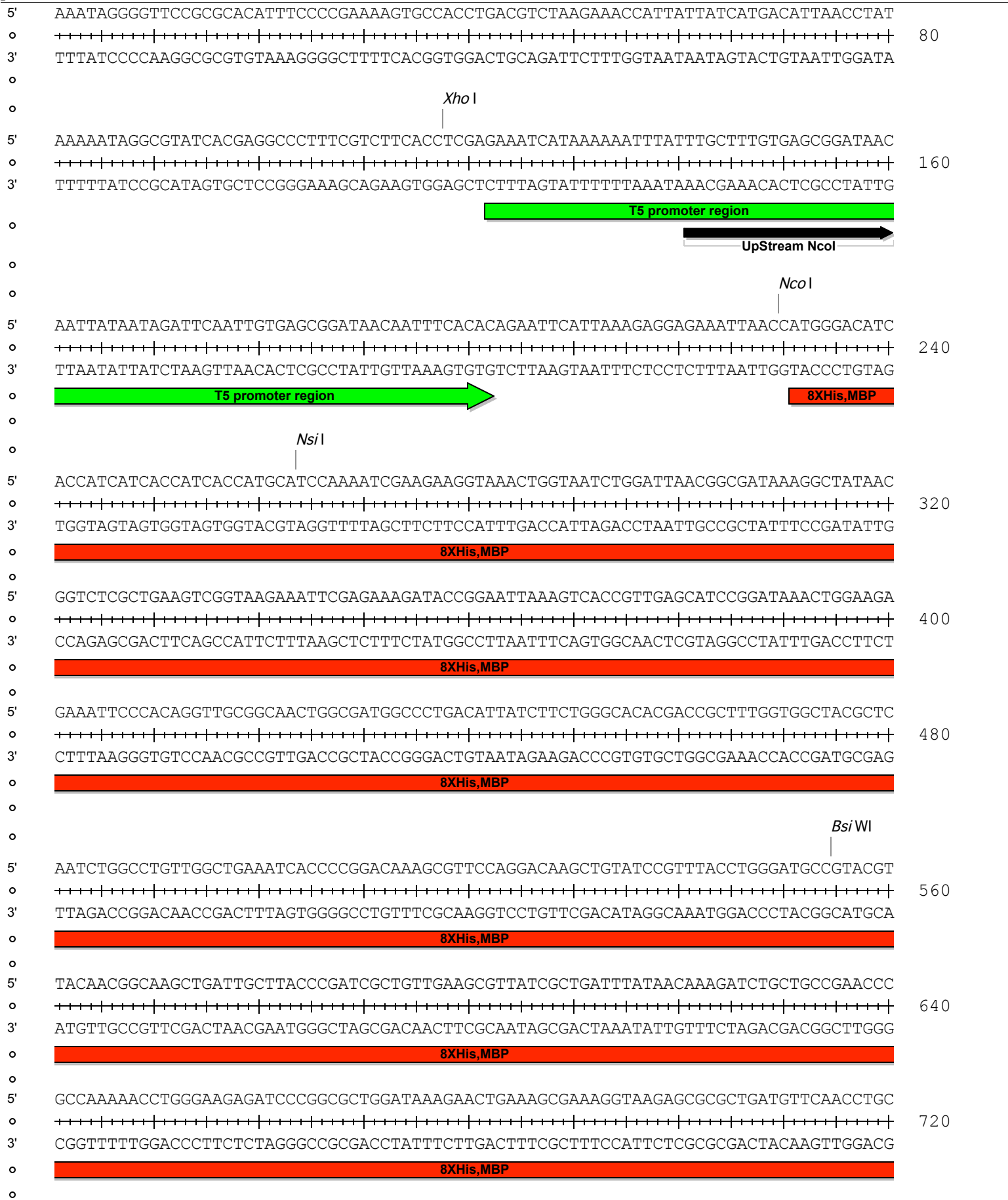
