

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

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CATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTG  
AAAAAGGAAGAGT
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>cat_promoter (variant -004) 103 bp

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TGATCGGCACGTAAGAGGTTCCAACCTTCACCATAATGAAATAAGATCACTACCGGGCG  
TATTTTTTGTAGTTATCGAGATTTTCAGGAGCTAAGGAAGCTAAA
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>Neor/KanR_promoter (consensus seq) 114 bp

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TCTGGTAAGGTTGGGAAGCCCTGCAAAGTAACTGGATGGCTTCTTGCCGCCAAGGAT  
CTGATGGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC
```

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

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GTGTCTCAAATCTCTGATGTTACATTGCACAAGATAAAAATATATCATCATGAACAAT  
AAAACGTCTGCTTACATAAACAGTAATAACAAGGGGTGTT
```

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

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GGTTTCAAATCGGCTCCGTCGATACTATGTTATACGCCAACTTTGAAAACAACCTTTGA  
AAAAGCTGTTTTCTGGTATTTAAGGTTTTAGAAATGCAAGGAACAGTGAATTGGAGTTCG  
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

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GGCTTACTAAAAGCCAGATAACAGTATGCGTATTTGCGCGCTGATTTTTGCGGTATAAG  
AATATATACTGATATGTATACCCGAAGTATGTCAAAAAGAGGTATGCT
```

>CMV_enhancer (variant -003) 304 bp
CGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCCAT
TGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCATTTGACGT
CAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCAGTACATCAAGTGTATCATAT
GCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCC
AGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCT
ATTACCATG

>CMV_promoter (variant -008) 199 bp
TGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTACTCACGGGGATTT
CCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGA
CTTCCAAAATGTCGTAACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTAC
GGTGGGAGGTCTATATAAGCAG

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

>SV40_promoter (variant -008) 196 bp
TGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTA
ACTCCGCCCAGTTCCGCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGC
AGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTG
GAGGCTAGGCTTTTGCAA

>SV40_enhancer-promoter (promoter variant -002) 303 bp
GGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAAT
TAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAG
CATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCC
TAACTCCGCCCAGTTCCGCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTAT
GCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTT
TGGAGGCC

>f1_ori_minimal (consensus seq) 381 bp
ACGCGCCCTGTAGCGGCGCATTAAGCGCGGGCGGTGTGGTGGTTACGCGCAGCGTGACC
GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTCTCGC
CACGTTTCGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT
TTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGT
GGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAA
TAGTGGACTCTTGTTCCAAACCTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTG
ATTTATAAGGGATTTTGCCGATTTTCGG

>f1_ori_plus-strand enhancer (consensus seq) 456 bp
ACGCGCCCTGTAGCGGCGCATTAAGCGCGGGCGGTGTGGTGGTTACGCGCAGCGTGACC
GCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCCCTTCTCGC
CACGTTTCGCCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGAT
TTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGT

GGGCCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAA
TAGTGGACTCTTGTTCCAAACCTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTG
ATTTATAAGGGATTTTTCGCCGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAA
AAATTTAACGCGAATTTTAACAAAATATTAACGTTTACAATTT

>pMB1-ColeE1_ori-high_copy (variant -014) 589 bp
TTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTAC
CAGCGGTGGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACCTGGC
TTCAGCAGAGCGCAGATAACAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCA
