



CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTT
 GTACTGGAATACCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAA
 CMV enhancer CMV promoter

375

TTGGCAGTACATCAATGGGCGTGGATAGCGGTTTACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAA
 AACCGTCATGTAGTTACCCGCACCTATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTT
 CMV promoter

450

TGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAT
 ACCCTCAAACAAAACCGTGTTTTAGTTGCCCTGAAAGGTTTTACAGCATTGTTGAGGCGGGGTAACCTGCGTTTA
 CMV promoter

525

GGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTGTAGTGAACCGTCAGATCCGCTAGCGCTA
 CCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
 CMV promoter

600

CCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGC
 GGCCAGCGGTGGTACCCTCGTTCCCGCTCCTCGACAAGTGCCCCACCACGGGTAGGACCAGCTCGACCTGCCG
 1 Met Val Ser Lys 5 Glu Glu Leu Phe 10 Thr Gly Val Val Pro 15 Ile Leu Val Glu Leu Asp Gly
 EGFP

675

GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAG
 CTGCATTTGCCGGTGTTC AAGTTCGCACAGGCCGCTCCCGCTCCCGCTACGGTGGATGCCGTTTCGACTGGGACTTC
 25 Asp Val Asn Gly His Lys Phe Ser 30 Val Ser Gly Glu Gly 35 Thr Gly Asp Ala Thr 40 Tyr Gly Lys Leu Thr Leu Lys
 EGFP

750

TTCATCTGCACCACCGGCAAGCTGCCCGTGCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGC
 AAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGACTGGATGCCGCACGTACAG
 50 Phe Ile Cys Thr Thr Gly Lys Leu 55 Pro Val Pro Trp Pro 60 Thr Leu Val Thr Thr 65 Leu Thr Tyr Gly Val Gln Cys
 EGFP

825

TTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAG
AAGTCGGCGATGGGGCTGGTGTACTTCGTCTGTCTGAAGAAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCCTC

900

Phe Ser Arg Tyr 75 Pro Asp His Met 80 Gln His Asp Phe 85 Lys Ser Ala Met 90 Glu Gly Tyr Val 95 Glu
EGFP

CGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTG
GCGTGGTAGAAGAAGTTCCTGCTGCCGTTGATGTTCTGGGCGCGGCTCCACTTCAAGTCCCGCTGTGGGACCAC

975

Arg Thr Ile Phe 100 Phe Lys Asp Asp 105 Gly Asn Tyr Lys Thr 110 Arg Ala Glu Val Lys Phe 115 Glu Gly Asp Thr 120 Leu Val
EGFP

AACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTAC
TTGGCGTAGCTCGACTTCCCGTAGCTGAAGTTCCTCCTGCCGTTGTAGGACCCCGTGTTCGACCTCATGTTGATG

1050

Asn Arg Ile Glu 125 Leu Lys Gly Ile 130 Asp Phe Lys Glu Asp 135 Gly Asn Ile Leu Gly His 140 Lys Leu Glu Tyr 145 Asn Tyr
EGFP

AACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAAC
TTGTCCGTTGTTGCAGATATAGTACCGGCTGTTCTGCTCTTGGCCGTAGTTCCACTTGAAGTTCCTAGGCGGTGTTG

1125

Asn Ser His 150 Asn Val Tyr Ile Met 155 Ala Asp Lys Gln Lys 160 Asn Gly Ile Lys Val 165 Asn Phe Lys Ile Arg 170 His Asn
EGFP

ATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGGCAGCGGCCCGTGCTGCTG
TAGCTCCTGCCGTCGCACGTGCAGCGGCTGGTGTATGGTCTTGTGGGGGTAGCCGCTGCCGGGGCAGCAGCAGC

1200

Ile Glu Asp Gly 175 Ser Val Gln Leu Ala 180 Asp His Tyr Gln 185 Asn Thr Pro Ile Gly 190 Asp Gly Pro Val 195 Leu Leu
EGFP

CCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTG
GGGCTGTTGGTGTATGGACTCGTGGGTCAGGCGGGACTCGTTTCTGGGGTTGCTCTTCGCGCTAGTGTACCAGGAC

1275

Pro Asp Asn 200 His Tyr Leu Ser Thr 205 Gln Ser Ala Leu Ser 210 Lys Asp Pro Asn Glu Lys 215 Arg Asp His Met 220 Val Leu
EGFP

CTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTCCGGACTCAGATCTCGAGCT
GACCTCAAGCACTGGCGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTTCAGGCCTGAGTCTAGAGCTCGA

1350

Leu Glu Phe Val 225 Thr Ala Ala Gly 230 Ile Thr Leu Gly Met Asp 235 Glu Leu Tyr Lys Ser Gly Leu Arg Ser Arg Ala
EGFP (in frame with EGFP) MCS

BglII XhoI SacI

CAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGATCTAGATAACTGATCATAATCAGC
GTTTGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCG

1425

Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly Ser Thr Gly Ser Arg
EGFP (in frame with EGFP) MCS

HindIII EcoRI PstI SalI KpnI XmaI BamHI

ApaI SmaI

..... (in frame with EGFP) ----->