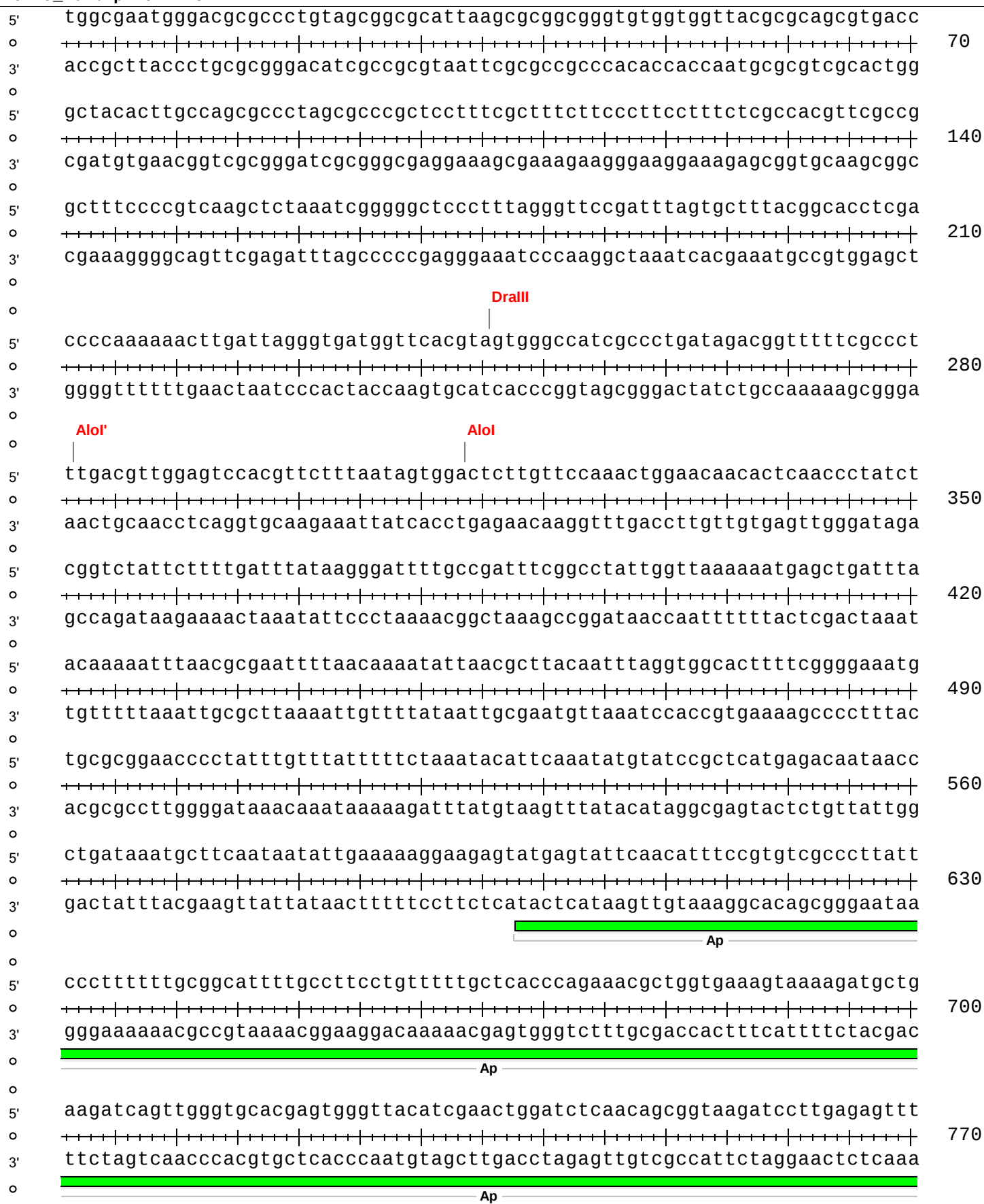
