CAAACGCCTATCGTTACGAGAACCTACAACCGAGATACATATCGCTACGAACAGTTCAAACCTGATCTTC

0   8   16   24   32   40   48   56   64

TTGTCTGTTGAAGTGCACCTCATCGTTATCTTCTGGCCCTATCTCCTTACATATGTGGGAAATTGCAAGT

72   80   88   96   104   112   120   128   136

EcorI site

GAACCTTGATTTGGTATCTCAGCTTTGTGAATGTCTCAGTCGACAGCTGCTCTTGATTTGCCGTAGGTTA

144   152   160   168   176   184   192   200   208

CATTATTAGGGGACACGCGCTGATTTGGATCGGCTTATTTTGCAGTGAGCACGTGTGCGCAAAGTACACC

216   224   232   240   248   256   264   272   280

Gene aaCI

TCTAGATAGTGCCTTTCAAGGGAACTTCTATCTGCGGTGGTTCTCGGTTAAGTATCACAGCTGGGGGGCA

280   288   296   304   312   320   328   336   344

Gene aaCI

CTGTGGTTCCCGACGGCAATCATGCGAACGAATTCTACCAGGGAGACGAGCCAGCCAACTCAATGGAAAA

352   360   368   376   384   392   400   408   416

Gene aaCI

CATCATCATTTGGTGTGGGTGCGACATGATGTGGGCACATCGAAGCCTCCGAGTCGTGATCCCCAGCTAT

424   432   440   448   456   464   472   480   488

Gene aaCl

AGAAGTACACTCTATCCTTAACAACTATAGCGTAGTAAGTGTCCTAGGTAAAGTCTAAAGCATGTATCAC

496   504   512   520   528   536   544   552   560

Gene aaCl

AGCACGCGCACGGTCTTAGGGCCGGCTTATTGTGAACTGGGTTACGGGGAAGGGCAGTTTTCATGTTCAA

560   568   576   584   592   600   608   616   624

Gene aaCl

CACGGTCACACACAAGGTGATAGGCTAGGGTGTTCCTGTTCCTTCCACGTAGCGGAGCATCAGAACTAGA

632   640   648   656   664   672   680   688   696

Gene aaCl

CCTCAAGCTGTTAAGAATGTTTTGAGGGACAGAGTAGCTTACGGGGCAAGCGAGGGCTAGACGCAAATTG

704   712   720   728   736   744   752   760   768

