SUPPLEMENTARY MATERIAL (FIGURES)

TBIO Method of Primer Design and PCR-Based Gene Synthesis

Figure 1S: Amino acid and DNA coding sequence of human protein kinase B-2 (PKB2). The synthetic DNA coding sequence for human PKB2 that was optimized for high-level protein expression in *E. coli* was generated by replacing the indicated amino acid codons.

```
                                       ctg                              cgtccgcgc      tta
   1  atgaatgaggtgtctgtcatcaaagaaggctggctccacaagcgtggtgaatacatcaagacctggaggccacggtacttcctgctgaag    90
   1   M  N  E  V  S  V  I  K  E  G  W  L  H  K  R  G  E  Y  I  K  T  W  R  P  R  Y  F  L  L  K     30
                                    cgtcca                  ctgccg
  91  agcgacggctccttcattgggtacaaggagaggcccgaggcccctgatcagactctacccccttaaacaacttctccgtagcagaatgc   180
  31   S  D  G  S  F  I  G  Y  K  E  R  P  E  A  P  D  Q  T  L  P  P  L  N  N  F  S  V  A  E  C     60
                        cgt   cgccct            attcgt                           cgt
 181  cagctgatgaagaccgagaggccgcgacccaacacctttgtcatacgctgcctgcagtggaccacagtcatcgagaggaccttccacgtg   270
  61   Q  L  M  K  T  E  R  P  R  P  N  T  F  V  I  R  C  L  Q  W  T  T  V  I  E  R  T  F  H  V     90
                     cgc            cgt                        ctg      cgc               ccg
 271  gattctccagacgagagggaggagtggatgcgggccatccagatggtcgccaacagcctcaagcagcgggccccaggcgaggaccccatg   360
  91   D  S  P  D  E  R  E  E  W  M  R  A  I  Q  M  V  A  N  S  L  K  Q  R  A  P  G  E  D  P  M    120
                        cca                              gtt               cgc
 361  gactacaagtgtggctcccccagtgactcctccacgactgaggagatggaagtggcggtcagcaaggcacgggctaaagtgaccatgaat   450
 121   D  Y  K  C  G  S  P  S  D  S  S  T  T  E  E  M  E  V  A  V  S  K  A  R  A  K  V  T  M  N    150
                  ctg   ttgctg      ggc                        cgt
 451  gacttcgactatctcaaactccttggcaagggaacctttggcaaagtcatcctggtgcgggagaaggccactggccgctactacgccatg   540
 151   D  F  D  Y  L  K  L  L  G  K  G  T  F  G  K  V  I  L  V  R  E  K  A  T  G  R  Y  Y  A  M    180
            cgt            attatc                                    cgc   ctg         cgt
 541  aagatcctgcgaaaggaagtcatcattgccaaggatgaagtcgctcacacagtcaccgagagccgggtcctccagaacaccaggcacccg   630
 181   K  I  L  R  K  E  V  I  I  A  K  D  E  V  A  H  T  V  T  E  S  R  V  L  Q  N  T  R  H  P    210
         tta                  ttt
 631  ttcctcactgcgctgaagtatgccttccagacccacgaccgcctgtgctttgtgatggagtatgccaacggggggtgagctgttcttccac   720
 211   F  L  T  A  L  K  Y  A  F  Q  T  H  D  R  L  C  F  V  M  E  Y  A  N  G  G  E  L  F  F  H    240
            cgt   cgc               cgtgcgcgc                           ctg               cgt
 721  ctgtcccgggagcgtgtcttcacagaggagcgggcccggttttatggtgcagagattgtctcggctcttgagtacttgcactcgcgggac   810
 241   L  S  R  E  R  V  F  T  E  E  R  A  R  F  Y  G  A  E  I  V  S  A  L  E  Y  L  H  S  R  D    270
                              gag   ctg                                          ttg      gaa
 811  gtggtataccgcgacatcaagctggaaaacctcatgctggacaaagatggccacatcaagatcactgactttggcctctgcaaagagggc   900
 271   V  V  Y  R  D  I  K  L  E  N  L  M  L  D  K  D  G  H  I  K  I  T  D  F  G  L  C  K  E  G    300
                                          acg            gcc                              cgt
 901  atcagtgacggggccaccatgaaaaccttctgtgggaccccggagtacctggcgcctgaggtgctggaggacaatgactatggccgggcc   990
 301   I  S  D  G  A  T  M  K  T  F  C  G  T  P  E  Y  L  A  P  E  V  L  E  D  N  D  Y  G  R  A    330
                                                            ccg                        ctg
 991  gtggactggtgggggctgggtgtggtcatgtacgagatgatgtgcggccgcctgcccttctacaaccaggaccacgagcgcctcttcgag  1080
 331   V  D  W  W  G  L  G  V  V  M  Y  E  M  M  C  G  R  L  P  F  Y  N  Q  D  H  E  R  L  F  E    360
```

```
      Figure 1S (continued)
      tta   ctg   gaggaa      ttt         tta   cca               ctg         tta         ccg
1081  ctcatcctcatggaagagatccgcttcccgcgcacgctcagccccgaggccaagtccctgcttgctgggctgcttaagaaggaccccaag  1170
 361   L  I  L  M  E  E  I  R  F  P  R  T  L  S  P  E  A  K  S  L  L  A  G  L  L  K  K  D  P  K    390
         cggctg         cca                           cgt      ctg
1171  cagaggcttggtgggggcccagcgatgccaaggaggtcatggagcacaggttcttcctcagcatcaactggcaggacgtggtccagaag  1260
 391   Q  R  L  G  G  G  P  S  D  A  K  E  V  M  E  H  R  F  F  L  S  I  N  W  Q  D  V  V  Q  K    420
         tta      ccg                                 cgc      gac
1261  aagctcctgccacccttcaaacctcaggtcacgtccgaggtcgacacaaggtacttcgatgatgaatttaccgcccagtccatcacaatc  1350
 421   K  L  L  P  P  F  K  P  Q  V  T  S  E  V  D  T  R  Y  F  D  D  E  F  T  A  Q  S  I  T  I    450
         cct            gat                           cgt      tttccg               gcg
1351  acacccccctgaccgctatgacagcctgggcttactggagctggaccagcggacccacttcccccagttctcctactcggccagcatccgc  1440
 451   T  P  P  D  R  Y  D  S  L  G  L  L  E  L  D  Q  R  T  H  F  P  Q  F  S  Y  S  A  S  I  R    480

1441  gagtga                                                                                      1443
 481   E                                                                                           481
```