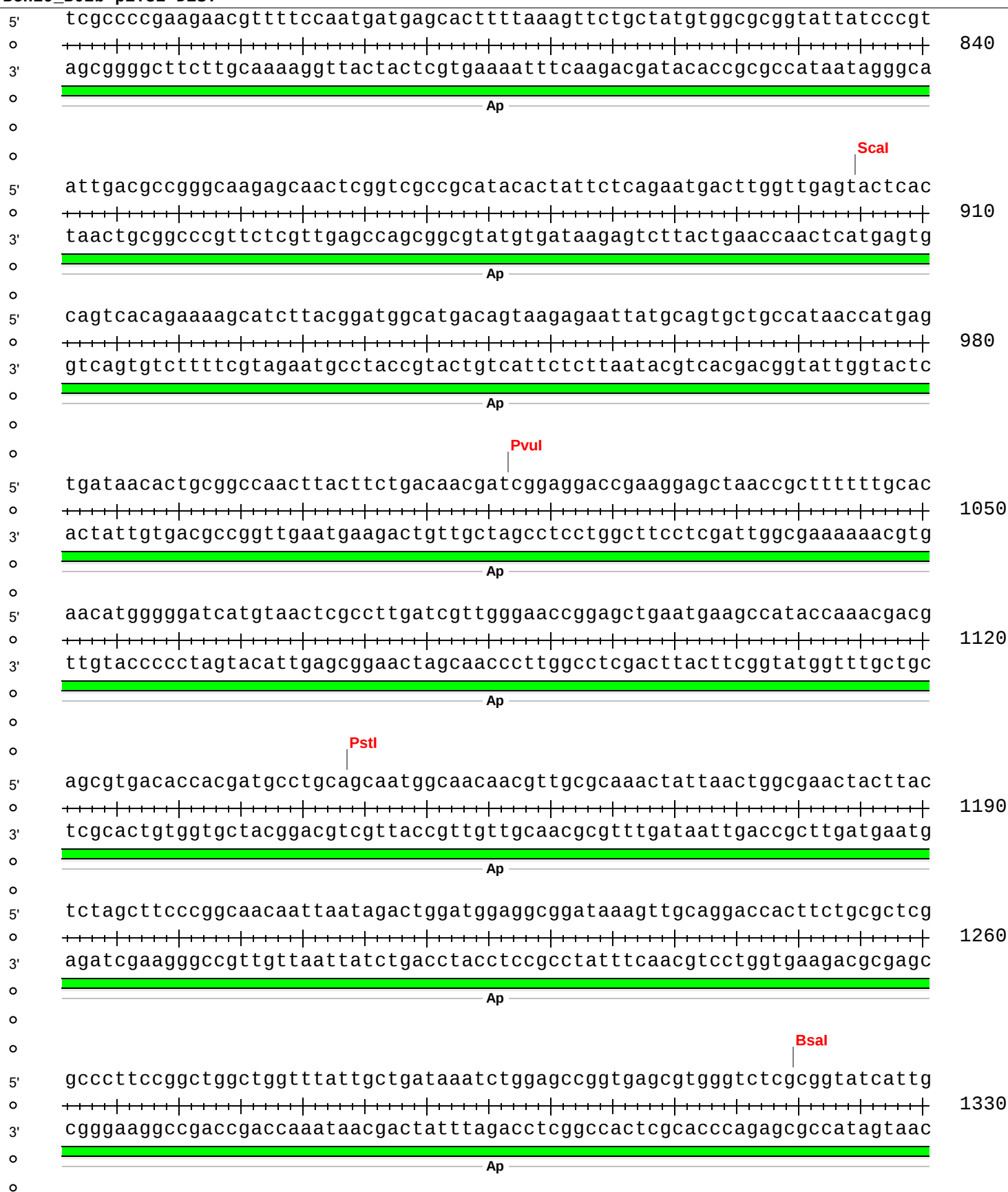
