

(Circular) MAP of: Peaw135.Seq check: 3436 from: 1 to: 5850

>>>pJS39

With 212 enzymes: *

MaxCuts: 3

June 17, 1998 11:18 ..

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E   c   N           X           C   d
o   s           b           l   I
R   p           a           a   I
I   V           I           I   I
gaattcgaagttcctatactttctagagaataggaacttcgggatcggccccatcgataa
1  -----+-----+-----+-----+-----+-----+ 60
cttaagcttcaaggatatgaaagatctcttatccttgaaggccctagccgggtagctatt

                        B
                AKS  EN  N  g
                vpm  ao  h  l
                ana  gt  e  I
                III  II  I  I
                /    /
gcttggtaccggggcggcctagcagatctagcttATGATAGTGATGTGCTTAAAAACT
61 -----+-----+-----+-----+-----+ 120
cgaacctggggcccggcggatcgtctagatcgaaTACTATCACTACACGAATTTTTGA

                        N
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                        I
TACTCAATGGCTGGTTTATGCATATCGCAATACATGCGAAAAACCTAAAAGAGCTTGCCG
121 -----+-----+-----+-----+-----+ 180
ATGAGTTACCGACCAAATACGTATAGCGTTATGTACGCTTTTTGGATTTTCTCGAACGGC

                        S
                        D  a
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                        a  I
                        I  I
ATAAAAAAGGCCAATTTATTGCTATTTACCGCGGCTTTTTATTGAGCTTGAAAGATAAAT
181 -----+-----+-----+-----+-----+ 240
TATTTTTTCCGGTTAAATAACGATAAATGGCGCCGAAAAATAACTCGAACTTTCTATTTA

AAAATAGATAGGTTTTATTGGAAGCTAAATCTTCTTTATCGTAAAAAATGCCCTCTTGGG
241 -----+-----+-----+-----+-----+ 300
TTTTATCTATCCAAAATAAACCCTTCGATTTAGAAGAAATAGCATTTTTTTACGGGAGAACCC

TTATCAAGAGGGTCATTATATTTTCGCGGAATAACATCATTTGGTGACGAAATAACTAAGC
301 -----+-----+-----+-----+-----+ 360
AATAGTTCTCCAGTAATATAAAGCGCCTTATTGTAGTAAACCACTGCTTTATTGATTCCG
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361 ACTTGTCTCCTGTTTACTCCCCTGAGCTTGAGGGGTTAACATGAAGGTCATCGATAGCAG
-----+-----+-----+-----+-----+-----+ 420
TGAACAGAGGACAAATGAGGGGACTCGAACTCCCAATTGTACTTCCAGTAGCTATCGTC

421 GATAATAATACAGTAAAACGCTAAACCAATAATCCAAATCCAGCCATCCCAAATTGGTAG
-----+-----+-----+-----+-----+-----+ 480
CTATTATTATGTCATTTTGCGATTTGGTTATTAGGTTTAGGTCGGTAGGGTTTAACCATC

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481 TGAATGATTATAAATAACAGTAAACAGTAATGGGCCAATAACACCGGTTGCATTGGTAAG
-----+-----+-----+-----+-----+-----+ 540
ACTTACTAATATTTATTGTCATTTGTCATTACCCGGTTATTGTGGCCAACGTAACCATTTC

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541 GCTCACCAATAATCCCTGTAAAGCACCTTGCTCATGACTCTTTGTTTGGATAGACATCAC
-----+-----+-----+-----+-----+-----+ 600
CGAGTGGTTATTAGGGACATTTTCGTGGAACGAGTACTGAGAAACAAACCTATCTGTAGTG

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601 TCCCTGTAATGCAGGTAAAGCGATCCCACCACCAGCCAATAAAAATTTAAAACAGGGAAATC
-----+-----+-----+-----+-----+-----+ 660
AGGGACATTACGTCCATTTTCGCTAGGGTGGTGGTTCGGTTATTTTAATTTTGTCCCTTTAG

661 TAACCAACCTTCAGATATAAACGCTAAAAAGGCAAATGCACTACTATCTGCAATAAATTC
-----+-----+-----+-----+-----+-----+ 720
ATTGGTTGGAAGTCTATATTTGCGATTTTTCCGTTTACGTGATGATAGACGTTATTTAAG

