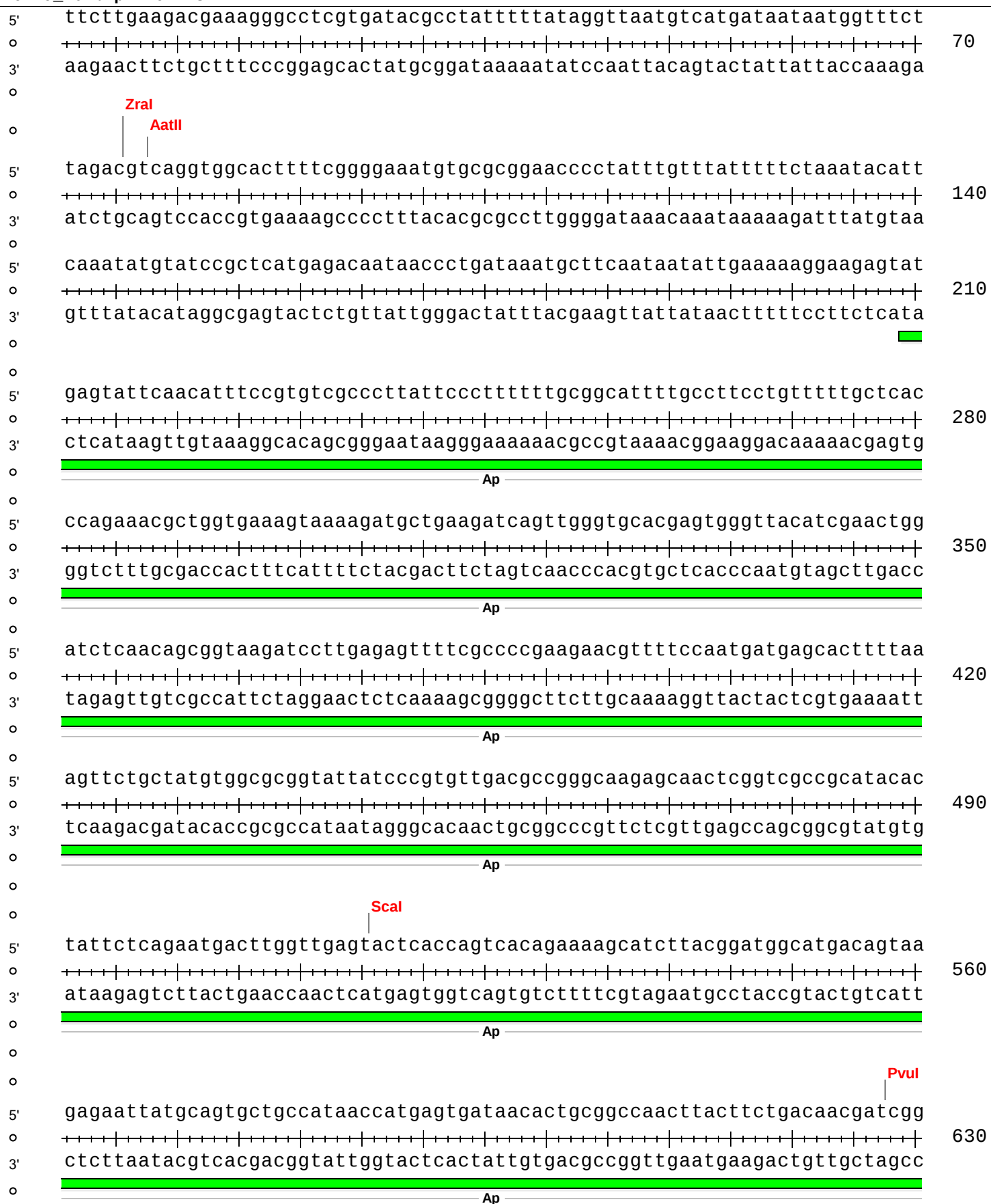


BGH29_B02b-pET16-DEST



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 Ori

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 Ori

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 Ori

