

Suggested Minimal Sequences for Highly Variant Features

These suggested sequences are identified as recommended in the GenoCAD parts library.

>AmpR_promoter (variant -004) 72 bp

CATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTG
AAAAAGGAAGAGT

>cat_promoter (variant -004) 103 bp

TGATCGGCACGTAAGAGGTTCCAACCTTTCACCATAATGAAATAAGATCACTACCGGGCG
TATTTTTTTGAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAA

>NeoR/KanR_promoter (consensus seq) 114 bp

TCTGGTAAGGTTGGGAAGCCCTGCAAAGTAACTGGATGGCTTCTTGCCGCCAAGGAT
CTGATGGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC

>KanR-aph(3')-Ia_promoter (consensus seq) 99 bp

GTGTCTCAAATCTCTGATGTTACATTGCACAAGATAAAAATATATCATCATGAACAAT
AAAACGTCTGCTTACATAAACAGTAATAACAAGGGGTGTT

>KanR-aphA-3_promoter (consensus seq) 182 bp

GGTTTCAAATCGGCTCCGTCGATACTATGTTATACGCCAACTTTGAAAACAACCTTTGA
AAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAATGCAAGGAACAGTGAATTGGAGTTCC
TCTTGTTATAATTAGCTTCTTGGGGTATCTTTAAATACTGTAGAAAAGAGGAAGGAAAT
AATAA

>SmR-PcS-P2S_promoter (consensus seq) 231 bp

ACCCAGTTGACATAAGCCTGTTTCGGTTCGTAACTGTAATGCAAGTAGCGTAACTGCCG
TCACGCAACTGGTCCAGAACCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGGT
TTTCATGGCTTCTTGTTATGACTGTTTTTTTTGGGGTACAGTCTATGCCTCGGGCATCCA
AGCAGCAAGCGCGTTACGCCGTGGGTCGATGTTTGATGTTATGGAGCAGCAACG

>SmR-PcW-P2S_promoter (consensus seq) 232 bp

ACCCAGTGGACATAAGCCTCGTTCGGTTCGTAAGCTGTAATGCAAGTAGCGTAACTGCC
GTCACGCAACTGGTCCAGAACCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGG
TTTTTCATGGCTTCTTGTTATGACTGTTTTTTTTGGGGTACAGTCTATGCCTCGGGCATCC
AAGCAGCAAGCGCGTTACGCCGTGGGTCGATGTTTGATGTTATGGAGCAGCAACG

>SmR-PcW-P2W_promoter (consensus seq) 233 bp

ACCCAGTGGACATAAGCCTCGTTCGGTTCGTAAGCTGTAATGCAAGTAGCGTAACTGCC
GTCACGCAACTGGTCCAGAACCTTGACCGAACGCAGCGGTGGTAACGGCGCAGTGGCGG
TTTTTCATGGCTTCTTGTTATGACATGTTTTTTTTGGGGTACAGTCTATGCCTCGGGCATC
CAAGCAGCAAGCGCGTTACGCCGTGGGTCGATGTTTGATGTTATGGAGCAGCAACG

>ccdB_promoter (consensus seq) 107 bp

GGCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAG
AATATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTATGCT

>CMV_enhancer (variant -003) 304 bp
CGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCAT
TGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTGACGT
CAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATAT
GCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCC
AGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCT
ATTACCATG

>CMV_promoter (variant -008) 199 bp
TGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTT
CCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGA
CTTTCCAAAATGTCGTAACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTAC
GGTGGGAGGTCTATATAAGCAG

>SV40_ori (variant -004) 136 bp
ATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTT
TTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAG
GAGGCTTTTTTGGAGGCC

>SV40_promoter (variant -008) 196 bp
TGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTA
ACTCCGCCCAGTTCCGCCCATTCTCCGCCCCTGGCTGACTAATTTTTTTTATTTATGC
AGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTG
GAGGCCTAGGCTTTTGCAA

>SV40_enhancer-promoter (promoter variant -002) 303 bp
GGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAAT
TAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAG
CATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCC
TAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCTGGCTGACTAATTTTTTTTATTTAT
GCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTT
TGGAGGCC

>f1_ori_minimal (consensus seq) 381 bp
ACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC
GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCTTTCTCGC
CACGTTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT
TTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGT
GGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAA
TAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTG
ATTTATAAGGGATTTTGCCGATTTTCGG

>f1_ori_plus-strand enhancer (consensus seq) 456 bp
ACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACC
GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCTTTCTCGC
CACGTTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT
TTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGT

GGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAA
TAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTG
ATTTATAAGGGATTTTGCCGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAA
AAATTTAACGCGAATTTTAACAAAATATTAACGTTTACAATTT

>pMB1-ColeE1_ori-high_copy (variant -014) 589 bp
TTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTAC
CAGCGGTGGTTTGTGTTTGC CGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACTGGC
TTCAGCAGAGCGCAGATAACCAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCA
CTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGG
CTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG
GATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG
AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTC
CCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGC
ACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTCGCCA
CCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA

>pMB1-ColeE1_ori-medium copy (variant -014) 589 bp
TTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTAC
CAGCGGTGGTTTGTGTTTGC CGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACTGGC
TTCAGCAGAGCGCAGATAACCAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCA
CTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGG
CTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG
GATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG
AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTC
CCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGC
ACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTCGCCA
CCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA

>EMCV-IRES_high_express (consensus seq) 589 bp
CCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAA
AGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAA
GACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGG
TGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCA
GTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAATGGCTCTCCTCAAGCGTAT
TCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGG
CCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAACGTCTAGGCCCCCG
AACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCACAACCATG

>EMCV-IRES_attenuated (consensus seq) 578 bp
CCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAA
AGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAA
GACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGG
TGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCA

GTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTAT
TCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGG
CCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCC
GAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATG

>EMCV-IRES_minimal_attenuated (consensus seq) 467 bp
GAGGGCCCCGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTC
TCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTCAGGCAGCGGAACCCCCCACCTGG
CGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCAC
AACCCACAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCA
AGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGA
TCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAG
GCCCCCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATG

>AmpR-bla (*E. coli*; variant -013) 861 bp
ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTTGCGGCATTTTGCCTTCC
TGTTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTG
CACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTTCGC
CCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATT
ATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCCGCATACACTATTCTCAGAATG
ACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGA
GAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGAC
AACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAA
CTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGAC
ACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACCTATTAAGTGGCGAACTACT
TACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGAC
CACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTTATTGCTGATAAATCTGGAGCCGGT
GAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTAT
CGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCG
CTGAGATAGGTGCCTCACTGATTAAGCATTGGTAA

>AmpR-bla(M) (variant -002) 795 bp
ATGGACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGT
GGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAG
AACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGT
ATTGACGCCGGGCAAGAGCAACTCGGTGCGCCGCATACACTATTCTCAGAATGACTTGGT
TGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTAT
GCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATC
GGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACCTCGCCT
TGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGA
TGCCTGTAGCAATGGCAACAACGTTGCGCAAACCTATTAAGTGGCGAACTACTTACTCTA
GCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCT
GCGCTCGGCCCTTCCGGCTGGCTGGTTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTG
GGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTT
ATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGAT
AGGTGCCTCACTGATTAAGCATTGGTAA

>BleoR-ble (*Streptoalloteichus*; variant -003) 375 bp
ATGGCCAAGTTGACCAAGTGCCGTTCCGGTGCTCACCGCGCGACGTCGCCGGAGCGGT
CGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGACTTCGCCG
GTGTGGTCCGGGACGACGTGACCCTGTTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCG
GACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTC
GGAGGTCGTGTCCACGAACCTTCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCG
AGCAGCCGTGGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTC
GTGGCCGAGGAGCAGGACTGA

>BlpR-bar (*Streptomyces*; variant -002) 552 bp
ATGAGCCCAGAACGACGCCCCGGCCGACATCCGCCGTGCCACCGAGGCGGACATGCCGGC
GGTCTGCACCATCGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGC
CGCAGGAACCGCAGGAGTGGACGGACGACCTCGTCCGTCTGCGGGAGCGCTATCCCTGG
CTCGTCGCCGAGGTGGACGGCGAGGTCGCCGGCATCGCCTACGCGGGCCCCCTGGAAGGC
ACGCAACGCCTACGACTGGACGGCCGAGTCGACCGTGTACGTCTCCCCCGCCACCAGC
GGACGGGACTGGGCTCCACGCTCTACACCCACCTGCTGAAGTCCCTGGAGGCACAGGGC
TTCAAGAGCGTGGTCGCTGTCATCGGGCTGCCCAACGACCCGAGCGTGCGCATGCACGA
GGCGCTCGGATATGCCCCCGCGGCATGCTGCGGGCGGCCGGCTTCAAGCACGGGAAC
GGCATGACGTGGGTTTTCTGGCAGCTGGACTTCAGCCTGCCGGTACCGCCCCGTCCGGTC
CTGCCCGTCACCGAGATTTGA

>BlpR-pat1 (SnapGene feature) 456 bp
ATGGCGGCGGTCTGCGACATCGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCG
TACGGAGCCGCAGACTCCGCAGGAGTGGATCGACGACCTGGAGCGCCTCCAGGACCGCT
ACCCCTGGCTCGTCGCCGAGGTGGAGGGCGTCGTGCGCCGGCATCGCCTACGCCGGCCCC
TGGAAGGCCCCGCAACGCCTACGACTGGACCGTCGAGTCGACGGTGTACGTCTCCACCG
GCACCAGCGGCTCGGACTGGGCTCCACCCTCTACACCCACCTGCTGAAGTCCATGGAGA
CCCAGGGCTTCAAGAGCGTGGTCGCCGTCATCGGACTGCCCAACGACCCGAGCGTGCGC
CTGCACGAGGCGCTCGGATACACCGCGCGCGGGACGCTGCGGGCAGCCGGCTACAAGCA
CGGGGGCTGGCACGACGTGGGGTTCTGGCAGCGCGACTTCTAG

>BSD (*Aspergillus*; variant -005) 396 bp
ATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTTGAAAGAGCAACGGCTACAAT
CAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACG
GCCGCATCTTCACTGGTGTCAATGTATATCATTTTTACTGGGGGACCTTGTGCAGAACTC
GTGGTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGAT
CGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCG
ATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTT
GGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAA

>ccdB (F plasmid; variant -004) 306 bp
ATGCAGTTTAAGGTTTACACCTATAAAAGAGAGACCGTTATCGTCTGTTTGTGGATGT
ACAGAGTGATATTATTGACACGCCCCGGGCGACGGATGGTGATCCCCCTGGCCAGTGAC
GTCTGCTGTCTAGATAAAGTCTCCCGTGAACTTTACCCGGTGGTGATATCGGGGATGAA
AGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGA

AGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCT
GGGGAATATAA

>CmR-cat (*E. coli*; variant -013) 660 bp

ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGA
ACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGG
ATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTT
ATTCACATTCTTGCCCCGCTGATGAATGCTCATCCGGAATTCCGTATGGCAATGAAAGA
CGGTGAGCTGGTGATATGGGATAGTGTTACCCCTTGTTACACCGTTTTCCATGAGCAAA
CTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACAC
ATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTT
TATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTGTATT
TAAACGTGGCCAATATGGACAACCTCTTCGCCCCCGTTTTTCACCATGGGCAATATTAT
ACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGTTTGTGA
TGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGG
GCGGGGCGTAA