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721 GAGCAGTACTGCCGTTTTTTTCGCCCCATTTAGTGGCTATTCTTCCTGCCACAAAGGCTTG
-----+-----+-----+-----+-----+-----+ 780
CTCGTCATGACGGCAAAAAAGCGGGGTAAATCACCGATAAGAAGGACGGTGTTCGCAAC

781 GAATACTGAGTGTAAGACCAAGACCCGCTAATGAAAAGCCAACCATCATGCTATTCCA
-----+-----+-----+-----+-----+-----+ 840
CTTATGACTCACATTTTCTGGTTCTGGGCGATTACTTTTCGGTTGGTAGTACGATAAGGT

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841 TCCAAAACGATTTTCGGTAAATAGCACCCACACCGTTGCGGGAATTTGGCCTATCAATTG
-----+-----+-----+-----+-----+-----+ 900
AGGTTTTGCTAAAAGCCATTTATCGTGGGTGTGGCAACGCCCTTAAACCGGATAGTTAAC

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901 CGCTGAAAAATAAATAATCAACAAAATGGGCATCGTTTTAAATAAAGTGATGTATACCGA
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GCGACTTTTTATTTATTAGTTGTTTTACCCGTAGCAAATTTATTTCACTACATATGGCT

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961 ATTCGATTGCGTCTCAACCCCTACTTCGGTATCTGTATTATCACGTGTATTTTTGGTTTT
-----+-----+-----+-----+-----+ 1020
TAAGCTAACGCAGAGTTGGGGATGAAGCCATAGACATAATAGTGCACATAAAAAACCAAAG

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1021 ACGGAACCAAAACATAACCACAAGGAAAGTGACAATATTTAGCAACGCAGCGATAAAAA
-----+-----+-----+-----+-----+ 1080
TGCCTTGGTTTTGTATTGGTGTTCCTTTCACTGTTATAAATCGTTGCGTCGCTATTTTTT

1081 GGGACTATGCGGTGAAATCTCTCCTGCAAAACCACCAATAATAGGCCCCGCTATTAACC
-----+-----+-----+-----+-----+ 1140
CCCTGATACGCCACTTTAGAGAGGACGTTTTGGTGGTTATTATCCGGGGCGATAATTTGG

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1141 AAGCCCAAAACTTGCCCCTAACCAACCGAACCCTTACGCGTTGAGAAGCTGAGGTGGT
-----+-----+-----+-----+-----+ 1200
TTCGGGTTTTGAACGGGATTGGTTGGCTTGGTGAAGTGCGCAACTCTTCGACTCCACCA

ATCGGCAATGACCGATGCCGCGACAGCCCCAGTAGCTCCTGTGATCCCTGAAAGCAAACG

1201 -----+-----+-----+-----+-----+-----+ 1260
TAGCCGTTACTGGCTACGGCGCTGTCTGGGGTCATCGAGGACACTAGGGACTTTCGTTTGC

GCCTAAATACAGCATCCAAAGCGCACTTGAAAAAGCCAGCAATAAGTAATCCAGCGATGC
1261 -----+-----+-----+-----+-----+-----+ 1320
CGGATTTATGTCTAGGTTTCGCGTGAACTTTTTCGGTCGTTATTCATTAGGTCGCTACG

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GCCTATTAATGACAACAACAGCACTGGGCGCCGACCAAATCGGTCAGACATTTTTCCAAG
1321 -----+-----+-----+-----+-----+-----+ 1380
CGGATAATTACTGTTGTTGTCTGTGACCCGCGGCTGGTTTAGCCAGTCTGTAAAAAGGTTT

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CCAAGGAGCAAAGATAACCTGCATTAACGCATAAAGTGCAAGCAATACGCCAAAGTGGTT
1381 -----+-----+-----+-----+-----+-----+ 1440
GGTTCCTCGTTTTCTATTGGACGTAATTGCGTATTTACGTTTCGTTATGCGGTTTTACCAA

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AGCGATATCTTCCGAAGCAATAAATTCACGTAATAACGTTGGCAAGACTGGCATGATAAG
1441 -----+-----+-----+-----+-----+-----+ 1500
TCGCTATAGAAGGCTTCGTTATTTAAGTGCATTATTGCAACCGTTCTGACCGTACTATTC