Gene aaCl

CCGAACTACTGGCAATATCAAGGCAGAATTCCAGACAGCCAAGACAAACATACCTAATGACGAGACAGGC

776   784   792   800   808   816   824   832   840

Gene aaCl

TATATCGGTGGATCTCTGGGCCTTAATGATCGACTCCCCGAATTACACGTTAGGAACCGGGCCTCGGCTT

840   848   856   864   872   880   888   896   904

BamHI site

Gene aaCl

TGAAAGGCCACAGCTTTGGCCGTAATGCAGCTATATGGTAAGTATGTTTCGGTAGATCGGCGCACATGAT

912   920   928   936   944   952   960   968   976

Gene aaCl

CGTGCAATGACCTAAATATATGCGCCTATCTGATATCGTAACCCTAACAGGCTAAACCGGCTATCGAGGG

984 992 1,000 1,008 1,016 1,024 1,032 1,040 1,048

Gene aaCl

TGCTTCGATTTTGATAGTCAGACAATAACCCTAGCCTTGACCGTGTGGACCGTGTCCGACTTTCATCACA

1,056 1,064 1,072 1,080 1,088 1,096 1,104 1,112 1,120

Gene aaCl

GGATATGCGCCCCGTGCATTCAGGGCTTGCCGGGGCTCCGAAGTGCAGCTCACCGGGATGTTCGTTGCGT

1,120 1,128 1,136 1,144 1,152 1,160 1,168 1,176 1,184

Gene aaCl   **AarI site**

CATCAAGCGTGACTCGGCTAGGCGACCCCTTAACACTGAGATACCCTTCATATGAAATGCCGCGGCACGA

1,192 1,200 1,208 1,216 1,224 1,232 1,240 1,248 1,256

AGATCCCTAGTGGGAGTACGTCTAAATTATGTCAATATATAAACCTACTGCTCATAAATCTGATTGAGAT

1,264 1,272 1,280 1,288 1,296 1,304 1,312 1,320 1,328

GAGGGCTCATCTGAACCCGCGACCTGCACCAACTGTCTAACGGATATATTACGTCCTCCTAGGCTGAAGG

1,336 1,344 1,352 1,360 1,368 1,376 1,384 1,392 1,400

Gene barK

AGTTGAAAGATCGCCTATTCGCGTCAGCAATTCAGATCAGGCACAATGAAATTTGCTTAGGGAGACTGCT

1,400 1,408 1,416 1,424 1,432 1,440 1,448 1,456 1,464

Gene barK