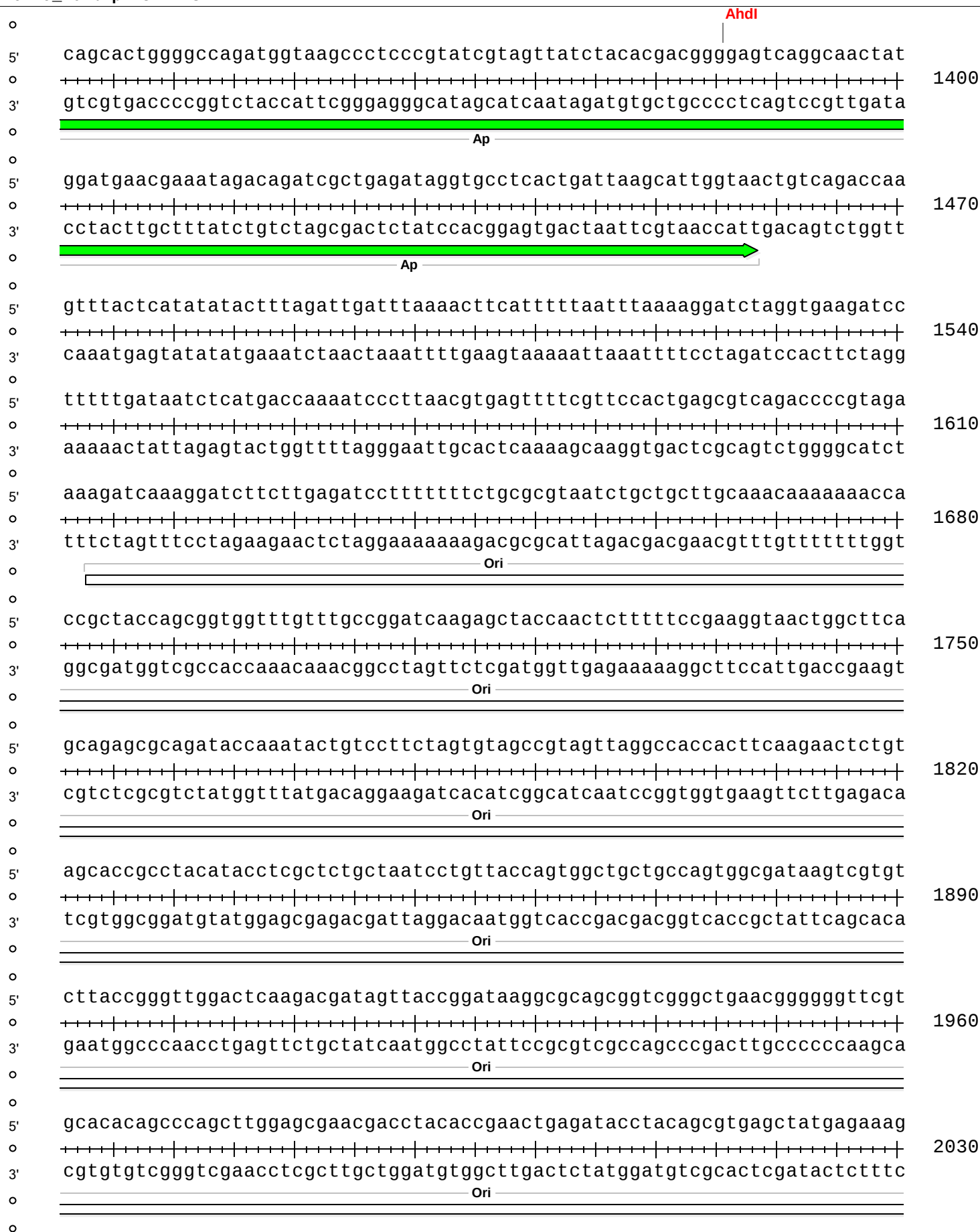


