

BGH39_B01a-pET32-DEST

5' tcgccccgaagaacgttttccaatgatgagcactttttaagttctgctatgtggcgcggtattatcccggt
 840
 3' agcggggcttcttgcaaaagggttactactcgtgaaaatttcaagacgatacacccgcgcataatagggca

Ap

5' attgacgccgggcaagagcaactcggtcgccgcatacactattctcagaatgacttgggtgagtactcac
 910
 3' taactgcgggcccggttctcgttgagccagcggcgtatgtgataagagtcttactgaaccaactcatgagtg

Ap

Scal

5' cagtcacagaaaagcatcttacggatggcatgacagtaagagaattatgcagtgctgccataaccatgag
 980
 3' gtcagtgtcttttcgtagaatgcctaccgtactgtcattctcttaatacgtcacgacgggtattgggtactc

Ap

5' tgataaactgcggccaaacttacttctgacaacgatcggaggaccgaaggagctaaccgcttttttgcac
 1050
 3' actattgtgacgccggttgaatgaagactgttgctagcctcctggcttctcgcattggcgaaaaaacgtg

Ap

PvuI

5' aacatgggggatcatgtaactcgccttgatcgttggggaaccggagctgaatgaagccataccaaacgacg
 1120
 3' ttgtaccccctagtacattgagcgggaactagcaacccttggcctcgacttacttcggtatggtttgctgc

Ap

5' agcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaaactattaactggcgaactacttac
 1190
 3' tcgcactgtggtgctacggacgtcgttaccgttgttgcaacgcggttgataattgaccgcttgatgaatg

Ap

PstI

5' tctagcttcccggcaacaattaatagactggatggaggcggataaagttgcaggaccacttctgcgctcg
 1260
 3' agatcgaagggccggttgtaattatctgacctacctccgcctatttcaacgtcctgggtgaagacgcgagc

Ap

5' gcccttccggctggctggtttattgctgataaatctggagccggtgagcgtgggtctcgcggtatcattg
 1330
 3' cgggaaggccgaccgaccaataacgactatthagacctcggccactcgcaccagagcgcctatagtaac

Ap

Bsal

o

5' cagcactggggccagatggtaagccctcccgtatcgtagttatctacacgacggggagtcaggcaactat 1400

o

3' gtcgtgacccccggtctaccattcgggagggcatagcatcaatagatgtgctgccctcagtcctgttgata

o

o

5' ggatgaacgaaatagacagatcgctgagataggtgcctcactgattaagcattggtaactgtcagaccaa 1470

o

3' cctacttgctttatctgtctagcgactctatccacggagtgactaattcgtaaccttgacagtcctggtt

o

o

5' gtttactcatatatacttttagattgatttaaacttcatttttaatttaaaggatctaggtgaagatcc 1540

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3' caaatgagtatatatgaaatctaactaaattttgaagtaaaaattaaattttcctagatccacttctagg

o

5' ttttgataatctcatgaccaaataccttaacgtgagttttcgttccactgagcgtcagaccccgtaga 1610

o

3' aaaaactattagagtactggttttagggaattgcactcaaaagcaagggtgactcgcagtcctggggcatct

o

5' aaagatcaaaggatcctcttgagatccttttttctgcgcgtaatctgctgcttgcaaacaaaaaacca 1680

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3' tttctagtttcctagaagaactctaggaaaaaagacgcgcattagacgacgaacgtttgtttttttgg