ACCCGTCCGAACTGTGGACCAGGAGGGGCCATATGTCACTCGCGGTAGCAAGTGTGCTTATACTTCGTT

1,472   1,480   1,488   1,496   1,504   1,512   1,520   1,528   1,536

Gene barK

TACAGTCCTCATGCGAAAGCTACGATCGCCAACCCTGTAAAAGATTATCTTCAGGAGACTCTATCACGT

1,544   1,552   1,560   1,568   1,576   1,584   1,592   1,600   1,608

Gene barK

TGTCATCATCCAAATGGGGAATGGACCGTGCTTCATCAATTGGAGTCGACGGTCGGGGAAAGCTACTTGC

1,616   1,624   1,632   1,640   1,648   1,656   1,664   1,672   1,680

Gene barK

ATCGACCGCTTCTTGCGGATCCGGGTCTTTATTACATGAGTAGCAGCCAATAGTCATGGGATGGTGTGTT

1,680   1,688   1,696   1,704   1,712   1,720   1,728   1,736   1,744

Gene barK   **promoter**

CCTGGTCCTTGGACGTGCCTTTAAATGCTGTACAACGAAATTCTGCTAGCATGTAGAGGACCGACGGGGA

1,752   1,760   1,768   1,776   1,784   1,792   1,800   1,808   1,816

promoter   **Gene kanR**

AACCCTGGACATAGGGAATCCCGTCGTTCGGACTAGCTATTAAAGCAGACCCACCTCGTTACGTCCACGG

1,824   1,832   1,840   1,848   1,856   1,864   1,872   1,880   1,888

Gene kanR

CACGAGGAATGATCTCGAGTTGCTTTGCTCGTGCCAAATACGAGGCCGGCTCAGCAACCTGGTTTAAAGT

1,896   1,904   1,912   1,920   1,928   1,936   1,944   1,952   1,960

Gene kanR

GGAACATACACCGGCAGCTAACCAACGGTGACGAGAGTGACTCTATGTCGCTGGACCGGCAGTGGCTTCG

1,960   1,968   1,976   1,984   1,992   2,000   2,008   2,016   2,024

Gene kanR

TTTCTAACGCGATCATACCGCTGCCACCGGTTGGTACGAAGGAACCCAGCGATCTCAAACCATGTCATTG

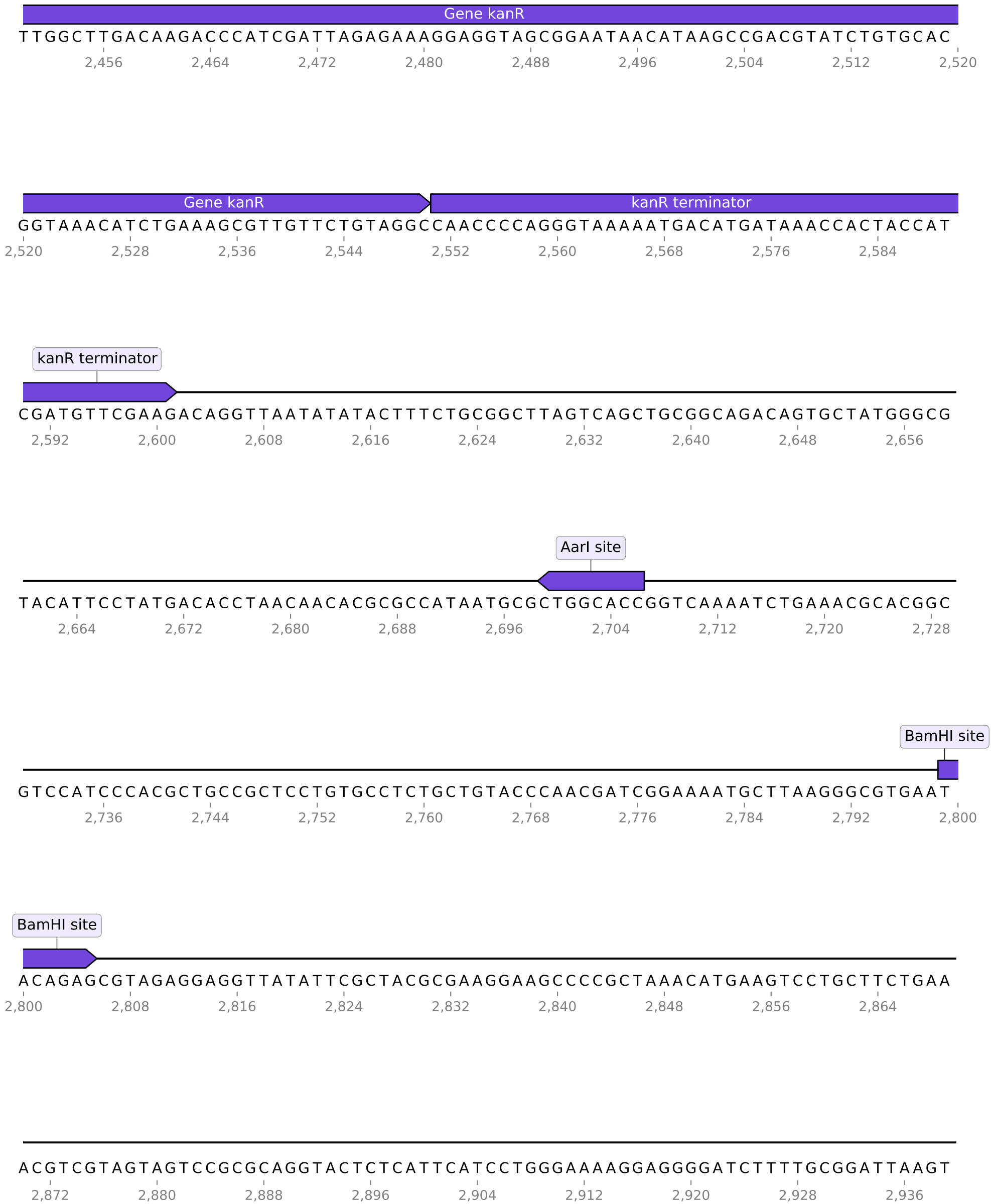2,032   2,040   2,048   2,056   2,064   2,072   2,080   2,088   2,096

