCCTTGACCAAGAGCA
6-6	TGCTGCCCATTTAGTTCCTCCTCGTGGGAGACCCGGAGTGAA
7-1	CGCCTATAACATGCGATCGTTACATACCTGGCTAAATAAGAC
7-2	AAACATTACGATGTTCTATGCAGCGCAGGCTTTGGCACTAGT
7-3	TTAACCACATTCGCGCTGGGCTGTAAAGCAACCGACCGCCTT

7-4	ATTGCACACCGATGATGAGCCTCGTTGGTGAGTAGCCCTGGT
7-5	TATGGTCTGACGTTTAGATGGTCTCCCACGAGGGCAGGTTCC
7-6	TTTTTTTTTTTTCACTCCGGGTGGGTCCAAGCTTTTTTTTTT
8-1	TTTTTTTTTTTCAATTATTTGTGTTATAGGCGTTTTTTTTTT
8-2	AAGCCTGCGCTAACGATCGCAACTGCTCCGAAGGCTATAAGG
8-3	CCCGCACTAGATCGTCTCACGAATGTGGTTAAACTAGTGCCA
8-4	CTCACCAACGAGCCCAGCGCGTGAATCCGGCCAGAACTGTCT
8-5	TGGTGCTGCAGTGAATCTGACGTCAGACCATAACCAGGGCTA
8-6	GCTTGGACCCACCATCTAAACCAACTCAGCGTGTTCGGAAGA
9-1	GATTGCTATCGATTTAGGTCGTCGGAGCAGTCAAATAATTGA
9-2	CTAGTGCGGGCCTTATAGCCTTTCTATAGTAGAGGATCCTAG
9-3	GTAAGATGAGAGATGCGTACGGCCGGATTCACGTGAGACGAT
9-4	TGCAGCACCAAGACAGTTCTGCCCATACACCTGGTCGAAGCG
9-5	AGGAGGCATTACCCACCACAACGCTGAGTTGGTCAGATTCAC
9-6	TTTTTTTTTTTCTTCCGAACAACGACGATAATTTTTTTTTTT
10-1	TTTTTTTTTTTAATGCATGTCCGATAGCAATCTTTTTTTTTT
10-2	CTACTATAGAACGACCTAAATTCCCGGTTTGCCCTCTACAAG
10-3	GACGCTGGGATTAATCTACCCTCTCATCTTACCTAGGATCCT
10-4	AGGTGTATGGGCGTACGCATCGAGTGCAAGCCTTGGACCGGA
10-5	CTGGCGCCTAAGGGCCTAGTCTAATGCCTCCTCGCTTCGACC
10-6	ATTATCGTCGTTTGTGGTGGGTGCTGCTAACCTAGTATCCAT
11-1	CAAACCGGGAGACATGCATTA
11-2	TCCCAGCGTCCTTGTAGAGGG
11-3	GCTTGCACTCGGGTAGATTAA
11-4	TAGGCGCCAGTCCGGTCCAAG
11-5	GTTAGCAGCAGACTAGGCCCT
11-6	TTTTTTTTTTATGGATACTAG

Motif 6.1 (10H×11T)

Name	Sequence
1-1	GTACCTACTTAAAGCGGTACC
1-2	AGCATTGGCAGGAGGCGGTGC
1-3	CTTGGAAGCCGTAGCCACGCC
1-4	AGTTAGTGCGCAGAATGGTCC
1-5	GTTCCTTCCAGGGACGATTTA
1-6	TCACACCCACTTTTTTTTTTT
2-1	TTTTTTTTTTTCTAAAGCTAGTTAAGTAGGTACTTTTTTTTT
2-2	CCTGCCAATGCTGGTACCGCTCCGATGGGCCCTAAAGTATCC
2-3	TGGCAAAGATAGATTCAAACGACGGCTTCCAAGGCACCGCCT
2-4	TGCGCACTAACTGGCGTGGCTGGATATTTGCGCAAAGTGTTT
2-5	AAACATTGCCGCGCTGTATTTCCTGGAAGGAACGGACCATTC
2-6	AAGTGGGTGTGATAAATCGTCAAAGCGTGTCGATGTCATCCC
3-1	AGGGCATATCGGAGGTCCCTTGGGCCCATCGGCTAGCTTTAG
3-2	TATCTTTGCCAGGATACTTTAATAACCGTCTTAGCAGATAGC
3-3	GGAACGCCTAAAGTACCATTCCGCAAATATCCCGTTTGAATC
3-4	CGGCAATGTTTAAACACTTTGGTACACTAATGGGACACAAGC
3-5	CCTCCCGCTACCGACAAAGGTCGACACGCTTTAAATACAGCG
3-6	TTTTTTTTTTTGGGATGACATTTAAGGATTAGATTTTTTTTT
4-1	TTTTTTTTTTTCAACCTGACTCCGATATGCCCTTTTTTTTTT
4-2	TAAGACGGTTATAAGGGACCTAACAGTGACGCAAGGTGCCTC
4-3	AGACGACATCAAATAAAGAAATTTAGGCGTTCCGCTATCTGC
4-4	CCATTAGTGTACGAATGGTACGTGTATTGATCGGGACCAGCG
4-5	CGTAGAAACTGAGTATTGGGCGGTAGCGGGAGGGCTTGTGTC
4-6	TCTAATCCTTAAACCTTTGTCCTTCGATGATATAACTGCGCT
5-1	TATAGAAGAAGCCGCAGCAGCGCGTCACTGTTAGTCAGGTTG
5-2	TGATGTCGTCTGAGGCACCTTAAAGAGGACGAAACTCCAATT
5-3	AGGCTAGCCCTCGTGCCCATCGATCAATACACTTTCTTTATT
5-4	CAGTTTCTACGCGCTGGTCCCTTCCGCAGTTGTCGCAGACTT
5-5	CAACCCGCGTCACACGCATGTTATCATCGAAGGCCCAATACT
5-6	TTTTTTTTTTTAGCGCAGTTAGCGAGCGCCGAGTTTTTTTTT
6-1	TTTTTTTTTTTTAACGGCGTGGCTTCTTCTATATTTTTTTTT
6-2	TTCGTCCTCTTTGCTGCTGCGGTCTTTAAATATGTAGGTGGT
6-3	AACTAGACGTTGGTAACTGGTGAGGGCTAGCCTAATTGGAGT
6-4	ACAACTGCGGAAGATGGGCACACCGCTATAAATCACATACGC
6-5	ACTCCCTACTGACGTTAGAACTGACGCGGGTTGAAGTCTGCG
6-6	CTCGGCGCTCGCACATGCGTGCCGGGCTACGCCTAGTTGGGC
7-1	TCCACATTAACAGCGGAGATCTATTTAAAGACCACGCCGTTA
7-2	AACGTCTAGTTACCACCTACAACCAAATATTCATTAAACTAT
7-3	TCAGACCCATAGCCTTTGAACTTTATAGCGGTACCAGTTACC

7-4	CAGTAGGGAGTGCGTATGTGAAAGCAGCACCAAGGCGCGTCG
7-5	GTTGGGCGACGGACCAACGTAGCGTAGCCCGGGTTCTAACGT
7-6	TTTTTTTTTTTGCCCAACTAGTTCTGTCGACAGTTTTTTTTT
8-1	TTTTTTTTTTTGCCCGGATTATGTTAATGTGGATTTTTTTTT
8-2	TGAATATTTGGTGATCTCCGCGTGGTTGCTAGCAGTAAAGAG
8-3	ATCTTTGCCACCCAAGAGAGGCTATGGGTCTGAATAGTTTAA
8-4	TTGGTGCTGCTTGTTCAAAGGCGGTGACACGATCGGAGCTGC
8-5	TGGAATAGCGCGGCCCACGCACCGTCGCCCAACCGACGCGCC
8-6	CTGTCGACAGAATACGTTGGTTTGAGCTTGTTCGCGGCTTAT
9-1	ATTGGGCGGAGCGTTTACCGTCTAGCAACCACTAATCCGGGC
9-2	GTGGCAAAGATCTCTTTACTGAAAGTTAATCACCGTCCGATT
9-3	CCAATCCTTGACAAACGGGCGTCGTGTCACCGCCTCTCTTGG
9-4	GCGCTATTCCAGCAGCTCCGACGGCATGGCTACTCCTCCCAT
9-5	ATGATACAATTGGCGGACCTGAACAAGCTCAATGCGTGGGCC
9-6	TTTTTTTTTTTATAAGCCGCGGTTACGCCTCCATTTTTTTTT
10-1	TTTTTTTTTTTATTTAACCCTGCTCCGCCCAATTTTTTTTTT
10-2	GTGATTAACTTTACGGTAAACCCTTCGGCGGCCTACCCGCAT
10-3	ACACCGACATAGGAGGTCTTCGTCAAGGATTGGAATCGGACG
10-4	GTAGCCATGCCGCGCCCGTTTATGACATGGAAACATAACCCG
10-5	CCCGCATGCGCTGTCAGGTGACAATTGTATCATATGGGAGGA
10-6	TGGAGGCGTAACCAGGTCCGCTCATCCAGTAATAACTTCCCT
11-1	GCCGCCGAAGGAGGGTTAAAT
11-2	TATGTCGGTGTATGCGGGTAG
11-3	TTCCATGTCATGAAGACCTCC
11-4	GCGCATGCGGGCGGGTTATGT
11-5	TTACTGGATGATCACCTGACA
11-6	TTTTTTTTTTTAGGGAAGTTA

Motif 6.2 (10H×11T)

Name	Sequence
1_1	TTTTTTTTGGCGCAATCTAGT
1_2	TACGCCCTGGTCACGTACTCG
1_3	ACGGGAACGCCGGTCTATAAA
1_4	GGGCACCCGAGGTAGGTCTCA
1_5	GCCGACACAAGTGCATGGCTG
1_6	TAGACAATGCTGACACGGTCG
2_1	TTTTTTTTTTTTTTCGCAGCGATTGTTGTCCAACCTGCGCCA
2_2	TTCCCGTCGAGTACGTGACCAGGGCGTAACTAGATGATACAC
2_3	CAGCTAACTTTGTACGACCCGACTATCACCACGATACCGGCG
2_4	TGTCGGCTGAGACCTACCTCGGGTGCCCTTTATAGTGAGGCG
2_5	CCCTAAGTAACGTTGGACGAGAAACGTCCGCGTTTGCACTTG
2_6	TTTTTTTTTTTTTTTGTCAGCATTGTCTACAGCCATAGTCTGA
3_2	TTTTTTTTTTATATCTTGTTACTATTTCTCTAACGTACAAAG
3_3	CTTAGGGCGCCTCAATCGTGGTGATAGTCGGGTCGTCTATAG
3_4	GAAAGTACTATGCTACATAATGATGTGGAAGACCCAACGTTA
3_5	TTTTTTTTCAGACTAAACGCGGACGTTTCTCGTCCGCTCTAG
3_6	TAATTAAGATCTAGTTTAATATTGGCGTCCCTAGCTTTTTTT
3_1	TTAGCTGGTGTATCGGTTGGACAACAATCGCTGCGTTTTTTT
4_1	TTTTTTTTTTTTTTTATAATTGACCAGGTAGTGAGCATATAAA
4_2	TACTTTCCTATAGACGTTAGAGAAATAGTAACAAGTCGCCTT
4_3	AGGTGGGCGTTCTGGTGCCTGGCTCGTTCGTCTGTAGCATAG
4_4	TTAATTACTAGAGCGGGTCTTCCACATCATTATGTCGTTCAT
4_5	TATTCGTAAGAATGGCGTTAATACCTAGCTTGCAGCTAGATC
4_6	TTTTTTTTTTTTTTTGCTAGGGACGCCAATATTAAACGTGCAT
5_2	TTTTTTTCCCGTAGACCTGGGAACCTGGTGAGTTACAGAACG
5_3	ACGAATAATGAACGACAGACGAACGAGCCAGGCACCTACACG
5_4	TGTCGAGATTGACTCTATCCTGGCAGTTATGCGGACATTCTT
5_5	TTTTTTTATGCACGCTGCAAGCTAGGTATTAACGCCGAGCGG
5_6	TGGATCTCAGCCTTTACCCGGTGTATTACTTGGCCTTTTTTT
5_1	CCCACCTAAGGCGAGCTCACTACCTGGTCAATTATTTTTTTT
6_1	TTTTTTTTTTTTTTTAATCAATGACACAACCGGTACCTACGGG
6_2	CTCGACACGTGTAGTAACTCACCAGGTTCCCAGGTACGGTGT
6_3	TGGTTCGCTGGAACGGCCCGTATCTCTAAAGTAGCAGTCAAT
6_4	AGATCCACCGCTCGTCCGCATAACTGCCAGGATAGAAGGAGC
6_5	TTACAAGCTCCGAGAGAAGCCTGGATGCCGGCGTTAAGGCTG
6_6	TTTTTTTTTTTTTTTGGCCAAGTAATACACCGGGTAACTGCCA
7_2	TTTTTTTAAATAATCACTCGCAGCAAATGTGGCGAGTTCCAG
7_3	CTTGTAAGCTCCTTGCTACTTTAGAGATACGGGCCTGTCCGA
7_4	CTGAACAAAGCAGGGCCCTACCTGAGTCGTTTGGTCTCGGAG

7_5	TTTTTTTTGGCAGTAACGCCGGCATCCAGGCTTCTTCCCTAG
7_6	TACCACTGAGACAAAGGACAATGTCTGGCCGGGTGTTTTTTT
7_1	CGAACCAACACCGTGTACCGGTTGTGTCATTGATTTTTTTTT
8_1	TTTTTTTTTTTTTTTCAAGTTTATACGTCTGACTTAATTATTT
8_2	TGTTCAGTCGGACATCGCCACATTTGCTGCGAGTGCTGTGCT
8_3	GGACTGCTGCAAGTGTGGGCCTCCCGGATACGCACCCTGCTT
8_4	AGTGGTACTAGGGAACCAAACGACTCAGGTAGGGCAGAGTGT
8_5	GCTATGGCCCTAGAATACATAGAAGAACACTGGTGTTGTCTC
8_6	TTTTTTTTTTTTTTTCACCCGGCCAGACATTGTCCTCACTCTG
9_2	TTTTTTTACTTTAAGCAGGAACCTTCTATGGGTTAACTTGCA
9_3	CCATAGCACACTCTGTGCGTATCCGGGAGGCCCACTTTCGGG
9_4	CTTTGGCCGTAATAGAGCCCTGTAGGTAGCGTTTGTCTAGGG
9_5	TTTTTTTCAGAGTGCACCAGTGTTCTTCTATGTATCTGTATA
9_6	TGATTCCGATGGAATCCGACCAAATATCTGTCGCTTTTTTTT
9_1	GCAGTCCAGCACAGTAAGTCAGACGTATAAACTTGTTTTTTT
10_1	TTTTTTTTTTTTTTTTTTAAGCGAACCCTTCGTCATTTAAAGT
10_2	GCCAAAGCCCGAAATAACCCATAGAAGGTTCCTGCCTTGCTC
10_3	CAGGTGCGAAGGAGACTCCACCGCTGCAGATTCTATATTACG
10_4	GGAATCATATACAGCAAACGCTACCTACAGGGCTCTTTCTTA
10_5	TTCAAATTTAGTGCGACTGAACGAGGCTCAGGGCCTTCCATC
10_6	TTTTTTTTTTTTTTTAGCGACAGATATTTGGTCGGATAATATT
11_3	TGCAGCGGTGGAGTCTCCTTC
11_4	ATTTGAATAAGAAATAGAATC
11_5	AGCCTCGTTCAGTCGCACTAA
11_6	TTTTTTTAATATTAGGCCCTG
11_1	AGGGTTCGCTTAAATTTTTTT
11_2	GCACCTGGAGCAAGATGACGA

Motif 6.3 (10H×11T)

Name	Sequence
1_1	TTTTTTTTTGTCGCACCTATT
1_2	GTTCTAGGACCACGTCGTTGT
1_3	TCTGGACGAGGATTGGGCGTA
1_4	ATGTCATTCCAATTTATGACT
1_5	TCAACCGGGTCACCCACTGCC
1_6	GCTAAACATTTATGGATCGAG
2_1	TTTTTTTTTTTTTTTAGGTACGTCCTCCTTACTCCTGCGACA
2_2	CGTCCAGAACAACGACGTGGTCCTAGAACAATAGGTTTGGCA
2_3	GTCGCAGACGCTTAGGTATAACCCTGGCCACTGAACAATCCT
2_4	CCGGTTGAAGTCATAAATTGGAATGACATTACGCCACCTAGC
2_5	CCGTCCGAATTTGATGTGATTCCGCTATCGCCCTTGGGTGAC
2_6	TTTTTTTTTTTTTTTTCATAAATGTTTAGCGGCAGTCTGAAGG
3_2	TTTTTTTTTTGTACCATGAGTTTAATATGCTTTAACTAAGCG
3_3	TCGGACGGGCTAGGTTTCAGTGGCCAGGGTTATACTGGGTCC
3_4	GGCTAGTCACCCACAATGACGGCCCGCTTCTTCATATCAAAT
3_5	TTTTTTTTCCTTCAGAAGGGCGATAGCGGAATCACGGCAAAC
3_6	GGATAGCAGGTCTCGTCGGCACGGCCCATTCCCTTTTTTTTT
3_1	CTGCGACTGCCAAAGGAGTAAGGAGGACGTACCTATTTTTTT
4_1	TTTTTTTTTTTTTTTTAAGCTCGTAGACATCCGGTGGGTACAA
4_2	GACTAGCCGGACCCATTAAAGCATATTAAACTCATATGATTA
4_3	AGGAGAGGTGTACCGCTCGAGGTTCGTCTACCCTATGTGGGT
4_4	TGCTATCCGTTTGCCATGAAGAAGCGGGCCGTCATCGGACCT
4_5	GTAGATTGCCTAATTTCAGGTGCTTCACTCGTGACCGAGACC
4_6	TTTTTTTTTTTTTTTTAAGGGAATGGGCCGTGCCGAGGAGTAC
5_2	TTTTTTTTTCGGGCGGGCACTTCCCTTAAACTGGACGGTACA
5_3	CAATCTACAGGTCCGTAGGGTAGACGAACCTCGAGCTGCGTT
5_4	GATCCGATTCCCTACCCGCCACAGCACCAAGAGCAAATTAGG
5_5	TTTTTTTTGTACTCCGTCACGAGTGAAGCACCTGAACGCACT
5_6	CATTGTTTGTAGAGATTCGAGCGGGTATGCCTCTGTTTTTTT
5_1	CTCTCCTTAATCATCACCGGATGTCTACGAGCTTCTTTTTTT
6_1	TTTTTTTTTTTTTTTTCCTGTAACAGGCTGGCAGTACGCCCGA
6_2	ATCGGATCAACGCAGTCCAGTTTAAGGGAAGTGCCCTCGGGT
6_3	TAGACCATGTCAAGGCAGCTAACCAGTTCACGAGTGTAGGGA
6_4	AAACAATGAGTGCGTTGCTCTTGGTGCTGTGGCGGGCGGAAT
6_5	AGGTACATCCCACACTACAGCCACATATTTAGTGTTCTCTAC
6_6	TTTTTTTTTTTTTTTTCAGAGGCATACCCGCTCGAATGCGTCG
7_2	TTTTTTTTGAGGCAAAGCCGTACGAAGGCCGTTCTCCTTGAC
7_3	ATGTACCTATTCCGCACTCGTGAACTGGTTAGCTGATTTGCA
7_4	GTCCTGGGCACGGGACCTTGGTGATCACTCAGAATGTGTGGG

7_5	TTTTTTTTCGACGCAACACTAAATATGTGGCTGTAGGAGGGT
7_6	TACCAGCACGTATTCTCGACCAAATGTATCGTCCCTTTTTTT
7_1	TGGTCTAACCCGAGTACTGCCAGCCTGTTACAGGGTTTTTTT
8_1	TTTTTTTTTTTTTTTTCCACCCTATAACTCCTGCCTTGCCTC
8_2	CCCAGGACTGCAAATAGAACGGCCTTCGTACGGCTATGCGTC
8_3	GCTTATTAGACTTCTGAGTTACCGGTTGAGAACGCTCCCGTG
8_4	TGCTGGTAACCCTCCATTCTGAGTGATCACCAAGGTAACTTC
8_5	TTAGACGCCTATCAGTGTGTTCTGCGTCCACTGCGGAATACG
8_6	TTTTTTTTTTTTTTTGGGACGATACATTTGGTCGACAAAGCT
9_2	TTTTTTTTCCTTGGTCCTCTAAACACGAATCGGTCAGAAGTC
9_3	GCGTCTAAGAAGTTAGCGTTCTCAACCGGTAACTCACGACAT
9_4	AGTCAAGGCTTGAGGGCGTCAGTAACAGATACGGTCTGATAG
9_5	TTTTTTTTAGCTTTGCGCAGTGGACGCAGAACACAAAGGGAA
9_6	CGTATATCATGGTGGTTAACGTACCTTGTTGGCTTTTTTTTT
9_1	AATAAGCGACGCATGGCAGGAGTTATAGGGTGGAGTTTTTTT
10_1	TTTTTTTTTTTTTTTTTAGTGATGGGCTGCCCAACGACCAAGG
10_2	CCTTGACTATGTCGTGACCGATTCGTGTTTAGAGGCATCCAC
10_3	TAACGTCGAGTAGTCTCACGAAATAGAAAGATTTACCTCAAG
10_4	GATATACGTTCCCTTACCGTATCTGTTACTGACGCGGTATAC
10_5	AGCCCTCAGTAGGTAGGATGCACTATTGGTGGTAACCACCAT
10_6	TTTTTTTTTTTTTTTTAAGCCAACAAGGTACGTTAACCCAGTC
11_3	TTTCTATTTCGTGAGACTACT
11_4	TGAGGGCTGTATACCTAAATC
11_5	CCAATAGTGCATCCTACCTAC
11_6	TTTTTTTTGACTGGGTTACCA
11_1	CAGCCCATCACTATTTTTTTT
11_2	GACGTTAGTGGATGCGTTGGG

Motif 7.1 (10H×11T)

Name	Sequence
1-1	AGCCCACTCGGGCGCGGACGG
1-2	TCAGCGATATTAGGCTGTTAA
1-3	ATCTCGACGATCGCATGCAGC
1-4	CAACGCTCCTAGTCATCTTTC
1-5	GATATAGCACCCGATTCACCT
2-1	TTTTTTTTTTTTTTTTTTTTTACTTTCTCTCGCAACTTAGTA
2-2	TTTTTTTTTTTTTTTTTTTTTCCGTCCGCGCCCGAGTGGGCT
2-3	TTAACAGAAGACAGGTGATAACCCTGGCACACCTCGATTAAC
2-4	GAGTTTACCTAATATCGCTGAGCTGCATGCGATCGTCGAGAT
2-5	GAAAGATGAAGGCGGGCGAGCCGGCTCACTAACGTCGGTTCG
2-6	TTTAGCAGACTAGGAGCGTTGAGGTGAATCGGGTGCTATATC
3-1	TTATCACCTGTCTTTAAACTCTACTAAGTTGCGAGGTGCCGA
3-2	TAGCAATGGATGACCCGGGATCATTCGGATTAGACAGAAAGT
3-3	GCTCGCCCGCCTTCTGCTAAAGTTAATCGAGGTGTAAATTGT
3-4	ACGTGTTTGTACGACCGTTGATGTGTCTGTGAGTTGCCAGGG
3-5	TTTTTTTTTTTTTTTTTTTTTCGAACCGACGTTAGCATAGTC
3-6	TTTTTTTTTTTTTTTTTTTTTCATTCCCTGTGGTCTGAGCCG
4-1	TTTTTTTTTTTTTTTTTTTTTGCCCACCCTCCCTTCAAGATC
4-2	TTTTTTTTTTTTTTTTTTTTTCGGCACGTCTAATCCGAATG
4-3	ATCCCGGCCATTGAGGTACCGTCGAAGCAGCGACCCAAGCTT
4-4	TCAATCTGTCATCCATTGCTAACAATTTAACTCACAGACACA
4-5	TCAACGGCAATGGTCACTACAGTACATGGTTGACAGGTTGGT
4-6	GGAGCACTCGTACAAACACGTGACTATGGACCACAGGGAATG
5-1	CGGTACCTCAATGGAGATTGAGATCTTGAAGGGAGTCTGAAG
5-2	CAGGATCCACGGTAAAGCTATTCCCTCTTCGAACAGGTGGGC
5-3	TGTAGTGACCATTGGTGCTCCAAGCTTGGGTCGCTAGCTGGT
5-4	CGAGTGTTTAACGAGCCCTAATCTCGAGTATCCCTGCTTCGA
5-5	TTTTTTTTTTTTTTTTTTTTTTACCAACCTGTCAACTTTAGCG
5-6	TTTTTTTTTTTTTTTTTTTTTCTCTACGGTGGGTACATGTAC
6-1	TTTTTTTTTTTTTTTTTTTTTACGGCGAAAGATGCATATACG
6-2	TTTTTTTTTTTTTTTTTTTTTCTTCAGATGTTCGAAGAGGGA
6-3	ATAGCTTGAATAGGGCGTTAATCTGGAAGGGATACCCTGACA
6-4	CGTTAAATACCGTGGATCCTGACCAGCTAGGGATACTCGAGA
6-5	TTAGGGCAAATTCCTCGAGCAGCCAGAGATCATGTCTCTAGA
6-6	TCCAGTTTCGTTAAACACTCGCGCTAAATACCCACCGTAGAG
7-1	TTAACGCCCTATTCTTTAACGCGTATATGCATCTTTAATTGT
7-2	TGTTACCCGTTATCATCGTATGGTCTACTCGGATTTCGCCGT
7-3	TGCTCGAGGAATTTAACTGGATGTCAGGGTATCCCAGGTTAA
7-4	GCGCTTTCGCTTGTGAATTAGACGAGACATCGAGCTTCCAGA

7-5	TTTTTTTTTTTTTTTTTTTTTTCTAGAGACATGATAAGGCAG
7-6	TTTTTTTTTTTTTTTTTTTTTATACTGCCGGTGAGCTCTGGC
8-1	TTTTTTTTTTTTTTTTTTTTTTTACTGCCGGAACGCTGCCCT
8-2	TTTTTTTTTTTTTTTTTTTTTTACAATTAAATCCGAGTAGACC
8-3	ATACGATCGATTTCTTAGCAGGCCAAAGGAGCGTTGGTCACA
8-4	GCTATTGGATAACGGGTAACATTAACCTGCTCGATGTCTCGT
8-5	CTAATTCGATATACGGGTTGCTGGCATTATACGAACTTGATT
8-6	TGGGCCCACAAGCGAAAGCGCCTGCCTTCTCACCGGCAGTAT
9-1	CTGCTAAGAAATCGCAATAGCAGGGCAGCGTTCCGGCTAAAT
9-2	TGTCGTGTATGGTGCAAAGACACTGAAGCTGGGCCGCAGTAA
9-3	GCAACCCGTATATCGGGCCCATGTGACCAACGCTCTTGGGTT
9-4	GACAAGGTCTAGCGTTACTTGGTACTGTGTGTGTACTTTGGC
9-5	TTTTTTTTTTTTTTTTTTTTTTAATCAAGTTCGTATAGCTCAG
9-6	TTTTTTTTTTTTTTTTTTTTTTTCTACGGACGCTCCAATGCCA
10-1	TTTTTTTTTTTTTTTTTTTTTTGGGCTACCGAGGGTCTGGGCC
10-2	TTTTTTTTTTTTTTTTTTTTTTATTTAGCGGCCCAGCTTCAGT
10-3	GTCTTTGGGTCCGCAGGGCTCGGAACGCTATGCCGCCCTCTA
10-4	GGTTCATCACCATACACGACAAACCCAATACACACACAGTAC
10-5	CAAGTAATCCGGCGCTCCCGCGCGCACATGGGCATACGCCTG
10-6	TATCGCGCGCTAGACCTTGTCCTGAGCTGGAGCGTCCGTAGA
11-1	GGCCCAGACCCTCGGTAGCCC
11-2	GAGCCCTGCGGACCATGAACC
11-3	TAGAGGGCGGCATAGCGTTCC
11-4	GCGGGAGCGCCGGACGCGATA
11-5	CAGGCGTATGCCCATGTGCGC

Motif 7.2 (10H×11T)

Name	Sequence
1-1	GTGCAGTAAGTCTGCCGAAGA
1-2	ATATGACTTCGGTCAACAACA
1-3	GGATCTTTGTGGGACAGAAGG
1-4	CCACAGATGCCGGGACCCGAT
1-5	AGAGGAGAGCATGATATGCTC
1-6	TTTTTTTTTTTTTTCCTTTCG
2-1	TTTTTTTTTTTTTTTCTTCGGCACCCGCACCACCGTTCCACG
2-2	TTTTTTTTTTTTTTGGGATTTCAGACTTACTGCACTGTTGTT
2-3	GACCGAAGTCATATCCTTCTGTGCGTTTGGTCGCGAATTTGC
2-4	GCCAGTAGCAGAAGCCGTTGATCCCACAAAGATCCATCGGGT
2-5	CCCGGCATCTGTGGGAGCATAACGTCTGTTGAGTTATCTGAG
2-6	CTTGCGGCTCTTAGACCCAAGTCATGCTCTCCTCTCGAAAGG
3-1	CTTCTGCTACTGGCCGTGGAAACTAAACCTCTCGAAACCGTC
3-2	TTCACGAGATTGATAGCGTAACGGTGGTGCGGGTGAAATCCC
3-3	CTAAGAGCCGCAAGGCAAATTGCCCTCTTACATACGCCAATA
3-4	GGCATGCGATTCGCGTAGGGCCGCGACCAAACGCATCAACGG
3-5	TTTTTTTTTTTTTTTCTCAGATGACGTCTCATTCATCGCACTG
3-6	TTTTTTTTTTTTTTTTCTAAGTAACTCAACAGACGTCTTGGGT
4-1	TTTTTTTTTTTTTTGACGGTTTAATCTCTCTCGCCACCCTCC
4-2	TTTTTTTTTTTTTTGTACCTATCGAGAGGTTTAGTTTACGCT
4-3	ATCAATCTCGTGAATATTGGCGATAATTACTTTAATTGATTT
4-4	ATGGAGGGTCTGTCCGGGCTGGTATGTAAGAGGGCGCCCTAC
4-5	GCGAATCGCATGCCCAGTGCGTCCTCGCTTCCGGCGCTGTCG
4-6	GAGCAAAGAGCGATGTCCGATATGAATGAGACGTCACTTAGA
5-1	GACAGACCCTCCATGGAGGGTATCTTAGGTCATTTATTCCCG
5-2	TTTACTTGATCCCATCTAGATGGCGAGAGAGATTATAGGTAC
5-3	ATCGCTCTTTGCTCAAATCAATCCGCATTGAACTGAAGCGGA
5-4	CTCTGTTTCTATATTAAGCTATTAAAGTAATTATCCAGCCCG
5-5	TTTTTTTTTTTTTTCGACAGCCATTTATGTACATCAATACGA
5-6	TTTTTTTTTTTTTTTGCCGATGCCGGAAGCGAGGAATCGGAC
6-1	TTTTTTTTTTTTTTCGGGAATCTAGACACGCCCGGAGACTTA
6-2	TTTTTTTTTTTTTTTAGGTCGAAATGACCTAAGATATCTAGA
6-3	TGGGATCAAGTAAATCCGCTTGAAGTTAATTCGATTGCGTCA
6-4	CCGAATCGAACATAGTTAGCTCAGTTCAATGCGGATAGCTTA
6-5	ATATAGAAACAGAGTCGTATTCATCATCCTCAGTTCAACTTC
6-6	CCCGATTAAGCGTCCGCTATCGATGTACATAAATGATCGGCA
7-1	TATGTTCGATTCGGTAAGTCTGGCACCTTGTGATGGGCGAGG
7-2	TCAAGCGAGCTCTTTGCCATGCCGGGCGTGTCTAGCGACCTA
7-3	GACGCTTAATCGGGTGACGCAACCTTTGCACTTCGGCTGCGA

7-4	ACATCGAGTCGACCGCAATCTATCGAATTAACTTCAGCTAAC
7-5	TTTTTTTTTTTTTTGAAGTTGTTCCCTGCCTGGATTCGGCTG
7-6	TTTTTTTTTTTTTTTATCAGTAACTGAGGATGATGGATAGCG
8-1	TTTTTTTTTTTTTTCCTCGCCCTACTCATATAGTGTTTGCGG
8-2	TTTTTTTTTTTTTTGTATCGTCATCACAAGGTGCCCATGGCA
8-3	AAGAGCTCGCTTGATCGCAGCATGACACCCTAAGATTCTGGT
8-4	ACGATATAGACGACGGACGTACGAAGTGCAAAGGTAGATTGC
8-5	GGTCGACTCGATGTCAGCCGATAACACTTCATACACTTCGCA
8-6	CTATACAGTTTGCGAGGACGGATCCAGGCAGGGAAACTGATA
9-1	GTCGTCTATATCGTCCGCAAAGAGAACGATTAGCGACGTAAG
9-2	CATTTGTTTCAGCGGACCGCGCACTATATGAGTAGACGATAC
9-3	CGCAAACTGTATAGACCAGAACGTCTATGTGGCCCTTGGGTC
9-4	CCGACTCTTACCGGCTGAATTTCTTAGGGTGTCATTACGTCC
9-5	TTTTTTTTTTTTTTTGCGAAGGTGGTTTGACGTCTTAAGGAA
9-6	TTTTTTTTTTTTTTACTGGTATGTATGAAGTGTTACCGTCCT
10-1	TTTTTTTTTTTTTTCTTACGTCGGCACACTAACATGGCCATA
10-2	TTTTTTTTTTTTTTACCACACCGCTAATCGTTCTCCGCGGTC
10-3	CGCTGAAACAAATGGACCCAATAATAGTTTAGGACTAAATTC
10-4	TAGGTATAGGATTCCAAGGGTGGGCCACATAGACGAATTCAG
10-5	CCGGTAAGAGTCGGTTCCTTAACTTAATCTATTAGGCCAGAT
10-6	TTTCTAGCCAAACAGTGCCGCAGACGTCAAACCACTACCAGT
11-1	ATGTTAGTGTGCCGGTGTGGT
11-2	GAATCCTATACCTATATGGCC
11-3	GTCCTAAACTATTAACCCTTG
11-4	TGTTTGGCTAGAAAGAATTTA
11-5	CTAATAGATTAAGTGCGGCAC
11-6	TTTTTTTTTTTTTTATCTGGC

Motif 8 (10H×11T)

Name	Sequence
1-1	TTTTTTTTTTGACGATGAGCG
1-2	ACTAGGTCTAGCTACCCGGGT
1-3	TTATGGCCGCTCGTGTGCACC
1-4	CGTCTGGGTCGGGTCCGCCTC
1-5	GACACGATCTTAAGCCGAATG
1-6	CGGACGTATGGCCCAACGTTG
2-1	CCACGCCATACCGGCGGATACTAGACCTAGTCGCTCATCGTC
2-2	ACGCGACAATCACCCTATTGGGCGGCCATAAACCCGGGTAGC
2-3	TAATAGCGTACGTGGGAAAGAGACCCAGACGGGTGCACACGA
2-4	ATTACCGGAACGGAAGATCACAGATCGTGTCGAGGCGGACCC
2-5	CGATGCTACTTGACGACGCATCATACGTCCGCATTCGGCTTA
2-6	ATTTACCGGACTTTTTTTTTTTTTTTTTTTCAACGTTGGGC
3-1	GTGTCGCCCATCAGTCGTTCTGTATGGCGTGGTTTTTTTTTT
3-2	CACAATGAATTAAGACTTGGCGATTGTCGCGTGTATCCGCCG
3-3	GCAAAGCACGTCAGTATTGGAGTACGCTATTACCAATAGGGT
3-4	AGGGCTTACGTTCTCCAAGGCGTTCCGGTAATTCTTTCCCAC
3-5	GCCGCTACCCTCCATAGCGGCAAGTAGCATCGGTGATCTTCC
3-6	TTTTTTTTTTTACCAGCGAGTGTCCGGTAAATATGCGTCGTC
4-1	TTTTTTTTTTTAGAACGACTGAAGGTAGCCGATCCCAGTCAC
4-2	ATGGGCGACACGCCAAGTCTTCATCGTTGAATGAGGTACATT
4-3	AATTCATTGTGTCCAATACTGTAAATGCCCAATCGGCGCTAA
4-4	ACGTGCTTTGCGCCTTGGAGATCTCGATTCGTTTGAGCCGGA
4-5	ACGTAAGCCCTGCCGCTATGGCATTCCAAGGACAAGGCTATC
4-6	AGGGTAGCGGCACTCGCTGGTTTTTTTTTTCTATGAACAGA
5-1	TTTTTTTTTTGTGACTGGGATACAACAACCGTATACACGTGT
5-2	CGGCTACCTTAATGTACCTCACAGAGGGCTCCCTCAAAGCGC
5-3	TTCAACGATGTTAGCGCCGATATCGCGGGCACGCGCCGCGGA
5-4	TGGGCATTTATCCGGCTCAAATTCGTCAGTGTCATTAAGGAC
5-5	CGAATCGAGAGATAGCCTTGTTGATGTCGCGGGCTTGGGAAT
5-6	CCTTGGAATGTCTGTTCATAGCACGACATAGTTTTTTTTTTT
6-1	CGGGCTCTCCCATAGTGGCCACGGTTGTTGTTTTTTTTTTTT
6-2	GCTGGCCGCCCACAACCACCGGAGCCCTCTGACACGTGTATA
6-3	AGCCGATTAAGAATGACGCACTGCCCGCGATGCGCTTTGAGG
6-4	CCTCCACTTTCTACATTGGGTCACTGACGAATCCGCGGCGCG
6-5	AGAATAAAGGTTGTGTATGAACGCGACATCAGTCCTTAATGA
6-6	AGGTAGGATGATTTTTTTTTTCTATGTCGTGATTCCCAAGCC
7-1	TTGGTGTTCGCCTACATAGAAGGGAGAGCCCGTTTTTTTTTT
7-2	CTCGGCGATTCGTGACACTGAGGGCGGCCAGCTGGCCACTAT
7-3	ACCTCCCTAAGATGGTTCGCGCTTAATCGGCTCGGTGGTTGT

7-4	CAAGACTGACGTATCCCGGAGGAAAGTGGAGGGTGCGTCATT
7-5	GATAGCGAGTACCTTCTTTACACCTTTATTCTACCCAATGTA
7-6	TTTTTTTTTTTCCAAGGTTCATCATCCTACCTTTCATACACA
8-1	TTTTTTTTTTTTTCTATGTAGTTCGCACTAGAAACAAGAGCG
8-2	GCGAACACCAATCAGTGTCACTATCCAGGCGGTATCGATGTA
8-3	GAATCGCCGAGCGCGAACCATGGTGAACCGCCAAGAAGAAAC
8-4	CTTAGGGAGGTCTCCGGGATAAAGGGCCTAAGGAGGGAGGCT
8-5	CGTCAGTCTTGGTAAAGAAGGAGCATATACGTTGAGGCGGGC
8-6	TACTCGCTATCTGAACCTTGGTTTTTTTTTTTAGCCTCCTGT
9-1	TTTTTTTTTTCGCTCTTGTTTATCTTCGGTTGGTCCCATGGG
9-2	CTAGTGCGAATACATCGATACCGAAAGTAACAAGAAGGTACG
9-3	CGCCTGGATAGTTTCTTCTTGGAGAAATTACGAATCTGAAAG
9-4	GCGGTTCACCAGCCTCCCTCCTGACAAGACGACACTGAGCGA
9-5	TTAGGCCCTTGCCCGCCTCAAATCTTTAAGGTGACATAAGAT
9-6	CGTATATGCTACAGGAGGCTACCCTCAGTAGTTTTTTTTTTT
10-1	CAGCTACATTATCGGTTGCCTAACCGAAGATTTTTTTTTTTT
10-2	TCGTACTGAACAAAGAGACTAGTTACTTTCGCCCATGGGACC
10-3	GTCACCTGTTCACACTCTAGTGTAATTTCTCCGTACCTTCTT
10-4	TATACTGCGCCCTAAAGCAACCGTCTTGTCACTTTCAGATTC
10-5	CGCGGTAATTTGCTGTACCGTCCTTAAAGATTCGCTCAGTGT
10-6	AAGTGCACAGATTTTTTTTTTCTACTGAGGGATCTTATGTCA
11-1	TAATGTAGCTGTTTTTTTTTT
11-2	GTTCAGTACGAAGGCAACCGA
11-3	GAACAGGTGACTAGTCTCTTT
11-4	GGCGCAGTATAACTAGAGTGT
11-5	AAATTACCGCGGTTGCTTTAG
11-6	TCTGTGCACTTACGGTACAGC

Motif 9 (10H×11T)

Name	Sequence
1-1	TAGAGTGTGCACGACAACACG
1-2	CTGGGCTAGTTTAACGCTAGT
1-3	GCGTGTCGGGCAGTCCACCCA
1-4	ATGTGATCACAACCACGCTAT
1-5	GGAATCATAGTACAAATGCAA
1-6	TTTTTTTTTTCTGGATATGAC
2-1	TTTTTTTTTTCGTGTTGTCGTGAAAGTTTGTGATGGCTCGTC
2-2	GCACACTCTAACTAGCGTTAATGGCTTCTGCACCGATAATCG
2-3	ACTAGCCCAGTGGGTGGACTGGTACTTCTTTGTCAGATGTGA
2-4	CCCGACACGCATAGCGTGGTTCGCAGAACAGACCAGATTAAG
2-5	GTGATCACATTTGCATTTGTAACGCTGTGCCCGTATCACAAT
2-6	CTATGATTCCGTCATATCCAGCGTCTCCGATTTTTTTTTTTT
3-1	TTTTTTTTTTTATCGAAAGAAACAAACTTTCTTTTTTTTTTT
3-2	TACCTTATTCAAGTTGTCGAGGCAGAAGCCAGACGAGCCATC
3-3	ACCACACCGAGTTTACAGATTAAAGAAGTACCGATTATCGGT
3-4	TGTTCCACCTAATGGGCCCACCTGTTCTGCGTCACATCTGAC
3-5	CGTTCGGCTCCCTATAGCCAGGGCACAGCGTCTTAATCTGGT
3-6	CTGATGAGACACTACAACCACATCGGAGACGATTGTGATACG
4-1	TGAATAAGGTATTCTTTCGATGATGGCGGCGGTTTTTTTTTT
4-2	CTCGGTGTGGTCTCGACAACTTAAGGATCTTCGAGCTCCGAG
4-3	TAGGTGGAACAAATCTGTAAAGGCCCGAACAACTAAATGGGC
4-4	GGAGCCGAACGGTGGGCCCATGAACAGGGCTCAGCGGACACA
4-5	TGTCTCATCAGCTGGCTATAGTCGGCTTACTTCTGCAAGGGC
4-6	TTTTTTTTTTTGTGGTTGTAGAATCATGGTTACACCAATCTG
5-1	CCCATTTATTCAAGGTGGACACCGCCGCCATCCTCGGAGCTC
5-2	CACAAGTCCATGGGCCAGCGTGAAGATCCTTAGCCCATTTAG
5-3	TTTAGACTGTACACTCAACGGTTGTTCGGGCCTGTGTCCGCT
5-4	GGAGAATTTGGGAGCGCGTTAGAGCCCTGTTCGCCCTTGCAG
5-5	TTCCGGCATGTCGGAGACCTCAAGTAAGCCGACAGATTGGTG
5-6	TTTTTTTTTTGAAATAGGTGATAACCATGATTTTTTTTTTTT
6-1	TTTTTTTTTTTGTCCACCTTGTGATCAGGCCGCTGGACACCG
6-2	AATAAATGGGACGCTGGCCCAAGACGTGCGGCACCCTTTAAG
6-3	TGGACTTGTGCCGTTGAGTGTATACCTTCAGCTAGACTCCAG
6-4	ACAGTCTAAATAACGCGCTCCTTGGCTAGGTGGGCTTAACTA
6-5	CAAATTCTCCGAGGTCTCCGACGTCTAACAGTATTCAGATCC
6-6	CATGCCGGAATCACCTATTTCCTGATTTAGCTTTTTTTTTTT
7-1	TTTTTTTTTTTCATGTACTACGGCCTGATCATTTTTTTTTTT
7-2	ACTAACGTAGTTTATTCTATCCCGCACGTCTCGGTGTCCAGC
7-3	TCACGCATAAAGTCCAAGCCTCTGAAGGTATCTTAAAGGGTG