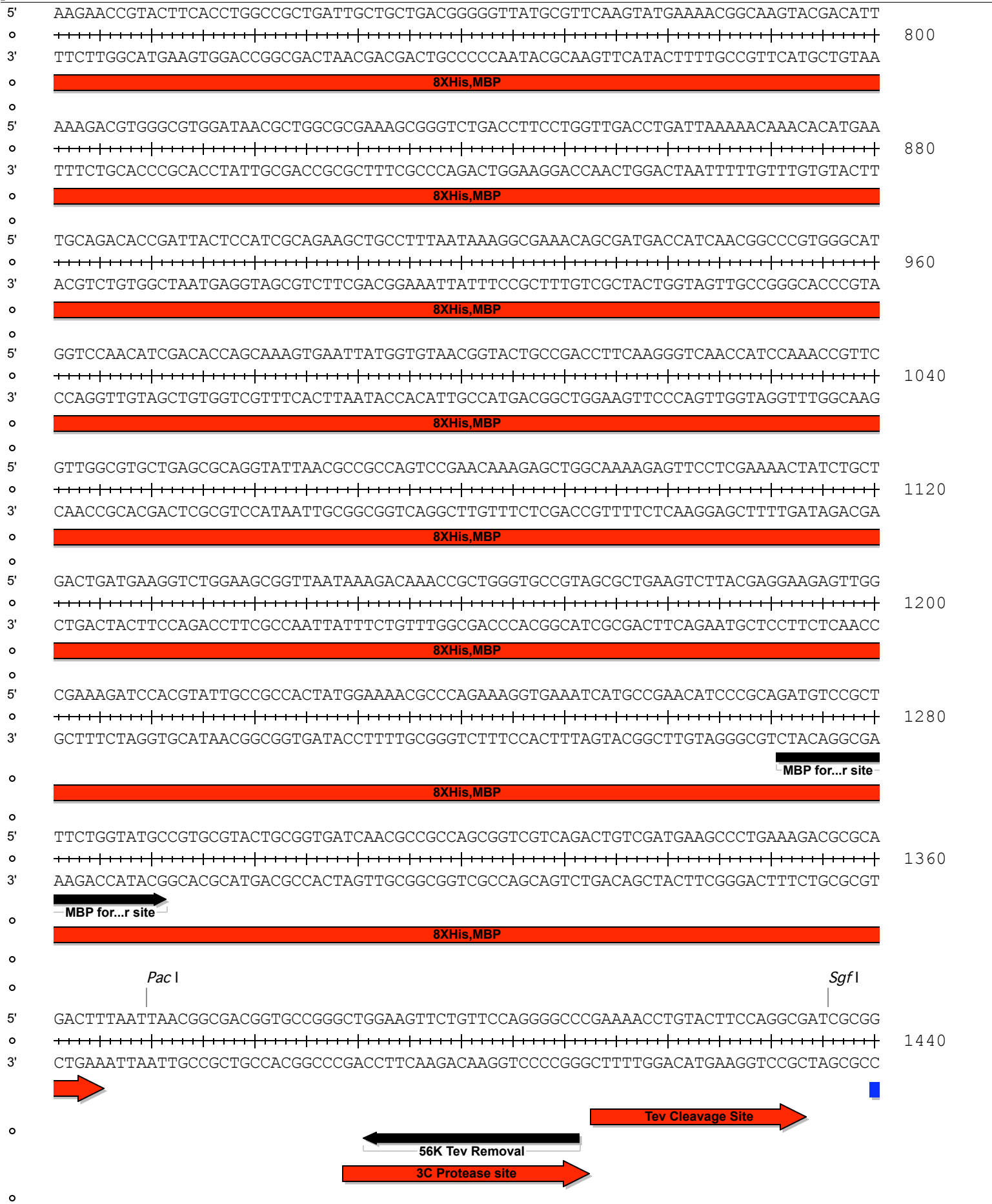


