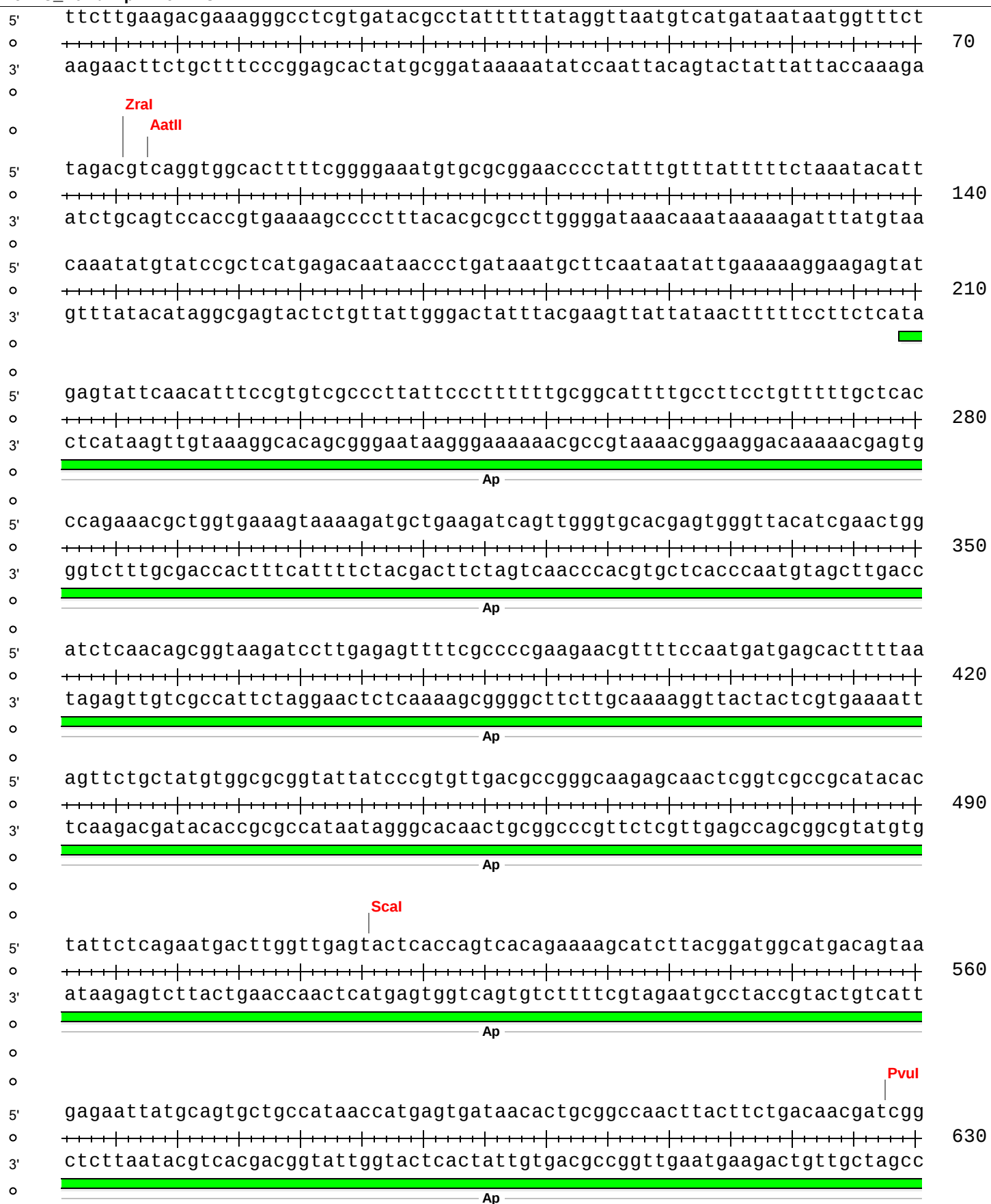