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 Ori

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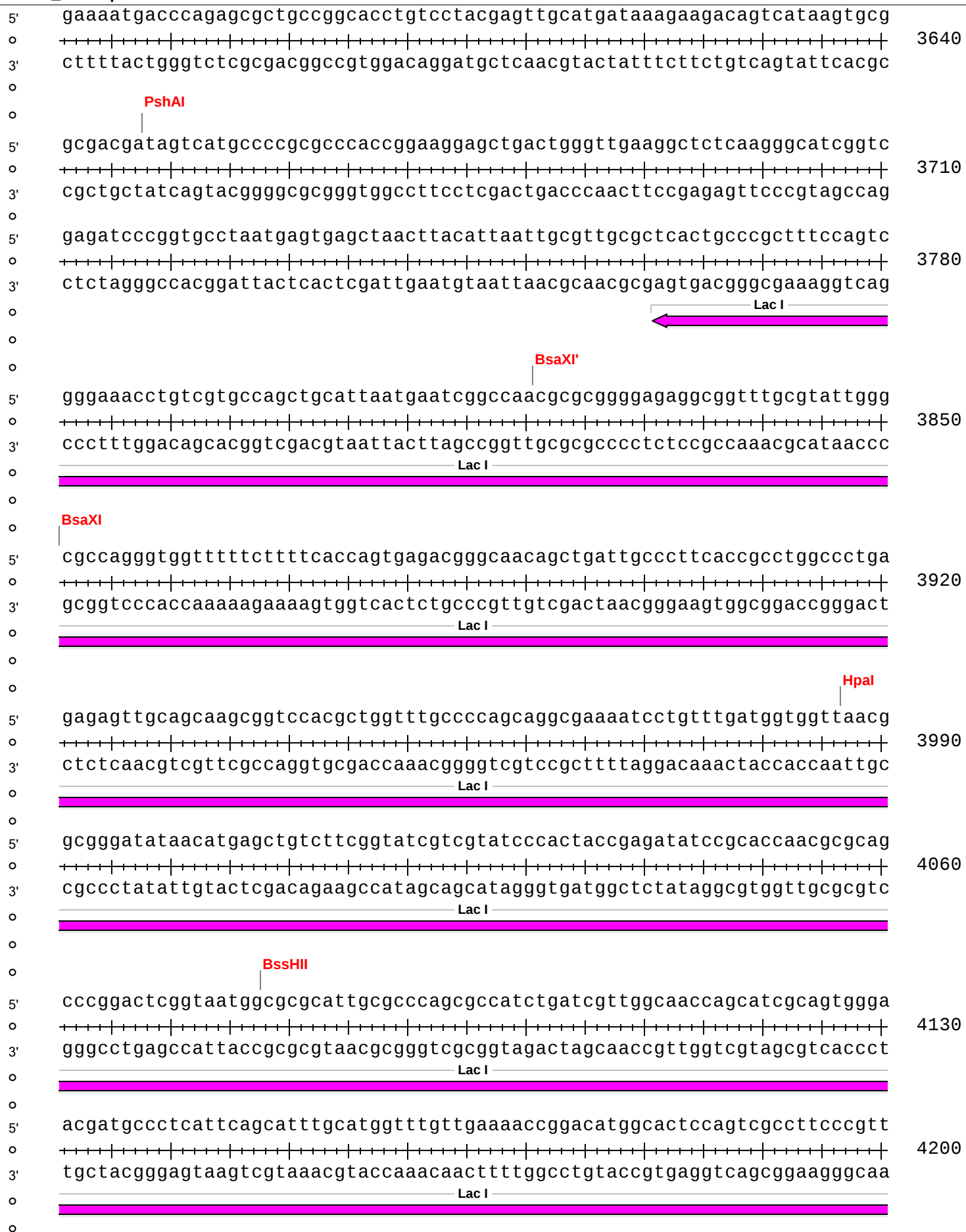
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 Ori -----> Pcil