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GCCAATCCCATGGCATCGAGTAACGTAATTACCAATGCGATCTTTGTCTGAACTATTCAT
1501 -----+-----+-----+-----+-----+-----+ 1560
CGGTTAGGGGTACCGTAGCTCATTGCATTAATGGTTACGCTAGAAACAGCTTGATAAGTA

TTCACTTTTCTCTATCACTGATAGGGAGTGGTAAAATAACTCTATCAATGATAGAGTGTC
1561 -----+-----+-----+-----+-----+-----+ 1620
AAGTGAAAAGAGATAGTGACTATCCCTCACCATTTTATTGAGATAGTTACTATCTCACAG

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AACAAAAATTAGGAATTAATGATGTCcAGATTAGATAAAAAGTAAAGTGATTAACAGCGCA
1621 -----+-----+-----+-----+-----+-----+ 1680
TTGTTTTTAATCCTTAATTACTACAGgTCTAATCTATTTTTCATTTCACTAATTGTCTCGCT

TTAGAGCTGCTTAATGAGGTCGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCAGAAG
1681 -----+-----+-----+-----+-----+-----+ 1740

AATCTCGACGAATTACTCCAGCCTTAGCTTCCAAATTGTTGGGCATTTGAGCGGGTCTTC
CTAGGTGTAGAGCAGCCTACATTGTATTGGCATGTAAAAAATAAGCGGGCTTTGCTCGAC
1741 -----+-----+-----+-----+-----+-----+ 1800
GATCCACATCTCGTCTGGATGTAACATAACCGTACATTTTTTTATTTCGCCCGAAACGAGCTG

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GCCTTAGCCATTGAGATGTTAGATAGGCACCATACTCACTTTTGCCCTTTAGAAGGGGAA
1801 -----+-----+-----+-----+-----+-----+ 1860
CGGAATCGGTAACTCTACAATCTATCCGTGGTATGAGTGAAAACGGGAAATCTTCCCCTT

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AGCTGGCAAGATTTTTTACGTAATAACGCTAAAAGTTTTAGATGTGCTTTACTAAGTCAT
1861 -----+-----+-----+-----+-----+-----+ 1920
TCGACCGTTCTAAAAAATGCATTATTGCGATTTTTCAAATCTACACGAAATGATTTCAGTA

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CGCGATGGAGCAAAAGTACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTC
1921 -----+-----+-----+-----+-----+-----+ 1980
GCGCTACCTCGTTTTTCATGTAAATCCATGTGCCGGATGTCTTTTTGTCATACTTTGAGAG

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GAAAATCAATTAGCCTTTTTATGCCAACAAGGTTTTTCACTAGAGAATGCATTATATGCA
1981 -----+-----+-----+-----+-----+-----+ 2040
CTTTTAGTTAATCGGAAAAATACGGTTGTTCCAAAAAGTGATCTCTTACGTAATATACGT

CTCAGCGCTGTGGGGCATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTC
2041 -----+-----+-----+-----+-----+-----+ 2100
GAGTCGCGACACCCCGTAAAATGAAATCCAACGCATAACCTTCTAGTTCTCGTAGTTCAG

GCTAAAGAAGAAAGGGAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCT
2101 -----+-----+-----+-----+-----+-----+ 2160
CGATTTCTTCTTTCCCTTTGTGGATGATGACTATCATACGGCGGTAATAATGCTGTTCCA

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ATCGAATTATTTGATCACCAAGGTGCAGAGCCAGCCTTCTTATTTCGGCCTTGAATTGATC

2161 -----+-----+-----+-----+-----+-----+ 2220
TAGCTTAATAAACTAGTGGTTCCACGTCTCGGTTCGGAAGAATAAGCCGGAACCTTAAGCTAG

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ATATGCGGATTAGAAAAACAACCTTAAATGTGAAAGTGGGTCTTAAAAGCAGCATAACCTT
2221 -----+-----+-----+-----+-----+ 2280
TATACGCCTAATCTTTTTGTTGAATTTACACTTTACCCAGAATTTTCGTCGTATTGGAA