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o

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o

o

5' gcacacagcccagcttggagcgaacgacctacaccgaactgagatacctacagcgtgagctatgagaaag 2030

o

3' cgtgtgtcgggtcgaacctcgcttgctggatgtggcttgactctatggatgtcgcactcgatactctttc

o

o

AhdI



Ap

Ap

Ori

Ori

Ori

Ori

Ori

Ori

```

5' cgccacgcttcccgaaggggaaaggcggacaggtatccggttaagcggcagggtcggaacaggagagcgc
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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         Ori
-----
5' acgaggagcttccagggggaaacgcctggtatctttatagtcctgtcgggttccgccacctctgacttg
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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         Ori
-----
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0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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         Ori
----->
5' acggttctggccttttgctggccttttgctcacatggtcttctcctgcgttatccccctgattctgtggat
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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5' aaccgtattaccgcctttgagtgagctgataccgctcgccgcagccgaacgaccgagcgcagcgagtcag
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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5' tgagcgaggaagcggaaagagcgctgatgcggtatcttctccttacgcactgtgcggtatctcacaccg
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3' actcgctccttcgccttctcgcggactacgccataaaagagggaatgcgtagacacgccataaagtgtggc
                                     BstZ171
                                     |
5' catatatggtgcactctcagtacaatctgctctgatgcccgatagttaagccagtatacactccgctatc
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3' gtataataccacgtgagagtcattgtagacgagactacggcgtatcaattcggtcatatgtgagggcatag
      Tth111
      |
5' gctacgtgactgggtcatggctgcgccccgacaccgccaacacccgctgacgcgcccctgacgggcttgt
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3' cgatgcactgaccagtgaccgacggggctgtgggcggttgtgggcgactgcgcgggactgccgaaca
5' ctgctcccggcatccgcttacagacaagctgtgaccgctctccgggagctgcatgtgtcagaggttttcac
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3' gacgagggccgtaggcgaatgtctgttcgacactggcagaggccctcgacgtacacagtcctcaaaaagtg
5' cgcatcaccgaaacgcgagcagcgtgctgaaagctcatcagcgtggtcgtgaagcgattcacagat