Figure 2S: Amino acid and DNA coding sequence of human p70 40S ribosomal protein S6 kinase-1 (S6K1). The synthetic DNA coding sequence for human S6K1 that was optimized for high-level protein expression in *E. coli* was generated by replacing the indicated amino acid codons.

```
         cgtcgccgtcgccgt                              cgc   cgt                              att
   1  atgaggcgacgaaggaggcgggacggcttttacccagccccggacttccgagacagggaagctgaggacatggcaggagtgtttgacata    90
   1   M  R  R  R  R  R  R  D  G  F  Y  P  A  P  D  F  R  D  R  E  A  E  D  M  A  G  V  F  D  I     30
                                                               ctgaacgag      gat   ggc
  91  gacctggaccagccagaggacgcgggctctgaggatgagctggaggagggggggtcagttaaatgaaagcatggaccatgggggagttgga   180
  31   D  L  D  Q  P  E  D  A  G  S  E  D  E  L  E  E  G  G  Q  L  N  E  S  M  D  H  G  G  V  G     60
         tac                                                      cgc               cgc
 181  ccatatgaacttggcatggaacattgtgagaaatttgaaatctcagaaactagtgtgaacagagggccagaaaaaatcagaccagaatgt   270
  61   P  Y  E  L  G  M  E  H  C  E  K  F  E  I  S  E  T  S  V  N  R  G  P  E  K  I  R  P  E  C     90
            ctg                                 gtg   caggtgcgc                           atcttc
 271  tttgagctacttcgggtacttggtaaagggggctatggaaaggtttttcaagtacgaaaagtaacaggagcaaatactgggaaaatattt   360
  91   F  E  L  L  R  V  L  G  K  G  G  Y  G  K  V  F  Q  V  R  K  V  T  G  A  N  T  G  K  I  F    120
                                 attgtgcgcaac
 361  gccatgaaggtgcttaaaaaggcaatgatagtaagaaatgctaaagatacagctcatacaaaagcagaacggaatattctggaggaagta   450
 121   A  M  K  V  L  K  K  A  M  I  V  R  N  A  K  D  T  A  H  T  K  A  E  R  N  I  L  E  E  V    150
            ccg            ctgatctac                                 ctg                    ctg
 451  aagcatcccttcatcgtggatttaatttatgcctttcagactggtggaaaactctacctcatccttgagtatctcagtggaggagaacta   540
 151   K  H  P  F  I  V  D  L  I  Y  A  F  Q  T  G  G  K  L  Y  L  I  L  E  Y  L  S  G  G  E  L    180
               ctggagcgt      att                     ttc   ctggcc      agc
 541  tttatgcagttagaaagagagggaatatttatggaagacactgcctgcttttacttggcagaaatctccatggctttggggcatttacat   630
 181   F  M  Q  L  E  R  E  G  I  F  M  E  D  T  A  C  F  Y  L  A  E  I  S  M  A  L  G  H  L  H    210
      cag               cgc                        ctgaac                  ctg         ggcctg
 631  caaaaggggatcatctacagagacctgaagccggagaatatcatgcttaatcaccaaggtcatgtgaaactaacagactttggactatgc   720
 211   Q  K  G  I  I  Y  R  D  L  K  P  E  N  I  M  L  N  H  Q  G  H  V  K  L  T  D  F  G  L  C    240
                                       acc            att                           cgc
 721  aaagaatctattcatgatggaacagtcacacacacatttgtggaacaatagaatacatggcccctgaaatcttgatgagaagtggccac   810
 241   K  E  S  I  H  D  G  T  V  T  H  T  F  C  G  T  I  E  Y  M  A  P  E  I  L  M  R  S  G  H    270
                              ctg                                ccg                cgcaaaaag
 811  aatcgtgctgtggattggtggagtttgggagcattaatgtatgacatgctgactggagcacccccattcactggggagaatagaaagaaa   900
 271   N  R  A  V  D  W  W  S  L  G  A  L  M  Y  D  M  L  T  G  A  P  P  F  T  G  E  N  R  K  K    300
               aag   ctgaagtgc               ccg                cgt                        cgc
 901  acaattgacaaaatcctcaaatgtaaactcaatttgcctccctacctcacacaagaagccagagatctgcttaaaaagctgctgaaaaga   990
 301   T  I  D  K  I  L  K  C  K  L  N  L  P  P  Y  L  T  Q  E  A  R  D  L  L  K  K  L  L  K  R    330
                                                                        cgc
 991  aatgctgcttctcgtctgggagctggtcctggggacgctggagaagttcaagctcatccattctttagacacattaactgggaagaactt  1080
 331   N  A  A  S  R  L  G  A  G  P  G  D  A  G  E  V  Q  A  H  P  F  F  R  H  I  N  W  E  E  L    360
```

Figure 2S (continued)

```
            cgc         ccaccg                     gaggaa                              cgc
1081  ctggctcgaaaggtggagcccccctttaaacctctgttgcaatctgaagaggatgtaagtcagtttgattccaagtttacacgtcagaca  1170
 361   L  A  R  K  V  E  P  P  F  K  P  L  L  Q  S  E  E  D  V  S  Q  F  D  S  K  F  T  R  Q  T    390
            gatagt                                                      tac
1171  cctgtcgacagcccagatgactcaactctcagtgaaagtgccaatcaggtctttctgggttttacatatgtggctccatctgtacttgaa  1260
 391   P  V  D  S  P  D  D  S  T  L  S  E  S  A  N  Q  V  F  L  G  F  T  Y  V  A  P  S  V  L  E    420
                     ttc   ttcgag         cgc      cgtcgc               cgt
1261  agtgtgaaagaaaagttttcctttgaaccaaaaatccgatcacctcgaagatttattggcagcccacgaacacctgtcagcccagtcaaa  1350
 421   S  V  K  E  K  F  S  F  E  P  K  I  R  S  P  R  R  F  I  G  S  P  R  T  P  V  S  P  V  K    450
         agc                  cgc         gca
1351  ttttctcctggggatttctggggaagaggtgcttcggccagcacagcaaatcctcagacacctgtggaatacccaatggaaacaagtggc  1440
 451   F  S  P  G  D  F  W  G  R  G  A  S  A  S  T  A  N  P  Q  T  P  V  E  Y  P  M  E  T  S  G    480
      att                                                attcgc                     aagaag   gcc
1441  atagagcagatggatgtgacaatgagtggggaagcatcggcaccacttccaatacgacagccgaactctggcccatacaaaaaacaagct  1530
 481   I  E  Q  M  D  V  T  M  S  G  E  A  S  A  P  L  P  I  R  Q  P  N  S  G  P  Y  K  K  Q  A    510
         ccg                                    ctg
1531  tttcccatgatctccaaacggccagagcacctgcgtatgaatctatga                                            1578
 511   F  P  M  I  S  K  R  P  E  H  L  R  M  N  L                                                 526
```