pVP56K





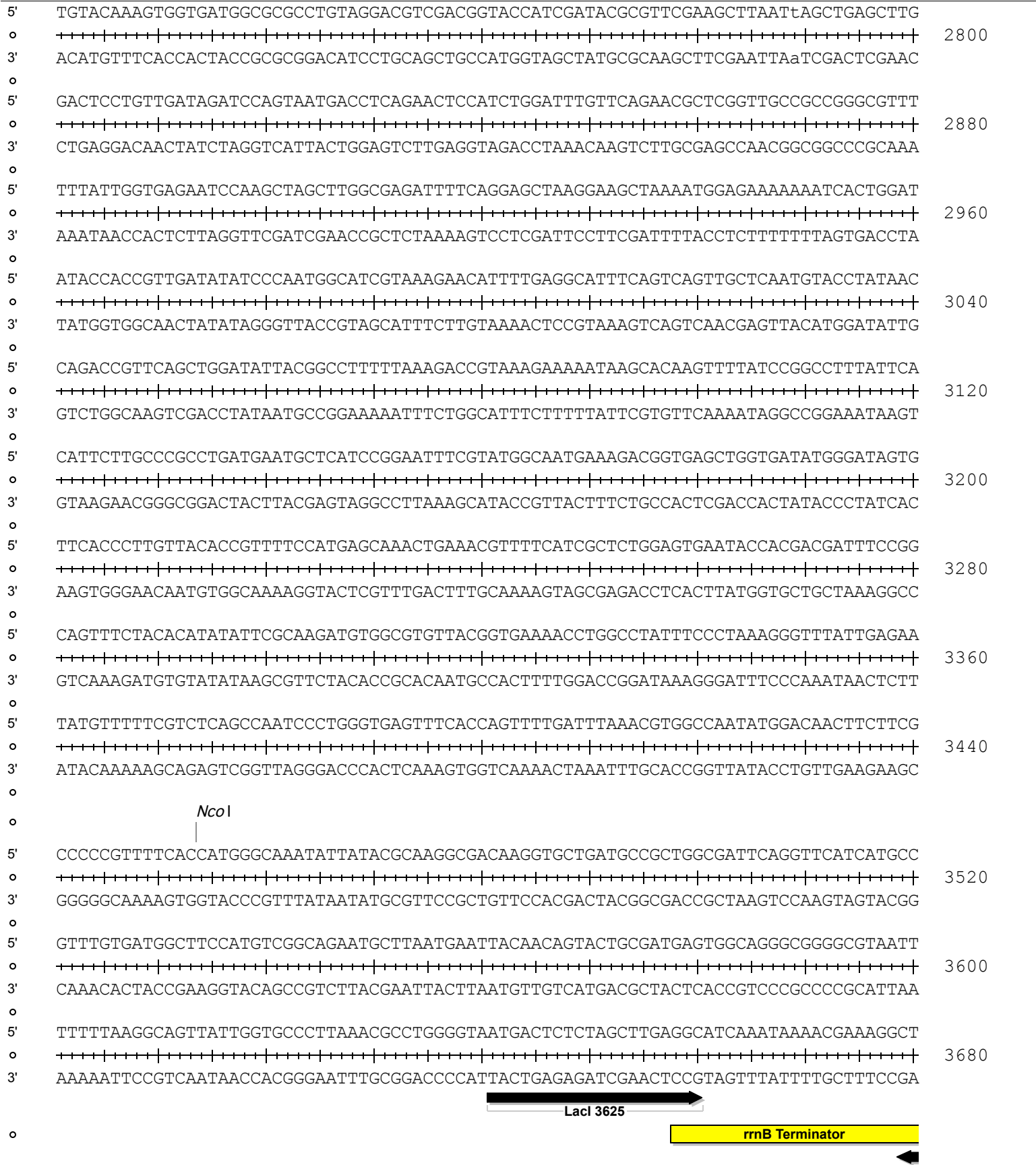
Genomic map of the BarCat locus on chromosome 1. The map shows the BarCat cassette (blue line) and the Barnase gene (red line). The BarCat cassette is divided into three regions: BarCat Mid Forward (black arrow), BarCat Mid Reverse (black arrow), and BarCat Mid Forward (black arrow). The Barnase gene is flanked by two BarCat cassettes. The map includes DNA sequence coordinates (5' to 3') and a scale bar (0 to 2080).