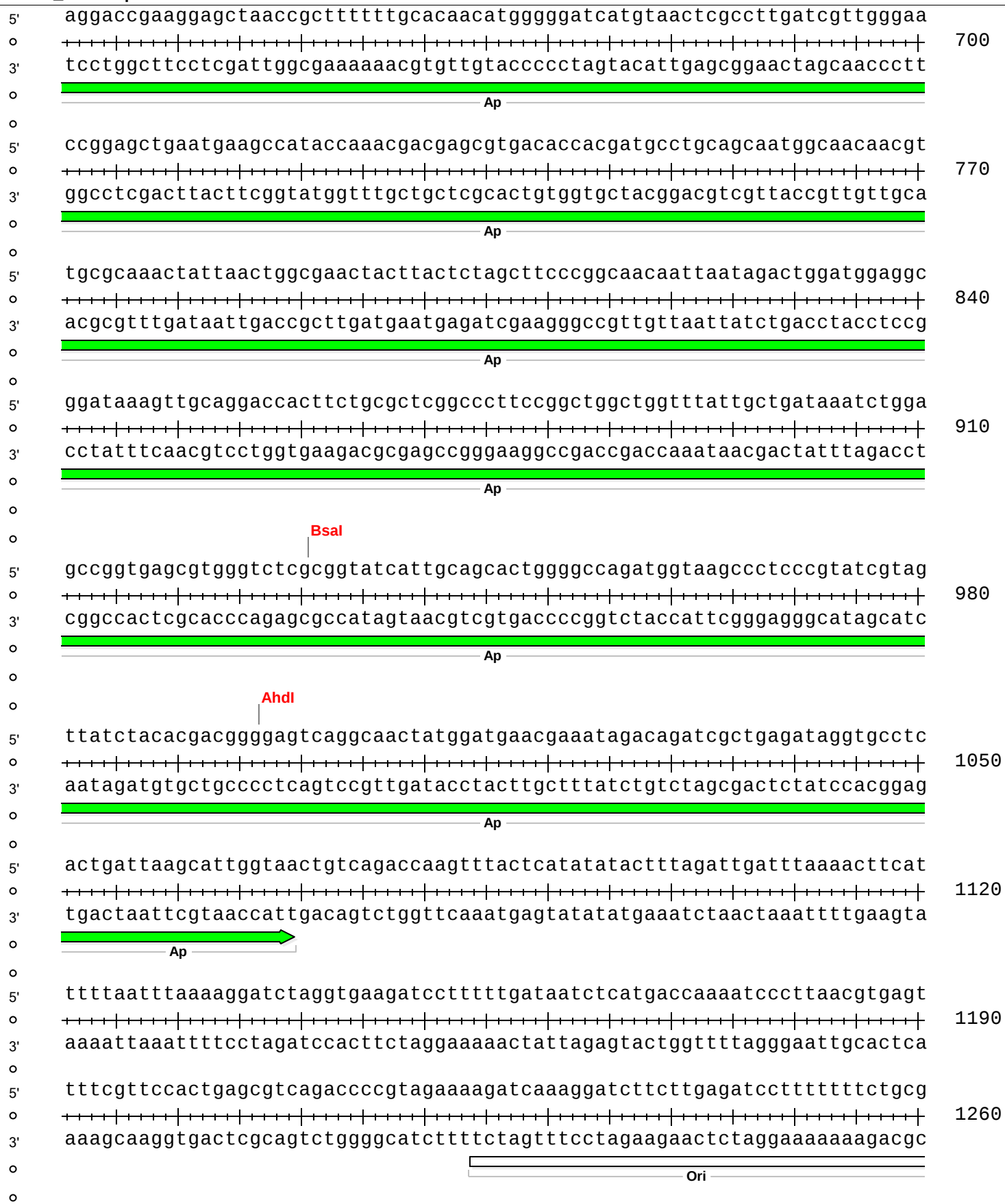