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3' gcagtagtggtttgcgcgctccgctcgcgcccatttcgagtagtcgcaccagcacttcgctaagtgtcta
5' gtctgctgttcatccgcgctccagctcggttagtttctccagaagcgtaaatgtctggcttctgataaag
0  | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3' cagacggacaagtaggcgcaggtcgagcaactcaaagaggtcttcgcaattacagaccgaagactatctc

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5'  cggggccatggttaagggcggttttttctctggttggtcactgatgcctccgtgtaagggggatttctggtc
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
3'  gcccggtaacaattcccgcataaaaggacaaaccagtgactacggaggcacattccccctaagacaagt

5'  tgggggtaatgataccgatgaaacgagagaggatgctcacgatacgggttactgatgatgaacatgcccg
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
3'  acccccattactatggctactttgctctctctctacgagtgctatgcccaatgactactacttgtacgggc

5'  gttactggaacggttgtgagggtaaacaactggcggatggatgcggcgggaccagagaaaaatcactcag
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
3'  caatgaccttgcaacactcccatttgttgaccgccatactacgccgccctggctctcttttttagtgagtc

5'  ggtcaatgccagcgcttcgttaatacagatgtaggtgttccacagggtagccagcagcatcctgcgatgc
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
3'  ccagttacggctcgcgaagcaattatgtctacatccacaaggtgtcccatcggtcgctcgtaggacgctacg

5'  agatccggaacataatgggtgcagggcgctgacttccgcgcttccagactttacgaaacacggaaaccgaa
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
3'  tctaggccttgtattaccacgtcccgcgactgaaggcgcaaaggtctgaaatgctttgtgcctttggctt

5'  gaccattcatgttgttctcaggtcgcagacgtttgcagcagcagtcgcttcacgttcgctcgcgtatc
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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5'  ggtgattcattctgctaaccagtaaggcaacccccgccagccttagccgggtcctcaacgacaggagcacga
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o

o  FspAI
   |
5'  tcatgcgacccccggtggggcccgccatgccggcgataatggcctgcttctcgccgaaacggttgggtggcggg
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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5'  accagtgcgaaggccttgagcaggggctgcaagattccgaataaccgcaagcgacaggccgatcatcgctc
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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5'  gcgctccagcgaagcggtcctcgccgaaaaatgaccagagcgtgcgggcacctgtcctacgagttgca