>FKBP12-DmrA (dimerizes w FRAP-DmrC; FKBP(DmrA)-005) 321 bp

GGAGTGCAGGTGGAAACCATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCACTACACCGGGATGCTTGAAGATGGAAAGAAATTTGATTCCTCCC
GGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCCAGATGAGTGTGGGTGAGAGAGCCAAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAAAACTGGAA

>FKBP12-DmrB (F36V; homodimerizes; DmrB-001) 321 bp

GGAGTGCAGGTGGAGACTATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCACTACACCGGGATGCTTGAAGATGGAAAGAAAGTTGATTCCTCCC
GGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCCAGATGAGTGTGGGTGAGAGAGCCAAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAAAACTGGAA

>FRAP-DmrC (wild-type; dimerizes w FKBP-DmrA; FRB) 279 bp

ATCCTCTGGCATGAGATGTGGCATGAAGGCCTGGAAGAGGCATCTCGTTTGTACTTTGG
GGAAAGGAACGTGAAAGGCATGTTTGAGGTGCTGGAGCCCTTGATGCTATGATGGAAC
GGGGCCCCCAGACTCTGAAGGAAACATCCTTTAATCAGGCCTATGGTCGAGATTTAATG
GAGGCCCAAGAGTGGTGCAGGAAGTACATGAAATCAGGGAATGTCAAGGACCTCACCCA
AGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCTCAAAG

>FRAP-DmrC (T2098L; dimerizes w FKBP-DmrA; FRB*) 279 bp

ATCCTCTGGCATGAGATGTGGCATGAAGGCCTGGAAGAGGCATCTCGTTTGTACTTTGG
GGAAAGGAACGTGAAAGGCATGTTTGAGGTGCTGGAGCCCTTGATGCTATGATGGAAC
GGGGCCCCCAGACTCTGAAGGAAACATCCTTTAATCAGGCCTATGGTCGAGATTTAATG
GAGGCCCAAGAGTGGTGCAGGAAGTACATGAAATCAGGGAATGTCAAGGACCTCCTCCA
AGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCTCAAAG

>FKBP-DmrD (F36M; AP21998 monomerizes; DmrD-001) 321 bp

GGAGTGCAGGTGGAGACTATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCCTACACCGGGATGCTTGAAGATGGAAAGAAAATGGATTCTCTCC
GGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCCAGATGAGTGTGGGTGAGAGAGCCAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAAAACCTGGAA

>FKBP-DD (F36V,L106P;Shield1 stabilizes; DD) 324 bp
ATGGGAGTGCAGGTGGAAACCATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGG
CCAGACCTGTGTGGTGCCTACACCGGGATGCTTGAAGATGGAAAGAAAGTCGATTCTCT
CCCGGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGC
TGGGAAGAAGGGGTTGCCCAGATGAGTGTGGGTGAGAGAGCCAACTGACTATATCTCC
AGATTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCG
TCTTCGATGTGGAGCTTCTAAAACCGGAA

>FKBP-DD-C (E31G,F36V,R71G,K105E; Shield1 stabilizes; DD-C)
324 bp
GGAGTGCAGGTGGAAACCATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCCTACACCGGGATGCTTGGAGATGGAAAGAAAGTTGACTCTCTCC
GGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCCAGATGAGTGTGGGTGAGGAGCCAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAGAACTGGAATAG

>GmR-aacC1 (Class 1 integron; variant -004) 543 bp
ATGTTACGCAGCAGCAACGATGTTACGCAGCAGGGCAGTCGCCCTAAAACAAAGTTAGG
TGGCTCAAGTATGGGCATCATTCGCACATGTAGGCTCGGCCCTGACCAAGTCAAATCCA
TGCGGGCTGCTCTTGATCTTTTCGGTCGTGAGTTCGGAGACGTAGCCACCTACTCCCAA
CATCAGCCGACTCCGATTACCTCGGGAACCTTGCTCCGTAGTAAGACATTCATCGCGCT
TGCTGCCTTCGACCAAGAAGCGGTTGTTGGCGCTCTCGCGGCTTACGTTCTGCCCAGGT
TTGAGCAGCCGCGTAGTGAGATCTATATCTATGATCTCGCAGTCTCCGGCGAGCACCGG
AGGCAGGGCATTGCCACCGCGCTCATCAATCTCCTCAAGCATGAGGCCAACGCGCTTGG
TGCTTATGTGATCTACGTGCAAGCAGATTACGGTGACGATCCCGCAGTGGCTCTCTATA
CAAAGTTGGGCATACGGGAAGAAGTGATGCACTTTGATATCGACCAAGTACCGCCACC
TAA

>HygR-aph(4)-Ia (*E. coli*; variant -008) 1026 bp
ATGAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCTGA
CAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTTTTCTAGCTTCG
ATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTACAAA
GATCGTTATGTTTATCGGCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGA
CATTTGGGGAATTCAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCA
CGTTGCAAGACCTGCCTGAAACCGAACTGCCCCGCTGTTCTGCAGCCGGTCGCGGAGGCC
ATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCATTCGGACC
GCAAGGAATCGGTCAATACTACATGGCGTGATTTTCATATGCGCGATTGCTGATCCCC
ATGTGTATCACTGGCAAACCTGTGATGGACGACACCGTCAGTGCGTCCGTGCGCAGGCT
CTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGACGCG
GGATTTGCGCTCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGACT

GGAGCGAGGCGATGTTCTGGGGATTCCCAATACGAGGTCGCCAACATCTTCTTCTGGAGG
CCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCGAGCGGAGGCATCCGGAGCT
TGCAGGATCGCCGCGGCTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATC
AGAGCTTGGTTGACGGCAATTTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCA
ATCGTCCGATCCGGAGCCGGGACTGTCTGGGCGTACACAAATCGCCCGCAGAAGCGCGGC
CGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAAACCGACGCCCCAGCA
CTCGTCCGAGGGCAAAGGAATAG