BGH13_B01b2-pET16-DEST



BGH13_B01b2-pET16-DEST



The diagram illustrates the pGEM-1 vector, a circular plasmid used for cloning. It features a multiple cloning site (MCS) with 10 fragments, each containing a unique restriction enzyme site. The fragments are labeled 1 through 10, and each is flanked by 'Ori' (origin of replication) markers. The fragments are as follows:

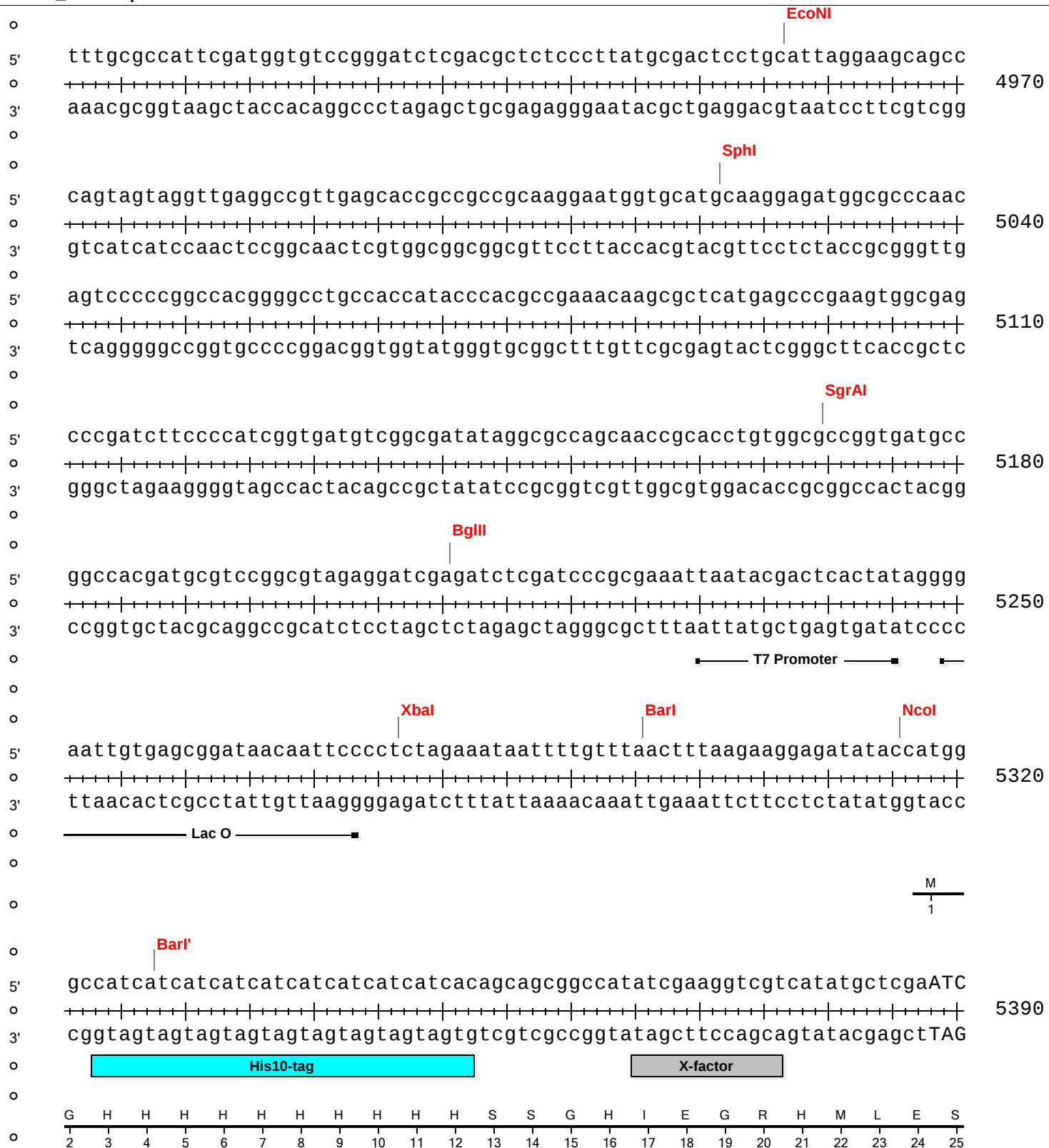
- Fragment 1: 5' cgtaatctgctgcttgcaaacacacacacagcggtgggtttgttttgccggatcaagagcta 3'
- Fragment 2: 5' ccaactctttttccgaaggtaactggcttcagcagagcgcagataccaaatactgtccttctagtgtagc 3'
- Fragment 3: 5' cgtagttaggccaccacttcaagaactctgtagcaccgcctacatacctcgctctgctaactctgttacc 3'
- Fragment 4: 5' agtggctgctgccagtggcgataagtcgtgtcttaccgggttggaactcaagacgatagttaccggataag 3'
- Fragment 5: 5' ggcgagcggtcgggctgaacggggggttcgtgcacacagcccagcttgagcgaacgacctacaccgaac 3'
- Fragment 6: 5' tgagatacctacagcgtgagctatgagaaagcgccacgcttcccgaaggagaaaggcggacaggtatcc 3'
- Fragment 7: 5' ggtaagcggcagggtcggaacaggagagcgcacgagggagcttccagggggaacgcctgggtatctttat 3'
- Fragment 8: 5' agtcctgtcgggtttcgccacctctgacttgagcgtcgatttttgtgatgctcgtcaggggggcggagcc 3'
- Fragment 9: 5' tatggaaaaacgccagcaacgcggcctttttacggttcctggccttttgctggccttttgctcacatgtt 3'
- Fragment 10: 5' ctttcctgcgttatcccctgattctgtggataaccgtattaccgcctttgagtgagctgataaccgctcgc 3'