7-4	ATGCTCGTTATATAAAGGACAACCTAGCCAACTGGAGTCTAG
7-5	GGGCATTATGATCAGAATTGTCTGTTAGACGTAGTTAAGCCC
7-6	GGACGTGGGCCTTTAGATCGAGCTAAATCAGGGATCTGAATA
8-1	ACTACGTTAGTGTAGTACATGAAAGTCCAGGATTTTTTTTTT
8-2	TTTATGCGTGAGATAGAATAAAGCAGAAGAAGTTCATGGGCG
8-3	ATAACGAGCATAGGCTTGGACGCACAGCGACAACCGATGCGT
8-4	TCATAATGCCCTGTCCTTTATGTTCAAGGGTCCTAACCTCGG
8-5	GGCCCACGTCCACAATTCTGATTATGAAACGGCTTTGCATAG
8-6	TTTTTTTTTTTTCGATCTAAAGATAGGTCTGCCAACTCCCAT
9-1	CTGAGCGTACACCTCCCAAAGTCCTGGACTTTCGCCCATGAA
9-2	GAAGCAGCCGGTTCACGTGGACTTCTTCTGCTACGCATCGGT
9-3	GTTAACGCGCCGCTGAGCGCATGTCGCTGTGCCCGAGGTTAG
9-4	CATCGATCTGTAGAGTAAATCGACCCTTGAACCTATGCAAAG
9-5	GGGTAAGAATCGGGCTCATGGCCGTTTCATAAATGGGAGTTG
9-6	TTTTTTTTTTCAGTGTTCGACGCAGACCTATCTTTTTTTTTT
10-1	TTTTTTTTTTCTTTGGGAGGTTGTCTGAAATGCAAAGAGCAT
10-2	GTACGCTCAGTCCACGTGAACGTCTTTGCACCTAGCACACCG
10-3	CGGCTGCTTCTGCGCTCAGCGGACTCGGCTGCGGGTGCCATT
10-4	GCGCGTTAACGATTTACTCTAGGATGCGGGATGGCAAAGTCA
10-5	CAGATCGATGCCATGAGCCCGCGCCAGGCGCGCTTACAGTGC
10-6	ATTCTTACCCGTCGAACACTGTATAACTCGATTTTTTTTTTT
11-1	TATTTCAGACTTTTTTTTTT
11-2	GTGCAAAGACATGCTCTTTGC
11-3	CAGCCGAGTCCGGTGTGCTAG
11-4	TCCCGCATCCAATGGCACCCG
11-5	GCGCCTGGCGTGACTTTGCCA
11-6	TCGAGTTATAGCACTGTAAGC

Motif 10 (10H×11T)

Name	Sequence
1-1	CCGGCTTAGACTGAGCAGCTC
1-2	AATCGCCGAGTATAGACTGAC
1-3	CTAAGCGGTCGTGGATGGTAG
1-4	GAAGTAATCTGACTACGGCCC
1-5	GTATGACTGTTAAGGCACTTA
1-6	AGCTAGACCTTTTTTTTTTTT
2-1	CTCGGCGATTGAGCTGCTCAGCTGTTCTCCCTTTTTTTTTT
2-2	TTCTGTCTGGAAACTATGACGTCTAAGCCGGTTTTTTTTTT
2-3	AGATTACTTCCTACCATCCACTCGGGATTAAAGAAGTTGCGC
2-4	CGTGAAGCTATGACCAGCCCAGACCGCTTAGGTCAGTCTATA
2-5	AGGTCTAGCTTAAGTGCCTTAGCTCCGTCACACCTGGCTTTA
2-6	GGAAACACTCTGTAGGCCGTTACAGTCATACGGGCCGTAGTC
3-1	GGGAGAACAGCGTCATAGTTTCTAGGAGCTACCGTATTTGAC
3-2	TCGCATTATCCCGCCGGCTACCCAGACAGAAGCGCAACTTCT
3-3	TTAATCCCGATGGGCTGGTCAATTTCGGATAAAGGGTAGGCC
3-4	GGCCGGAGGAGCAGCGATGAATAGCTTCACGTAAAGCCAGGT
3-5	GTGACGGAGCAACGGCCTACAAATAGCACAGATTCCGGGAAG
3-6	TTTTTTTTTTTGATTCTCAATGAGTGTTTCCTTTTTTTTTT
4-1	TTTTTTTTTTTGTCAAATACGAGTGAAAGGGCGGCTGTGGTG
4-2	TTTTTTTTTTTTCGCCGTTCAGTAGCTCCTAGGTAGCCGGCG
4-3	GGATAATGCGAGGCCTACCCTATCAATGCTATCAACCGGCTT
4-4	TTTCCCTCACTGGCCCTAGGCTTATCCGAAATTTCATCGCTG
4-5	CTCCTCCGGCCCTTCCCGGAATACACTTAGTATTTACTCCTT
4-6	CAACACGCTTAAACATAAGGGTCTGTGCTATTATTGAGAATC
5-1	TCAACATACGTTATATGCTCGGCCCTTTCACTTGAACGGCGA
5-2	AGTGAGGGAAACACCACAGCCCGTGGTGGTCAGTAGACTTTA
5-3	AGCTAACACTCCTGTCGTGGCATAGCATTGATGCCTAGGGCC
5-4	TAAGCGTGTTGAAGCCGGTTGCCTGTTTGTTATGTATCCGTC
5-5	GCTGGTCAGAGGGTACTGCCATACTAAGTGTACCCTTATGTT
5-6	TTTTTTTTTTTAAGGAGTAAATTTGTGATGGTTTTTTTTTT
6-1	GACCACCACGCGAGCATATAATTATACGCTTTTTTTTTTTT
6-2	AGTCGCTCTCCCTCGTTCATCCGTATGTTGATTTTTTTTTT
6-3	AACAAACAGGGCCACGACAGGGCTTAGTATTATCCGACGAGG
6-4	CTAGTACCCACAGGCGAGCAGAGTGTTAGCTTAAAGTCTACT
6-5	CCATCACAAATGGCAGTACCCGTTTGGGAAGCACGCAAATTA
6-6	CGATTTCACAGCGGCTAAATCTCTGACCAGCGACGGATACAT
7-1	AAGCGTATAAGATGAACGAGGTCTTATAACCCTTGTATTAAT
7-2	CAGCGAAAGTGTACTCGCGTGGAGAGCGACTCCTCGTCGGAT
7-3	AATACTAAGCCTGCTCGCCTGTCAGACCAAGTAGCACAGGTG

7-4	AGGGCCGATCCCATAGTCTAATGGGTACTAGTAATTTGCGTG
7-5	CTTCCCAAACGATTTAGCCGCGTTCGAAACTATTTGAACTAT
7-6	TTTTTTTTTTTCACCCGATGGTGTGAAATCGTTTTTTTTTTT
8-1	TTTTTTTTTTTATTAATACAAATGCGACATAATCGACTGTGA
8-2	TTTTTTTTTTTTCTAGCTAGAGGGTTATAAGACACGCGAGTA
8-3	CACTTTCGCTGCACCTGTGCTGTCCGATTTGACTGATTCCGT
8-4	TAACGCATTCGAGGTACGTTTACTTGGTCTGATTAGACTATG
8-5	GGATCGGCCCTATAGTTCAAATTGCCTGTCCTTCTATTGAAA
8-6	TGGAGCGTGGAGCTCTCGGTATAGTTTCGAACCCATCGGGTG
9-1	ACGTAACCGACATAGGCGCGTTTATGTCGCATTCTAGCTAGA
9-2	CGAATGCGTTATCACAGTCGACCCTACCCGAGACTTCTCGCG
9-3	TCTACATAGGCCAGTATTCACTCAAATCGGACAAACGTACCT
9-4	TCCACGCTCCAACGGAATCAGACTAGGCGTAAATTCTCAACG
9-5	AATGCAATCTGTTGTAACCTAAGGACAGGCAATACCGAGAGC
9-6	TTTTTTTTTTTTTTTCAATAGAAGAATTTATGTTTTTTTTTT
10-1	TCGGGTAGGGACGCGCCTATGGAAGCCGTCCTTTTTTTTTTT
10-2	ACTTCCTATAAACATGCACCGTCGGTTACGTTTTTTTTTTTT
10-3	TACGCCTAGTGTGAATACTGGAGCTTCGCACCACCACGCACT
10-4	ATGTGAATGTCGTATCTGCGCCCTATGTAGACGCGAGAAGTC
10-5	CATAAATTCTTAGGTTACAACAGTTCTAGTATTGTGCGGTAG
10-6	ATTATAAAGCTAATGAAACTAAGATTGCATTCGTTGAGAATT
11-1	GGACGGCTTCCGGTGCATGTT
11-2	ATAGGAAGTAGTGCGTGGTGA
11-3	GTGCGAAGCTGCGCAGATACG
11-4	CATTCACATCTACCGCACAAT
11-5	TACTAGAACTTAGTTTCATTA
11-6	GCTTTATAATTTTTTTTTTTT

Motif 11.1 (10H×11T)

Name	Sequence
1-1	TCCGCCGTCGGCGTCTCGGGA
1-2	ACTTGTACCAAGAGGCCAGTG
1-3	GTCTGTGCCCTAGCTGCATCG
1-4	CGTAGACGTTAAGACCTCGGA
1-5	AGGTGGTTTATACGGACTGTA
1-6	TTTTTTTTTTTTTAATACCCA
2-1	TTTTTTTTTTGCCCAATGCGTTTTTTTTTTTTTTTTTTTTTTCCGACGGCGGATTTTTTTTTT
2-2	GTGCAGCAAGTCCGTTAACCATTTTTTTTTTTTTTTTTTTTTTGGTACAAGTTCCCGAGACG
2-3	GAATGAACTAGGGATAATAAGTTTTTTTTTTTTTTTTTTTTTAGGGCACAGACCACTGGCCTC
2-4	ACCGACTAAATGATTGAGTCCTTTTTTTTTTTTTTTTTTTTTTAACGTCTACGCGATGCAGCT
2-5	TACAAAGTTCAACCATAGACGTTTTTTTTTTTTTTTTTTTTTATAAACCACCTTCCGAGGTCT
2-6	TGGGATAGTAGACACCTGCCCTTTTTTTTTTTTTTTTTTTTTACGCATAGTCCTACAGTCCGT
3-1	AGTTATCCCTCATCGGTTACTTTTTTTTTTTTTTTTTTTTTCTTGCTGCACACGCATTGGGC
3-2	TAGAAGGGCCCTCAAGATGCATTTTTTTTTTTTTTTTTTTTTTAGTTCATTCTGGTTAACGGA
3-3	ATGCGGGCCTAGCATGTAAGCTTTTTTTTTTTTTTTTTTTTTTAGTCGGTCTTATTATCCC
3-4	TCCGTAAATTTAGTTTAGGACTTTTTTTTTTTTTTTTTTTTTGAACTTTGTAGGACTCAATCA
3-5	GTTTACTGCACCAACTTGAAGTTTTTTTTTTTTTTTTTTTTTACTATCCCACGTCTATGGTT
3-6	ACTCGCAGCACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC
4-1	TTTTTTTTTTCACGTGGGCATTTTTTTTTTTTTTTTTTTTTTGAGGGATAACTTTTTTTTTTT
4-2	CGAGTCCGCGAGGTCCGAATCTTTTTTTTTTTTTTTTTTTTTGGGCCCTTCTAAGTAACCGAT
4-3	CGCGCCAACGGGTGGAGCTGTTTTTTTTTTTTTTTTTTTTTTAGGCCCGCATTGCATCTTGA
4-4	CCATCGCGCCCTAAGTGTATGTTTTTTTTTTTTTTTTTTTTTAAATTTACGGAGCTTACATGC
4-5	GGTACCGGACCGTGGTCACCGTTTTTTTTTTTTTTTTTTTTTGTGCAGTAAACGTCCTAAACT
4-6	AGGTAATCTAATAGCAGCAGTTTTTTTTTTTTTTTTTTTTTGTGCTGCGAGTCTTCAAGTTG
5-1	ACATAGCGAGTCAAACGGTGATTTTTTTTTTTTTTTTTTTTCGCGGACTCGATGCCCACGTG
5-2	ATGGGCGGGCCGGTCACAAGTTTTTTTTTTTTTTTTTTTTCGTTGGCGCGGATTCGGACCT
5-3	CCGGAGCCCTAAGTCCGAGGTTTTTTTTTTTTTTTTTTTTGGCGCGATGGACAGCTCCACC
5-4	AAGGATCTGGAGGAAGTTCCATTTTTTTTTTTTTTTTTTTTGTCCGGTACCCATACACTTAG
5-5	TTAGGGAAATAAAGGATTGACTTTTTTTTTTTTTTTTTTTTTAGATTACCTCGGTGACCACG
5-6	TCAGCGCTTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACTGCTGCTAT
6-1	TTTTTTTTTTGTATCTGCACATTTTTTTTTTTTTTTTTTTTTACTCGCTATGTTTTTTTTTTT
6-2	CCGCATGATCCGCAAGAGCTTTTTTTTTTTTTTTTTTTTTTGGCCCGCCCATTCACCGTTTG
6-3	AGTGCTTATGACCCTAAATTGTTTTTTTTTTTTTTTTTTTTTAGGGCTCCGGACTTGTGACC
6-4	CGTCAGAAAGATAAAGAGGGCTTTTTTTTTTTTTTTTTTTTTCCAGATCCTTACCTCGGACT
6-5	CATACGCTGTCCCTAACGTTATTTTTTTTTTTTTTTTTTTTTATTTCCCTAATGGAACTTCC
6-6	GCCAATCCAGGTTTAAAGAGATTTTTTTTTTTTTTTTTTTTTGAAGCGCTGAGTCAATCCTT
7-1	TATTTGGCATCTGACTATAGGTTTTTTTTTTTTTTTTTTTTGATCATGCGGTGTGCAGATAC
7-2	GTACGCCCTGACCCACCGATGTTTTTTTTTTTTTTTTTTTTTCATAAGCACTAAGCTCTTGCG
7-3	GTTAAAGGCGTTCGCGAAATTTTTTTTTTTTTTTTTTTTTTCTTTCTGACGCAATTTAGGGT

7-4	CCTTTGACTTTCACTGAACAGTTTTTTTTTTTTTTTTTTTTTACAGCGTATGGCCCTCTTTAT
7-5	GCCCTGACGGGAGCTGCGGGCTTTTTTTTTTTTTTTTTTTTCTGGATTGGCTAACGTTAGGG
7-6	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC
8-1	TTTTTTTTTTACAGAAAGGTCTTTTTTTTTTTTTTTTTTTTGATGCCAAATATTTTTTTTTT
8-2	TGGCGGTTGGATTAATTAGGCTTTTTTTTTTTTTTTTTTTTCAGGGCGTACCCTATAGTCA
8-3	AATCCCTGTGGCTACCGAGGCTTTTTTTTTTTTTTTTTTTTACGCCTTTAACCATCGGTGGG
8-4	AACTGAAGCGGCTTGGCCACTTTTTTTTTTTTTTTTTTTTAAAGTCAAAGGAATTTCGCGA
8-5	ACCGTGACGCAACTAAACAATTTTTTTTTTTTTTTTTTTTCCCGTCAGGGCCTGTTCAGTG
8-6	GGACTCTATCCCTACGGAACCTTTTTTTTTTTTTTTTTTTTAATTCAACGTCGCCCGCAGCT
9-1	GGGACCCTTCACTAACGACCATTTTTTTTTTTTTTTTTTTTCCAACCGCCAGACCTTTCTGT
9-2	GCCTGATATTGCAATCACTCCTTTTTTTTTTTTTTTTTTTCACAGGGATTGCCTAATTAAT
9-3	GGGTACCGACTCCCTTTACGGTTTTTTTTTTTTTTTTTTTCGCTTCAGTTGCCTCGGTAGC
9-4	CTTCCGAGAAGTCATTTGGAATTTTTTTTTTTTTTTTTTTTGCGTCACGGTAGTGGCCAAGC
9-5	GTCTCAGGCGCTTGAGAATGATTTTTTTTTTTTTTTTTTTTGATAGAGTCCATTGTTTAGTT
9-6	TCGAACACTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
10-1	TTTTTTTTTTCACATAGGCCGTTTTTTTTTTTTTTTTTTTTGAAGGGTCCCTTTTTTTTTT
10-2	CCCACCTAGAAGAAGAAAGGGTTTTTTTTTTTTTTTTTTTCAATATCAGGCTGGTCGTTAG
10-3	TAGAACTGAGAGACAGGGCTATTTTTTTTTTTTTTTTTTTTAGTCGGTACCCGGAGTGATTG
10-4	TATAGCGCGTCTGTGGCGCGATTTTTTTTTTTTTTTTTTTTCTTCTCGGAAGCCGTAAAGGG
10-5	CTGGCGGTACCATAAACTCGCTTTTTTTTTTTTTTTTTTTTGCGCCTGAGACTTCCAAATGA
10-6	ATTTCCCTGACCTTGAGGGAGTTTTTTTTTTTTTTTTTTTTGAAGTGTTCGATCATTCTCAA
11-1	TCTAGGTGGGCGGCCTATGTG
11-2	CTCAGTTCTACCCTTTCTTCT
11-3	ACGCGCTATATAGCCCTGTCT
11-4	GTACCGCCAGTCGCGCCACAG
11-5	TCAGGGAAATGCGAGTTTATG
11-6	TTTTTTTTTTCTCCCTCAAGG

Motif 11.2 (10H×11T)

Name	Sequence
1-1	TCCGCCGTCGGCGTCTCGGGA
1-2	ACTTGTACCAAGAGGCCAGTG
1-3	GTCTGTGCCCTAGCTGCATCG
1-4	CGTAGACGTTAAGACCTCGGA
1-5	AGGTGGTTTATACGGACTGTA
1-6	TTTTTTTTTTTTTAATACCCA
2-1	TTTTTTTTTTGCCCAATGCGTTGGAAGGGATGGAGGATCCGACGGCGGATTTTTTTTTT
2-2	GTGCAGCAAGTCCGTTAACCATGGAAGGGATGGAGGATTTGGTACAAGTTCCCGAGACG
2-3	GAATGAACTAGGGATAATAAGTGGAAGGGATGGAGGATAGGGCACAGACCACTGGCCTC
2-4	ACCGACTAAATGATTGAGTCCTGGAAGGGATGGAGGATTAACGTCTACGCGATGCAGCT
2-5	TACAAAGTTCAACCATAGACGTGGAAGGGATGGAGGATATAAACCACCTTCCGAGGTCT
2-6	TGGGATAGTAGACACCTGCCCTGGAAGGGATGGAGGATACGCATAGTCCTACAGTCCGT
3-1	AGTTATCCCTCATCGGTTACTTGGAAGGGATGGAGGATCTTGCTGCACACGCATTGGGC
3-2	TAGAAGGGCCCTCAAGATGCATGGAAGGGATGGAGGATTAGTTCATTCTGGTTAACGGA
3-3	ATGCGGGCCTAGCATGTAAGCTGGAAGGGATGGAGGATTTTAGTCGGTCTTATTATCCC
3-4	TCCGTAAATTTAGTTTAGGACTGGAAGGGATGGAGGATGAACTTTGTAGGACTCAATCA
3-5	GTTTACTGCACCAACTTGAAGTGGAAGGGATGGAGGATTACTATCCCACGTCTATGGTT
3-6	ACTCGCAGCACTTTTTTTTTTTGGAAGGGATGGAGGATTTTTTTTTTTGGGCAGGTGTC
4-1	TTTTTTTTTTCACGTGGGCATTGGAAGGGATGGAGGATGAGGGATAACTTTTTTTTTTT
4-2	CGAGTCCGCGAGGTCCGAATCTGGAAGGGATGGAGGATGGGCCCTTCTAAGTAACCGAT
4-3	CGCGCCAACGGGTGGAGCTGTTGGAAGGGATGGAGGATTAGGCCCGCATTGCATCTTGA
4-4	CCATCGCGCCCTAAGTGTATGTGGAAGGGATGGAGGATAAATTTACGGAGCTTACATGC
4-5	GGTACCGGACCGTGGTCACCGTGGAAGGGATGGAGGATGTGCAGTAAACGTCCTAAACT
4-6	AGGTAATCTAATAGCAGCAGTTGGAAGGGATGGAGGATGTGCTGCGAGTCTTCAAGTTG
5-1	ACATAGCGAGTCAAACGGTGATGGAAGGGATGGAGGATCGCGGACTCGATGCCCACGTG
5-2	ATGGGCGGGCCGGTCACAAGTTGGAAGGGATGGAGGATCGTTGGCGCGGATTCGGACCT
5-3	CCGGAGCCCTAAGTCCGAGGTTGGAAGGGATGGAGGATGGCGCGATGGACAGCTCCACC
5-4	AAGGATCTGGAGGAAGTTCCATGGAAGGGATGGAGGATGTCCGGTACCCATACACTTAG
5-5	TTAGGGAAATAAAGGATTGACTGGAAGGGATGGAGGATTAGATTACCTCGGTGACCACG
5-6	TCAGCGCTTCATTTTTTTTTTTGGAAGGGATGGAGGATTTTTTTTTTTACTGCTGCTAT
6-1	TTTTTTTTTTGTATCTGCACATGGAAGGGATGGAGGATACTCGCTATGTTTTTTTTTTT
6-2	CCGCATGATCCGCAAGAGCTTTGGAAGGGATGGAGGATGGCCCGCCCATTCACCGTTTG
6-3	AGTGCTTATGACCCTAAATTGTGGAAGGGATGGAGGATTAGGGCTCCGGACTTGTGACC
6-4	CGTCAGAAAGATAAAGAGGGCTGGAAGGGATGGAGGATTCCAGATCCTTACCTCGGACT
6-5	CATACGCTGTCCCTAACGTTATGGAAGGGATGGAGGATTATTTCCCTAATGGAACTTCC
6-6	GCCAATCCAGGTTTAAAGAGATGGAAGGGATGGAGGATTGAAGCGCTGAGTCAATCCTT
7-1	TATTTGGCATCTGACTATAGGTGGAAGGGATGGAGGATGATCATGCGGTGTGCAGATAC
7-2	GTACGCCCTGACCCACCGATGTGGAAGGGATGGAGGATCATAAGCACTAAGCTCTTGCG
7-3	GTTAAAGGCGTTCGCGAAATTTGGAAGGGATGGAGGATCTTTCTGACGCAATTTAGGGT

7-4	CCTTTGACTTTCACTGAACAGTGGAAGGGATGGAGGATACAGCGTATGGCCCTCTTTAT
7-5	GCCCTGACGGGAGCTGCGGGCTGGAAGGGATGGAGGATCTGGATTGGCTAACGTTAGGG
7-6	GACGTTGAATTTTTTTTTTTTTGGAAGGGATGGAGGATTTTTTTTTTTTTCTCTTTAAAC
8-1	TTTTTTTTTTACAGAAAGGTCTGGAAGGGATGGAGGATGATGCCAAATATTTTTTTTTT
8-2	TGGCGGTTGGATTAATTAGGCTGGAAGGGATGGAGGATTCAGGGCGTACCCTATAGTCA
8-3	AATCCCTGTGGCTACCGAGGCTGGAAGGGATGGAGGATACGCCTTTAACCATCGGTGGG
8-4	AACTGAAGCGGCTTGGCCACTTGGAAGGGATGGAGGATAAAGTCAAAGGAATTTCGCGA
8-5	ACCGTGACGCAACTAAACAATTGGAAGGGATGGAGGATCCCGTCAGGGCCTGTTCAGTG
8-6	GGACTCTATCCCTACGGAACCTGGAAGGGATGGAGGATAATTCAACGTCGCCCGCAGCT
9-1	GGGACCCTTCACTAACGACCATGGAAGGGATGGAGGATCCAACCGCCAGACCTTTCTGT
9-2	GCCTGATATTGCAATCACTCCTGGAAGGGATGGAGGATCACAGGGATTGCCTAATTAAT
9-3	GGGTACCGACTCCCTTTACGGTGGAAGGGATGGAGGATCGCTTCAGTTGCCTCGGTAGC
9-4	CTTCCGAGAAGTCATTTGGAATGGAAGGGATGGAGGATGCGTCACGGTAGTGGCCAAGC
9-5	GTCTCAGGCGCTTGAGAATGATGGAAGGGATGGAGGATGATAGAGTCCATTGTTTAGTT
9-6	TCGAACACTTCTTTTTTTTTTTGGAAGGGATGGAGGATTTTTTTTTTTGGTTCCGTAGG
10-1	TTTTTTTTTTCACATAGGCCGTGGAAGGGATGGAGGATTGAAGGGTCCCTTTTTTTTTT
10-2	CCCACCTAGAAGAAGAAAGGGTGGAAGGGATGGAGGATCAATATCAGGCTGGTCGTTAG
10-3	TAGAACTGAGAGACAGGGCTATGGAAGGGATGGAGGATAGTCGGTACCCGGAGTGATTG
10-4	TATAGCGCGTCTGTGGCGCGATGGAAGGGATGGAGGATCTTCTCGGAAGCCGTAAAGGG
10-5	CTGGCGGTACCATAAACTCGCTGGAAGGGATGGAGGATGCGCCTGAGACTTCCAAATGA
10-6	ATTTCCCTGACCTTGAGGGAGTGGAAGGGATGGAGGATGAAGTGTTCGATCATTCTCAA
11-1	TCTAGGTGGGCGGCCTATGTG
11-2	CTCAGTTCTACCCTTTCTTCT
11-3	ACGCGCTATATAGCCCTGTCT
11-4	GTACCGCCAGTCGCGCCACAG
11-5	TCAGGGAAATGCGAGTTTATG
11-6	TTTTTTTTTTCTCCCTCAAGG

Motif 11.3 (10H×11T)

Name	Sequence
1-1	TCCGCCGTCGGCGTCTCGGGA
1-2	ACTTGTACCAAGAGGCCAGTG
1-3	GTCTGTGCCCTAGCTGCATCG
1-4	CGTAGACGTTAAGACCTCGGA
1-5	AGGTGGTTTATACGGACTGTA
1-6	TTTTTTTTTTTTTAATACCCA
2-1	TTTTTTTTTTGCCCAATGCGTTTTTTTTTTTCCGACGGCGGATTTTTTTTTT
2-2	GTGCAGCAAGTCCGTTAACCATTTTTTTTTTTTGGTACAAGTTCCCGAGACG
2-3	GAATGAACTAGGGATAATAAGTTTTTTTTTTAGGGCACAGACCACTGGCCTC
2-4	ACCGACTAAATGATTGAGTCCTTTTTTTTTTTTAACGTCTACGCGATGCAGCT
2-5	TACAAAGTTCAACCATAGACGTTTTTTTTTTTATAAACCACCTTCCGAGGTCT
2-6	TGGGATAGTAGACACCTGCCCTTTTTTTTTTTACGCATAGTCCTACAGTCCGT
3-1	AGTTATCCCTCATCGGTTACTTTTTTTTTTTTCTTGCTGCACACGCATTGGGC
3-2	TAGAAGGGCCCTCAAGATGCATTTTTTTTTTTTAGTTCATTCTGGTTAACGGA
3-3	ATGCGGGCCTAGCATGTAAGCTTTTTTTTTTTTTAGTCGGTCTTATTATCCC
3-4	TCCGTAAATTTAGTTTAGGACTTTTTTTTTTGAACTTTGTAGGACTCAATCA
3-5	GTTTACTGCACCAACTTGAAGTTTTTTTTTTTACTATCCCACGTCTATGGTT
3-6	ACTCGCAGCACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC
4-1	TTTTTTTTTTCACGTGGGCATTTTTTTTTTTTGAGGGATAACTTTTTTTTTTT
4-2	CGAGTCCGCGAGGTCCGAATCTTTTTTTTTTTGGGCCCTTCTAAGTAACCGAT
4-3	CGCGCCAACGGGTGGAGCTGTTTTTTTTTTTTTAGGCCCGCATTGCATCTTGA
4-4	CCATCGCGCCCTAAGTGTATGTTTTTTTTTTTAAATTTACGGAGCTTACATGC
4-5	GGTACCGGACCGTGGTCACCGTTTTTTTTTTTGTGCAGTAAACGTCCTAAACT
4-6	AGGTAATCTAATAGCAGCAGTTTTTTTTTTTGTGCTGCGAGTCTTCAAGTTG
5-1	ACATAGCGAGTCAAACGGTGATTTTTTTTTTTCGCGGACTCGATGCCCACGTG
5-2	ATGGGCGGGCCGGTCACAAGTTTTTTTTTTTTCGTTGGCGCGGATTCGGACCT
5-3	CCGGAGCCCTAAGTCCGAGGTTTTTTTTTTTTGGCGCGATGGACAGCTCCACC
5-4	AAGGATCTGGAGGAAGTTCCATTTTTTTTTTTGTCCGGTACCCATACACTTAG
5-5	TTAGGGAAATAAAGGATTGACTTTTTTTTTTTTAGATTACCTCGGTGACCACG
5-6	TCAGCGCTTCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACTGCTGCTAT
6-1	TTTTTTTTTTGTATCTGCACATTTTTTTTTTTACTCGCTATGTTTTTTTTTTT
6-2	CCGCATGATCCGCAAGAGCTTTTTTTTTTTTTGGCCCGCCCATTCACCGTTTG
6-3	AGTGCTTATGACCCTAAATTGTTTTTTTTTTTTAGGGCTCCGGACTTGTGACC
6-4	CGTCAGAAAGATAAAGAGGGCTTTTTTTTTTTTCCAGATCCTTACCTCGGACT
6-5	CATACGCTGTCCCTAACGTTATTTTTTTTTTTTATTTCCCTAATGGAACTTCC
6-6	GCCAATCCAGGTTTAAAGAGATTTTTTTTTTTTGAAGCGCTGAGTCAATCCTT
7-1	TATTTGGCATCTGACTATAGGTTTTTTTTTTTGATCATGCGGTGTGCAGATAC
7-2	GTACGCCCTGACCCACCGATGTTTTTTTTTTTCATAAGCACTAAGCTCTTGCG
7-3	GTTAAAGGCGTTCGCGAAATTTTTTTTTTTTCTTTCTGACGCAATTTAGGGT

7-4	CCTTTGACTTTCACTGAACAGTTTTTTTTTTACAGCGTATGGCCCTCTTTAT
7-5	GCCCTGACGGGAGCTGCGGGCTTTTTTTTTTCTGGATTGGCTAACGTTAGGG
7-6	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC
8-1	TTTTTTTTTTACAGAAAGGTCTTTTTTTTTTGATGCCAAATATTTTTTTTT
8-2	TGGCGGTTGGATTAATTAGGCTTTTTTTTTTTCAGGGCGTACCCTATAGTCA
8-3	AATCCCTGTGGCTACCGAGGCTTTTTTTTTTACGCCTTTAACCATCGGTGGG
8-4	AACTGAAGCGGCTTGGCCACTTTTTTTTTTTAAAGTCAAAGGAATTTCGCGA
8-5	ACCGTGACGCAACTAAACAATTTTTTTTTTTCCCGTCAGGGCCTGTTCAGTG
8-6	GGACTCTATCCCTACGGAACCTTTTTTTTTTAATTCAACGTCGCCCGCAGCT
9-1	GGGACCCTTCACTAACGACCATTTTTTTTTTCCAACCGCCAGACCTTTCTGT
9-2	GCCTGATATTGCAATCACTCCTTTTTTTTTTCACAGGGATTGCCTAATTAAT
9-3	GGGTACCGACTCCCTTTACGGTTTTTTTTTTCGCTTCAGTTGCCTCGGTAGC
9-4	CTTCCGAGAAGTCATTTGGAATTTTTTTTTTGCGTCACGGTAGTGGCCAAGC
9-5	GTCTCAGGCGCTTGAGAATGATTTTTTTTTTTGATAGAGTCCATTGTTTAGTT
9-6	TCGAACACTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
10-1	TTTTTTTTTTCACATAGGCCGTTTTTTTTTTTGAAGGGTCCCTTTTTTTTTT
10-2	CCCACCTAGAAGAAGAAAGGGTTTTTTTTTTCAATATCAGGCTGGTCGTTAG
10-3	TAGAACTGAGAGACAGGGCTATTTTTTTTTTTAGTCGGTACCCGGAGTGATTG
10-4	TATAGCGCGTCTGTGGCGCGATTTTTTTTTTCTTCTCGGAAGCCGTAAAGGG
10-5	CTGGCGGTACCATAAACTCGCTTTTTTTTTTGCGCCTGAGACTTCCAAATGA
10-6	ATTTCCCTGACCTTGAGGGAGTTTTTTTTTTGAAGTGTTCGATCATTCTCAA
11-1	TCTAGGTGGGCGGCCTATGTG
11-2	CTCAGTTCTACCCTTTCTTCT
11-3	ACGCGCTATATAGCCCTGTCT
11-4	GTACCGCCAGTCGCGCCACAG
11-5	TCAGGGAAATGCGAGTTTATG
11-6	TTTTTTTTTTCTCCCTCAAGG

Motif 11.4 (10H×11T)

Name	Sequence
1-1	TCCGCCGTCGGCGTCTCGGGA
1-2	ACTTGTACCAAGAGGCCAGTG
1-3	GTCTGTGCCCTAGCTGCATCG
1-4	CGTAGACGTTAAGACCTCGGA
1-5	AGGTGGTTTATACGGACTGTA
1-6	TTTTTTTTTTTTTAATACCCA
2-1	TTTTTTTTTTGCCCAATGCGTTTCCGACGGCGGATTTTTTTTTT
2-2	GTGCAGCAAGTCCGTTAACCATTTTGGTACAAGTTCCCGAGACG
2-3	GAATGAACTAGGGATAATAAGTTAGGGCACAGACCACTGGCCTC
2-4	ACCGACTAAATGATTGAGTCCTTTAACGTCTACGCGATGCAGCT
2-5	TACAAAGTTCAACCATAGACGTTATAAACCACCTTCCGAGGTCT
2-6	TGGGATAGTAGACACCTGCCCTTACGCATAGTCCTACAGTCCGT
3-1	AGTTATCCCTCATCGGTTACTTTCTTGCTGCACACGCATTGGGC
3-2	TAGAAGGGCCCTCAAGATGCATTTAGTTCATTCTGGTTAACGGA
3-3	ATGCGGGCCTAGCATGTAAGCTTTTTAGTCGGTCTTATTATCCC
3-4	TCCGTAAATTTAGTTTAGGACTTGAACTTTGTAGGACTCAATCA
3-5	GTTTACTGCACCAACTTGAAGTTTACTATCCCACGTCTATGGTT
3-6	ACTCGCAGCACTTTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC
4-1	TTTTTTTTTTCACGTGGGCATTTGAGGGATAACTTTTTTTTTTT
4-2	CGAGTCCGCGAGGTCCGAATCTTGGGCCCTTCTAAGTAACCGAT
4-3	CGCGCCAACGGGTGGAGCTGTTTTAGGCCCGCATTGCATCTTGA
4-4	CCATCGCGCCCTAAGTGTATGTTAAATTTACGGAGCTTACATGC
4-5	GGTACCGGACCGTGGTCACCGTTGTGCAGTAAACGTCCTAAACT
4-6	AGGTAATCTAATAGCAGCAGTTTGTGCTGCGAGTCTTCAAGTTG
5-1	ACATAGCGAGTCAAACGGTGATTCGCGGACTCGATGCCCACGTG
5-2	ATGGGCGGGCCGGTCACAAGTTTCGTTGGCGCGGATTCGGACCT
5-3	CCGGAGCCCTAAGTCCGAGGTTTGGCGCGATGGACAGCTCCACC
5-4	AAGGATCTGGAGGAAGTTCCATTGTCCGGTACCCATACACTTAG
5-5	TTAGGGAAATAAAGGATTGACTTTAGATTACCTCGGTGACCACG
5-6	TCAGCGCTTCATTTTTTTTTTTTTTTTTTTTTTACTGCTGCTAT
6-1	TTTTTTTTTTGTATCTGCACATTACTCGCTATGTTTTTTTTTTT
6-2	CCGCATGATCCGCAAGAGCTTTTGGCCCGCCCATTCACCGTTTG
6-3	AGTGCTTATGACCCTAAATTGTTTAGGGCTCCGGACTTGTGACC
6-4	CGTCAGAAAGATAAAGAGGGCTTTCCAGATCCTTACCTCGGACT
6-5	CATACGCTGTCCCTAACGTTATTTATTTCCCTAATGGAACTTCC
6-6	GCCAATCCAGGTTTAAAGAGATTTGAAGCGCTGAGTCAATCCTT
7-1	TATTTGGCATCTGACTATAGGTTGATCATGCGGTGTGCAGATAC
7-2	GTACGCCCTGACCCACCGATGTTCATAAGCACTAAGCTCTTGCG
7-3	GTTAAAGGCGTTCGCGAAATTTTCTTTCTGACGCAATTTAGGGT

7-4	CCTTTGACTTTCACTGAACAGTTACAGCGTATGGCCCTCTTTAT
7-5	GCCCTGACGGGAGCTGCGGGCTTCTGGATTGGCTAACGTTAGGG
7-6	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC
8-1	TTTTTTTTTTACAGAAAGGTCTTGATGCCAAATATTTTTTTTTT
8-2	TGGCGGTTGGATTAATTAGGCTTTCAGGGCGTACCCTATAGTCA
8-3	AATCCCTGTGGCTACCGAGGCTTACGCCTTTAACCATCGGTGGG
8-4	AACTGAAGCGGCTTGGCCACTTTAAAGTCAAAGGAATTTCGCGA
8-5	ACCGTGACGCAACTAAACAATTTCCCGTCAGGGCCTGTTCAGTG
8-6	GGACTCTATCCCTACGGAACCTTAATTCAACGTCGCCCGCAGCT
9-1	GGGACCCTTCACTAACGACCATTCCAACCGCCAGACCTTTCTGT
9-2	GCCTGATATTGCAATCACTCCTTCACAGGGATTGCCTAATTAAT
9-3	GGGTACCGACTCCCTTTACGGTTCGCTTCAGTTGCCTCGGTAGC
9-4	CTTCCGAGAAGTCATTTGGAATTGCGTCACGGTAGTGGCCAAGC
9-5	GTCTCAGGCGCTTGAGAATGATTGATAGAGTCCATTGTTTAGTT
9-6	TCGAACACTTCTTTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
10-1	TTTTTTTTTTCACATAGGCCGTTTGAAGGGTCCCTTTTTTTTTT
10-2	CCCACCTAGAAGAAGAAAGGGTTCAATATCAGGCTGGTCGTTAG
10-3	TAGAACTGAGAGACAGGGCTATTAGTCGGTACCCGGAGTGATTG
10-4	TATAGCGCGTCTGTGGCGCGATTCTTCTCGGAAGCCGTAAAGGG
10-5	CTGGCGGTACCATAAACTCGCTTGCGCCTGAGACTTCCAAATGA
10-6	ATTTCCCTGACCTTGAGGGAGTTGAAGTGTTCGATCATTCTCAA
11-1	TCTAGGTGGGCGGCCTATGTG
11-2	CTCAGTTCTACCCTTTCTTCT
11-3	ACGCGCTATATAGCCCTGTCT
11-4	GTACCGCCAGTCGCGCCACAG
11-5	TCAGGGAAATGCGAGTTTATG
11-6	TTTTTTTTTTCTCCCTCAAGG

Motif 12 (5 square × 5 square)

Name	Sequence
1_1	TCCGCCGTCGGTTTTTTTTTTCGTCTCGGGA
1_2	ACTTGTACCAATTTTTTTTTTGAGGCCAGTG
1_3	GTCTGTGCCCTTTTTTTTTTTAGCTGCATCG
1_4	CGTAGACGTTATTTTTTTTTTAGACCTCGGA
1_5	AGGTGGTTTATTTTTTTTTTTACGGACTGTA
1_6	TTTTTTTTTTTTTTTTTTTTTTAATACCCA
2_1	TTTTTTTTTTTTTTTTTTTTGCCCAATGCGTTTTTTTTTTTCCGACGGCGGATTTTTTTTTTTTTTTTTT
2_2	GTGCAGCAAGTTTTTTTTTTCCGTTAACCATTTTTTTTTTTTGGTACAAGTTTTTTTTTTTCCCGAGACG
2_3	GAATGAACTATTTTTTTTTTGGGATAATAAGTTTTTTTTTTAGGGCACAGACTTTTTTTTTCACTGGCCTC
2_4	ACCGACTAAATTTTTTTTTTGATTGAGTCCTTTTTTTTTTAACGTCTACGTTTTTTTTTCGATGCAGCT
2_5	TACAAAGTTCTTTTTTTTTAACCATAGACGTTTTTTTTTATAAACCACCTTTTTTTTTTCCGAGGTCT
2_6	TGGGATAGTATTTTTTTTTGACACCTGCCCTTTTTTTTTACGCATAGTCCTTTTTTTTTTACAGTCCGT
3_2	AGTTATCCCTCTTTTTTTTTCATCGGTTACTTTTTTTTTCTTGCTGCACTTTTTTTTTACGCATTGGGC
3_3	TAGAAGGGCCCTTTTTTTTTCTCAAGATGCTTTTTTTTTTAGTTCATTCTTTTTTTTTGGTTAACGGA
3_4	ATGCGGGCCTATTTTTTTTTAGCATGTAAGTTTTTTTTTTAGTCGGTTTTTTTTTCTTATTATCCC
3_5	TCCGTAAATTTTTTTTTTTAGTTTAGGATTTTTTTTGAACTTTGTATTTTTTTTGGACTCAATCA
3_6	GTTTACTGCACTTTTTTTTCCAACTTGAATTTTTTTTTACTATCCCATTTTTTTTCGTCTATGGTT
3_1	ACTCGCAGCACTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGCAGGTGTC
4_1	TTTTTTTTTTTTTTTTTTTCACGTGGGCATTTTTTTTTTGAGGGATAACTTTTTTTTTTTTTTTTTT
4_2	CGAGTCCGCGTTTTTTTTTAGGTCCGAATCTTTTTTTTTGGGCCCTTCTATTTTTTTTTAGTAACCGAT
4_3	CGCGCCAACGTTTTTTTTTGGTGGAGCTGTTTTTTTTTTTAGGCCCGCATTTTTTTTTTGCATCTTGA
4_4	CCATCGCGCCTTTTTTTTTCTAAGTGTATGTTTTTTTTTAAATTTACGGATTTTTTTTTGCTTACATGC
4_5	GGTACCGGACTTTTTTTTTCGTGGTCACCGTTTTTTTTTGTGCAGTAAACTTTTTTTTGTCCTAAACT
4_6	AGGTAATCTATTTTTTTTTATAGCAGCAGTTTTTTTTTGTGCTGCGAGTTTTTTTTTCTTCAAGTTG
5_2	ACATAGCGAGTTTTTTTTTTCAAACGGTGTTTTTTTTTCGCGGACTCGTTTTTTTTATGCCCACGTG
5_3	ATGGGCGGGCCTTTTTTTTTCGGTCACAAGTTTTTTTTTCGTTGGCGCGTTTTTTTTGATTCGGACCT
5_4	CCGGAGCCCTATTTTTTTTTAAGTCCGAGGTTTTTTTTGGCGCGATGGTTTTTTTTACAGCTCCACC
5_5	AAGGATCTGGATTTTTTTTTAGGAAGTTCCTTTTTTTTTGTCCGGTACCTTTTTTTTCATACACTTAG
5_6	TTAGGGAAATATTTTTTTTTAAAGGATTGATTTTTTTTTAGATTACCTTTTTTTTTCGGTGACCACG
5_1	TCAGCGCTTCATTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACTGCTGCTAT
6_1	TTTTTTTTTTTTTTTTTTTGTATCTGCACATTTTTTTTTACTCGCTATGTTTTTTTTTTTTTTTTTT
6_2	CCGCATGATCTTTTTTTTTCGCAAGAGCTTTTTTTTTTGGCCCGCCCATTTTTTTTTTCACCGTTTG
6_3	AGTGCTTATGTTTTTTTTTACCCTAAATTGTTTTTTTTTAGGGCTCCGGTTTTTTTTTACTTGTGACC
6_4	CGTCAGAAAGTTTTTTTTTATAAAGAGGGCTTTTTTTTTCCAGATCCTTTTTTTTTACCTCGGACT
6_5	CATACGCTGTTTTTTTTTTCCCTAACGTTATTTTTTTTTATTTCCCTAATTTTTTTTTGGAACTTCC
6_6	GCCAATCCAGTTTTTTTTTGTTTAAAGAGATTTTTTTTTGAAGCGCTGATTTTTTTTTGTCAATCCTT
7_2	TATTTGGCATCTTTTTTTTTCTGACTATAGTTTTTTTTTGATCATGCGGTTTTTTTTTGTGCAGATAC
7_3	GTACGCCCTGATTTTTTTTTACCCACCGATTTTTTTTTCATAAGCACTTTTTTTTTAAGCTCTTGCG
7_4	GTTAAAGGCGTTTTTTTTTTCGCGAAATTTTTTTTTCTTTCTGACGTTTTTTTTTCAATTTAGGGT