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TTTCCGTGATGGTAACTTCACGGTAACCAAGATGTGAGTTAACCACCCTTTAGATTCAT
2281 -----+-----+-----+-----+-----+ 2340
AAAGGCACTACCATTGAAGTGCCATTGGTTCTACAGCTCAATTGGTGGGAAATCTAAGTA

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AAAGCGAAAATAATGCGGCTCCAACGTACCCACCTAAATGGAAACGGCGTTCACTCCAAT
2341 -----+-----+-----+-----+-----+ 2400
TTTCGCTTTTATTACGCCGAGGTTGCATGGGTGGATTTACCTTTGCCGCAAGTGAGGTTA

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CTAAACACGCACAACAGATTTTACGTGAATGTTTGGAAAGGAACGTCAATTCCTTTTTCAT
2401 -----+-----+-----+-----+-----+ 2460
GATTTGTGCGTGTTGTCTAAAATGCACCTTACAAACCTTCCTTGCAGTTAAGGGTAAAGTA

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GAAAATATTGAATACCACTTAATGTGATCATTGAACCATTTTCAGTGATCCATTGCTGTT
2461 -----+-----+-----+-----+-----+ 2520
CTTTTATAACTTATGGTGAATTACACTAGTAACCTTGGTAAAAGTCACTAGGTAACGACAA

GACAAAGGGAATCATAGATCCTGCAAGCCTCGTCGTCCTGGCCGGACCACGCTATCTGTG
2521 -----+-----+-----+-----+-----+ 2580
CTGTTTTCCCTTAGTATCTAGGACGTTTCGGAGCAGCAGGACCGGCCTGGTGCGATAGACAC

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CAAGGTCCCCGGCCCCGGACGCGCGCTCCATGAGCAGAGCGCCCCGCCGAGGCGAAGA
2581 -----+-----+-----+-----+-----+-----+ 2640
GTTCCAGGGGCCGGGCCTGCGCGGAGGTAICTCGTCTCGCGGGCGGCGGCTCCGCTTCT

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CTCGGGCGGCGCCCTGCCCGTCCCACCAGGTCAACAGGCGGTAACCGGCCTCTTCATCGG
2641 -----+-----+-----+-----+-----+-----+ 2700
GAGCCCCGCCGCGGGACGGGCAGGGTGGTCCAGTTGTCCGCCATTGGCCGGAAGTAGCC

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GAATGCGCGCGACCTTCAGCATCGCCGGCATGTCCCCCTGGCGGACGGGAAGTATCCAGC
2701 -----+-----+-----+-----+-----+-----+ 2760
CTTACGCGCGCTGGAAGTCGTAGCGGCCGTACAGGGGACCGCCTGCCCTTCATAGGTCG

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TCGAGTGGGTGGTGAGCAGCTCGCCGTCGCGCAGCAGGCGCCAGCGCTCCATCCACGCAG
2761 -----+-----+-----+-----+-----+-----+ 2820
AGCTCACCCACCACTCGTCGAGCGGCAGCGCGTCGTCCGCGGTTCGCGAGGTAGGTGCGTC

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TGACCTCAGGCGGAAAACGGGAAGACACACTCATGAGATGCCTGCAAGCAATTCGTTCTG
2821 -----+-----+-----+-----+-----+-----+ 2880
ACTGGAGTCCGCCTTTTGCCTTCTGTGTGAGTACTCTACGGACGTTTCGTTAAGCAAGAC

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TATCAGGCGCAGGAGCGTCCCGTCCGGGTCGAtcgaccaattcgaagttcctatactttc
2881 -----+-----+-----+-----+-----+-----+ 2940
ATAGTCCGCGTCCTCGCAGGGCAGGCCAGCTagctggttaagcttcaaggatatgaaag