The origin of replication (Ori) is located between each fragment. The PciI restriction site is located at the end of the 10th fragment, indicated by a red line and the label 'PciI'.

5' gcagcagtcgcttcacggttcgctcgcgtatcgggtgattcatttctgctaaccagtaaggcaaccccgccag 2870
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' cgtcgtcagcgaagtgcgaagcgagcgcatagccactaagtaagacgattgggtcattccggtggggcggtc
o
o
o
o
5' cctagccgggtcctcaacgacaggagcacgatcatgcgccaccgctggccaggaccaacgctgcccgaga 2940
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ggatcggcccaggagttgctgtcctcgtgctagtagcgctgggcaccggctcctgggttgcgacgggctct
o
o
o
o
5' tgcgccgctgctgggctgctggagatggcggacgcgatggatatgttctgccaagggttggtttgcgcatt 3010
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' acgcggcgcacgccgacgacctctaccgcctgcgctacctatacaagacgggttcccaaccaaacgcgtaa
o
o
o
o
5' cacagtctccgcaagaattgattggctccaattcttggagtgggtgaatccgtagcgaggtgccgccgg 3080
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gtgtcaagaggcggttcttaactaaccgaggttaagaacctcaccacttaggcaatcgctccacggcgggc
o
o
o
o
5' cttccattcaggtcgaggtggcccggtccatgcaccgcgacgcaacgcggggaggcagacaaggtatag 3150
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gaaggtaagtccagctccaccgggcccaggtacgtggcgctgcgttgcgccccctccgtctgttccatatc
o
o
o
o
5' ggccggcgctacaatccatgccaaaccggttccatgtgctcgccgaggcggcataaatcgccgtgacgatc 3220
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ccgccgcggatgttaggtacggttgggcaaggtacacgagcggctccgccgtatttagcggcactgctag
o
o
o
o
5' agcgggtccagtgatcgaagttaggctggtaagagccgcgagcgatccttgaagctgtccctgatggtcgt 3290
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' tcgccagggtcactagcttcaatccgaccttctcggcgctcgctaggaacttcgacagggactaccagca
o
o
o
o
5' catctacctgcctggacagcatggcctgcaacgcgggcatcccgatgccgccggaagcgagaagaatcat 3360
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gtagatggacggacctgtcgtagcggttgcgcccgtagggctacggcggccttcgctcttcttagta
o
o
o
o
5' aatggggaaggccatccagcctcgctcggaacgccagcaagacgtagcccagcgctcgcccgccatg 3430
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ttacccttccggtaggctcgagcgcagcgcttgcggctggttctgcatcgggtcgcgagccggcggtac
o
o
o
o
5' ccggcgataatggcctgcttctcgccgaaacgtttggtggcgggaccagtgacgaaggcttgagcgaggg 3500
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ggccgctattaccggacgaagagcggctttgcaaaccaccgccctggtcactgcttccgaactcgctccc
o
o
o
o
5' cgtgcaagattccgaataaccgcaagcgacaggccgatcatcgctcgctccagcgaaagcggtcctcgcc 3570
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gcacgttctaaggcttatggcgttcgctgtccggctagtagcagcgcgaggtcgctttcgccaggagcgg
o
o
o
o
5' gaaaatgaccagagcgctgccggcacctgtcctacgagttgcatgataaagaagacagtcataagtgcg 3640
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' cttttactgggtctcgcgacggccgtggacaggatgctcaacgtactatttcttctgtcagtattcacgc
o
o
o
o