Figure 3S: Amino acid and DNA coding sequence of human phosphoinositide-dependent kinase-1 (PDK1). The synthetic DNA coding sequence for human PDK1 that was optimized for high-level protein expression in *E. coli* was generated by replacing the indicated amino acid codons.

```
            cgt                           ccg      agctccgtt               ccg               cgt
   1  atggccaggaccaccagccagctgtatgacgccgtgcccatccagtccagcgtggtgttatgttcctgcccatccccatcaatggtgagg     90
   1   M  A  R  T  T  S  Q  L  Y  D  A  V  P  I  Q  S  S  V  V  L  C  S  C  P  S  P  S  M  V  R      30
                  agctcc   ccg                     cgt      ccg                           cgcccg
  91  acccagactgagtccagcacgccccctggcattcctggtggcagcaggcagggccccgccatggacggcactgcagccgagcctcggccc    180
  31   T  Q  T  E  S  S  T  P  P  G  I  P  G  G  S  R  Q  G  P  A  M  D  G  T  A  A  E  P  R  P      60
                                       cca         aaa   cgc         ttt      ggt      ggt
 181  ggcgccggctccctgcagcatgcccagcctccgccgcagcctcggaagaagcggcctgaggacttcaagtttgggaaaatccttggggaa    270
  61   G  A  G  S  L  Q  H  A  Q  P  P  P  Q  P  R  K  K  R  P  E  D  F  K  F  G  K  I  L  G  E      90
                                 cgt               cgt         atc               cgt      att
 271  ggctcttttccacggttgtcctggctcgagaactggcaacctccagagaatatgcgattaaaattctggagaagcgacatatcataaaa    360
  91   G  S  F  S  T  V  V  L  A  R  E  L  A  T  S  R  E  Y  A  I  K  I  L  E  K  R  H  I  I  K     120
      gaa         ccg         cgt                              ccg
 361  gagaacaaggtcccctatgtaaccagagagcgggatgtcatgtcgcgcctggatcacccccttctttgttaagctttacttcacatttcag    450
 121   E  N  K  V  P  Y  V  T  R  E  R  D  V  M  S  R  L  D  H  P  F  F  V  K  L  Y  F  T  F  Q     150
                                                ggt   ctg
 451  gacgacgagaagctgtatttcggccttagttatgccaaaaatggagaactacttaaatatattcgcaaaatcggttcattcgatgagacc    540
 151   D  D  E  K  L  Y  F  G  L  S  Y  A  K  N  G  E  L  L  K  Y  I  R  K  I  G  S  F  D  E  T     180
            cgt                                                            cgt
 541  tgtacccgatttacacggctgagatcgtgtctgctttagagtacttgcacggcaagggcatcattcacagggaccttaaaccggaaaac    630
 181   C  T  R  F  Y  T  A  E  I  V  S  A  L  E  Y  L  H  G  K  G  I  I  H  R  D  L  K  P  E  N     210
                              att               ggt                                    cgt
 631  atttgttaaatgaagatatgcacatccagatcacagatttggaacagcaaaagtcttatccccagagagcaaacaagccagggccaac    720
 211   I  L  L  N  E  D  M  H  I  Q  I  T  D  F  G  T  A  K  V  L  S  P  E  S  K  Q  A  R  A  N     240
               ggt                                                                        ggt
 721  tcattcgtgggaacagcgcagtacgtttctccagagctgctcacggagaagtccgcctgtaagagttcagacctttgggctcttggatgc    810
 241   S  F  V  G  T  A  Q  Y  V  S  P  E  L  L  T  E  K  S  A  C  K  S  S  D  L  W  A  L  G  C     270
      attatt               ggt   cct   cgt   ggt               att
 811  ataatataccagcttgtggcaggactcccaccattccgagctggaaacgagtatcttatatttcagaagatcattaagttggaatatgac    900
 271   I  I  Y  Q  L  V  A  G  L  P  P  F  R  A  G  N  E  Y  L  I  F  Q  K  I  I  K  L  E  Y  D     300
                  tttttt         cgt                                       cgc
 901  tttccagaaaaattcttccctaaggcaagagacctcgtggagaaacttttggttttagatgccacaaagcggttaggctgtgaggaaatg    990
 301   F  P  E  K  F  F  P  K  A  R  D  L  V  E  K  L  L  V  L  D  A  T  K  R  L  G  C  E  E  M     330
         ggt   ggt                     ttt                              caa
 991  gaaggatacggacctcttaaagcacacccgttcttcgagtccgtcacgtgggagaacctgcaccagcagacgcctccgaagctcaccgct   1080
 331   E  G  Y  G  P  L  K  A  H  P  F  F  E  S  V  T  W  E  N  L  H  Q  Q  T  P  P  K  L  T  A     360
```

Figure 3S (continued)

```
                              gat
1081  tacctgccggctatgtcggaagacgacgaggactgctatggcaattatgacaatctcctgagccagtttggctgcatgcaggtgtcttcg  1170
 361   Y  L  P  A  M  S  E  D  D  E  D  C  Y  G  N  Y  D  N  L  L  S  Q  F  G  C  M  Q  V  S  S    390
      agc                                       ccg   cgt            atc
1171  tcctcctcctcacactccctgtcagcctccgacacgggcctgccccagaggtcaggcagcaacatagagcagtacattcacgatctggac  1260
 391   S  S  S  S  H  S  L  S  A  S  D  T  G  L  P  Q  R  S  G  S  N  I  E  Q  Y  I  H  D  L  D    420
                                                   cgtctg   ctg               ggt
1261  tcgaactcctttgaactggacttacagttttccgaagatgagaagaggttgttgttggagaagcaggctggcggaaacccttggcaccag  1350
 421   S  N  S  F  E  L  D  L  Q  F  S  E  D  E  K  R  L  L  L  E  K  Q  A  G  G  N  P  W  H  Q    450
                  aac   attgtg                                       cgtcgc
1351  tttgtagaaaataatttaatactaaagatgggcccagtggataagcggaagggtttatttgcaagacgacgacagctgttgctcacagaa  1440
 451   F  V  E  N  N  L  I  L  K  M  G  P  V  D  K  R  K  G  L  F  A  R  R  R  Q  L  L  L  T  E    480
      ggt            tac   gac                                                ggt
1441  ggaccacatttatattatgtggatcctgtcaacaaagttctgaaaggtgaaattccttggtcacaagaacttcgaccagaggccaagaat  1530
 481   G  P  H  L  Y  Y  V  D  P  V  N  K  V  L  K  G  E  I  P  W  S  Q  E  L  R  P  E  A  K  N    510
                                    cgt   tac            ccg   ggt                  cgt
1531  tttaaaactttctttgtccacacgcctaacaggacgtattatctgatggaccccagcgggaacgcacacaagtggtgcaggaagatccag  1620
 511   F  K  T  F  F  V  H  T  P  N  R  T  Y  Y  L  M  D  P  S  G  N  A  H  K  W  C  R  K  I  Q    540
               cgtcaacgt
1621  gaggtttggaggcagcgataccagagccacccggacgccgctgtgcagtga                                         1668
 541   E  V  W  R  Q  R  Y  Q  S  H  P  D  A  A  V  Q                                              556
```