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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5'  tgataaagaagacagtcataagtgcggcgacgatagtcatgccccgcgccaccggaaggagctgactgg
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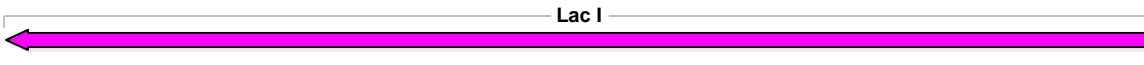
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o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
3'  caacttccgagagttcccgtagccagctctagggccacggattactcactcgattgaatgtaattaacgc

5'  ttgcgctcactgcccgtttccagtcgggaaacctgctcgtgccagctgcattaatgaatcggccaacgcg
o  +++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|++++|
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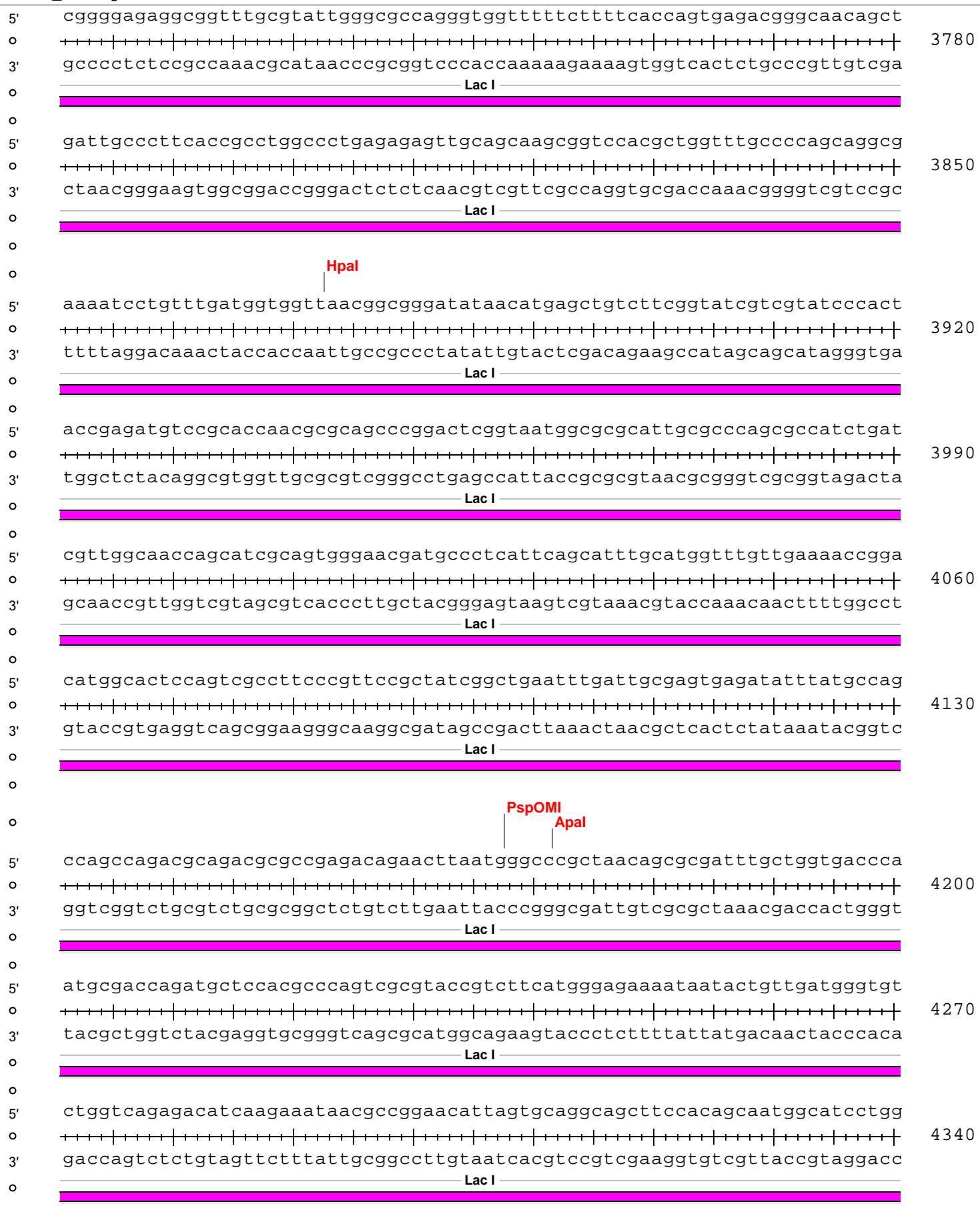
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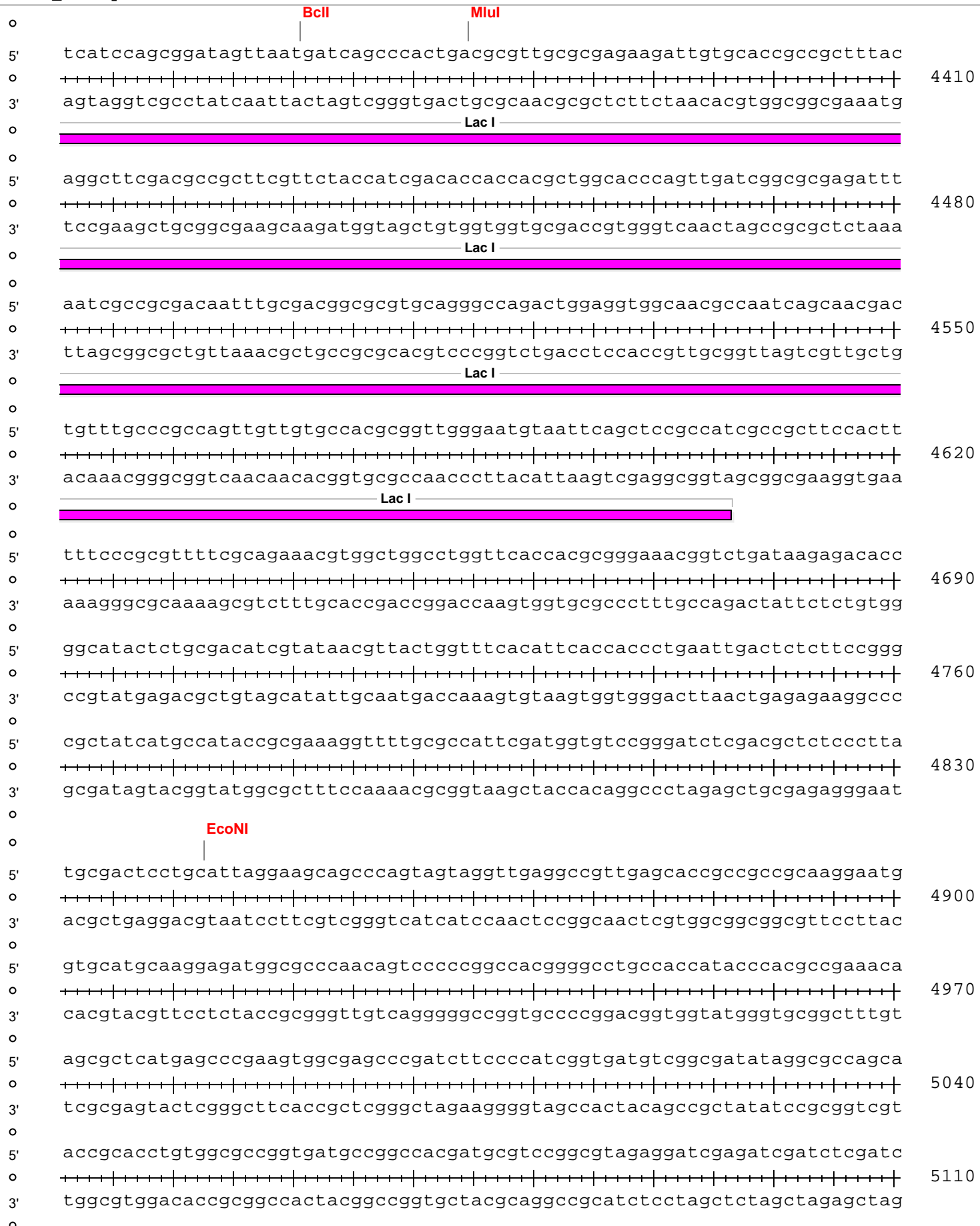
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BGH39_B01a-pET32-DEST



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 3' ggcgctttaattatgctgagtgatattccccttaacactcgcctattgttaaggggagatctttattaa

← T7 Promoter →
← Lac Operator →

XbaI

5180

5' gtttaactttaagaaggagatatacatatgagcgataaaattattcacctgactgacgacagtttgaca
 3' caaattgaaattcttcctctatatgtataactcgcctattttaataagtgagactgactgctgtcaaaactgt

BamHI

BamHI'

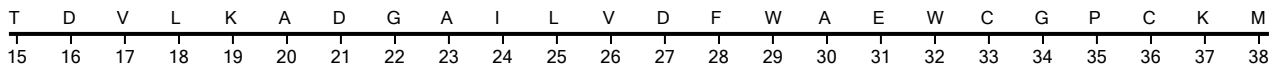
5250



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5320

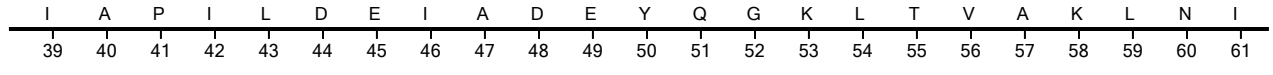
Trx Tag



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5390

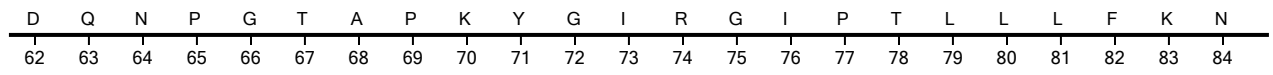
Trx Tag



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5460

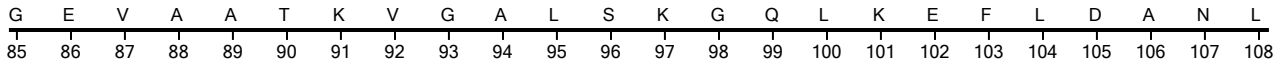
Trx Tag



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 3' cacttcaccgcccgttggtttcaccacgtgacagatttcagtcactttctcaaggagctgcgattgga

5530

Trx Tag



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5' ggccggttctggttctggccatatgcaccatcatcatcattcttctggtctggtgccaacgcggttct
 3' cccggccaagaccaagaccggtatacgtggttagtagtagtaagaagaccagaccacggtgcgccaaga

MscI

His6-tag **Thrombin**

A G S G S G H M H H H H H S S G L V P R G S
 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131

5600

5' ggtatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg
 3' ccatactttctttggcgacgacgatttaagcttgcggtcgtgtacctgctcggtctagaccatggctgc

BglIII **Acc65I** **KpnI**

G M K E T A A A K F E R Q H M D S P D L G T D
 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154