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          H                A
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2941 tagagaataggaacttcgggatccTCTACGCCGACGCATCGTGGCCGGCATCACCGGCG
-----+-----+-----+-----+-----+-----+ 3000
2941 atctcttatccttgaagccctaggAGATGCGGCCTGCGTAGCACCGGCCGTAGTGGCCCG
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3001 CCACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCCACCGATGGGGAAGATCGGGCT
-----+-----+-----+-----+-----+ 3060
3001 GGTGTCCACGCCAACGACCGCGGATATAGCGGCTGTAGGTGGCTACCCCTTCTAGCCCGA
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        I                               I
3061 CGCCACTTCGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCGGTGGCC
-----+-----+-----+-----+-----+ 3120
3061 GCGGTGAAGCCCCGAGTACTCGGAACAAAGCCGCACCCATACCACCGTCCGGGGCACCGG
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                S
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3121 GGGGGACTGTTGGGCGCCATCTCCTTGCATGCACCATTCTTGGCGGCGGGTGTGCTCAAC
-----+-----+-----+-----+-----+ 3180
3121 CCCCCTGACAACCCGCGGTAGAGGAACGTACGTGGTAAGGAACGCCCGCCACGAGTTG
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                E                               SA
                c                               ac
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3181 GGCTCAACCTACTACTGGCGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCTG
-----+-----+-----+-----+-----+ 3240
3181 CCGGAGTTGGATGATGACCGCGACGAAGGATTACGTCTCAGCGTATTCCCTCTCGCAGC
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3241 ACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGAC
-----+-----+-----+-----+-----+ 3300
3241 TGGCTACGGGAACTCTCGGAAGTTGGGTGTCAGTCGAGGAAGGCCACCCGCGCCCCGTACTG
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                P
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3301 TATCGTCGCCGCACTTATGACTGTCTTCTTTTATCATGCAACTCGTAGGACAGGTGCCGGC
-----+-----+-----+-----+-----+ 3360
3301 ATAGCAGCGGCGTGAATACTGACAGAAGAAATAGTACGTTGAGCATCCTGTCCACGGCCG
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3361 AGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATGATCGGCCT 3420
 -----+-----+-----+-----+-----+-----+
 TCGCGAGACCCAGTAAAAGCCGCTCCTGGCGAAAGCGACCTCGCGCTGCTACTAGCCGGA

3421 GTCGCTTGCGGTATTTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCACTGGTCCCGC 3480
 -----+-----+-----+-----+-----+-----+
 CAGCGAACGCCATAAGCCTTAGAACGTGCGGGAGCGAGTTCGGAAGCAGTGACCAGGGCG

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3481 CACCAAACGTTTTTCGGCGAGAAGCAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGG 3540
 -----+-----+-----+-----+-----+-----+
 GTGGTTTGCAAAGCCGCTCTTCGTCCGGTAATAGCGGCCGTACCGCCGGCTGCGCGACCC

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3541 CTACGTCTTGCTGGCGTTCGCGACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCT 3600
 -----+-----+-----+-----+-----+-----+
 GATGCAGAACGACCGCAAGCGCTGCGCTCCGACCTACCGGAAGGGTAATACTAAGAAGA

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3601 CGCTTCCGGCGGCATCGGGATGCCCCGCTTGCAGGCCATGCTGTCCAGGCAGGTAGATGA 3660
 -----+-----+-----+-----+-----+-----+
 GCGAAGGCCCGCCGTAGCCCTACGGGCGCAACGTCCGGTACGACAGGTCCGTCCATCTACT

3661 CGACCATCAGGGACAGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATCAC 3720
 -----+-----+-----+-----+-----+-----+
 GCTGGTAGTCCCTGTCTGAAGTTCCTAGCGAGCGCCGAGAATGGTTCGGATTGAAGCTAGTG

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3721 TGGACCGCTGATCGTCACGGCGATTTATGCCGCTCGGCGAGCACATGGAACGGGTTGGC 3780
 -----+-----+-----+-----+-----+-----+
 ACCTGGCGACTAGCAGTGCCGCTAAATACGGCGGAGCCGCTCGTGTACCTTGCCCAACCG

3781 ATGGATTGTAGGCGCCGCCCTATACCTTGTCTGCCTCCCCGCTTTCGCTCGCGGTGCATG 3840
 -----+-----+-----+-----+-----+-----+
 TACCTAACATCCGCGGCGGGATATGGAACAGACGGAGGGGCGCAACGCAGCGCCACGTAC

3841 GAGCCGGGCCACCTCGACCTGAATGGAAGCCGGCGGCACCTCGCTAACGGATTACCACT 3900
 -----+-----+-----+-----+-----+-----+
 CTCGGCCCCGTGGAGCTGGACTTACCTTCGGCCCGCGTGGAGCGATTGCCTAAGTGGTGA