SUPPLEMENTARY MATERIAL (TABLES)

Tables 1S-3S: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the codon-optimized PKB2 (Table 1S), S6K1 (Table 2S), and PDK1 (Table 3S) gene sequences. In each table, the coding- or "sense"-strand oligonucleotide primers (5'→3') and the noncoding- or "antisense"-strand oligonucleotide primers (3'←5') designed for both the TBC and TBIO strategies are listed for (A) the amino-terminal half and (B) the carboxy-terminal half of the gene sequence. For each primer, the overall length (nt), the coding region of the gene sequence, the melting temperature, T_m, and the number of base pairs (bp) for each overlapping region are given. For each primer, the 5'-terminal overlapping nucleotides are indicated in blue color, and the 3'-terminal nucleotides are indicated in red color. Green colored regions of primers indicate nucleotides that are common to both the 5'- and 3'-overlapping regions. The start and stop codons are capitalized in the primer sequences.

Table 1AS: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the amino-terminal half of the codon-optimized protein kinase B-2 (PKB2) gene sequence.

TBC name	coding or "sense" (S) oligonucleotide primers (5'→3') noncoding or "antisense" (A) primers (3'←5')	T_m (°C)	overlap (bp)	length (nt)	coding region	TBIO name
C-S01	gggggggggcatATGaatgaggtgtctgtcatcaaagaaggctggctgcacaagcgtggt	64.8	19	60	-12-48	IO-S19
C-A01	gaccgacgtgttcgcaccacttatgtagttctggaccgcaggcgcgatgaagaatgactt	63.4	22	60	29-89	IO-S18rc
C-A01rc	ctggctgcacaagcgtggtgaatacatcaagacctggcgtccgcgctacttcttactgaa					IO-S18
C-S02	gtccgcgctacttcttactgaagagcgacggctccttcattgggtacaaggagcgtccag	65.2	22	60	68-127	IO-S17
C-A02	taacccatgttcctcgcaggtctccggggactagtctgagacggcgggaatttgttgaag	65.4	24	60	106-165	IO-S16rc
C-A02rc	attgggtacaaggagcgtccagaggcccctgatcagactctgccgcccttaaacaacttc					IO-S16
C-S03	actctgccgcccttaaacaacttctccgtagcagaatgccagctgatgaagaccgagcgt	65.3	21	60	142-201	IO-S15
C-A03	gtcgactacttctggctcgcaggcgcgggattgtggaaacagtaagcaacggacgtcacc	65.3	21	60	181-240	IO-S14rc
C-A03rc	cagctgatgaagaccgagcgtccgcgccctaacacctttgtcattcgttgcctgcagtgg					IO-S14
C-S04	gtcattcgttgcctgcagtggaccacagtcatcgagcgtaccttccacgtggattctcca	63.4	22	60	220-279	IO-S13
C-A04	atggaaggtgcacctaagaggtctgctcgcgctcctcacctacgcacggtaggtctacca	65.3	21	60	258-317	IO-S12rc
C-A04rc	taccttccacgtggattctccagacgagcgcgaggagtggatgcgtgccatccagatggt					IO-S12
C-S05	gatgcgtgccatccagatggtcgccaacagcctgaagcagcgcgccccaggcgaggacccgatggacta	64.8	19	69	297-365	IO-S11
C-A05	cgctcctgggctacctgatgttcacaccgagggggttcactgaggaggtgc	64.8	19	50	347-396	IO-S10rc
C-A05rc	gcgaggacccgatggactacaagtgtggctcccccaagtgactcctccacg					IO-S10
C-S06	cccaagtgactcctccacgactgaggagatggaagttgcggtcagcaaggcacgcgctaa	64.5	20	60	378-437	IO-S09
C-A06	cagtcgttccgtgcgcgatttcactggtacttactgaagctgatagactttaacgacccg	64.8	26	60	418-477	IO-S08rc
C-A06rc	gtcagcaaggcacgcgctaaagtgaccatgaatgacttcgactatctgaaattgctgggc					IO-S08
C-S07	acttcgactatctgaaattgctgggcaagggcacctttggcaaagtcatcctggtgcgtg	65.3	21	60	452-511	IO-S07
C-A07	cgtttcagtaggaccacgcactcttccggtgaccggcgatgatgcggtacttctaggacg	63.4	22	60	491-550	IO-S06rc
C-A07rc	gcaaagtcatcctggtgcgtgagaaggccactggccgctactacgccatgaagatcctgc					IO-S06
C-S08	tactacgccatgaagatcctgcgtaaggaagtcattatcgccaaggatgaagtcgctcac	65.3	21	60	529-588	IO-S05
C-A08	cggttcctacttcagcgagtgtgtcagtggctctcggcgcaggacgtcttgtgggcagtg	64.8	19	60	568-627	IO-S04rc
C-A08rc	gccaaggatgaagtcgctcacacagtcaccgagagccgcgtcctgcagaacacccgtcac					IO-S04
C-S09	cctgcagaacacccgtcacccgttcttaactgcgctgaagtatgcctttcagacccacga	63.5	23	60	609-668	IO-S03
C-A09	ttcatacggaaagtctgggtgctggcggacacgaaacactacctcatacggttgcccccca	64.5	20	60	646-705	IO-S02rc
C-A09rc	aagtatgcctttcagacccacgaccgcctgtgctttgtgatggagtatgccaacgggggt					IO-S02
C-S10	tggagtatgccaacgggggtgagctgttcttccacctgtcccgtgagcgcgtcttcacag	64.8	19	60	686-745	IO-S01

Table 1BS: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the carboxy-terminal half of the codon-optimized protein kinase B-2 (PKB2) gene sequence.