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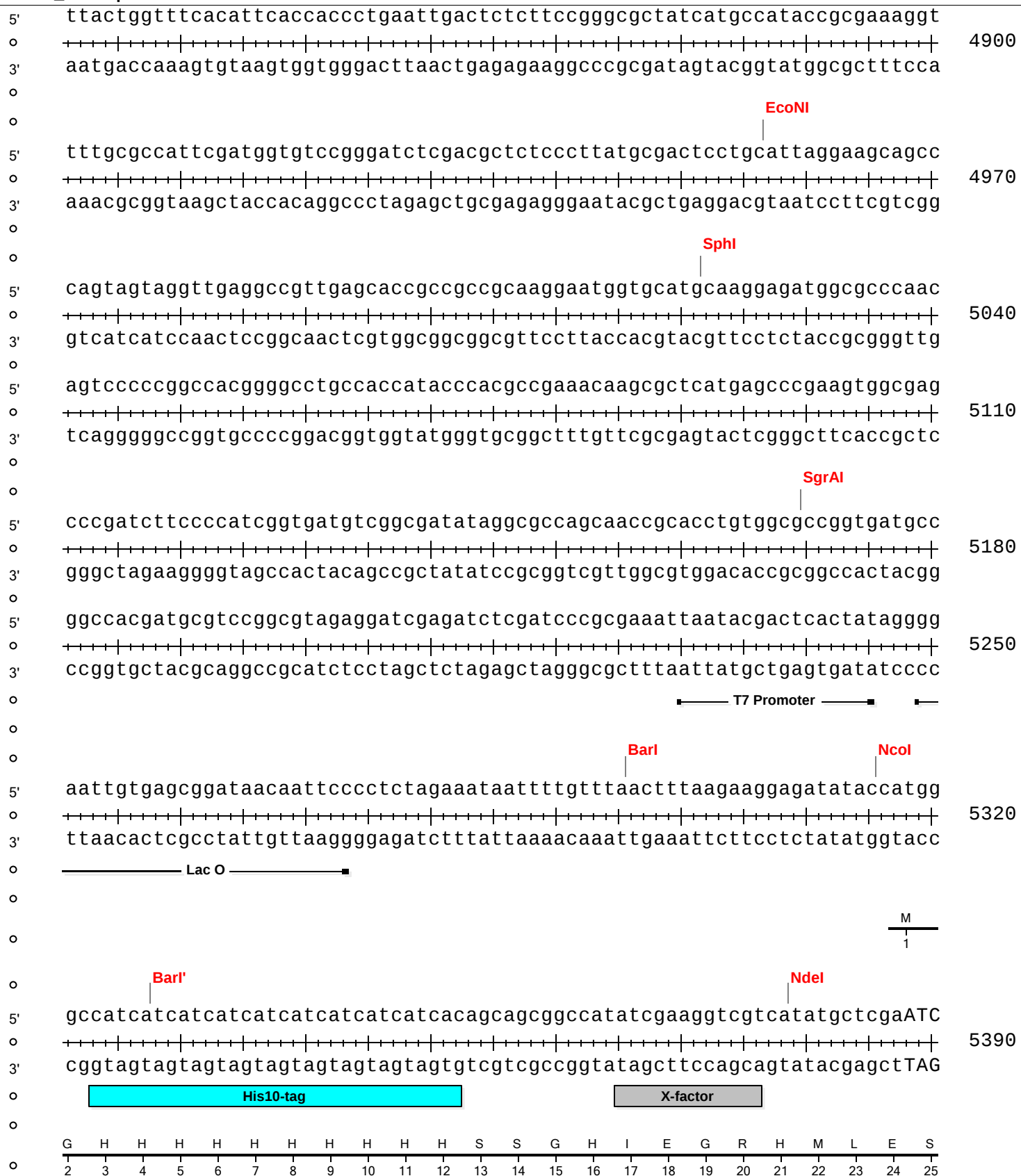
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[illegible]