En...e

5670

5' acgacgacaaggccatggcgatATCAACAAGTTTGTACAAAAAAGCAGGCTctgaaaacttgtactttca
 3' tgctgctgttccggtaccgctaTAGTTGTTCAAACATGTTTTTTCGTCCGAgacttttgaacatgaaagt

NcoI

Enterokinase **attB1** **TEV site**

BGH39_B01a-pDONR221

D D D K A M A I S T S L Y K K A G S E N L Y F Q
 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178

5740

5' aggcCGTGAACGTACGCGAATAAGCGTTGATGCCAGTGAAGCGGTACGCCCGTTCAACCGTTCTGGCGC
 3' tccgGCACTTGCAATGCGCTTATTCGCAACTACGGTCACTTCGCCATGCGGGCAAGTTGGCCAAGACCGCG

BsiWI **AgeI**

T... **BGH39_B01a** **BGH39_B01a-pDONR221**

G R E R T R I S V D A S E A V R P F N R F W R
 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201

5810

5' GGCACCGGCTTTTCGCCGGCCGAGCTGCTGCTCGAGCCCGAGATGCGCCAGATGCTTGCCTATATCGGTG
 3' CCGTGGCCGAAAAGCGGCCGGCTCGACGACGAGCTCGGGCTCTACGCGGTCTACGAACGGATATAGCCAC

BGH39_B01a **BGH39_B01a-pDONR221**

G T G F S P A E L L L E P E M R Q M L A Y I G
 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224

5880

BGH39_B01a-pET32-DEST

5' GCCTGCCGAATGAGGGCATCAAGTTCCTGCGGGTGCATTATCTCTACAATCTGCTGAGCGCGAAGGGCGA
 3' CGGACGGCTTACTCCCCTAGTTC AAGGACGCCACGTAATAGAGATGTTAGACGACTCGCGCTTCCCCT

5950

BGH39_B01a

BGH39_B01a-pDONR221

G L P N E G I K F L R V H Y L Y N L L S A K G E
 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248

BmgBI

5' GGTCGGCTACGACTGGTCGCTGCTCGACCGCGCGCTCGACGTGATGATCGAACACCGCCTGAAGCCGTT
 3' CCAGCCGATGCTGACCAGCGACGAGCTGGCGCGCGAGCTGCACTACTAGCTTGTGGCGGACTTCGGCAAG

6020

BGH39_B01a

BGH39_B01a-pDONR221

V G Y D W S L L D R A L D V M I E H R L K P F
 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271

5' TTCGAACTGATGGGCAACCCATCCGGCCTGTTACCGACTATGAGGACATGGATCAGGTCAGGCGCTGGC
 3' AAGCTTGACTACCCGTTGGGTAGGCCGGACAAGTGGCTGATACTCCTGTACCTAGTCCAGTCCGCGACCG

6090

BGH39_B01a

BGH39_B01a-pDONR221

F E L M G N P S G L F T D Y E D M D Q V R R W
 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294

5' GGGATCTCGTGACGGCAACGGTCGACCGTTATGGCGCGGTTACGGCATGGACGAATTGCGCACATGGTA
 3' CCCTAGAGCACTGCCGTTGCCAGCTGGCAATACCGCGCGCAATGCCGTACCTGCTTAACGCGTGTACCAT

6160

BGH39_B01a

BGH39_B01a-pDONR221

R D L V T A T V D R Y G A R Y G M D E L R T W Y
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5' TTTCGAAACGACGAACGAGGCCGACTCCGGCTGGTGGACCTACGGGATCAAGGGTTACACCAACTACTAC