TBC name	coding region	length (nt)	overlap (bp)	T_m (°C)	coding or "sense" (S) oligonucleotide primers (5'→3') noncoding or "antisense" (A) primers (3'←5')	TBIO name
C-A10	**727–786**	**60**	**19**	**64.8**	**gcactcgcgcagaagtgtctcctcgcacgcgcgaaaataccacgtctctaacagagccga**	**IO-A01**
C-S11	**761–820**	**60**	**26**	**64.8**	**tttatggtgcagagattgtctcggctctggagtacttgcactcgcgtgacgtggtatacc**	**IO-A02rc**
C-S11rc					**aaataccacgtctctaacagagccgagacctcatgaacgtgagcgcactgcaccatatgg**	**IO-A02**
C-A11	**801–860**	**60**	**20**	**64.5**	**gagcgcactgcaccatatggcgctgtagttcgacctcttggactacgacctgtttctacc**	**IO-A03**
C-S12	**839–898**	**60**	**22**	**63.4**	**acctgatgctggacaaagatggccacatcaagatcactgactttggcttgtgcaaagaag**	**IO-04rc**
C-S12rc					**tggactacgacctgtttctaccggtgtagttctagtgactgaaaccgaacacgtttcttc**	**IO-A04**
C-A12	**875–934**	**60**	**24**	**63.7**	**gactgaaaccgaacacgtttcttccgtagtcactgccccggtggtacttttggaagacac**	**IO-A05**
C-S13	**912–971**	**60**	**23**	**65.3**	**ggccaccatgaaaaccttctgtgggacgccggagtacctggcccctgaggtgctggagga**	**IO-A06rc**
C-S13rc					**ccggtggtacttttggaagacaccctgcggcctcatggaccgggactccacgacctcct**	**IO-A06**
C-A13	**954–1013**	**60**	**18**	**65.3**	**gggactccacgacctcctgttactgataccggcacggcacctgaccacccccgacccaca**	**IO-A07**
C-S14	**995–1054**	**60**	**19**	**66.9**	**actggtgggggctgggtgtggtcatgtacgagatgatgtgcggccgcctgccgttctaca**	**IO-A08rc**
C-S14rc					**tgaccacccccgacccacaccagtacatgctctactacacgccggcggacggcaagatgt**	**IO-A08**
C-A14	**1037–1096**	**60**	**18**	**65.2**	**cggcggacggcaagatgttggtcctggtgctcgcggacaagatcaattaggactacctcc**	**IO-A09**
C-S15	**1072–1131**	**60**	**25**	**64.6**	**ctgttctagttaatcctgatggaggaaatccgctttccgcgcacgttaagcccagaggcc**	**IO-A10rc**
C-S15rc					**gacaagatcaattaggactacctcctttaggcgaaaggcgcgtgcaattcgggtctccgg**	**IO-A10**
C-A15	**1113–1172**	**60**	**19**	**64.8**	**gtgcaattcgggtctccggttcagggacgaccgacccgacaatttcttcctgggcttcgt**	**IO-A11**
C-S16	**1150–1209**	**60**	**23**	**63.5**	**ctgttaaagaaggacccgaagcagcgcctgggtgggggccaagcgatgccaaggaggtc**	**IO-A12rc**
C-S16rc					**gacaatttcttcctgggcttcgtcgcggacccacccccggttcgctacggttcctccag**	**IO-A12**
C-A16	**1190–1249**	**60**	**20**	**64.5**	**gttcgctacggttcctccagtacctcgtggcaaagaaggactcgtagttgaccgtcctgc**	**IO-A13**
C-S17	**1230–1289**	**60**	**20**	**64.5**	**gagcatcaactggcaggacgtggtccagaagaagttactgccaccgttcaaacctcaggt**	**IO-A14rc**
C-S17rc					**ctcgtagttgaccgtcctgcaccaggtcttcttcaatgacggtggcaagtttggagtcca**	**IO-A14**
C-A17	**1269–1328**	**60**	**21**	**65.3**	**cggtggcaagtttggagtccagtgcaggctccagctgtgtgcgatgaagctgctacttaa**	**IO-A15**
C-S18	**1303–1362**	**60**	**26**	**64.8**	**gacacacgctacttcgacgatgaatttaccgcccagtccatcacaatcacacctcctgac**	**IO-A16rc**
C-S18rc					**ctgtgtgcgatgaagctgctacttaaatggcgggtcaggtagtgttagtgtggaggactg**	**IO-A16**
C-A18	**1341–1400**	**60**	**22**	**63.4**	**gtagtgttagtgtggaggactggcgatactatcggacccgaatgacctcgacctggtcgc**	**IO-A17**
C-S19	**1381–1440**	**60**	**20**	**64.5**	**ttactggagctggaccagcgtacccactttccgcagttctcctactcggcgagcatccgc**	**IO-A18rc**
C-S19rc					**aatgacctcgacctggtcgcatgggtgaaaggcgtcaagaggatgagccgctcgtaggcg**	**IO-A18**
C-A19	**1423–1482**	**60**	**18**	**65.2**	**atgagccgctcgtaggcgctcACTattactgagctcctaggccgcgactcgcgcgcgcgc**	**IO-A19**

Table 2AS: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the amino-terminal half of the codon-optimized p70 40S ribosomal protein S6 kinase-1 (S6K1) gene sequence.