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BGH29_B02b-pET32-DEST





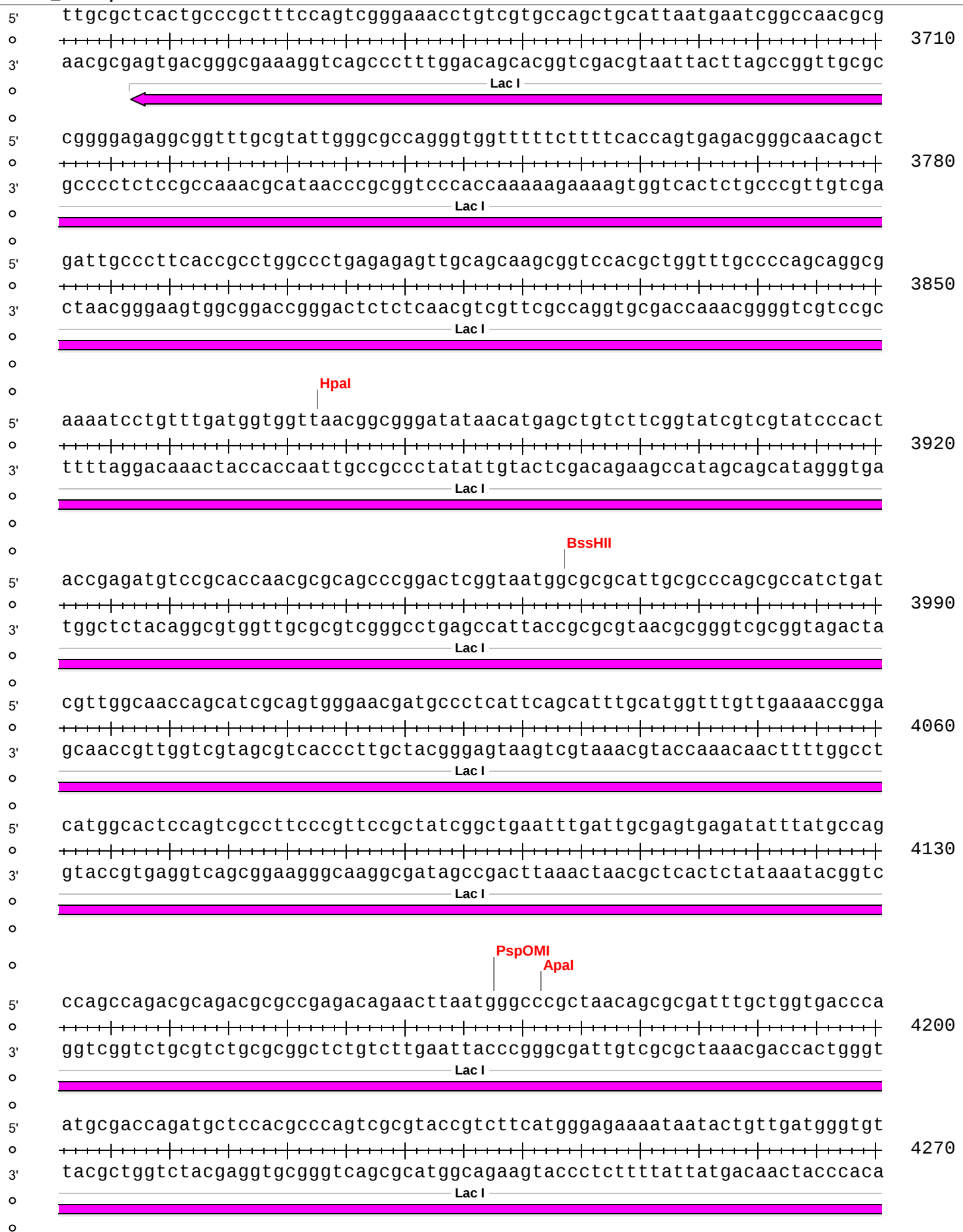
5' cgccacgcttcccgaagggagaaaaggcggacaggtatccggtaagcggcaggggtcggaacaggagagcgc
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gcggtgcaagggcttccctctttccgcctgtccataggccattcgccgtcccagccttgctctctcgcg
Ori
5' acgagggagcttccaggggaaacgcctggtatctttatagtcctgtcgggtttcgccacctctgacttg
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' tgctccctcgaagggtccccctttgcggaaccatagaaatatcaggacagccaaagcgggtggagactgaac
Ori
5' agcgtcgatttttgtgatgctcgtcagggggcggagcctatggaaaaacgccagcaacgcggccttttt
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' tcgcagctaaaaacactacgagcagtcccccgcctcggatacctttttgcggtcgttgcgccggaaaaa
Ori
5' acggttcctggccttttgctggccttttgctcacatgttctttcctgcgttatcccctgattctgtggat
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' tgccaaggaccggaacgaccggaacgagtgtaagaaggacgcaataggggactaagacaccta
5' aaccgtattaccgcctttgagtgagctgataccgctcgccgcagccgaacgaccgagcgcagcagtgag
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' ttggcataatggcggaactcactcgactatggcgagcggcgctcggcttgctggctcgctcgctcagtc
5' tgagcgaggaagcgggaagagcgctgatgcggtattttctccttacgcacatctgtgcggtatttcacaccg