CTTCAAGAACTCTGTAGCACCGCCTACATACTCGCTCTGCTAATCCTGTTACCAGTGG
CTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG
GATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG
AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTC
CCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGC
ACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCA
CCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA

>pMB1-ColeE1_ori-medium copy (variant -014) 589 bp
TTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTAC
CAGCGGTGGTTTGTTCGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACCTGGC
TTCAGCAGAGCGCAGATAACAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCA
CTTCAAGAACTCTGTAGCACCGCCTACATACTCGCTCTGCTAATCCTGTTACCAGTGG
CTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCG
GATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG
AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTC
CCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGC
ACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCA
CCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA

>EMCV-IRES_high_express (consensus seq) 589 bp
CCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAA
AGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAA
GACAAACAACGTCGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGG
TGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCA
GTGCCACGTTGTGAGTTGGATAGTTGTGGAAGAGTCAAATGGCTCTCCTCAAGCGTAT
TCAACAAGGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGG
CCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAACGTCCTAGGCCCCCCG
AACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATGGCCACAACCATG

>EMCV-IRES_attenuated (consensus seq) 578 bp
CCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCTCTCGCCAA
AGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAA
GACAAACAACGTCGTAGCGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGG
TGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCA

GTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTAT
TCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGG
CCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAGGCCCCC
GAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATG

>EMCV-IRES_minimal_attenuated (consensus seq) 467 bp
GAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCCTAGGGGTCTTTCCCTC
TCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTCAGGCAGCGGAACCCCCACCTGG
CGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCAC
AACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCA
AGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTTGTATGGGATCTGA
TCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAACGTCTAG
GCCCCCGAACCACGGGGACGTGGTTTTCTTTGAAAAACACGATGATAATATG

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

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

>BleoR-ble (*Streptoalloteichus*; variant -003) 375 bp
ATGGCCAAGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGACGTCGCCGGAGCGGT
CGAGTTCTGGACCGACCGGCTCGGGTTCCTCCGGGACTTCGTGGAGGACGACTTCGCCG
GTGTGGTCCGGGACGACGTGACCCTGTTTCATCAGCGCGGTCCAGGACCAGGTGGTGCCG
GACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTC
GGAGGTCGTGTCCACGAACCTCCGGGACGCCTCCGGGCCGGCCATGACCAGATCGGGC
AGCAGCCGTGGGGCGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTC
GTGGCCGAGGAGCAGGACTGA

>BlpR-bar (*Streptomyces*; variant -002) 552 bp
ATGAGCCCAGAACGACGCCCGGCCGACATCCGCCGTGCCACCGAGCGGACATGCCGGC
GGTCTGCACCATCGTCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGC
CGCAGGAACCGCAGGAGTGGACGGACGACCTCGTCCGTCTGCGGGAGCGCTATCCCTGG
CTCGTCCCGAGGTGGACGGCGAGGTCGCCGGCATCGCCTACGCGGGCCCCCTGGAAGGC
ACGCAACGCCTACGACTGGACGGCCGAGTCGACCGTGTACGTCTCCCCCGCCACCAGC
GGACGGGACTGGGCTCCACGCTCTACACCCACCTGCTGAAGTCCCTGGAGGCACAGGGC
TTCAAGAGCGTGGTCGCTGTCATCGGGCTGCCAACGACCCGAGCGTGCGCATGCACGA
GGCGCTCGGATATGCCCGCGGCATGCTGCGGGCGGCCGGCTTCAAGCACGGGAAC
GGCATGACGTGGGTTTTCTGGCAGCTGGACTTCAGCCTGCCGGTACCGCCCCGTCCGGTC
CTGCCCGTCACCGAGATTTGA

>BlpR-pat1 (SnapGene feature) 456 bp
ATGGCGGCGGTCTGCGACATCGTCAATCACTACATCGAGACGAGCACGGTCAACTTCCG
TACGGAGCCGCAGACTCCGCAGGAGTGGATCGACGACCTGGAGCGCCTCCAGGACCCT