Gene kanR

TCGTCTTGAATTATGCCTTTATGGAAACCAAACTAAGAGTCTGTAATAGACATCAATCGACCACGGAGGA

2,104   2,112   2,120   2,128   2,136   2,144   2,152   2,160   2,168

Gene kanR

GGCCGTCGTAGTGGCCGGGCTTTATTACCCGGAAAGGGTACCTTATCGAGTCATGAGGTATGGAGAAATA

2,176   2,184   2,192   2,200   2,208   2,216   2,224   2,232   2,240

Gene kanR

GGTCTCAAATGGCCTAAAAGCAGAACATCATGTGATTCACTTCATTTATAAGGAATTGCCGAACACCGCC

2,240   2,248   2,256   2,264   2,272   2,280   2,288   2,296   2,304

Gene kanR

TAAGCTAGCTATGCTGAATGCGACTCACCATAACACGCTGTCTATTTGATGATGCGTCGTGTGACTCGGG

2,312   2,320   2,328   2,336   2,344   2,352   2,360   2,368   2,376

Gene kanR

CCGCGCGCACCAAAGGACGGACAAATTCGACAATCCTGTTGATCGCCGGGGCGCAATACATGTTGACGAA

2,384   2,392   2,400   2,408   2,416   2,424   2,432   2,440   2,448

Gene kanR

TTGGCTTGACAAGACCCATCGATTAGAGAAAGGAGGTAGCGGAATAACATAAGCCGACGTATCTGTGCAC

2,456 2,464 2,472 2,480 2,488 2,496 2,504 2,512 2,520

Gene kanR | **kanR terminator**

GGTAAACATCTGAAAGCGTTGTTCTGTAGGCCAACCCCAGGGTAAAAATGACATGATAAACCACTACCAT

2,520 2,528 2,536 2,544 2,552 2,560 2,568 2,576 2,584

kanR terminator

CGATGTTCGAAGACAGGTTAATATATACTTTCTGCGGCTTAGTCAGCTGCGGCAGACAGTGCTATGGGCG

2,592 2,600 2,608 2,616 2,624 2,632 2,640 2,648 2,656

AarI site

TACATTCCTATGACACCTAACAACACGCGCCATAATGCGCTGGCACCGGTCAAAATCTGAAACGCACGGC

2,664 2,672 2,680 2,688 2,696 2,704 2,712 2,720 2,728

BamHI site

GTCCATCCCACGCTGCCGCTCCTGTGCCTCTGCTGTACCCAACGATCGGAAAATGCTTAAGGGCGTGAAT

2,736 2,744 2,752 2,760 2,768 2,776 2,784 2,792 2,800

BamHI site

ACAGAGCGTAGAGGAGGTTATATTCGCTACGCGAAGGAAGCCCCGCTAAACATGAAGTCCTGCTTCTGAA

2,800 2,808 2,816 2,824 2,832 2,840 2,848 2,856 2,864

ACGTCGTAGTAGTCCGCGCAGGTACTCTCATTCATCCTGGGAAAAGGAGGGGATCTTTTGCGGATTAAGT

2,872 2,880 2,888 2,896 2,904 2,912 2,920 2,928 2,936

CATAACCCGCTACAAGTCGTTCGGCCAGTTCCTGTAGTCGGAAGCGCAAACTCCTCCTATTTAGCCTTGC

2,944 2,952 2,960 2,968 2,976 2,984 2,992 3,000 3,008

CATGTGTTCTAGTGACGCAGGCCCGCTGCAGAATGTACCATAACTTATTGTGGATCTACTGCCCCTCTGT

3,016 3,024 3,032 3,040 3,048 3,056 3,064 3,072 3,080

ATTGCCTACGGACCGGCCCGCGAGACCTGCATTGTCATCGTCAGTTTATAGGAGGATCATCGCATCCGTC

3,080 3,088 3,096 3,104 3,112 3,120 3,128 3,136 3,144

Gene aaCI

TGCCCTGCCGCTGCAATCCACGCGTGCTTCAAACGACCAGTTTGCATCATGGTGTGAGACGCTAGCCTTA

3,152 3,160 3,168 3,176 3,184 3,192 3,200 3,208 3,216

Gene aaCI

TCCCCTATTAGTTAGGAGAACGGAACGGGGAGGCGTGACAAAGCAGGAGGTGGTGAGCTCCGAAACCCGC

3,224 3,232 3,240 3,248 3,256 3,264 3,272 3,280 3,288

Gene aaCI

GCTACTTTTAGACGGAATTAACGGCCGAACGCTATTAACTTCTCGGTCCCACGATGAATTTCTGAGGGGA

3,296 3,304 3,312 3,320 3,328 3,336 3,344 3,352 3,360

Gene aaCI

CACCCGATGTCGGAAAGGTACGGTTGAAGAATGAACCATTGTGCTGTAAATGCAGAACGCTCCCGCCCCG

3,360 3,368 3,376 3,384 3,392 3,400 3,408 3,416 3,424

Gene aaCI