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' actcgctccttcgccttctcgcggactacgccataaaagaggaatgcgtagacacgccataaagtgtggc
SapI
5' catatatggtgcactctcagtacaatctgctctgatgccgcatagttaagccagttacactccgctatc
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gtatataccacgtgagagtcattgtagacgagactacggcgatcaattcggtcatatgtgaggcgatag
BstZ17I
5' gctacgtgactgggtcatggctgcgccccgacaccgccaacaccgctgacgcgccctgacgggcttgt
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' cgatgcactgaccagtagcagcggggctgtgggcgggttggtgggcgactgcgcgggactgccgaaca
Tth111I
5' ctgctcccggcatccgcttacagacaagctgtgaccgtctccgggagctgcatgtgtcagagggttttac
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gacgagggccgtaggcgaatgtctgttcgacactggcagaggccctcgacgtacacagtcctccaaaagt
5' cgtcatcaccgaaacgcgcgaggcagctgcggtaaagctcatcagcgtggcgtgaagcgattcacagat
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' gcagtagtggttttgcgcgtccgtcgacgccatttcgagtagtcgcaccagcacttcgctaagtgtcta
5' gtctgcctgttcatccgcgtccagctcgttgagtttctccagaagcggttaatgtctggcttctgataaag
+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
3' cagacggacaagtaggcgcaggtcgagcaactcaaagaggtcttcgcaattacagaccgaagactatttc