>KanR-aph(3')-Ia (*E. coli*; variant -009) 816 bp
ATGAGCCATATTCAACGGGAAACGTCTTGCTCGAGGCCGCGATTAAATTCCAACATGGA
TGCTGATTTATATGGGTATAAATGGGCTCGCGATAATGTCGGGCAATCAGGTGCGACAA
TCTATCGATTGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAACATGGCAAAGGT
AGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAAACTGGCTGACGGAATTTAT
GCCTCTTCCGACCATCAAGCATTTTATCCGTACTCCTGATGATGCATGGTTACTCACCA
CTGCGATCCCCGGGAAAACAGCATTCAGGTATTAGAAGAATATCCTGATTCAGGTGAA
AATATTGTTGATGCGCTGGCAGTGTTCCTGCGCCGGTTGCATTCGATTCCTGTTTGTA
TTGTCTTTTAAACAGCGATCGCGTATTTTCGTCTCGCTCAGGCGCAATCACGAATGAATA
ACGGTTTGGTTGATGCGAGTGATTTTGATGACGAGCGTAATGGCTGGCCTGTTGAACAA
GTCTGGAAAGAAATGCATAAACTTTTGCCATTCTCACCGGATTCAGTCGTCATCATGG
TGATTTCTCACTTGATAACCTTATTTTTGACGAGGGGAAATTAATAGGTTGTATTGATG
TTGGACGAGTCGGAATCGCAGACCGATACCAGGATCTTGCCATCCTATGGAACGCTC
GGTGAGTTTTCTCCTTCATTACAGAAACGGCTTTTTTCAAAAATATGGTATTGATAATCC
TGATATGAATAAATTGCAGTTTCATTTGATGCTCGATGAGTTTTTCTAA

>KanR-aphA-3 (*Staphylococcus*; variant -020) 795 bp
ATGGCTAAAATGAGAATATCACCGGAATTGAAAAAACTGATCGAAAAATACCGCTGCGT
AAAAGATACGGAAGGAATGTCTCCTGCTAAGGTATATAAGCTGGTGGGAGAAAATGAAA
ACCTATATTTAAAAATGACGGACAGCCGGTATAAAGGGACCACCTATGATGTGGAACGG
GAAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCCTGTTCCAAAGGTCCTGCACTT
TGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGGCCGATGGCGTCTTTTGCT
CGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCGGAGTGC
ATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTATACGAATAGCTTAGACAG
CCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGCCGATGTGGATTGCGAAA
ACTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTATGATTTTTTAAAGACG
GAAAAGCCCGAAGAGGAACTTGTCTTTTCCCACGGCGACCTGGGAGACAGCAACATCTT
TGTGAAAGATGGCAAAGTAAGTGGCTTTATTGATCTTGGGAGAAGCGGCAGGGCGGACA
AGTGGTATGACATTGCCTTCTGCGTCCGGTTCGATCAGGGAGGATATCGGGGAAGAACAG
TATGTGAGCTATTTTTTGACTTACTGGGGATCAAGCCTGATTGGGAGAAAATAAAATA
TTATATTTTACTGGATGAATTGTTTTAG

>lacI (GTG START codon; variant -002) 1083 bp
GTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGT
TTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGAAG
CGGCGATGGCGGAGCTGAATTACATTTCCCAACCGCGTGGCACAACAACTGGCGGGCAAA
CAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGAAAT
TGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGTGATGG
TAGAACGAAGCGGCGTCAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGC
GTCAGTGGGCTGATCATTAACCTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGC

TGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACA
GTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTG
GGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCG
TCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGG
AAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGC
ATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGC
CATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATA
CCGAAGACAGCTCATGTTATATCCCGCCGT**T**AACCACCATCAAACAGGATTTTCGCCTG
CTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGG
CAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGGCGCCAATACGC
AAACCGCTCTCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCC
CGACTGGAAAGCGGGCAGTGA

lacI-003 and -004 have a T-C transition (red highlight shows position)
that results in L286S. According to Markiewicz et al. (1994) *J. Mol.*
Biol. **240**:421-433, this impairs lacI function.

>Luciferase-luc (*Photinus*; wild-type variant -005 w PTS1
signal) 1653 bp
ATGGAAGACGCCAAAAACATAAAGAAAGGCCCGGCCATTCTATCCTCTAGAGGATGG
AACCGCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCTGGAACAA
TTGCTTTTACAGATGCACATATCGAGGTGAACATCACGTACGCGGAATACTTCGAAATG
TCCGTTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGT
CGTATGCAGTGAAAACCTCTCTTCAATTCTTTATGCCGGTGTTGGGCGCGTTATTTATCG
GAGTTGCAGTTGCGCCCGCAACGACATTTATAATGAACGTGAATTGCTCAACAGTATG
AACATTTTCGCAGCCTACCGTAGTGTTTGTTCAAAAAGGGTTGCAAAAAATTTTGAA
CGTGCAAAAAAATTACCAATAATCCAGAAAATTATTATCATGGATTCTAAACGGATT
ACCAGGGATTTTCAGTCGATGTACACGTTTCGTCACATCTCATCTACCTCCCGGTTTTAAT
GAATACGATTTTGTACCAGAGTCCTTTGATCGTGACAAAACAATTGCACTGATAATGAA
TTCTCTGGATCTACTGGGTTACCTAAGGGTGTGGCCCTTCCGCATAGAACTGCCTGCG
TCAGATTCTCGCATGCCAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCG
ATTTTAAAGTGTTGTTCCATTCCATCACGGTTTTTGGAATGTTTACTACACTCGGATATTT
GATATGTGGATTTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTTTACGAT
CCCTTCAGGATTACAAAATTCAAAGTGCGTTGCTAGTACCAACCCTATTTTTCATTCTTC
GCCAAAAGCACTCTGATTGACAAATACGATTTATCTAATTTACACGAAATTGCTTCTGG
GGGCGCACCTCTTTCGAAAGAAGTCGGGGAAGCGGTTGCAAAACGCTTCCATCTTCCAG
GGATACGACAAGGATATGGGCTCACTGAGACTACATCAGCTATTCTGATTACACCCGAG
GGGATGATAAACCGGGCGCGGTTCGGTAAAGTTGTTCCATTTTTTTGAAGCGAAGGTTGT
GGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAGAGAGGCGAATTATGTGTCAGAG
GACCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGAC
AAGGATGGATGGCTACATTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTT
CATAGTTGACCGCTTGAAGTCTTTAATTAAATACAAAGGATATCAGGTGGCCCCCGCTG
AATTGGAATCGATATTGTTACAACACCCCAACATCTTCGACGCGGGCGTGGCAGGTCTT
CCCGACGATGACGCCGGTGAACCTCCCGCCGCCGTTGTTGTTTTGGAGCACGGAAAGAC
GATGACGGAAAAAGAGATCGTGGATTACGTGCCAGTCAAGTAACAACCGCGAAAAAGT
TGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGTCTTACCGGAAAACTCGAC
GCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGTCCAAATTGTA
A