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CCAAGAATTGGAGCCAATCAATTCTTGCGGAGAACTGTGAATGCGCAAACCAACCCTTGG
 3901 -----+-----+-----+-----+-----+-----+-----+ 3960
 GGTTCTTAACCTCGGTTAGTTAAGAACGCCTCTTGACACTTACGCGTTTTGGTTGGGAACC

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CAGAACATATCCATCGCGTCCGCCATCTCCAGCAGCCGCACGCGGCATCGCGTTGCTG
 3961 -----+-----+-----+-----+-----+-----+-----+ 4020
 GTCTTGTATAGGTAGCGCAGGCGGTAGAGGTCGTCGGCGTGCGCCGCTAGCGCAACGAC

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GCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAG
 4021 -----+-----+-----+-----+-----+-----+-----+ 4080
 CGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTC

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AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTC
 4081 -----+-----+-----+-----+-----+-----+-----+ 4140
 TCCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAG

GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCG
 4141 -----+-----+-----+-----+-----+-----+-----+ 4200
 CACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGC

GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT
 4201 -----+-----+-----+-----+-----+-----+-----+ 4260
 CCTTCGCACCGCGAAAGAGTATCGAGTGCACATCCATAGAGTCAAGCCACATCCAGCAA

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CGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCC
 4261 -----+-----+-----+-----+-----+-----+-----+ 4320
 GCGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGG

GGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC
 4321 -----+-----+-----+-----+-----+-----+-----+ 4380
 CCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGG

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ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG
4381 -----+-----+-----+-----+-----+-----+ 4440
TGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACC

TGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA
4441 -----+-----+-----+-----+-----+-----+ 4500
ACCGGATTGATGCCGATGTGATCTTCCTGTCTATAAACCATAGACGCGAGACGACTTCGGT

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GTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC
4501 -----+-----+-----+-----+-----+-----+ 4560
CAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGGTGGCGACCATCG

GGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT
4561 -----+-----+-----+-----+-----+-----+ 4620
CCACCAAAAAACAAACGTTTCGTCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTA

CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACACGTTAAGGGATT
4621 -----+-----+-----+-----+-----+-----+ 4680
GGAAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAA

TTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATGAAGT
4681 -----+-----+-----+-----+-----+-----+ 4740
AACCAGTACTCTAATAGTTTTTCTAGAAGTGGATCTAGGAAAATTTAATTTTTACTTCA

TTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATC
4741 -----+-----+-----+-----+-----+-----+ 4800
AAATTTAGTTAGATTTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAG

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AGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCC
4801 -----+-----+-----+-----+-----+-----+ 4860
TCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCAACGGACTGAGGGG

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GTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA
4861 -----+-----+-----+-----+-----+-----+ 4920
CAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTACGACGTTACTAT

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 4921 CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGG 4980
 -----+-----+-----+-----+-----+-----+
 GGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCC

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 4981 GCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGC 5040
 -----+-----+-----+-----+-----+-----+
 CGGCTCGCGTCTTACCAGGACGTTGAAATAGGCGGAGGTAGGTCAGATAATTAACAACG

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 5041 CGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCT 5100
 -----+-----+-----+-----+-----+-----+
 GCCCTTCGATCTCATTTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGA

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 5101 GCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAA 5160
 -----+-----+-----+-----+-----+-----+
 CGTCCGTAGCACCCACAGTGCAGCAGCAAACCATAACCGAAGTAAGTCGAGGCCAAGGGTT

5161 CGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGT 5220
 -----+-----+-----+-----+-----+-----+
 GCTAGTTCGGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCA

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 5221 CCTCCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCA 5280
 -----+-----+-----+-----+-----+-----+
 GGAGGCTAGCAACAGTCTTCAATCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGT

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 5281 CTGCATAATTCTTTACTGTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTAC 5340
 -----+-----+-----+-----+-----+-----+
 GACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATG

5341 TCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCA 5400
 -----+-----+-----+-----+-----+-----+
 AGTTGGTTCAGTAAGACTCTTATCACATACCGCTGGCTCAACGAGAACGGGCCGAGT