Sequence coordinates (5' to 3'):

- 1520: CCGCGTTGGAATAAGTAAAGGAATCACATGGCAGGTTTATCAACACGTTTGACGGGGTTGCGGATTATCTTCAGACATA
- 1600: TCATAAGCTACCTGATAATTACATTACAAAATCAGAAGCACAGCCCTCGGCTGGGTGGCATCAAAAGGGAACCTTGCAG
- 1680: ACGTCGCTCCGGGGAAAAGCATCGGCGGAGACATCTTCTCAAACAGGGAAGGCAAACTCCCGGGCAAAAAGCGGACGAACA
- 1760: TGGCGTGAAGCGGATATTAAC TATACATCAGGCTTCAGAAATTCAGACCGGATTCTTTACTCAAGCGACTGGCTGATTTA
- 1840: CAAAACAACGGACCATTATCAGACCTTTACAAAAATCAGATAAATTAGGCACCCAGGCTTTACACTTTATGCTTTTCGGCT
- 1920: CGTATAATGTGTGGATTTTGAGTTAGGATCCGTCGAGATTTTCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAAAATCACT
- 2000: GGATATAACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTA
- 2080: TAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTA

5' TTCACATTTCTTGCCCGCCTGATGAATGCTCATCCGGAATTCCTGTGGCAATGAAAGACGGTGAGCTGGTGATATGGGAT  
 2160  
 3' AAGTGTAAAGAACGGGCGGACTACTTACGAGTAGGCCTTAAGGCATACCGTTACTTTCTGCCACTCGACCACTATACCCTA  
 BarCat Cassette  
 CAT  
 5' AGTGTTCACCCCTTGTTACACCGTTTTCCATGAGCAAACCTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTT  
 2240  
 3' TCACAAGTGGGAACAATGTGGCAAAAGGTACTCGTTTTGACTTTGCAAAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAA  
 BarCat Cassette  
 CAT  
 5' CCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTG  
 2320  
 3' GGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAATGCCACTTTTGGACCGGATAAAGGGATTTCCTCAAATAAC  
 BarCat Cassette  
 CAT  
 5' AGAATATGTTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACCTTC  
 2400  
 3' TCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAACTAAATTTGCACCGGTTATACCTGTTGAAG  
 BarCat Cassette  
 CAT  
 5' TTCGCCCCCGTTTTTCACGATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCA  
 2480  
 3' AAGCGGGGGCAAAGTGCTACCCGTTTATAATATGCGTTCCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGT  
 BarCat Cassette  
 CAT  
 5' TGCCGTTTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGT  
 2560  
 3' ACGGCAAACACTACCGAAGGTACAGCCGCTTACGAATTACTTAATGTTGTCATGACGCTACTCACCGTCCCGCCCCGCA  
 BarCat Cassette  
 CAT  
 Pme I Xba I  
 5' AATGTTTAAACGAATTCGAGCTCGGTACCCGGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTGATCCGGCTGCTA  
 2640  
 3' TTACAAATTTGCTTAAGCTCGAGCCATGGGCCCCCTAGGAGATCTCAGCTGGACGTCCGTACGTTTCGACTAGGCCGACGAT  
 Ba...e  
 PmeI Forward  
 T7 terminator reverse  
 pF1K Homology  
 5' ACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCAAACCTCGTTTCTCGTTCAGCTTTCT  
 2720  
 3' TGTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTATTGATCGTTTGAGCAAAGAGCAAGTCGAAAGA  
 pF1K Homology

