



5' TTGGGGTTGCGCCTTTTCCAAGGCAGCCCTGGGTTTGCGCAGGGACGCGGCTGCTCTGGGGCGTGGTTCCGGGAAA
 3' AACCCCAACGCGGAAAAGGTTCCGTCGGGACCCAAACGCGTCCCTGCGCCGACGAGACCCGCACCAAGGCCCTTT
 hPGK promoter

75

CGCAGCGGCGCCGACCCTGGGTCTCGCACATTCTTCACGTCCGTTTCGCAGCGTCACCCGGATCTTCGCCGCTACC
 GCGTCGCCGCGGCTGGGACCCAGAGCGTGTAAGAAAGTGCAGGCAAGCGTCGCAGTGGGCTAGAAAGCGGCGATGG
 hPGK promoter

150

CTTGTGGGCCCCCGGCGACGCTTCTGCTCCGCCCTAAGTCGGGAAGGTTTCTTGCGGTTCGCGGCGTGCCGG
 GAACACCCGGGGGGCCGCTGCGAAGGACGAGGCGGGGATTTCAGCCCTTCCAAGGAACGCCAAGCGCCGCACGGCC
 hPGK promoter

225

ACGTGACAAACGGAAGCCGCACGTCTCACTAGTACCCTCGCAGACGGACAGCGCCAGGGAGCAATGGCAGCGCGC
 TGCACTGTTTGCCTTTCGGCGTGCAAGTGATCATGGGAGCGTCTGCCTGTGCGGGTCCCTCGTTACCGTTCGCGCG
 hPGK promoter

300

CGACCGCGATGGGCTGTGGCCAATAGCGGCTGCTCAGCAGGGCGCGCCGAGAGCAGCGGCCGGGAAGGGCGGTG
 GCTGGCGCTACCCGACACCGTTATCGCCGACGAGTCGTCCCGCGCGGCTCTCGTTCGCCGGCCCTTCCCCGCCAC
 hPGK promoter

375

CGGGAGGCGGGGTGTGGGGCGGTAGTGTGGGCCCTGTTCTGCCGCGCGGTGTTCCGCATTCTGCAAGCCTCCG
 GCCCTCCGCCCCACACCCCGCCATCACACCCGGGACAAGGACGGGCGCGCCACAAGGCGTAAGACGTTTCGGAGGC
 hPGK promoter

450

GAGCGCACGTCGGCAGTCGGCTCCCTCGTTGACCGAATCACCGACCTCTCTCCCCAGGGGGATCCACCGGAGCTT
CTCGCGTGCAGCCGTCAGCCGAGGGAGCAACTGGCTTAGTGGCTGGAGAGAGGGGTCCCCCTAGGTGGCCTCGAA

BamHI

hPGK promoter

ACCATGACCGAGTACAAGCCCACGGTGC GCCTCGCCACCCGCGACGACGTC CCCAGGGCCGTACGCACCCCTCGCC
TGGTACTGGCTCATGTTCTGGGTGCCACGCGGAGCGGTGGGCGCTGCTGCAGGGGTCCCGGCATGCGTGGGAGCGG

AspI

BsiWI

1 Met Thr Glu Tyr 5 Lys Pro Thr Val Arg Leu 10 Ala Thr Arg Asp 15 Asp Val Pro Arg Ala 20 Val Arg Thr Leu Ala
PuroR

GCCGCGTTCGCCGACTACCCCGCCACGCGCCACACCGTCGATCCGGACCGCCACATCGAGCGGGTCCACCGAGCTG
CGGCGCAAGCGGCTGATGGGGCGGTGCGCGGTGTGGCAGCTAGGCCTGGCGGTGTAGCTCGCCAGTGGCTCGAC