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ACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGT
5401 -----+-----+-----+-----+-----+-----+ 5460
TGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGTAACCTTTTGCA

TCTTCGGGGCGAAAACCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCC
5461 -----+-----+-----+-----+-----+-----+ 5520
AGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAACCTCTAGGTCAAGCTACATTGGG

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ACTCGTGCACCCAACCTGATCTTCAGCATCTTTTACTTTACCAGCGTTTCTGGGTGAGCA
5521 -----+-----+-----+-----+-----+-----+ 5580
TGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGAAAGACCCACTCGT

AAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATA
5581 -----+-----+-----+-----+-----+-----+ 5640
TTTTGTCTTCCGTTTTACGGCGTTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTAT

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CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGC
5641 -----+-----+-----+-----+-----+-----+ 5700
GAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCG

GGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCC
5701 -----+-----+-----+-----+-----+-----+ 5760
CCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAAGGG

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CGAAAAGTGCCACCTGACGTCTAAGAAACCATTTATCATGACATTAACCTATAAAAAT
5761 -----+-----+-----+-----+-----+-----+ 5820
GCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTTTA

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AGGCGTATCACGAGGCCCTTTTCGTCTTCAA
5821 -----+-----+-----+ 5850
TCCGCATAGTGCTCCGGGAAAGCAGAAGTT

Enzymes that do cut and were not excluded:

AatII	AccI	AflIII	AhdI	AlwNI	ApaLI	AvaI	BaeI
BamHI	BanII	BclI	BglII	BpmI	Bpu10I	BsaI	BsaBI
BsaXI	BsbI	BsgI	BsmI	BsmBI	BspGI	BspMI	BsrBI
BssHII	BssSI	Bst1107I	BstEII	BstXI	Bsu36I	ClaI	DraIII
DrdI	DrdII	DsaI	EagI	EarI	EcoNI	EcoRI	EcoRV
FspI	HgiEII	HindIII	HpaI	KpnI	MluI	MunI	NcoI
NdeI	NheI	NotI	NruI	NsiI	NspV	Pfl1108I	PflMI
PinAI	PmlI	PpuMI	PshAI	PstI	PvuI	RleAI	SacII
SalI	ScaI	SexAI	SgrAI	SmaI	SnaBI	SphI	SspI
TatI	UbaDI	VspI	XbaI	XhoI	XmnI		

Enzymes that do not cut:

AflII	ApaI	AscI	AvrII	BmgI	BplI	Bpu1102I	BseRI
BspEI	BspLU11I	BsrGI	FseI	MscI	PacI	PmeI	PvuII
RsrII	SanDI	SapI	SfiI	SgfI	SpeI	SrfI	Sse8387I
Sse8647I	SstI	StuI	SunI	SwaI	Tth111I	XcmI	

Enzymes excluded; MinCuts: 1 MaxCuts: 3

AceIII	AciI	AluI	AlwI	Alw26I	ApaBI	ApoI	AvaII
BanI	BbsI	BbvI	BccI	Bce83I	BcefI	BcgI	BcgI
BfaI	BfiI	BglI	BsaAI	BsaHI	BsaJI	BsaWI	BscGI
BsiEI	BsiHKAI	BslI	BsmFI	Bsp24I	Bsp24I	Bsp1286I	BsrI
BsrDI	BsrFI	BstYI	Cac8I	CjeI	CjeI	CjePI	CjePI
CviJI	CviRI	DdeI	DpnI	DraI	EaeI	EciI	Eco47III
Eco57I	EcoO109I	EcoRII	FauI	Fnu4HI	FokI	GdiII	HaeI
HaeII	HaeIII	HgaI	HhaI	Hin4I	HincII	HinfI	HphI
MaeIII	MboII	MmeI	MnlI	MseI	MslI	MspI	MspA1I
MwoI	NarI	NciI	NgoAIV	NlaIII	NlaIV	NspI	PleI
Psp1406I	RcaI	RsaI	Sau96I	Sau3AI	ScrFI	SfaNI	SfcI
SimI	StyI	TaiI	TaqI	TaqII	TaqII	TauI	TfiI
ThaI	TseI	Tsp45I	Tsp4CI	Tsp509I	TspRI	Tth1111I	