>Luciferase-luc+ (*Photinus*; N50D,N119G, ΔPTS1 enhanced variant -008) 1653 bp
ATGGAAGACGCCAAAAACATAAAGAAAGGCCCGCGCCATTCTATCCGCTGGAAGATGG
AACCCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAA
TTGCTTTTACAGATGCACATATCGAGGTGGACATCACTTACGCTGAGTACTTCGAAATG
TCCGTTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGT
CGTATGCAGTGAAAACCTCTCTTCAATTCTTTATGCCGGTGTGGGCGCGTTATTTATCG
GAGTTGCAGTTGCGCCCGCGAACGACATTTATAATGAACGTGAATTGCTCAACAGTATG
GGCATTTTCGCAGCCTACCGTGGTGTTCGTTTTCCAAAAAGGGGTGCAAAAAATTTTGAA
CGTGCAAAAAAAGCTCCCAATCATCAAAAAATTTATTATCATGGATTCTAAAACGGATT
ACCAGGGATTTTCAGTCGATGTACACGTTTCGTCACATCTCATCTACCTCCCGGTTTTAAT
GAATACGATTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAATTGCACTGATCATGAA
CTCCTCTGGATCTACTGGTCTGCCTAAAGGTGTCGCTCTGCCTCATAGAACTGCCTGCG
TGAGATTCTCGCATGCCAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCG
ATTTTAAAGTGTTGTTCCATTCCATCACGGTTTTTGGAAATGTTTACTACACTCGGATATTT
GATATGTGGATTTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTCTGAGGA
GCCTTTCAGGATTACAAGATTCAAAGTGCGCTGCTGGTGCCAACCCTATTCTCCTTCTTC
GCCAAAAGCACTCTGATTGACAAATACGATTTTATCTAATTTACACGAAATTGCTTCTGG
TGGCGCTCCCCTCTCTAAGGAAGTCGGGGAAGCGGTTGCCAAGAGGTTCCATCTGCCAG
GTATCAGGCAAGGATATGGGCTCACTGAGACTACATCAGCTATTCTGATTACACCCGAG
GGGGATGATAAACCGGGCGCGGTTCGGTAAAGTTGTTCCATTTTTTGAAGCGAAGGTTGT
GGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAAAGAGGCGAACTGTGTGTGAGAG
GTCCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGAC
AAGGATGGATGGCTACATTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTT
CATCGTTGACCGCCTGAAGTCTCTGATTAAGTACAAAGGCTATCAGGTGGCTCCCGCTG
AATTGGAATCCATCTTGCTCCAACACCCCAACATCTTCGACGCAGGTGTCGCAGGTCTT
CCCGACGATGACGCCGGTGAACCTCCCGCCGCCGTTGTTGTTTTGGAGCACGGAAAGAC
GATGACGGAAAAAGAGATCGTGGATTACGTGCCAGTCAAGTAACAACCGCGAAAAAGT
TGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGTCTTACCGGAAAACCTCGAC
GCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTA
A

>Luciferase-luc2 (N50D,N119G, ΔPTS1 enhanced synthetic variant -006) 1650 bp
ATGGAAGATGCCAAAAACATTAAGAAGGGGCCAGCGCCATTCTACCCACTCGAAGACGG
GACCGCCGGCGAGCAGCTGCACAAAGCCATGAAGCGCTACGCCCTGGTGCCCGGCACCA
TCGCCTTTACCGACGCACATATCGAGGTGGACATTACCTACGCCGAGTACTTCGAGATG
AGCGTTCGGCTGGCAGAAGCTATGAAGCGCTATGGGCTGAATACAAACCATCGGATCGT
GGTGTGCAGCGAGAATAGCTTGCAGTTCTTCATGCCCGTGTTGGGTGCCCTGTTTCATCG
GTGTGGCTGTGGCCCCAGCTAACGACATCTACAACGAGCGCGAGCTGCTGAACAGCATG
GGCATCAGCCAGCCCACCGTCGTATTCTGTGAGCAAGAAAGGGCTGCAAAAGATCCTCAA
CGTGCAAAAGAAGCTACCGATCATACAAAAGATCATCATCATGGATAGCAAGACCGACT
ACCAGGGCTTCCAAAGCATGTACACCTTCGTGACTTCCCATTGTCACCCGGCTTCAAC
GAGTACGACTTCGTGCCCCGAGAGCTTCGACCGGGACAAAACCATCGCCCTGATCATGAA
CAGTAGTGGCAGTACCGGATTGCCCAAGGGCGTAGCCCTACCGCACCGCACCGCTTG
TCCGATTTCAGTCATGCCCGCGACCCCATCTTCGGCAACCAGATCATCCCCGACACCGCT
ATCCTCAGCGTGGTGCCATTTTACCACGGCTTCGGCATGTTTACCACGCTGGGCTACTT
GATCTGCGGCTTTCGGGTCGTGCTCATGTACCGCTTCGAGGAGGAGCTATTCTTGCGCA

