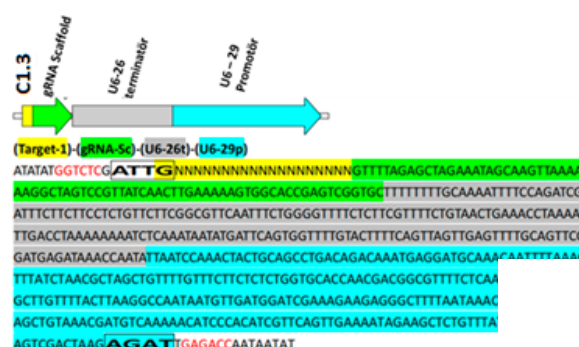


**Supplementary File S2:** Experimental procedure for multiplex CRISPR targeting all functional genes of BCTIV genes named as; C1 (RepA), C2(RepB) and overlapping region between V1/V2( CP-MP) and V2/V3 (MP/ssDNA).

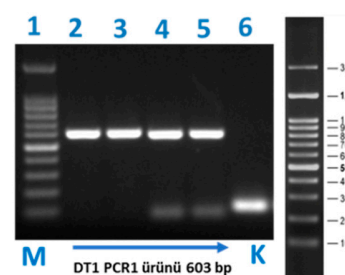
**Supp. File Table S1:** gRNA sequences for multiplex CRISPR

gRNA	Sequence
DT1-BsF: 3. gRNA_C1	5'- AATAATGGTCTCTATTGTGCTGTTGCCAATACTGTTGTT-3'
DT1-F0: 3. gRNA_C1	5'- TGTGCTGCTTGCCAATACTGTTGTTT TAGAGCTAGAAATAGC -3'
DT2-BsF2: 15.gRNA_V1/V2	5' AATAATGGTCTCTAGATTGGGAAGAGGAAGACGACCGGTGTT 3'
DT2-F0: 15.gRNA_V1/V2	5'- TGGGAAGAGGAAGACGACCGGTGTTT TAGAGCTAGAAATAGC -3'
DT3-BsF3: 6. gRNA_C2	5'- AATAATGGTCTCTGTGATTGGCAATACAAGGTCTTCCGCCGTT -3'
DT3-F0: 6. gRNA_C2	5'- TGGCAATACAAGGTCTTCCGCCGTTT TAGAGCTAGAAATAGC -3'
DT4-R0: 19. gRNA_V3/V2	5'-AAC TTCAGAGT GAGCGAATTTCCAATCACTACTTCGACTCTAGCTGTAT -3'
DT4-BsR: 19. gRNA_V3/V2	5'- ATTATTGGTCTCTAAACTTCAGAGTGAGCGAATTTCC -3'

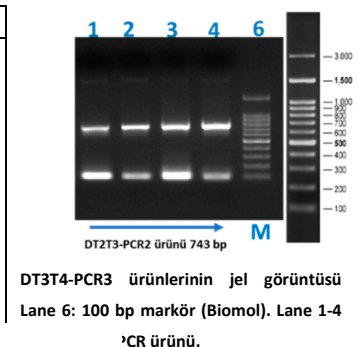
**Supp. File\_Table S2.** PCR conditions for cloning of gRNA\_C1 by using pCBC-DT1T2 vector



Components	( $\mu$ l)	PCR conditions
10 $\times$ Q5 polimeraz Buffer	5	1. One cycle: 98 $^{\circ}$ C, 30 sec.
MgSO <sub>4</sub> (25mM)	3	
dNTPs (2mM)	4	
Q5 polimeraz	1	
pCBC-DT1T2 (diluted to 200 times)	1	2. 34 cycles: 98 $^{\circ}$ C, 10 sec; 65 $^{\circ}$ C, 30 sec; 72 $^{\circ}$ C, 30 sec.
plazmid (adgene 50590)		
DT1-BsF (20 $\mu$ M) gRNA C1.3	1	3. One cycle: 72 $^{\circ}$ C, 7 min
DT1-F0 (1 $\mu$ M) gRNA C1.3	1	
DT0-BsR (20 $\mu$ M) primer	1	
ddH <sub>2</sub> O	33	
Total volume	50 $\mu$ l	



**Supp. File Table S3.** PCR conditions for cloning of gRNA V1/V2 by using pCBC-DT2T3



Components	Quantity (ul)	Cycle
Purified DT1 PCR1 fragments (~17 ng/μl)	4	<b>1. 30 cycles</b> 5 min at 37°C <b>2. 30 cycles</b> 5 min at 16 °C <b>2.</b> 5 min at 55°C <b>3.</b> 5 min at 80°C
Purified DT2T3-PCR2 fragments (~12 ng/μl)	5	
Purified DT3T4-PCR3 fragments (~11 ng/μl)	6	
pHSE401 (~160 ng/μl)	2	
10× T4 DNA Ligase Buffer (NEB)	1.5	
10× BSA	1.5	
BsaI (NEB)	1	
T4 DNA Ligase (HC, NEB)	1	
ddH2O	3	
Total volume	25	

**pHE401**  
16,653 bp

Restriction sites and coordinates (bp):

- (59) PmeI
- M13 pUC Forward (233 - 255)
- M13 Forward (247 - 264)
- AflIII (503)
- BstEII (1135)
- BssHII (1699)
- SwaI (3028)
- XbaI (3098)
- SgrDI (3835)
- AbsI (5065)
- AhdI (5238)
- TspMI - XmaI (5510)
- SmaI (5512)
- KflI (5594)
- MluI (6176)
- EcoRI (8014)
- Eco3kI (7375)
- SacI (7377)
- RsrII (9404)
- AsiSI (9440)
- SacII (10,660)
- (12,564 - 12,580) pGEX 3
- (12,466 - 12,483) 14,440
- (12,213 - 12,232) pR322ori-F
- (12,797) MreI - SgrAI
- (12,724 - 12,748) pGEX 3
- (12,599) pStZ177
- (13,695) BsiWI

Genetic elements and coordinates (bp):

- 16,000
- 14,000
- 12,000
- 10,000
- 8,000
- 6,000
- 4,000
- 2,000
- 0
- CaMV 35S promoter
- Shine-Dalgarno sequence
- CaMV 35S promoter (enhanced)
- HygR
- CaMV poly(A) signal
- King
- lacZ
- bam
- pSV1 StaA
- pGEX 3
- pR322ori-F

U6-29p-F: TTAATCCAACTACTGCAGCCTGAC and U6-1t-R: AACGGACCAATCACTTTGTCTTAGC

U6-29p-F: TTAATCCAACTACTGCAGCCTGAC and U6-1t-R: AACGGACCAATCACTTTGTCTTAGC