BGH13_B01b2-pET16-DEST

5' AACAAGTTTGTACAAAAAGCAGGCTctgaaaacttgtacttttcaaggcCAACGCGAACCGCGTTCGTT
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' TTGTTCAAACATGTTTTTTCGTCGAgacttttgaacatgaaagtccgGTTGGCGCTTGGCGCAAGCAA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
attB1 TEV site BGH13_B01b2
BGH13_B01b2-pDONR221
T S L Y K K A G S E N L Y F Q G Q P R T A F V
26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48

5460

BstBI

5' CATTTGTTTGAATGGCAGTGGAAACGATATTGCTAGCGAGTGCGAAAATGTACTGGGGCCAAAAGGCTATG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GTAAACAAGCTTACCGTCACCTTGCTATAACGATCGCTCACGCTTTTACATGACCCCGGTTTTTCCGATAC
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
BGH13_B01b2
BGH13_B01b2-pDONR221
H L F E W Q W N D I A S E C E N V L G P K G Y
49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71

5530

5' CGGCAGTGCAGGTATCCCCACCCCAAAAATCGGTTAGTAGCAGCCAATGGTGGAGTCGTTACCAACCTGT
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' GCCGTCACGTCCATAGGGGTGGGGTTTTTAGCCAATCATCGTCGGTTACCACCTCAGCAATGGTTGGACA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
BGH13_B01b2
BGH13_B01b2-pDONR221
A A V Q V S P P Q K S V S S S Q W W S R Y Q P V
72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95

5600

5' TAGCTATGCCATAGAGGGCCGTTCTGGCAATCGCAACGAATTCGCCAGCATGGTAAGCCGGTGTAAAAAT
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ATCGATACGGTATCTCCCGGCAAGACCGTTAGCGTTGCTTAAGCGGTCGTACCATTTCGGCCACATTTTTTA
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
BGH13_B01b2
BGH13_B01b2-pDONR221
S Y A I E G R S G N R N E F A S M V S R C K N
96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118

5670

SnaBI

5' GCTGGGGTGGATATATACGTAGATGCCGTAATTAATCATATGGCTGCCGGCGGGCGCTATTACCCAGAAG
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' CGACCCACCTATATATGCATCTACGGCATTAAATAGTATACCGACGGCCGCCCGCGATAATGGGTCTTC
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
BGH13_B01b2
BGH13_B01b2-pDONR221
A G V D I Y V D A V I N H M A A G G R Y Y P E
119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141

5740

○
○
5' TGCCTTACTACGCAGAGCATTTTTCACACGTGCTACGGCCAAATTGATTACGGTAACCGCTGGCAGGTACA
○
3' ACGGAATGATGCGTCTCGTAAAAGTGTGCACGATGCCGGTTTAACTAATGCCATTGGCGACCGTCCATGT
○
BGH13_B01b2
○
BGH13_B01b2-pDONR221

5810

○
○
V P Y Y A E H F H T C Y G Q I D Y G N R W Q V Q
○
142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165
○
5' AAAC TGTGACTTGGTAGGGCTAAACGATTTAGCAACAGAACAAGACTATGTACGCACAAAAATAGCCAAT
○
3' TTTGACACTGAACCATCCCGATTTGCTAAATCGTTGTCTTGTTCTGATACATGCGTGTTTTTATCGGTTA
○
BGH13_B01b2
○
BGH13_B01b2-pDONR221

5880

○
○
N C D L V G L N D L A T E Q D Y V R T K I A N
○
166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188
○
5' TACTTAAACGACTTAACTAACCTTGGCGTAGCTGGCTTCCGCTTTGATGCTGCGAAACATATCCCCGTGG
○
3' ATGAATTTGCTGAATTGATTGGAACCGCATCGACCGAAGGCGAAACTACGACGCTTTGTATAGGGGCACC
○
BGH13_B01b2
○
BGH13_B01b2-pDONR221