7_5	CCTTTGACTTTTTTTTTTTTTTCACTGAACATTTTTTTTTTTACAGCGTATGTTTTTTTTTTGCCCTCTTTAT
7_6	GCCCTGACGGGTTTTTTTTTTGAGCTGCGGGTTTTTTTTTTCTGGATTGGCTTTTTTTTTTTAACGTTAGGG
7_1	GACGTTGAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCTTTAAAC
8_1	TTTTTTTTTTTTTTTTTTTTTACAGAAAGGTCTTTTTTTTTTTGATGCCAAATATTTTTTTTTTTTTTTTTTT
8_2	TGGCGGTTGGTTTTTTTTTTTATTAATTAGGCTTTTTTTTTTTTCAGGGCGTACTTTTTTTTTTTCCTATAGTCA
8_3	AATCCCTGTGTTTTTTTTTTTGCTACCGAGGCTTTTTTTTTTTACGCCTTTAACTTTTTTTTTTTCATCGGTGGG
8_4	AACTGAAGCGTTTTTTTTTTTGCTTGGCCACTTTTTTTTTTTTAAAGTCAAAGGTTTTTTTTTTTAATTTCGCGA
8_5	ACCGTGACGCTTTTTTTTTTTAACTAAACAATTTTTTTTTTTTCCCGTCAGGGCTTTTTTTTTTTCTGTTCAGTG
8_6	GGACTCTATCTTTTTTTTTTTCCTACGGAACCTTTTTTTTTTTAATTCAACGTCTTTTTTTTTTTGCCCGCAGCT
9_2	GGGACCCTTCATTTTTTTTTTTACTAACGACCTTTTTTTTTTTCCAACCGCCATTTTTTTTTTTGACCTTTCTGT
9_3	GCCTGATATTGTTTTTTTTTTTGCAATCACTCTTTTTTTTTTTCACAGGGATTTTTTTTTTTTTGCCTAATTAAT
9_4	GGGTACCGACTTTTTTTTTTTTTCCCTTTACGTTTTTTTTTTTCGCTTCAGTTTTTTTTTTTTTGCCTCGGTAGC
9_5	CTTCCGAGAAGTTTTTTTTTTTGTCATTTGGATTTTTTTTTTTGCGTCACGGTTTTTTTTTTTTAGTGGCCAAGC
9_6	GTCTCAGGCGCTTTTTTTTTTTCTTGAGAATGTTTTTTTTTTTGATAGAGTCCTTTTTTTTTTTATTGTTTAGTT
9_1	TCGAACACTTCTTTTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGTTCCGTAGG
10_1	TTTTTTTTTTTTTTTTTTTTTCACATAGGCCGTTTTTTTTTTTTGAAGGGTCCCTTTTTTTTTTTTTTTTTTT
10_2	CCCACCTAGATTTTTTTTTTTAGAAGAAAGGGTTTTTTTTTTTCAATATCAGGCTTTTTTTTTTTTGGTCGTTAG
10_3	TAGAACTGAGTTTTTTTTTTTAGACAGGGCTATTTTTTTTTTTAGTCGGTACCCTTTTTTTTTTTGGAGTGATTG
10_4	TATAGCGCGTTTTTTTTTTTTCTGTGGCGCGATTTTTTTTTTTCTTCTCGGAAGTTTTTTTTTTTCCGTAAAGGG
10_5	CTGGCGGTACTTTTTTTTTTTCATAAACTCGCTTTTTTTTTTTGCGCCTGAGACTTTTTTTTTTTTTCCAAATGA
10_6	ATTTCCCTGATTTTTTTTTTTCCTTGAGGGAGTTTTTTTTTTTGAAGTGTTCGATTTTTTTTTTTTCATTCTCAA
11_3	TCTAGGTGGGTTTTTTTTTTCGGCCTATGTG
11_4	CTCAGTTCTATTTTTTTTTTCCCTTTCTTCT
11_5	ACGCGCTATATTTTTTTTTTTTAGCCCTGTCT
11_6	GTACCGCCAGTTTTTTTTTTTCGCGCCACAG
11_1	TCAGGGAAATTTTTTTTTTTGCGAGTTTATG
11_2	TTTTTTTTTTTTTTTTTTTTCTCCCTCAAGG

Motif 13 (3 hexagon × 7 hexagon)

Name	Sequence
1-2	GATCCGACCTGTGGTCGTCAC
1-3	CAGTACACGCAGATGTTGCTT
1-4	CGTACACCTGAAGTTCAGTTC
1-5	GAGGCAGTAGAGTACCACACC
1-6	TACTTGCCTTGTGGGATCCTG
1-7	TATGCGTCTGGACATCTAACT
1-8	
2-1	GTGACGACCACAGGTCGGATCTCGCGAGATCATACGTCTGACCATAGGACTCTGCCACGTGCA
2-2	AGGCTATGAAACCCATAAGGGGTCAGACGTATGATCTCGCGAAAGCAACATCTGCGTGTACTG
2-3	GAACTGAACTTCAGGTGTACGTTACGTCAGATGCTTCTTAAGGCACAATACCATGTGTTCAGA
2-4	CCCTCTAACCGAGTGTTATAGCTTAAGAAGCATCTGACGTAAGGTGTGGTACTCTACTGCCTC
2-5	CAGGATCCCACAAGGCAAGTATTCGCAATCAAGTTCTCAAGGAACGGGAAGCCTGACGAGAAT
2-6	CCAGCTGCAATTTCCGCACGACCTTGAGAACTTGATTGCGAAAGTTAGATGTCCAGACGCATA
2-7	
3-1	TATTGGGTCTAGAAGACTCAC
3-2	TCGAGCTTGCCAGATCAAGATGTGAGTCTTCTAGACCCAATATGCACGTGGCAGAGTCCTATG
3-3	CCCTTATGGGTTTCATAGCCTGGGCGTCTCGAAGTGGCTGCACAGGAAATCCTGAACCCAAGG
3-4	CCGAAAGTTTCAAGTCGGGATTGCAGCCACTTCGAGACGCCCTCTGAACACATGGTATTGTGC
3-5	CTATAACACTCGGTTAGAGGGCTTTGAGTACGCTAGCAGCTTTGACTAGCAAAGTGGTCTACG
3-6	ACTGCAAAGAGACGACGAGTAAAGCTGCTAGCGTACTCAAAGATTCTCGTCAGGCTTCCCGTT
3-7	TCGTGCGGAAATTGCAGCTGGCAGCTCGCCTTGAACAGTGAAGGTTACCTCATTGGGCTTGTG
3-8	TTCACTGTTCAAGGCGAGCTG
4-1	ATCTTGATCTGGCAAGCTCGACAATCCATTGGCTTATTGAGTTCCGGGATGATTTGACAACTC
4-2	TGTCGTGAAGTCAATCTCGTTACTCAATAAGCCAATGGATTGCCTTGGGTTCAGGATTTCCTG
4-3	ATCCCGACTTGAAACTTTCGGTGGATGTTCATCGCACAACTGATACGGCCTGAGTCCATCCCA
4-4	ATCTGGAAGCAGTGCACCAATCAGTTGTGCGATGAACATCCACGTAGACCACTTTGCTAGTCA
4-5	TACTCGTCGTCTCTTTGCAGTTGCGGCTATACAGAAGATGAGCATACCTATTGCGTGATCGTC
4-6	AATAGCCCGACAGTTATCATACTCATCTTCTGTATAGCCGCACACAAGCCCAATGAGGTAACC
4-7	
5-1	GGCGCAAGGTGTTAGCATCCC
5-2	TCCGAACAACAACCCACACGGGGGATGCTAACACCTTGCGCCGAGTTGTCAAATCATCCCGGA
5-3	AACGAGATTGACTTCACGACAGTTAATCCGGAAGCGATGGTCTGGCTATCCTCGAGAACATGC
5-4	CTGGAAATACTGCTCAGCTCCGACCATCGCTTCCGGATTAACTGGGATGGACTCAGGCCGTAT
5-5	ATTGGTGCACTGCTTCCAGATACAATCAGTGGGTGGTAATCCAAGTCTTGAGGAAACGGAAAC
5-6	ATGAACTAGTGAACTCCCAAGGGATTACCACCCACTGATTGTGACGATCACGCAATAGGTATG
5-7	TATGATAACTGTCGGGCTATTAACTACACGGACTACGTTACGAACGCTCCCTGTCCATTTAGG
5-8	CGTAACGTAGTCCGTGTAGTT
6-1	CCGTGTGGGTTGTTGTTCGGAGATATGCCTATCTGGTCCATGTCGCAACGCAACCTGGGACAT
6-2	TGCTCGAAATAGGCTGCGTTCCATGGACCAGATAGGCATATCGCATGTTCTCGAGGATAGCCA

6-3	GGAGCTGAGCAGTATTTCCAGTATGCTTATAGACGTTTGTTGCACTTTCAACAGTTCTGTCTA
6-4	CCGACACCATCTGGGAACTAACAACAAACGTCTATAAGCATAGTTTCCGTTTCCTCAAGACTT
6-5	CTTGGGAGTTCACTAGTTCATGTGTATACCTGCAAGATCTATTCAGCTACTTTGTGCTCCCGA
6-6	GCTAGCCAAGGTAAAGCACATATAGATCTTGCAGGTATACACCCTAAATGGACAGGGAGCGTT
6-7	
7-1	TCATGGGACCTCGTGATATGA
7-2	GAAGAGGCACTGGTTAACTCGTCATATCACGAGGTCCCATGAATGTCCCAGGTTGCGTTGCGA
7-3	GAACGCAGCCTATTTCGAGCAACGCACTTACAACGTGTAAGGCGTAACAACGATGTGAATGCC
7-4	AGCTTCACACACCCTGTGTCGCCTTACACGTTGTAAGTGCGTTAGACAGAACTGTTGAAAGTG
7-5	TTAGTTCCCAGATGGTGTCGGCTCACCTATATCGGATTGAACTGGTAAACGGCCACAGACTCG
7-6	TTGCCTGATGCTCCAGTCAACGTTCAATCCGATATAGGTGAGTCGGGAGCACAAAGTAGCTGA
7-7	ATGTGCTTTACCTTGGCTAGCTTCTACTCCGACGTTGGTGGCATCTCGGTACTGAATGGAGGT
7-8	GCCACCAACGTCGGAGTAGAA
8-1	CGAGTTAACCAGTGCCTCTTCTTCCATGACGCTTAGATCGTTCTCCGTTAGACAACCATGGAG
8-2	TTTCCCATAGCGCTGGCTCATAACGATCTAAGCGTCATGGAAGGCATTCACATCGTTGTTACG
8-3	CGACACAGGGTGTGTGAAGCTGAAGCGTGTCTGAGTAGGGAGTCCCAACGAATGAAGGCAGGT
8-4	CACCTTATCCTGCTTGTTAGGCTCCCTACTCAGACACGCTTCCGAGTCTGTGGCCGTTTACCA
8-5	GTTGACTGGAGCATCAGGCAATTAGTGACTCGATGGGATAGAGTTCTAAGAGCACTATGGCTA
8-6	AGACCAATGCCTTTCTAGTGTTCTATCCCATCGAGTCACTAAACCTCCATTCAGTACCGAGAT
8-7	
9-1	GGACCTTTATGGAGACACTTG
9-2	CTTTGTCACGCTCTACGGCTACAAGTGTCTCCATAAAGGTCCCTCCATGGTTGTCTAACGGAG
9-3	ATGAGCCAGCGCTATGGGAAAATTGCTGCTCTATGTCATGCCGTACGCAAGCACTTCTTGCCG
9-4	GAATCTACTTACTGCGAATGTGGCATGACATAGAGCAGCAATACCTGCCTTCATTCGTTGGGA
9-5	CCTAACAAGCAGGATAAGGTGCTCAACGACTAGGGCTTCGGTTCACAGCCAAACACAACGGCA
9-6	CTCAACATGGGTACACTCTCAACCGAAGCCCTAGTCGTTGAGTAGCCATAGTGCTCTTAGAAC
9-7	ACACTAGAAAGGCATTGGTCTATGTGAGCAAGGAGATTTCGTCTACAACCTTAGCAATCGCCT
9-8	ACGAAATCTCCTTGCTCACAT
10-1	TAGCCGTAGAGCGTGACAAAGAGAACCGTTCAGCGAACATAGCATGAGATTCGTCATTCCTAC
10-2	GAGTGGTAGGATCTGATGTACCTATGTTCGCTGAACGGTTCTCGGCAAGAAGTGCTTGCGTAC
10-3	ACATTCGCAGTAAGTAGATTCGGGTACGTGTGCATGTGCACGCTACAGACGAGCGATCCAATC
10-4	CCAGCTATTCCCGGGTTGCTACGTGCACATGCACACGTACCCTGCCGTTGTGTTTGGCTGTGA
10-5	TGAGAGTGTACCCATGTTGAGTAGGAGTTATTGTAGCCTACGTCCACTCCTTCAGTCCCTCAT
10-6	CAAAGGTATCAACGTTCTGCGCGTAGGCTACAATAACTCCTAAGGCGATTGCTAAGGTTGTAG
10-7	
11-1	
11-2	GTAGGAATGACGAATCTCATG
11-3	GTACATCAGATCCTACCACTC
11-4	GATTGGATCGCTCGTCTGTAG
11-5	TAGCAACCCGGGAATAGCTGG
11-6	ATGAGGGACTGAAGGAGTGGA
11-7	CGCAGAACGTTGATACCTTTG

Motif 14 (4 hexagon × 6 hexagon)

Name	Sequence
1-1	
1-2	CTCCATATTGATGACCCAACTCTACGGCTT
1-3	GTCCAAATGGTCCTGAACCCAGCGACTTCG
1-4	GTTGATAGTCTGCAACTTGGCGTTGCTTGG
1-5	TGCTGCATTAGAAGCACATAACAGTGGGCT
2-1	TCGCTAGTCCCATCACTCGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCCGTAGA
2-2	GACATTTCCCGGTAAAGCAGGATTGAACAGCAATATGGAGTTTTTTTTTTCGAAGTCGCT
2-3	ATCACGCACCTTGAGGCGAGGATGGCGATTCCATTTGGACTTTTTTTTTTCCAAGCAACG
2-4	GTGGTCGACTCGAAGAGGCACAACTGGCCAGACTATCAACTTTTTTTTTTAGCCCACTGT
2-5	TTGTCTAGCATAATGCAGCA
3-1	
3-2	CTAAGCGATACGACAACACCTAGTGTACGCGGACTAGCGAGTTGGGTCATCTGTTCAATC
3-3	AAGTCTTCCTAAGTGTCTTGGGATGTGGCTGGGAAATGTCGGGTTCAGGAAATCGCCATC
3-4	TACGCGCACTCTCGTCTGACTGGGAATGCTGGTGCGTGATCCAAGTTGCATGGCCAGTTG
3-5	GGACTGTCACTGCACACTGAGATTCTAGAGAGTCGACCACTATGTGCTTCTGCTAGACAA
4-1	GAGGTGACGACGAATGTAGCTTTTTTTTTTTTTTTTTTTTTGCGAGTGATGGCGTACACTA
4-2	GTTCACGTTTACTAGATGCGAACCGCCAGATATCGCTTAGCTGCTTTACCAGCCACATCC
4-3	GCAGTCTACAAGTACATGACGGTCTCACGAAGGAAGACTTCTCGCCTCAAAGCATTCCCA
4-4	TGTCCGCATGAACTCAACAGCCAATCAAAGAGTGCGCGTATGCCTCTTCGCTCTAGAATC
4-5	AAGGTAGGGTGTGACAGTCC
5-1	
5-2	TACGTTCCCTCACTATGGTAGTGGAGCAATTCGTCACCTCGGTGTTGTCGTCTGGCGGTT
5-3	CTATGCACTGGTTGGCAGCTATCCGGAGTCAAACGTGAACCAAGACACTTTCGTGAGACC
5-4	TCCAGTACTAACATCAGGGTAAGAGAGAACTGTAGACTGCGTCAGACGAGCTTTGATTGG
5-5	GGATCCAGGAGTACGTGGATAACGCGGTCACATGCGGACATCAGTGTGCAACCCTACCTT
6-1	CACGAGGTCAAGTGAAGGAATTTTTTTTTTTTTTTTTTTTGCTACATTCGATTGCTCCAC
6-2	TACCGCAATTAGGGAGTTTAGTCGTGGTTAAGGGAACGTACGCATCTAGTGACTCCGGAT
6-3	ATCCATTCTCCTTGTGTGGACGATCAGTATCAGTGCATAGGTCATGTACTGTTCTCTCTT
6-4	GTTGGAAACTGAAAGATGAGGTTAGGTTCTTAGTACTGGACTGTTGAGTTTGACCGCGTT
6-5	GCTATGTATCTCCTGGATCC
7-1	
7-2	CTACAGTAGCTAGGCATTGCATGGAACTACTGACCTCGTGTACCATAGTGTAACCACGAC
7-3	ACGGTTATAGTAGGTAACGTCAAACCCGCTAATTGCGGTAAGCTGCCAACATACTGATCG
7-4	AACGGTGAGCATGTCAGTCGGCATAAGTCCGAGAATGGATACCCTGATGTAGAACCTAAC
7-5	TCCGAAACGACCTATAGCGCCCTGTGAATGAGTTTCCAACATCCACGTACGATACATAGC
8-1	AGCGTCAGGTACCCACAGAATTTTTTTTTTTTTTTTTTTTTCCTTCACTGTAGTTCCAT
8-2	AGTGGCACGTGTTCCTGTTTAACGATAGAGGCTACTGTAGTAAACTCCCTAGCGGGTTTG
8-3	CCATAAAGTCACGGAGATAATGACACCATCCTATAACCGTTCCACACAAGGGACTTATGC
8-4	TCGACAGACAGGTTTATCGAATCCCGCACAGCTCACCGTTCTCATCTTTCCATTCACAGG

8-5	GCTCTCATACTCGTTTCGGA
9-1	
9-2	AGCAGCGTGTCCTATTAGCCAGCCTTCGTGACCTGACGCTGCAATGCCTACTCTATCGTT
9-3	CAAGGGATCAAGAGCGAGCTTTCGAACGAAACGTGCCACTACGTTACCTAGATGGTGTCA
9-4	ATCACATGGTTTCTCGCAAACACTCCAAGGGACTTTATGGCGACTGACATTGTGCGGGAT
9-5	CCTACGTCGATTCCGCGAATATCAGCCGAGTGTCTGTCGAGCGCTATAGGGTATGAGAGC
10-1	ACGCAGATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTGTGGGTCACGAAGGCT
10-2	GACTACTTTGTTTTTTTTTTCTACCCGTTTACACGCTGCTAAACAGGAACTTCGTTCGAA
10-3	GGTACAGAGTTTTTTTTTTTCAATGAAGCTTGATCCCTTGTTATCTCCGTCCTTGGAGTG
10-4	GGTGAAATACTTTTTTTTTTTACGCTTGCCACCATGTGATTCGATAAACCCTCGGCTGAT
10-5	CGTACCGACATCGACGTAGG
11-1	
11-2	ATATCTGCGTGGCTAATAGGAAACGGGTAG
11-3	CAAAGTAGTCAGCTCGCTCTAGCTTCATTG
11-4	ACTCTGTACCTTTGCGAGAAGGCAAGCGTA
11-5	GTATTTCACCATTCGCGGAATGTCGGTACG

Motif 0 (24H×28T)

Name	Sequence
1-1	CAGGGTGGTACTATTTATCGT
1-2	CCTCCGGGCACTCAGCTTACT
1-3	CAACCGATCTCTGGATAATAT
1-4	CCCGTCAAAGCTTATATTTCT
1-5	CTATTTAGAACTCCAGGAAGT
1-6	CCAGGCCCACCTATATGGATT
1-7	CTTAAAGGCTCTGGTTGAAGT
1-8	CAGATCACGACTAACACACCT
1-9	CGCCTCTATCCTGTGAACACT
1-10	CGGCTGAGAACTTAAGTTTCT
1-11	CGGTCTCGCCCTTAGAATGAT
1-12	CGGGCGCCAACTGAAGCCCTT
1-13	CGGGACATCCCTTTAGTCGAT
1-14	CGGAGATGCGCTCAGATGTAT
2-1	TTTTTTTTTTTGGGTGCCCATGTACCACCCTGTTTTTTTTTT
2-2	CGGGCTGGTCTCCGAAGGACTGTGCCCGGAGGACGATAAATA
2-3	CGAAGTTTCCTGCATTATGATGAGATCGGTTGAGTAAGCTGA
2-4	CTTCAAGTGCTCCCTGCAGCTGCTTTGACGGGATATTATCCA
2-5	CGATTTCAGCTAAAGTTGTGTGTTCTAAATAGAGAAATATAA
2-6	CCAATGCGCCTGCACCTGTATGGTGGGCCTGGACTTCCTGGA
2-7	CATCACATCCTCGTTCGTACTGAGCCTTTAAGAATCCATATA
2-8	CACAGTCTGCTACTGCAGATTGTCGTGATCTGACTTCAACCA
2-9	CTTGGATACCTCAGTCTGACTGGATAGAGGCGAGGTGTGTTA
2-10	CAACTCTAGCTCCTCCGCACTGTTCTCAGCCGAGTGTTCACA
2-11	CTCACATAACTTCCCTCTTCTGGGCGAGACCGAGAAACTTAA
2-12	CTTGCGAGGCTAAAGAATGCTGTTGGCGCCCGATCATTCTAA
2-13	CAGCGGACTCTAGTGGGCTATGGGATGTCCCGAAGGGCTTCA
2-14	CATCGTGTGCTTATTCCTCTTGCGCATCTCCGATCGACTAAA
2-15	CCTATTTGTCTTTTTTTTTTTTTTTTTTTTTTATACATCTGA
3-1	CGCCGCGTGTCTATCGTGGTTGACCAGCCCGATGGGCACCCA
3-2	CCATTAGGGCCTAAGCAGCCTGGAAACTTCGAGTCCTTCGGA
3-3	CATATATCGACTCGTCAAGGTGCACTTGAAGATCATAATGCA
3-4	CGAAAGTTGGCTAAACGACATGCTGAAATCGAGCTGCAGGGA
3-5	CATACGGTTTCTAGAAAGATTGGCGCATTGGACACAACTTTA
3-6	CAAGGCTCGGCTTATGCAATTGGATGTGATGATACAGGTGCA
3-7	CAACTTAGCTCTGAAAGTCGTGCAGACTGTGAGTACGAACGA
3-8	CACTTCCCATCTAAACCAGGTGGTATCCAAGAATCTGCAGTA
3-9	CAAGTCCGCGCTCGTCAGATTGCTAGAGTTGAGTCAGACTGA
3-10	CGTGTAGAATCTAGAGCTGATGTTATGTGAGAGTGCGGAGGA

3-11	CAGCTGAGAGCTTTGGTCGGTGCCTCGCAAGAGAAGAGGGAA
3-12	CATCTTAGGGCTGCTGTGTATGAGTCCGCTGAGCATTCTTTA
3-13	CCTTTCTCGACTCTGAAGTGTGCACACGATGATAGCCCACTA
3-14	CGCCCTGTTTCTGAGTCCCTTGACAAATAGGAAGAGGAATAA
4-1	TTTTTTTTTTTGGGAGTGGATGACACGCGGCGTTTTTTTTTT
4-2	CAGGCTCTACTGGGAGGATATGGCCCTAATGGAACCACGATA
4-3	CGCGCTAGACTACATTTATATGTCGATATATGAGGCTGCTTA
4-4	CTACGCTATCTTTACCATTATGCCAACTTTCGACCTTGACGA
4-5	CGGAGTAAACTTGTGCCTTGTGAAACCGTATGATGTCGTTTA
4-6	CAGATAAAGCTACTAGCATTTGCCGAGCCTTGAATCTTTCTA
4-7	CGCCTCCTTCTCAATAATAATGAGCTAAGTTGAATTGCATAA
4-8	CCAACTAGGCTGGACCATCGTGATGGGAAGTGACGACTTTCA
4-9	CTAATGATGCTAATGAACTATGCGCGGACTTGACCTGGTTTA
4-10	CCGCCAGTACTAAATACCTGTGATTCTACACGAATCTGACGA
4-11	CGTGGCGTTCTACCATTGTTTGCTCTCAGCTGATCAGCTCTA
4-12	CACTTTATTCTATGAGTTAATGCCCTAAGATGACCGACCAAA
4-13	CCCGACCGTCTGCCCTCGCTTGTCGAGAAAGGATACACAGCA
4-14	CGGATTTGACTCACAGAGACTGAAACAGGGCGACACTTCAGA
4-15	CATGCTCGCCTTTTTTTTTTTTTTTTTTTTTAAGGGACTCA
5-1	CGGACTTCATCTATGGTTTATGTAGAGCCTGATCCACTCCCA
5-2	CCGTTGATGACTGGGCGGATTGTCTAGCGCGATATCCTCCCA
5-3	CTAATGGGACCTCTGGTCCCTGATAGCGTAGATATAAATGTA
5-4	CCACTTCCTTCTTGGTTGCGTGTTTACTCCGATAATGGTAAA
5-5	CAGTACATAGCTAGGATGCATGCTTTATCTGACAAGGCACAA
5-6	CGAAGGGAGCCTGGCATTTGTGAAGGAGGCGAAATGCTAGTA
5-7	CGCCAAGTAGCTAGTCCGCATGCCTAGTTGGATTATTATTGA
5-8	CTAGCAGCATCTAATCCATTTGCATCATTAGACGATGGTCCA
5-9	CAAGCGCGTACTTACCTGACTGTACTGGCGGATAGTTCATTA
5-10	CCCTGCGCACCTTCGCCACGTGAACGCCACGACAGGTATTTA
5-11	CCCTAACCCTCTTTAGGTACTGAATAAAGTGAAACAATGGTA
5-12	CTGCAAACATCTTACTGACCTGACGGTCGGGATTAACTCATA
5-13	CATGGTACGGCTAACATATCTGTCAAATCCGAAGCGAGGGCA
5-14	CATGCGGCTGCTACCGGGCATGGCGAGCATGAGTCTCTGTGA
6-1	TTTTTTTTTTTGGAGGATTCTGATGAAGTCCGTTTTTTTTTT
6-2	CCCGTGGTCCTCGCCCGAAATGTCATCAACGGATAAACCATA
6-3	CTTTATTGGCTTCTCAGTTATGGTCCCATTAGAATCCGCCCA
6-4	CACTAGAAGCTTAAGGGTAATGAAGGAAGTGGAGGGACCAGA
6-5	CGCGAGAGCCTTCCTGTTATTGCTATGTACTGACGCAACCAA
6-6	CGCGTCCTTCTACGGCGAGATGGCTCCCTTCGATGCATCCTA
6-7	CCAGTTAGTCTCAATGCAGTTGCTACTTGGCGACAAATGCCA
6-8	CCAATACTCCTCGGAGGCAGTGATGCTGCTAGATGCGGACTA
6-9	CCAATCGGCCTGCAGGCTGTTGTACGCGCTTGAAATGGATTA

6-10	CCCTATATTCTCTTGGGCAATGGTGCGCAGGGAGTCAGGTAA
6-11	CGGTGGCCGCTACAACCAATTGAGGGTTAGGGACGTGGCGAA
6-12	CTGTTGCTTCTTTAGTTCTTTGATGTTTGCAGAGTACCTAAA
6-13	CAGCGTTGGCTGAAACTCGCTGCCGTACCATGAGGTCAGTAA
6-14	CGTGGTCAGCTTGCTCTAGTTGCAGCCGCATGAGATATGTTA
6-15	CCCTGACGCCTTTTTTTTTTTTTTTTTTTTTTATGCCCGGTA
7-1	CGATTGGTCTCTGAGACTTATGGACCACGGGAGAATCCTCCA
7-2	CGGGCCGGCTCTATTGACAATGCCAATAAAGATTTCGGGCGA
7-3	CAGAGGATGGCTTTCCGATGTGCTTCTAGTGATAACTGAGAA
7-4	CACCAAAGGGCTCAACAACTTGGCTCTCGCGATTACCCTTAA
7-5	CTTGTTCAGACTCGAATTCCTGAAGGACGCGAATAACAGGAA
7-6	CAGAGCATCCCTACAGATGCTGACTAACTGGATCTCGCCGTA
7-7	CGTACTGGTTCTGACAGGTCTGGAGTATTGGAACTGCATTGA
7-8	CCTCGGACGCCTAACTTCTGTGGCCGATTGGACTGCCTCCGA
7-9	CCACCAAACTCTATAGCCCGTGAATATAGGGAACAGCCTGCA
7-10	CATGAGTGAACTGTTAGGTCTGCGGCCACCGATTGCCCAAGA
7-11	CTAGAGTACACTACCCGCATTGAAGCAACAGAATTGGTTGTA
7-12	CGAGAAGTATCTATGCACCCTGCCAACGCTGAAAGAACTAAA
7-13	CTATTGAGGACTATCCAATCTGCTGACCACGAGCGAGTTTCA
7-14	CCGACTGCTGCTGCGAATAGTGGCGTCAGGGAACTAGAGCAA
8-1	TTTTTTTTTTTTGCTTGGGTTGAGACCAATCGTTTTTTTTTT
8-2	CCGCACAGCCTCATACCCTCTGAGCCGGCCCGATAAGTCTCA
8-3	CTAGGTTCCCTTCCTTATAATGCCATCCTCTGATTGTCAATA
8-4	CTATGGCTACTCACAACCGTTGCCCTTTGGTGACATCGGAAA
8-5	CGTGTTGTCCTATATCACGCTGTCTGAACAAGAAGTTGTTGA
8-6	CGAGCGTCTCTTGTTGTCTTTGGGATGCTCTGAGGAATTCGA
8-7	CTGACGCTCCTCTGGACCTATGAACCAGTACGAGCATCTGTA
8-8	CACATTTAACTAACTTATCCTGGCGTCCGAGGAGACCTGTCA
8-9	CAACATACGCTTCGAGCCAGTGAGTTTGGTGGACAGAAGTTA
8-10	CAATACTTCCTACACCTATCTGTTCACTCATGACGGGCTATA
8-11	CTTCCAGCCCTTAAAGCGGATGTGTACTCTAGAGACCTAACA
8-12	CCCTATCCACTTAGTTCGACTGATACTTCTCGAATGCGGGTA
8-13	CTCCAAGCCCTCACGAAACATGTCCTCAATAGAGGGTGCATA
8-14	CCTACGGATCTGATGCACATTGCAGCAGTCGGAGATTGGATA
8-15	CCAGCAACGCTTTTTTTTTTTTTTTTTTTTTACTATTCGCA
9-1	CCTTACCGGACTTTCCGTAATGGCTGTGCGGAACCCAAGCAA
9-2	CTTACCGCGGCTAGTGCTCATGGGAACCTAGAGAGGGTATGA
9-3	CTTGATCGAACTTGTCATATTGTAGCCATAGATTATAAGGAA
9-4	CTGGTTTGATCTCGTACCAATGGACAACACGAACGGTTGTGA
9-5	CCCGTGTTGACTGCATAGTATGAGACGCTCGAGCGTGATATA
9-6	CCGCTAGATCCTCCTTGTGCTGGAGCGTCAGAAAGACAACAA
9-7	CGCAGGCTAGCTTACGTTAGTGTTAAATGTGATAGGTCCAGA

9-8	CTCCGGTCAACTAGTTAGTATGCGTATGTTGAGGATAAGTTA
9-9	CGGTCTTTAACTGGGATTACTGGAAGTATTGACTGGCTCGAA
9-10	CAGTTCGTCACTGGCTACCTTGGGCTGGAAGAGATAGGTGTA
9-11	CATACTGTCTCTAACTGCAATGTGGATAGGGATCCGCTTTAA
9-12	CTTGGCTTTACTTATCGGCGTGGGCTTGGAGAGTCGAACTAA
9-13	CGTAAGGGCACTATCGTTTATGATCCGTAGGATGTTTCGTGA
9-14	CTCGCTTTAGCTGGAGACCGTGCGTTGCTGGAATGTGCATCA
10-1	TTTTTTTTTTTAGTGCAGAATGTCCGGTAAGGTTTTTTTTTT
10-2	CATACCTCTCTTAGGTCAATTGCCGCGGTAAGATTACGGAAA
10-3	CACACCACACTCAGTAGGTTTGTTCGATCAAGATGAGCACTA
10-4	CCACGCAGTCTGGTCATCACTGATCAAACCAGAATATGACAA
10-5	CAACGCAAGCTTTCTGATTATGTCAACACGGGATTGGTACGA
10-6	CGTAGTGGCCTTACTAGGGTTGGATCTAGCGGATACTATGCA
10-7	CTCGTGGAACTCAGGGCTCGTGCTAGCCTGCGAGCACAAGGA
10-8	CACCGCCCTCTTACGCCCACTGTTGACCGGAGACTAACGTAA
10-9	CGAATTAAACTAGACGAGTATGTTAAAGACCGATACTAACTA
10-10	CATAAGCGACTTTGATCGGCTGTGACGAACTGAGTAATCCCA
10-11	CATGCAACCCTGTAAGCAAATGAGACAGTATGAAGGTAGCCA
10-12	CACTACTGGCTTGTAAGCGCTGTAAAGCCAAGATTGCAGTTA
10-13	CTGTAAGGTCTCGAGATGTGTGTGCCCTTACGACGCCGATAA
10-14	CCGTCTAACCTATAATATTGTGCTAAAGCGAGATAAACGATA
10-15	CGGCAACGTCTTTTTTTTTTTTTTTTTTTTTTACGGTCTCCA
11-1	CCTTTGCTTCCTTGACCAAGTGAGAGGTATGATTCTGCACTA
11-2	CGTGGAGGCGCTCACCCTCCTGTGTGGTGTGAATTGACCTAA
11-3	CTCGCCAACCCTTGTCCAGGTGACTGCGTGGAAACCTACTGA
11-4	CGCTTCTTCACTGCATGCGATGCTTGCGTTGAGTGATGACCA
11-5	CAGATATAGCCTAGCCCTCGTGGCCACTACGATAATCAGAAA
11-6	CATCCGCAGCCTTACACTAATGTTCCACGAGAACCCTAGTAA
11-7	CGATGCAGATCTTCTGCCTTTGAGGGCGGTGACGAGCCCTGA
11-8	CAATAGCCATCTCACTTGATTGTTTAATTCGAGTGGGCGTAA
11-9	CGTCCTTGGACTCAACGTCCTGTCGCTTATGATACTCGTCTA
11-10	CTGCGAAGGCCTACAGGCACTGGGTTGCATGAGCCGATCAAA
11-11	CTTCTTCGAACTGGACATCTTGCCAGTAGTGATTTGCTTACA
11-12	CAGTCGTGTCCTTATGACTATGACCTTACAGAGCGCTTACAA
11-13	CATTACATGGCTAATGCTGATGGTTAGACGGACACATCTCGA
11-14	CCAGCATCCACTGCGGTAACTGACGTTGCCGACAATATTATA
12-1	TTTTTTTTTTTCTGTGCATATGGAAGCAAAGGTTTTTTTTTT
12-2	CTGGCGACGCTCTGACCGTGTGCGCCTCCACGACTTGGTCAA
12-3	CTTGGTCTACTGTTTATAGATGGGTTGGCGAGAGGAGGGTGA
12-4	CGCGCGCCACTCATTAGGAGTGTGAAGAAGCGACCTGGACAA
12-5	CCAGATTTACTTGTACCCAGTGGCTATATCTGATCGCATGCA
12-6	CGGCGCGCTCTGCTAGCTGGTGGCTGCGGATGACGAGGGCTA

12-7	CGCGCTCCGCTCACTCGGAATGATCTGCATCGATTAGTGTAA
12-8	CATCGGTACCTTTGGGCGGGTGATGGCTATTGAAAGGCAGAA
12-9	CAAATTGATCTTATAACTACTGTCCAAGGACGAATCAAGTGA
12-10	CTTCACGGACTCCGGATTCATGGCCTTCGCAGAGGACGTTGA
12-11	CGCGCCTGACTCTGGCTGTATGTTCGAAGAAGAGTGCCTGTA
12-12	CTCAAACCTCTCGTCGAGTGTGGACACGACTGAAGATGTCCA
12-13	CATACATCACTCGAGAATCGTGCCATGTAATGATAGTCATAA
12-14	CCACGGGTGCTGATCGTCCGTGTGGATGCTGGATCAGCATTA
12-15	CCACCTCCTCTTTTTTTTTTTTTTTTTTTTTTAGTTACCGCA
13-1	CCCGAAGTACCTCTGCAGGATGCGTCGCCAGATATGCACAGA
13-2	CGTTACCAGGCTACGATGAGTGTAGACCAAGACACGGTCAGA
13-3	CTGTCCCACTCTCCTTCAAATGTGGCGCGCGATCTATAAACA
13-4	CATTATATTGCTCCTGAGGGTGTAAATCTGGACTCCTAATGA
13-5	CGTGCATGCCCTCCCAAACTTGAGCGCGCCGACTGGGTACAA
13-6	CATTGCACTGCTCTACCCTTTGCGGAGCGCGACCAGCTAGCA
13-7	CTTCATCGACCTGTTTAGGTTGGTACCGATGATTCCGAGTGA
13-8	CTACCGGCGTCTGGACACCATGATCAATTTGACCCGCCCAAA
13-9	CCGCGGTGTGCTGCATTCGCTGTCCGTGAAGAGTAGTTATAA
13-10	CCCGAGGTTCCTGATCTCCATGTCAGGCGCGATGAATCCGGA
13-11	CATGAGCGTGCTACCCGTTATGAGGTTTGAGATACAGCCAGA
13-12	CTCTGGAATACTAAGAATGTTGTGATGTATGACACTCGACGA
13-13	CTATTCGTTGCTCTGTCCTGTGCACCCGTGGACGATTCTCGA
13-14	CCCTCGCAGACTCCCGACAGTGAGGAGGTGGACGGACGATCA
14-1	TTTTTTTTTTTGTTACTTGATGGTACTTCGGGTTTTTTTTTT
14-2	CCGATGCGACTTGATATGTCTGCCTGGTAACGATCCTGCAGA
14-3	CGCTGCCAGCTTCAGGGCCTTGAGTGGGACAGACTCATCGTA
14-4	CAGAAGGGTCTGTGTAACTGTGCAATATAATGATTTGAAGGA
14-5	CGAGCGCCGCTGCGGCTATTTGGGCATGCACGACCCTCAGGA
14-6	CAGGAGGCTCTCCAACCGCTTGCAGTGCAATGAAGTTTGGGA
14-7	CTGGGACGACTGGCACGTCATGGTCGATGAAGAAAGGGTAGA
14-8	CTGCACCAGCTGCGTCGTTGTGACGCCGGTAGAACCTAAACA
14-9	CAAAGGAAACTAACAGTGTCTGCACACCGCGGATGGTGTCCA
14-10	CTCTGCTCTCTTTACTGGTGTGGAACCTCGGGAGCGAATGCA
14-11	CATGTAAGACTACGAATCGCTGCACGCTCATGATGGAGATCA
14-12	CTTTAGGAACTAATCTTTGTTGTATTCCAGAGATAACGGGTA
14-13	CCCAGCGATCTGTTGCATCGTGCAACGAATAGAACATTCTTA
14-14	CACGAACAGCTAACCTTAACTGTCTGCGAGGGACAGGACAGA
14-15	CTATAGTAACTTTTTTTTTTTTTTTTTTTTTACTGTCGGGA
15-1	CTGGGCAAGCCTTATTGCGATGTCGCATCGGATCAAGTAACA
15-2	CGTGCGGTCCCTACGCGCAGTGCTGGCAGCGAGACATATCAA
15-3	CGCGGGCCGCCTTTCAATTATGACCCTTCTGAAGGCCCTGAA
15-4	CTATCTTGTACTGCACCGGTTGCGGCGCTCGACAGTTACACA

15-5	CCAAACCGTCCTCCTACGTTTGAGCCTCCTGAAATAGCCGCA
15-6	CATGTCCCAACTGGAGTCTTTGTCGTCCCAGAAGCGGTTGGA
15-7	CCAGCGCGTTCTGTGTCTTATGCTGGTGCAGATGACGTGCCA
15-8	CTTGACCGCTCTGGAGATTCTGTTTCCTTTGACAACGACGCA
15-9	CTGCGGGCCACTCGCGCCATTGAGAGCAGAGAGACACTGTTA
15-10	CTACCTTAGTCTAAAGTAATTGTCTTACATGACACCAGTAAA
15-11	CTACTTGCTGCTCGTTCCTCTGTTCCTAAAGAGCGATTCGTA
15-12	CAGTATCTGCCTAATTTGCGTGATCGCTGGGAACAAAGATTA
15-13	CGCTTTGGCACTAGTAGCGGTGCTGTTCGTGACGATGCAACA
15-14	CGGTGTTGCACTTAACAGCTTGTTACTATAGAGTTAAGGTTA
16-1	TTTTTTTTTTTGGCCCATCATGGCTTGCCCAGTTTTTTTTTT
16-2	CAAGACATACTATTCTGTATTGGGACCGCACGATCGCAATAA
16-3	CTAGACCACCTCTTTCTTTATGGCGGCCCGCGACTGCGCGTA
16-4	CCCTTGTGGCTAAGGAGGTCTGTACAAGATAGATAATTGAAA
16-5	CACCGAACCCTTCCGCTCGCTGGACGGTTTGGAACCGGTGCA
16-6	CCTGAAGTTCTTGATCCCGATGTTGGGACATGAAACGTAGGA
16-7	CTGAGTGACCTTCCATCCATTGAACGCGCTGGAAAGACTCCA
16-8	CCCTCAGCACTCACTTCTGGTGAGCGGTCAAGATAAGACACA
16-9	CTGGTAGGACTCCATCCGTATGTGGCCCGCAGAGAATCTCCA
16-10	CGTGCCCTGCTAAACCGCGTTGACTAAGGTAGAATGGCGCGA
16-11	CCAACATTACTTCCGCGGGATGCAGCAAGTAGAATTACTTTA
16-12	CGACAAACACTTGCATTACGTGGCAGATACTGAGAGGAACGA
16-13	CGCCCACCGCTAAGTGCGTCTGTGCCAAAGCGACGCAAATTA
16-14	CGGGACGAGCTCAACGCTTGTGTGCAACACCGACCGCTACTA
16-15	CATTGTACTCTTTTTTTTTTTTTTTTTTTTTTAAGCTGTTAA
17-1	CTTTGGGTACCTAGACGGGTTGTATGTCTTGATGATGGGCCA
17-2	CGCATGTCCGCTCCAGAAAGTGGTGGTCTAGAATACAGAATA
17-3	CTAAGGACGTCTCCAATTCATGCCACAAGGGATAAAGAAAGA
17-4	CAAATGCATACTTTGTTTAGTGGGTTCGGTGAGACCTCCTTA
17-5	CACTTAGAGTCTGGGCCCGGTGAACTTCAGGAGCGAGCGGAA
17-6	CTCTCATGTACTATGTTCAGTGGTCACTCAGATCGGGATCAA
17-7	CCAGCTGTCACTGCGCCACCTGTGCTGAGGGAATGGATGGAA
17-8	CATCTGATATCTCGGAACGATGTCCTACCAGACCAGAAGTGA
17-9	CTACTATTGCCTGCTCGAGGTGCAGGGCACGATACGGATGGA
17-10	CTGCAGAAACCTGCTCCTCGTGTAATGTTGGAACGCGGTTTA
17-11	CTTGAGGGATCTGTAAATTATGTGTTTGTCGATCCCGCGGAA
17-12	CAGGAGTCACCTATGCTCATTGCGGTGGGCGACGTAATGCAA
17-13	CAAACTACTACTCGCGTAAATGCTCGTCCCGAGACGCACTTA
17-14	CGAATGGGCTCTAGATGTCATGAGTACAATGACAAGCGTTGA
18-1	TTTTTTTTTTTTCCAGACTATGGTACCCAAAGTTTTTTTTTT
18-2	CGTTCGCTTCTGCTGGGCCGTGCGGACATGCGAACCCGTCTA
18-3	CACCCTTACCTTTCTGCCAATGACGTCCTTAGACTTTCTGGA