ACCCCTGGCTCGTCCCGAGGTGGAGGGCGTCTGCGCCGGCATCGCCTACGCCGGCCCC
TGGAAGCCCCGCAACGCCTACGACTGGACCGTCGAGTCGACGGTGTACGTCTCCACCG
GCACCAGCGGCTCGGACTGGGCTCCACCCTCTACACCCACCTGCTGAAGTCCATGGAGA
CCCAGGGCTTCAAGAGCGTGGTCGCCGTCATCGGACTGCCAACGACCCGAGCGTGCGC
CTGCACGAGGCGCTCGGATACACCGCGCGGGACGCTGCGGGCAGCCGGCTACAAGCA
CGGGGGCTGGCACGACGTGGGGTTCTGGCAGCGCGACTTCTAG

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

>ccdB (F plasmid; variant -004) 306 bp
ATGCAGTTTAAGGTTTACACCTATAAAAGAGAGCCGTTATCGTCTGTTTGTGGATGT
ACAGAGTGATATTATTGACACGCCCGGGCGACGGATGGTGATCCCCCTGGCCAGTGAC
GTCTGCTGTTCAGATAAAGTCTCCCGTGAACCTTACCCGGTGGTGCATATCGGGGATGAA
AGCTGGCGCATGATGACCACCGATATGGCCAGTGTGCCGGTCTCCGTTATCGGGGAAGA

AGTGGCTGATCTCAGCCACCGCGAAAATGACATCAAAAACGCCATTAACCTGATGTTCT
GGGAATATAA

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

ATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGA
ACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGG
ATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTT
ATTACATTCCTTGCCCCGCTGATGAATGCTCATCCGGAATTCGGTATGGCAATGAAAGA
CGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACCGTTTTCCATGAGCAAA
CTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACAC
ATATATTCGCAAGATGTGGCGTGTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTT
TATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTACCAGTTTTGATT
TAAACGTGGCCAATATGGACAACCTTCTCGCCCCGTTTTCCACCATGGGCAAAATATTAT
ACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGTTTGTGA
TGGCTTCATGTTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGG
GCGGGGCGTAA

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

GGAGTGCAGGTGGAAACCATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCCTACACCGGGATGCTTGAAGATGGAAAGAAATTTGATTCCTCCC
GGGACAGAAACAAGCCCTTTAAGTTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCAGATGAGTGTGGGTGAGAGAGCCAAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAAAACCTGGAA

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

GGAGTGCAGGTGGAGACTATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCCTACACCGGGATGCTTGAAGATGGAAAGAAAGTTGATTCCTCCC
GGGACAGAAACAAGCCCTTTAAGTTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCAGATGAGTGTGGGTGAGAGAGCCAAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAAAACCTGGAA

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

ATCCTCTGGCATGAGATGTGGCATGAAGGCCTGGAAGAGGCATCTCGTTTGTACTTTGG
GGAAAGGAACGTGAAAGGCATGTTTGAGGTGCTGGAGCCCTTGCATGCTATGATGGAAC
GGGGCCCCCAGACTCTGAAGGAAACATCCTTTAATCAGGCCTATGGTCGAGATTTAATG
GAGGCCCAAGAGTGGTGCAGGAAGTACATGAAATCAGGGAATGTCAAGGACCTCACCCA
AGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCTCAAAG

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

ATCCTCTGGCATGAGATGTGGCATGAAGGCCTGGAAGAGGCATCTCGTTTGTACTTTGG
GGAAAGGAACGTGAAAGGCATGTTTGAGGTGCTGGAGCCCTTGCATGCTATGATGGAAC
GGGGCCCCCAGACTCTGAAGGAAACATCCTTTAATCAGGCCTATGGTCGAGATTTAATG
GAGGCCCAAGAGTGGTGCAGGAAGTACATGAAATCAGGGAATGTCAAGGACCTCTCCA
AGCCTGGGACCTCTATTATCATGTGTTCCGACGAATCTCAAAG

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

GGAGTGCAGGTGGAGACTATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCA
GACCTGCGTGGTGCCTACACCGGGATGCTTGAAGATGGAAAGAAAATGGATTCTCC
GGGACAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGG
GAAGAAGGGGTTGCCAGATGAGTGTGGGTGAGAGAGCCAAACTGACTATATCTCCAGA
TTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCT
TCGATGTGGAGCTTCTAAAACCTGGAA

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

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

>GmR-aacC1 (Class 1 integron; variant -004) 543 bp
ATGTTACGCAGCAGCAACGATGTTACGCAGCAGGGCAGTCGCCCTAAAACAAAAGTTAGG
TGGCTCAAGTATGGGCATCATTCGCACATGTAGGCTCGGCCCTGACCAAGTCAAATCCA
TGCGGGCTGCTCTTGATCTTTTCGGTCTGTAGTTCGGAGACGTAGCCACCTACTCCCAA
CATCAGCCGACTCCGATTACCTCGGGAACCTTGCTCCGTAGTAAGACATTCATCGCGCT
TGCTGCCTTCGACCAAGAAGCGGTTGTTGGCGCTCTCGCGGCTTACGTTCTGCCAGGT
TTGAGCAGCCGCGTAGTGAGATCTATATCTATGATCTCGCAGTCTCCGGCGAGACCCGG
AGGCAGGGCATTGCCACCGCGCTCATCAATCTCCTCAAGCATGAGGCCAACCGCGTTGG
TGCTTATGTGATCTACGTGCAAGCAGATTACGGTGACGATCCCGCAGTGGCTCTCTATA