BGH29_B02b-pET16-DEST



5460

5530

5600

5670

5740

○

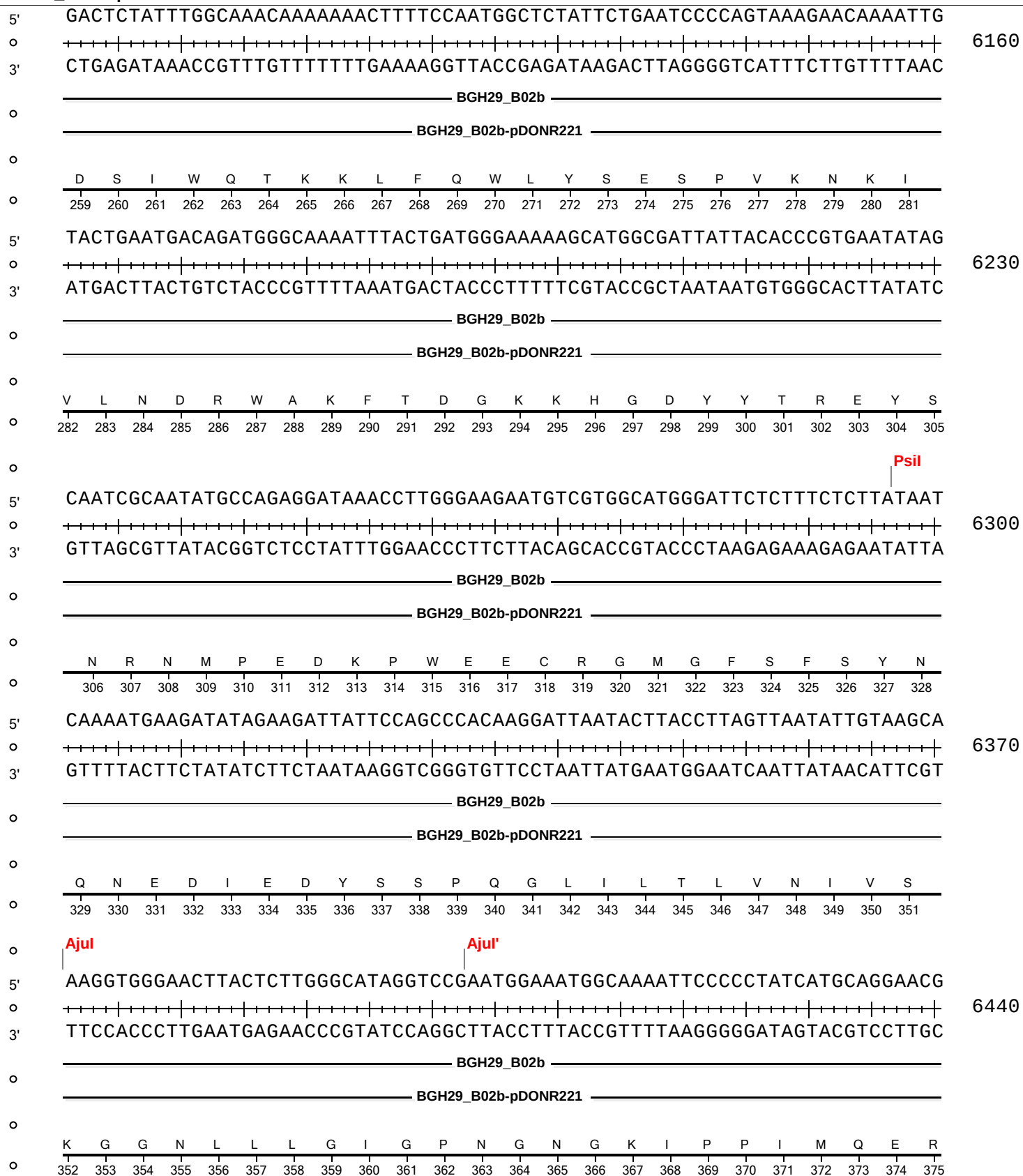
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BstBI

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

BGH29_B02b-pET16-DEST



5' CTTATTGCAAATGGGAGAATGGCTAAAAGTAAATGGAGAACAATCTATGATACTTACAAATGGAAACAA
+ + + + +
3' GAATAACGTTTACCCTCTTACCGATTTTCATTTACCTCTTCGTTAGATACTATGAATGTTTACCTTTGTT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