TBC name	coding or "sense" (S) oligonucleotide primers (5'→3') noncoding or "antisense" (A) primers (3'←5')	T_m (°C)	overlap (bp)	length (nt)	coding region	TBIO name
C-S01	gaaggtcgtcatATGcgtcgccgtcgccgtcgggacggctttacccagccccggacttc	64.5	20	60	−12–48	IO-S22
C-A01	aaatgggtcggggcctgaaggcgctggcacttcgactcctgtaccgtcctcacaaactgt	63.4	22	60	29–88	IO-S21rc
C-A01rc	tttacccagccccggacttccgcgaccgtgaagctgaggacatggcaggagtgtttgaca					IO-S21
C-S02	gacatggcaggagtgtttgacattgacctggaccagccagaggacgcgggctctgaggatgagctggag	64.5	20	69	67–135	IO-S20
C-A02	cgagactcctactcgacctcctccccccagtcgacttgctctcgtacctagtacc	63.4	21	55	116–170	IO-S19rc
C-A02rc	gctctgaggatgagctggaggaggggggtcagctgaacgagagcatggatcatgg					IO-S19
C-S03	gaacgagagcatggatcatggcggagttggaccatacgaacttggcatggaacattgtga	63.6	27	60	150–209	IO-S18
C-A03	tatgcttgaaccgtaccttgtaacactctttaaactttagagtctttgatcacacttggc	63.2	26	60	183–242	IO-S17rc
C-A03rc	atacgaacttggcatggaacattgtgagaaatttgaaatctcagaaactagtgtgaaccg					IO-S17
C-S04	gaaatctcagaaactagtgtgaaccgcgggccagaaaaaatccgcccagaatgttttgag	63.6	27	60	217–276	IO-S16
C-A04	ctttttttaggcgggtcttacaaaactcgacgaagcccatgaaccatttcccccgatacct	63.3	21	60	250–309	IO-S15rc
C-A04rc	gaaaaaatccgcccagaatgttttgagctgcttcgggtacttggtaaagggggctatgga					IO-S15
C-S05	cttggtaaagggggctatggaaaggtgtttcaggtgcgcaaagtaacaggagcaaatact	63.2	26	60	289–348	IO-S14
C-A05	acgcgtttcattgtcctcgtttatgacccttttagaagcggtacttccacgaattttcc	63.5	23	60	323–382	IO-S13rc
C-A05rc	tgcgcaaagtaacaggagcaaatactgggaaaatcttcgccatgaaggtgcttaaaaagg					IO-S13
C-S06	cgccatgaaggtgcttaaaaaggcaatgattgtgcgcaacgctaaagatacagctcatac	64.8	26	60	360–419	IO-S12
C-A06	gcgttgcgatttctatgtcgagtatgttttcgtcttgccttataagacctccttcatttc	63.6	27	60	394–453	IO-S11rc
C-A06rc	cgcaacgctaaagatacagctcatacaaaagcagaacggaatattctggaggaagtaaag					IO-S11
C-S07	gaacggaatattctggaggaagtaaagcatccgttcatcgtggatctgatctacgccttt	63.5	23	60	427–486	IO-S10
C-A07	agcacctagactagatgcggaaagtctgaccacctttttgagatggagtaggacctcatag	63.5	23	60	464–523	IO-S09rc
C-A07rc	tcgtggatctgatctacgcctttcagactggtggaaaactctacctcatcctggagtatc					IO-S09
C-S08	actctacctcatcctggagtatctcagtggaggagaactgtttatgcagctggagcgtga	63.4	22	60	501–560	IO-S08
C-A08	acaaatacgtcgacctcgcactcccttaaaaataccttctgtgacggacgaagatggacc	64.5	20	60	539–598	IO-S07rc
C-A08rc	tgtttatgcagctggagcgtgagggaatttttatggaagacactgcctgcttctacctgg					IO-S07
C-S09	cactgcctgcttctacctggccgaaatcagcatggctttggggcatttacatcagaaggg	63.5	23	60	579–638	IO-S06
C-A09	aaccccgtaaatgtagtcttcccctagtagatggcgctggacttcggcctcttatagtac	63.4	22	60	616–675	IO-S05rc
C-A09rc	ttggggcatttacatcagaagggatcatctaccgcgacctgaagccggagaatatcatg					IO-S05
C-S10	cctgaagccggagaatatcatgctgaaccaccaaggtcatgtgaaactgacagactttgg	64.8	26	60	654–713	IO-S04
C-A10	ccagtacactttgactgtctgaaaccggacacgtttcttagataagtactaccttgtcag	63.5	29	60	688–747	IO-S03rc
C-A10rc	ggtcatgtgaaactgacagactttggcctgtgcaaagaatctattcatgatggaacagtc					IO-S03
C-S11	gcaaagaatctattcatgatggaacagtcacacacaccttttgtggaacaattgaataca	63.9	30	60	719–778	IO-S02
C-A11	gtgtgtggaaaacaccttgttaacttatgtaccggggactttagaactacgcgtcaccgg	63.4	21	60	749–808	IO-S01rc
C-A11rc	cacacaccttttgtggaacaattgaatacatggcccctgaaatcttgatgcgcagtggcc					IO-S01

Table 2BS: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the carboxy-terminal half of the p70 40S ribosomal protein S6 kinase-1 (S6K1) gene sequence.

TBC name	coding region	length (nt)	overlap (bp)	T_m (°C)	coding or "sense" (S) oligonucleotide primers (5'→3') noncoding or "antisense" (A) primers (3'←5')	TBIO name
C-S12	788–847	60	21	63.4	aaatcttgatgcgcagtggccacaatcgtgctgtggattggtggagtctgggagcattaa	IO-A01rc
C-S12rc					tttagaactacgcgtcaccggtgttagcacgacacctaaccacctcagaccctcgtaatt	IO-A01
C-A12	822–882	60	25	64.6	ctaaccacctcagaccctcgtaattacatactgtacgactgacctcgtggcggtaagtga	IO-A02
C-S13	863–922	60	20	64.5	ctggagcaccgccattcactggggagaatcgcaaaaagacaattgacaagatcctgaagt	IO-A03rc
C-S13rc					gacctcgtggcggtaagtgacccctcttagcgtttttctgttaactgttctaggacttca	IO-A03
C-A13	890–949	60	33	64.8	tagcgtttttctgttaactgttctaggacttcacgtttgagttaaacggaggcatggagt	IO-A04
C-S14	924–983	60	26	64.8	caaactcaatttgcctccgtacctcacacaagaagcccgtgatctgcttaaaaagctgct	IO-A05rc
C-S14rc					gtttgagttaaacggaggcatggagtgtgttcttcgggcactagacgaatttttcgacga	IO-A05
C-A14	956–1018	60	25	64.6	gggcactagacgaatttttcgacgactttgcgttacgacgaagagcagaccctcgaccag	IO-A06
C-S15	999–1058	60	20	64.5	ttctcgtctgggagctggtcctggggacgctggagaagttcaagctcatccattctttcg	IO-A07rc
C-S15rc					aagagcagaccctcgaccaggacccctgcgacctcttcaagttcgagtaggtaagaaagc	IO-A07
C-A15	1032–1091	60	27	63.6	tcttcaagttcgagtaggtaagaaagcggtgtaattgacccttcttgaagaccgagcgtt	IO-A08
C-S16	1071–1130	60	21	63.4	ggaagaacttctggctcgcaaggtggagccaccgtttaaacctctgttgcaatctgagga	IO-A09rc
C-S16rc					ccttcttgaagaccgagcgttccacctcggtggcaaatttggagacaacgttagactcct	IO-A09
C-A16	1104–1163	60	27	63.6	caaatttggagacaacgttagactcctctacattcagtcaaactaaggttcaaatgtgc	IO-A10
C-S17	1135–1194	60	29	63.5	gtaagtcagtttgattccaagtttacacgccagacacctgtcgatagtccagatgactca	IO-A11rc
C-S17rc					cattcagtcaaactaaggttcaaatgtgcggtctgtggacagctatcaggtctactgagt	IO-A11
C-A17	1172–1231	60	23	63.5	gacagctatcaggtctactgagttgagagtcactttcacggttagtccagaaagacccaa	IO-A12
C-S18	1210–1269	60	22	63.4	gccaatcaggtctttctgggtttacatacgtggctccatctgtacttgaaagtgtgaaa	IO-A13rc
C-S18rc					cggttagtccagaaagacccaaaatgtatgcaccgaggtagacatgaactttcacacttt	IO-A13
C-A18	1243–1302	60	27	63.6	cgaggtagacatgaactttcacactttcttttcaagaggaagctcggttttaggcgagt	IO-A14
C-S19	1281–1340	60	22	63.4	cttcgagccaaaaatccgctcacctcgtcgctttattggcagcccacgtacacctgtcag	IO-A15rc
C-S19rc					gaagctcggtttttaggcgagtggagcagcgaaataaccgtcgggtgcatgtggacagtc	IO-A15
C-A19	1321–1380	60	20	64.5	tcgggtgcatgtggacagtcgggtcagtttaaatcgggaccctaaagacccctgcgcca	IO-A16
C-S20	1362–1421	60	19	64.8	ggatttctggggacgcggtgcttcggcaagcacagcaaatcctcagacacctgtggaata	IO-A17rc
C-S20rc					cctaaagacccctgcgccacgaagccgttcgtgtcgtttaggagtctgtggacaccttat	IO-A17
C-A20	1396–1455	60	26	64.8	cgtttaggagtctgtggacaccttatgggttacctttgttcaccgtaactcgtctaccta	IO-A18
C-S21	1433–1492	60	23	63.5	caagtggcattgagcagatggatgtgacaatgagtggggaagcatcggcaccacttccaa	IO-A19rc
C-S21rc					gttcaccgtaactcgtctaccacactgttactcacccttcgtagccgtggtgaaggtt	IO-A19
C-A21	1472–1531	60	21	63.4	ttcgtagccgtggtgaaggttaagcggtcggcttgagacccggtatgttcttcgttcgga	IO-A20
C-S22	1511–1570	60	21	63.4	ggccatacaagaagcaagccttccgatgatctccaaacggccagagcacctgcgtatga	IO-A21rc
C-S22rc					ccggtatgttcttcgttcggaaaggctactagaggtttgccggtctcgtggacgcatact	IO-A21
C-A22	1551–1610	60	20	64.5	cggtctcgtggacgcatacttagacACTattatcccgacgacgctggcgactcgttattg	IO-A22