Bpu10I

FspAI

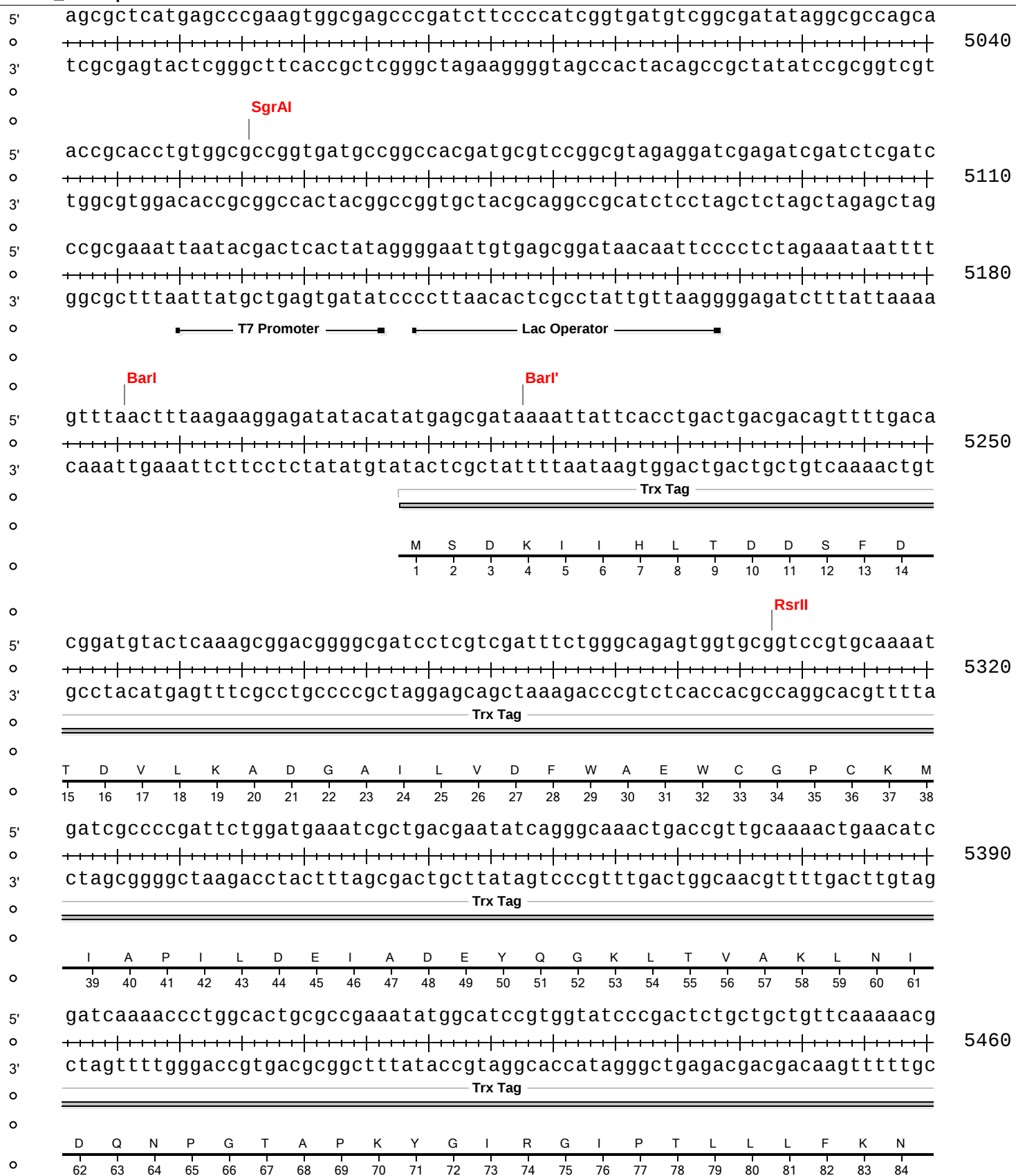
PshAI

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[illegible]