5950

○
○
Y L N D L T N L G V A G F R F D A A K H I P V
○
189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211
○
5' GTGACATTGCTGCAATTAAAGCAAACTTATTGGCAACCCGTATATATTCCAAGAAGTGATAGGTGCGCC
○
3' CACTGTAACGACGTTAATTTCTGTTTTGAATAACCGTTGGGCATATATAAGGTTCTTCACTATCCACGCGG
○
BGH13_B01b2
○
BGH13_B01b2-pDONR221

6020

○
○
G D I A A I K A K L I G N P Y I F Q E V I G A P
○
212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235
○
5' GGGCGAGCCCATCCAACCATCAGAATATACCTACTTAGCAGACGTAACAGAGTTTAACTTTACCAAATCG
○
3' CCCGCTCGGGTAGGTTGGTAGTCTTATATGGATGAATCGTCTGCATTGTCTCAAATTGAAATGGTTTAGC
○
BGH13_B01b2
○
BGH13_B01b2-pDONR221

6090

○
○
G E P I Q P S E Y T Y L A D V T E F N F T K S
○
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258

5' GTTAGCCATTTTAAAGGGCGCGGACCAATTAAGAGTTAAAAAATATTGGTACTTGGGGCGGTTGGG
 3' CAATCGGTAAAAAATTTCCCGCGCCTGGTTAATTTCTCAATTTTTTATAACCATGAACCCCGCCAACCC
 BGH13_B01b2
 BGH13_B01b2-pDONR221

5' TTGCAAGTGCAGACGCCGTAACCTTTGTTGCCAACCACGATAACCAGCGCCAGGATACAAACAACACCAT
 3' AACGTTACGTCTGCGGCATTGGAAACAACGTTGGTGCTATTGGTCGCGGTCCTATGTTTGTGTGGTA
 BGH13_B01b2
 BGH13_B01b2-pDONR221

V S H F F K G R G P I K E L K N I G T W G G W
 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281

V A S A D A V T F V A N H D N Q R Q D T N N T I
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6230