GCTTGCAAGACTATAAGATTCAATCTGCCCTGCTGGTGCCCACTATTTAGCTTCTTC
GCTAAGAGCACTCTCATCGACAAGTACGACCTAAGCAACTTGCACGAGATCGCCAGCGG
CGGGGCGCCGCTCAGCAAGGAGGTAGGTGAGGCCGTGGCCAAACGCTTCCACCTACCAG
GCATCCGCCAGGGCTACGGCCTGACAGAAACAACCAGCGCCATTCTGATCACCCCCGAA
GGGACGACAAGCCTGGCGCAGTAGGCAAGGTGGTGCCCTTCTTCGAGGCTAAGGTGGT
GGACTTGACACCGGTAAGACACTGGGTGTGAACCAGCGCGGCGAGCTGTGCGTCCGTG
GCCCCATGATCATGAGCGGCTACGTTAACAACCCCGAGGCTACAAACGCTCTCATCGAC
AAGGACGGCTGGCTGCACAGCGGCGACATCGCCTACTGGGACGAGGACGAGCACTTCTT
CATCGTGGACCGGCTGAAGAGCCTGATCAAATACAAGGGCTACCAGGTAGCCCCAGCCG
AACTGGAGAGCATCCTGCTGCAACACCCCAACATCTTCGACGCCGGGGTCGCCGGCCTG
CCCGACGACGATGCCGGCGAGCTGCCCGCCGAGTCGTCGTGCTGGAACACGGTAAAC
CATGACCGAGAAGGAGATCGTGGACTATGTGGCCAGCCAGGTTACAACCGCCAAGAAGC
TGCGCGGTGGTGTGTTGTGTTGTCGTGGACGAGGTGCCTAAAGGACTGACCGGCAAGTTGGAC
GCCCCGAAGATCCGCGAGATTCTCATTAAGGCCAAGAAGGGCGGCAAGATCGCCGTG

Luciferase-002 and -005 are wild-type. Luciferase -007 and -008 are enhanced luciferase. Luciferase-001, -003, -004 and -006 are synthetic enhanced.

>MBP (variant -004) 1101 bp

ATGAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAAACGGCGATAAAGGCTATAACGG
TCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGC
ATCCGGATAAACTGGAAGAGAAATTTCCACAGGTTGCGGCAACTGGCGATGGCCCTGAC
ATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGA
AATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTAC
GTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTAT
AACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAA
AGAAGTGAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCA
CCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTAC
GACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGT
TGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTG
CCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCCGTGGGCATGGTCCAACATC
GACACCAGCAAAGTGAATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATC
CAAACCGTTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGC
TGGCAAAAGAGTTCCTCGAAAACATCTGCTGACTGATGAAGGTCTGGAAGCGGTAAAT
AAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGA
TCCACGTATTGCCGCCACCATGGAACCGCCAGAAAGGTGAAATCATGCCGAACATCC
CGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGT
CGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT

>nos-nptII (KanR variant -016) 822 bp

ATGGCAATTACCTTATCCGCAACTTCTTTACCTATTTCCGCCCCGATCCGGGCAGGTTC
TCCGGCCGCTTGCGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCT
GCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCT
GGCCACGACGGGCGTTCTTGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGG
ACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCT
GCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGC
TACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGG

AAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCC
GAACTGTTCCGCCAGGCTCAAGGCGCGCATGCCCCGACGGCGAGGATCTCGTCTGACCCA
TGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCG
ACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGAT
ATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGC
CGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGA

>NeoR-KanR-nptII (variant -002) 795 bp

ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT
CGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGT
CAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAA
CTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGC
TGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGG
GGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGAT
GCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAA
ACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC
TGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGC
ATGCCCCGACGGCGAGGATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATATCAT
GGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACC
GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGG
GCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTT
CTATCGCCTTCTTGACGAGTTCTTCTGA

>PuroR-pac (*Streptomyces*; variant -006) 600 bp

ATGACCGAGTACAAGCCCACGGTGCGCCTCGCCACCCGCGACGACGTCCCCCGGGCCGT
ACGCACCCCTCGCCGCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGACCCGG
ACCGCCACATCGAGCGGGTCACCGAGCTGCAAGAACTCTTCCTCACGCGCGTCGGGCTC
GACATCGGCAAGGTGTGGGTTCGCGGACGACGGCGCCGCGGTGGCGGTCTGGACCACGCC
GGAGAGCGTCGAAGCGGGGGCGGTGTTTCGCCGAGATCGGCCCCGCGCATGGCCGAGTTGA
GCGGTTCCCGGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCC
AAGGAGCCCGCGTGGTTCCTGGCCACCGTCGGCGTCTCGCCCGACCACCAGGGCAAGGG
TCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCGGAGCGCGCCGGGGTGCCCCG
CCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTCACC
GTCACCGCCGACGTCGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCC
CGGTGCCTGA

>TcR-tetA1 (Tn10; variant -001) 1206 bp

ATGAATAGTTCGACAAAGATCGCATTTGGTAATTACGTTACTCGATGCCATGGGGATTGG
CCTTATCATGCCAGTCTTGCCAACGTTATTACGTGAATTTATTGCTTCGGAAGATATCG
CTAACCACTTTGGCGTATTGCTTGCACTTTATGCGTTAATGCAGGTTATCTTTGCTCCT
TGGCTTGGA AAAATGTCTGACCGATTTGGTTCGGCGCCCAGTGCTGTTGTTGTCATTAAT
AGGCGCATCGCTGGATTACTTATTGCTGGCTTTTTCAAGTGCGCTTTGGATGCTGTATT
TAGGCCGTTTGCTTTCAGGGATCACAGGAGCTACTGGGGCTGTCGCGGCATCGGTCATT
GCCGATAACACCTCAGCTTCTCAACGCGTGAAGTGGTTCGGTTGGTTAGGGGCAAGTTT
TGGGCTTGGTTTAATAGCGGGGCTATTATTGGTGGTTTTGCAGGAGAGATTTACCGC
ATAGTCCCTTTTTTATCGCTGCGTTGCTAAATATTGTCACCTTTCCTTGTTGGTTATGTTT
TGGTTCCGTGAAACCAAAAATACACGTGATAATACAGATAACCGAAGTAGGGGTGAGAC
GCAATCAAATTCGGTGTACATCACTTTATTTAAACGATGCCCATTTTGTGATTATTT