 3' AAAGCTTTGCTGCTTGCTCCGGCTGAGGCCGACCACCTGGATGCCCTAGTTCCCAATGTGGTTGATGATG

6230

BGH39_B01a

BGH39_B01a-pDONR221

F E T T N E A D S G W W T Y G I K G Y T N Y Y
 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341

BGH39_B01a-pET32-DEST

5' GACGCCTGCGTCGCGGGGCTCGATGCCATCGATCCCACCTTGCCGATGGGCGGACCCGGAACCGCCCGCA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' CTGCGGACGCAGCGCCCCGAGCTACGGTAGCTAGGGTGAACGGCTACCCGCCTGGGCCTTGCGGGGCGT

6300

BGH39_B01a

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D A C V A G L D A I D P T L P M G G P G T A R
342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364

5' CGCTCTCGCCGATCTTTTCGCGCCCTGATGGCCATTGCGACAGCGGCACGAGCTGCCTCAGCGATGACGG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GCGAGAGCGGCTAGAAAGCGCGGACTACCGGGTAACGCTGTGCGCGTGTCTGACGGAGTCGCTACTGCC

6370

BGH39_B01a

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T L S P I F R A L M A H C D S G T S C L S D D G
365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388

5' CCCGCCGCGCATCGATTACATCTCGATCCACGAAAAGGGCGTCAACGGCAGCAAGGAAGACCTGACCCCG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GGGCGGCGCGTAGCTAATGTAGAGCTAGGTGCTTTTCCCGCAGTTGCCGTCGTTCTTCTGGACTGGGGC

6440

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P P R I D Y I S I H E K G V N G S K E D L T P
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5' AAAACCAACGGTATCGTCGACCGCACTTTGCTCGTCGTCGACTATCTGAAGGAGCATCACCCGCGCCTGG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' TTTTGATTGCCATAGCAGCTGGCGTGAAACGAGCAGCAGCTGATAGACTTCCCTCGTAGTGGGCGCGGACC

6510

BGH39_B01a

BGH39_B01a-pDONR221

K T N G I V D R T L L V V D Y L K E H H P R L
412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434

5' CGGGCTTGCCCATCGTCAACGATGAATGCGATCCGCAGCTTGGCTGGAGCGATCATCATAGCTGGCACGG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GCCCGAACGGGTAGCAGTTGCTACTTACGCTAGGCGTCGAACCGACCTCGCTAGTAGTATCGACCGTGCC

6580

BGH39_B01a

BGH39_B01a-pDONR221

A G L P I V N D E C D P Q L G W S D H H S W H G
435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458

BGH39_B01a-pET32-DEST

5' CAAAGCCTATTACGCCGGTATCATCGCCCGCATCATCGAACAGCAGCACCACCGGCGCATCATCGCCCCGAAA
 3' GTTTCGGATAATGCGGCCATAGTAGCGGGCGTAGTAGCTTGTCTGCTGGCCGCGTAGTAGCGGGGCTTT

6650

BGH39_B01a