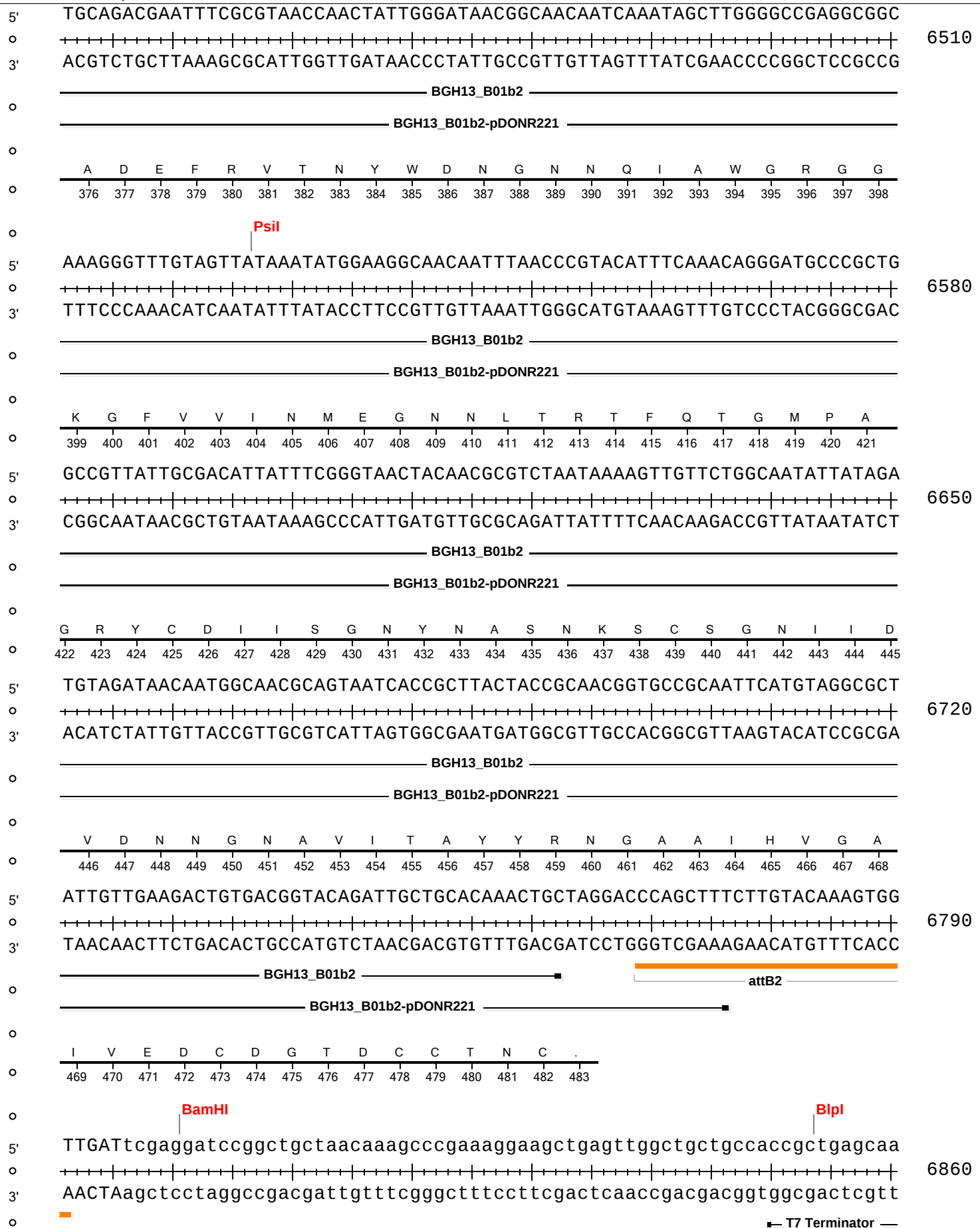
6300

6370

6440

5' TACCCATAAAGATGGTGATAACCGCAATACTATGGCGCACGTATTTATGCTGGGCTGGCCCTATGGGTAC
 3' ATGGGTATTTCTACCACTATTGGCGTTATGATACCGCGTGCATAAATACGACCCGACCGGGATACCCATG
 BGH13_B01b2
 BGH13_B01b2-pDONR221
 T H K D G D N R N T M A H V F M L G W P Y G Y
 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328
 KpnI
 5' CCTAAAGTAATGTCTAGTTATGAGTGGTACGATCACGACCAAGGCCCTCCCGCCACGGTGCTAGCAGCT
 3' GGATTTCAATTACAGATCAATACTCACCATGCTAGTGCTGGTTCCGGGAGGGCGGGTGCCACGATCGTCGA
 BGH13_B01b2
 BGH13_B01b2-pDONR221
 P K V M S S Y E W Y D H D Q G P P A H G A S S
 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351
 5' GTAACAGCGGCTGGTTATGTGAACACCGCACGCCAGCTATCGCCAATATGGTTGCTTTTCGCAATTTAC
 3' CATTGTCGCCGACCAATACACTTGTGGCGTGCGGTTCGATAGCGTTATACCAACGAAAAGCGTTAAAGTG
 BGH13_B01b2
 BGH13_B01b2-pDONR221
 C N S G W L C E H R T P A I A N M V A F R N F T
 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375

BGH13_B01b2-pET16-DEST



5' taactagcataaaccccttggggcctctaaacgggtcttgaggggttttttgcgtgaaaggaggaactatat 6930
 3' attgatcgtattggggaaccccgagatttggccagaactccccaaaaacgactttcctccttgatata
 T7 Terminator
 5' ccggatatcccgaagaggcccggcagtaccggcataaccaagcctatgcctacagcatccaggggtgacg 7000
 3' ggcctatagggcgttctccggggccgtcatggccgtattggttcggatacggatgtcgtagggtccactgc
 5' gtgccgaggatgacgatgagcgcattgttagatttcatacacggtgcctgactgcgttagcaatttaact 7070
 3' cacggctcctactgctactcgcgtaacaatctaaagtatgtgccacggactgacgcaatcgtaaattga
 HindIII Clal
 5' gtgataaactaccgcattaaagcttatcgatgataagctgtcaaacatgagaa 7123
 3' cactatttgatggcgtaatttcgaatagctactattcgacagtttgtaactctt