ATTTTTCAGCGCAATTGATAGGCCAAATTCCCGCAACGGTGTGGGTGCTATTTACCGAA
AATCGTTTTGGATGGAATAGCATGATGGTTGGCTTTTCATTAGCGGGTCTTGGTCTTTT
ACACTCAGTATTCCAAGCCTTTGTGGCAGGAAGAATAGCCACTAAATGGGGCGAAAAAA
CGGCAGTACTGCTCGAATTTATTGCAGATAGTAGTGCATTTGCCTTTTATAGCGTTTATA
TCTGAAGGTTGGTTAGATTTCCCTGTTTTAATTTTATTGGCTGGTGGTGGGATCGCTTT
ACCTGCATTACAGGGAGTGATGTCTATCCAAACAAAGAGTCATGAGCAAGGTGCTTTAC
AGGGATTATTGGTGAGCCTTACCAATGCAACCGGTGTTATTGGCCCATTACTGTTTACT
GTTATTTATAATCATTCACTACCAATTTGGGATGGCTGGATTGATTATTGGTTTAGC
GTTTTACTGTATTATTATCCTGCTATCAATGACCTTCATGTTGACCCCTCAAGCTCAGG
GGAGTAAACAGGAGACAAGTGCTTAG

>TcR-tetA2 (IncP- α plasmids; ATG START codon; variant -003)
1200 bp

ATGAAACCCAACATACCCCTGATCGTAATTCTGAGCACTGTCGCGCTCGACGCTGTCGG
CATCGGCCTGATTATGCCGGTGCTGCCGGGCCTCCTGCGCGATCTGGTTCACCTCGAACG
ACGTCACCGCCCACTATGGCATTCTGCTGGCGCTGTATGCGTTGGTGCAATTTGCCTGC
GCACCTGTGCTGGGCGCGCTGTCGGATCGTTTCGGGCGGCGGCCAATCTTGCTCGTCTC
GCTGGCCGGCGCCACTGTCGACTACGCCATCATGGCGACAGCGCCTTTCCTTTGGGTTT
TCTATATCGGGCGGATCGTGGCCGGCATCACCGGGGCGACTGGGGCGGTAGCCGGCGCT
TATATTGCCGATATCACTGATGGCGATGAGCGCGCGCGGCACTTCGGCTTCATGAGCGC
CTGTTTTCGGGTTTCGGGATGGTCGCGGGACCTGTGCTCGGTGGGCTGATGGGCGGTTTCT
CCCCCACGCTCCGTTCTTCGCCGCGGCAGCCTTGAACGGCCTCAATTTCTGACGGGC
TGTTTTCTTTTGGCGGAGTCGCACAAAGGCGAACGCCGGCCGTTACGCCGGGAGGCTCT
CAACCCGCTCGCTTCGTTCCGGTGGGCCCGGGGCATGACCGTCGTCGCCGCCCTGATGG
CGGTCTTCTTCATCATGCAACTTGTGCGACAGGTGCCGGCCGCGCTTTGGGTCATTTTC
GGCGAGGATCGCTTTCACCTGGGACGCGACCACGATCGGCATTTTCGCTTGCCGCATTTGG
CATTTCTGCATTCACCTCGCCAGGCAATGATCACCGGCCCTGTAGCCGCCCGGCTCGGCG
AAAGGCGGGCACTCATGCTCGGAATGATTGCCGACGGCACAGGCTACATCCTGCTTGCC
TTCGCGACACGGGGATGGATGGCGTTCCCGATCATGGTCCTGCTTGCTTCGGGTGGCAT
CGGAATGCCGGCGCTGCAAGCAATGTTGTCCAGGCAGGTGGATGAGGAACGTCAGGGGC
AGCTGCAAGGCTCACTGGCGGCGCTCACCAGCCTGACCTCGATCGTCGGACCCCTCCTC
TTCACGGCGATCTATGCGGCTTCTATAACAACGTGGAACGGGTGGGCATGGATTGCAGG
CGCTGCCCTCTACTTGCTCTGCCGCGCGCTGCGTCGCGGGCTTTGGAGCGGCGCAG
GGCAACGAGCCGATCGCTGA

>TcR-tetC (pSC101; variant -005) 1191 bp

ATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGCTGTAGG
CATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCGTCCATTCCGACA
GCATCGCCAGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGC
GCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCGCCAGTCCTGCTCGCTTC
GCTACTTGGAGCCACTATCGACTACGCGATCATGGCGACCACACCCGTCCTGTGGATCC
TCTACGCCGGACGCATCGTGGCCGGCATCACCGGCGCCACAGGTGCGGTTGCTGGCGCC
TATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGC
TTGTTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGGGGACTGTTGGGCGCCATCT
CCTTGCAATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAACCTACTACTGGGC
TGCTTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCCTT
CAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCACTTATGA
CTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGGGTCATTTTC

GGCGAGGACCGCTTTCGCTGGAGCGCGACGATGATCGGCCTGTCGCTTGCGGTATTTCGG
AATCTTGACGCCCCTCGCTCAAGCCTTCGTCACTGGTCCCGCCACCAAACGTTTCGGCG
AGAAGCAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCG
TTCGCGACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGGCAT
CGGGATGCCCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGAC
AGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATCATTGGACCGCTGATC
GTCACGGCGATTTATGCCGCTCGGCGAGCACATGGAACGGGTGGCATGGATTGTAGG
CGCCGCCCTATACCTTGTCTGCCTCCCCGCGTTGCGTCGCGGTGCATGGAGCCGGGCCA
CCTCGACCTGA