18-4	CGCCTCACACTGTCAGAGTTTGTATGCATTTGATGAATTGGA
18-5	CTAACCTGCCTGACCGATCGTGACTCTAAGTGACTAAACAAA
18-6	CGACGATACCTAAGGCGTGGTGTACATGAGAGACCGGGCCCA
18-7	CTTCGCCTGCTTACCATGTCTGTGACAGCTGGACTGAACATA
18-8	CTATACGGCCTGGTGGTAATTGATATCAGATGAGGTGGCGCA
18-9	CACGCACGCCTATGCCTTGGTGGCAATAGTAGATCGTTCCGA
18-10	CGACATGTGCTAGTGTTCGCTGGTTTCTGCAGACCTCGAGCA
18-11	CACTACGTTCTCGCACAAAGTGATCCCTCAAGACGAGGAGCA
18-12	CCACAGCAACTAAGTCCATATGGTGACTCCTGATAATTTACA
18-13	CTTCTGCGCCTTGACTGTCATGTAGTAGTTTGAATGAGCATA
18-14	CGATCACCGCTCGTAAACTATGAGCCCATTCGATTTACGCGA
18-15	CTAACCGCACTTTTTTTTTTTTTTTTTTTTTTATGACATCTA
19-1	CTGAGATGATCTCAAACGAATGAAGCGAACGATAGTCTGGAA
19-2	CCCTTCCCGCCTTAGGCGGCTGGTAAGGGTGACGGCCCAGCA
19-3	CCTGGCTAGTCTATTGTTAATGTGTGAGGCGATTGGCAGAAA
19-4	CTACGTGGAGCTATTAGGGATGGCAGGTTAGAAACTCTGACA
19-5	CTGACATTACCTCACAATCCTGGTATCGTCGACGATCGGTCA
19-6	CTAGGCGTTTCTTATGTCCTTGCAGGCGAAGACCACGCCTTA
19-7	CTTAAGGTGCCTATATAATTTGGCCGTATAGAGACATGGTAA
19-8	CAACACTGGACTAGAACAACTGGCGTGCGTGAATTACCACCA
19-9	CCCTCGTTTACTTCTTAGGCTGCACATGTCGACCAAGGCATA
19-10	CGACAGTCGCCTGTGGTTAGTGAACGTAGTGAGCGAACACTA
19-11	CCGTACATCTCTAAAGCAGATGTTGCTGTGGACTTTGTGCGA
19-12	CGGACCAGGGCTGGGCTCGATGGCGCAGAAGATATGGACTTA
19-13	CTCGGAAGCTCTCCTACATATGCGGTGATCGATGACAGTCAA
19-14	CGCCCGGGAACTTCGGCCTATGTGCGGTTAGATAGTTTACGA
20-1	TTTTTTTTTTTTACCTTGCTTGATCATCTCAGTTTTTTTTTT
20-2	CGCTTAAGTCTTGGCGCTAATGGCGGGAAGGGATTCGTTTGA
20-3	CCCTAGGCCCTAGCTGCATGTGACTAGCCAGGAGCCGCCTAA
20-4	CTAAGCCTTCTGTTAATTCTTGCTCCACGTAGATTAACAATA
20-5	CGGGCTCCACTGTAAGTGCTTGGTAATGTCAGATCCCTAATA
20-6	CTCTGTTATCTGGTAGTAGGTGAAACGCCTAGAGGATTGTGA
20-7	CCCGTGCGACTACAATTAGATGGCACCTTAAGAAGGACATAA
20-8	CACCAACGGCTAGGCACGGCTGTCCAGTGTTGAAATTATATA
20-9	CTGGGCAGTCTACGAACTCTTGTAAACGAGGGAGTTGTTCTA
20-10	CGAGCGATACTCACCCATTGTGGCGACTGTCGAGCCTAAGAA
20-11	CGTTATGCCCTTCAAGATTATGAGATGTACGGACTAACCACA
20-12	CTGAAGGTCCTCCAGAGTGCTGCCCTGGTCCGATCTGCTTTA
20-13	CGGGCTTTGCTGAGCTGTGTTGAGCTTCCGAGATCGAGCCCA
20-14	CGGCTACTTCTGATCTTGGGTGTTCCCGGGCGATATGTAGGA
20-15	CGTCATATCCTTTTTTTTTTTTTTTTTTTTTATAGGCCGAA
21-1	CTTGCTTTGCCTCCTAACGATGACTTAAGCGAAGCAAGGTAA

21-2	CAATACACCGCTGCAAGACCTGGGCCTAGGGATTAGCGCCAA
21-3	CTTGGGACGGCTTTGGAAATTGAAGGCTTAGACATGCAGCTA
21-4	CCAATTAGGACTAATTTAGATGTGGAGCCCGAAGAATTAACA
21-5	CTTTGGCCATCTTATCCAAATGATAACAGAGAAGCACTTACA
21-6	CCCTGGTTATCTCCTATCCTTGTCGCACGGGACCTACTACCA
21-7	CTATTGTCCTCTAAGGGTCCTGCCGTTGGTGATCTAATTGTA
21-8	CTTTGCAATACTACCGGAACTGACTGCCCAGAGCCGTGCCTA
21-9	CCTACAGCGTCTATGGCAAATGTATCGCTCGAAGAGTTCGTA
21-10	CGGATCACCTCTCACAGGCCTGGGCATAACGACAATGGGTGA
21-11	CCTAGCATCTCTCTGGTGTTTGGACCTTCAGATAATCTTGAA
21-12	CATAGCGGAACTTTAACAAGTGCAAAGCCCGAGCACTCTGGA
21-13	CGACCGCCATCTATCTCAGGTGAAGTAGCCGAACACAGCTCA
21-14	CTGTGATGGACTACGGAACATGGATATGACGACCCAAGATCA
22-1	TTTTTTTTTTTGTTGTTTGTTGGCAAAGCAAGTTTTTTTTTT
22-2	CTCTGACGGCTACATTGAGGTGCGGTGTATTGATCGTTAGGA
22-3	CGGAAGTGCCTCCATGATTGTGCCGTCCCAAGAGGTCTTGCA
22-4	CTACCATGGCTGCTCACGAGTGTCCTAATTGGAATTTCCAAA
22-5	CTTAGTCGGCTGCCGATAGTTGATGGCCAAAGATCTAAATTA
22-6	CGCAAGCGCCTGTATCAGGTTGATAACCAGGGATTTGGATAA
22-7	CTGGTGACGCTTCTAATTCGTGAGGACAATAGAAGGATAGGA
22-8	CAGGAGAACCTCTTCAACAATGTATTGCAAAGAGGACCCTTA
22-9	CCCTCTACACTTCGGTGCTATGACGCTGTAGGAGTTCCGGTA
22-10	CGGACTTAACTCGAGCTCCGTGAGGTGATCCGATTTGCCATA
22-11	CCTGGCGATCTCACAAAGCGTGAGATGCTAGGAGGCCTGTGA
22-12	CGTGAGTCGCTAAAGGGCGCTGTTCCGCTATGAAACACCAGA
22-13	CCCTCCCTACTGTATGCCACTGATGGCGGTCGACTTGTTAAA
22-14	CTAGAATTGCTGCCTCTCATTGTCCATCACAGACCTGAGATA
22-15	CGGCTGGGACTTTTTTTTTTTTTTTTTTTTTATGTTCCGTA
23-1	CATGCCTGCCCTTGCTAACTTGCCGTCAGAGAACAAACAACA
23-2	CAAGACTATACTCAGGACGCTGGCACTTCCGACCTCAATGTA
23-3	CACGCGCATCCTCCGTTTATTGCCATGGTAGACAATCATGGA
23-4	CGTAAAGCTGCTATGGTCTATGCCGACTAAGACTCGTGAGCA
23-5	CGTGAATGCACTCGGTAGACTGGCGCTTGCGAACTATCGGCA
23-6	CTCGGTAATACTTTATGCTATGCGTCACCAGAACCTGATACA
23-7	CAAGAGTCTCCTTTAGACAGTGGTTCTCCTGACGAATTAGAA
23-8	CCGGCTGGCCCTGGGCTGCGTGTGTAGAGGGATTGTTGAAGA
23-9	CCTATGGACACTACGCACGTTGTTAAGTCCGATAGCACCGAA
23-10	CAGAGATGAACTTGACTCGTTGATCGCCAGGACGGAGCTCGA
23-11	CACCCTAGCGCTGGGCACTTTGCGACTCACGACGCTTTGTGA
23-12	CCTGCCCGTACTATACATAGTGTAGGGAGGGAGCGCCCTTTA
23-13	CGAAGAGACCCTTGATTTGGTGCAATTCTAGAGTGGCATACA
23-14	CCTTTGCCGGCTTCTATACTTGTCCCAGCCGAATGAGAGGCA

24-1	TTTTTTTTTTTCAGTATGTATGGGCAGGCATGTTTTTTTTTT
24-2	CTGTATCGGCTTTAGTATAATGTATAGTCTTGAAGTTAGCAA
24-3	CATCTGGGTCTACAAGACCCTGGATGCGCGTGAGCGTCCTGA
24-4	CACAGATGTCTATTTGCGAGTGCAGCTTTACGAATAAACGGA
24-5	CAGCGTGGACTCGTAACAATTGTGCATTCACGATAGACCATA
24-6	CCGGCTCGCCTCTGGGTAGCTGTATTACCGAGAGTCTACCGA
24-7	CGCCTAGCTCTAGCAAACTGTGGAGACTCTTGATAGCATAAA
24-8	CCCGGCTATCTAGTGCGACGTGGGCCAGCCGGACTGTCTAAA
24-9	CCAGAATGACTCGACCTCGGTGTGTCCATAGGACGCAGCCCA
24-10	CAAAGACGACTCTATTCCGTTGTTCATCTCTGAACGTGCGTA
24-11	CTGGGCCAACTACGGGCCTCTGCGCTAGGGTGAACGAGTCAA
24-12	CGTGTGTGACTGTTCGGACCTGTACGGGCAGGAAAGTGCCCA
24-13	CACCGTTTCCTAAGTAGTCATGGGTCTCTTCGACTATGTATA
24-14	CCCAGGCTTCTGTAAGAGTATGCCGGCAAAGGACCAAATCAA
24-15	CTTGGAAGACTTTTTTTTTTTTTTTTTTTTTAAGTATAGAA
25-1	GCCGATACAGATACATACTGA
25-2	GACCCAGATGATTATACTAAA
25-3	GACATCTGTGAGGGTCTTGTA
25-4	GTCCACGCTGACTCGCAAATA
25-5	GGCGAGCCGGAATTGTTACGA
25-6	GAGCTAGGCGAGCTACCCAGA
25-7	GATAGCCGGGACAGTTTGCTA
25-8	GTCATTCTGGACGTCGCACTA
25-9	GTCGTCTTTGACCGAGGTCGA
25-10	GTTGGCCCAGAACGGAATAGA
25-11	GTCACACACGAGAGGCCCGTA
25-12	GGAAACGGTGAGGTCCGAACA
25-13	GAAGCCTGGGATGACTACTTA
25-14	GTCTTCCAAGATACTCTTACA

Motif 1 (24H×29T)

Name	Sequence
1-1	GCCGGTGTCATAGGACCAGAG
1-2	GCCTCAACGGCTTTAGCACGT
1-3	AACAGAGAGGTACTCCAAAGA
1-4	ACTTAGTTACCGGCTCGTTGA
1-5	GTGTAAAGCTGGCGGTGACGC
1-6	GGTTACAGATACCTTGACGTG
1-7	GCACGAGTCGAACTTTATTAT
1-8	GGGTTGCCCGAGCTCCATAGT
1-9	AAACACGAAGTTAAACGGGCA
1-10	TGCGCGCTTATCGATGCAGCC
1-11	CGCTACCCTCACAATAATATT
1-12	CATGTAGACGTTCCCACCATG
1-13	CCCGTATCCTACGGGCAGTTC
1-14	ATCTTATGATCCAGGATTTAT
1-15	TCTTTACAACGTTTTTTTTT
2-1	TTTTTTTTTTGCCATTGAGCTATGACACCGGCTTTTTTTT
2-2	GAGACGGCGTCGTCGGCGAACAGCCGTTGAGGCCTCTGGTCC
2-3	CTGGGCGGATGTTACAGTGCGTACCTCTCTGTTACGTGCTAA
2-4	TCCGATTGCTAGACGCATTGTCGGTAACTAAGTTCTTTGGAG
2-5	CAACATCTGCAGCAGCTGTAGCCAGCTTTACACTCAACGAGC
2-6	ATCTGCCGCGGTAGTTGCTGCGTATCTGTAACCGCGTCACCG
2-7	ATTTATGTGACGTTGAAAGGCTTCGACTCGTGCCACGTCAAG
2-8	CATGTATACGAAGTCAGAGGTCTCGGGCAACCCATAATAAAG
2-9	TGGAGCTTTGCCGCCCGTCCTAACTTCGTGTTTACTATGGAG
2-10	GAATCTGGGATTGAACACCTCGATAAGCGCGCATGCCCGTTT
2-11	TAGTCAGGCGTTATTCACAAAGTGAGGGTAGCGGGCTGCATC
2-12	CCGAATAAGGTCGCCCGTAATAACGTCTACATGAATATTATT
2-13	ACGAAATGGCGAATTGCCTTTGTAGGATACGGGCATGGTGGG
2-14	CAGGATAATGTGTGTCCTTCAGGATCATAAGATGAACTGCCC
2-15	TTAATAGGACGCAACGGATCAACGTTGTAAAGAATAAATCCT
3-1	CACGGAACGGCATCGAACGTGGACGCCGTCTCGCTCAATGGC
3-2	TCGTCCTAGGCCCTGGACTTCCATCCGCCCAGGTTCGCCGAC
3-3	TTCCGGATCGACCCTCGCCATTAGCAATCGGACGCACTGTAA
3-4	TTACCTAGAAATACCCGATGATGCAGATGTTGACAATGCGTC
3-5	GAAGCTGGCAAGGTTGCTATACCGCGGCAGATCTACAGCTGC
3-6	CGGGAAGATGGAGACAGTCGTGTCACATAAATGCAGCAACTA
3-7	CTTCTCCAAGAGGGTTAGCGTTCGTATACATGGCCTTTCAAC
3-8	CAGTTTAACCGGCTTTACTGCGCAAAGCTCCAACCTCTGACT
3-9	AACAGCGCCACCGAGACAAGTATCCCAGATTCAGGACGGGCG

3-10	AGGCTAACAAGTCAATAGATAACGCCTGACTAGAGGTGTTCA
3-11	ATAGCCTGTTTCAGGGTCCCTACCTTATTCGGTTTGTGAATA
3-12	AACAATGGCTCTTTAAAGTTGCGCCATTTCGTATTACGGGCG
3-13	ACGTTCTCCCGTCCCTCCATTACATTATCCTGAAAGGCAATT
3-14	AAATCATATGGTGGAGCTGACCGTCCTATTAATGAAGGACAC
3-15	CAAACAAGTATCTTTTTTTTTTTTTTTTTTTTTTGATCCGTTG
4-1	TTTTTTTTTTTGGTTTCGAGATGCCGTTCCGTGTTTTTTTTT
4-2	GATTAGAGCATAATCTCTTTCGGCCTAGGACGACACGTTCGA
4-3	GCTGAGGTGTGCCGAGAAACAGTCGATCCGGAAGAAGTCCAG
4-4	TCTAGGAAACCCGGATATGTGATTTCTAGGTAAATGGCGAGG
4-5	CGGCAGTTTAAGACCTGCTCTCTTGCCAGCTTCTCATCGGGT
4-6	GAACAAATATCTACACCCTATTCCATCTTCCCGTATAGCAAC
4-7	ACCACCAGGGCTTGAACTTTCCTCTTGGAGAAGACGACTGTC
4-8	AGGGTGAGGAACAGTCACATTCCGGTTAAACTGACGCTAACC
4-9	TGCCACCCGTTTCCCTTCATCGGTGGCGCTGTTGCAGTAAAG
4-10	AGAGCATGCGCCTGAACGTTAACTTGTTAGCCTACTTGTCTC
4-11	GCAGACGGTAAGGAGGATGTGGAAACAGGCTATTATCTATTG
4-12	CGCATTTATGCCGTTATAACAAGAGCCATTGTTAGGGACCCT
4-13	CAAACGTTGAATAGGGCGACTACGGGAGAACGTCAACTTTAA
4-14	CGAGCACGCCCTCGGTTATGGACCATATGATTTAATGGAGGG
4-15	GCTATACGGGTTATTTGATGAGATACTTGTTTGGTCAGCTCC
5-1	GGTCGGATCACTCCCGCCAACATGCTCTAATCTCTCGAAACC
5-2	GAACTCGTCTCCGCTCAGGGTCACACCTCAGCGAAAGAGATT
5-3	CTAATAATAAGCGTGCCTAGCGGTTTCCTAGATGTTTCTCGG
5-4	TGAGCAAAGCAGACACAAAGGTTAAACTGCCGCACATATCCG
5-5	ACCATCACCCTACGATTCTCAGATATTTGTTCAGAGCAGGTC
5-6	TAGCAAACTCAGAGGATTCTTGCCCTGGTGGTATAGGGTGTA
5-7	ATCTCAAACCAACCCTCGGGATTCCTCACCCTGAAAGTTCAA
5-8	GGTCCCTTGTCGTTCTCCCTGAACGGGTGGCAAATGTGACTG
5-9	GTATACTTTATTGAGGCCCAGGCGCATGCTCTGATGAAGGGA
5-10	AATTTCCTATACGTTGGGTCATTACCGTCTGCTAACGTTCAG
5-11	TAAACCCAGGCCCGGCCAGCTGCATAAATGCGCACATCCTCC
5-12	GACAACTTACTGTAAACAAGGTTCAACGTTTGTGTTATAACG
5-13	GACCTGTGAACCAATGATAGTGGGCGTGCTCGAGTCGCCCTA
5-14	ATGGGCCAAGCATGTATACAAACCCGTATAGCCCATAACCGA
5-15	CCTAAGTCCGAGTTTTTTTTTTTTTTTTTTTTTCATCAAATA
6-1	TTTTTTTTTTTCTAGCTCACCAGTGATCCGACCTTTTTTTTT
6-2	ACTTCACTATTTAAGGTGTTGGGAGACGAGTTCGTTGGCGGG
6-3	ATTTAGACTAGTCGCCTGGATGCTTATTATTAGACCCTGAGC
6-4	CAGAAAGTGAGGGCCTCAGGTCTGCTTTGCTCAGCTAGGCAC
6-5	GGTCAGGTCAACGGTCATCTCTAGGGTGATGGTCCTTTGTGT
6-6	AAAGCTCGGATTAGCGCCCGGCTGAGTTTGCTATGAGAATCG

6-7	AATTCCAGCGGGCTAATCATATTGGTTTGAGATAAGAATCCT
6-8	CTCTTTCAGCTGAGTGGTGTCCGACAAGGGACCTCCCGAGGG
6-9	GCCATGCATCGCTCCACAACAAATAAAGTATACCAGGGAGAA
6-10	GCTACCCTTTATCTGTGAGCCGTATAGGAAATTCTGGGCCTC
6-11	AAGGCATTTAAGGAGGAGTTAGGCCTGGGTTTATGACCCAAC
6-12	AACTTATGGGCGTAATTGGCCCAGTAAGTTGTCAGCTGGCCG
6-13	ACTCCTCAGATCTTACTGCACGGTTCACAGGTCCCTTGTTTA
6-14	TCGTGACCGACCGGAGGCTCCTGCTTGGCCCATACTATCATT
6-15	ATATCGGCCACCTAGCGCATACTCGGACTTAGGTTGTATACA
7-1	TTGCACGACCGTATCGTCTCTAATAGTGAAGTGGTGAGCTAG
7-2	ACTTACAACGCCTGAAATAAGCTAGTCTAAATCAACACCTTA
7-3	AATAATTACCTCACATACGCTCTCACTTTCTGATCCAGGCGA
7-4	CTGGTCATCTCAGAATGAGAATTGACCTGACCACCTGAGGCC
7-5	TAGCGTGAATGGATGAGACGCATCCGAGCTTTGAGATGACCG
7-6	GTCACTCAAGTCATTGGAAGCCCGCTGGAATTCCGGGCGCTA
7-7	TGTATTGTGATCTAACCCGACAGCTGAAAGAGTATGATTAGC
7-8	ACACCTGCTTGGTCTGGGCTGCGATGCATGGCGACACCACTC
7-9	ACGTACCGTCATCAATCAACGTAAAGGGTAGCTGTTGTGGAG
7-10	AGGGACCTCTCAACGCGACGATTAAATGCCTTGGCTCACAGA
7-11	GCGCGCTGTTGGGATGCCATTGCCCATAAGTTTAACTCCTCC
7-12	CGTCCGGACCTCATCTGACCGATCTGAGGAGTGGCCAATTAC
7-13	TCGGCTCAAGCATAGCGGACCGTCGGTCACGAGTGCAGTAAG
7-14	AATGGCCTTCGCAGAATTCACGTGGCCGATATGGAGCCTCCG
7-15	TCGTCGTTTCCGTTTTTTTTTTTTTTTTTTTTTATGCGCTAG
8-1	TTTTTTTTTTTGGACATTCCTACGGTCGTGCAATTTTTTTTT
8-2	TGCGAAGGCCGAAGCTGGCAGGGCGTTGTAAGTAGAGACGAT
8-3	TGCAGGCGGGCCAAAGGATAAGAGGTAATTATTCTTATTTCA
8-4	GCTTCCGTTGCTGATGCCATTTGAGATGACCAGAGCGTATGT
8-5	CAGGCGAAATCAGCGTTGGCTCCATTCACGCTATTCTCATTC
8-6	AGCGCTGGAGGGCTCAATGTTGACTTGAGTGACGCGTCTCAT
8-7	AATGGTGTGCCGAAGTCGTGCGATCACAATACAGCTTCCAAT
8-8	CAGCCTCTTCGCTCGGATACACCAAGCAGGTGTGTCGGGTTA
8-9	AGCGTCGCTTCCAGTGATAGCATGACGGTACGTCAGCCCAGA
8-10	AATCAGGTGGGAAAGTACTGCTGAGAGGTCCCTCGTTGATTG
8-11	TACAGATTAGTTTCGGCAGGACCAACAGCGCGCTCGTCGCGT
8-12	GGGCGCTTCGCCGTGCCCATTGAGGTCCGGACGAATGGCATC
8-13	CCAGTCGAGGAAAGTATCGAATGCTTGAGCCGACGGTCAGAT
8-14	AGTGGGAGTCTTACAGAGCCCGCGAAGGCCATTGGTCCGCTA
8-15	GCCCGGAAACGCATAGCTATTCGGAAACGACGAGTGAATTCT
9-1	AATCTCCCACGCATTGGACCTCGGCCTTCGCAAGGAATGTCC
9-2	TCAGTGTATACCGACTGTAAAGCCCGCCTGCACTGCCAGCTT
9-3	GCCTTCGCACAGTGGTCTGACGCAACGGAAGCTTATCCTTTG

9-4	GTCTAGGTATCCCTGCTGGGAGATTTCGCCTGAATGGCATCA
9-5	GCCGGAATTTGCTAGCATTTACCTCCAGCGCTAGCCAACGCT
9-6	ATTACCTTTATTATATTACGCGGCACACCATTAACATTGAGC
9-7	GACATATTCCCGTGGCTGGACCGAAGAGGCTGGCACGACTTC
9-8	TGTTATAGGTACACTGGAACTGAAGCGACGCTTGTATCCGAG
9-9	TTCCCACTGGTCCGGTCATCTCCCACCTGATTGCTATCACTG
9-10	CCAGTTAAAGGACCACCTGAGACTAATCTGTAGCAGTACTTT
9-11	CGGGTATTCCTGCCAATCCCTGCGAAGCGCCCTCCTGCCGAA
9-12	CTATTAACCACTTGTGCGCGCTCCTCGACTGGAATGGGCACG
9-13	TATCTTGCTACCAAGCAATCGAGACTCCCACTTTCGATACTT
9-14	TGACGACGAGGGTGAGCGGATCGTTTCCGGGCGGGCTCTGTA
9-15	TCCGTAATTCGTTTTTTTTTTTTTTTTTTTTTAATAGCTATG
10-1	TTTTTTTTTTTCTGTCTCGTAGCGTGGGAGATTTTTTTTTTT
10-2	TAGTAAACTCCAAGGCTACCCGGTATACACTGAAGGTCCAAT
10-3	TGTAAGTCGATTAAACCACTGCTGTGCGAAGGCTTTACAGTC
10-4	CAGAAATATTGAACTGTGATTGGATACCTAGACGTCAGACCA
10-5	TGAGAGCTCTGATGAATTCGCGCAAATTCCGGCTCCCAGCAG
10-6	TTTCCTAGTTGAATATCCACGAATAAAGGTAATTAAATGCTA
10-7	CTGGGCGGAATCCCTTCAGTCCGGGAATATGTCGCGTAATAT
10-8	CTGTGCGATGGCGTAGGAGGAGTACCTATAACAGTCCAGCCA
10-9	ATCGCATTGAAACTGGACGAGGACCAGTGGGAAAGTTCCAGT
10-10	CAGAGTGCCGTCAGGTGAGGTTCCTTTAACTGGAGATGACCG
10-11	ACGCCTACTCTTGTACCTGGGCAGGAATACCCGCTCAGGTGG
10-12	TCAGAATACCAAGGATTCAGTAGTGGTTAATAGAGGGATTGG
10-13	ATGGGCTGTATTGGCCCATTCGGTAGCAAGATAGCGCGCACA
10-14	GTATGAGACAATATGAGAGATCCCTCGTCGTCACGATTGCTT
10-15	CGACCGCTGCAGGCGCACATCACGAATTACGGAATCCGCTCA
11-1	CGTCCTGTGAAATTGGACAGTGGAGTTTACTATACGAGACAG
11-2	CGGCTACGGCTGTGCCTGTCGATCGACTTACAGGGTAGCCTT
11-3	GATTATCTCGGATACCACGCTCAATATTTCTGCAGTGGTTTA
11-4	CTGTAGGTATACATTAAATAACAGAGCTCTCAAATCACAGTT
11-5	CTAGAGGTCTCCGAGGGCTTGCAACTAGGAAAGCGAATTCAT
11-6	CCGATTACAGTTTGACTCGTTATTCCGCCCAGCGTGGATATT
11-7	ACATCGTTGCATGTTCCTGGACCATCGCACAGGACTGAAGGG
11-8	GCTACGGAACATCCAGTCTCCTTCAATGCGATTCCTCCTACG
11-9	ACAGACGAGCTATCGATCTGAACGGCACTCTGCTCGTCCAGT
11-10	AGCGGACGGAGGCTTTACGCAAGAGTAGGCGTACCTCACCTG
11-11	GTTGACACGACCCTCTGTTTGTGGTATTCTGACCCAGGTACA
11-12	CCGCGATTATACGGTTACAAGATACAGCCCATACTGAATCCT
11-13	CGCGGTCTCGAGTGTTAACCATTGTCTCATACGAATGGGCCA
11-14	ACCGATGCTAAATCAATGGTTTGCAGCGGTCGATCTCTCATA
11-15	TCGGACCGCAACTTTTTTTTTTTTTTTTTTTTGATGTGCGCC

12-1	TTTTTTTTTTTCCACAACCAGTTTCACAGGACGTTTTTTTTT
12-2	ACGTGTTACCCAAGGAGAGTCCAGCCGTAGCCGACTGTCCAA
12-3	AGTGCACGAGGAGGGCGTCTCTCCGAGATAATCCGACAGGCA
12-4	ATAGCATGTGCGGCAGGAATTGTATACCTACAGAGCGTGGTA
12-5	CCTAGTGCATCAGCGCACGACGGAGACCTCTAGTTATTTAAT
12-6	GAGATCTAGAGAGGGTTTACGAACTGTAATCGGCAAGCCCTC
12-7	CTCATATCTTTAGTTAGTGGTATGCAACGATGTAACGAGTCA
12-8	AGAAATGAGCCGTGACCCAACATGTTCCGTAGCTCCAGGAAC
12-9	CAACCGAGGGCGCAATCGCGGTAGCTCGTCTGTGGAGACTGG
12-10	TGAAGTTTACGCCTAGTATCGCCTCCGTCCGCTTCAGATCGA
12-11	GATCGGTGCGTGCTCAATTACGGTCGTGTCAACTGCGTAAAG
12-12	GATTACGACAGACAGTATTTCGTATAATCGCGGCAAACAGAG
12-13	GATACTGACTTCGAAGATGTGCTCGAGACCGCGCTTGTAACC
12-14	TTGAGAGCAGCACGCACCTCATTTAGCATCGGTTGGTTAACA
12-15	ATGTATCGTATAAGACAGAATGTTGCGGTCCGAAACCATTGA
13-1	CATGACACTTAAACATCTAATGGGTAACACGTCTGGTTGTGG
13-2	TCCGAAAGGTCGGTGGCCTCTCCTCGTGCACTGACTCTCCTT
13-3	TTCAATATGGGCTGGGACGCCGCACATGCTATGAGACGCCCT
13-4	CTGGACATGTGGGCATCAAGAGATGCACTAGGAATTCCTGCC
13-5	TCATCCTACATCCCTAAAGGTCTCTAGATCTCGTCGTGCGCT
13-6	GGGTCGGTTCAACGAAAGACTAAAGATATGAGCGTAAACCCT
13-7	CAGGGCGTAGCAAATATTTACGGCTCATTTCTACCACTAACT
13-8	TCTAATGTTATTACCTTGCGAGCCCTCGGTTGGTTGGGTCAC
13-9	ATCAAGCCGCCTGTGATTATCCGTAAACTTCACCGCGATTGC
13-10	GCTGCAGAGCCCTCTTGCACAACGCACCGATCCGATACTAGG
13-11	AATTGGTTATCTAAGGACTGGCTGTCGTAATCGTAATTGAGC
13-12	GAAAGGATTATAGAGGACTATAAGTCAGTATCGAAATACTGT
13-13	GAAAGCAGAATGATTTACTAAGCTGCTCTCAACACATCTTCG
13-14	GCATGCGTGATACTAACTACAATACGATACATTGAGGTGCGT
13-15	AACTATCGATGGTTTTTTTTTTTTTTTTTTTTATTCTGTCTT
14-1	TTTTTTTTTTTGCGCTAAGCATTAAGTGTCATGTTTTTTTTT
14-2	ACGATTTAGGCCACTACTAATCGACCTTTCGGAATTAGATGT
14-3	CACGGGCTCGAATCGTTAACTGCCCATATTGAAAGAGGCCAC
14-4	AAACAGGAGAACCCTGAGTCGCCACATGTCCAGGGCGTCCCA
14-5	CTCATCCCGGGCGTTTGGACCGATGTAGGATGATCTTGATGC
14-6	GAGCTTGCGAGGTCCCAATGGTTGAACCGACCCACCTTTAGG
14-7	GAAATTCCGATAGCCGTGCGATGCTACGCCCTGAGTCTTTCG
14-8	GACTCATGGTCTGTCGTGCCAAATAACATTAGAGTAAATATT
14-9	GCGAGATACACGGTTCAGGATAGGCGGCTTGATTCGCAAGGT
14-10	CTTAGAACTATCGGAGCGCTCGGGCTCTGCAGCGATAATCAC
14-11	GGACGATCCTTGTGTCTCCCAAGATAACCAATTTGTGCAAGA
14-12	CTTAGTGGGCAAATAAACGTGTATAATCCTTTCCCAGTCCTT

14-13	GGTAAGTGACGTGTTTAGAATCATTCTGCTTTCATAGTCCTC
14-14	TAGTATAACCGTCACAGAGGTTATCACGCATGCTTAGTAAAT
14-15	TTGCAAACTCAGAATGGCACTCCATCGATAGTTTGTAGTTAG
15-1	ACGCATATTGCCGGCACCTAAGCCTAAATCGTTGCTTAGCGC
15-2	GCAGCGGTCCTGCCAGAACCGTCGAGCCCGTGATTAGTAGTG
15-3	GGACATTATATGCTGCCATGGTTCTCCTGTTTAGTTAACGAT
15-4	CACGTGACTCAGTCCTATTATCCCGGGATGAGCGACTCAGGG
15-5	TACACTAATCTTCGAGGCTGCCTCGCAAGCTCGGTCCAAACG
15-6	TTGAGGTTGGAGGACATATCCATCGGAATTTCCCATTGGGAC
15-7	GAGCTCGGACGCGTCCGCGTGGACCATGAGTCTCGCACGGCT
15-8	GCTTAGTCGCCGAGAAAGATAGTGTATCTCGCTGGCACGACA
15-9	ACGGTAGACTCTCGTGCTTGGATAGTTCTAAGATCCTGAACC
15-10	TCGCCCTACTGTTTACAGTTGAAGGATCGTCCGAGCGCTCCG
15-11	CTTTCGTAACAGTCCTCGTTCTGCCCACTAAGTGGGAGACAC
15-12	TGGAAACGGTGTGGCGCCCATCGTCACTTACCCACGTTTATT
15-13	TATGCGAGTTTAATGGGCTCTCGGTTATACTAATTCTAAACA
15-14	AGGACACACAGCTTTCCCTGCTGAGTTTGCAAACCTCTGTGA
15-15	CAGTCCAAGGCGTTTTTTTTTTTTTTTTTTTTAGTGCCATTC
16-1	TTTTTTTTTTCTTCATTCTCGGCAATATGCGTTTTTTTTTT
16-2	GACGGGCGGGACTGTTGGAGTCAGGACCGCTGCTTAGGTGCC
16-3	GTAAGATCGTTTACCCTAGTTCATATAATGTCCCGGTTCTGG
16-4	CCCATAGTTTGAGGGTTCCCACTGAGTCACGTGCCATGGCAG
16-5	AGATGCGCTCATAACATCTCAAAGATTAGTGTAATAATAGGA
16-6	TACGGTCGCAGATTAATTCTACTCCAACCTCAAGCAGCCTCG
16-7	GACTCTGAACCCTACCTAAGTGCGTCCGAGCTCGGATATGTC
16-8	ACGTGACATAAGCATCAACCTCGGCGACTAAGCCACGCGGAC
16-9	TCTTTAGCATGCATCGTGTAGAGAGTCTACCGTTATCTTTCT
16-10	GGCGTTATCATTAGATTTACCACAGTAGGGCGACCAAGCACG
16-11	CTGTCGGGCGAACGACTTAGGCTGTTACGAAAGCAACTGTAA
16-12	TTTCTTTATGCCGCGTATTTCACACCGTTTCCAGAACGAGGA
16-13	GACTTTGGCTTCCTTGACGCTTAAACTCGCATAATGGGCGCC
16-14	GCAGATCCAATCGTTATTCCAGCTGTGTGTCCTAGAGCCCAT
16-15	CACCCTTAGACGAGAGTTGTACGCCTTGGACTGGCAGGGAAA
17-1	CTTAGTATAGGCCTTCTCGCTTCCCGCCCGTCGAGAATGAAG
17-2	CTTAGGTTGCGAGGTGTTCCTAACGATCTTACACTCCAACAG
17-3	TCTCTTATGAGTGCAGTCCTGCAAACTATGGGAACTAGGGTA
17-4	TCTTCTAAATGCGACCGGTACTGAGCGCATCTTGGGAACCCT
17-5	CCTTAAGCTGGGCCAAGGTATCTGCGACCGTATGAGATGTTA
17-6	AAATGATGCTCTATACAAAGCGGTTCAGAGTCTAGAATTAAT
17-7	CGTCGCCTTGAGGGTCCTGCCTTATGTCACGTACTTAGGTAG
17-8	AACAATATTGGCGACTGTCGTCATGCTAAAGAAGGTTGATGC
17-9	TTACCGAGGTAGACTTTCACTATGATAACGCCCTACACGATG

17-10	TTAATCATGTTGGTACTACGTTCGCCCGACAGGGTAAATCTA
17-11	TACGTGGAGGTGCGTAAGGCAGCATAAAGAAACCTAAGTCGT
17-12	GTCGCGCATCGTTAAGCCCGTAAGCCAAAGTCGAAATACGCG
17-13	CCATGCATCGGCTGTAGTCCAATTGGATCTGCAGCGTCAAGG
17-14	GGGCCTATTCATGGTCCTACTGTCTAAGGGTGTGGAATAACG
17-15	GTATTATCGATATTTTTTTTTTTTTTTTTTTTTACAACTCTC
18-1	TTTTTTTTTTTCATACTCCCGGCCTATACTAAGTTTTTTTTT
18-2	GCTTCCATATTGTATACTGTATCGCAACCTAAGAGCGAGAAG
18-3	GCAGAGTAGTAGACCATCGAAACTCATAAGAGAAGGAACACC
18-4	GCTACTTTCACCCTTTAGCGAGCATTTAGAAGACAGGACTGC
18-5	AAGCGCAAAGAACGGCCCATGCCCAGCTTAAGGGTACCGGTC
18-6	CGTCTCATGTCGCCCTCGCTAAGAGCATCATTTATACCTTGG
18-7	CTCTATCCACCCTTCGTAGGACTCAAGGCGACGGCTTTGTAT
18-8	TTTAGTTGAACTCGAGTGAAGGCCAATATTGTTGGCAGGACC
18-9	AGCCAGGATCAACCAACTCTGCTACCTCGGTAAACGACAGTC
18-10	CAAGGAAAGCATTTCCCTGCTCAACATGATTAAAGTGAAAGT
18-11	GGCTAAGCGTTGCGAACTCCGCACCTCCACGTAACGTAGTAC
18-12	ATGACTGTTTCACACTGGAGCACGATGCGCGACTGCCTTACG
18-13	TTCCAAATCCACAAGTGAAGGGCCGATGCATGGACGGGCTTA
18-14	AACCTACGGTCTGTACCCTATATGAATAGGCCCTGGACTACA
18-15	TTGCTCAATTTACACGCAGATTATCGATAATACAGTAGGACC
19-1	GGACTCGGTAGCGTTTAATTGAATATGGAAGCCGGGAGTATG
19-2	AGCTTTATCGACTCGAGTCTCTACTACTCTGCTACAGTATAC
19-3	ACAGATCGACGTTTAGGGTATGTGAAAGTAGCTTCGATGGTC
19-4	ATTAGCGATTGAGAAGCTGTTTCTTTGCGCTTTCGCTAAAGG
19-5	GTCTAAGCCGATAGTAGATAGGACATGAGACGCATGGGCCGT
19-6	GGCTGTAAAGAACAAATTGTTGGTGGATAGAGTAGCGAGGGC
19-7	GACATGCGCCAGGTGGTAGGAGTTCAACTAAATCCTACGAAG
19-8	ATTGAAGTGCGTCCCTGCGTGTGATCCTGGCTCTTCACTCGA
19-9	AAAGCGACCTAATTCTAATAGTGCTTTCCTTGCAGAGTTGGT
19-10	CGGACACCAGATGCTGATCTCAACGCTTAGCCAGCAGGGAAA
19-11	GCGCTATCTGCTCAGTATCTAGAAACAGTCATCGGAGTTCGC
19-12	GGCCGCGTTCGACTAGACCCGTGGATTTGGAAGCTCCAGTGT
19-13	CTAAGGACGTACTATACCCTCGACCGTAGGTTCCTTCACTTG
19-14	CTGGAAGTTCCGCTATCCCGCAAATTGAGCAAATAGGGTACA
19-15	CTGTATCATATCTTTTTTTTTTTTTTTTTTTTATCTGCGTGT
20-1	TTTTTTTTTTTAATGCCCATCGCTACCGAGTCCTTTTTTTTT
20-2	AGCAATACTTTCTGTGGGAGGGTCGATAAAGCTCAATTAAAC
20-3	AGAGCTGAGTGTTTACACGGCACGTCGATCTGTGAGACTCGA
20-4	TGCCAAGAGTCCATACCGTGCTCAATCGCTAATATACCCTAA
20-5	CATAACCAACAATTTAGTTGTATCGGCTTAGACAACAGCTTC
20-6	GAATTATTCAATGCAACGAGCTTCTTTACAGCCCTATCTACT

20-7	ACGCGCGGGCCTGTCGGAGCCCTGGCGCATGTCAACAATTTG
20-8	TCTAGTGCATACAAATTCGGTACGCACTTCAATTCCTACCAC
20-9	TAATTGCATTGCAGTAGGCTCTTAGGTCGCTTTCACGCAGGG
20-10	GTTTCTGTTCCGTACCGATGGATCTGGTGTCCGCTATTAGAA
20-11	GACGCGGGCGTACAAATTCGCAGCAGATAGCGCGAGATCAGC
20-12	GTAGGAAACTAACGCTCTTGATCGAACGCGGCCTAGATACTG
20-13	TTTAAGAAGCTGAGCGTAGCTGTACGTCCTTAGCGGGTCTAG
20-14	CAATTATAGTAATGGTAACCACGGAACTTCCAGGAGGGTATA
20-15	CTTTCAGTGATAGATGAAAGAGATATGATACAGGCGGGATAG
21-1	CTGCTTATCCAGACCATTTCCAAAGTATTGCTGATGGGCATT
21-2	ACAGTCCCGTCTACGGGCCAGCACTCAGCTCTCCTCCCACAG
21-3	GCGTGGTACGTAGCCGGAGCAGACTCTTGGCAGCCGTGTAAA
21-4	TGTATTTCTACAACTTGTACGTGTTGGTTATGGCACGGTATG
21-5	CATGCATGTCTAACGTCGCGATTGAATAATTCACAACTAAAT
21-6	GGTCTTCTACTGTAGGAGGACGGCCCGCGCGTGCTCGTTGCA
21-7	GCATCTTTCAGCGCTCAATCATATGCACTAGAGGCTCCGACA
21-8	CCCTGAAACTCTACAGAGGGCCAATGCAATTAACCGAATTTG
21-9	CATCTAGAAAGGGCGTTGGGTGGAACAGAAACGAGCCTACTG
21-10	ATCTTTGATCTGCGGGACATAACGCCCGCGTCCCATCGGTAC
21-11	TGGTAGTTCCTTCTTTCGGCGTAGTTTCCTACGCGAATTTGT
21-12	GAACGAAGGTTTACTGTGACTAGCTTCTTAAATCAAGAGCGT
21-13	TGGGACAAGACATATACACCTTACTATAATTGAGCTACGCTC
21-14	GTTGCGACCACGCAAGATAGCATCACTGAAAGTGGTTACCAT
21-15	CTTTAAGCCGGATTTTTTTTTTTTTTTTTTTTCTTTCATCT
22-1	TTTTTTTTTTTGCGGGCGAAACTGGATAAGCAGTTTTTTTTT
22-2	GTACCAGCTGGTGCTTGATAGAGACGGGACTGTGGAAATGGT
22-3	TAGAGGGCTATTGGAGGGAGTTACGTACCACGCCTGGCCCGT
22-4	TGGATGTTTAGGGCGGACAGTTGTAGAAATACATGCTCCGGC
22-5	TCTGTATTGGACCCTATGAAATAGACATGCATGCGTACAAGT
22-6	GGCCCTTTAATAAACCTAGGCCAGTAGAAGACCTCGCGACGT
22-7	TTGGTCCTCATCAGAGATGCGGCTGAAAGATGCGTCCTCCTA
22-8	CGAGCGGGCATTTATAGCGACAGAGTTTCAGGGTGATTGAGC
22-9	AGCATGTAGTGGGCCGTGGAGCCTTTCTAGATGGCCCTCTGT
22-10	GAAGTCGTTTATTATTAGTCACAGATCAAAGATACCCAACGC
22-11	GGTGCAGGAGGAGCAGACTCAAAGGAACTACCATATGTCCCG
22-12	TTACTTGCTTCATTTAGCGATAAACCTTCGTTCCGCCGAAAG
22-13	GGCAATTAGAGAATTGTATCCTGTCTTGTCCCAAGTCACAGT
22-14	CTTACGCTGAAGCGCCTTTAGCGTGGTCGCAACAGGTGTATA
22-15	CCAAAGACGAAAGACCGTTTATCCGGCTTAAAGGCTATCTTG
23-1	TTCTAAAGTGGCTCTAATCGACCAGCTGGTACTTTCGCCCGC
23-2	CAGAAGGTGATAACTTCCAAGATAGCCCTCTACTATCAAGCA
23-3	GCCTCGCCCTGTCTGACTCGTCTAAACATCCAACTCCCTCCA