BstEII

25 Ala Ala Phe Ala Asp 30 Tyr Pro Ala Thr Arg 35 His Thr Val Asp Pro 40 Asp Arg His Ile Glu 45 Val Thr Glu Leu
PuroR

CAAGAACTCTTCTCACGCGCGTCGGGCTCGACATCGGCAAGGTGTGGGTCGCGGACGACGGCGCCGCGGTGGCG
GTTCTTGAGAAGGAGTGC GCGCAGCCCGAGCTGTAGCCGTTCCACACCCAGCGCCTGCTGCCGCGGCGCCACCGC

50 Gln Glu Leu Phe Leu 55 Thr Arg Val Gly Leu 60 Asp Ile Gly Lys Val 65 Trp Val Ala Asp Asp 70 Gly Ala Ala Val Ala
PuroR

GTCTGGACCACGCCGGAGAGCGTCAAGCGGGGGCGGTGTTCCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGC
CAGACCTGGTGGCGCCTCTCGCAGCTTCGCCCCCGCCACAAGCGGCTCTAGCCGGGCGCGTACCGGCTCAACTCG

75 Val Trp Thr Thr Pro 80 Glu Ser Val Glu Ala 85 Gly Ala Val Phe Ala 90 Glu Ile Gly Pro Arg 95 Thr Ala Glu Leu Ser
PuroR

GAGCGCACGTCGGCAGTCGGCTCCCTCGTTGACCGAATCACCGACCTCTCTCCCCAGGGGGATCCACCGGAGCTT
CTCGCGTGCAGCCGTCAGCCGAGGGAGCAACTGGCTTAGTGGCTGGAGAGAGGGGTCCCCCTAGGTGGCCTCGAA

BamHI

hPGK promoter

CCAAGGGCCGACCGGCGCGTCTGTTGTCTACCTTCCGGAGGACCGCGGCGTGGCCGGGTTCTCGGGCGCACCAAG

100 Gly Ser Arg Leu Ala 105 Ala Gln Gln Gln Met 110 Glu Gly Leu Leu Ala 115 Pro His Arg Pro Lys 120 Glu Pro Ala Trp Phe
PuroR

CTGGCCACCGTCGGCGTCTCGCCCGACCACCAGGGCAAGGGTCTGGGCAGCGCGTCTGCTCCCCGGAGTGGAG
GACCGGTGGCAGCCGCAGAGCGGGCTGGTGGTCCCGTCCAGACCCGTCGCGGCAGCACGAGGGGCTCACCTC

125 Leu Ala Thr Val Gly 130 Val Ser Pro Asp His 135 Gln Gly Lys Gly Leu 140 Gly Ser Ala Val Val 145 Leu Pro Gly Val Glu
PuroR

GCGGCCGAGCGCGCCGGGGTGCCCGCCTTCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTC
CGCCGGCTCGCGCGGCCCCACGGGCGGAAGGACCTCTGGAGGCGCGGGGCGTTGGAGGGGAAGATGCTCGCCGAG

150 Ala Ala Glu Arg Ala 155 Gly Val Pro Ala Phe 160 Leu Glu Thr Ser Ala 165 Pro Arg Asn Leu Pro 170 Phe Tyr Glu Arg Leu
PuroR

GGTTTACCGTCACCGCCGACGTCGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGACCCGCAAGCCCGGTGCC
CCGAAGTGGCAGTGGCGGCTGCAGCTCCACGGGCTTCTGGCGCGTGGACCACGTA CTGGGCGTTCCGGCCACGG

175 Gly Phe Thr Val Thr 180 Ala Asp Val Glu Val 185 Pro Glu Gly Pro Arg 190 Thr Trp Cys Met Thr 195 Arg Lys Pro Gly Ala
PuroR

KpnI

TGACGCCCGCCCCACGACCCGCGAGCGCCCGACCGAAAGGAGCGCACGACCCCATGCATCGGTACCTTTAAGACCA
ACTGCGGGCGGGGTGCTGGGCGTCGCGGGCTGGCTTTCCTCGCGTGTGGGGTACGTAGCCATGGA AATTCTGGT

200
PuroR