AGTTGCGGTAGTTTACATTGGCGCACGTGCGCTAACAGGGAGGAAATGTTCAGGCTGGCCATGTACCTCT

3,432   3,440   3,448   3,456   3,464   3,472   3,480   3,488   3,496

Gene aaCI

GTGATGACATGCTCATGAACAAATAACAGATACAACCGTCTCCCCAGTGGCGTGAACCGTGCAGGAGTCG

3,504   3,512   3,520   3,528   3,536   3,544   3,552   3,560   3,568

Gene aaCI

AATGATGGGAAAAGGCATGAACTATTTCGTACGTAGTCAGTTCTTAGAAGATGTCTATCATCCAGCGCTA

3,576   3,584   3,592   3,600   3,608   3,616   3,624   3,632   3,640

AarI site
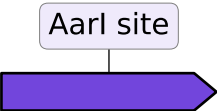
Gene aaCI

TTTAACCTAAACAGCCTGATGCGGAACGGGCCAGATCCCTTTATAGGTCCCAGGAGTGAATGCCCTCAGA

3,640   3,648   3,656   3,664   3,672   3,680   3,688   3,696   3,704

Gene aaCI

CCTTTGAATCCCTAGGGCAATGATCAAAGAGAACTAATGAGACAGTCGGGCTGCCTGGCCTTGTTGACAG

3,712   3,720   3,728   3,736   3,744   3,752   3,760   3,768   3,776

Gene aaCI

GATAGCTGTGAATATGCGTAGGCATCCAAGCAAGTGGGAGCAATCATACTGTTTCCCTACATCCGGGACT

3,784   3,792   3,800   3,808   3,816   3,824   3,832   3,840   3,848

Gene aaCI

CCGAGCGACGATGAGCGGGCATTACGCGCATGGTTGATCGAAACGTGGGGTTTCTGTAGTCTGAAACGCT

3,856   3,864   3,872   3,880   3,888   3,896   3,904   3,912   3,920

Gene aaCl

TTTTCGGTGACAGCTTTTGTAAGAGGCTCCATGTCTCACATTTCTACCCGGCCATAGAAGAGTTAACGC

3,920   3,928   3,936   3,944   3,952   3,960   3,968   3,976   3,984

Gene aaCl

TTTAATGGGCCGGTTAAGCCCTGGTCACGATGCGGTCGCACACGCCTGGCAGCTAGGATCGGATAACTA

3,992   4,000   4,008   4,016   4,024   4,032   4,040   4,048   4,056

Gene aaCl

ACGTCACGCTCCGTGAGGTCGTACCTTCTGACTTCTTGCTAAAGCCAGGCGACTATACCTTTAGTATCTC

4,064   4,072   4,080   4,088   4,096   4,104   4,112   4,120   4,128

Gene aaCl

GTCACTAGAAGCTAGCCATTGAGTGCTCCCGGGGTTTTCAAGACTTATCACCGTTTTGGCATTTAAGTCG

4,136   4,144   4,152   4,160   4,168   4,176   4,184   4,192   4,200

TGAACTCGCCAGTCTACTGATAAGTTTTCGACAGGAAGAAAGTAATATGACTCTCCCAGCTTTTCCCCGA

4,200   4,208   4,216   4,224   4,232   4,240   4,248   4,256   4,264

CTTTGTTCAAACTCCATCATAGATTAACGCCGAACTAAGAAGACCGTGTCTCTCTGTATAGGTTTTACTG

4,272   4,280   4,288   4,296   4,304   4,312   4,320   4,328   4,336

EcorI site

CAGTCTCCAGTAACGCCGCCACATAGACCTAAAACGAATAGATAGGGTAGCCTGTAACGCGATATCCAAC

4,344   4,352   4,360   4,368   4,376   4,384   4,392   4,400   4,408

TTTCACCATGTCGACTCCTCTCACGTCGCTCGAACACTACTGCGCAAAAGTCGCTGAGTCAAATCGCGT

4,416 4,424 4,432 4,440 4,448 4,456 4,464 4,472 4,480

ACTGTACTCCTCTATAGTTTTGGCGGAAGTACTGAGATCTTTAACATGGGAATTCGCTCGATATCTGTGC

4,480 4,488 4,496 4,504 4,512 4,520 4,528 4,536 4,544

CGGCTTGTTGTTGACCATAAAGACTGGAGGTACACAGTAGAGAGTTGAGCTTCATTCTAGACCATGTCTT

4,552 4,560 4,568 4,576 4,584 4,592 4,600 4,608 4,616

CCTCGCATTAGCCATCACCCGACTCGTCTCAATACGCAGTCCGTCTGCTGCGAGGATCACGGACATGCCG

4,624 4,632 4,640 4,648 4,656 4,664 4,672 4,680 4,688

CACGTGACATAGCGAAATCCCTTCAACTTA

4,696 4,704 4,712 4,720