23-4	CTGAAGCTCCCTCGACACGTGTCCAATACAGAACTGTCCGCC
23-5	CAGCGGAGTCTATATCTACGTATTAAAGGGCCTTTCATAGGG
23-6	GACCCACTAAGTGGTTTCCGCATGAGGACCAAGCCTAGGTTT
23-7	GACTGTGCTCCCTGGACCCGAATGCCCGCTCGCGCATCTCTG
23-8	TGAGGTACAGCGTTCGTGTCACACTACATGCTGTCGCTATAA
23-9	GAGTAGCATTAGGCACAGCAGTAAACGACTTCCTCCACGGCC
23-10	TGCTGCGTCGTGCGTGCTTCTCCTCCTGCACCTGACTAATAA
23-11	CGTTGGCAGCACTTCTACCTAGAAGCAAGTAATGAGTCTGCT
23-12	AATTCTCGTGCGCGGGTGAGTCTCTAATTGCCATCGCTAAAT
23-13	TGGTAGAAAGAAGGGAGGCTCTTCAGCGTAAGGGATACAATT
23-14	GACCCAGGGTTAGTTCCGGAGTTCGTCTTTGGCTAAAGGCGC
23-15	ACTTCGTGCTTGTTTTTTTTTTTTTTTTTTTTTAAACGGTCT
24-1	TTTTTTTTTTTAGGTAGGCAGGCCACTTTAGAATTTTTTTTT
24-2	TACAAACGTGTCCTTGTCCTTTATCACCTTCTGTCGATTAGA
24-3	GTCCCTGGAGCGTTCCGAAATACAGGGCGAGGCCTTGGAAGT
24-4	GGTACGACACAGCGTGTCCTGAGGGAGCTTCAGACGAGTCAG
24-5	GTCCAGGTCTACTAAATTGTCTAGACTCCGCTGCACGTGTCG
24-6	GGCGTGGTACGTGCATCACCAACTTAGTGGGTCACGTAGATA
24-7	AAGGGCAAAGCCATTGACGACGGGAGCACAGTCGCGGAAACC
24-8	ACAACGGGTACTATAGTATCGCGCTGTACCTCATCGGGTCCA
24-9	GTGGAAGCCCGTTCGGTGTCTCTAATGCTACTCTGACACGAA
24-10	ACCTGGAAACCGCCCGATAGGCACGACGCAGCACTGCTGTGC
24-11	TCACGGTACCAGTCGGAGATGGTGCTGCCAACGAGAAGCACG
24-12	TCTTTCCGTGCGGTCGTCCGGCGCACGAGAATTTAGGTAGAA
24-13	AGGGCACGCATAGCTGCCAGCTTCTTTCTACCAACTCACCCG
24-14	CAGCAAAGCAATGGCTGAAATTAACCCTGGGTCGAGCCTCCC
24-15	TTGCTCTACTATTATGTGCATCAAGCACGAAGTCTCCGGAAC
25-1	ACACGTTTGTACTGCCTACCT
25-2	GCTCCAGGGACAAGGACAAGG
25-3	TGTGTCGTACCATTTCGGAAC
25-4	TAGACCTGGACCAGGACACGC
25-5	CGTACCACGCCGACAATTTAG
25-6	GCTTTGCCCTTTGGTGATGCA
25-7	GTACCCGTTGTGTCGTCAATG
25-8	CGGGCTTCCACCGATACTATA
25-9	GGTTTCCAGGTAGACACCGAA
25-10	TGGTACCGTGACCTATCGGGC
25-11	GCACGGAAAGACATCTCCGAC
25-12	ATGCGTGCCCTCCGGACGACC
25-13	TTGCTTTGCTGGCTGGCAGCT
25-14	TAGTAGAGCAAATTTCAGCCA
25-15	TTTTTTTTTTTATGCACATAA

Motif 3.1 (24H×29T)

Name	Sequence
1-1	CGGGCATCAGCAGAGGGCTGT
1-2	ATCAGCAGTTCCGAGAATGTC
1-3	AAACTTCTACCAACCCTATGG
1-4	CAGTGTATCCCTCTTTGAGTC
1-5	GATCATGAACTTACATAGAAA
1-6	GGGCAAGGAGAGCGACGTGAT
1-7	GCACCTTCGGGACTTCGTCTC
1-8	ACCGGTAGGTACTACGGGCTT
1-9	ATCAACCGTTGTAAGTGAAGT
1-10	GTTGCGAGATCACGTTTAGTC
1-11	GCTGCGGGAGACGTTCTCCTA
1-12	TATGCGGCCTTTCATCTCATC
1-13	TTGGCCTATGGCTGAGGGACT
1-14	CACGGCGAGACCGACGACTAC
1-15	TTTTTTTTTGTGTGCATCCGA
2-1	TTTTTTTTTACAGCCCTCTGCATACTGCTGACATTTCCGAGG
2-2	TGATGCCCGGACATTCTCGGACTGGGCCTCCTCGTACAACTA
2-3	ACTGCTGATCCATAGGGTTGGGTGTCTACAATACTTCGGAAA
2-4	TAGAAGTTTGACTCAAAGAGGCTCGGGAGTGTGCTGGACACC
2-5	GATACACTGTTTCTATGTAAGTAGCGACGTAACGTTGCACAC
2-6	TTCATGATCATCACGTCGCTCAGGGTAGAAATCGTCTGAACG
2-7	TCCTTGCCCGAGACGAAGTCCACGCGTACCGCTAAGTCCTAT
2-8	CGAAGGTGCAAGCCCGTAGTATGATTACCGCTGACGGCCGTT
2-9	CCTACCGGTACTTCACTTACAACAGGCAGATCGCCGATTAGC
2-10	ACGGTTGATGACTAAACGTGAGAAATTGGAGAGTCTAATTCA
2-11	TCTCGCAACTAGGAGAACGTCGGACTTTAAAGCCGAATGCAT
2-12	TCCCGCAGCGATGAGATGAAAGACGGGTACCGGCTTAAGTTT
2-13	GGCCGCATAAGTCCCTCAGCCCTATCCCAGCCCATCCCATGT
2-14	ATAGGCCAAGTAGTCGTCGGTCCCTGCTTTAGGAATAAGTAG
2-15	CTCGCCGTGTCGGATGCACACGTCGCTTCAAATTTTTTTTTT
3-1	ACCCTCGGATAGTATTAATGGGTCAGCAGTATTTTTTTTTTT
3-2	TTATTTAACATACGCGAAACAAGGAGGCCCAGCCTCGGAAAT
3-3	ACTAAGTCCCTCGCTGGCATGATTGTAGACACTAGTTGTACG
3-4	CCGACCCTCTCCCTGCTTGAGACACTCCCGAGTTTCCGAAGT
3-5	GCACGGTTCCTTGATAGATATTTACGTCGCTAGGTGTCCAGC
3-6	GACCACGTTCGCAACTTCACTATTTCTACCCTGTGTGCAACG
3-7	TTCATTTATGGAAAGTTCCCGGCGGTACGCGTCGTTCAGACG
3-8	TTGTCTTAGACAGTGCAATTAAGCGGTAATCAATAGGACTTA
3-9	CTGTTGTCCTTCTTCTACGGCGATCTGCCTGTAACGGCCGTC

3-10	TAGAGTACAAAGCCATCATAGTCTCCAATTTCGCTAATCGGC
3-11	CAGCAAGTGATCAGGACACTGCTTTAAAGTCCTGAATTAGAC
3-12	GATACTCTAAGGATTTATCCGCGGTACCCGTCATGCATTCGG
3-13	TGCACTGAAGCGAAACTATAAGGCTGGGATAGAAACTTAAGC
3-14	AGACAAGGTTTAGTATATGATCTAAAGCAGGGACATGGGATG
3-15	TTTTTTTTTAGCTCGAGACACTTTGAAGCGACCTACTTATTC
4-1	TTTTTTTTTCCATTAATACTATAACGGCGAGATCACGTCATC
4-2	TCCGAGGGTTGTTTCGCGTATTATCAATGGCTCTGTGCCGAC
4-3	GTTAAATAACATGCCAGCGAGTGAGAGAAAGTGTCGGTATTT
4-4	GGACTTAGTCTCAAGCAGGGAACCCAGATCGACTTATGCTTC
4-5	GAGGGTCGGATATCTATCAAGTATCTCACCCTATGAGATCGC
4-6	GAACCGTGCAGTGAAGTTGCGGGTCCCGTAAGGAAGGGTTGT
4-7	AACGTGGTCCGGGAACTTTCCATACGCATTGCCCTCCAGGTG
4-8	ATAAATGAATAATTGCACTGTACAGTCTGGGAGTCGTCGCAA
4-9	CTAAGACAAGCCGTAGAAGAATTGGGATCTTGTAAGGTTCTG
4-10	GGACAACAGCTATGATGGCTTTACGTTTACGTAGGCTTGGTC
4-11	TGTACTCTACAGTGTCCTGATTCCGCTTATGATACCATCGGG
4-12	CACTTGCTGCGGATAAATCCTAACGGTTGCACGTTCAGAATC
4-13	TAGAGTATCTTATAGTTTCGCGACCGGAGTTACACGAGCTTT
4-14	TTCAGTGCAATCATATACTAAGGGCAGATAGAACGCAATAGT
4-15	ACCTTGTCTGTGTCTCGAGCTTCCGAACACACTTTTTTTTTT
5-1	AGAGCGTATGGTCATCTGAGATCTCGCCGTTATTTTTTTTTT
5-2	CCGTTTACCTCCTCCTTATAGAGCCATTGATAGATGACGTGA
5-3	CGGGTCCCGACCAGGGTTCTAACTTTCTCTCAGTCGGCACAG
5-4	AGCCAATCCCTACCGCCGTGATCGATCTGGGTAAATACCGAC
5-5	CCAGCTGTCCGGTGTGCCTTTAGGGTGAGATAGAAGCATAAG
5-6	CTGATTGTAGCAGGGCTTTAGCTTACGGGACCGCGATCTCAT
5-7	CCACCTGGTTTGAGCGAGGAGGCAATGCGTATACAACCCTTC
5-8	GGATATGTTGTTGCTGAGATGTCCCAGACTGTCACCTGGAGG
5-9	GATATTTCCGATAAAGAACATCAAGATCCCAATTGCGACGAC
5-10	AAGACACGGTCGGACCGGGACACGTAAACGTACAGAACCTTA
5-11	TCCTGTTTCCCGGGCTACATATCATAAGCGGAGACCAAGCCT
5-12	AATGGCCCTACTGCCCGTTAAGTGCAACCGTTCCCGATGGTA
5-13	GCGCAGTACAGTTCTCTGTTATAACTCCGGTCGATTCTGAAC
5-14	CTACGCTAGTATTTAGAGCGATCTATCTGCCCAAAGCTCGTG
5-15	TTTTTTTTTGGCTCCCGATCGGTGTGTTCGGAACTATTGCGT
6-1	TTTTTTTTTTCTCAGATGACCCGCGCCAAACTTCGATCATAT
6-2	ATACGCTCTCTATAAGGAGGACGATCGACGCGACTTAGAAAG
6-3	GGTAAACGGTAGAACCCTGGTATTTCAAGATACAGCCTGTTA
6-4	CGGGACCCGTCACGGCGGTAGCATATACTGATGTCACGCTGC
6-5	GGATTGGCTAAAGGCACACCGACGTCGATAAATAGTGCCTCT
6-6	GACAGCTGGCTAAAGCCCTGCCTGTAAATGCGCCTGCCTAGG

6-7	TACAATCAGCTCCTCGCTCAAAGTGGGCTTCCCTGAACATCC
6-8	ACCAGGTGGCATCTCAGCAACAAATTGCGACGAATGGCCCTT
6-9	AACATATCCATGTTCTTTATCCGAGTGCTAATGTGCTCAGTG
6-10	GGAAATATCGTCCCGGTCCGATCTCAATACCCTGTCTAGCGT
6-11	CCGTGTCTTTATGTAGCCCGGCGCGTAGGGCCTGCTTCCCGA
6-12	GAAACAGGATTAACGGGCAGTGTATTTAAATGGGCTGACAGG
6-13	AGGGCCATTTAACAGAGAACTTTCAGCGGGCCAGTGAGACAG
6-14	GTACTGCGCTCGCTCTAAATAGGCATATAATTCGCCCTTAAG
6-15	CTAGCGTAGCGATCGGGAGCCGAAGGTAAAGCTTTTTTTTTT
7-1	CGCGGCCGAAGACGTCTTCGGAGTTTGGCGCGTTTTTTTTTT
7-2	TAAGTCTTAAACTATATATACCGCGTCGATCGATATGATCGA
7-3	CTTTGTGACCCGGAAGCGTTATATCTTGAAATCTTTCTAAGT
7-4	CCGTGATCCCACGATTCCGCGATCAGTATATGTAACAGGCTG
7-5	TGATGACACATGTCTATACTGTTTATCGACGTGCAGCGTGAC
7-6	GGCACTTTGAAGGAGAACTTACGCATTTACAGAGAGGCACTA
7-7	TAATTAACCGCTTCTGCAGGCGGAAGCCCACTCCTAGGCAGG
7-8	TCGTAATTTGCTCACCGGTAACGTCGCAATTTGGATGTTCAG
7-9	CTGAGATCAGCAGTGTCTATAATTAGCACTCGAAGGGCCATT
7-10	AAGATCGAGCGACACACCCTAGGGTATTGAGACACTGAGCAC
7-11	CCATCTGCTTGGTCGAGATACGGCCCTACGCGACGCTAGACA
7-12	TAGAGATACCGGCGGATGTCTCATTTAAATACTCGGGAAGCA
7-13	CCGCCTTTACCCAACGTGCTGGGCCCGCTGAACCTGTCAGCC
7-14	GTCGACCAGATCCTTGTCGGTAATTATATGCCCTGTCTCACT
7-15	TTTTTTTTTGTCTTTATTCTTGCTTTACCTTCCTTAAGGGCG
8-1	TTTTTTTTTCCGAAGACGTCTCGTGCGTGTCCGGGTCCTCAG
8-2	TCGGCCGCGGTATATATAGTTTGATTCCGCTTTAGCGCCTTC
8-3	TAAGACTTATAACGCTTCCGGTGTAACACCAATAGCAACCGT
8-4	GTCACAAAGCGCGGAATCGTGGAGGATATGTGTACTCTGAAC
8-5	GGATCACGGCAGTATAGACATAGGGTAAACCGGTAAAGTGGG
8-6	GTGTCATCATAAGTTCTCCTTTAACGGTTTCAGCAATGTCTT
8-7	CAAAGTGCCGCCTGCAGAAGCAAGGGCGTTAGTTGTCGGTCC
8-8	GGTTAATTATTACCGGTGAGCGACAGTGGCCGAAGTAAGGTT
8-9	AAATTACGATATAGACACTGCTCGTGCCAAATCACACCTAGT
8-10	TGATCTCAGTAGGGTGTGTCGGTTGCGTCATGCCGGATCCTT
8-11	CTCGATCTTGTATCTCGACCAGATTAAATGTTGCAACAAGGC
8-12	AGCAGATGGAGACATCCGCCGCCGGGTAGGCATTTCTTCCTC
8-13	GTATCTCTACAGCACGTTGGGCTCAATAGACAGGCCGCGTAA
8-14	TAAAGGCGGACCGACAAGGATGCATTCAGCAGGAACCCGTGC
8-15	CTGGTCGACAAGAATAAAGACTCCAACGGGTGTTTTTTTTTT
9-1	CGCGCTCCGTTCTGGCGTTCAGGACACGCACGTTTTTTTTTT
9-2	TCTGCTATACCATTCTAGAGGAAGCGGAATCACTGAGGACCC
9-3	CAGTTATGTGCCAAATCTAGTTTGGTGTTACAGAAGGCGCTA

9-4	GCTACGCCACGTGACGATTGTCACATATCCTCACGGTTGCTA
9-5	ACGGATTGACGGACGTTGGGCCGGTTTACCCTGTTCAGAGTA
9-6	CAGCCACACATCCGCGACTTATGAAACCGTTACCCACTTTAC
9-7	ACGGGCTCCTCGCCGGAATTGCTAACGCCCTTAAGACATTGC
9-8	CCACGGCTTCCCATCTTCAGCCGGCCACTGTCGGACCGACAA
9-9	AATACGCGTGACCTCGCCCAGATTTGGCACGAAACCTTACTT
9-10	GATAACCTGCAGGCTTTCGCTCATGACGCAACACTAGGTGTG
9-11	CCTCCCTCAAGGAATGGTATAAACATTTAATCAAGGATCCGG
9-12	ATTCATAGTGTGTCCATACATTGCCTACCCGGGCCTTGTTGC
9-13	GGTGTCTCCGTCCCATTTGTTTGTCTATTGAGGAGGAAGAAA
9-14	TTTAACAGAAGGCACGGTGACCTGCTGAATGCTTACGCGGCC
9-15	TTTTTTTTTATTCTAGACTTGCACCCGTTGGAGCACGGGTTC
10-1	TTTTTTTTTTGAACGCCAGAATCACCGAACAGTATTTCTGGG
10-2	CGGAGCGCGCCTCTAGAATGGCCAATAAGGTTTGCGAATTAA
10-3	TATAGCAGAACTAGATTTGGCTAGGTGGGTTTAATGAACATT
10-4	ACATAACTGACAATCGTCACGCAAGCAATTACGAGGGCCTAA
10-5	TGGCGTAGCGCCCAACGTCCGAGCATTAGAAGGGTATCGAGT
10-6	TCAATCCGTTAAGTCGCGGATGATAACTGCGGAAGTCGTTGT
10-7	GTGTGGCTGCAATTCCGGCGAATAAGCAGAAGATAGAGGTCT
10-8	GGAGCCCGTGCTGAAGATGGGAGTAAGACCTCACTCAGAAAC
10-9	AAGCCGTGGCTGGGCGAGGTCCTTCGTTTACAGATTTAGACG
10-10	ACGCGTATTAGCGAAAGCCTGCGTGGGTCAGCCGTAATGATG
10-11	CAGGTTATCTATACCATTCCTGAGGGCGAACAGGGACATAAA
10-12	TGAGGGAGGATGTATGGACACTACCCGCCCAAACCGAGTTCG
10-13	ACTATGAATAACAAATGGGACAAGCCGGTCTCGCAACTCAGT
10-14	GGAGACACCGTCACCGTGCCTTGTCATTCAGACCCGTGGGCA
10-15	TCTGTTAAACAAGTCTAGAATGTTGACAATTATTTTTTTTTT
11-1	ATCTTACCGCCTGTCGAGCCGCTGTTCGGTGATTTTTTTTTT
11-2	CCCACGGGTTTAGAGGTAAGGAACCTTATTGGCCCAGAAATA
11-3	TGGCAGGGCTAGGATATGCAGAAACCCACCTATTAATTCGCA
11-4	ATCCCTGGGTAGGATGAGAACGTAATTGCTTGAATGTTCATT
11-5	CTCCTTCGATCACTCGATCACCTTCTAATGCTTTAGGCCCTC
11-6	CGCATTCCATCATGCCACAGCCCGCAGTTATCACTCGATACC
11-7	CGTTATCCTAGTAGCTATTCTCTTCTGCTTATACAACGACTT
11-8	CGAGTAACTGGTGTATTGTATGAGGTCTTACTAGACCTCTAT
11-9	CGCTGACAGTGAGAAATGATCTGTAAACGAAGGTTTCTGAGT
11-10	TGGAGCTGAGTCGCTGGCCTAGCTGACCCACGCGTCTAAATC
11-11	TTAAGGACCGAAGGGTGAAAGTGTTCGCCCTCCATCATTACG
11-12	AAAGGCTTGTCCTCCAAGTGGTTGGGCGGGTATTTATGTCCC
11-13	GTACGAAGGAAGAACTCTATGGAGACCGGCTTCGAACTCGGT
11-14	ACAATTCTATGCTTTAATCTCTCTGAATGACAACTGAGTTGC
11-15	TTTTTTTTTTGAGAACAGTGGTAATTGTCAACTGCCCACGGG

12-1	TTTTTTTTTCGGCTCGACAGGAACCCGCACGCGGTAACCTCC
12-2	CGGTAAGATCCTTACCTCTAATAATATGTTCTTCCTGTTCTC
12-3	ACCCGTGGGCTGCATATCCTATACGTAAGATAAACTACTCGT
12-4	GCCCTGCCAGTTCTCATCCTAGCGCGGTCTTGACCGCTGAGG
12-5	CCCAGGGATGTGATCGAGTGAACAAACACATGCTGCCACCCT
12-6	TCGAAGGAGGCTGTGGCATGAACATCATTCCAAGGAGTGGCG
12-7	TGGAATGCGAGAATAGCTACTTAATCTTCCTGACAGTGATGA
12-8	AGGATAACGATACAATACACCTGCTGAGTGTACCTTCGATCA
12-9	AGTTACTCGGATCATTTCTCAAGTTCTCGACGAGTCCTTCTA
12-10	CTGTCAGCGTAGGCCAGCGACCTCCGGGCAGAATCCTAAGGA
12-11	TCAGCTCCACTTTCACCCTTCATCCTCCTGCTTGGTATCACG
12-12	GGTCCTTAACCACTTGGAGGAGGATGGGTAGGTTCCTCCGAT
12-13	CAAGCCTTTCATAGAGTTCTTGAATGGTAGGCGCGCTAAAGG
12-14	CCTTCGTACGAGATTAAAGCAGTGATAACTAAGATGGCGCAC
12-15	TAGAATTGTCCACTGTTCTCAGCAACCCTGCCTTTTTTTTTT
13-1	AGTATGTATGCCCTGTGACGGGCGTGCGGGTTTTTTTTTTT
13-2	TTCACCTCTGTGCGTACCTCTAGAACATATTAGGAGGTTACC
13-3	TTAAGCTGCTGCGCAACGATCTATCTTACGTAGAGAACAGGA
13-4	CCGTTAGATTTAGCTGGTTACCAAGACCGCGCACGAGTAGTT
13-5	TCGTATACCAGAGCATGATGACATGTGTTTGTCCTCAGCGGT
13-6	GGCCACTATTACAGTGGGCTGTGGAATGATGTAGGGTGGCAG
13-7	CTCTTCTCAACTCATCCACGTCAGGAAGATTACGCCACTCCT
13-8	CACAATGTGTTTGTATTCTGTTACACTCAGCATCATCACTGT
13-9	CGGCACCCGAACGTACCAGTTCGTCGAGAACTTGATCGAAGG
13-10	TGGGCCCTACCCTGCACTAAATCTGCCCGGAGTAGAAGGACT
13-11	GTGATAGGGCGGATCCTGGTCAGCAGGAGGATTCCTTAGGAT
13-12	AAAGGCTACTTCTGAAGCCAGCCTACCCATCCCGTGATACCA
13-13	AATCTTCTGTAGACGCCAGCGGCCTACCATTCATCGGAGGAA
13-14	GAAAGGAGGGTTGATGGCTTCTTAGTTATCACCCTTTAGCGC
13-15	TTTTTTTTTCTAAAGAAATTCGGCAGGGTTGCGTGCGCCATC
14-1	TTTTTTTTTCCGTCACAGGGCTTCCGGGCACTAGTACGAATT
14-2	ATACATACTAGAGGTACGCACAAGCTGTGAGATTTATAGGTA
14-3	AGAGGTGAAGATCGTTGCGCACGATTCACTACAAGGTCATGT
14-4	GCAGCTTAAGTAACCAGCTAAGTATGCCACTTCTCCACCGCA
14-5	ATCTAACGGTCATCATGCTCTATCAATAACGGTAGTACTCTA
14-6	GGTATACGACAGCCCACTGTACTCAGTTTAGGACACTTGCTC
14-7	ATAGTGGCCACGTGGATGAGTCGGTCCGTTCGCCCGCATATT
14-8	TGAGAAGAGACAGAATACAAATACTAGCTTCTTGTTTAGTGC
14-9	CACATTGTGAACTGGTACGTTACGGGCTCAGGATCTACACGC
14-10	CGGGTGCCGTTTAGTGCAGGGTGCCATAAGGGAGGTTTAGGT
14-11	TAGGGCCCAGACCAGGATCCGCGCATACTGTGAAAGGAGAGG
14-12	CCCTATCACCTGGCTTCAGAAAGAGCTGAGTTATCGTCCCTC

14-13	GTAGCCTTTCGCTGGCGTCTATGGAGTGGATGGCCTCTTATT
14-14	CAGAAGATTGAAGCCATCAACTGCTTCCCTCCAATCGTGGCT
14-15	CCTCCTTTCGAATTTCTTTAGGTTGTATTCCATTTTTTTTTT
15-1	GGATAGGGACAGGGCTAACTCAGTGCCCGGAATTTTTTTTTT
15-2	GTCAACCTTGGCACGGCGACCTCTCACAGCTTAATTCGTACT
15-3	CAGGTCCCTAATCTATGCCGGGTAGTGAATCGTACCTATAAA
15-4	TGGTTCACATTGGTTTAACCTAAGTGGCATACACATGACCTT
15-5	GACGCGGCGTATGCGAGTCCTCCGTTATTGATTGCGGTGGAG
15-6	GGATCGACGGGCCTCATAACTCCTAAACTGAGTAGAGTACTA
15-7	TCTCTGCAGGAATTCATAGATCGAACGGACCGGAGCAAGTGT
15-8	ACGCCGAGCGAGGGTCGCTAAAGAAGCTAGTAAATATGCGGG
15-9	AGGACCTCTGTCCCTCGAATTCCTGAGCCCGTGCACTAAACA
15-10	CTTTGTTAACTTATCTGTATTCCCTTATGGCAGCGTGTAGAT
15-11	TCTCACCCTTTATCGTACGTGCACAGTATGCGACCTAAACCT
15-12	CTCCAGTCTAGGTTACTAACCAACTCAGCTCTCCTCTCCTTT
15-13	TTGCCGTTGTGGGTTCCGTCACATCCACTCCAGAGGGACGAT
15-14	AACATGGGATTCTAAGTTCCTGGAGGGAAGCAAATAAGAGGC
15-15	TTTTTTTTTAATGCGGCCCTCTGGAATACAACAGCCACGATT
16-1	TTTTTTTTTGAGTTAGCCCTGCTCATGAGTCGATGACGAAAG
16-2	TCCCTATCCGGTCGCCGTGCCGAGGACGAATAAAGTTAAGGA
16-3	AAGGTTGACCCGGCATAGATTCCTACACCTCTGTTCGCAATT
16-4	AGGGACCTGAGGTTAAACCAAAGCCAATGATGAATCCACTCC
16-5	TGTGAACCAAGGACTCGCATAGTCGAGCGTGGTGGATCGCGC
16-6	CGCCGCGTCAGTTATGAGGCCATTTCTGAGATAGTCCCTATA
16-7	CGTCGATCCATCTATGAATTCTCATGAATTGTTATCGAAAGC
16-8	CTGCAGAGATTAGCGACCCTCCTCAGCGTCCAACGTTATGTA
16-9	GCTCGGCGTAATTCGAGGGACCCATAATAACAAAGAGATGCA
16-10	AGAGGTCCTAATACAGATAAGGACTTAATTCGTGGAACGTCG
16-11	TTAACAAAGCACGTACGATAATTTCCGATCCCTCGGCATGCG
16-12	AGGGTGAGAGGTTAGTAACCTTCGAGGCACACATTTGACCGA
16-13	AGACTGGAGTGACGGAACCCAGTCATTTACCGAGTAAACAGC
16-14	CAACGGCAAAGGAACTTAGAAGGCGACTAGAGGCCCTGGATC
16-15	TCCCATGTTGAGGGCCGCATTGAATCTATTAATTTTTTTTTT
17-1	AAGACTTCCGGGCTTGACATCCGACTCATGAGTTTTTTTTTT
17-2	GAGTTGCCTGCGTAAACTGGTTATTCGTCCTCCTTTCGTCAT
17-3	GGCTGCTTCAAGGCGGGCGTCAGAGGTGTAGGTCCTTAACTT
17-4	AACCTCATCGTTCGCGACCTCCATCATTGGCTAATTGCGAAC
17-5	GTCCAGAATGCTCTATAGGCTCCACGCTCGACGGAGTGGATT
17-6	GACCACGTGGGCCATCGTCGGATCTCAGAAATGCGCGATCCA
17-7	ACTACCTCCAAATTATTTATAACAATTCATGATATAGGGACT
17-8	CCACATTCCCTTTAATATGTGTGGACGCTGAGGCTTTCGATA
17-9	CCCTGCGGGTCGATAATGAGTTGTTATTATGGTACATAACGT

17-10	CCTGTGGGCTCTTAATGCAAACGAATTAAGTCTGCATCTCTT
17-11	TTGTTAATAGACCACCAGCACGGGATCGGAAACGACGTTCCA
17-12	ACTGCCAAACGCACTCGAGCAGTGTGCCTCGACGCATGCCGA
17-13	TTATTCAGGCCAGGATCAGGTCGGTAAATGACTCGGTCAAAT
17-14	CCGAGTGTGCCTGCAGCACAACTCTAGTCGCCGCTGTTTACT
17-15	TTTTTTTTTCACAGATATGTCTTAATAGATTCGATCCAGGGC
18-1	TTTTTTTTTGATGTCAAGCCCTCCAAAGCCTGTGATCGTTCA
18-2	GGAAGTCTTACCAGTTTACGCTAAATAGCTGCTACTCCATTA
18-3	AGGCAACTCGACGCCCGCCTTTCTATGCATGAAACTACATTT
18-4	GAAGCAGCCGAGGTCGCGAACATGAAAGAATTGGTATAACCG
18-5	GATGAGGTTAGCCTATAGAGCACCCTGAGAGTCTATGTCGGG
18-6	ATTCTGGACCCGACGATGGCCACTGCGTTGTATGGGTATTGA
18-7	CACGTGGTCTATAAATAATTTAAGAACTATTTAAACCCGGAA
18-8	GGAGGTAGTCACATATTAAAGAGAGAACTGCACCTCTAAAGC
18-9	GGAATGTGGACTCATTATCGAGAGAGCCTCCGGGTAACCTCT
18-10	CCCGCAGGGTTTGCATTAAGAACGGGCTCGTTCCCATCCGGG
18-11	GCCCACAGGGTGCTGGTGGTCATCGCCGGATGACTAGTTGGT
18-12	TATTAACAATGCTCGAGTGCGTATATCGACCTGAGAATAGTA
18-13	TTTGGCAGTACCTGATCCTGGGTGCCAAGTTCCTAGATGAGT
18-14	CCTGAATAATTGTGCTGCAGGTTACCAGATTGTATCTCTTAG
18-15	CACACTCGGGACATATCTGTGGTAGTATGACATTTTTTTTTT
19-1	GGATGACCCGAGAGACGTACGCAGGCTTTGGATTTTTTTTTT
19-2	GTTAAATTTCTTGACACTCGAGCAGCTATTTATGAACGATCA
19-3	GAGCTAATTACAGGGTCGGAATCATGCATAGATAATGGAGTA
19-4	GGTCGAGTCGTAGCATAATCGAATTCTTTCATAAATGTAGTT
19-5	TTCCAGTCGTGTCTACTTCCTACTCTCAGGGTCGGTTATACC
19-6	GCGGTCCAAAGAGGGTGCGCGTACAACGCAGTCCCGACATAG
19-7	ATTGATCTGAGCCCGACGACTAAATAGTTCTTTCAATACCCA
19-8	AAACCGGCGAATTGATCACTATGCAGTTCTCTTTCCGGGTTT
19-9	TTGGGCAGCGCTTTAATAGTGCGGAGGCTCTCGCTTTAGAGG
19-10	AAGGATTTACAGTATGTTATAAACGAGCCCGTAGAGGTTACC
19-11	AGACGAATGTGTGTAATAAGCCATCCGGCGATCCCGGATGGG
19-12	GCTGGGTATACAACTGCCTCAAGGTCGATATAACCAACTAGT
19-13	GCACCTCTCCAAACACCGGCAGAACTTGGCACTACTATTCTC
19-14	TAGTCACTAAGCGTTCGATTTCAATCTGGTAAACTCATCTAG
19-15	TTTTTTTTTATACTTCAATTGTGTCATACTACCTAAGAGATA
20-1	TTTTTTTTTCGTACGTCTCTCACATCTTGACTCTGGATCTTT
20-2	GGGTCATCCTCGAGTGTCAAGACGAATTAAGAGATATTTATA
20-3	AAATTTAACTTCCGACCCTGTATCCGGGCGATCACCCAGGTG
20-4	AATTAGCTCCGATTATGCTACCTAGACGGTTTAGTAGAGTGG
20-5	GACTCGACCAGGAAGTAGACAGTAGCATTACACCGATTCTAC
20-6	CGACTGGAACGCGCACCCTCTTCGGTGAACGAGGCACACTAT

20-7	TTGGACCGCAGTCGTCGGGCTCCCTCAGAAGAAATAAATAAA
20-8	CAGATCAATTAGTGATCAATTGTCGGCCGAAACACCGGATGC
20-9	CGCCGGTTTCACTATTAAAGCCTGGGCTTCCACGAGAAGAGG
20-10	GCTGCCCAATATAACATACTGGAGGCTCCGCCACCCTTTAAT
20-11	TAAATCCTTGCTTATTACACAAGTGAAAGGGAGAAGGTCCCA
20-12	CATTCGTCTTGAGGCAGTTGTTTATGCGTTTCCAGTCCATAA
20-13	ATACCCAGCTGCCGGTGTTTGCGCCGTAATATTACGAAGCAC
20-14	GAGAGGTGCAAATCGAACGCTTGGGAACATCATTAACACTAA
20-15	TAGTGACTACAATTGAAGTATGTTTCAAGTTTTTTTTTTTTT
21-1	CATTGTCGTTATAAAGCTAGAAGTCAAGATGTTTTTTTTTTT
21-2	ACTAAGACAATAAGGAATCTATCTTAATTCGTAAAGATCCAG
21-3	CGTACCCAAACTCAGAGAGGTATCGCCCGGATTATAAATATC
21-4	ACCATGAAGTAGAATGGTCAGAAACCGTCTAGCACCTGGGTG
21-5	ACTCCCTATGGCGGGCCTCTGTGTAATGCTACCCACTCTACT
21-6	CAGTAGCAGTTCTCGTAATTATCGTTCACCGAGTAGAATCGG
21-7	ACACAAGGGTCGCCGGCGTGGTCTTCTGAGGGATAGTGTGCC
21-8	AACCCGGTCAACCAGACTAACTTTCGGCCGACTTTATTTATT
21-9	ACACCACCCTTAGAACAACGGTGGAAGCCCAGGCATCCGGTG
21-10	CGACTTCCCTTATTTAGAAATGGCGGAGCCTCCCTCTTCTCG
21-11	TAATAGAAAGGATTAACGGTCTCCCTTTCACTATTAAAGGGT
21-12	ACCCACGTCCGATTGTGGTCTGAAACGCATAATGGGACCTTC
21-13	TGGGCGGAGATAGTCGCCAGTATATTACGGCGTTATGGACTG
21-14	TTAGCTGGGAGCGGCCAGCGCTGATGTTCCCAGTGCTTCGTA
21-15	TTTTTTTTTGCCTATTAGATGAAACTTGAAACTTAGTGTTAA
22-1	TTTTTTTTTTCTAGCTTTATAAAGTTGCACCGACGAAACGAC
22-2	ACGACAATGTAGATTCCTTATAAGAAGTCTCTCGCTTCTGGT
22-3	TGTCTTAGTACCTCTCTGAGTGTCAATTGTATGTTGACATGC
22-4	TTGGGTACGCTGACCATTCTAGAAATCTTCTGAAGACACATC
22-5	CTTCATGGTCAGAGGCCCGCCCAGCAGAATCATCCAGTTAAC
22-6	ATAGGGAGTTAATTACGAGAACGCCAGCCTGCTGGCTGGTCC
22-7	CTGCTACTGCCACGCCGGCGACTATATACGCAGGTCGCTTGT
22-8	CCCTTGTGTGTTAGTCTGGTTTCATGAAGCTGTAGACTAGGT
22-9	GACCGGGTTCCGTTGTTCTAACCTGTTTCCATAAGTGCTAAA
22-10	GGGTGGTGTATTTCTAAATAATACTCCCGCTATAATAATGAC
22-11	GGGAAGTCGGACCGTTAATCCCAGCGAGAAAGATTACCCTTA
22-12	TTTCTATTAAGACCACAATCGGGCACAGCCGTAACCTTGGTA
22-13	GACGTGGGTACTGGCGACTATACTAGACGGCCCTCATCCGAC
22-14	CTCCGCCCAGCGCTGGCCGCTCGTACGCTTATACAGGACTCT
22-15	CCCAGCTAACATCTAATAGGCAGATAACCAATTTTTTTTTTT
23-1	TGCATGTACTTGCTGGCGCAACGGTGCAACTTTTTTTTTTTT
23-2	CAGAGCATGCGAAGTTATTCCAGAGACTTCTTGTCGTTTCGT
23-3	CATTGCGGTGGGCGTGCACACATACAATTGACACCAGAAGCG

23-4	CCCTATTTAGCCAACAATTCTCAGAAGATTTCGCATGTCAAC
23-5	GCCTACGAAGTTACTCCTAGGTGATTCTGCTGGATGTGTCTT
23-6	GGATGAGTCCAAATCTGGTGGGCAGGCTGGCGGTTAACTGGA
23-7	TTTGGCTGTCTAGAAGAATGATGCGTATATAGGGACCAGCCA
23-8	CCCTTTCCACTTAAGCGTAAACAGCTTCATGAACAAGCGACC
23-9	TGTTCCCTACTCTTATCGCGTATGGAAACAGGACCTAGTCTA
23-10	ACAGGCTCATCGTTCAAGGCTTAGCGGGAGTATTTAGCACTT
23-11	TCGGTGAATTGACCGATAGTACTTTCTCGCTGGTCATTATTA
23-12	AGAAGCACGATTGGTTCTCCAACGGCTGTGCCTAAGGGTAAT
23-13	TGCCGGGCATAGGAGATAATAGGCCGTCTAGTTACCAAGGTT
23-14	GTTTCACGCGTGGATTGCCGTATAAGCGTACGGTCGGATGAG
23-15	TTTTTTTTTATGCACTGTATTATTGGTTATCTAGAGTCCTGT
24-1	TTTTTTTTTTTGCGCCAGCAACCGACTACACACTGCGTGGTA
24-2	GTACATGCAGGAATAACTTCGGTCCAAAGGATAGTAGCTACT
24-3	CATGCTCTGGTGTGCACGCCCATTAGGGCTTCAAACCGTTCA
24-4	ACCGCAATGAGAATTGTTGGCGTTTCGTTTACGCGTGACGAA
24-5	TAAATAGGGCCTAGGAGTAACGTCCGCTACTTCCGTGCAGTT
24-6	TTCGTAGGCCCACCAGATTTGCGGGAGTGATTCTCGACCATC
24-7	GACTCATCCTCATTCTTCTAGCACGATTTAGGACTTGTCCCT
24-8	ACAGCCAAATTTACGCTTAAGTATAGGTTTAAAGGTAGAAAT
24-9	TGGAAAGGGACGCGATAAGAGGACAGCTAAGACCCATCAGTG
24-10	TAGGGAACAAGCCTTGAACGATGAGGGCAGCAGAGAACCCGT
24-11	TGAGCCTGTTACTATCGGTCAGAATTGAAAGTAGACCGTCAT
24-12	ATTCACCGATGGAGAACCAATACACCAGGTAGGTCCACAATC
24-13	CGTGCTTCTTATTATCTCCTATTCTGGCGAATCTCTTGGATG
24-14	TGCCCGGCAACGGCAATCCACCTAGTTCATCGTGAATAGCGG
24-15	GCGTGAAACAATACAGTGCATCGTAATTTCTATTTTTTTTTT
25-1	TGTGTAGTCGGTTTTTTTTT
25-2	ATCCTTTGGACTACCACGCAG
25-3	GAAGCCCTAATAGTAGCTACT
25-4	GTAAACGAAACTGAACGGTTT
25-5	AAGTAGCGGACTTCGTCACGC
25-6	AATCACTCCCGAACTGCACGG
25-7	CCTAAATCGTGGATGGTCGAG
25-8	TTAAACCTATAAGGGACAAGT
25-9	TCTTAGCTGTCATTTCTACCT
25-10	TGCTGCCCTCACACTGATGGG
25-11	ACTTTCAATTCACGGGTTCTC
25-12	CTACCTGGTGTATGACGGTCT
25-13	ATTCGCCAGAAGATTGTGGAC
25-14	CGATGAACTAGCATCCAAGAG
25-15	TAGAAATTACGCCGCTATTCA

Motif 3.2 (24H×29T)

Name	Sequence
1-1	GTGGTATTTCTACTTCAATAC
1-2	TTCAAGCATCATCGCAAATCC
1-3	GGAACTGGCTGGACTACTGCT
1-4	CGCCGGGCTATATCTCTACTG
1-5	ATAAGCTAAACAAAGTCAAGG
1-6	TATGGCGACCTTGGGACGTAG
1-7	GGTGAATCACTGTTCAGGAAT
1-8	ACCTAAACCCTGGGCCGGGTT
1-9	CGCTCGACCCTCGACAAGTCT
1-10	GCTTAACAACTCGAATTCATA
1-11	CCTCAAAGGATTACAAGCTTC
1-12	ATCCAATCTCAGGCGCCTTTC
1-13	GACCAGCCTATAGCATTCGAT
1-14	CGTACATCACGAGGATTCAGC
1-15	TTTTTTTTTTTGATGCTTTCG
2-1	TTTTTTTTTTGTATTGAAGTAATCGGTAAGGTGTCCAAGGAC
2-2	GAAATACCACGGATTTGCGATCAGCTTAATCCTTGGAGGCAC
2-3	GATGCTTGAAAGCAGTAGTCCGCCAGACATCGGCTGGACGGG
2-4	AGCCAGTTCCCAGTAGAGATACTCGTCCAAAGGACAGGTGCT
2-5	TAGCCCGGCGCCTTGACTTTGGTGGCCTCCAGCTAAATTCTG
2-6	TTTAGCTTATCTACGTCCCAATTTAGGGCAAGTCAAGCTCCG
2-7	GGTCGCCATAATTCCTGAACAGCCTGCCACGTAAACTTTAGG
2-8	GTGATTCACCAACCCGGCCCAGATGGATGTATTGATTACGTG
2-9	GGGTTTAGGTAGACTTGTCGACCCAAGCAGGCGTCGAGCATA
2-10	GGGTCGAGCGTATGAATTCGATGGCGATTAGCAAATTGGGCG
2-11	GTTGTTAAGCGAAGCTTGTAACGTTAACCATCGGGCATACTG
2-12	TCCTTTGAGGGAAAGGCGCCTAGATGAGCTAGCCTTCACGGC
2-13	GAGATTGGATATCGAATGCTAAGGCTCGATCTTGTTCGTAGA
2-14	TAGGCTGGTCGCTGAATCCTCGTGTCTTCGTGTGGGATGCCG
2-15	GTGATGTACGCGAAAGCATCAACTGTAGTGGCTTTTTTTTTT
3-1	TTACACGCGTCTCTTGATAATACCTTACCGATTTTTTTTTTT
3-2	AGGTACTTGGCCCAATATGCTGGATTAAGCTGGTCCTTGGAC
3-3	AAAGGAGGTGAACTCTTTCGTCGATGTCTGGCGTGCCTCCAA
3-4	AGAGAGCCCAGGCTTTAGCATCTTTGGACGAGCCCGTCCAGC
3-5	TTAACGGGTCAGATCCTGGGCCTGGAGGCCACAGCACCTGTC
3-6	CCGACCAAGCTGAGGCATCAGCTTGCCCTAAACAGAATTTAG
3-7	TTCAAACCGATGTCCGAACAGACGTGGCAGGCCGGAGCTTGA
3-8	GTTGAGCTGATATTGTGCGAGATACATCCATCCCTAAAGTTT
3-9	GTAAATGCGAATATTTGCGGCGCCTGCTTGGGCACGTAATCA