Table 3AS: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the amino-terminal half of the codon-optimized phosphoinositide-dependent protein kinase-1 (PDK1) gene sequence.

TBC name	coding or "sense" (S) oligonucleotide primers (5'→3') noncoding or "antisense" (A) primers (3'←5')	T_m (°C)	overlap (bp)	length (nt)	coding region	TBIO name
C-S01	actgactcatATGgcccgtaccaccagccagctgtatgacgccgtg	66.5	20	46	−10–36	IO-S24
C-A01	cggtcgacatactgcggcacggctaggtctcgaggcaacacaatacaaggacgggcaggg	64.5	20	60	17–76	IO-S23rc
C-A01rc	gccagctgtatgacgccgtgccgatccagagctccgttgtgttatgttcctgcccgtccc					IO-S23
C-S02	gttatgttcctgcccgtccccatcaatggtgcgtacccagactgagagctccacgccgcc	68.6	20	60	57–116	IO-S22
C-A02	tgactctcgaggtgcggcggaccgtaaggaccaccgtcggcagtcccgggccggtacctg	67.2	16	60	97–156	IO-S21rc
C-A02rc	actgagagctccacgccgcctggcattcctggtggcagccgtcagggcccggccatggac					IO-S21
C-S03	gggcccggccatggacggcactgcagccgagcctcgcccgggcgccggctccctgcagca	67.2	17	60	141–200	IO-S20
C-A03	cggccgagggacgtcgtacgggtcggaggcggtgtcggagcgtttttcgcgggactcctg	63.6	26	60	184–243	IO-S19rc
C-A03rc	gccggctccctgcagcatgcccagcctccgccacagcctcgcaaaaagcgccctgaggac					IO-S19
C-S04	agcctcgcaaaaagcgccctgaggactttaagtttggtaaaatccttggtgaaggctctt	63.6	27	60	218–277	IO-S18
C-A04	aaccattttaggaaccacttccgagaaaaaggtgccaacaggaccgagcacttgaccgtt	65.3	21	60	251–310	IO-S17rc
C-A04rc	ttggtaaaatccttggtgaaggctcttttccacggttgtcctggctcgtgaactggcaa					IO-S17
C-S05	tcctggctcgtgaactggcaacctcccgtgaatatgcgatcaaaattctggagaagcgtc	64.8	26	60	290–349	IO-S16
C-A05	acgctagttttaagacctcttcgcagtatagtaatttcttttgttccagggcatacattg	64.0	32	60	324–383	IO-S15rc
C-A05rc	tgcgatcaaaattctggagaagcgtcatatcattaaagaaaacaaggtcccgtatgtaac					IO-S15
C-S06	atcattaaagaaaacaaggtcccgtatgtaacccgtgagcgcgatgtcatgtcgcgcctg	66.5	20	60	352–411	IO-S14
C-A06	cgctacagtacagcgcggacctagtgggcaagaaacaattcgaaatgaagtgtaaagtcc	65.3	25	60	392–451	IO-S13rc
C-A06rc	gcgatgtcatgtcgcgcctggatcacccgttctttgttaagctttacttcacatttcagg					IO-S13
C-S07	gttaagctttacttcacatttcaggacgacgagaagctgtatttcggccttagttatgcc	63.7	24	60	427–486	IO-S12
C-A07	gacataaagccggaatcaatacggttttaccacttgacgaatttatataagcgttttag	63.3	36	60	463–522	IO-S11rc
C-A07rc	ctgtatttcggccttagttatgccaaaaatggtgaactgcttaaatatattcgcaaaatc					IO-S11
C-S08	aaaaatggtgaactgcttaaatatattcgcaaaatcggttcattcgatgagacctgtacc	65.4	24	60	487–546	IO-S10
C-A08	ccaagtaagctactctggacatgggcaaaaatgtgccgactctagcacagacgaaatctc	65.4	24	60	523–582	IO-S09rc
C-A08rc	ggttcattcgatgagacctgtacccgtttttacacggctgagatcgtgtctgctttagag					IO-S09
C-S09	gctgagatcgtgtctgctttagagtacttgcacggcaagggcatcattcaccgtgacctt	65.4	24	60	559–618	IO-S08
C-A09	ttcccgtagtaagtggcactggaatttggccttttgtaaaacaatttacttctatacgtg	63.8	35	60	595–654	IO-S07rc
C-A09rc	aagggcatcattcaccgtgaccttaaaccggaaaacattttgttaaatgaagatatgcac					IO-S07
C-S10	aaccggaaaacattttgttaaatgaagatatgcacattcagatcacagattttggtacag	64.0	28	60	620–679	IO-S06
C-A10	gtgtaagtctagtgtctaaaaccatgtcgttttcagaataggggtctctcgtttgttcgg	65.3	27	60	652–711	IO-S05rc
C-A10rc	cacattcagatcacagattttggtacagcaaaagtcttatccccagagagcaaacaagcc					IO-S05
C-S11	gtcttatccccagagagcaaacaagcccgtgccaactcattcgtgggtacagcgcagtac	65.3	21	60	685–744	IO-S04
C-A11	aagcacccatgtcgcgtcatgcaaagaggtctcgacgagtgcctcttcaggcggacattc	65.3	21	60	724–783	IO-S03rc
C-A11rc	ttcgtgggtacagcgcagtacgtttctccagagctgctcacggagaagtccgcctgtaag					IO-S03
C-S12	acggagaagtccgcctgtaagagttcagacctttgggctcttggttgcattatttaccag	63.0	26	60	763–822	IO-S02
C-A12	cccgagaaccaacgtaataaatggtcgaacaccgtccagagggtggaaaggcacgaccat	64.5	20	60	797–856	IO-S01rc
C-A12rc	gggctcttggttgcattatttaccagcttgtggcaggtctcccacctttccgtgctggta					IO-S01