>TcR-tetL (*Bacillus*; GTG START codon; variant -006) 1377 bp
GTGAATACATCCTATTACAAATCGAATTTACGACACAACCAAATTTTAATTTGGCTTTG
CATTTTATCTTTTTTTTAGCGTATTAAATGAAATGGTTTTGAACGTCTCATTACCTGATA
TTGCAAATGATTTTAATAAACACCTGCGAGTACAACTGGGTGAACACAGCCTTTATG
TTAACCTTTTCCATTGGAACAGCTGTATATGGAAAGCTATCTGATCAATTAGGCATCAA
AAGGTTACTCCTATTTGGAATTATAATAAATTGTTTCGGGTCGGTAATTGGGTTTGTG
GCCATTCTTTCTTTTCTTACTTATTATGGCTCGTTTTATTCAAGGGGCTGGTGCAGCT
GCATTTCCAGCACTCGTAATGGTTGTAGTTGCGCGCTATATTCAAAGGAAAATAGGGG
TAAAGCATTTGGTCTTATTGGATCGATAGTAGCCATGGGAGAAGGAGTCGGTCCAGCGA
TTGGTGGAATGATAGCCATTATATTCATTGGTCCTATCTTCTACTCATTCTTATGATA
ACAATTATCACTGTTCCGTTTTCTTATGAAATTATTAAAGAAAGAAGTAAGGATAAAAGG
TCATTTTGATATCAAAGGAATTATACTAATGTCTGTAGGCATTGTATTTTTTTATGTTGT
TTACAACATCATATAGCATTTCTTTTCTTATCGTTAGCGTGCTGTCATTCTCTGATATTT
GTAAACATATCAGGAAAGTAACAGATCCTTTTGTTGATCCCGGATTAGGGAAAAATAT
ACCTTTTATGATTGGAGTCTTTGTGGGGGAATTATATTTGGAACAGTAGCAGGGTTTG
TCTCTATGGTTCCTTATATGATGAAAGATGTTCCACCAGCTAAGTACTGCCGAAATCGGA
AGTGTAATTATTTTCCCTGGAACAATGAGTGTCATTATTTTCGGCTACATTGGTGGGAT
ACTTGTTGATAGAAGAGGTCCTTTATACGTGTTAAACATCGGAGTTACATTTCTTTCTG
TTAGCTTTTTAACTGCTTCCTTTCTTTTAGAAACAACATCATGGTTCATGACAATTATA
ATCGTATTTGTTTTAGGTGGGCTTTCGTTACCAAACAGTTATATCAACAATTGTTTC
AAGTAGCTTGAAACAGCAGGAAGCTGGTGCTGGAATGAGTTTGCTTAACTTTACCAGCT
TTTTATCAGAGGGAACAGGTATTGCAATTGTAGGTGGTTTATTATCCATACCTTACTT
GATCAAAGGTTGTTACCTATGGAAGTTGATCAGTCAACTTATCTGTATAGTAATTTGTT
ATTACTTTTTTCAGGAATCATTGTCATTAGTTGGCTGGTTACCTTGAATGTATATAAAC
ATTCTCAAAGGGATTTCTAA

>TetR (*Pseudomonas* RP4; variant -001) 651 bp
ATGACAAAGTTGCAGCCGAATACAGTGATCCGTGCCGCCCTGGACCTGTTGAACGAGGT
CGGCGTAGACGGTCTGACGACACGCAAACCTGGCGGAACGGTTGGGGGTTTCAGCAGCCGG
CGCTTTACTGGCACTTCAGGAACAAGCGGGCGCTGCTCGACGCACTGGCCGAAGCCATG
CTGGCGGAGAATCATACGCATTTCGGTGCCGAGAGCCGACGACGACTGGCGCTCATTTCT
GATCGGGAATGCCCCGAGCTTCAGGCAGGCGCTGCTCGCCTACCGCGATGGCGCGCGCA
TCCATGCCGGCACGCGACCGGGCGCACCGCAGATGGAAACGGCCGACGCGCAGCTTCGC
TTCCTCTGCGAGGCGGGTTTTTCGGCCGGGACGCCGTCAATGCGCTGATGACAATCAG
CTACTTCACTGTTGGGGCCGTGCTTGAGGAGCAGGCCGGCGACAGCGATGCCGGCGAGC
GCGGCGGCACCGTTGAACAGGCTCCGCTCTCGCCGCTGTTGCGGGCCGCGATAGACGCC
TTCGACGAAGCCGGTCCGGACGCAGCGTTCGAGCAGGGACTCGCGGTGATTGTCTGATG

ATTGGCGAAAAGGAGGCTCGTTGTCAGGAACGTTGAAGGACCGAGAAAGGGTGACGATT
GA

>TetR (Tn10; variant -004) 624 bp

ATGTCTAGATTAGATAAAAAGTAAAGTGATTAACAGCGCATTAGAGCTGCTTAATGAGGT
CGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCCAGAAGCTAGGTGTAGAGCAGCCTA
CATTGTATTGGCATGTAAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAGATG
TTAGATAGGCACCATACTCACTTTTGCCCTTTAGAAGGGGAAAGCTGGCAAGATTTTTT
ACGTAATAACGCTAAAAGTTTTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAAAG
TACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCGAAAATCAATTAGCC
TTTTTATGCCAACAAGGTTTTTCACTAGAGAATGCATTATATGCACTCAGCGCTGTGGG
GCATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAA
GGGAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTATCGAATTATTT
GATCACCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATT
AGAAAAACAACCTTAAATGTGAAAGTGGGTCTTAA

TetR-003 was mis-annotated and is actually a unique variant of TcR