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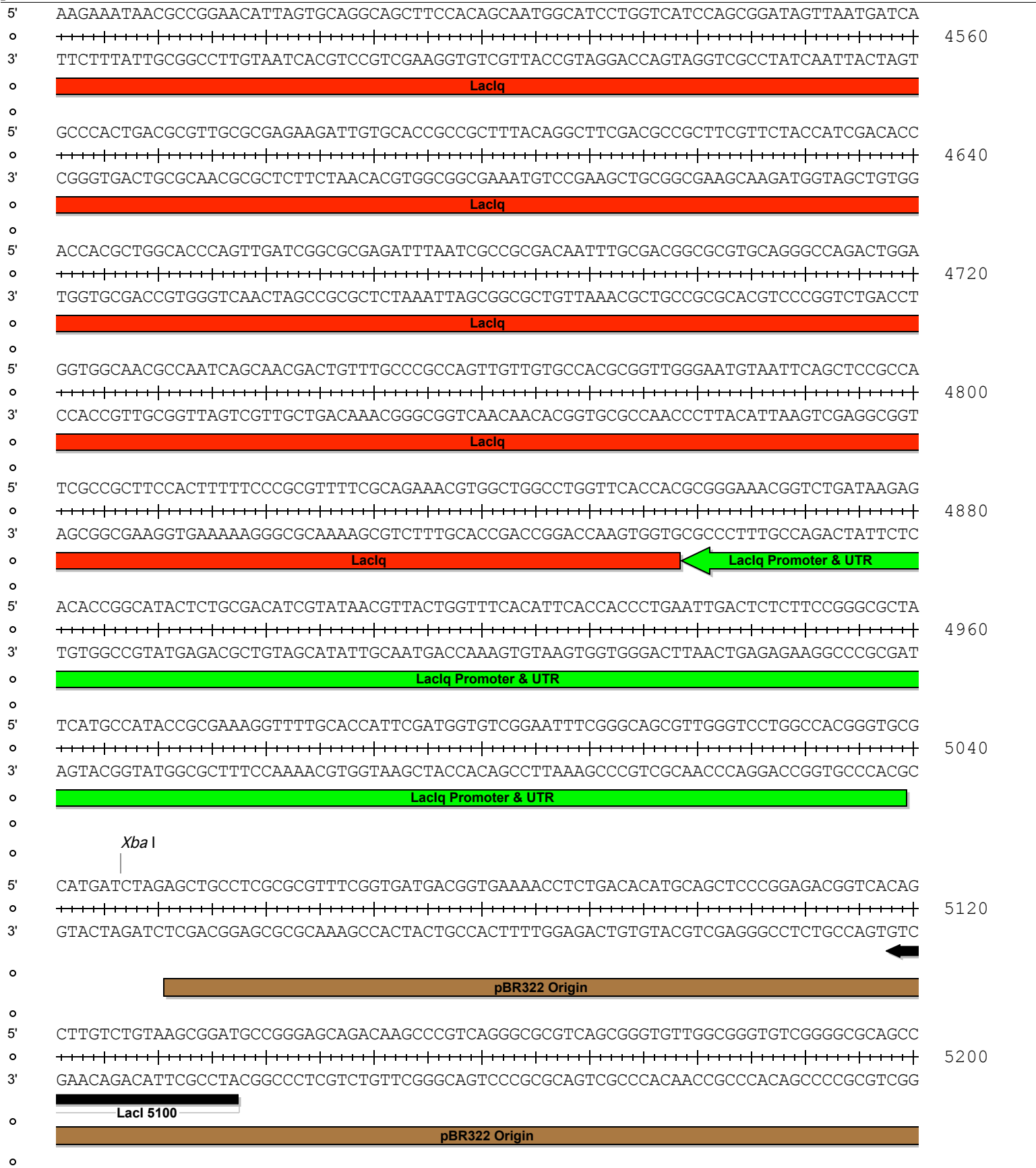