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K A Y Y A G I I A R I I E Q H D R R I I A P K
 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481

5' GCGGCGAATTTACCTTCCTCAGCAATGACCACGCCTTTATCGGCGGCTGGAGCCAGCGCACGATCTTTG
 3' CGCCGCTTAAAGTGAAGGAGTCGTTACTGTTGCGGAAATAGCCGCCGACCTCGGTGCGGTGCTAGAAAC

6720

BGH39_B01a

BGH39_B01a-pDONR221

A A N F T F L S N D H A F I G G W S Q R T I F
 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504

5' CCTATTTTCGGTTCGCGCAATTTACCAAGGCGCAGTGGGAGCACAAAGACCAATCTGGATATGCTGGTCAC
 3' GGATAAAGCCAAGCGCGTTAAAGTGGTTCGCGCTACCCTCGTGTCTGGTTAGACCTATACGACCAGTG

6790

BGH39_B01a

BGH39_B01a-pDONR221

A Y F G S R N F T K A Q W E H K T N L D M L V T
 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528

5' CGATGTCGACAGGGCGCCGCCCTTCGACATCATCAAGAAGCCCGGCCTCACATCGATGGAAGCTGCTGGCA
 3' GCTACAGCTGTCCCGCGGCGGAAGCTGTAGTAGTTCTTCGGGCGGAGTGTAGCTACCTTGACGACCGT

6860

BGH39_B01a

BGH39_B01a-pDONR221

D V D R A P P F D I I K K P G L T S M E L L A
 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551

5' ACGCTTGCGGATACCGTTTGCAAGGTGACGGCCGAACCGCCGCTTGCGCCCGACCAGGATGGCCTGGCGA
 3' TGCGAACCGCTATGGCAAACGTTCCACTGCCGGCTTGGCGGCGAACGCGGGCTGGTCCCTACCGGACCGCT

6930

BGH39_B01a

BGH39_B01a-pDONR221

T L G D T V C K V T A E P P L A P D Q D G L A
 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574

BGH39_B01a-pET32-DEST

5' TCCTGCCGACGCGGCTGCCGGGCGGGCGGTGTTTCCATCAGCCTCATCCATAGCGTCGATGCCATCAACCG
 0 ++++++
 3' AGGACGGCTGCGCCGACGGCCC GCCCACAAAGGTAGTCGAGTAGGTATCGCAGCTACGGTAGTTGGC

7000

BGH39_B01a

BGH39_B01a-pDONR221

I L P T R L P G G G V S I S L I H S V D A I N R
 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598

5' CTCGGGCGCGACCGCCGTCCGTCTCGAGGTGAGCGGCTTGGTTCCCGGCCGCCACGCGCTTTGCCTGCTG
 0 ++++++
 3' GAGCCCGGCCTGGCGGCAGGCAGAGCTCCACTCGCCGAACCAAGGGCCGGCGGTGCGCGAAACGGACGAC

7070

BGH39_B01a

BGH39_B01a-pDONR221

S G R T A V R L E V S G L V P G R H A L C L L
 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621

5' CGCATCGACGAGGAATTCACCAATCCGATGGAGGTCTGGGAAGCCAGCACGATGAAAGCAACCCGCGTG
 0 ++++++
 3' GCGTAGCTGCTCCTTAAGTGGTTAGGCTACCTCCAGACCCTTCGGGTCGTGCTACTTTTCGTTGGGCGCAC

7140

BGH39_B01a

BGH39_B01a-pDONR221

R I D E E F T N P M E V W E A Q H D E S N P R
 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644