3-10	ACTCGTAGCGCTGGAGCATGGGCTAATCGCCATATGCTCGAC
3-11	TGTAGCGCCACGGCCGGTTTAGATGGTTAACGCGCCCAATTT
3-12	GAAGCTTGCACTAAACCTCAACTAGCTCATCTCAGTATGCCC
3-13	CTGCATCCGCAACCTCCGGCAAGATCGAGCCTGCCGTGAAGG
3-14	AATATGTCAGTACCAGGTCCTCACGAAGACACTCTACGAACA
3-15	TTTTTTTTTTCAATCATAACTGCCACTACAGTCGGCATCCCA
4-1	TTTTTTTTTTATTATCAAGAGATGAGAATCAGGAGGTTCTGG
4-2	ACGCGTGTAAAGCATATTGGGAACTCACTCCGTCTCCGCTGT
4-3	CCAAGTACCTACGAAAGAGTTCAAAGTCTTAGCCTTCTGGTG
4-4	CACCTCCTTTATGCTAAAGCCAATTGCCCTCGGCCTCTCGTA
4-5	TGGGCTCTCTGCCCAGGATCTTGTAACCTAACGACAGCAGAC
4-6	GACCCGTTAACTGATGCCTCACTATCCTCTATTTGGTTAAAG
4-7	GCTTGGTCGGCTGTTCGGACAGACTCGGTCGGCAAATTTCTT
4-8	TCGGTTTGAACTCGCACAATATCCTTTCACACTGGGCAGGAA
4-9	TCAGCTCAACGCCGCAAATATGTGACATCGGATTACAGATCA
4-10	TCGCATTTACCCATGCTCCAGACACTAATTGGAGAAACTTTA
4-11	CGCTACGAGTTAAACCGGCCGCCTTGGAACGCATAGAGAGAT
4-12	TGGCGCTACATTGAGGTTTAGAGTCCAAGACGCCCTAGAGGT
4-13	TGCAAGCTTCTGCCGGAGGTTTCACGTGACAAAGACTAAAGG
4-14	GCGGATGCAGAGGACCTGGTAAACCGAGTGCACTCGCATGGA
4-15	CTGACATATTAGTTATGATTGGCGATAATGTCTTTTTTTTTT
5-1	CCTGTAACTTTAAAGCTACGGCTGATTCTCATTTTTTTTTT
5-2	TGGGCCTGCCGACGATTTAGCCGGAGTGAGTTCCAGAACCTC
5-3	GGCTCATGCCAGAACTCTGCCCTAAGACTTTGACAGCGGAGA
5-4	CAGCATCTCCATACCGTATGCCGAGGGCAATTCACCAGAAGG
5-5	TGTGAATAAGCGCGTGGAGTCGTTAGGTTACATACGAGAGGC
5-6	GTGACCTGGAATTATCAGCGTATAGAGGATAGGTCTGCTGTC
5-7	TCCATGCAATCTATTCATAGCCCGACCGAGTCCTTTAACCAA
5-8	CAGTCCCAGCGAGCACACTTGGTGTGAAAGGAAAGAAATTTG
5-9	ATTTGTCTTACTAAGAGGCTATCCGATGTCACTTCCTGCCCA
5-10	GGTCACGGTATCGAATTCCTTCCAATTAGTGTTGATCTGTAA
5-11	CGTACTTTCTGGCGAAAGACTGCGTTCCAAGGTAAAGTTTCT
5-12	CTCCGTTGCTTTCGTATGATTCGTCTTGGACTATCTCTCTAT
5-13	ATATTCGACCTCACCGATTGCTTGTCACGTGAACCTCTAGGG
5-14	CTACAGGCCTCAGGCTTCGGCTGCACTCGGTTCCTTTAGTCT
5-15	TTTTTTTTTTGCAACCGCTGCGACATTATCGCTCCATGCGAG
6-1	TTTTTTTTTTCCGTAGCTTTATTATCGCGTTGCGGGCACCCT
6-2	AAGTTACAGGGCTAAATCGTCCTGGCCAATGCAGTTACAAGT
6-3	GGCAGGCCCAGGCAGAGTTCTGTGGGACGGCCAACGTCCGCT
6-4	GGCATGAGCCGCATACGGTATACCAAGGTATTGCCAAAGGGT
6-5	GGAGATGCTGGACTCCACGCGACCCTAGACAACTCTATACCC
6-6	CTTATTCACAACGCTGATAATTGTGGGATTCGATACCCAAGC

6-7	TCCAGGTCACGCTATGAATAGTCTAGTCCATAGGGCCCGGGT
6-8	ATTGCATGGACAAGTGTGCTCGGGAGAGGCACAGTCAGCGAT
6-9	GCTGGGACTGTAGCCTCTTAGGATCAGTGTAAGTTCGCCGAT
6-10	TAAGACAAATAAGGAATTCGACATCGTACTACCCGTTCAGGG
6-11	TACCGTGACCAGTCTTTCGCCCACCGCTCGTCTCCCGAAACA
6-12	AGAAAGTACGAATCATACGAATTTATGACATCCATAACGGTT
6-13	AGCAACGGAGGCAATCGGTGAACCACATTTCGCTGCGCTAAC
6-14	GGTCGAATATGCCGAAGCCTGGCATGGTGTGAGCTGAATAGC
6-15	AGGCCTGTAGGCAGCGGTTGCACACCCTCGATTTTTTTTTTT
7-1	CGGTATTTAGCCCGGAGTAGACAACGCGATAATTTTTTTTTT
7-2	CACGGCGTAGGGCTAACTGTTGCATTGGCCAGAGGGTGCCCG
7-3	GTTCGTGTTATGTGTGGAACAGGCCGTCCCACACTTGTAACT
7-4	TGTCCAGCTCCTTTAATGTGAAATACCTTGGTAGCGGACGTT
7-5	GCGGGAGTTGCGCTAGAGAATTTGTCTAGGGTACCCTTTGGC
7-6	CCGCGGGCTATTCCCTTCCTACGAATCCCACAGGGTATAGAG
7-7	GCGGTCGAGCCCTGCGTCTGATATGGACTAGAGCTTGGGTAT
7-8	CATCCCATTATTCTTGCACAGGTGCCTCTCCCACCCGGGCCC
7-9	TGTGATCCAACAACCGAACCGTTACACTGATCATCGCTGACT
7-10	ACTGAACTACCCTCGTAATGCGTAGTACGATGATCGGCGAAC
7-11	TTCCCACTCCGTTAGGCCTTCGACGAGCGGTGCCCTGAACGG
7-12	AGGACGTACTGGCGTTCTGCAGATGTCATAAATGTTTCGGGA
7-13	TGTTTAGAGCATACATCCGTACGAAATGTGGTAACCGTTATG
7-14	TAGTGGTGAAACAGCGAGGCTTCACACCATGCGTTAGCGCAG
7-15	TTTTTTTTTTATACAATAGACATCGAGGGTGTGCTATTCAGC
8-1	TTTTTTTTTTTCTACTCCGGGAGCACCACGAGTGATGCGGCC
8-2	CTAAATACCGAACAGTTAGCCCTTATCAACGATCTCAGCCGT
8-3	CTACGCCGTGTGTTCCACACAGTTGTCCTCGATTTAATGATG
8-4	TAACACGAACTCACATTAAAGAATAGCGGTATCCTGCTCGTA
8-5	GAGCTGGACAATTCTCTAGCGAACGCATGCACAGCTGCGCAG
8-6	CAACTCCCGCTAGGAAGGGAAATATCCTCTGTTATTCTGAGA
8-7	TAGCCCGCGGTCAGACGCAGGCACTAAATTAGAATTTCCTAA
8-8	GCTCGACCGCCTGTGCAAGAAAGGGTTGCCTAGTACAAAGCT
8-9	TAATGGGATGCGGTTCGGTTGGCTGAGTTTGGAAGGACCACA
8-10	TTGGATCACAGCATTACGAGGTTCCCAAGGGACCCGACTTAT
8-11	GTAGTTCAGTGAAGGCCTAACTTAGAGGAGAGACCACACTCC
8-12	GGAGTGGGAATGCAGAACGCCTAGTGGCCCGCAACTCTCTGG
8-13	AGTACGTCCTTACGGATGTATCTGCTAATTGTTTGGAAAGGC
8-14	GCTCTAAACAAGCCTCGCTGTGGTAATCACATCAATCTTCAC
8-15	TTCACCACTAGTCTATTGTATCGCGGGACAACTTTTTTTTTT
9-1	AGCCGTCTCGATCGTTTGTACCTCGTGGTGCTTTTTTTTTTT
9-2	TTACCTACCATGTGGATTCCATCGTTGATAAGGGCCGCATCA
9-3	GTTGCGTTGGTGGTGTCTCTATCGAGGACAACACGGCTGAGA

9-4	AATGTTTAAATCCTGCCACACATACCGCTATTCATCATTAAA
9-5	CTCACCCTTATTCGTAGCTCCGTGCATGCGTTTACGAGCAGG
9-6	GTTCATGTTCACCGACGCGGCACAGAGGATATCTGCGCAGCT
9-7	CGCTTAAGTACGAGCAACCCACTAATTTAGTGTCTCAGAATA
9-8	TTTGCAGCTATAAGTTCACACTAGGCAACCCTTTAGGAAATT
9-9	CTATACTATCCGACTGGTACACCAAACTCAGCAGCTTTGTAC
9-10	AAGCTAGGTCAGTTCTGTTGGTCCCTTGGGAATGTGGTCCTT
9-11	CGTAGAATGGGTAAAGCCTTGCTCTCCTCTAAATAAGTCGGG
9-12	GAGTGTATCCCTGCTTCCAATGCGGGCCACTAGGAGTGTGGT
9-13	GGCAGAATCATATGTTTCCGAACAATTAGCAGCCAGAGAGTT
9-14	CGCATCTGTGAGGCTGAATGCATGTGATTACCGCCTTTCCAA
9-15	TTTTTTTTTTCGCAGGTGGGAGTTGTCCCGCGGTGAAGATTG
10-1	TTTTTTTTTTGTACAAACGATCGGCCTGGATCCAGCACGCTT
10-2	CGAGACGGCTTGGAATCCACAAGTGAGTGACGCTCTTGATTC
10-3	TGGTAGGTAATAGAGACACCATATATATAACTTACGGACTAG
10-4	CCAACGCAACGTGTGGCAGGATCTAGCACTTCCCAAATTCAG
10-5	TTTAAACATTGGAGCTACGAAACACATTGTTCCATAATAGCA
10-6	TAAGGGTGAGGCCGCGTCGGTGGGACTAAAGACCGTCTGATG
10-7	GAACATGAACTGGGTTGCTCGACGCTGGTTACAATTATCGGT
10-8	TACTTAAGCGGTGTGAACTTAGATGCCCAGGCCGGGCGTGCA
10-9	TAGCTGCAAATGTACCAGTCGCGCTGGAAGTCCAAAGTTTAT
10-10	GATAGTATAGCCAACAGAACTTGAGCGGATTTGACATAAATG
10-11	GACCTAGCTTCAAGGCTTTACGCGGCGCTGGCAATGTCGGGC
10-12	CCATTCTACGATTGGAAGCAGGGCGGTTGTGCCGTACTATAT
10-13	GGATACACTCTCGGAAACATACGCAGCGAGACCATACACTCA
10-14	TGATTCTGCCGCATTCAGCCTAGCCTTAGTTAGCTCTAGTTG
10-15	CACAGATGCGTCCCACCTGCGGCTAGGCCCTGTTTTTTTTTT
11-1	AGCATATGCCCTCGTGGGTTAGATCCAGGCCGTTTTTTTTTT
11-2	GGATAGCTCTGCGTGTCGAGACGTCACTCACTAAGCGTGCTG
11-3	GCGGGACTGCGTGGAGACTTAAGTTATATATAGAATCAAGAG
11-4	GAAACGTGGGCATGAGGGTGAGAAGTGCTAGACTAGTCCGTA
11-5	CTGTCTACCGAACCCAAGGTTGAACAATGTGTCTGAATTTGG
11-6	GTGCCGGAATTGGATTATAGCTCTTTAGTCCCTGCTATTATG
11-7	TGAGCTCAGACGGCAATCCAGGTAACCAGCGTCATCAGACGG
11-8	TATCCAATACACGTCAACCTAGCCTGGGCATCACCGATAATT
11-9	GGACTGGTCCGACAACGGGCGGACTTCCAGCGTGCACGCCCG
11-10	GTACGCCCTTCAGCGTTACGTAAATCCGCTCAATAAACTTTG
11-11	GCGACCGACCCGTCCCATGTTGCCAGCGCCGCCATTTATGTC
11-12	TATGTCCCGAACTTCAGAGATGCACAACCGCCGCCCGACATT
11-13	AGGCATACTCCCGCAAACTTCGTCTCGCTGCGATATAGTACG
11-14	CTCAACGATTAGAGTGCAAGTTAACTAAGGCTTGAGTGTATG
11-15	TTTTTTTTTTAACGGAATGCTCAGGGCCTAGCCAACTAGAGC

12-1	TTTTTTTTTTTAACCCACGAGAAGCGCAAACAATAGTGGATG
12-2	GGCATATGCTTCTCGACACGCTTTACGACCTTTACGGTAGGA
12-3	AGAGCTATCCTAAGTCTCCACACGGTAGCATCGGCGGCATCT
12-4	GCAGTCCCGCTCACCCTCATGCACTAACGACGAGTGTTAGAT
12-5	CCCACGTTTCAACCTTGGGTTTACTGAGCTTGCGAATCCGAA
12-6	CGGTAGACAGGCTATAATCCAGGCTGGAGGACGGCGTACGAA
12-7	ATTCCGGCACCTGGATTGCCGGCACCACCATCACCACAAGGT
12-8	TCTGAGCTCATAGGTTGACGTAGCATGGTCCGGCATTTACGC
12-9	GTATTGGATACGCCCGTTGTCCAAAGCAAAGTTTGAAAGGGT
12-10	GGACCAGTCCACGTAACGCTGTAGAGCCAACGATTCGTGACG
12-11	AAGGGCGTACAACATGGGACGGTGAAGCTCCTTAAGCAACTA
12-12	GGTCGGTCGCATCTCTGAAGTAAGAAACTTATTACCAGCGTT
12-13	TCGGGACATAGAAGTTTGCGGAAACGGCTAGGTTACTAAGTT
12-14	GAGTATGCCTACTTGCACTCTCCCAGAAAGACGCCTCGTATC
12-15	AATCGTTGAGAGCATTCCGTTGCCAGGTATCATTTTTTTTTT
13-1	ATGTGGCACCGAGGCCCTCCATGTTTGCGCTTTTTTTTTTT
13-2	TCAGCCACTCGGATTAGAAATAAGGTCGTAAACATCCACTAT
13-3	ACGTATGCGCCGTAGTCCACGGATGCTACCGTTCCTACCGTA
13-4	TCGCAATGGTCTCCATTTAGTCGTCGTTAGTGAGATGCCGCC
13-5	ACGTTTATATTTCGACTGGAGCAAGCTCAGTAATCTAACACT
13-6	GCCTCTGTTGTTCGTTATAATGTCCTCCAGCCTTCGGATTCG
13-7	CTGGGCAGCGGAGTGCGACACGATGGTGGTGCTTCGTACGCC
13-8	CGACAACAACGAGCGTAGACTCGGACCATGCTACCTTGTGGT
13-9	CCTACAAGGTACATATATAATACTTTGCTTTGGCGTAAATGC
13-10	TATTATGAGTATTGGAAAGCTCGTTGGCTCTAACCCTTTCAA
13-11	CAGGATCCATATAGGGAGGAAAGGAGCTTCACCGTCACGAAT
13-12	CTGTAGTAGGGCCTGGGCGGTATAAGTTTCTTTAGTTGCTTA
13-13	TAGAGTGCTGTAAGTCAACACCCTAGCCGTTTAACGCTGGTA
13-14	CGAGCCAGATAATACATAAGGGTCTTTCTGGGAACTTAGTAA
13-15	TTTTTTTTTTCCAACCCAAAGTGATACCTGGCGATACGAGGC
14-1	TTTTTTTTTTTGGAGGGCCTCAAACTACAGGAACTAAGCATG
14-2	GGTGCCACATATTTCTAATCCGACCGGAAATCAGGTCCCGGT
14-3	GAGTGGCTGACGTGGACTACGAGGCAAATTAACACTCTCCGT
14-4	GCGCATACGTACTAAATGGAGGAATCTGATACCCACGGGACA
14-5	ACCATTGCGACTCCAGTCGAAGGTAAACGGGAGTTATCGCCG
14-6	ATATAAACGTATTATAACGAAGCATTCAATAGGTCATGCGGC
14-7	CAACAGAGGCGTGTCGCACTCATTGGCTATTGTCCACTCGTT
14-8	CGCTGCCCAGAGTCTACGCTCCTTCAGCAGAGTTAACGGTTG
14-9	GTTGTTGTCGATTATATATGTATATTGAGTCACGTGCTAAGC
14-10	ACCTTGTAGGAGCTTTCCAATACGTCAGTGCCAAACCGGTCT
14-11	ACTCATAATATTCCTCCCTATGTGAGACTTTCAGTTAATACG
14-12	ATGGATCCTGACCGCCCAGGCGGCCTACGTTTAATGTTAGAG

14-13	CCTACTACAGGTGTTGACTTAGTGAGCTCCGATCGGACGCAG
14-14	CAGCACTCTACCTTATGTATTTGCTGCAGCTAACACGTACAG
14-15	ATCTGGCTCGCTTTGGGTTGGGCCATGGTGGGTTTTTTTTTT
15-1	CAACTCCATTGGTTCATCTGATCCTGTAGTTTTTTTTTTTTT
15-2	TACCGGATCTCGCCATGCGGTGATTTCCGGTCCATGCTTAGT
15-3	ACTAGTCCCTCCTGTCTCCAGTTAATTTGCCTACCGGGACCT
15-4	CACCTAAGAGCCTGGACGGTAGTATCAGATTCACGGAGAGTG
15-5	CCAGGTAATAAATTGCGTAGTTCCCGTTTACCTGTCCCGTGG
15-6	CGAGAGCGAGAGCCGCAAAGGCTATTGAATGCCGGCGATAAC
15-7	TTATATATCCTACCAGGCTCACAATAGCCAATGCCGCATGAC
15-8	GGCAATTACCGTGATCGCCCTCTCTGCTGAAGAACGAGTGGA
15-9	AGGCAGGCTTCTAAGTACTATTGACTCAATATCAACCGTTAA
15-10	GAACTCTTGGGAAGTCTGACCGGCACTGACGTGCTTAGCACG
15-11	GCGTTACACGGAGTCGAGCGAGAAAGTCTCACAGACCGGTTT
15-12	TGGACAAACACCGACTTAGAGAAACGTAGGCCCGTATTAACT
15-13	TTCTGGCGCTAGGATATGTCATCGGAGCTCACCTCTAACATT
15-14	GCCCTGGCGCGAAAGAAGTAATAGCTGCAGCACTGCGTCCGA
15-15	TTTTTTTTTTAAGGCCTTGCACCCACCATGGCCTGTACGTGT
16-1	TTTTTTTTTTTCAGATGAACCATTTCGCATCGTATATATGAG
16-2	AATGGAGTTGACCGCATGGCGCAGCATAGGAACACTCTGTTA
16-3	AGATCCGGTACTGGAGACAGGAAGAGCAGGCCTCCCTCCTCT
16-4	AGGGACTAGTTACCGTCCAGGATCGTGCGTGTCCCTCCCAAC
16-5	CTCTTAGGTGACTACGCAATTTAAACGATTTGTATTCGTACC
16-6	TATTACCTGGCCTTTGCGGCTCATGAACTCATCTGTGGAGAA
16-7	CTCGCTCTCGTGAGCCTGGTATTGACACTGTTCTAGATAGCG
16-8	GGATATATAAAGGGCGATCACGAGATATCGTGAATCGTCCAC
16-9	GGTAATTGCCATAGTACTTAGACGACTTAAGGCGTAGGCCTA
16-10	AAGCCTGCCTGGTCAGACTTCTAGATGCTCCCTATCGCATGC
16-11	CCAAGAGTTCTCGCTCGACTCCATTCCCGCTGACGAGGTTGG
16-12	CGTGTAACGCCTCTAAGTCGGCTGAGGAAACATTAGAGTCGG
16-13	TGTTTGTCCATGACATATCCTTCTGCACGTGTTCACTAGATG
16-14	AGCGCCAGAATTACTTCTTTCGTTCGCATCTTGCCCTCTCGA
16-15	GCGCCAGGGCTGCAAGGCCTTTAGGGCTCTCATTTTTTTTTT
17-1	CCGGGTGGTAGTGAGAACGAGCGATGCGAAATTTTTTTTTTT
17-2	GCTTTAGCTGACTTATATGCATTCCTATGCTGCTCATATATA
17-3	GGCTAATCACACGAATATTGCGGCCTGCTCTTTAACAGAGTG
17-4	GAAACGTTCGGACCAATCTGAACACGCACGATAGAGGAGGGA
17-5	CTACCTAAGCGATTCACTACCCAAATCGTTTAGTTGGGAGGG
17-6	TTGGGAAAGGTTCCCGAAGAAATGAGTTCATGGGTACGAATA
17-7	CTGTGTATGTACTATAACTTGAACAGTGTCAATTCTCCACAG
17-8	CAAGTCTAACGATTTCTTAAACACGATATCTCCGCTATCTAG
17-9	AAGCCAGAGTCACGCAGGGTTCCTTAAGTCGTGTGGACGATT

17-10	GGTTCGCCATACGTTGTCCTTGGGAGCATCTATAGGCCTACG
17-11	ATTCCGTATACGGTGCCATCCCAGCGGGAATGGCATGCGATA
17-12	AACCAATGAATGGCTCAGATCTGTTTCCTCAGCCAACCTCGT
17-13	TGGAATCAGGGTTGTATGCGTACACGTGCAGACCGACTCTAA
17-14	GCACCCAGTCCGAAACACGGTAAGATGCGAACCATCTAGTGA
17-15	TTTTTTTTTTTTACGTCGTTCGTGAGAGCCCTATCGAGAGGGC
18-1	TTTTTTTTTTCTCGTTCTCACTATTATTGCCTCCTCCCTCTC
18-2	TACCACCCGGTGCATATAAGTATACAGAGGTAATTATTGATG
18-3	CAGCTAAAGCGCAATATTCGTCTGGGAGATCAGTCTTTACTA
18-4	GTGATTAGCCTCAGATTGGTCCCACATCGACCGCTCGGTATG
18-5	CGAACGTTTCGGTAGTGAATCGGACGTTGATCATGGTGGCAA
18-6	GCTTAGGTAGTTCTTCGGGAATATTTCCATCCGGTCTAAGCA
18-7	CCTTTCCCAACAAGTTATAGTGAAAGGGCCGTGTTGGGTCCC
18-8	ACATACACAGTTTAAGAAATCGAAGTAACACTCCTGACGGGA
18-9	GTTAGACTTGAACCCTGCGTGGCACAATAGGCATAACGGACC
18-10	ACTCTGGCTTAAGGACAACGTAAGAATGTTGACTACTGAAAG
18-11	ATGGCGAACCGGATGGCACCGGTTCGGAACTTGTCCGAAATT
18-12	TATACGGAATGATCTGAGCCAGGTACAGGAAGGAGTTCGTCT
18-13	TTCATTGGTTACGCATACAACAGGAGTTCTGAGTCGACGCCC
18-14	CCTGATTCCAACCGTGTTTCGGCGGAGAAAGTTTGCCAAGAA
18-15	GACTGGGTGCCGAACGACGTACGTAGGTTGTATTTTTTTTTT
19-1	TGGCAGGCATGATTGCTGTACAGGCAATAATATTTTTTTTTT
19-2	CAATCTGGTGCCGTGGAACCATACCTCTGTATGAGAGGGAGG
19-3	GGCTTGTGTGGCGTAACTTCGTGATCTCCCAGCATCAATAAT
19-4	GTGCACGCAAATCGCCCGTTAGGTCGATGTGGTAGTAAAGAC
19-5	CGGCCGGGACGTGCCACCTCAGATCAACGTCCCATACCGAGC
19-6	AGTGACTCTCCTCGAGCGAAGGGATGGAAATATTGCCACCAT
19-7	CCAGCGGGTCTATTCTAGACGACGGCCCTTTCTGCTTAGACC
19-8	TGCAGGCTACGATGGACGCTAAGTGTTACTTCGGGACCCAAC
19-9	GCTGAGTTCCGCGAATGTCCGGCCTATTGTGCTCCCGTCAGG
19-10	TTATCCCGGCACCGCGTATGATCAACATTCTTGGTCCGTTAT
19-11	TCTTCGCACAAGAATTGCTTCAAGTTCCGAACCTTTCAGTAG
19-12	TCGCACGCCTTGGGCAATCAACTTCCTGTACCAATTTCGGAC
19-13	ACGGCCATGTGTGTGACAACATCAGAACTCCTAGACGAACTC
19-14	CCTGCGAGGCGTACCCTACTAACTTTCTCCGCGGGCGTCGAC
19-15	TTTTTTTTTTGGTGCGTGTATTACAACCTACGTTCTTGGCAA
20-1	TTTTTTTTTTGTACAGCAATCTCCTATATGAAGCCAGGATAG
20-2	ATGCCTGCCATGGTTCCACGGTCCTCCCGATGGAAGGATAAG
20-3	CACCAGATTGCGAAGTTACGCTCAATCCATAGTGTGCATACT
20-4	CACACAAGCCTAACGGGCGATCGCTCCGACACGGCAACGAGC
20-5	TTGCGTGCACTGAGGTGGCACAGAACGTGATCAAGGACCCAG
20-6	GTCCCGGCCGCTTCGCTCGAGTGCTGATGATCCAATCAGCTC

20-7	GAGAGTCACTCGTCTAGAATAGCTCATGTGCCTATGAGATAG
20-8	GACCCGCTGGTAGCGTCCATCGGCATCTCCTAACTGTGCTCG
20-9	GTAGCCTGCACGGACATTCGCAAGGGCTGATACACCACTACA
20-10	GGAACTCAGCTCATACGCGGTAACCTATAGACCAAATAGACG
20-11	GCCGGGATAAGAAGCAATTCTAATTTCGTGCGGAAAGAGCCA
20-12	TGTGCGAAGATTGATTGCCCACCACAGGTGACTGTTCCCGCT
20-13	AGGCGTGCGATGTTGTCACACCACAGCAAAGGGTAAAGTCTC
20-14	ACATGGCCGTTAGTAGGGTACTTAAGTATTCGTTCCGACGTC
20-15	GCCTCGCAGGATACACGCACCAGAGTTCCGTATTTTTTTTTT
21-1	CGGGACGCGGTGACTCCCGACTTCATATAGGATTTTTTTTTT
21-2	TGAACGCTAGCCCTGTCTTGGCATCGGGAGGACTATCCTGGC
21-3	AGGTTTATCGGAACGCTGGATCTATGGATTGACTTATCCTTC
21-4	CCTCCCTGGAAGATGTACGACGTGTCGGAGCGAGTATGCACA
21-5	GCTTCAGAAAGATAGGCCATAGATCACGTTCTGCTCGTTGCC
21-6	GAACGGCTCAATAGCCTCAATGATCATCAGCACTGGGTCCTT
21-7	GAGCTTCTCTCCTGTATAATTGGCACATGAGCGAGCTGATTG
21-8	GATAATAAGCGGTAGTTAAGTTAGGAGATGCCCTATCTCATA
21-9	TACAGGTTCGCGGTGCTCCAATATCAGCCCTTCGAGCACAGT
21-10	CCGACAACTATATACGTTAGCGTCTATAGGTTTGTAGTGGTG
21-11	GACCGAACCTGACCGGTCGTCCGCACGAAATTCGTCTATTTG
21-12	TTCATTGGGTCGCGTAGGCGAGTCACCTGTGGTGGCTCTTTC
21-13	AATGAACTTGCTCTGGCATTCCCTTTGCTGTGAGCGGGAACA
21-14	CACACTGCCCGTCAATGGGACCGAATACTTAAGAGACTTTAC
21-15	TTTTTTTTTTAACGTAGCTAATACGGAACTCTGACGTCGGAA
22-1	TTTTTTTTTTGTCGGGAGTCACTTTGTATCTGAATTGGGCCT
22-2	CCGCGTCCCGCCAAGACAGGGTAGCTACCTATTAGGCCTGAC
22-3	CTAGCGTTCAATCCAGCGTTCCTCGACACCACGTAATGGCTG
22-4	CGATAAACCTGTCGTACATCTTGTGGGTCAGCGGGTACTAGG
22-5	TCCAGGGAGGTATGGCCTATCTAGAAGGAATAAATTCAGCGG
22-6	TTTCTGAAGCATTGAGGCTATTAGAATCTCTTATCAAAGAGG
22-7	TGAGCCGTTCAATTATACAGGACAATCTCCGGCTTCTAGTAA
22-8	AGAGAAGCTCACTTAACTACCCATGATATGGGCACCTCCGTT
22-9	GCTTATTATCTTGGAGCACCGCCCACCCTCGTCGAGCGGGAT
22-10	CGAACCTGTAGCTAACGTATATTATTAAGAAAGAATGTGTGT
22-11	TAGTTGTCGGGACGACCGGTCCACACGTTCTTCTCATTGAAT
22-12	AGGTTCGGTCTCGCCTACGCGCGCGCTTGGCCGAATTGCAGC
22-13	ACCCAATGAAGAATGCCAGAGATGAAATACTTGGTGAGTTAA
22-14	CAAGTTCATTGTCCCATTGACACACGTGTCAAGCGAAACTAT
22-15	GGGCAGTGTGTTAGCTACGTTGTGCGTCTAGGTTTTTTTTTT
23-1	GAGTAGCATTCTCATGGGCGCCAGATACAAAGTTTTTTTTTT
23-2	GGGACTCATGAGGTTTGATGCATAGGTAGCTAAGGCCCAATT
23-3	TTAAACTCTAGCGGGACCGCCGTGGTGTCGAGGTCAGGCCTA

23-4	ATGACCGCAACCAGTGTACGCGCTGACCCACACAGCCATTAC
23-5	ATCAGGGCAGTATTACATCATTATTCCTTCTACCTAGTACCC
23-6	CTTAAGTAGCGAAACCCTATTAAGAGATTCTACCGCTGAATT
23-7	TGGATGCTCCTATTCCCGGACCCGGAGATTGTCCTCTTTGAT
23-8	GAAGCCCTGCCCGAGGGTACACCCATATCATGTTACTAGAAG
23-9	AAGTTAGATAATCCGTAGCACACGAGGGTGGGAACGGAGGTG
23-10	CAAATTGGCTGACCTTAGTTGTTTCTTAATAAATCCCGCTCG
23-11	ACAACCAGGTCTGATTGTCTCAAGAACGTGTGACACACATTC
23-12	CTTATTTGAGACTATCCATTCGGCCAAGCGCGATTCAATGAG
23-13	GATCGATTTAGTAATCATCTAAAGTATTTCATGCTGCAATTC
23-14	AGTCTACTGCCGGTATCCCATTTGACACGTGTTTAACTCACC
23-15	TTTTTTTTTTCGTGCGGTAAGCCTAGACGCACATAGTTTCGC
24-1	TTTTTTTTTTGCGCCCATGAGTCAGACAGACTGGCTCCGCAG
24-2	AATGCTACTCGCATCAAACCTGAATAGGGTAAACCCTAAGGC
24-3	CATGAGTCCCGGCGGTCCCGCCCACTCCAGTTGCGTCCTACT
24-4	TAGAGTTTAAGCGTACACTGGTTCTCTGGTAGTGCGCGTATC
24-5	TTGCGGTCATATGATGTAATATATGTCTTAATACGTCGTGAC
24-6	CTGCCCTGATAATAGGGTTTCTCGAGCATTAATGGTCATCTA
24-7	GCTACTTAAGGTCCGGGAATAAGGGCGTGTCAACTACTCAAA
24-8	GGAGCATCCATGTACCCTCGGCTATCTACGATGCACTAGCAC
24-9	GCAGGGCTTCGTGCTACGGATTGGAGCCAAATCATTAACCTG
24-10	TATCTAACTTCAACTAAGGTCACAATGAGTCACCGTCGAGGA
24-11	AGCCAATTTGGAGACAATCAGGGCGTTTAAACCAAGCTACGT
24-12	ACCTGGTTGTGAATGGATAGTCGTGCATGGTGGTTCACTACA
24-13	CTCAAATAAGTAGATGATTACGGCTCCTGCTTATCGTCTCCT
24-14	TAAATCGATCATGGGATACCGTGGGCCTGTCGGTACCGACTC
24-15	GCAGTAGACTCTTACCGCACGCCAACAACTGTTTTTTTTTTT
25-1	AGTCTGTCTGATTTTTTTTT
25-2	TTACCCTATTCCTGCGGAGCC
25-3	AACTGGAGTGGGCCTTAGGGT
25-4	CTACCAGAGAAAGTAGGACGC
25-5	ATTAAGACATAGATACGCGCA
25-6	TTAATGCTCGAGTCACGACGT
25-7	TGACACGCCCTTAGATGACCA
25-8	ATCGTAGATAGTTTGAGTAGT
25-9	ATTTGGCTCCAGTGCTAGTGC
25-10	TGACTCATTGTCAGGTTAATG
25-11	GTTTAAACGCCTCCTCGACGG
25-12	CACCATGCACGACGTAGCTTG
25-13	AAGCAGGAGCCTGTAGTGAAC
25-14	CGACAGGCCCAAGGAGACGAT
25-15	ACAGTTGTTGGGAGTCGGTAC

Motif 4.1 (24H×29T)

Name	Sequence
1-1	GGTCGAGGGATTTTTTTTTTT
1-2	TGCCGCTCGACGATATCGAGC
1-3	CACTTAGTTTGGGAGGGCCTC
1-4	TGAAGCATCCTAAAGCGTATC
1-5	GGGAATATCCAATCTTAGGTG
1-6	GATATGCTTAGGCCAATAAAC
1-7	CCCTTAGGCTCCAACAAGGTG
1-8	CGTGCTATGATTGCACTCACT
1-9	CTATTAGGAAGTACATCCGTT
1-10	AACATACAGGCCTTAGGAGTT
1-11	CTCCGGTCGGGAATAGTTGAT
1-12	TTTAACACGTGTAGGGATTTC
1-13	TGATAACCTAAGTATGAGCTG
1-14	GACGTCCGTAGGTCAAAGCGA
1-15	TCCTACCGATCCGCGGAAGCC
2-1	TCCCTCGACCGCTCGATATCGTTTACTCTGAGCTTAAAGGCC
2-2	TCGAGCGGCAGAGGCCCTCCCAGAAAGCAATCGGCCTATCAA
2-3	AAACTAAGTGGATACGCTTTATCAGAACGCTCGGCCATGTTT
2-4	GGATGCTTCACACCTAAGATTCCTCCAGCTCCACGCCTTGTG
2-5	GGATATTCCCGTTTATTGGCCTGTCATATTTCGCGGGACTGA
2-6	TAAGCATATCCACCTTGTTGGAGAGGATTAAACCTACCGTGC
2-7	AGCCTAAGGGAGTGAGTGCAAATATATGAATTAGGTATCGTA
2-8	TCATAGCACGAACGGATGTACGGGATACTCTGGACGGGCTTC
2-9	TTCCTAATAGAACTCCTAAGGGCATCAACACGCGCGATGATG
2-10	CCTGTATGTTATCAACTATTCAGCATCATATAACGTATTTCT
2-11	CCGACCGGAGGAAATCCCTACACAGCAGACCCAATCCTCCTG
2-12	ACGTGTTAAACAGCTCATACTATACGCGTAGTTTAGGCACTG
2-13	TAGGTTATCATCGCTTTGACCGCGTTTGCGCCCATGCGGTTG
2-14	TACGGACGTCGGCTTCCGCGGCAACTCTACTAACGGGCGTGA
2-15	ATCGGTAGGATTTTTTTTTTTTCTGGGCGTTTTTTTTTTTTT
3-1	TCAGAGTAAATTTTTTTTTTTCGGCATTTCATTTTTTTTTTT
3-2	ATTGCTTTCTGGCCTTTAAGCTATCCTAGCCGAATCAGGAAC
3-3	AGCGTTCTGATTGATAGGCCGCAGAGGCAATACCCGCTTATA
3-4	GAGCTGGAGGAAACATGGCCGAGAACTACTTCATTAAAGTCG
3-5	AAATATGACACACAAGGCGTGGTCCGTACAGTTTGCCTCGAG
3-6	TTAATCCTCTTCAGTCCCGCGTATCGTACGAGTCGGGTGTAA
3-7	ATTCATATATGCACGGTAGGTAGCTGCCCTGTACACCTCTGC
3-8	AGAGTATCCCTACGATACCTATTCTCCGTGGCGTGGCCGATT
3-9	GTGTTGATGCGAAGCCCGTCCTTGAAGCCAACGCAATTTCGA

3-10	ATATGATGCTCATCATCGCGCACGTCCCAAATAATCTAAGGA
3-11	GGTCTGCTGTAGAAATACGTTCAAACTTGATACGAGAGTTTA
3-12	CTACGCGTATCAGGAGGATTGTTGGCAATATAGTAGATGGCC
3-13	GCGCAAACGCCAGTGCCTAAATCTGCGAAGAGGAAGGAACAT
3-14	AGTAGAGTTGCAACCGCATGGCGTGGGTGGACTTCTTGCTGC
3-15	AACGCCCAGATCACGCCCGTTTGAAGGCCTACGGAAACACGC
4-1	TGAAATGCCGGTTCCTGATTCCCTGAAGCGGCTCCCTAGATA
4-2	GGCTAGGATATATAAGCGGGTGCTAGGGAGTAGTTCCCTCCT
4-3	ATTGCCTCTGCGACTTTAATGCCTACGTCGTTGTGCAACCTG
4-4	AAGTAGTTCTCTCGAGGCAAAGTACAACTATAGAGCTGTTCT
4-5	CTGTACGGACTTACACCCGACATAGTGGTGGTACAGGGCCGA
4-6	TCGTACGATAGCAGAGGTGTAATTTATTAATGTTCTATACTA
4-7	CAGGGCAGCTAATCGGCCACGGCGCAGTGACCATGTGCCATT
4-8	CCACGGAGAATCGAAATTGCGCAGGAATGAGGGTACACATGC
4-9	TTGGCTTCAATCCTTAGATTATTCATATGACGTGCTCTGGCT
4-10	TTTGGGACGTTAAACTCTCGTTCGCTCGGTCCTGGGCTTCCC
4-11	ATCAAGTTTGGGCCATCTACTGGCTTGATGGCGTGCTACGCA
4-12	ATATTGCCAAATGTTCCTTCCAGCCCGGGCGGCTGTGTTACT
4-13	TCTTCGCAGAGCAGCAAGAAGAAAGCATGTATGTCGATTCCT
4-14	TCCACCCACGGCGTGTTTCCGGATAAACTTAATTGAGTTAGT
4-15	TAGGCCTTCATTTTTTTTTTTGACCGACCCTTTTTTTTTTTT
5-1	CCGCTTCAGGTTTTTTTTTTTACGCACATTGTTTTTTTTTTT
5-2	ACTCCCTAGCTATCTAGGGAGACGAGACTACGGGATCCTAAG
5-3	ACGACGTAGGAGGAGGGAACTGGCAAAGACCTAGTTAATCAC
5-4	ATAGTTGTACCAGGTTGCACAAGGTCCTGTGTCCGAAGCGAC
5-5	CCACCACTATAGAACAGCTCTAGATAAGCGTCTTTGCAAATG
5-6	ATTAATAAATTCGGCCCTGTAGAAGGCGAGCGTGTGAAAGTC
5-7	GTCACTGCGCTAGTATAGAACTTATTGTATTACAAAGCTATA
5-8	CTCATTCCTGAATGGCACATGAAAGAGGATCGCTTTCGGCCG
5-9	GTCATATGAAGCATGTGTACCTGTGAACTTGGAAACTTTATG
5-10	GACCGAGCGAAGCCAGAGCACAGTAGAGCCCTATCGCCCTTA
5-11	CCATCAAGCCGGGAAGCCCAGAAGTGCTTGTGGGAGCGGAGA
5-12	CGCCCGGGCTTGCGTAGCACGGCTGCTTTAAGACCCGCGTGA
5-13	TACATGCTTTAGTAACACAGCTTGACCCGATGCCTCTATACA
5-14	TAAGTTTATCAGGAATCGACAACCGCCGGAAGTAATACGCAC
5-15	AGGGTCGGTCACTAACTCAATTGTACAGCAACTACTTTAATA
6-1	CAATGTGCGTCTTAGGATCCCAATCCCTATCATAAAGCCCAC
6-2	GTAGTCTCGTGTGATTAACTATAACGGCTAGTTTACTCATAT
6-3	GGTCTTTGCCGTCGCTTCGGATCAGAACTGTATAAAGCATCA
6-4	CACAGGACCTCATTTGCAAAGGGCCCGTTACTAGGGTAGCAA
6-5	ACGCTTATCTGACTTTCACACCGTGCCATTGGGTCGTCCACG
6-6	GCTCGCCTTCTATAGCTTTGTCCTAATCGGTGGCTTCATGAG

6-7	AATACAATAACGGCCGAAAGCATCGGTCCTCGGGTGCTCAGA
6-8	GATCCTCTTTCATAAAGTTTCACGTACAGGTTGAGATCGTCC
6-9	CAAGTTCACATAAGGGCGATACTCCGCCGACCGACAGGAGTA
6-10	GGGCTCTACTTCTCCGCTCCCTGGTTCTCCTCGATGGTCAGC
6-11	ACAAGCACTTTCACGCGGGTCGAGTATTAGGTAATCGAATCG
6-12	TTAAAGCAGCTGTATAGAGGCAAACCATCCGCGACGCTTCGC
6-13	ATCGGGTCAAGTGCGTATTACTAATTAGAACCCTAACTTTCT
6-14	TTCCGGCGGTTATTAAAGTAGGTTTAGGAATACTGAATCTCG
6-15	TTGCTGTACATTTTTTTTTTTCACGTAAGAGTTTTTTTTTTT
7-1	GATAGGGATTTTTTTTTTTTTCAACTCCCATTTTTTTTTTT
7-2	CTAGCCGTTAGTGGGCTTTATCGCTGGCAGCTGAATCGGGAG
7-3	ACAGTTCTGAATATGAGTAAAGACAACTCGATAGTAATAACA
7-4	GTAACGGGCCTGATGCTTTATGTCTCTTTCCTTCCCGACTCC
7-5	CAATGGCACGTTGCTACCCTATCAAGTTACGGGTAGACACGT
7-6	ACCGATTAGGCGTGGACGACCTAACTGACAGGAATGGAAAGG
7-7	GAGGACCGATCTCATGAAGCCTTGTTAAGGGTCAAAGAATTG
7-8	ACCTGTACGTTCTGAGCACCCTAGAGTAAGCCCTCGACGACA
7-9	GTCGGCGGAGGGACGATCTCAAACGAAAGTCTCCGTATTACA
7-10	AGGAGAACCATACTCCTGTCGTCCCTTAATAGCTCTCTATAT
7-11	CCTAATACTCGCTGACCATCGGGCGCGTTTGTTCCAACTTCA
7-12	CGGATGGTTTCGATTCGATTAGCGGCTTCCTGGTTCATCAGC
7-13	GTTCTAATTAGCGAAGCGTCGCCTCCTACCACCTAACGCGCT
7-14	ATTCCTAAACAGAAAGTTAGGGTTTACGGTGGCATTCATCTA
7-15	CTCTTACGTGCGAGATTCAGTCTTTGCTCTCGAACTGGAATT
8-1	ATGGGAGTTGCTCCCGATTCACGGAGGTAAACACTGCAAGCG
8-2	GCTGCCAGCGTGTTATTACTAGGCTTGACTATTCGGTTCTGC
8-3	TCGAGTTGTCGGAGTCGGGAAACGCACGGTCTTTAAGAAACA
8-4	GGAAAGAGACACGTGTCTACCTTGCACCTCCCTCCCTGCACT
8-5	CGTAACTTGACCTTTCCATTCGTCTCTAGGGCAAATGCAAAG
8-6	CTGTCAGTTACAATTCTTTGAATCGATTTAACAGGCCGGATC
8-7	CCCTTAACAATGTCGTCGAGGGCTCGCGGATACCTGTGGTCT
8-8	GCTTACTCTATGTAATACGGATCGGATACGCACCTGCCCATT
8-9	GACTTTCGTTATATAGAGAGCGTCAAAGTTACCGCGACCCAT
8-10	TATTAAGGGATGAAGTTGGAACCGGCTCTTTAATACCTCCAA
8-11	CAAACGCGCCGCTGATGAACCGATACGCAGGAGTCGATGACG
8-12	AGGAAGCCGCAGCGCGTTAGGTCTTTACGCGGTTACATACGG
8-13	TGGTAGGAGGTAGATGAATGCCCAATTCCGAGCTGCGCAGAA
8-14	CACCGTAAACAATTCCAGTTCAGTGGGAACCTGGGAGCCGTG
8-15	GAGAGCAAAGTTTTTTTTTTTGCGCGGTTGATTTTTTTTTTT
9-1	TTTACCTCCGTTTTTTTTTTTACCGAAGGAATTTTTTTTTTT
9-2	TAGTCAAGCCCGCTTGCAGTGTCCAGAAGAAGCGTGGCTGCG
9-3	GACCGTGCGTGCAGAACCGAAGTTGATAGGTGGTGCTTTGCA