The diagram illustrates the genomic organization of the *lac* operon. The DNA sequence is presented in 100 bp fragments, with the top strand in 5' to 3' orientation and the bottom strand in 3' to 5' orientation. Key features include:

- rrnB Terminator:** A yellow bar indicating the terminators for the *rrnB* operon, located upstream of the *lac* operon.
- DownStream BsiWI:** A black bar indicating a BsiWI restriction site located downstream of the *rrnB* terminator.
- LacIq:** Red bars representing the *LacI* quaternary complex binding sites, located at various positions along the DNA sequence.
- LacI Mid Reverse:** A black bar with a white arrow pointing left, representing the mid-reverse binding site for the *LacI* protein.

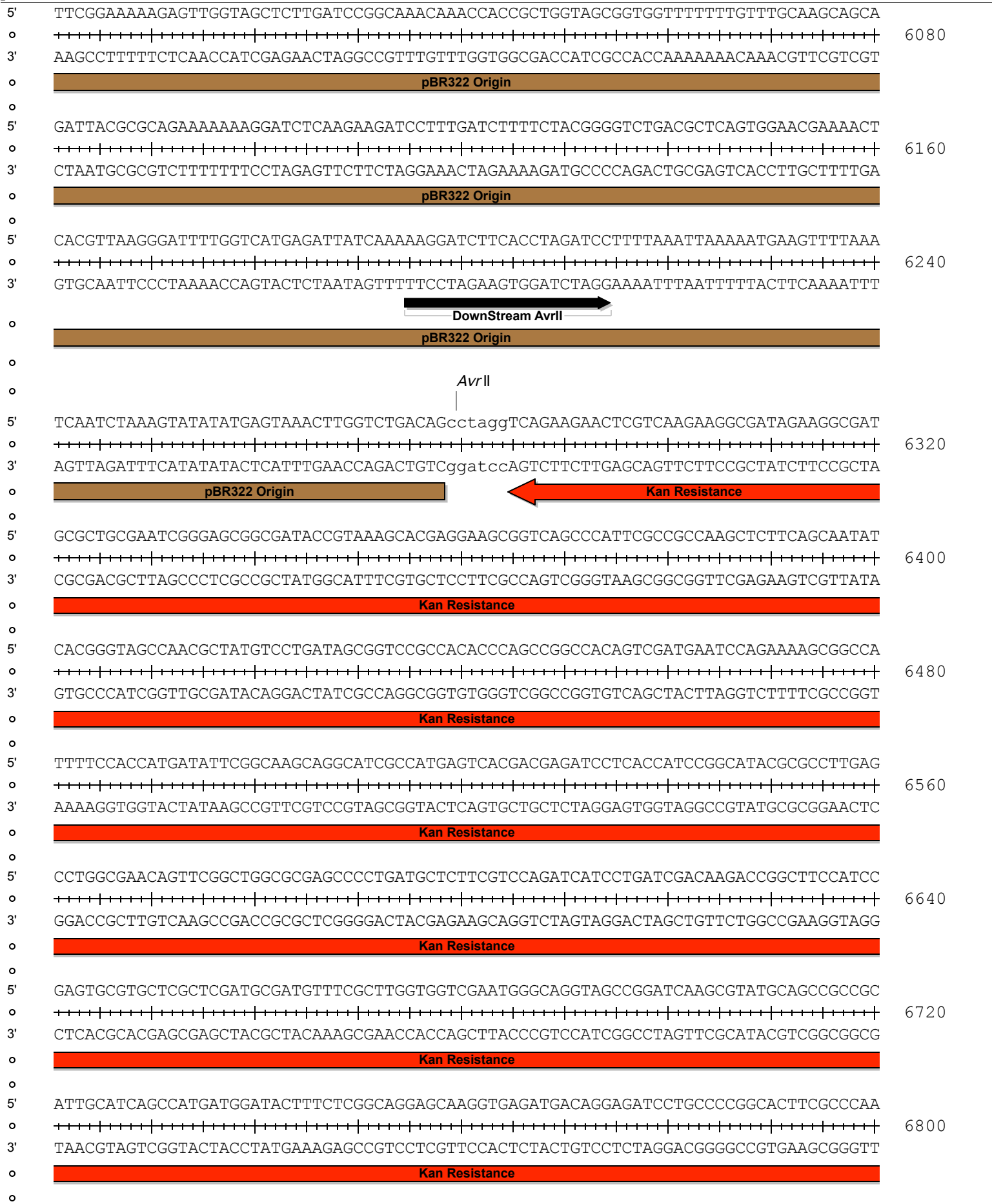
Distances in base pairs (bp) are indicated on the right side of the diagram, corresponding to the start of each 100 bp fragment:

- 3760
- 3840
- 3920
- 4000
- 4080
- 4160
- 4240
- 4320
- 4400
- 4480



Genomic map of the pBR322 plasmid showing the origin of replication and various restriction sites. The map is a circular representation with a scale from 0 to 6000 base pairs. Key features include the pBR322 Origin (a thick black bar), the NdeI site (a vertical line), and the LacI Seq from pBR322 (a horizontal bar). The sequence is shown in 5' to 3' orientation, with the 5' end at the top and the 3' end at the bottom. The map is divided into segments by vertical lines, with the origin of replication spanning from approximately 1000 to 2000 base pairs.





pVP56K

5'	TAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCAGCCACGATA	
o	+++++	6880
3'	ATCGTCGGTCAGGGAAGGGCGAAGTCACTGTTGCAGCTCGTGTGACGCGTTCCCTGCGGGCAGCACCGGTCGGTGCTAT	
o	Kan Resistance	
o		
5'	GCCGCGCTGCCTCGTCCTGCAGTTCATTTCAGGGCACCGGACAGGTCGGTCTTGACAAAAAGAACCGGGCGCCCCTGCGCT	
o	+++++	6960
3'	CGGCGCGACGGAGCAGGACGTCAAGTAAGTCCCGTGGCCTGTCCAGCCAGAACTGTTTTTCTTGCCCCGCGGGGACGCGA	
o	Kan Resistance	
o		
5'	GACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCAGTCATAGCCGAATAGCCTCTCCACCCAAGC	
o	+++++	7040
3'	CTGTCGGCCTTGTGCCCGCGTAGTCTCGTCGGCTAACAGACAACACGGGTCAGTATCGGCTTATCGGAGAGGTGGGTTCG	
o	Kan Resistance	
o		
5'	GGCCGGAGAACCTGCGTGCAATCCATCTTGTTCAAGCATGCGAAACGACCGTCATCCTGTCTCTTGATCAGATCTTGATC	
o	+++++	7120
3'	CCGGCCTCTTGACGCACGTTAGGTAGAACAAAGTTTCGTACGCTTTGCTGGCAGTAGGACAGAGAACTAGTCTAGAACTAG	
o	Kan Resistance	
o		
5'	CCCTGCGCCATCAGATCCTTGCGGCAAGAAAGCCATCCAGTTTACTTTGCAGGGCTTCCCAACCTTACCAGAGGGCGCC	
o	+++++	7200
3'	GGGACGCGGTAGTCTAGGAACCGCCGTTCTTTCGGTAGGTCAAATGAAACGTCCCGAAGGGTTGGAATGGTCTCCCGCGG	
o		
o		
		BsiWI
5'	CCAGCTGGCAATTCTTTTGAAGCTCACGCTGCCGCAAGCACTCAGGGcgtagc	
o	+++++	7253
3'	GGTCGACCGTTAAGAAAACCTTCAGTGCGACGGCGTTTCGTGAGTCCCgcatgc	
o		