5' GGCTCTTCGAGCCGGTCGGCGCACCCGCTGCACCTGATGAAGCGCAGTTTGCCGAAATGCGCCGCGCGCA
 0 ++++++
 3' CCGAGAAGCTCGGCCAGCCGCGTGGCGGACGTGGACTACTTCGCGTCAAACGGCTTTACGCGGCGCGCGT

7210

BGH39_B01a

BGH39_B01a-pDONR221

G L F E P V G A P P A P D E A Q F A E M R R A Q
 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668

5' GGAGCCCGCCCTGCTGCATCCGATCAGCGTCGTCGCGTGCAGCAAGGCCGGATCAGTGTGACCTGGAT
 0 ++++++
 3' CCTCGGGCGGGACGACGTAGGCTAGTCGCAGCAGCGCACGCTGCTTCCGGCCTAGTCACAGCTGGACCTA

7280

BGH39_B01a

BGH39_B01a-pDONR221

E P A L L H P I S V V A C D E G R I S V D L D
 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691

BspMI
AarI

5' GTGCCATTGCCGTCGCTGACGCAGGTGCTTGTCTGTTCCCGATATCGGCGTGCCACCGGCGGCACCGAGCG
3' CACGGTAACGGCAGCGACTGCGTCCACGAACAGCAAGGGCTATAGCCGCACGGTGGCCGCCGTGGCTCGC

7350

————— **BGH39_B01a** —————

————— **BGH39_B01a-pDONR221** —————

V P L P S L T Q V L V V P D I G V P P A A P S
692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714

BseRI

5' GCCTTGTCTGTCGAACGCTATCTCGGCCTCGGCGGTGCGGAGGAGCGCATGCTGTTCTGGGCTGCCGGCGA
3' CGGAACAGCAGCTTGCATAGAGCCGGAGCCGCCAGCCCTCCTCGCGTACGACAAGACCCGACGGCCGCT

7420

————— **BGH39_B01a** —————

————— **BGH39_B01a-pDONR221** —————

G L V V E R Y L G L G G R E E R M L F W A A G D
715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738

5' TGCCAGCCCGGCCATCTTCTACGATGTCTGGTACAGCACCAGTGGCGCGGCTTTTGAAAAGGTCAGTTCA
3' ACGGTCGGGCCCGGTAGAAGATGCTACAGGACCAGTCGTGGCTACCGCGCCGAAAACCTTTTCCAGTCAAGT

7490

————— **BGH39_B01a** —————

————— **BGH39_B01a-pDONR221** —————

A S P A I F Y D V L V S T D G A A F E K V S S
739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761

5' GCGCCGCTGATCTCGACGGCATTCCTGCACATGTCCGCCCGCAGGGCGTGCGTTATGCGGTGCGCGCCC
3' CGCGGCGACTAGAGCTGCCGTAAGGACGTGTACAGCGGCGGCGTCCCGCACGCAATACGCCACGCGCGGG

7560

————— **BGH39_B01a** —————

————— **BGH39_B01a-pDONR221** —————

A P L I S T A F L H M S P P Q G V R Y A V R A
762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784

NsiI

5' GCGATGCATTCCGGTCGCCGACGCGAGCTTTGTCTCTCCCGCTAGGACCCAGCTTTCTTGTACAAAGTGGT
3' CGCTACGTAAGCCAGCGGCGTCGCTCGAAACAGAGAGGGCGATCCTGGGTCGAAAGAACATGTTTCACCA

7630

————— **BGH39_B01a** —————

————— **attB2** —————

————— **BGH39_B01a-pDONR221** —————

R D A F G R R S E L C L S R
785 786 787 788 789 790 791 792 793 794 795 796 797 798 799