Table 3BS: Oligonucleotide primers designed for the thermodynamically-balanced conventional (TBC) (11,12) and thermodynamically-balanced inside-out (TBIO) methods of PCR-based synthesis of the carboxy-terminal half of the codon-optimized phosphoinositide-dependent protein kinase-1 (PDK1) gene sequence.

TBC name	coding region	length (nt)	overlap (bp)	T_m (°C)	coding or "sense" (S) oligonucleotide primers (5'→3') noncoding or "antisense" (A) primers (3'←5')	TBIO name
C-S13	837–896	60	20	64.5	cccacctttccgtgctggtaacgagtatcttattttcagaagatcattaagttggaata	IO-A01rc
C-S13rc					gggtggaaaggcacgaccattgctcatagaataaaagtcttctagtaattcaaccttat	IO-A01
C-A13	859–918	60	38	62.7	ctcatagaataaaagtcttctagtaattcaaccttatactgaaaggtcttttaagaag	IO-A02
C-S14	882–941	60	37	64.1	cattaagttggaatatgactttccagaaaattcttccctaaggcacgtgacctcgtgga	IO-A03rc
C-S14rc					gtaattcaaccttatactgaaaggtcttttaagaagggattccgtgcactggagcacct	IO-A03
C-A14	922–981	60	20	64.5	ttccgtgcactggagcacctctttgaaaaccaaaatctacggtgtttcgcgaatccgaca	IO-A04
C-S15	960–1019	60	22	65.3	tgccacaaagcgcttaggctgtgaggaaatggaaggttacggtcctcttaaagcacaccc	IO-A05rc
C-S15rc					acggtgtttcgcgaatccgacactcctttaccttccaatgccaggagaatttcgtgtggg	IO-A05
C-A15	998–1057	60	22	65.3	tgccaggagaatttcgtgtgggcaagaaactcaggcagtgcaccctcttggacgtggtcg	IO-A06
C-S16	1040–1099	60	18	65.2	gggagaacctgcaccagcaaacgcctccgaagctcaccgcttacctgccggctatgtcgg	IO-A07rc
C-S16rc					ccctcttggacgtggtcgtttgcggaggcttcgagtggcgaatggacggccgatacagcc	IO-A07
C-A16	1082–1141	60	18	65.2	tggacggccgatacagccttctgctactcctgacgataccgttaatactgttagaggact	IO-A08
C-S17	1113–1172	60	29	64.9	ctgctatggcaattatgacaatctcctgagccagtttggctgtatgcaggtgtcttcgag	IO-A09rc
C-S17rc					gacgataccgttaatactgttagaggactcggtcaaaccgacatacgtccacagaagctc	IO-A09
C-A17	1152–1211	60	21	63.4	gacatacgtccacagaagctcgaggaggagtgtgagggacagtcggaggctgtgcccgga	IO-A10
C-S18	1196–1255	60	16	64.7	cctccgacacgggcctgccgcagcgttcaggcagcaacatcgagcagtacattcacgatc	IO-A11rc
C-S18rc					ggaggctgtgcccggacggcgtcgcaagtccgtcgttgtagctcgtcatgtaagtgctag	IO-A11
C-A18	1233–1292	60	23	63.5	gtagctcgtcatgtaagtgctagacctgagcttgaggaaacttgacctgaatgtcaaaag	IO-A12
C-S19	1266–1325	60	27	63.6	ctcctttgaactggacttacagttttccgaagatgagaagcgtctgttgctggagaagca	IO-A13rc
C-S19rc					gaggaaacttgacctgaatgtcaaaaggcttctactcttcgcagacaacgacctcttcgt	IO-A13
C-A19	1304–1363	60	22	65.3	tcgcagacaacgacctcttcgtccgaccgccattgggaaccgtggtcaaacatcttttat	IO-A14
C-S20	1334–1393	60	30	65.3	gtaacccttggcaccagtttgtagaaaataacttaattctgaagatgggcccagtggata	IO-A15rc
C-S20rc					cattgggaaccgtggtcaaacatcttttattgaattaagacttctacccgggtcacctat	IO-A15
C-A20	1372–1431	60	22	65.3	gacttctacccgggtcacctattcgcgttcccaaataaacgtgcagcggctgtcgacaac	IO-A16
C-S21	1413–1472	60	19	64.8	acgtcgccgacagctgttgctcacagaaggtccacatttatattacgtggaccctgtcaa	IO-A17rc
C-S21rc					tgcagcggctgtcgacaacgagtgtcttccaggtgtaaatataatgcacctgggacagtt	IO-A17
C-A21	1445–1504	60	28	64.0	gtgtaaatataatgcacctgggacagttgtttcaagactttccactttaaggaaccagtg	IO-A18
C-S22	1480–1539	60	25	62.9	ctgaaaggtgaaattccttggtcacaagaacttcgtccagaggccaagaattttaaaact	IO-A19rc
C-S22rc					gactttccactttaaggaaccagtgttcttgaagcaggtctccggttcttaaaattttga	IO-A19
C-A22	1512–1571	60	28	64.0	agcaggtctccggttcttaaaattttgaaagaaacaggtgtgcggattggcatgcatgat	IO-A20
C-S23	1551–1610	60	21	63.3	cacgcctaaccgtacgtactatctgatggacccgagcggtaacgcacacaagtggtgccg	IO-A21rc
C-S23rc					gtgcggattggcatgcatgatagactacctgggctcgccattgcgtgtgttcaccacggc	IO-A21
C-A23	1592–1651	60	19	64.8	tgcgtgtgttcaccacggcattctaggtcctccaaaccgcagttgcaatggtctcggtgg	IO-A22
C-S24	1631–1690	60	21	65.3	gtcaacgttaccagagccacccggacgccgctgtgcagTAAtgatagctcgaggatccgc	IO-A23rc
C-S24rc					cagttgcaatggtctcggtgggcctgcggcgacacgtcATTactatcgagctcctaggcg	IO-A23
C-A24	1673–1702	60	18	63.0	ctatcgagctcctaggcgagtcgaatttat	IO-A24