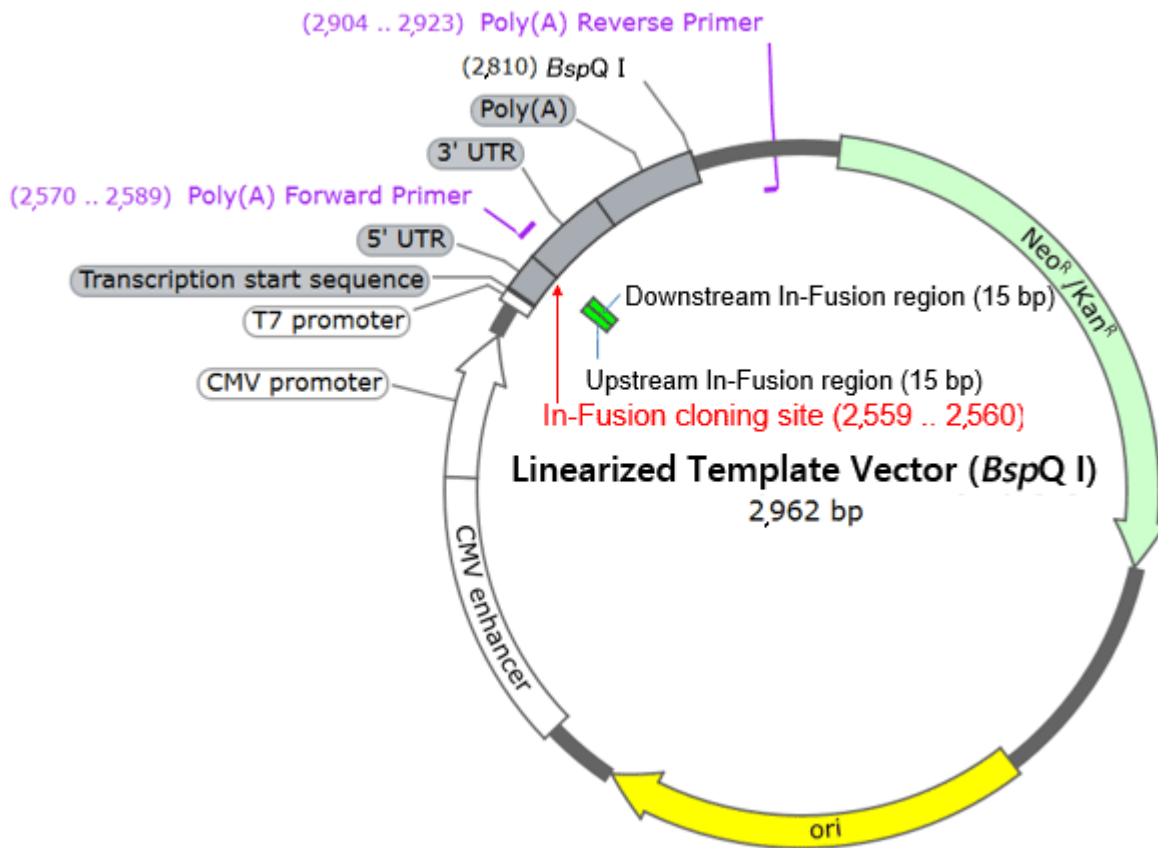


■ Linearized_Template_Vector_BspQ 벡터맵



Neo^R/Kan^R: 53 ~ 847

Ori: 1,172 ~ 1,760

T7 promoter sequence: 2,489 ~ 2,505

Transcription start sequence (AGG): 2,506 ~ 2,508

5'UTR: 2,509 ~ 2,559

Upstream In-Fusion region (15 bp): 2,545 ~ 2,559

▼In-Fusion cloning site (linearized site): between 2,559 and 2,560

Downstream In-Fusion region (15 bp): 2,560 ~ 2,574

3'UTR: 2,560 ~ 2,672

Poly(A)₁₄₁ : 2,673 ~ 2,813

BspQ I: 2,810

Poly(A) Forward Primer: 2,570 ~ 2,589

Poly(A) Reverse Primer: 2,904 ~ 2,923

T7 promoter 이후의 서열 정보

CTAACTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAAGGAATAAACTAGTA
 GATTGATCTCTTGGGTGACGAATGACCGAATAGCTTTAATTATGCTGAGTGATATTCCTTATTTGATCAT

T7 promoter 5' UTR

Transcription start sequence

Poly(A) Forward Primer
 CCTCGGTGGCCTAGCTTCTT

TTCTTCTGGTCCCCACAGACTCAGAGAGAACCCGCCACCTGAGCTGGAGCCTCGGTGGCCTAGCTTCTTG
 AAGAAGACCAGGGGTGTCTGAGTCTCTCTTGGGCGGTGGACTCGACCTCGGAGCCACCGGATCGAAGAAC

5' UTR 3' UTR

Upstream In-Fusion region (15 b) Downstream In-Fusion region (15 b)

CCCCTTGGGCCTCCCCCAGCCCCTCCTCCCCTTCTGCACCCGTACCCCGTGGTCTTTGAATAAAGTC
 GGGGAACCCGGAGGGGGGTCTGGGGAGGAGGGGAAGGACGTGGGCATGGGGGCACCAGAACTTATTTTCAG

3' UTR

TGAGTGGGCGGCAA
 ACTCACCCGCCGTT

3' UTR Poly(A)

AA
 TTT

Poly(A)

BspQI 認識配列

AAAAAAAAAAAAAgaagagcTCTCGAGTCGACCTAGGATCCCTTCTACTGGGCGGTTTTATGGACAGCA
 TTTTTTTTTTTTTTcttctcgAGAGCTCAGCTGGATCCTAGGGAAGATGACCCGCCAAAATACCTGTCGT

Poly(A)

AGCGAACCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGG
 TCGCTTGGCCTTAACGGTCGACCCCGCGGGAGACCATTCCAACCTTTCGGGACGTTTCATTTGACCTACC

CCATTCCAACCTTCGGGAC

Poly(A) Reverse Primer

CTTTCTTGCCGCCAAGGATCTG 3'
 ... 2,962
 GAAAGAACGGCGGTTCTAGAC 5'