L L Q M G E W L K V N G E A I Y D T Y K W K Q
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5' TCTGAACAATGGTCTGAAGGTGACAGAAATTGGAAAGATAAAGGAAAACATTATGTAGGAGGAAACTCTA
+ + + + +
3' AGACTTGTTACCAGACTTCCACTGTCTTTAACCTTTCTATTTCTTTTGTAAATACATCCTCCTTTGAGAT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

S E Q W S E G D R N W K D K G K H Y V G G N S
399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421

5' TTTTAAAACAAACAGTAGATCCCGATCCCGGCTTTGCCGTAAAAGAAGCCTTTTTTACAGCTAAAAATAA
+ + + + +
3' AAAATTTTGTGTTGTCATCTAGGGCTAGGGCCGAAACGGCATTCTTTCGAAAAAGTGTCGATTTTATT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

I L K Q T V D P D P G F A V K E A F F T A K N N
422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445

5' TGCAGTATATGCCATTCTGCCTAAATTTCCGGAAAATCAAGTCATACTGAAAGACATTAGAACAAGTTCC
+ + + + +
3' ACGTCATATACGGTAAGACGGATTTAAAGGCCTTTTAGTTCAGTATGACTTTCTGTAATCTTGTTCAAGG

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

A V Y A I L P K F P E N Q V I L K D I R T S S
446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468

5' AAAACAAAAATAACTTTATTAGGATATGACAAAACATTGAAATGGAAACAGAATGGAAATAATATAGTAA
+ + + + +
3' TTTTGTTTTTATTGAAATAATCCTATACTGTTTTGTAACCTTTACCTTTGTCTTACCTTTATTATATCATT

————— BGH29_B02b —————

————— BGH29_B02b-pDONR221 —————

K T K I T L L G Y D K T L K W K Q N G N N I V
469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491

5' TAGAAATTCCCACTATTTCCTTACAGCAAAGTTCCTTGTCTAGTATGCATGGACACTTAAATTAGAATATGT
○
3' ATCTTTAAGGGTGATAAGGAATGTCGTTTCAAGGAACAGTCATACGTACCTGTGAATTTAATCTTATACA
○
○
○
○
I E I P T I P Y S K V P C Q Y A W T L K L E Y V
○
492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515

5' TGAATAGGACCCAGCTTTCTTGTACAAAGTGGTTGATtcgaggatccggctgctaacaagcccgaaagg 6930
 3' ACTTATCCTGGGTCGAAAGAACATGTTTCACCAACTAagctcctaggccgacgattgtttcgggctttcc



Diagram of the T7 promoter region. The top strand (5' to 3') is aagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtctt. The bottom strand (3' to 5') is ttcgactcaaccgacgacggtggcgactcgttattgatcgtattggggaaccccgagatttgcccagaa. A red 'BlpI' restriction site is indicated above the top strand at the sequence 'gagcaata'. A 'T7 Terminator' is indicated below the bottom strand at the sequence 'ggggaaccccgag'. A scale bar on the right indicates 7000 base pairs.

5' gaggggttttttgcTgaaaggaggaactatatccggatatcccgaagaggcccggcagtaccggcataa 7070
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 3' ctcccaaaaaacgacttttcctccttgatataggcctatagggcgttctccgggcccgtcatggccgtatt
 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
 T7 Terminator

5' ccaagcctatgcctacagcatccagggtgacggtgccgaggatgacgatgagcgcattgttagatttcatt
 ++++++
 3' ggttcggatacggatgtcgtagggtccactgccacggctcctactgctactcgcgtaacaatctaaagta

5' acacggtgcctgactgcgtagcaatttaactgtgataaactaccgcattaaagcttatcgatgataagc
 HindIII Clal
 3' tgtgccacggactgacgcaatcgttaaattgacactatgtgatggcgtaatttcgaatagctactattcg

5' tgtcaaacatgagaa
 EcoRI
 3' acagtttgtactctt