CAAAGTTGGGCATACGGGAAGAAGTGTGCACTTTGATATCGACCAAGTACCGCCACC
TAA

>HygR-aph(4)-Ia (*E. coli*; variant -008) 1026 bp
ATGAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGA
CAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTTTCAGCTTCG
ATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTACAAA
GATCGTTATGTTTATCGGCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGA
CATTTGGGAATTCAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCA
CGTTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGCAGCCGGTTCGCGGAGGCC
ATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCATTCGGACC
GCAAGGAATCGGTCAATACTACTACATGGCGTGATTTTCATATGCGCGATGCTGATCCCC
ATGTGTATCACTGGCAAACCTGTGATGGACGACACCGTCAGTGCGTCCGTTCGCGCAGGCT
CTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCGAAGTCCGGCACCTCGTGCACGC
GGATTTTCGGCTCCAACAATGTCTGACGGACAATGGCCGCATAACAGCGGTCATTGACT

GGAGCGAGGCGATGTTCTGGGGATTCCCAATACGAGGTCGCCAACATCTTCTTCTGGAGG
CCGTGGTTGGCTTGTATGGAGCAGCAGACGCGTACTTCGAGCGGAGGCATCCGGAGCT
TGCAGGATCGCCGCGGCTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATC
AGAGCTTGGTTGACGGCAATTTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCA
ATCGTCCGATCCGGAGCCGGGACTGTCTGGGCGTACACAAATCGCCCGCAGAAGCGCGGC
CGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAAACCGACGCCCCAGCA
CTCGTCCGAGGGCAAAGGAATAG

>KanR-aph(3')-Ia (*E. coli*; variant -009) 816 bp
ATGAGCCATATTCAACGGGAAACGTCTTGCTCGAGGCCGCGATTAAATTC AACATGGA
TGCTGATTTATATGGGTATAAATGGGCTCGCGATAATGTCGGGCAATCAGGTGCGACAA
TCTATCGATTGTATGGGAAGCCCGATGCGCCAGAGTTGTTTCTGAAACATGGCAAAGGT
AGCGTTGCCAATGATGTTACAGATGAGATGGTCAGACTAAACTGGCTGACGGAATTTAT
GCCTCTTCCGACCATCAAGCATTTTATCCGTACTCCTGATGATGCATGGTTACTCACCA
CTGCGATCCCCGGGAAAACAGCATTCCAGGTATTAGAAGAATATCCTGATTCAGGTGAA
AATATTGTTGATGCGCTGGCAGTGTTCCTGCGCCGGTTGCATTCGATTCCTGTTTGTA
TTGTCCTTTTAAACAGCGATCGCGTATTTTCGTCTCGCTCAGGCGCAATCACGAATGAATA
ACGGTTTGGTTGATGCGAGTGATTTTGTATGACGAGCGTAATGGCTGGCCTGTTGAACAA
GTCTGGAAAGAAATGCATAAACTTTTGCATTCTCACCGGATTCAGTCGTCACTCATGG
TGATTTCTCACTTGATAACCTTATTTTTGACGAGGGGAAATTAATAGGTTGTATTGATG
TTGGACGAGTCGGAATCGCAGACCGATAACCAGGATCTTGCCATCCTATGGAACGCCTC
GGTGAGTTTTCTCCTTCATTACAGAAACGGCTTTTTTCAAAAATATGGTATTGATAATCC
TGATATGAATAAATTGCAGTTTCATTTGATGCTCGATGAGTTTTTTCTAA

>KanR-aphA-3 (*Staphylococcus*; variant -020) 795 bp
ATGGCTAAAATGAGAATATCACCGGAATTGAAAAAACTGATCGAAAAATACCGCTGCGT
AAAAGATACGGAAGGAATGTCTCCTGCTAAGGTATATAAGCTGGTGGGAGAAAATGAAA
ACCTATATTTAAAAATGACGGACAGCCGGTATAAAGGGACCACCTATGATGTGGAACGG
GAAAAGGACATGATGCTATGGCTGGAAGGAAAGCTGCCGTGTTCAAAGGTCCTGCACTT
TGAACGGCATGATGGCTGGAGCAATCTGCTCATGAGTGAGGCCGATGGCGTCCTTTGCT
CGGAAGAGTATGAAGATGAACAAAGCCCTGAAAAGATTATCGAGCTGTATGCGGAGTGC
ATCAGGCTCTTTCACTCCATCGACATATCGGATTGTCCCTATACGAATAGCTTAGACAG
CCGCTTAGCCGAATTGGATTACTTACTGAATAACGATCTGGCCGATGTGGATTGCGAAA
ACTGGGAAGAAGACACTCCATTTAAAGATCCGCGCGAGCTGTATGATTTTTTAAAGACG
GAAAAGCCCGAAGAGGAACTTGTCTTTTCCCACGGCGACCTGGGAGACAGCAACATCTT
TGTGAAAGATGGCAAAGTAAGTGGCTTTATTGATCTTGGGAGAAGCGGCAGGGCGGACA
AGTGGTATGACATTCCTTCTGCGTCCGGTTCGATCAGGGAGGATATCGGGGAAGAACAG
TATGTGAGCTATTTTTTACTTACTGGGGATCAAGCCTGATTGGGAGAAAATAAAATA
TTATATTTTACTGGATGAATTGTTTTAG

>lacI (GTG START codon; variant -002) 1083 bp
GTGAAACCAGTAACGTTATACGATGTCGAGAGTATGCCGGTGTCTTATCAGACCGT
TTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACCGGGAAAAAGTGGAAAG
CGGCGATGGCGGAGCTGAATTACATTTCCCAACCGCGTGGCACAACAACGGCGGGCAAA
CAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGAAAT
TGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGTGATGG
TAGAACGAAGCGGCGTCAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGC
GTCAGTGGGCTGATCATTAACCTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGC

TGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACA
GTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTG
GGTCACCAGCAAATCGCGCTGTTAGCGGGCCATTAAAGTTCTGTCTCGGCGGTCTGCG
TCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGG
AAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGC
ATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGC
CATTACCGAGTCCGGGCTGCGCGTTGGTGCCGATATCTCGGTAGTGGGATACGACGATA
CCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTG
CTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGG
CAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCAATACGC
AAACCGCTCTCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTC
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
AACCGCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAA
TTGCTTTTACAGATGCACATATCGAGGTGAACATCACGTACGCGGAATACTTCGAAATG
TCCGTTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGT
CGTATGCAGTGAAAACCTCTCTTCAATTCCTTATGCCGGTGTGGGCGCGTTATTTATCG
GAGTTGCAGTTGCGCCCGCAACGACATTTATAATGAACGTGAATTGCTCAACAGTATG
AACATTTTCGCAGCCTACCGTAGTGTGTTTCCAAAAAGGGTTGCAAAAAATTTTGAA
CGTGCAAAAAAATTACCAATAATCCAGAAAATTATTATCATGGATTCTAAAACGGATT
ACCAGGGATTTTCAGTCGATGTACACGTTTCGTCACATCTCATCTACCTCCCGGTTTTAAT
GAATACGATTTTGTACCAGAGTCCTTTGATCGTGACAAAACAATTGCACTGATAATGAA
TTCCTCTGGATCTACTGGGTTACCTAAGGGTGTGGCCCTTCCGCATAGAACTGCCTGCG
TCAGATTTCTCGCATGCCAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCG
ATTTTAAGTGTTGTTCCATTCCATCACGGTTTTTGGAAATGTTTACTACACTCGGATATTT
GATATGTGGATTTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTTTACGAT
CCCTTCAGGATTACAAAATTCAAAGTGCCTTGCTAGTACCAACCCTATTTTTCATTCTTC
GCCAAAAGCACTCTGATTGACAAATACGATTTATCTAATTTACACGAAATTGCTTCTGG
GGGCGCACCTCTTTCGAAAGAAGTCGGGGAAGCGGTTGCAAAACGCTTCCATCTTCCAG
GGATACGACAAGGATATGGGCTCACTGAGACTACATCAGCTATTTCTGATTACACCCGAG
GGGATGATAAACCGGGCGCGGTTCGGTAAAGTTGTTCCATTTTTTTGAAGCGAAGGTTGT
GGATCTGGATACCGGAAAACGCTGGGCGTTAATCAGAGAGGCGAATTATGTGTCAGAG
GACCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGAC
AAGGATGGATGGCTACATTTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTT
CATAGTTGACCGCTTGAAGTCTTTAATTAATAACAAAGGATATCAGGTGGCCCCCGCTG
AATTGGAATCGATATTGTTACAACACCCCAACATCTTCGACGCGGGCGTGGCAGGTCTT
CCCGACGATGACGCCGGTGAACCTCCCGCCGCGTGTGTTGTTTTGGAGCACGGAAAGAC
GATGACGGAAAAAGAGATCGTGGATTACGTCCGAGTCAAGTAACAACCGCGAAAAAGT
TGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGCTTACCGGAAAACCTCGAC
GCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGTCCAAATTGTA
A

>Luciferase-luc+ (*Photinus*; N50D,N119G, ΔPTS1 enhanced variant -008) 1653 bp

ATGGAAGACGCCAAAAACATAAAGAAAGGCCCGGCCATTCTATCCGCTGGAAGATGG
AACCGCTGGAGAGCAACTGCATAAGGCTATGAAGAGATACGCCCTGGTTCCTGGAACAA
TTGCTTTTACAGATGCACATATCGAGGTGGACATCACTTACGCTGAGTACTTCGAAATG
TCCGTTTCGGTTGGCAGAAGCTATGAAACGATATGGGCTGAATACAAATCACAGAATCGT
CGTATGCAGTGAAAACCTCTCTCAATTCTTTATGCCGGTGTGGGCGCGTTATTTATCG
GAGTTGCAGTTGCGCCCGCGAACGACATTTATAATGAACGTGAATTGCTCAACAGTATG
GGCATTTTCGCAGCCTACCGTGGTGTTCGTTTTCCAAAAAGGGTTGCAAAAAATTTTGAA
CGTGCAAAAAAAGCTCCCAATCATCAAAAAATTTATTATCATGGATTCTAAAACGGATT
ACCAGGGATTTTCAGTCGATGTACACGTTTCGTCACATCTCATCTACCTCCCGGTTTTAAT
GAATACGATTTTGTGCCAGAGTCCTTCGATAGGGACAAGACAATTGCACTGATCATGAA
CTCCTCTGGATCTACTGGTCTGCCTAAAGGTGTGCGTCTGCCTCATAGAAGTGCCTGCG
TGAGATTCTCGCATGCCAGAGATCCTATTTTTGGCAATCAAATCATTCCGGATACTGCG
ATTTTAAAGTGTTGTTCCATTCCATCACGGTTTTTGGAAATGTTTACTACACTCGGATATTT
GATATGTGGATTTTCGAGTCGTCTTAATGTATAGATTTGAAGAAGAGCTGTTTCTGAGGA
GCC TTCAGGATTACAAGATTCAAAGTGCCTGCTGGTGCCAACCTATTTCTCCTTCTTC
GCCAAAAGCACTCTGATTGACAAATACGATTTTATCTAATTTACACGAAATTGCTTCTGG
TGCGCTCCCCTCTCTAAGGAAGTCGGGGAAGCGGTTGCCAAGAGGTTCCATCTGCCAG
GTATCAGGCAAGGATATGGGCTCACTGAGACTACATCAGCTATTTCTGATTACACCCGAG
GGGATGATAAACCGGGCGCGGTCGGTAAAGTTGTTCCATTTTTTGAAGCGAAGGTTGT
GGATCTGGATACCGGGAAAACGCTGGGCGTTAATCAAAGAGGCGAACTGTGTGTGAGAG
GTCCTATGATTATGTCCGGTTATGTAAACAATCCGGAAGCGACCAACGCCTTGATTGAC
AAGGATGGATGGCTACATTTCTGGAGACATAGCTTACTGGGACGAAGACGAACACTTCTT
CATCGTTGACCGCCTGAAGTCTCTGATTAAGTACAAAGGCTATCAGGTGGCTCCCGCTG
AATTGGAATCCATCTTGCTCCAACACCCCAACATCTTCGACGCAGGTGTCGCAGGTCTT
CCCGACGATGACGCCGGTGAACCTCCCGCCGCGTGTGTTGTTTTGGAGCACGGAAAGAC
GATGACGGAAAAAGAGATCGTGGATTACGTGCCAGTCAAGTAACAACCGCGAAAAAGT
TGCGCGGAGGAGTTGTGTTTGTGGACGAAGTACCGAAAGGCTTACCGGAAAACCTCGAC
GCAAGAAAAATCAGAGAGATCCTCATAAAGGCCAAGAAGGGCGGAAAGATCGCCGTGTA
A

>Luciferase-luc2 (N50D,N119G, ΔPTS1 enhanced synthetic variant -006) 1650 bp

ATGGAAGATGCCAAAAACATTAAGAAGGGCCAGCGCCATTCTACCCACTCGAAGACGG
GACCGCCGGCGAGCAGCTGCACAAAGCCATGAAGCGCTACGCCCTGGTGCCTGGCACCA
TCGCCTTTACCGACGCACATATCGAGGTGGACATTACCTACGCCGAGTACTTCGAGATG