BGH29_B02b-pET32-DEST



5530

5' ggatgaaagaaaccgctgctgctaaattcgaacgccagcacatggacagcccagatctgggtaccgacg 5670

3' ccatactttctttggcgacgacgatttaagcttgcggtcgtgtacctgtcgggtctagacccatggctgc

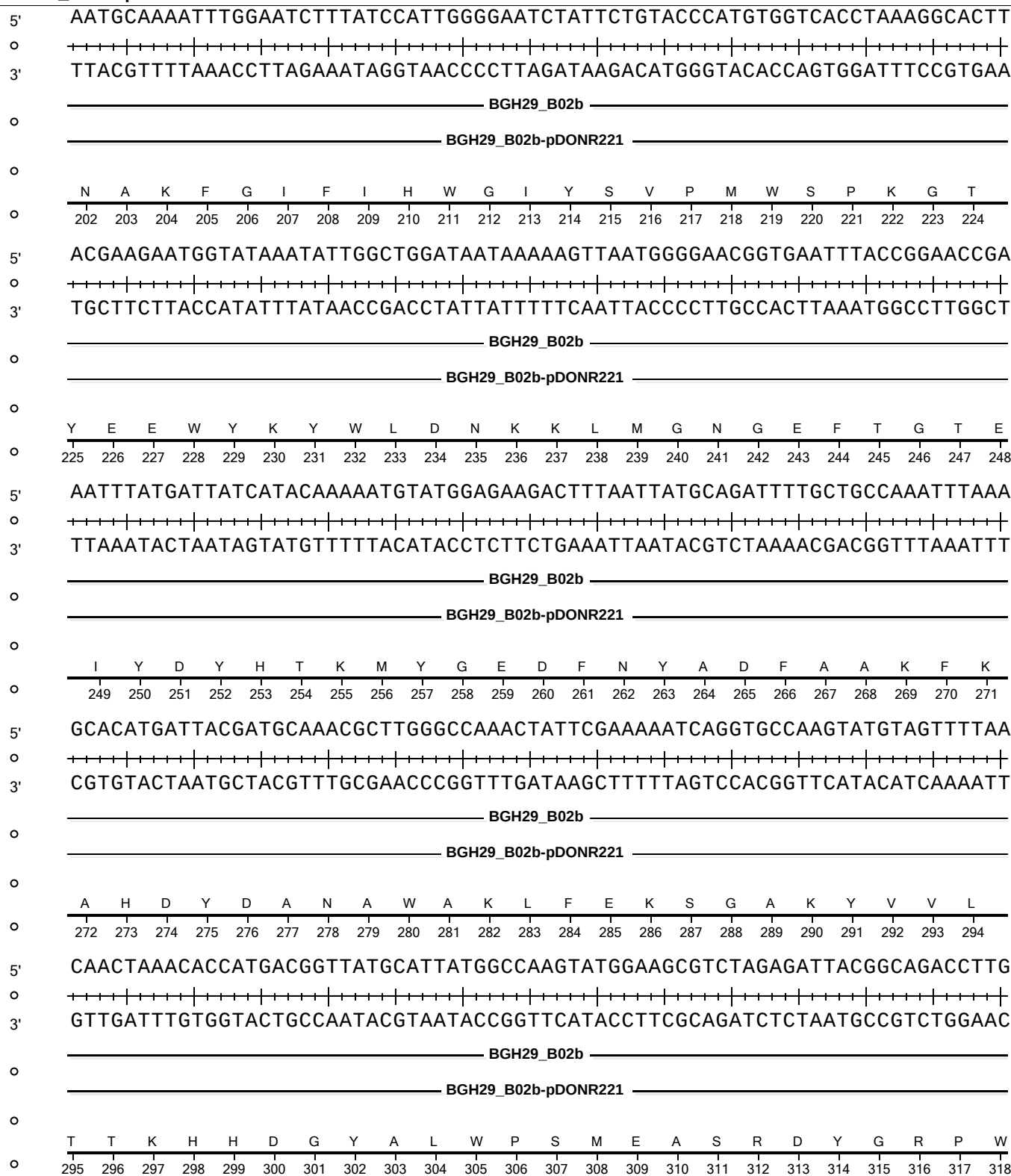
En...e

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

Genomic map of the BGH29_B02b gene region. The top track shows the DNA sequence from position 155 to 178, with amino acid codes (D, D, D, K, A, M, A, I, S, T, S, L, Y, K, A, G, S, E, N, L, Y, F, Q) above. The sequence is 5'-aggcCAAACAATATCTACCAACCAACATGGAATCGCTCGATACTCGCCCTACCCCTGCATGGTTCAA-3'. Below the sequence is a red arrow pointing right, labeled 'T...', indicating a transcription start site. The gene is labeled 'BGH29_B02b' and the promoter is labeled 'BGH29_B02b-pDONR221'. The bottom track shows the DNA sequence from position 179 to 201, with amino acid codes (G, Q, N, N, I, Y, Q, P, T, W, E, S, L, D, T, R, P, T, P, A, W, F, K) above. The sequence is 5'-GTCGCTCGATACTCGCCCTACCCCTGCATGGTTCAA-3'.