9-4	GGAGGTGCAATGTTTCTTAAAGGTCAATCCCTCCCACTAGGC
9-5	CCCTAGAGACAGTGCAGGGAGCTTATAATTATCCCTTTACGA
9-6	TTAAATCGATCTTTGCATTTGTGAGCTGGCCGATCTACTTCC
9-7	ATCCGCGAGCGATCCGGCCTGCCACCATGCACGAGCGACCTG
9-8	GCGTATCCGAAGACCACAGGTCCCTAACGACAGGCCTAGTCT
9-9	TAACTTTGACAATGGGCAGGTATTGTCAGACCCTTTAGAGTT
9-10	AAAGAGCCGGATGGGTCGCGGTAGTAATGTGGATTGCGACAC
9-11	CCTGCGTATCTTGGAGGTATTGGAGGCTACCGCGAACTTGTC
9-12	CGCGTAAAGACGTCATCGACTGGGCCGGTAGCCTTAAAGTGC
9-13	TCGGAATTGGCCGTATGTAACTACTGCGACGCAAGATCTTCC
9-14	GGTTCCCACTTTCTGCGCAGCGGCTCTTCGCTATTGGTTGAC
9-15	TCAACCGCGCCACGGCTCCCAATGTACCACTATCCCGCGCTG
10-1	TTCCTTCGGTCGCAGCCACGCGTAGACCGCTGTTTCTTCGGT
10-2	TTCTTCTGGATGCAAAGCACCATCACAGACGAAATGGTACTC
10-3	ACCTATCAACGCCTAGTGGGATTACCCTCAGGGCCTCAGCCC
10-4	GGGATTGACCTCGTAAAGGGAATACCAGAATCAATGTGACTC
10-5	TAATTATAAGGGAAGTAGATCTGCATTTCAGCGGCACCTCCT
10-6	GGCCAGCTCACAGGTCGCTCGGCGCTGACCCTGTTCGGTGTA
10-7	TGCATGGTGGAGACTAGGCCTAGAGAATTTAGCTTACATCTC
10-8	GTCGTTAGGGAACTCTAAAGGCCTGTCTTTACCCACGTAAGG
10-9	GTCTGACAATGTGTCGCAATCAAGGAGCCCTGCCCTAAGCAC
10-10	CACATTACTAGACAAGTTCGCGTACACGAAGATGATGACGCA
10-11	GGTAGCCTCCGCACTTTAAGGATAGATAGGGAAAGACTGGCT
10-12	CTACCGGCCCGGAAGATCTTGAGCGCCAGAAGGGAAGAAGTA
10-13	CGTCGCAGTAGTCAACCAATAAAGTGGCCTAATAACAGTGCT
10-14	GCGAAGAGCCCAGCGCGGGATTATCAACATAGGGCTTTGGCC
10-15	AGTGGTACATTTTTTTTTTTATTTAGTGCTTTTTTTTTTTT
11-1	AGCGGTCTACTTTTTTTTTTTTTCGCATCTCTTTTTTTTTT
11-2	CGTCTGTGATACCGAAGAAACTCGCGAGCCGCTAGGTGTGGA
11-3	CTGAGGGTAAGAGTACCATTTAGTCTCAGAGCCATCCTGCCT
11-4	ATTCTGGTATGGGCTGAGGCCCTGGTATGTATGTACGTGTCC
11-5	CTGAAATGCAGAGTCACATTGTCTGAAAGGGTCTCATATGGC
11-6	GGGTCAGCGCAGGAGGTGCCGGTAGGACCGTCTGAAACAGGC
11-7	TAAATTCTCTTACACCGAACACAACCATGACAGCTCCCGCTG
11-8	TAAAGACAGGGAGATGTAAGCGAGCCCTTCGAGCTTCTGCAC
11-9	AGGGCTCCTTCCTTACGTGGGTGCAGGTAGGCCGTTTCTTAC
11-10	CTTCGTGTACGTGCTTAGGGCCTTGTACAATTTACCGGTCAT
11-11	CCCTATCTATTGCGTCATCATCTTCACTGACTCCATATCCCG
11-12	TTCTGGCGCTAGCCAGTCTTTAGAACAACACACGCCACTGTA
11-13	TAGGCCACTTTACTTCTTCCCATTACGGGAAAGCGTGACTTA
11-14	TATGTTGATAAGCACTGTTATTTAGAACGGACAGAATAAATA
11-15	AGCACTAAATGGCCAAAGCCCAGGTTAGTTGTGGAACCTCGC

12-1	GAGATGCGAATCCACACCTAGTTGAGTCGTTATGTAGCCTCT
12-2	CGGCTCGCGAAGGCAGGATGGGCAGACGCGTTCAATCACATG
12-3	CTCTGAGACTGGACACGTACATGACGACAATCTTGTTTATGC
12-4	TACATACCAGGCCATATGAGACTTAGCGGAGATTGGTCACCT
12-5	CCCTTTCAGAGCCTGTTTCAGGTTAGCCGTATTGTCGCTTCA
12-6	ACGGTCCTACCAGCGGGAGCTGCTTATTACTTATGAGGGCTA
12-7	GTCATGGTTGGTGCAGAAGCTGAGTTATCTCCGCGGACCGCT
12-8	CGAAGGGCTCGTAAGAAACGGTCGGGTAGTACTTAACTCACT
12-9	CCTACCTGCAATGACCGGTAAAGAGAAACACATATAGTCAGG
12-10	ATTGTACAAGCGGGATATGGACCGTGAAAGCTTACCTAAGAG
12-11	GTCAGTGAAGTACAGTGGCGTTACGGTTGGGCGCGAGGGCAT
12-12	GTGTTGTTCTTAAGTCACGCTATGCAGACTAAATATCGTATG
12-13	TTCCCGTAATTATTTATTCTGTTGAGGCCCATTAGCATCCAC
12-14	TCCGTTCTAAGCGAGGTTCCAGACCATCCATATAAGGAACGC
12-15	CAACTAACCTTTTTTTTTTTTCGTTTATATTTTTTTTTTTTT
13-1	AACGACTCAATTTTTTTTTTTTTAAGGTCCATTTTTTTTTTT
13-2	ACGCGTCTGCAGAGGCTACATACAAGCCTATATGCTTTACTG
13-3	ATTGTCGTCACATGTGATTGATCACCTCAGTATGAAAGCATA
13-4	CTCCGCTAAGGCATAAACAAGCCGTGTCTGGGCGCTACCAAG
13-5	TACGGCTAACAGGTGACCAATGTATTGAGGTGTGGGCGGGCT
13-6	AGTAATAAGCTGAAGCGACAACGACCCTTAGGACGGCATTTG
13-7	GAGATAACTCTAGCCCTCATAACCTCCAACCGGCTTTGTGTA
13-8	TACTACCCGAAGCGGTCCGCGTCACGAACTGCAACTGAATCG
13-9	GTGTTTCTCTAGTGAGTTAAGGATGGTCACGAGGGTCGTGGT
13-10	GCTTTCACGGCCTGACTATATGTACCGCTCAATCGCCGTTAG
13-11	CCCAACCGTACTCTTAGGTAACTGCAGCGTCGACACAATCGT
13-12	TAGTCTGCATATGCCCTCGCGTTAACCAGCCAGACGTTCAGG
13-13	TGGGCCTCAACATACGATATTGGATATGTTTAGCATAGACCG
13-14	ATGGATGGTCGTGGATGCTAATGTTAATACACAAGGTATGGA
13-15	AATATAAACGGCGTTCCTTATGCAGTGATTTACAGGGCTCAA
14-1	TGGACCTTAACAGTAAAGCATTAGGAGTCCAGGTAATCATAA
14-2	ATAGGCTTGTTATGCTTTCATGTGCAGAATTGAACATTATCA
14-3	ACTGAGGTGACTTGGTAGCGCCGATTCGAGTACAATTAGAAA
14-4	CCAGACACGGAGCCCGCCCACCTTTCTCTGTGCACCCAGATA
14-5	ACCTCAATACCAAATGCCGTCGAAAGACGAATAGAAATTGAC
14-6	CTAAGGGTCGTACACAAAGCCTTCCTCTAAAGCAGTCGCTCT
14-7	GGTTGGAGGTCGATTCAGTTGACCTTATAGCCGTCGCGTGGC
14-8	CAGTTCGTGAACCACGACCCTATATACACGTCCTGAGCATTT
14-9	CGTGACCATCCTAACGGCGATAGCCGCACGTTAGTAACTGTG
14-10	TGAGCGGTACACGATTGTGTCGTATAATTCAAGCGGGCCTCT
14-11	GACGCTGCAGCCTGAACGTCTTGGCTGGCCTGGAATGGTAAA
14-12	GGCTGGTTAACGGTCTATGCTCGGCCGGTACTCTTGTCCAGA

14-13	AAACATATCCTCCATACCTTGCGCGAGCCTGGCATATTTAGC
14-14	TGTATTAACATTGAGCCCTGTGTCACCAGATCTATGGGTATC
14-15	AAATCACTGCTTTTTTTTTTTCTTCTGGAAGTTTTTTTTTTT
15-1	TGGACTCCTATTTTTTTTTTTATCTTGCCCTTTTTTTTTTT
15-2	AATTCTGCACTTATGATTACCCATACCCATGCTGTTTATGTA
15-3	ACTCGAATCGTGATAATGTTCCCTACCTCTACGCTCGCGTTG
15-4	ACAGAGAAAGTTTCTAATTGTGCTTGGGAAACGGCCTGGAGA
15-5	TTCGTCTTTCTATCTGGGTGCCGTCTATATATAAAGTTCTGA
15-6	TTTAGAGGAAGTCAATTTCTATTTCCATGGCCAGCCCAAGAG
15-7	GCTATAAGGTAGAGCGACTGCTTAATAGGGCGAATTACGGTA
15-8	ACGTGTATATGCCACGCGACGTTCCACTTTCCCTTTGACGTA
15-9	ACGTGCGGCTAAATGCTCAGGGCATACAACCACAACCGATCT
15-10	TGAATTATACCACAGTTACTATGGACTAAATGTGAGTGTCCC
15-11	AGGCCAGCCAAGAGGCCCGCTCTAGTACAAAGCAAAGAGTAA
15-12	GTACCGGCCGTTTACCATTCCAGTAACAATCATGCCAAAGGA
15-13	CAGGCTCGCGTCTGGACAAGAGAACACGGTCTCTCAGCCGCG
15-14	ATCTGGTGACGCTAAATATGCATAGAGCAAACATGGTGTGTC
15-15	CTTCCAGAAGGATACCCATAGGCATGAGCTCCTGGCGTTGCT
16-1	AGGGCAAGATTACATAAACAGAGAGTTGCGCCGGACCGACTC
16-2	CATGGGTATGCAACGCGAGCGCCAATATCACCTATCAGAGAT
16-3	TAGAGGTAGGTCTCCAGGCCGATACTATGACTAGCCCAAACA
16-4	TTTCCCAAGCTCAGAACTTTAAATAAGATTCGTAACCTGCCC
16-5	TATATAGACGCTCTTGGGCTGGCTCTGTCTATTAACCTAGAT
16-6	GCCATGGAAATACCGTAATTCTGATGTGTGCGACGCGAGACC
16-7	GCCCTATTAATACGTCAAAGGATGATAGGTCGAGTGGTGCAA
16-8	GAAAGTGGAAAGATCGGTTGTCGAAGCTTATGCACTCATTGG
16-9	GGTTGTATGCGGGACACTCACACCCGGTAGAGAGTGGTCCAA
16-10	ATTTAGTCCATTACTCTTTGCCAACAGATCGACGTTTGATTG
16-11	TTTGTACTAGTCCTTTGGCATGTAAAGTTTGTTCTCGGTCTG
16-12	GATTGTTACTCGCGGCTGAGACCTCGGTCGCTGTTCGTACTG
16-13	GACCGTGTTCGACACACCATGTTCGGAGATCGTTTATTCAGC
16-14	TTTGCTCTATAGCAACGCCAGAGGCTGAGCGAACGTAGGCCG
16-15	GAGCTCATGCTTTTTTTTTTTTCCGGGAGTAGTTTTTTTTTT
17-1	GCGCAACTCTTTTTTTTTTTTTAGTGTATGAGTTTTTTTTTT
17-2	GTGATATTGGGAGTCGGTCCGATGCACGGGTAAGCACATAAT
17-3	GTCATAGTATATCTCTGATAGATCACCGCGAATGCAGACGTC
17-4	GAATCTTATTTGTTTGGGCTAAGGGCTTCCTCGGCATTTACC
17-5	TAGACAGAGCGGGCAGGTTACTACTGCAAACGAGTGAATTTA
17-6	GCACACATCAATCTAGGTTAACTTGTGAGACGGCGAGTACCG
17-7	GACCTATCATGGTCTCGCGTCGCATGTGATAATCCTCCCGCT
17-8	ATAAGCTTCGTTGCACCACTCCAGAAGTCTTGAGTGTGGAGA
17-9	TCTACCGGGTCCAATGAGTGCCACCGTGCACGCAGTCCCTAC

17-10	CGATCTGTTGTTGGACCACTCGGCCCTCCATGAGGGTTTAGC
17-11	CAAACTTTACCAATCAAACGTTTATCAATAAGCTCGCGTATG
17-12	GCGACCGAGGCAGACCGAGAAGTTAGAGTGCTCCATCTCTCT
17-13	GATCTCCGAACAGTACGAACACGATATAGTATGGTCGTAAGG
17-14	CGCTCAGCCTGCTGAATAAACCGTTGTTTAAGCGACCGGACC
17-15	CTACTCCCGGCGGCCTACGTTATCTCTCTAACCTATCCCTGA
18-1	CTCATACACTATTATGTGCTTATTGCCGGGTCTGTTGCTCTT
18-2	ACCCGTGCATGACGTCTGCATCGAAATCATTGGCCGCGCCCT
18-3	TCGCGGTGATGGTAAATGCCGCTCATCAATCAATATAAGCTT
18-4	AGGAAGCCCTTAAATTCACTCAACTAACTGGAAACCACCAAC
18-5	GTTTGCAGTACGGTACTCGCCAGGTCATACGAATAATGTGCG
18-6	GTCTCACAAGAGCGGGAGGATCAAAGAGAGGCCTAATTTCCT
18-7	TATCACATGCTCTCCACACTCGGGTCACCACGTCGTTAAATG
18-8	AAGACTTCTGGTAGGGACTGCTCTCATTGGCGACAGCGATGG
18-9	GTGCACGGTGGCTAAACCCTCCCATCACGTCTACCGATGCAT
18-10	ATGGAGGGCCCATACGCGAGCCCATTACCGAGACAACTTTGG
18-11	TTATTGATAAAGAGAGATGGAGCACGTGGGTACCATCTGCTA
18-12	GCACTCTAACCCTTACGACCACCGCACCGCTGTACGACGGCT
18-13	TACTATATCGGGTCCGGTCGCGTGCTCCAATTGCCGCTGTTG
18-14	TTAAACAACGTCAGGGATAGGTGCTAACGTTTAACGCTAGAT
18-15	TTAGAGAGATTTTTTTTTTTTCTCGGTCATGTTTTTTTTTTT
19-1	ACCCGGCAATTTTTTTTTTTTAGTGAGCGGATTTTTTTTTT
19-2	AATGATTTCGAAGAGCAACAGATAGAACTATTGATTGTAAAG
19-3	GATTGATGAGAGGGCGCGGCCATGGACGTCGTCGTCTCAAAC
19-4	CCAGTTAGTTAAGCTTATATTCTACGATAACGCTCTAGCCTT
19-5	CGTATGACCTGTTGGTGGTTTGTGACTTACGCTACCCTCGAT
19-6	CCTCTCTTTGCGCACATTATTCTTAAACAGGCGGTAGTTCTT
19-7	GTGGTGACCCAGGAAATTAGGTGGAATAATATCTGATCCACA
19-8	GCCAATGAGACATTTAACGACCACTCTACAGAGCATTTGCTC
19-9	GACGTGATGGCCATCGCTGTCTCACCCTACTCATTCATACTC
19-10	TCGGTAATGGATGCATCGGTAGCGTGGAGATCGAGATTTGAA
19-11	ACCCACGTGCCCAAAGTTGTCTGGCGTGTAGGCTACTCTGTT
19-12	AGCGGTGCGGTAGCAGATGGTTTGCTTCGCGCGAGACTCCTA
19-13	ATTGGAGCACAGCCGTCGTACCCTACACGATACGGGTCCTCA
19-14	AACGTTAGCACAACAGCGGCAACAGAACGACCAGAAACGAAT
19-15	CATGACCGAGATCTAGCGTTATGAAGGATGTAGTGGTTTAGA
20-1	TCCGCTCACTCTTTACAATCACTATTTACGTGAATGTACAAT
20-2	ATAGTTCTATGTTTGAGACGAAACGTACCGCCTTAGCTAGGT
20-3	CGACGTCCATAAGGCTAGAGCGTTACGTCTAGGTGAGGACCA
20-4	GTTATCGTAGATCGAGGGTAGGGCAGTCATCCGCTCAGTAAC
20-5	CGTAAGTCACAAGAACTACCGAACCGACAAGGCACGAAACGA
20-6	CCTGTTTAAGTGTGGATCAGAGTACTGTACATACGCGTCCTT

20-7	TATTATTCCAGAGCAAATGCTCGACAGGTGTAAGCCGCCCTC
20-8	CTGTAGAGTGGAGTATGAATGAACCCACCGTCAAAGCTAGCG
20-9	AGTAGGGTGATTCAAATCTCGAGGTTTAAGTTTCCGGGACTG
20-10	ATCTCCACGCAACAGAGTAGCGACACGGTCGATGCAATACCG
20-11	CTACACGCCATAGGAGTCTCGGGTCGACCTCTTTGGAGGTGA
20-12	CGCGAAGCAATGAGGACCCGTGCGGGTTAGTACAATCTACAT
20-13	ATCGTGTAGGATTCGTTTCTGAAAGAATCAAAGCATCTTTAT
20-14	GTCGTTCTGTTCTAAACCACTCGTCCAGGGACCTAATAAACT
20-15	ACATCCTTCATTTTTTTTTTTTGCATGCTGGTTTTTTTTTTT
21-1	ACGTAAATAGTTTTTTTTTTTTCTTCTATGATTTTTTTTTT
21-2	GCGGTACGTTATTGTACATTCGGTGCCGACTCTTTCCCATCG
21-3	TAGACGTAACACCTAGCTAAGCAGATCTAATACGAGGCTAAA
21-4	GATGACTGCCTGGTCCTCACCTAACCCGGGCACAGTAACCAC
21-5	CTTGTCGGTTGTTACTGAGCGCAAGGCCAGTACCCTGGAAGG
21-6	TGTACAGTACTCGTTTCGTGCCGCCCGGTAAGAAATAGTCGG
21-7	ACACCTGTCGAAGGACGCGTACCCGATAATTCCGGAGATAGT
21-8	ACGGTGGGTTGAGGGCGGCTTGACGAGCCTCCTCTGTTAGTT
21-9	ACTTAAACCTCGCTAGCTTTGCGCGACCTTGCATCACGGAGA
21-10	CGACCGTGTCCAGTCCCGGAATCCTTATTGCTAATAGACTTG
21-11	GAGGTCGACCCGGTATTGCATGGATTAGGCAGACATGTCAAT
21-12	ACTAACCCGCTCACCTCCAAAGGGCATATCGTAGGAAGCGCC
21-13	TTGATTCTTTATGTAGATTGTATAAGAGCACATTGGTGGGCT
21-14	TCCCTGGACGATAAAGATGCTGTTGGGCACCAATAGGCGGGA
21-15	CCAGCATGCAAGTTTATTAGGCGGCACCCGGAAGCACATTCT
22-1	TCATAGAAGACGATGGGAAAGCCGTCTCGATGATGTACAACG
22-2	AGTCGGCACCTTTAGCCTCGTTTGCCAGCCAGGCAGTTTAAG
22-3	ATTAGATCTGGTGGTTACTGTGTACGAACGGTAGCTCGGGCC
22-4	GCCCGGGTTACCTTCCAGGGTTAGCGCCTGCTATAAGCCGCT
22-5	ACTGGCCTTGCCGACTATTTCTAGCACTCAATCGAGTTGGTT
22-6	TTACCGGGCGACTATCTCCGGAATATGCCTAGACATTCTACA
22-7	AATTATCGGGAACTAACAGAGGAGATAGGACCACCACTCTTT
22-8	GAGGCTCGTCTCTCCGTGATGCACCTAGGTCGCAGAACCCGC
22-9	CAAGGTCGCGCAAGTCTATTATACAAAGAGGAATCAGTAATT
22-10	GCAATAAGGAATTGACATGTCTAGTGGATAATATGCTCTTTG
22-11	TGCCTAATCCGGCGCTTCCTAACAGGCGACTAATGTATTTAC
22-12	CGATATGCCCAGCCCACCAATGATGTCATTGTCCCACACGCA
22-13	GTGCTCTTATTCCCGCCTATTTGACTATAAGGATGTGATGCC
22-14	GGTGCCCAACAGAATGTGCTTCAGACCGTTCGCTGTACCCGT
22-15	CCGGGTGCCGTTTTTTTTTTTCGCTGCACAATTTTTTTTTTT
23-1	ATCGAGACGGTTTTTTTTTTTTAGAGTATACTTTTTTTTTTT
23-2	TGGCTGGCAACGTTGTACATCGTTGGACCGCGTCTACCTAGT
23-3	CCGTTCGTACCTTAAACTGCCGTTTATCTATGGTATACGCTG

23-4	GCAGGCGCTAGGCCCGAGCTAACCCTGACGAGACAAAGCCCG
23-5	TTGAGTGCTAAGCGGCTTATAAAGAGGGCGTGCCGCAGGGCC
23-6	TAGGCATATTAACCAACTCGAGTATACAACGTCTCCCAACCG
23-7	GTCCTATCTCTGTAGAATGTCGACCGGTTATGCCGCTGAGGT
23-8	GACCTAGGTGAAAGAGTGGTGTTCCATTGTAGAATAAAGAAG
23-9	CCTCTTTGTAGCGGGTTCTGCGTGACACGCAAGGAAGCTATC
23-10	TTATCCACTAAATTACTGATTCAACGTGCGCACTAAGACCCA
23-11	AGTCGCCTGTCAAAGAGCATACTCATAATCCAGTGATAAATC
23-12	CAATGACATCGTAAATACATTCAACGCAGACAAGGGCTGTCA
23-13	CTTATAGTCATGCGTGTGGGAGATTAATGACGGAGGTGCTTG
23-14	GAACGGTCTGGGCATCACATCTTGATACTGTTTAAACCCACG
23-15	TTGTGCAGCGACGGGTACAGCCTAACTTCCTAAGTAAACCTG
24-1	GTATACTCTAACTAGGTAGACCCGTGGTCGAGTCCGGGAAGT
24-2	GCGGTCCAACCAGCGTATACCATTATGCCCTTTATGGAGTTA
24-3	ATAGATAAACCGGGCTTTGTCATTACCTCGGTGACGGAATAG
24-4	TCGTCAGGGTGGCCCTGCGGCAGTCCCGAGTATCGCGGTTTA
24-5	ACGCCCTCTTCGGTTGGGAGAATTGGCTATGTGCACAATCTG
24-6	CGTTGTATACACCTCAGCGGCTGGTTGAGAGGGTCCAGGGCC
24-7	ATAACCGGTCCTTCTTTATTCATGGTATATGTTCCTGTTTAT
24-8	TACAATGGAAGATAGCTTCCTACACTAAGCTTGAGGAAGGGC
24-9	TGCGTGTCACTGGGTCTTAGTGCACGCCCAAGTAAGGATTTA
24-10	GCGCACGTTGGATTTATCACTTTCGAGAGATACTTTAACATC
24-11	GGATTATGAGTGACAGCCCTTGATCCAGCAAGCAAGCGCTAA
24-12	GTCTGCGTTGCAAGCACCTCCGTGCACCAGTTGAAACTACCT
24-13	GTCATTAATCCGTGGGTTTAAATGTTTGATTTCATTTGCGTC
24-14	ACAGTATCAACAGGTTTACTTCAAGGGCCTTTAGTCAGCTAA
24-15	AGGAAGTTAGTTTTTTTTTTTGAAGAGGTACTTTTTTTTTTT
25-1	TCGACCACGGTTTTTTTTTT
25-2	AGGGCATAATACTTCCCGGAC
25-3	CCGAGGTAATTAACTCCATAA
25-4	ACTCGGGACTCTATTCCGTCA
25-5	CATAGCCAATTAAACCGCGAT
25-6	CTCTCAACCACAGATTGTGCA
25-7	CATATACCATGGCCCTGGACC
25-8	AGCTTAGTGTATAAACAGGAA
25-9	TTGGGCGTGCGCCCTTCCTCA
25-10	ATCTCTCGAATAAATCCTTAC
25-11	TTGCTGGATCGATGTTAAAGT
25-12	ACTGGTGCACTTAGCGCTTGC
25-13	AATCAAACATAGGTAGTTTCA
25-14	AAGGCCCTTGGACGCAAATGA
25-15	GTACCTCTTCTTAGCTGACTA

Motif 11.1 (24H×29T)

Name	Sequence
1-1	TCCGCCGTCGGCGTCTCGGGA
1-2	ACTTGTACCAAGAGGCCAGTG
1-3	GTCTGTGCCCTAGCTGCATCG
1-4	CGTAGACGTTAAGACCTCGGA
1-5	AGGTGGTTTATACGGACTGTA
1-6	GGACTATGCGTTTAATACCCA
1-7	GTGTAATCTTAGAAGGAGTCA
1-8	CGTTCCTAAAGCGCGGATTTA
1-9	TGTAACACGACTGGAGACTTT
1-10	AGGTTTGTACGTGCGTAGCCT
1-11	CACGTATCAAGTAGTCGACTC
1-12	ACTGTAACCCATGCAATGGTC
1-13	TGCATAGGGCCAGGGTCGCTA
1-14	GAACACATTCTAAATAGAATC
1-15	TTTTTTTTTTTCCATGAACCT
2-1	TTTTTTTTTTGCCCAATGCGTTTTTTTTTTTTTTTTTTTTTTCCGACGGCGGATTTTTTTTTT
2-2	GTGCAGCAAGTCCGTTAACCATTTTTTTTTTTTTTTTTTTTTTGGTACAAGTTCCCGAGACG
2-3	GAATGAACTAGGGATAATAAGTTTTTTTTTTTTTTTTTTTTTAGGGCACAGACCACTGGCCTC
2-4	ACCGACTAAATGATTGAGTCCTTTTTTTTTTTTTTTTTTTTTAACGTCTACGCGATGCAGCT
2-5	TACAAAGTTCAACCATAGACGTTTTTTTTTTTTTTTTTTTTTATAAACCACCTTCCGAGGTCT
2-6	TGGGATAGTAGACACCTGCCCTTTTTTTTTTTTTTTTTTTTTACGCATAGTCCTACAGTCCGT
2-7	TTAGCTATTTAGTTCGGAGTTTTTTTTTTTTTTTTTTTTTTAAGATTACACTGGGTATTAA
2-8	GAAAGAACTGGGCCGTTGAAGTTTTTTTTTTTTTTTTTTTTTCTTTAGGAACGTGACTCCTTC
2-9	TCTGAATATATTTCGACTTATTTTTTTTTTTTTTTTTTTTTGTCGTGTTACATAAATCCGCG
2-10	TTACAGTTCGCATATAAAGGCTTTTTTTTTTTTTTTTTTTTTCGTACAAACCTAAAGTCTCCA
2-11	ATGACGTCACTTTCGTGCGCGTTTTTTTTTTTTTTTTTTTTTCTTGATACGTGAGGCTACGCA
2-12	TAGCCCGACGTTCCATTACAATTTTTTTTTTTTTTTTTTTTTTGGGTTACAGTGAGTCGACTA
2-13	GAACTCCTTAGCACCCAACGCTTTTTTTTTTTTTTTTTTTTTTGGCCCTATGCAGACCATTGCA
2-14	TCAGCTACAAAGTCAGGGAGTTTTTTTTTTTTTTTTTTTTTTAGAATGTGTTCTAGCGACCCT
2-15	TAAGCCGTGATGTGGTCGAGATTTTTTTTTTTTTTTTTTTTTTAATATATCTATGATTCTATTT
3-1	AGTTATCCCTCATCGGTTACTTTTTTTTTTTTTTTTTTTTTTCTTGCTGCACACGCATTGGGC
3-2	TAGAAGGGCCCTCAAGATGCATTTTTTTTTTTTTTTTTTTTTTAGTTCATTCTGGTTAACGGA
3-3	ATGCGGGCCTAGCATGTAAGCTTTTTTTTTTTTTTTTTTTTTTAGTCGGTCTTATTATCCC
3-4	TCCGTAAATTTAGTTTAGGACTTTTTTTTTTTTTTTTTTTTTGAACTTTGTAGGACTCAATCA
3-5	GTTTACTGCACCAACTTGAAGTTTTTTTTTTTTTTTTTTTTTTACTATCCCACGTCTATGGTT
3-6	ACTCGCAGCACCCGTGGAGTTTTTTTTTTTTTTTTTTTTTTAAATAGCTAAGGGCAGGTGTC
3-7	TAAAGGGCAGCCCTTGTTTCATTTTTTTTTTTTTTTTTTTTTCAGTTCTTTCAACTCCGAACT
3-8	TTTAAGCCCGGTGCTTGCGCTTTTTTTTTTTTTTTTTTTTTTATATTCAGACTTCAACGGCC
3-9	GGAATTGTCATGGTGAGTCCGTTTTTTTTTTTTTTTTTTTTTCGAACTGTAAATAAGTCGAAA

3-10	CCATGATCTAGGGCGCCAGTGTTTTTTTTTTTTTTTTTTTTTGTGACGTCATGCCTTTATATG
3-11	TGCGGTTGCTGCCTAAGTTCATTTTTTTTTTTTTTTTTTTTTCGTCGGGCTACGCGCACGAAA
3-12	CTAGATAGGATCGTCCGTGACTTTTTTTTTTTTTTTTTTTTTTAAGGAGTTCTTGTAATGGAA
3-13	ACCCTAAATAAGTCGTGCCGCTTTTTTTTTTTTTTTTTTTTTTGTAGCTGAGCGTTGGGTGC
3-14	TTCAACAATTTATGGGAGACTTTTTTTTTTTTTTTTTTTTTTCACGGCTTAACTCCCTGACT
3-15	GTAACATGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTCGACCACA
4-1	TTTTTTTTTTCACGTGGGCATTTTTTTTTTTTTTTTTTTTTGAGGGATAACTTTTTTTTTTT
4-2	CGAGTCCGCGAGGTCCGAATCTTTTTTTTTTTTTTTTTTTTGGGCCCTTCTAAGTAACCGAT
4-3	CGCGCCAACGGGTGGAGCTGTTTTTTTTTTTTTTTTTTTTTAGGCCCGCATTGCATCTTGA
4-4	CCATCGCGCCCTAAGTGTATGTTTTTTTTTTTTTTTTTTTTAAATTTACGGAGCTTACATGC
4-5	GGTACCGGACCGTGGTCACCGTTTTTTTTTTTTTTTTTTTTGTGCAGTAAACGTCCTAAACT
4-6	AGGTAATCTAATAGCAGCAGTTTTTTTTTTTTTTTTTTTTGTGCTGCGAGTCTTCAAGTTG
4-7	GCGGCTCTAAGCTCTTTGGCGTTTTTTTTTTTTTTTTTTTTGCTGCCCTTTAAACTCCACGG
4-8	CCAAAGGAATCTCGCTTCATATTTTTTTTTTTTTTTTTTTTCCGGGCTTAAATGAAACAAGG
4-9	GAGTCTTATCATGTTTGACGCTTTTTTTTTTTTTTTTTTTTATGACAATTCCAGCGCAAGCA
4-10	CGGACGTGAATTCTTCGGAGATTTTTTTTTTTTTTTTTTTTCTAGATCATGGCGGACTCACC
4-11	TAACTACTACTAGGAGTCGAATTTTTTTTTTTTTTTTTTTTCAGCAACCGCACACTGGCGCC
4-12	GGATGGAAAGTCTTCCCTTGGTTTTTTTTTTTTTTTTTTTTATCCTATCTAGTGAACTTAGG
4-13	GTGGAAACTCCCTCTGACTTATTTTTTTTTTTTTTTTTTTTTATTTAGGGTGTCACGGACG
4-14	AGGAAACTCGAAAGGATAGGTTTTTTTTTTTTTTTTTTTTTAAATTGTTGAAGCGGCACGAC
4-15	GTAACCTACTCGTTCAAGATATTTTTTTTTTTTTTTTTTTTTAGACATGTTACAGTCTCCCAT
5-1	ACATAGCGAGTCAAACGGTGATTTTTTTTTTTTTTTTTTTTCGCGGACTCGATGCCCACGTG
5-2	ATGGGCGGGCCGGTCACAAGTTTTTTTTTTTTTTTTTTTTCGTTGGCGCGGATTCGGACCT
5-3	CCGGAGCCCTAAGTCCGAGGTTTTTTTTTTTTTTTTTTTTGGCGCGATGGACAGCTCCACC
5-4	AAGGATCTGGAGGAAGTTCCATTTTTTTTTTTTTTTTTTTTGTCCGGTACCCATACACTTAG
5-5	TTAGGGAAATAAAGGATTGACTTTTTTTTTTTTTTTTTTTTTAGATTACCTCGGTGACCACG
5-6	TCAGCGCTTCAAGCCCTGGGTTTTTTTTTTTTTTTTTTTTTAGAGCCGCACTGCTGCTAT
5-7	AGAGTTACATCCTCCTCTTGTTTTTTTTTTTTTTTTTTTTATTCCTTTGGCGCCAAAGAGC
5-8	TCGAATCACCGATACGCGCATTTTTTTTTTTTTTTTTTTTGATAAGACTCTATGAAGCGAG
5-9	AACGTTGGTATGGGTGACTTATTTTTTTTTTTTTTTTTTTTCACGTCCGGCGTCAAACAT
5-10	TGCGCCTTATCAAATTACCGCTTTTTTTTTTTTTTTTTTTTGTAGTAGTTATCTCCGAAGAA
5-11	ACCGAATGCCCTTCTACATTGTTTTTTTTTTTTTTTTTTTTCTTTCCATCCTTCGACTCCTA
5-12	ACAGATGGGTACCGACACGGCTTTTTTTTTTTTTTTTTTTTGAGTTTCCACCCAAGGGAAGA
5-13	GGGCCGATCAATGCGAGCGAATTTTTTTTTTTTTTTTTTTTCGAGTTTCCTTAAGTCAGAGG
5-14	TCTAAACTTTATCGGAGGAGCTTTTTTTTTTTTTTTTTTTTAGTAGGTTACACCTATCCTTT
5-15	GCAGTTTACGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATCTTGAACG
6-1	TTTTTTTTTTGTATCTGCACATTTTTTTTTTTTTTTTTTTTACTCGCTATGTTTTTTTTTTT
6-2	CCGCATGATCCGCAAGAGCTTTTTTTTTTTTTTTTTTTTTGGCCCGCCCATTCACCGTTTG
6-3	AGTGCTTATGACCCTAAATTGTTTTTTTTTTTTTTTTTTTTAGGGCTCCGGACTTGTGACC
6-4	CGTCAGAAAGATAAAGAGGGCTTTTTTTTTTTTTTTTTTTTCCAGATCCTTACCTCGGACT
6-5	CATACGCTGTCCCTAACGTTATTTTTTTTTTTTTTTTTTTTATTTCCCTAATGGAACTTCC
6-6	GCCAATCCAGGTTTAAAGAGATTTTTTTTTTTTTTTTTTTTGAAGCGCTGAGTCAATCCTT

6-7 ACCTCTGCCATCGAGCATGCCTTTTTTTTTTTTTTTTTTTTTGATGTAACTCTACCCAGGGCT
6-8 GGACCGTCGAGCCGATTCACCTTTTTTTTTTTTTTTTTTTTCGGTGATTCGAACAAGAGGAG
6-9 ATTCCACTTCCACATTTGATTTTTTTTTTTTTTTTTTTTTTATACCAACGTTATGCGCGTAT
6-10 CTTCGGAGGGCCAGGATGAGCTTTTTTTTTTTTTTTTTTTTTGATAAGGCGCATAAGTCACCC
6-11 TGACAGAGACAGGTACTACGCTTTTTTTTTTTTTTTTTTTTTGGGCATTCGGTGCGGTAATTT
6-12 CCTGGCCGCCCTGTTAATATGTTTTTTTTTTTTTTTTTTTTTTACCCATCTGTCAATGTAGAA
6-13 CGTCTCAGCGAGATTAAATTATTTTTTTTTTTTTTTTTTTTTGATCGGCCCGCCGTGTCGG
6-14 TCCATTGCGACAAGGGCGTGCTTTTTTTTTTTTTTTTTTTTTTAAAGTTTAGATTCGCTCGCA
6-15 GCCTCTATCTGGTTAACTGGGTTTTTTTTTTTTTTTTTTTTTCCGTAAACTGCGCTCCTCCGA
7-1 TATTTGGCATCTGACTATAGGTTTTTTTTTTTTTTTTTTTTGATCATGCGGTGTGCAGATAC
7-2 GTACGCCCTGACCCACCGATGTTTTTTTTTTTTTTTTTTTTCATAAGCACTAAGCTCTTGCG
7-3 GTTAAAGGCGTTCGCGAAATTTTTTTTTTTTTTTTTTTTTCTTTCTGACGCAATTTAGGGT
7-4 CCTTTGACTTTCACTGAACAGTTTTTTTTTTTTTTTTTTTTACAGCGTATGGCCCTCTTTAT
7-5 GCCCTGACGGGAGCTGCGGGCTTTTTTTTTTTTTTTTTTTTCTGGATTGGCTAACGTTAGGG
7-6 GACGTTGAATTAAGTCAATCTTTTTTTTTTTTTTTTTTTTTGGCAGAGGTTCTCTTTAAAC
7-7 TATGACTTTATAAAGGTGTGTTTTTTTTTTTTTTTTTTTTCGACGGTCCGGCATGCTCGA
7-8 ACATCTCTAGGGCCCTGGATGTTTTTTTTTTTTTTTTTTTTGAAGTGGAATGGTGAATCGGC
7-9 GTCAGCAGGCAATCTGCCCGATTTTTTTTTTTTTTTTTTTTCCCTCCGAAGAATCAAATGTG
7-10 TCGGCTCTAAGCAGCGTTTACTTTTTTTTTTTTTTTTTTTTGTCTCTGTCAGCTCATCCTGG
7-11 CGATGTTGTTTGTGGTACTCTTTTTTTTTTTTTTTTTTTTGGCGGCCAGGGCGTAGTACCT
7-12 ATACACAATCCCTAAGAGTCTTTTTTTTTTTTTTTTTTTTCGCTGAGACGCATATTAACAG
7-13 TGTGTACTGAGAATAGGTCCATTTTTTTTTTTTTTTTTTTTCGCAATGGATAATTTAATCT
7-14 CACCTTATTACACACCCGGTTTTTTTTTTTTTTTTTTTTTAGATAGAGGCGCACGCCCTTG
7-15 ATGAACATTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCCAGTTAACC
8-1 TTTTTTTTTTACAGAAAGGTCTTTTTTTTTTTTTTTTTTTTGATGCCAAATATTTTTTTTTT
8-2 TGGCGGTTGGATTAATTAGGCTTTTTTTTTTTTTTTTTTTTCAGGGCGTACCCTATAGTCA
8-3 AATCCCTGTGGCTACCGAGGCTTTTTTTTTTTTTTTTTTTTACGCCTTTAACCATCGGTGGG
8-4 AACTGAAGCGGCTTGGCCACTTTTTTTTTTTTTTTTTTTTTAAAGTCAAAGGAATTTCGCGA
8-5 ACCGTGACGCAACTAAACAATTTTTTTTTTTTTTTTTTTTCCCGTCAGGGCCTGTTCAGTG
8-6 GGACTCTATCCCTACGGAACCTTTTTTTTTTTTTTTTTTTTAATTCAACGTCGCCCGCAGCT
8-7 TTTCATCTTCCATTAGTTGCCTTTTTTTTTTTTTTTTTTTTATAAAGTCATAAGATTGACTT
8-8 CGTGGGTGTTGGGCAACACCGTTTTTTTTTTTTTTTTTTTTCCTAGAGATGTACACACCTTT
8-9 GCCGAGGACGAGCAGACTTTCTTTTTTTTTTTTTTTTTTTTTGCCTGCTGACCATCCAGGGC
8-10 GAGCAAATGTTCCCGATGAACTTTTTTTTTTTTTTTTTTTTCTTAGAGCCGATCGGGCAGAT
8-11 GTTGGCGGTCAGCCATGGCTTTTTTTTTTTTTTTTTTTTTAAACAACATCGGTAAACGCTG
8-12 ACTGTCAACGGACAACGGACATTTTTTTTTTTTTTTTTTTTGGATTGTGTATAGAGTACCAC
8-13 CAAGCGTGGAAATCCGTCTGATTTTTTTTTTTTTTTTTTTTCTCAGTACACAAGACTCTTAG
8-14 GTATCAAAGCGGTCCAGACCCTTTTTTTTTTTTTTTTTTTTGTAATAAGGTGTGGACCTATT
8-15 AGGAAAGCTAGTGGTCCGCGTTTTTTTTTTTTTTTTTTTTTAATGTTCATAACCGGGTGT
9-1 GGGACCCTTCACTAACGACCATTTTTTTTTTTTTTTTTTTTCCAACCGCCAGACCTTTCTGT
9-2 GCCTGATATTGCAATCACTCCTTTTTTTTTTTTTTTTTTTTCACAGGGATTGCCTAATTAAT
9-3 GGGTACCGACTCCCTTTACGGTTTTTTTTTTTTTTTTTTTTCGCTTCAGTTGCCTCGGTAGC

9-4 CTTCCGAGAAGTCATTTGGAATTTTTTTTTTTTTTTTTTTTGCGTCACGGTAGTGGCCAAGC
9-5 GTCTCAGGCGCTTGAGAATGATTTTTTTTTTTTTTTTTTTTGATAGAGTCCATTGTTTAGTT
9-6 TCGAACACTTCCGTTGCGTTTTTTTTTTTTTTTTTTTTTTTGAAGATGAAAGGTTCCGTAGG
9-7 GGCACATTCACGGCTAGGAACTTTTTTTTTTTTTTTTTTTTAACACCCACGGGCAACTAATG
9-8 GCTCGCCAGTCGGACCTCGCCTTTTTTTTTTTTTTTTTTTCGTCCTCGGCCGGTGTTGCCC
9-9 GCATCCATGAGCGCTGGGAGATTTTTTTTTTTTTTTTTTTTACATTTGCTCGAAAGTCTGCT
9-10 TCTAACTTAAGCGATTAGGGTTTTTTTTTTTTTTTTTTTTGACCGCCAACGTTCATCGGGA
9-11 GGTGATTCGCAAGGGCCGATATTTTTTTTTTTTTTTTTTTTCGTTGACAGTAAGCCATGGCT
9-12 CTCGTTTGTCTAATAGCAAGTTTTTTTTTTTTTTTTTTTTCCACGCTTGTGTCCGTTGTC
9-13 CGCATGGGAATGCCCTGCGTCTTTTTTTTTTTTTTTTTTTGCTTTGATACTCAGACGGATT
9-14 GTGTGATTCTTCACCTGTACTTTTTTTTTTTTTTTTTTTTTAGCTTTCCTGGGTCTGGACC
9-15 GGACCTGGGCATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTACGCGGACCAC
10-1 TTTTTTTTTTCACATAGGCCGTTTTTTTTTTTTTTTTTTTTGAAGGGTCCCTTTTTTTTTT
10-2 CCCACCTAGAAGAAGAAAGGGTTTTTTTTTTTTTTTTTTTCAATATCAGGCTGGTCGTTAG
10-3 TAGAACTGAGAGACAGGGCTATTTTTTTTTTTTTTTTTTTTAGTCGGTACCCGGAGTGATTG
10-4 TATAGCGCGTCTGTGGCGCGATTTTTTTTTTTTTTTTTTTCTTCTCGGAAGCCGTAAAGGG
10-5 CTGGCGGTACCATAAACTCGCTTTTTTTTTTTTTTTTTTTTGCGCCTGAGACTTCCAAATGA
10-6 ATTTCCCTGACCTTGAGGGAGTTTTTTTTTTTTTTTTTTTTGAAGTGTTCGATCATTCTCAA
10-7 AACACAGCGATCACGTGCCCTTTTTTTTTTTTTTTTTTTTGTGAATGTGCCAAACGCAACG
10-8 GGGCCTGAGTGGTCCCGCCAGTTTTTTTTTTTTTTTTTTTTGACTGGCGAGCGTTCCTAGCC
10-9 GTGCCTAGCTTCGGCATCCACTTTTTTTTTTTTTTTTTTTCTCATGGATGCGGCGAGGTCC
10-10 AGTACTTACTGTTGACCAGGCTTTTTTTTTTTTTTTTTTTCTTAAGTTAGATCTCCCAGCG
10-11 TTCTTCATTGTTCTTGAGCATTTTTTTTTTTTTTTTTTTTGCGAATCACCACCCTAATCG
10-12 GCATTGCAACGTATCATAAACTTTTTTTTTTTTTTTTTTTAGACAAACGAGTATCGGCCCT
10-13 GCGGAAAGCGGAAATTTAGTGTTTTTTTTTTTTTTTTTTTATTCCCATGCGACTTGCTATT
10-14 AATCCGTCAGTAACCATGACTTTTTTTTTTTTTTTTTTTTAAGAATCACACGACGCAGGGC
10-15 GGCACGTTCATCGCCCGGCTTTTTTTTTTTTTTTTTTTTGCCCAGGTCCAGTACAGGTG
11-1 TTGTCGATAGAAGTCCGAGTGTTTTTTTTTTTTTTTTTTTCTAGGTGGGCGGCCTATGTG
11-2 TCCATCGTCTTTAGTGTATGGTTTTTTTTTTTTTTTTTTTCTCAGTTCTACCCTTTCTTCT
11-3 CTCGGCGAGCGCCAAAGAGGCTTTTTTTTTTTTTTTTTTTACGCGCTATATAGCCCTGTCT
11-4 GACCCTCCGCATACCTTGGGATTTTTTTTTTTTTTTTTTTGTACCGCCAGTCGCGCCACAG
11-5 CGAGTATAACCAATGACAAGTTTTTTTTTTTTTTTTTTTTCAGGGAAATGCGAGTTTATG
11-6 GTAGGGCCGTCGAAAGATGGATTTTTTTTTTTTTTTTTTTTCGCTGTGTTCTCCCTCAAGG
11-7 ATTCACAGCCAATTGTAATTTTTTTTTTTTTTTTTTTTTACTCAGGCCCAGGGCACGTGA
11-8 ACTCGGAAAGCAACTGCATTTTTTTTTTTTTTTTTTTTTAGCTAGGCACCTGGCGGGACC
11-9 GGTGAGTAACTCCCTCTGGATTTTTTTTTTTTTTTTTTTAGTAAGTACTGTGGATGCCGA
11-10 CTTTGAGAAATTCTTCGTAGCTTTTTTTTTTTTTTTTTTTCAATGAAGAAGCCTGGTCAAC
11-11 GCGGAGACAAGACCGCGACCTTTTTTTTTTTTTTTTTTTTGTTGCAATGCATGCTCAAGAA
11-12 CAACAACACGTCTGTTCGCGGTTTTTTTTTTTTTTTTTTTCGCTTTCCGCGTTTATGATAC
11-13 ACAGAACTTTGTCAGCCCTTTTTTTTTTTTTTTTTTTTCTGACGGATTCACTAAATTTC
11-14 ACCGGACCTAATCCAGCGCCATTTTTTTTTTTTTTTTTTTGAACGTGCCAGTCATGGTTA
11-15 TTTACCATAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAGCCGGGCGA

12-1 TTTTTTTTTTACGGAAGCAAATTTTTTTTTTTTTTTTTTTTTCTATCGACAATTTTTTTTTT

12-2 GGTAGACAGTCATGCAAGATTTTTTTTTTTTTTTTTTTTTTAAGACGATGGACACTCGGACT

12-3 CTTCAGGTCATACCTGTAGATTTTTTTTTTTTTTTTTTTTCGCTCGCCGAGCCATACACTA

12-4 ATCTCTCGCGTATTTAGATTCTTTTTTTTTTTTTTTTTTTTGCGGAGGGTCGCCTCTTTGG

12-5 TCTGCTCCTTTCCGGGAGGGATTTTTTTTTTTTTTTTTTTTGGTTATACTCGTCCCAAGGTA

12-6 GCTCTCGCCTCCTACAACGTTTTTTTTTTTTTTTTTTTTTGACGGCCCTACACTTGTCATT

12-7 AGCAGTGTAGCTTGACGCAGCTTTTTTTTTTTTTTTTTTTTGGCTGTGAATTCCATCTTTC

12-8 CCTCAATCCCTCTGCCTCCCATTTTTTTTTTTTTTTTTTTTGCTTTCCGAGTAAATTACAAT

12-9 CGGCTATCTGGGCCTCCGTAGTTTTTTTTTTTTTTTTTTTTAGTTACTCACCAAATGCAGTT

12-10 ACATTCCGGGATGCAGGCATGTTTTTTTTTTTTTTTTTTTTATTTCTCAAAGATCCAGAGGG

12-11 ACCCTAATCCTCTTTCGCCTCTTTTTTTTTTTTTTTTTTTTCTTGTCTCCGCGCTACGAAGA

12-12 TCGTTACATACGCGGCGGTCTTTTTTTTTTTTTTTTTTTTACGTGTTGTTGAGGTCGCGGT

12-13 ATCAGTAGAAGCTCGTACGGCTTTTTTTTTTTTTTTTTTTTCAAAGTTCTGTCCGCGAACAG

12-14 CCTAGAGCGAGGTCGTAGACCTTTTTTTTTTTTTTTTTTTTTAGGTCCGGTAAAGGGCTGA

12-15 GCGGATTGTGGCGCGACAAGATTTTTTTTTTTTTTTTTTTTCCTATGGTAAATGGCGCTGGA

13-1 GATCATCACCCTCCAATCCTATTTTTTTTTTTTTTTTTTTTACTGTCTACCTTTGCTTCCGT

13-2 TTAAAGGAAACGAATAACAATTTTTTTTTTTTTTTTTTTTTGACCTGAAGAATCTTGCATG

13-3 GGTTCCCTCGTTCGCTGCTTTTTTTTTTTTTTTTTTTTTCGCGAGAGATATCTACAGGTA

13-4 GGTAAAGGGCAGCAATGAAAGTTTTTTTTTTTTTTTTTTTAAGGAGCAGAGAATCTAAATA

13-5 CTAACTGCGTCACAAGTCATCTTTTTTTTTTTTTTTTTTTAGGCGAGAGCTCCCTCCCGGA

13-6 CAAACCGCCAAGGTGCCGGCATTTTTTTTTTTTTTTTTTTTCTACACTGCTAACGTTGTAGG

13-7 AACGCCGTGCAGGGACCAATCTTTTTTTTTTTTTTTTTTTTGGGATTGAGGGCTGCGTCAAG

13-8 TGTAGCTCCATGCTTCAAGAATTTTTTTTTTTTTTTTTTTCAGATAGCCGTGGGAGGCAGA

13-9 TCTTCGATATTGTGGAACACTTTTTTTTTTTTTTTTTTTTCCCGGAATGTCTACGGAGGCC

13-10 ATATTTATACCTGTTACAACCTTTTTTTTTTTTTTTTTTTGGATTAGGGTCATGCCTGCAT

13-11 CGAGACCGTCCGTTGGGTCTTTTTTTTTTTTTTTTTTTTATGTAACGAGAGGCGAAAGA

13-12 ACACCTGAGAGAGATTGTATATTTTTTTTTTTTTTTTTTTCTACTGATAGACCGCCGCG

13-13 CGCCACCCTATACCGAGAGGATTTTTTTTTTTTTTTTTTTCGCTCTAGGGCCGTACGAGC

13-14 GCTGGCTGGTCTCAACACTCCTTTTTTTTTTTTTTTTTTTCACAATCCGCGGTCTACGACC

13-15 GTCTTCAGGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTGTCGCGC

14-1 TTTTTTTTTTATGGCGGCTGTTTTTTTTTTTTTTTTTTTTGGGTGATGATCTTTTTTTTTT

14-2 CTGTCATTGGAGGCAACTTTATTTTTTTTTTTTTTTTTTTGTTTCCTTTAATAGGATTGGA

14-3 GCTCCAGGGCCCGGTACCGCTTTTTTTTTTTTTTTTTTTTTACGAGGGAACCATTGTTATTC

14-4 GGGCACAACTTTGTTTCGTGTTTTTTTTTTTTTTTTTTTTGCCCTTTACCAAAGCAGCGA

14-5 TGAGTCCGAACTGAGCCTATCTTTTTTTTTTTTTTTTTTTGACGCAGTTAGCTTTCATTGC

14-6 CAGCGACTTCCTCGTTCCTGTTTTTTTTTTTTTTTTTTTTGGCGGTTTGGATGACTTGT

14-7 CGATCCCACTTTGGTATTGGCTTTTTTTTTTTTTTTTTTTTGCACGGCGTTTGCCGGCACC

14-8 ACACTCGCGTGTGATAGAAATTTTTTTTTTTTTTTTTTTTATGGAGCTACAGATTGGTCCC

14-9 ATGAAGTACAGAGGTAGACGCTTTTTTTTTTTTTTTTTTTTAATATCGAAGATTCTTGAAGC

14-10 ACGAGGTCCCTTTCTTCTACCTTTTTTTTTTTTTTTTTTTTGGTATAAATATAGTGTTCCAC

14-11 GCTAGCCTCAGCTATTTACATTTTTTTTTTTTTTTTTTTTGGACGGTCTCGGGTTGTAACA

14-12 GTGGCTTCGCCGAGTATCCCTTTTTTTTTTTTTTTTTTTTCTCTCAGGTGTAAGACCCAAC

14-13 TACAGCGCGTAGCGGATGGAGTTTTTTTTTTTTTTTTTTTTTATAGGGTGGCGTATACAATCT
14-14 GCTGATACAATTCCCTGTACATTTTTTTTTTTTTTTTTTTTTGACCAGCCAGCTCCTCTCGGT
14-15 TAAAGCTCACGATTCCGGTCGTTTTTTTTTTTTTTTTTTTTTCACCTGAAGACGGAGTGTTGA
15-1 CAGCGCGCCAACCACGGGTAGTTTTTTTTTTTTTTTTTTTTTCCAATGACAGACAGCCGCCAT
15-2 GGTGTGTCCATTAATATGTTATTTTTTTTTTTTTTTTTTTTGCCCTGGAGCTAAAGTTGCCT
15-3 GAAACCGAGCCCAGGTGGAGCTTTTTTTTTTTTTTTTTTTTTAGTTGTGCCCAGCGGTACCGG
15-4 TATATCGGACGCGCACGGCTATTTTTTTTTTTTTTTTTTTTTTCGGACTCAACACGAAACAA
15-5 ACTCGAGGGCTTTAAAGATTTTTTTTTTTTTTTTTTTTTTTGAAGTCGCTGGATAGGCTCAG
15-6 CCTATCCGCCATGAAGTTGTGTTTTTTTTTTTTTTTTTTTTTAGTGGGATCGACAGGAACGAG
15-7 CGTACGGCTCACAAACTTCACTTTTTTTTTTTTTTTTTTTTTACGCGAGTGTGCCAATACCAA
15-8 TTTGGGCCGATTCTTAAACGGTTTTTTTTTTTTTTTTTTTTTGTACTTCATATTTCTATCAC
15-9 AGACCTCCATATATGCTGTACTTTTTTTTTTTTTTTTTTTTGGGACCTCGTGCGTCTACCTC
15-10 CAAGGCGCTTGTTTGAAAGTGTTTTTTTTTTTTTTTTTTTTTGAGGCTAGCGGTAGAAGAAA
15-11 GAGTCGACCCTGCTGCCGGTGTTTTTTTTTTTTTTTTTTTTGCGAAGCCACATGTAAATAGC
15-12 TCGGATATCGTTGGGTTTAGATTTTTTTTTTTTTTTTTTTTACGCGCTGTAAGGGATACTCG
15-13 TTTAATAGTTAAGGTACATTGTTTTTTTTTTTTTTTTTTTTGTATCAGCCTCCATCCGCT
15-14 AATTCAGGGCTAACTTTCCAATTTTTTTTTTTTTTTTTTTTGTGAGCTTTATGTACAGGGAA
15-15 CTGAACTTGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGACCGGAATC
16-1 TTTTTTTTTTGCGAAAGGGCATTTTTTTTTTTTTTTTTTTTTTGGCGCGCTGTTTTTTTTTT
16-2 TAACAATGTATAACATGCTTTTTTTTTTTTTTTTTTTTTTTATGGACACACCCTACCCGTGG
16-3 GTGGCTTCGACAAATTCTTGCTTTTTTTTTTTTTTTTTTTTTGGCTCGGTTTCTAACATATTA
16-4 CACGATGCATCGCTTGGTATTTTTTTTTTTTTTTTTTTTTCGTCCGATATAGCTCCACCTG
16-5 GTAGGTGCTCAGTAGCCATTCTTTTTTTTTTTTTTTTTTTTAGCCCTCGAGTTAGCCGTGCG
16-6 CATATCGGAAGAATTCTATAATTTTTTTTTTTTTTTTTTTTGGCGGATAGGAAATCTTTAA
16-7 GTAGGTGAGAAAGCGGGCTCGTTTTTTTTTTTTTTTTTTTTGAGCCGTACGCACAACTTCA
16-8 TTGAAATCTGGTTCGCCGAATTTTTTTTTTTTTTTTTTTTATCGGCCCAAAGTGAAGTTTG
16-9 CGGACCCAATGGAGATCTTCGTTTTTTTTTTTTTTTTTTTTATGGAGGTCTCCGTTTAAGA
16-10 AAGCCTAACCTTATCTCATTATTTTTTTTTTTTTTTTTTTCAAGCGCCTTGGTACAGCATA
16-11 GCTAGCGTGACTCAAACTCCCTTTTTTTTTTTTTTTTTTTTAGGGTCGACTCCACTTTCAAA
16-12 TTAATGTTGTTGTCCTCTGCATTTTTTTTTTTTTTTTTTTTACGATATCCGACACCGGCAGC
16-13 CATTACCGCGTTAATAACCGCTTTTTTTTTTTTTTTTTTTTAACTATTAAATCTAAACCCA
16-14 TCTTTCTTGACTTAGCATGACTTTTTTTTTTTTTTTTTTTTAGCCCTGAATTCAATGTACCT
16-15 CCTGCCAACTAATTGGATAACTTTTTTTTTTTTTTTTTTTTAGCAAGTTCAGTTGGAAAGTT
17-1 ACATATATCCGATCCAAGCGCTTTTTTTTTTTTTTTTTTTTTACATTGTTATGCCCTTTCGC
17-2 CTTTGCGGGACTCCGCTAGAGTTTTTTTTTTTTTTTTTTTTTCGAAGCCACAAAGCATGTTA
17-3 ACGTTGGTTTGGGCGTTCACCTTTTTTTTTTTTTTTTTTTTTATGCATCGTGGCAAGAATTTG
17-4 TAGGCAGCACAAATGACACTCTTTTTTTTTTTTTTTTTTTTGAGCACCTACAATACCAAGCG
17-5 CCAAGAGCGAGTGCAGTGTCATTTTTTTTTTTTTTTTTTTTTCCGATATGGAATGGCTACT
17-6 TTTCTCAACCCTTGGCTTATGTTTTTTTTTTTTTTTTTTTTCTCACCTACTTATAGAATTC
17-7 CGAGTTGTTGCTGCCTCATCCTTTTTTTTTTTTTTTTTTTTCAGATTTCAACGAGCCCGCTT
17-8 TTGGACCGGGACTTGGGTAATTTTTTTTTTTTTTTTTTTTATTGGGTCCGATTCGGCGAAC
17-9 TCCTTAGCTGCAGTGAAAGTTTTTTTTTTTTTTTTTTTTGGTTAGGCTTCGAAGATCTCC

17-10 TAAACTTTAGTCTTGGTCCCTTTTTTTTTTTTTTTTTTTTTTTCACGCTAGCTAATGAGATAA
17-11 GTGTTTCGTCCCGTCTTTGAGTTTTTTTTTTTTTTTTTTTTTACAACATTAAGGGAGTTTGAG
17-12 GGAGGTGATCTCATGTATCAGTTTTTTTTTTTTTTTTTTTTCGCGGTAATGTGCAGAGGACA
17-13 TGGTGCAAGGGATCTTTCACTTTTTTTTTTTTTTTTTTTTTTCAAGAAAGAGCGGTTATTAA
17-14 CTTCATATAGGCCGTGACGGATTTTTTTTTTTTTTTTTTTTTAGTTGGCAGGGTCATGCTAAG
17-15 TCCTACTGACGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTTATCCAATT
18-1 TTTTTTTTTTCCCGTCAGGGCTTTTTTTTTTTTTTTTTTTTTCGGATATATGTTTTTTTTTTT
18-2 TGCGGCTACCATATAAGATTTTTTTTTTTTTTTTTTTTTTTGTCCCGCAAAGGCGCTTGGAT
18-3 AGCCTAAAGCCGAGTGATGGCTTTTTTTTTTTTTTTTTTTTTCAAACCAACGTCTCTAGCGGA
18-4 CCACTCCGTACCTGCCTTTAATTTTTTTTTTTTTTTTTTTTTGTGCTGCCTAGGTGAACGCC
18-5 TTCTGGGTGACAGGCCGTTCTTTTTTTTTTTTTTTTTTTTTCTCGCTCTTGGGAGTGTCATT
18-6 AATCGCAACACCCGCTGGCACTTTTTTTTTTTTTTTTTTTTTGGGTTGAGAAATGACACTGCA
18-7 GGTGGGCGAATCCAGCAGAGATTTTTTTTTTTTTTTTTTTTTGCAACAACTCGCATAAGCCAA
18-8 CATGACTTGTCGTTGGCATCCTTTTTTTTTTTTTTTTTTTTTCCCGGTCCAAGGATGAGGCA
18-9 ATGGCGGCCGCCCGGGCCTACTTTTTTTTTTTTTTTTTTTTTGCAGCTAAGGAATTACCCAAG
18-10 CCACGTATGCCGTAGGACATATTTTTTTTTTTTTTTTTTTTTACTAAAGTTTAAACTTTCACT
18-11 GGTTCTTCGTACAGCCTCGCCTTTTTTTTTTTTTTTTTTTTGGACGAAACACAGGGACCAAG
18-12 CAAATGCGTGAGGTGCGTCTCTTTTTTTTTTTTTTTTTTTTAGATCACCTCCCTCAAAGACG
18-13 TGTTAGTTAGCACGTGTCTCGTTTTTTTTTTTTTTTTTTTTCCCTTGCACCACTGATACATG
18-14 CCTCCGCGTTGTCAAACCCTATTTTTTTTTTTTTTTTTTTTCCTATATGAAGAGTGAAAGAT
18-15 GCCAGATCATGCGGACAGATCTTTTTTTTTTTTTTTTTTTTCGTCAGTAGGATCCGTCACGG
19-1 CATCACTGCTACTTCGACAACTTTTTTTTTTTTTTTTTTTTGGTAGCCGCAGCCCTGACGGG
19-2 ACAGAGGAGCTTGCGCCTGATTTTTTTTTTTTTTTTTTTTTGCTTTAGGCTAAATCTTATAT
19-3 GGCGTGGTCCGCCAAGCTATCTTTTTTTTTTTTTTTTTTTTACGGAGTGGGCCATCACTCG
19-4 GCATTAAGGCCGCGGCTGGGATTTTTTTTTTTTTTTTTTTTCACCCAGAATTAAAGGCAGG
19-5 TAACTACCAATGACTTATAGCTTTTTTTTTTTTTTTTTTTTGTTGCGATTAGAACGGCCTG
19-6 GTACTACACATTACGAGAGCATTTTTTTTTTTTTTTTTTTTCGCCCACCGTGCCAGCGGG
19-7 GGACAGCACAACACTACCATTTTTTTTTTTTTTTTTTTTACAAGTCATGTCTCTGCTGGA
19-8 GCTGCTAGCATGCCGGATTAATTTTTTTTTTTTTTTTTTTCGGCCGCCATGGATGCCAACG
19-9 GTTTGCACTCCGGGTGCCTTTTTTTTTTTTTTTTTTTTTGCATACGTGGGTAGGCCCGGG
19-10 AATTTGATATATTAGGCCGGGTTTTTTTTTTTTTTTTTTTTACGAAGAACCTATGTCCTACG
19-11 AACAGAAAGTGATGTGTTAATTTTTTTTTTTTTTTTTTTTCACGCATTTGGGCGAGGCTGT
19-12 CTACGTCCGAAAGACGAGATCTTTTTTTTTTTTTTTTTTTCTAACTAACAGAGACGCACCT
19-13 CCTCAGGGCCATGCATTTAAGTTTTTTTTTTTTTTTTTTTTAACGCGGAGGCGAGACACGTG
19-14 ATTGTGACATGAGCGCCCGGTTTTTTTTTTTTTTTTTTTTATGATCTGGCTAGGGTTTGAC
19-15 GAATTCTAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGATCTGTCCGC
20-1 TTTTTTTTTTATGTTCAAGTTTTTTTTTTTTTTTTTTTTTTTAGCAGTGATGTTTTTTTTTT
20-2 AATCGGTTTATGTGCATAGATTTTTTTTTTTTTTTTTTTTTAGCTCCTCTGTGTTGTCGAAG
20-3 ATCTCCCATCCTGGAGACCACTTTTTTTTTTTTTTTTTTTTCGGACCACGCCATCAGGCGCA
20-4 GGGAGCTTCTCAAGGAAACGTTTTTTTTTTTTTTTTTTTTGGCCTTAATGCGATAGCTTGG
20-5 CAGCCGAAACCTAGCCTTACATTTTTTTTTTTTTTTTTTTTATTGGTAGTTATCCCAGCCGC
20-6 AGCTAAAGCGTCCACCATTCGTTTTTTTTTTTTTTTTTTTTATGTGTAGTACGCTATAAGTC

20-7 GCGTAGAATCGTTTCCTAAACTTTTTTTTTTTTTTTTTTTTTTGTGCTGTCCTGCTCTCGTA
20-8 GGCTACGCGTTTGGCCCTCGTTTTTTTTTTTTTTTTTTTTTTATGCTAGCAGCAATGGTAGTG
20-9 TCTACGCCCATGGCCCGAAGCTTTTTTTTTTTTTTTTTTTTTGGAGTGCAAACTTAATCCGGC
20-10 AATTCATGTTCGGACCTTAAGTTTTTTTTTTTTTTTTTTTTTATATCAAATTAAAGGCACCC
20-11 GAACCGTATACGCCAGTTGAGTTTTTTTTTTTTTTTTTTTTCACTTTCTGTTCCCGGCCTAA
20-12 TGCATTCTGGAGCAAGGACTCTTTTTTTTTTTTTTTTTTTTTTCGGACGTAGATTAACACAT
20-13 ACATAAGCCAAAGTGGGCTCATTTTTTTTTTTTTTTTTTTTTGGCCCTGAGGGATCTCGTCT
20-14 TCGGAGGACCTCTTTATGGGCTTTTTTTTTTTTTTTTTTTTCATGTCACAATCTTAAATGCA
20-15 ATTTCGAAAGCCTTAGAGTGCTTTTTTTTTTTTTTTTTTTTATTTAGAATTCACCGGGCGCT
21-1 ACGTCCTTGTTTCTGCGTAATTTTTTTTTTTTTTTTTTTTTAAACCGATTAACTTGAACAT
21-2 GTAGCGATGTAAACTGCAGCATTTTTTTTTTTTTTTTTTTTGATGGGAGATATCTATGCACA
21-3 TTCCCTACTCAACGGCTATCATTTTTTTTTTTTTTTTTTTTAGAAGCTCCCGTGGTCTCCAG
21-4 TTAGGATGCGAACTCCACTCCTTTTTTTTTTTTTTTTTTTTGTTTCGGCTGACGTTTCCTTG
21-5 CGGAATATGAGCGCAGGGCGCTTTTTTTTTTTTTTTTTTTTCGCTTTAGCTTGTAAGGCTAG
21-6 CCTACACTCTCTCGGGTCCTATTTTTTTTTTTTTTTTTTTTGATTCTACGCCGAATGGTGGA
21-7 TCGTGTGCATTTGAAGTCGCATTTTTTTTTTTTTTTTTTTTACGCGTAGCCGTTTAGGAAAC
21-8 GCTGTCTTAGGGTCCTAATGCTTTTTTTTTTTTTTTTTTTTGGGCGTAGAACGAGGGCCAA
21-9 GCGGACGGCTCTAATGACTTATTTTTTTTTTTTTTTTTTTAACATGAATTGCTTCGGGCCA
21-10 CTAGTTACGCAGAGAGATCAGTTTTTTTTTTTTTTTTTTTTATACGGTTCCTTAAGGTCCG
21-11 CAGACGACCGTTGGCGTTGTTTTTTTTTTTTTTTTTTTTCCAGAATGCACTCAACTGGCG
21-12 TCTGATCCTGTGCAAACTTATTTTTTTTTTTTTTTTTTTTGGCTTATGTGAGTCCTTGCT
21-13 GCGTTACATAGTGGGCAGTCTTTTTTTTTTTTTTTTTTTTGGTCCTCCGATGAGCCCACTT
21-14 CCTGTCGGTAGGGTCTGCTTTTTTTTTTTTTTTTTTTTTCTTTCGAAATGCCCATAAAGA
21-15 AGTGTATCAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGCACTCTAAGG
22-1 TTTTTTTTTTCGGTCGCTCCCTTTTTTTTTTTTTTTTTTTTAACAAGGACGTTTTTTTTTT
22-2 TACATAGCTAATGTGGCTAGGTTTTTTTTTTTTTTTTTTTTACATCGCTACATTACGCAGA
22-3 GCCGCAATGGTGGCGGTCGTCTTTTTTTTTTTTTTTTTTTTGAGTAGGGAATGCTGCAGTT
22-4 ACTGACCTGGGCATGTGGGATTTTTTTTTTTTTTTTTTTTCGCATCCTAATGATAGCCGT
22-5 AAGTTCAATTTATACCTCTAGTTTTTTTTTTTTTTTTTTTCTCATATTCCGGGAGTGGAGT
22-6 GTAGCATGGCTGCTACTTCTCTTTTTTTTTTTTTTTTTTTGAGAGTGTAGGGCGCCCTGCG
22-7 GGCCTACGATCCGGGCGTGGGTTTTTTTTTTTTTTTTTTTAATGCACACGATAGGACCCGA
22-8 ATCATGGGTATGTGTGCCAGTTTTTTTTTTTTTTTTTTTTCCTAAGACAGCTGCGACTTCA
22-9 TTAGGACTCAATGCTTATATGTTTTTTTTTTTTTTTTTTTGAGCCGTCCGCGCATTAGGAC
22-10 GCCGAAGACGCCCGCAATCTCTTTTTTTTTTTTTTTTTTTTGCGTAACTAGTAAGTCATTA
22-11 CATGAGCGAGTGCAGTAAGCATTTTTTTTTTTTTTTTTTTTACGGTCGTCTGCTGATCTCTC
22-12 ATATCTGCGTACACTTCGGAATTTTTTTTTTTTTTTTTTTTACAGGATCAGAAACAACGCCA
22-13 CTTACCGGTCACGGGTATAAGTTTTTTTTTTTTTTTTTTTTCTATGTAACGCATAAGTTTGC
22-14 CCTGCCTAGATGTGCACTAGTTTTTTTTTTTTTTTTTTTTCTACCGACAGGAGACTGCCCA
22-15 GTCCAGAGCATGGTCCATCCCTTTTTTTTTTTTTTTTTTTTGCTGATACACTAAAGCAGACC
23-1 TGGACTTCATTCAGAGCGTTATTTTTTTTTTTTTTTTTTTTAGCTATGTAGGGAGCGACCG
23-2 ACCTAATTTAGGCGGGCGGACTTTTTTTTTTTTTTTTTTTTCCATTGCGGCCCTAGCCACAT
23-3 GCATATCATGCTCGAGCGCTTTTTTTTTTTTTTTTTTTTTCCAGGTCAGTGACGACCGCCA

23-4	ACGCGTTCCTTCTATAAGTTATTTTTTTTTTTTTTTTTTTTTAATTGAACTTATCCCACATGC
23-5	GTGCCGTGGCCAGTTAAAGGCTTTTTTTTTTTTTTTTTTTTTGCCATGCTACCTAGAGGTATA
23-6	GGGTAAGAGAGTGTCGTAGTATTTTTTTTTTTTTTTTTTTTTATCGTAGGCCGAGAAGTAGCA
23-7	TAAGTGACACTATTATTTAGTTTTTTTTTTTTTTTTTTTTTTTACCCATGATCCCACGCCCGG
23-8	AGGCTCCAGGTTATAAGGGATTTTTTTTTTTTTTTTTTTTTTGAGTCCTAAACTGGCACACA
23-9	GGGACCGAGTTGCTCCGATGTTTTTTTTTTTTTTTTTTTTTTCGTCTTCGGCCATATAAGCAT
23-10	TAGGGTTCATGGCAATGTTCGTTTTTTTTTTTTTTTTTTTTTCTCGCTCATGGAGATTGCGGG
23-11	GAAGTTGAATTAAATATTCAATTTTTTTTTTTTTTTTTTTTTACGCAGATATTGCTTACTGCA
23-12	TGACAACTAAGCTTATGGAGGTTTTTTTTTTTTTTTTTTTTGACCGGTAAGTTCCGAAGTGT
23-13	AATGTAATATGTTTAGCCTGATTTTTTTTTTTTTTTTTTTTTCTAGGCAGGCTTATACCCGT
23-14	CCACTAGCTTTCTAAATGCGGTTTTTTTTTTTTTTTTTTTTTGCTCTGGACACTAGTGCACA
23-15	GCAATGGATTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGGGATGGACCA
24-1	TTTTTTTTTTATATGTCAGGATTTTTTTTTTTTTTTTTTTTAATGAAGTCCATTTTTTTTTT
24-2	ACACCCTCTTAAGGCGATCAGTTTTTTTTTTTTTTTTTTTTCTAAATTAGGTTAACGCTCTG
24-3	CTTGCCTTGCACAGTCAAACGTTTTTTTTTTTTTTTTTTTTGCATGATATGCGTCCGCCCGC
24-4	CCGATGCCGTCGACCAGAGTCTTTTTTTTTTTTTTTTTTTTAAGGAACGCGTAAGCGCTCGA
24-5	TGGAGTGGCTAGTAGCCCGCATTTTTTTTTTTTTTTTTTTTGGCCACGGCACTAACTTATAG
24-6	GTTCGTCACTCGGTCGAAGGCTTTTTTTTTTTTTTTTTTTTCTCTCTTACCCGCCTTTAACT
24-7	TTTGGCTCTACACATGTACCTTTTTTTTTTTTTTTTTTTTAGTGTCACTTATACTACGACA
24-8	GTGTATCCCAGGCCATCCTCGTTTTTTTTTTTTTTTTTTTTACCTGGAGCCTACTAAATAAT
24-9	TCTGATAGTACTGTCAACTCATTTTTTTTTTTTTTTTTTTTAACTCGGTCCCATCCCTTATA
24-10	CCTTATGACATCTCTACGTGTTTTTTTTTTTTTTTTTTTTCATGAACCCTAACATCGGAGC
24-11	ATCCTCGCAAACGTTCTAGCTTTTTTTTTTTTTTTTTTTTAATTCAACTTCCGAACATTGC
24-12	GATACTATGACATCTTCGACATTTTTTTTTTTTTTTTTTTTCTTAGTTGTCATTGAATATTT
24-13	ATACTACAGAGTACGGCGGCATTTTTTTTTTTTTTTTTTTTCATATTACATTCCTCCATAAG
24-14	GCTCGATGCCTAGCCAATGCTTTTTTTTTTTTTTTTTTTTAAAGCTAGTGGTCAGGCTAAA
24-15	GCTCGAATGAGGGCCCTCCGGTTTTTTTTTTTTTTTTTTTTAATCCATTGCCCGCATTTAG
25-1	AAGAGGGTGTTCCTGACATAT
25-2	GCAAGGCAAGCTGATCGCCTT
25-3	ACGGCATCGGCGTTTGACTGT
25-4	AGCCACTCCAGACTCTGGTCG
25-5	AGTGACGAACTGCGGGCTACT
25-6	TAGAGCCAAAGCCTTCGACCG
25-7	TGGGATACACAGGTACATGTG
25-8	TACTATCAGACGAGGATGGCC
25-9	TGTCATAAGGTGAGTTGACAG
25-10	TTGCGAGGATACACGTAGAGA
25-11	TCATAGTATCAGCTAGAACGT
25-12	TCTGTAGTATTGTCGAAGATG
25-13	GGCATCGAGCTGCCGCCGTAC
25-14	TCATTCGAGCAGCATTGGCTA
25-15	TTTTTTTTTTCCGGAGGGCCC

Motif 4.1X

Name	Sequence
1-1	ACTAAGCACTTACCAGTCGTC
1-2	TGTATAGTATCCAGCAGCTTA
1-3	CATCGTTACCGAGATTGATGG
1-4	GGACTAGACCGTTAACCAGTT
1-5	AATTCAAGCGTAGCCATCCTC
1-6	TGGAGTTTCACCTGATGTTCG
2-1	AGTGCTTAGTTAAGCTGCTGGGCCTGCTGGATCGGCATGTAG
2-2	ATACTATACACCATCAATCTCAGAAAGACTTTGACGATACTC
2-3	GGTAACGATGAACTGGTTAACTCGCGCGAGCGACCCTCAGTG
2-4	GGTCTAGTCCGAGGATGGCTAACTATTATTTATGGACCGAAA
2-5	CGCTTGAATTCGAACATCAGGGTATGCTCCCTACTGAAATAG
2-6	TGAAACTCCAGACGACTGGTACCTCAGCTTTTAACCGTAGTC
3-1	TCCAGCAGGCGACTACGGTTATACCGTTTGTTATTTCTATGG
3-2	AAGTCTTTCTCTACATGCCGACTTTAACCTAGATGCTCATTC
3-3	GCTCGCGCGAGAGTATCGTCATGCTTAATACGAATCCTGACT
3-4	AAATAATAGTCACTGAGGGTCTTCCCATCAAGTGGTTTGCCA
3-5	GGGAGCATACTTTCGGTCCATTCCCGTACAGAGGTACGAGGT
3-6	AAAGCTGAGGCTATTTCAGTATAGCCATACTCGAAGGTCTTA
4-1	ACAAACGGTAGAATGAGCATCCAGGGCGTGAGCCCTTGAGTT
4-2	TAGGTTAAAGAGTCAGGATTCAGACATAGCGTCCGCGATCAG
4-3	GTATTAAGCATGGCAAACCACGCCAGTATGTAAATCCCGGGC
4-4	TTGATGGGAAACCTCGTACCTCGGCTCGGCCCAGTGGTCAAG
4-5	CTGTACGGGATAAGACCTTCGGTGGTAGCCCACCACTCGCCT
4-6	AGTATGGCTACCATAGAAATACCCGACCACTTCCCTGGCCCT
5-1	TCACGCCCTGAGGGCCAGGGACCTACACTCACGGACTCCTAA
5-2	CGCTATGTCTAACTCAAGGGCCAGTTACGTAAATCCGCGCAA
5-3	ACATACTGGCCTGATCGCGGACCATAGACCATCGGACCCGCA
5-4	GGCCGAGCCGGCCCGGGATTTATTCCTGCTGCTCAGATCAGA
5-5	GGGCTACCACCTTGACCACTGCTTAGATTTATGTGTTCGTAC
5-6	AGTGGTCGGGAGGCGAGTGGTATGAGTGGCACATCGCATTTA
6-1	TGAGTGTAGGTTGCGCGGATTGACCCATGTGCGCACGACTCC
6-2	TACGTAACTGTGCGGGTCCGATCCCGTCTGAGTCTATTCATC
6-3	TGGTCTATGGTCTGATCTGAGAGTGCACTTCAAGCAAAGTTG
6-4	CAGCAGGAATGTACGAACACATAGTGACACGGTGCGGAGCGT
6-5	TAAATCTAAGTAAATGCGATGGGCACAACCCTCCACAATGAA
6-6	TGCCACTCATTTAGGAGTCCGATTGCACTTTTTAATATAAAT
7-1	CACATGGGTCATTTATATTAACCTCCGATAGACAGAAGCCAT
7-2	TCAGACGGGAGGAGTCGTGCGGTTCGCATTACGAGGTAAGTA
7-3	GAAGTGCACTGATGAATAGACAAACTGTTTAGGCTAGGATAT

7-4	CGTGTCACTACAACTTTGCTTATAGGTCCTGGGCCGCCTCCT
7-5	GGGTTGTGCCACGCTCCGCACGATACTTATTCTAGAACTAGC
7-6	AAAGTGCAATTTCATTGTGGAATCCGGTTTCCATTTGTTCTA
8-1	CTATCGGAGGTACTTACCTCGAGAAAGGGCGATTCCGATCGC
8-2	TAATGCGAACATATCCTAGCCACCTTTCAGCATGCAAAGTTC
8-3	TAAACAGTTTAGGAGGCGGCCAGAACTCCACCTGCCACGTGA
8-4	CAGGACCTATGCTAGTTCTAGTAGCTAGTCGTAGAATCTACT
8-5	AATAAGTATCTAGAACAAATGGTGGCTTGTACCCGGAATGTG
8-6	GAAACCGGATATGGCTTCTGTTCGACCGTGTCGCCTATTCCA
9-1	CGCCCTTTCTTGGAATAGGCGATAGAATTCAACCCTTTATGT
9-2	GCTGAAAGGTGCGATCGGAATGACGTAAACGACAAAGTAAGG
9-3	GTGGAGTTCTGAACTTTGCATAGTGAAATGTTGGAACATTGG
9-4	CGACTAGCTATCACGTGGCAGGTGCACAGAATGAGCGGAAAT
9-5	TACAAGCCACAGTAGATTCTATTTGATCATCGATGCCCGCAG
9-6	ACACGGTCGACACATTCCGGGAACCAAGTCTGTTTAAAGTAC
10-1	TGAATTCTATCCTTACTTTGTTTCGAAAGTAATCCCATTGTC
10-2	CGTTTACGTCCCAATGTTCCACGACTGTGACGACAATTGTCG
10-3	ACATTTCACTATTTCCGCTCAGGCTATGGCATGCAACGATAC
10-4	TTCTGTGCACCTGCGGGCATCCATCCAGTGCCGTATGATACT
10-5	GATGATCAAAGTACTTTAAACTCATCCCTGTTCAACTCTGCA
10-6	AGACTTGGTTACATAAAGGGTGCAAGACATCGGGCGCGATGA
11-1	TACTTTCGAATCATCGCGCCC
11-2	GTCACAGTCGGACAATGGGAT
11-3	TGCCATAGCCCGACAATTGTC
11-4	GCACTGGATGGTATCGTTGCA
11-5	ACAGGGATGAAGTATCATACG
11-6	GATGTCTTGCTGCAGAGTTGA

Motif 4.2X

Name	Sequence
1-1	TTCAGCCTTCAACGAACACC
1-2	AAACACGGCAAAGGTCGAAG
1-3	CCATGTACCAACCTGACAAG
1-4	GTCTCCTGGCCCAGACGAAT
1-5	CATTTGGTCTCCGGATAAGG
1-6	ACGAACTTCGGGATTGACTA
2-1	GAAGGCTGAACTTCGACCTTCTTGTTCAGCACGGGACAGG
2-2	TGCCGTGTTTCTTGTCAGGTTCAGACGACGGTCCAAAGCA
2-3	TGGTACATGGATTCGTCTGGTGGCCTTCTGTCCGAGATCA
2-4	GCCAGGAGACCCTTATCCGGGCAACCCGATGCGGGCGGAA
2-5	AGACCAAATGTAGTCAATCCCAATCGGCCCTCGGAACGAC
2-6	CGAAGTTCGTGGTGTTCGTTGCGTCGTCTTTTTCCACAAA
3-1	GCTGAACAAGTTTGTGGAAAGCTTAAGACAAATAGCTAAC
3-2	CGTCGTCTGACCTGTCCCGTCGCCACTTGTCTTCTAACGA
3-3	CAGAAGGCCATGCTTTGGACTGGTTAATGGATCATACGTC
3-4	ATCGGGTTGCTGATCTCGGAGGTACCGCACCCAGCGAGCA
3-5	GGGCCGATTGTTCCGCCCGCTCAACAGGCCGTAAACGCAA
3-6	AAGACGACGCGTCGTTCCGACATGTACTCCAATCATCCGC
4-1	TGTCTTAAGCTCGTTAGAAGTATGAGAGAGTATCCTTATG
4-2	ACAAGTGGCGGACGTATGATAGCATCTGAGGACGCCACCA
4-3	CCATTAACCATGCTCGCTGGGAGTCCCTCGAACAAAGAGA
4-4	GTGCGGTACCTTGCGTTTACGTGCGGTGATGCAGGACACA
4-5	GGCCTGTTGAGCGGATGATTACATGCACTCTCGGTCATGT
4-6	GGAGTACATGGTTAGCTATTTCCCAACCGCGGAAATATGA
5-1	CTCTCTCATATCATATTTCCTCTCTAGGCGCTTCTGGGTG
5-2	CTCAGATGCTCATAAGGATAGGTCCGTGTAAAGCATGAAG
5-3	CGAGGGACTCTGGTGGCGTCGTTCTCCAGTCTGGCACACA
5-4	ATCACCGCACTCTCTTTGTTCTCGACCGGCTTTCTTTGTA
5-5	GAGTGCATGTTGTGTCCTGCTCTTGTCGTCCTTGGGACGT
5-6	GCGGTTGGGAACATGACCGAGAAGATTCGGGTCCCTGTAT
6-1	CGCCTAGAGACTTCATGCTTTAGGAGCGTTTCTAAAGGAG
6-2	TACACGGACCTGTGTGCCAGCAGTAATACGTTATGGCGGT
6-3	ACTGGAGAACTACAAAGAAATCTAAGGCAGTTACAGTGCA
6-4	GCCGGTCGAGACGTCCCAAGAGGGAAAGGCAAACCACCCT
6-5	GACGACAAGAATACAGGGACCCTCAACCCTTCACAAGTGT
6-6	CCGAATCTTCCACCCAGAAGGCTTTATCTTCCCTTCAGGG
7-1	AACGCTCCTACCCTGAAGGGCCTAATTCTCTTTAAACACC
7-2	CGTATTACTGCTCCTTTAGACCTCCCTTTAATGTGGATTT
7-3	CTGCCTTAGAACCGCCATAAAGCTTATTCCTTGCGAAGGC

7-4	GCCTTTCCCTTGCACTGTAAGACCCACTTCGCCAAAGTAG
7-5	AGGGTTGAGGAGGGTGGTTTAAATACAGATCTCAGACTGG
7-6	AAGATAAAGCACACTTGTGAACTCCGATCTTCTTGAAGGG
8-1	GAGAATTAGGAAATCCACATCTAGTGCTAAGTTAAACAGT
8-2	TAAAGGGAGGGCCTTCGCAACGGCCATCCCGGAGGTCCAC
8-3	GGAATAAGCTCTACTTTGGCTACCGCAATCTCATGAGCCG
8-4	GAAGTGGGTCCCAGTCTGAGCTGTGAACATATAGTCCTCG
8-5	ATCTGTATTTCCCTTCAAGAGGAAGGTTTGTTCGCTCCTA
8-6	AGATCGGAGTGGTGTTTAAACGGGCTGAATTCCCGGCTTT
9-1	TTAGCACTAGAAAGCCGGGAGCGTCGTTGTGAAAGACTAT
9-2	GGGATGGCCGACTGTTTAACCAGGGCAGTTAGAAGCCAGC
9-3	GATTGCGGTAGTGGACCTCCTCTAGGGCGTTTAACAAGCG
9-4	ATGTTCACAGCGGCTCATGACTGTGACCACTGGACAGTAT
9-5	CAAACCTTCCCGAGGACTATTAAGGAGTGCAGGCTGCCTT
9-6	ATTCAGCCCGTAGGAGCGAACCTTGGATCCCACACCAAAT
10-1	ACAACGACGCGCTGGCTTCTTTGTGAGCGATGCAGCGATC
10-2	AACTGCCCTGCGCTTGTTAATCGCAATTGGCAGTCCCATA
10-3	ACGCCCTAGAATACTGTCCAATGGGATGAAGCGTCCCATT
10-4	GTGGTCACAGAAGGCAGCCTGCCTACTCGCACGACAAAGT
10-5	GCACTCCTTAATTTGGTGTGCATCGTCTGCAGACGAAGCG
10-6	GGATCCAAGGATAGTCTTTCTTCGCTCACTGCGATGCTCA
11-1	TCGCTCACAATGAGCATCGC
11-2	CCAATTGCGAGATCGCTGCA
11-3	TTCATCCCATTATGGGACTG
11-4	GCGAGTAGGCAATGGGACGC
11-5	GCAGACGATGACTTTGTCGT
11-6	AGTGAGCGAACGCTTCGTCT