AGCGTTCGGCTGGCAGAAGCTATGAAGCGCTATGGGCTGAATACAAACCATCGGATCGT
GGTGTGCAGCGAGAATAGCTTGCAGTTCCTCATGCCCGTGTGGGTGCCCTGTTTCATCG
GTGTGGCTGTGGCCCCAGCTAACGACATCTACAACGAGCGCGAGCTGCTGAACAGCATG
GGCATCAGCCAGCCCACCGTTCGTATTCGTGAGCAAGAAAGGGCTGCAAAAGATCCTCAA
CGTGCAAAAGAAGCTACCGATCATACAAAAGATCATCATCATGGATAGCAAGACCGACT
ACCAGGGCTTCAAAGCATGTACACCTTCGTGACTTCCATTTGCCACCCGGCTTCAAC
GAGTACGACTTCGTGCCCCGAGAGCTTCGACCGGGACAAAACCATCGCCCTGATCATGAA
CAGTAGTGGCAGTACCGGATTGCCAAGGGCGTAGCCCTACCGCACCGCACCGCTTGTG
TCCGATTCAGTCATGCCCGCGACCCCATCTTCGGCAACCAGATCATCCCCGACACCGCT
ATCCTCAGCGTGGTGCCATTTTACCACGGCTTCGGCATGTTTACCACGCTGGGCTACTT
GATCTGCGGCTTTCGGGTCGTGCTCATGTACCGCTTCGAGGAGGAGCTATTCTTGCGCA

GCTTGCAAGACTATAAGATTCAATCTGCCCTGCTGGTGCCACACTATTTAGCTTCTTC
GCTAAGAGCACTCTCATCGACAAGTACGACCTAAGCAACTTGCACGAGATCGCCAGCGG
CGGGGCGCCGCTCAGCAAGGAGGTAGGTGAGGCCGTGGCCAAACGCTTCCACCTACCAG
GCATCCGCCAGGGCTACGGCCTGACAGAAACAACCAGCGCCATTCTGATCACCCCGAA
GGGACGACAAGCCTGGCGCAGTAGGCAAGGTGGTGCCCTTCTTCGAGGCTAAGGTGGT
GGACTTGGACACCGGTAAGACACTGGGTGTGAACCAGCGCGGCGAGCTGTGCGTCCGTG
GCCCCATGATCATGAGCGGCTACGTTAACAACCCCGAGGCTACAAACGCTCTCATCGAC
AAGGACGGCTGGCTGCACAGCGGCGACATCGCCTACTGGGACGAGGACGAGCACTTCTT
CATCGTGGACCGGCTGAAGAGCCTGATCAAATACAAGGGCTACCAGGTAGCCCCAGCCG
AACTGGAGAGCATCCTGCTGCAACACCCCAACATCTTCGACGCCGGGGTCGCCGGCCTG
CCCGACGACGATGCCGGCGAGCTGCCCGCCGAGTCGTCGTGCTGGAACACGGTAAAC
CATGACCGAGAAGGAGATCGTGGACTATGTGGCCAGCCAGGTTACAACCGCCAAGAAGC
TGCGCGGTGGTGTGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
GCCCCGAAGATCCGCGAGATTCTCATTAAAGCCAAGAAGGGCGGCAAGATCGCCGTG

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

ATGAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGG
TCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGC
ATCCGGATAAACTGGAAGAGAAATTTCCACAGGTTGCGGCAACTGGCGATGGCCCTGAC
ATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGA
AATCACCCCGACAAAGCGTTCAGGACAAGCTGTATCCGTTTACCTGGGATGCCGTAC
GTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATCGCTGATTTAT
AACAAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAAGAGATCCCGGCGCTGGATAA
AGAAGTGAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCA
CCTGGCCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTAC
GACATTAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGT
TGACCTGATTAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTG
CCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATC
GACACCAGCAAAGTGAATTATGGTGTAAACGGTACTGCCGACCTTCAAGGGTCAACCATC
CAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGC
TGGCAAAAGAGTTCCTCGAAAACATCTGCTGACTGATGAAGGTCTGGAAGCGGTAAAT
AAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGA
TCCACGTATTGCCGCCACCATGAAAACGCCAGAAAGGTGAAATCATGCCGAACATCC
CGCAGATGTCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGT
CGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT

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

ATGGCAATTACCTTATCCGCAACTTCTTTACCTATTTCCGCCCGGATCCGGGCAGGTTT
TCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCT
GCTCTGATGCCCGCGTGTTCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCT
GGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGG
ACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCT
GCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGC
TACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTIONCGGATGG

AAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCC
GAACTGTTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTTCGTGACCCA
TGGCGATGCCTGCTTGGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCG
ACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGAT
ATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGC
CGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGA

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

ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATT
CGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGT
CAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAA
CTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGC
TGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGG
GGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGAT
GCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAA
ACATCGCATCGAGCGAGCACGTA CTGGATGGAAGCCGGTCTTGTTCGATCAGGATGATC
TGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGC
ATGCCCGACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCAT
GGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACC
GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGG
GCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTT
CTATCGCCTTCTTGACGAGTTCTTCTGA

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

ATGACCGAGTACAAGCCCACGGTGCGCCCTCGCCACCCGCGACGACGTCCCCGGGCCGT
ACGCACCCCTCGCCGCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGACCCGG
ACCGCCACATCGAGCGGGTCAACGAGCTGCAAGAACTCTTCCTCACGCGCGTCGGGCTC
GACATCGGCAAGGTGTGGGTTCGCCGACGACGGCGCCGCGGTGGCGGTCTGGACCACGCC
GGAGAGCGTCAAGCGGGGGCGGTGTTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGA
GCGGTTCCCGGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCCGCC
AAGGAGCCCGCGTGGTTCCTGGCCACCGTCGGCGTCTCGCCGACCACCAGGGCAAGGG
TCTGGGCAGCGCCGTTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGGGGTGC
CCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGGCTTACC
GTCACCGCCGACGTCGAGGTGCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCC
CGGTGCCTGA

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

ATGAATAGTTTCGACAAAGATCGCATTGGTAATTACGTTACTCGATGCCATGGGGATTGG
CCTTATCATGCCAGTCTTGCCAACGTTATTACGTGAATTTATTGCTTCGGAAGATATCG
CTAACCACTTTGGCGTATTGCTTGCACCTTATGCGTTAATGCAGTTATCTTTGCTCCT
TGGCTTGGAAAAATGTCTGACCGATTTGGTTCGGCGCCAGTGCTGTTGTTGTCATTAAT
AGGCGCATCGCTGGATTACTTATTGCTGGCTTTTTCAAGTGCCTTTGGATGCTGTATT
TAGGCCGTTTGTCTTTCAGGGATCACAGGAGCTACTGGGGCTGTCGCGGCATCGGTCATT
GCCGATAACACCTCAGCTTCTCAACGCGTGAAGTGGTTCGGTTGGTTAGGGGCAAGTTT
TGGGCTTGGTTTAATAGCGGGCCTATTATTGGTGGTTTTGCAGGAGAGATTTACCCG
ATAGTCCCTTTTTTATCGCTGCGTTGCTAAATATTGTCACCTTTCCTTGTTGTTATGTTT
TGGTTCCGTGAAACCAAAAATACACGTGATAATACAGATAACCGAAGTAGGGGTTGAGAC
GCAATCAAATTCGGTGTACATCACTTTATTTAAACGATGCCCATTTTGTGATTATTT

ATTTTTTCAGCGCAATTGATAGGCCAAATTCCCGCAACGGTGTGGGTGCTATTTACCGAA
AATCGTTTTGGATGGAATAGCATGATGGTTGGCTTTTCATTAGCGGGTCTTGGTCTTTT
ACACTCAGTATTTCCAAGCCTTTGTGGCAGGAAGAATAGCCACTAAATGGGGCGAAAAAA
CGGCAGTACTGCTCGAATTTATTGCAGATAGTAGTGCATTTGCCTTTTATAGCGTTTATA
TCTGAAGGTTGGTTAGATTTCCCTGTTTTAATTTTATTGGCTGGTGGTGGGATCGCTTT
ACCTGCATTACAGGGAGTGATGTCTATCCAAACAAAGAGTCATGAGCAAGGTGCTTTAC
AGGGATTATTGGTGAGCCTTACCAATGCAACCGGTGTTATTGGCCCATTACTGTTTACT
GTTATTTATAATCATTCACTACCAATTTGGGATGGCTGGATTTGGATTATTGGTTTACG
GTTTTACTGTATTATTATCCTGCTATCAATGACCTTCATGTTGACCCCTCAAGCTCAGG
GGAGTAAACAGGAGACAAGTGCTTAG

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

ATGAAACCCAACATACCCCTGATCGTAATTCTGAGCACTGTTCGCGCTCGACGCTGTTCGG
CATCGGCCCTGATTATGCCGGTGTGCCGGGCTCCTGCGCGATCTGGTTCACTCGAACG
ACGTCACCCGCCACTATGGCATTCTGCTGGCGCTGTATGCGTTGGTGAATTTGCCTGC
GCACCTGTGCTGGGCGCGCTGTCGGATCGTTTCGGGCGGCGGCAATCTTGCTCGTCTC
GCTGGCCGGCGCCACTGTGCGACTACGCCATCATGGCGACAGCGCCTTTCCTTTGGGTTT
TCTATATCGGGCGGATCGTGGCCGGCATCACCGGGGCGACTGGGGCGGTAGCCGGCGCT
TATATTGCCGATATCACTGATGGCGATGAGCGCGCGGCACTTCGGCTTCATGAGCGC
CTGTTTTCGGGTTCGGGATGGTTCGCGGGACCTGTGCTCGGTGGGCTGATGGGCGGTTTCT
CCCCCACGCTCCGTTCTTCGCCGCGGCAGCCTTGAACGGCCTCAATTTCTGACGGGC
TGTTTTCTTTTGCCGGAGTCGCACAAAGGCCGAACGCCGGCCGTTACGCCGGGAGGCTCT
CAACCCGCTCGCTTCGTTCCGGTGGGCCCGGGGCATGACCGTCGTGCGCCCTGATGG
CGGTCTTCTTCATCATGCAACTTGTCCGACAGGTGCCGGCCGCGCTTTGGGTCATTTTC
GGCGAGGATCGCTTTCACTGGGACGCGACCACGATCGGCATTTTCGCTTGCCGCATTTGG
CATTCTGCATTCACTCGCCAGGCAATGATCACCGGCCCTGTAGCCGCCCGGCTCGGCG
AAAGGCGGGCACTCATGCTCGGAATGATTGCCGACGGCACAGGCTACATCCTGCTTGCC
TTCGCGACACGGGGATGGATGGCGTTCCCGATCATGGTCCTGCTTGCTTCGGGTGGCAT
CGGAATGCCGGCGCTGCAAGCAATGTTGTCCAGGCAGGTGGATGAGGAACGTCAGGGGC
AGCTGCAAGGCTCACTGGCGGCGCTCACAGCCTGACCTCGATCGTCCGACCCCTCCTC
TTCACGGCGATCTATGCGGCTTCTATAACAACGTGGAACGGGTGGGCATGGATTGCAGG
CGCTGCCCTCTACTTGCTCTGCCGCGGCTGCGTCCGCGGGCTTTGGAGCGGCGCAG
GGCAACGAGCCGATCGCTGA

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

ATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGCTGTAGG
CATAGGCTTGGTTATGCCGGTACTGCCGGGCTCCTTGCGGGATATCGTCCATTCCGACA
GCATCGCCAGTCACTATGGCGTGCTGCTAGCGCTATATGCGTTGATGCAATTTCTATGC
GCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCGCCAGTCCTGCTCGCTTC
GCTACTTGGAGCCACTATCGACTACGCGATCATGGCGACCACACCCGTCCTGTGGATCC
TCTACGCCGGACGCATCGTGGCCGGCATCACCGGCGCCACAGGTGCGGTTGCTGGCGCC
TATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGC
TTGTTTTCGGCGTGGGTATGGTGGCAGGCCCGTGGCCGGGGGACTGTTGGGCGCCATCT
CCTTGCATGCACCATTCCTTTCGCGCGGCGGTGCTCAACGGCCTCAACCTACTACTGGGC
TGCTTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCCTT
CAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCCCGCACTTATGA
CTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGGGTCATTTTC

GGCGAGGACCGCTTTCGCTGGAGCGCGACGATGATCGGCCTGTCGCTTGCGGTATTCGG
AATCTTGCACGCCCTCGCTCAAGCCTTCGTCACTGGTCCCGCCACCAAACGTTTCGGCG
AGAAGCAGGCCATTATCGCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCG
TTCGCGACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGGCAT
CGGGATGCCCGCGTTGCAGGCCATGCTGTCCAGGCAGGTAGATGACGACCATCAGGGAC
AGCTTCAAGGATCGCTCGCGGCTCTTACCAGCCTAACTTCGATCATTGGACCGCTGATC
GTCACGGCGATTTATGCCGCTCGGCGAGCACATGGAACGGGTGGCATGGATTGTAGG
CGCCGCCCTATACCTTGTCTGCCCTCCCGCGGTTGCGTCGCGGTGCATGGAGCCGGGCCA
CCTCGACCTGA

>TcR-tetL (*Bacillus*; GTG START codon; variant -006) 1377 bp
GTGAATACATCCTATTACAAATCGAATTTACGACACAACCAAATTTTAATTTGGCTTTG
CATTTTATCTTTTTTTTAGCGTATTAATGAAATGGTTTTGAACGTCTCATTACCTGATA
TTGCAAATGATTTAATAAACACCTGCGAGTACAACTGGGTGAACACAGCCTTTATG
TTAACCTTTTCCATTGGAACAGCTGTATATGGAAAGCTATCTGATCAATTAGGCATCAA
AAGGTTACTCCTATTTGGAATTATAATAAATTGTTTTCGGGTCGGTAATTGGGTTTGTG
GCCATTTCTTTCTTTTCTTACTTATTATGGCTCGTTTTATTCAAGGGGCTGGTGCAGCT
GCATTTCCAGCACTCGTAATGGTTGTAGTTGCGCGCTATATTCAAAGGAAAATAGGGG
TAAAGCATTTGGTCTTATTGGATCGATAGTAGCCATGGGAGAAGGAGTCGGTCCAGCGA
TTGGTGGAAATGATAGCCATTATATTCATTGGTCCTATCTTCTACTCATTCTTATGATA
ACAATTATCACTGTTCCGTTTTCTTATGAAATTATTAAGAAAGAAGTAAGGATAAAAAG
TCATTTTGATATCAAAGGAATTATACTAATGTCTGTAGGCATTGTATTTTTTTATGTTGT
TTACAACATCATATAGCATTCTTTTCTTATCGTTAGCGTGCTGTCAATCCTGATATTT
GTAAAACATATCAGGAAAGTAACAGATCCTTTTGTGATCCCGGATTAGGGAAAAATAT
ACCTTTTATGATTGGAGTCTTTTGTGGGGGAATTATATTTGGAACAGTAGCAGGGTTG
TCTCTATGGTTCCTTATATGATGAAAGATGTTCCACCAGCTAAGTACTGCCGAAATCGGA
AGTGTAATTATTTTCCCTGGAACAATGAGTGTCATTATTTTTCGGCTACATTGGTGGGAT
ACTTGTGATAGAAGAGGTCCTTTATACGTGTTAAACATCGGAGTTACATTTCTTTCTG
TTAGCTTTTTAACTGCTTCTTTCTTTTAGAAACAACATCATGGTTCATGACAATTATA
ATCGTATTTGTTTTAGGTGGGCTTTCGTTACCAAACAGTTATATCAACAATTGTTTC
AAGTAGCTTGAAACAGCAGGAAGCTGGTGCTGGAATGAGTTTGCTTAACTTTACCAGCT
TTTTATCAGAGGGAACAGGTATTGCAATTGTAGGTGGTTTATTATCCATACCTTACTT
GATCAAAGGTTGTTACCTATGGAAGTTGATCAGTCAACTTATCTGTATAGTAATTTGTT
ATTACTTTTTTCAGGAATCATTGTCATTAGTTGGCTGGTTACCTTGAATGTATATAAAC
ATTCTCAAAGGGATTTCTAA

>TetR (*Pseudomonas* RP4; variant -001) 651 bp
ATGACAAAGTTGCAGCCGAATACAGTGATCCGTGCCGCCCTGGACCTGTTGAACGAGGT
CGGCGTAGACGGTCTGACGACACGAACTGGCGGAACGGTTGGGGGTTACAGCAGCCGG
CGCTTTACTGGCACTTCAGGAACAAGCGGGCGCTGCTCGACGCACTGGCCGAAGCCATG
CTGGCGGAGAATCATAACGATTCGGTGCCGAGAGCCGACGACGACTGGCGCTCATTTCT
GATCGGGAATGCCCGCAGCTTCAGGCAGGCGCTGCTCGCCTACCGCGATGGCGCGCGCA
TCCATGCCGGCACGCGACCGGGCGCACCAGATGGAAACGGCCGACGCGCAGCTTCGC
TTCCTCTGCGAGGCGGGTTTTTTCGGCCGGGACGCCGTCAATGCGCTGATGACAATCAG
CTACTTCACTGTTGGGGCCGTGCTTGAGGAGCAGGCCGGCGACAGCGATGCCGGCGAGC
GCGGCGGCACCGTTGAACAGGCTCCGCTCTCGCCGCTGTTGCGGGCCGCGATAGACGCC
TTCGACGAAGCCGGTCCGGACGCGAGCGTTCGAGCAGGGACTCGCGGTGATTGTGCGATGG

ATTGGCGAAAAGGAGGCTCGTTGTCAGGAACGTTGAAGGACCGAGAAAGGGTGACGATT
GA

>TetR (Tn10; variant -004) 624 bp

ATGTCTAGATTAGATAAAAAGTAAAGTGATTAACAGCGCATTAGAGCTGCTTAATGAGGT
CGGAATCGAAGGTTTAAACAACCCGTAAACTCGCCCAGAAGCTAGGTGTAGAGCAGCCTA
CATTGTATTGGCATGTAAAAAATAAGCGGGCTTTGCTCGACGCCTTAGCCATTGAGATG
TTAGATAGGCACCATACTCACTTTTTGCCCTTTAGAAGGGGAAAGCTGGCAAGATTTTTT
ACGTAATAACGCTAAAAGTTTTAGATGTGCTTTACTAAGTCATCGCGATGGAGCAAAAG
TACATTTAGGTACACGGCCTACAGAAAAACAGTATGAAACTCTCGAAAATCAATTAGCC
TTTTTATGCCAACAAGGTTTTTCACTAGAGAATGCATTATATGCACTCAGCGCTGTGGG
GCATTTTACTTTAGGTTGCGTATTGGAAGATCAAGAGCATCAAGTCGCTAAAGAAGAAA
GGGAAACACCTACTACTGATAGTATGCCGCCATTATTACGACAAGCTATCGAATTATTT
GATCACCAAGGTGCAGAGCCAGCCTTCTTATTCGGCCTTGAATTGATCATATGCGGATT
AGAAAAACAACCTTAAATGTGAAAGTGGGTCTTAA

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