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5880

5950

6020

6090

6160

5' GAACAGTATGGAAATAGGTCCTAAACGCGATTGGTGAATATACCACAGCTCTTAGAAAAACAGAC
 3' CTTGTCATACCTTTATCCAGGATTTGCGCTAAACCATCCACTTATATGGTGTGCGAGAATCTTTTTGTCTG
 BGH29_B02b
 BGH29_B02b-pDONR221
 N S M E I G P K R D L V G E Y T T A L R K T D
 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341
 5' ATTAAGGTGGGATTCTACATTTTCATGCAGAGAATGGGGAAGTCCGTTATATTGCCCGGAGTTACTTAATA
 3' TAATTCCACCCTAAGATGTAAAGTACGTCTCTTACCCCTTCAGGCAATATAACGGGCCTCAATGAATTAT
 BGH29_B02b
 BGH29_B02b-pDONR221
 I K V G F Y I S C R E W G S P L Y C P E L L N
 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364
 5' TATATGTATCCCGTCATTTTATACCGCAAGTTAAAGATCTGGTAAATCGGTATGAACCCGATATTCTTTG
 3' ATATACATAGGGCAGTAAATATGGCGTTCAATTTCTAGACCATTTAGCCATACTTGGGCTATAAGAAAC
 BGH29_B02b
 BGH29_B02b-pDONR221
 I Y V S R H F I P Q V K D L V N R Y E P D I L W
 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' GTCAGACGGTCCCGATAATTACAGTGACTCTATTTGGCAAACAAAAAACTTTTCCAATGGCTCTATTCT
 3' CAGTCTGCCAGGGCTATTAATGTCAGTGAATAAACCGTTTGTTTTTTTGAAAAGGTTACCGAGATAAGA
 BGH29_B02b
 BGH29_B02b-pDONR221
 S D G P D N Y S D S I W Q T K K L F Q W L Y S
 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411
 5' GAATCCCCAGTAAAGAACAAAATTGTACTGAATGACAGATGGGCAAAATTTACTGATGGGAAAAAGCATG
 3' CTTAGGGGTCATTTCTTGTTTTAACATGACTTACTGTCTACCGTTTTTAAATGACTACCTTTTTTCGTAC
 BGH29_B02b
 BGH29_B02b-pDONR221
 E S P V K N K I V L N D R W A K F T D G K K H
 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434

BGH29_B02b-pET32-DEST

5' GCGATTATTACACCCGTGAATATAGCAATCGCAATATGCCAGAGGATAAACCTTGGGAAGAATGTCGTGG
 3' CGCTAATAATGTGGGCACTTATATCGTTAGCGTTATACGGTCTCCTATTTGGAACCCTTCTTACAGCACC

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

6580

G D Y Y T R E Y S N R N M P E D K P W E E C R 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

5' CATGGGATTCTCTTTCTCTTATAATCAAAATGAAGATATAGAAGATTATTCCAGCCCACAAGGATTAATA
 3' GTACCCCTAAGAGAAAGAGAATATTAGTTTTACTTCTATATCTTCTAATAAGGTCGGGTGTTCTTAATTAT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

M G F S F S Y N Q N E D I E D Y S S P Q G L I
 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481

6650

Ajul Ajul'

5' CTTACCTTAGTTAATATTGTAAGCAAAGGTGGGAACCTTACTCTTGGGCATAGGTCCGAATGGAAATGGCA
 3' GAATGGAATCAATTATAACATTCGTTTCCACCCTTGAATGAGAACCCGTATCCAGGCTTACCTTTACCGT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

6720

L T L V N I V S K G G N L L L G I G P N G N G
 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504

5' AAATTCCCCCTATCATGCAGGAACGCTTATTGCAAATGGGAGAATGGCTAAAAGTAAATGGAGAAGCAAT
 3' TTTAAGGGGGATAGTACGTCCTTGCGAATAACGTTTACCCTCTTACCGATTTTCATTTACCTCTTCGTTA

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

6790

K I P P I M Q E R L L Q M G E W L K V N G E A I
 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' CTATGATACTTACAAATGGAACAATCTGAACAATGGTCTGAAGGTGACAGAAATTGGAAAGATAAAGGA
 3' GATACTATGAATGTTTACCTTTGTTAGACTTGTTACCAGACTTCCACTGTCTTTAACCTTTCTATTTCT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

6860

Y D T Y K W K Q S E Q W S E G D R N W K D K G
 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551

BGH29_B02b-pET32-DEST

