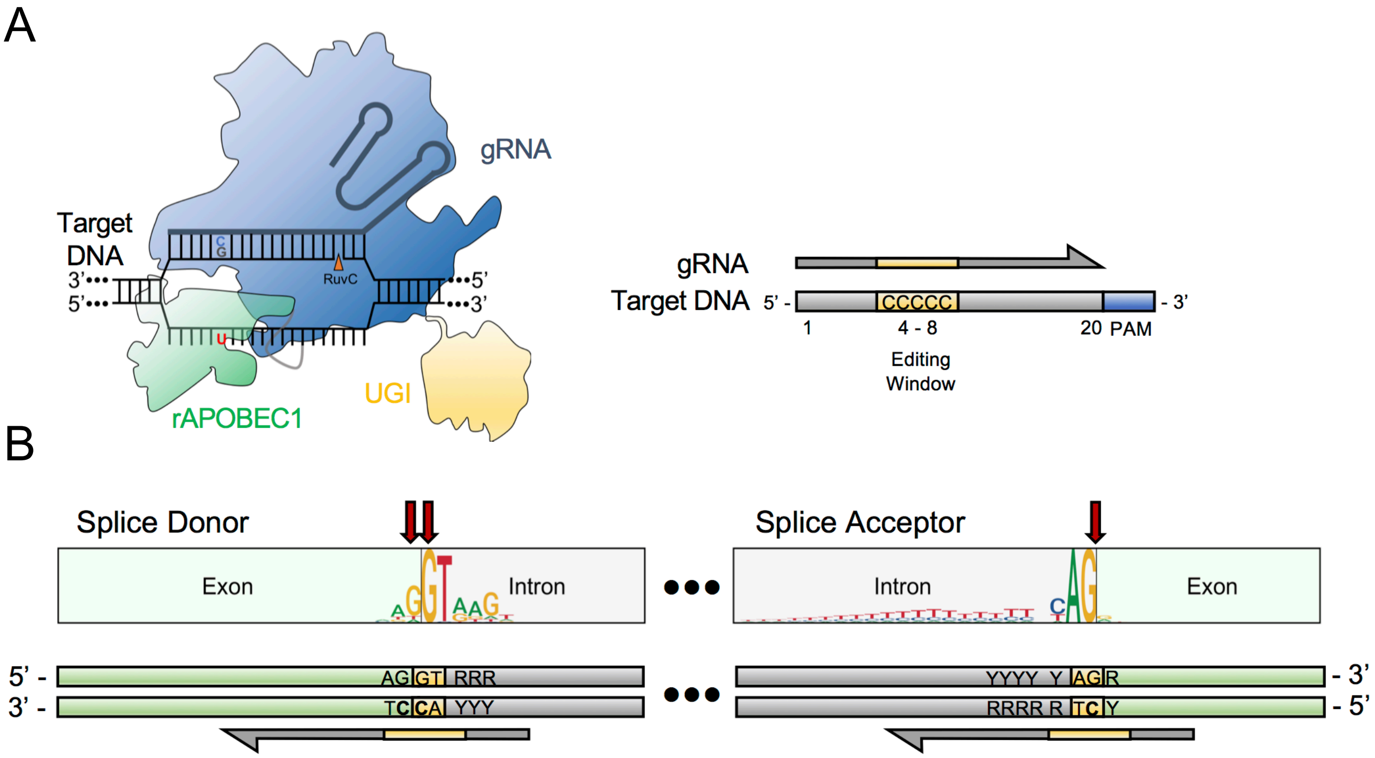
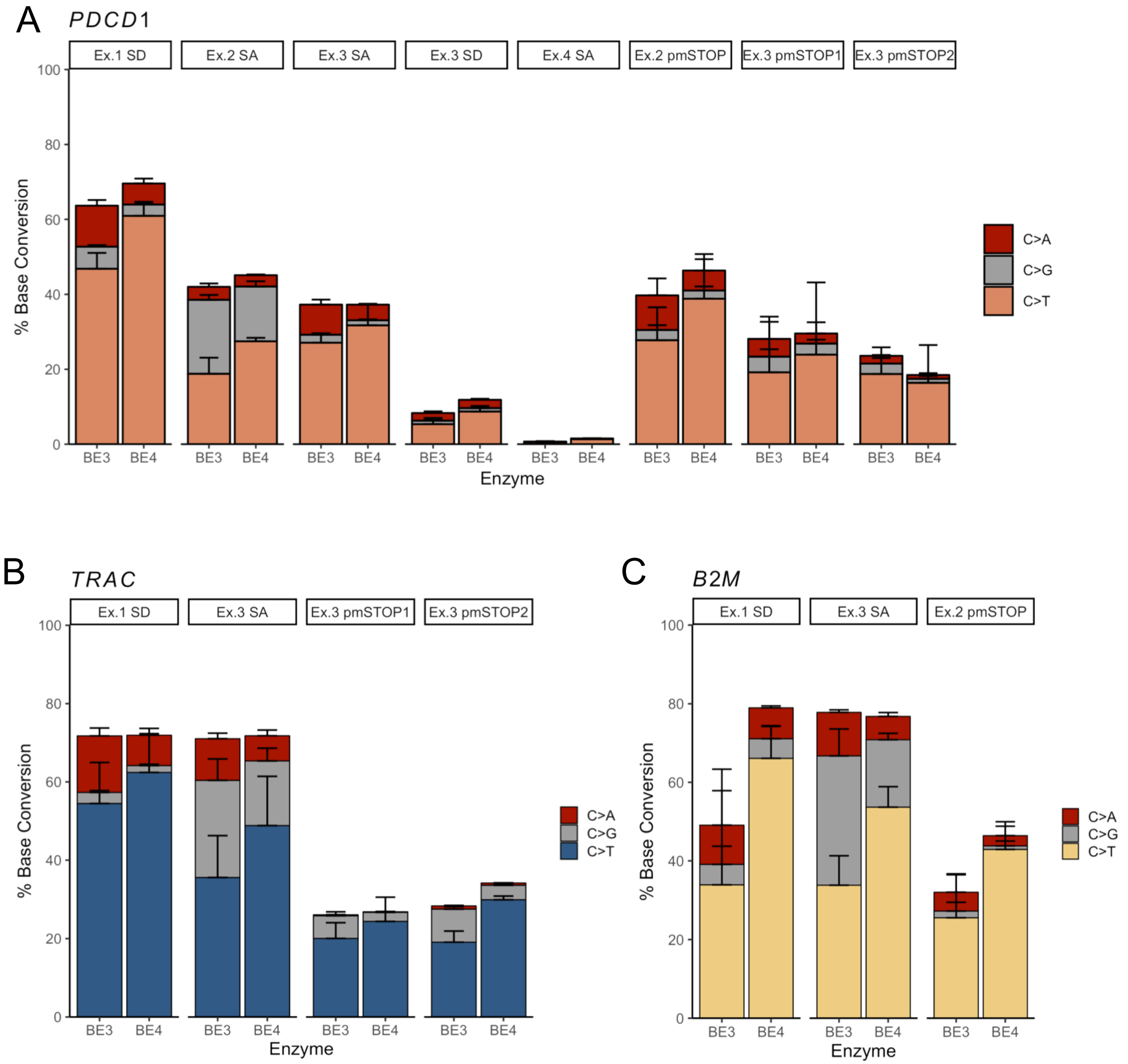
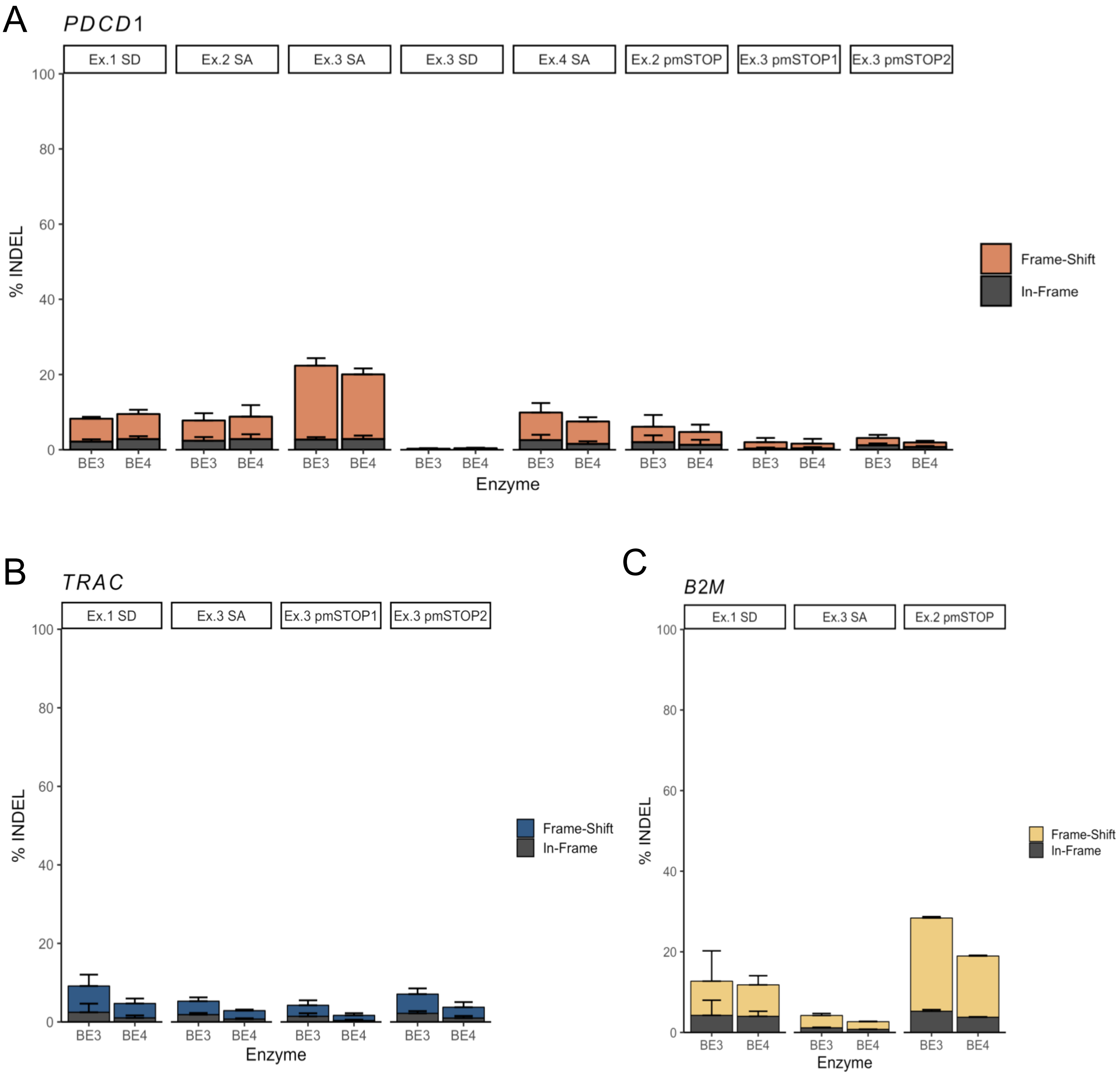


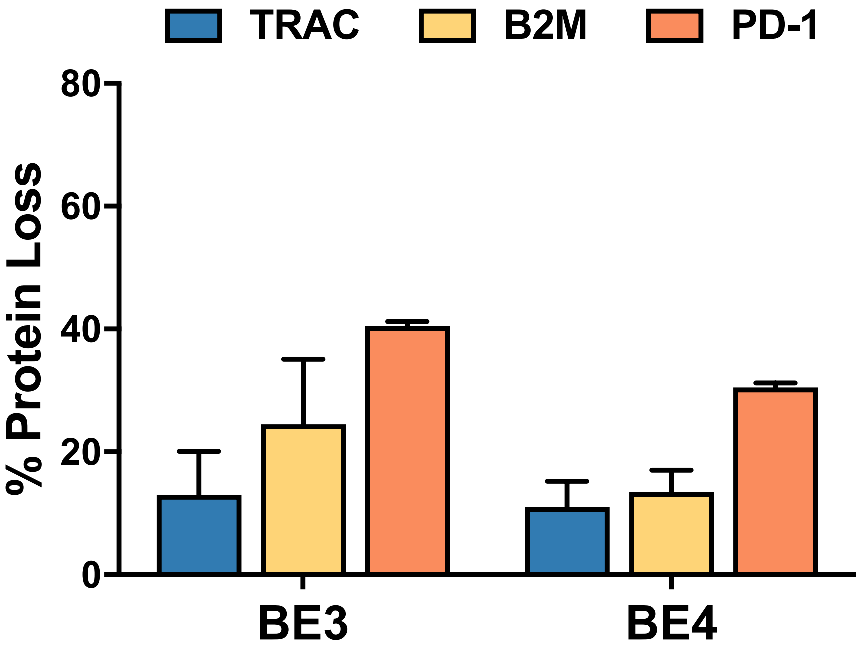
Supplementary Figure 1: **Targeting splice sites using base editor. A.** Diagram depicting Cas9 base editor (BE) bound to target DNA (left) and protospacer depicting the purported base editing window achieved with BE3 and BE4 (right). **B.** Logo diagrams depicting the consensus sequence of mammalian splice donor (SD) and splice acceptor (SA) elements and the related orientation of protospacers utilized for BE knockout via splice site disruption. Red arrows indicate target Cs (G antisense) predicted to disrupt splicing following conversion.



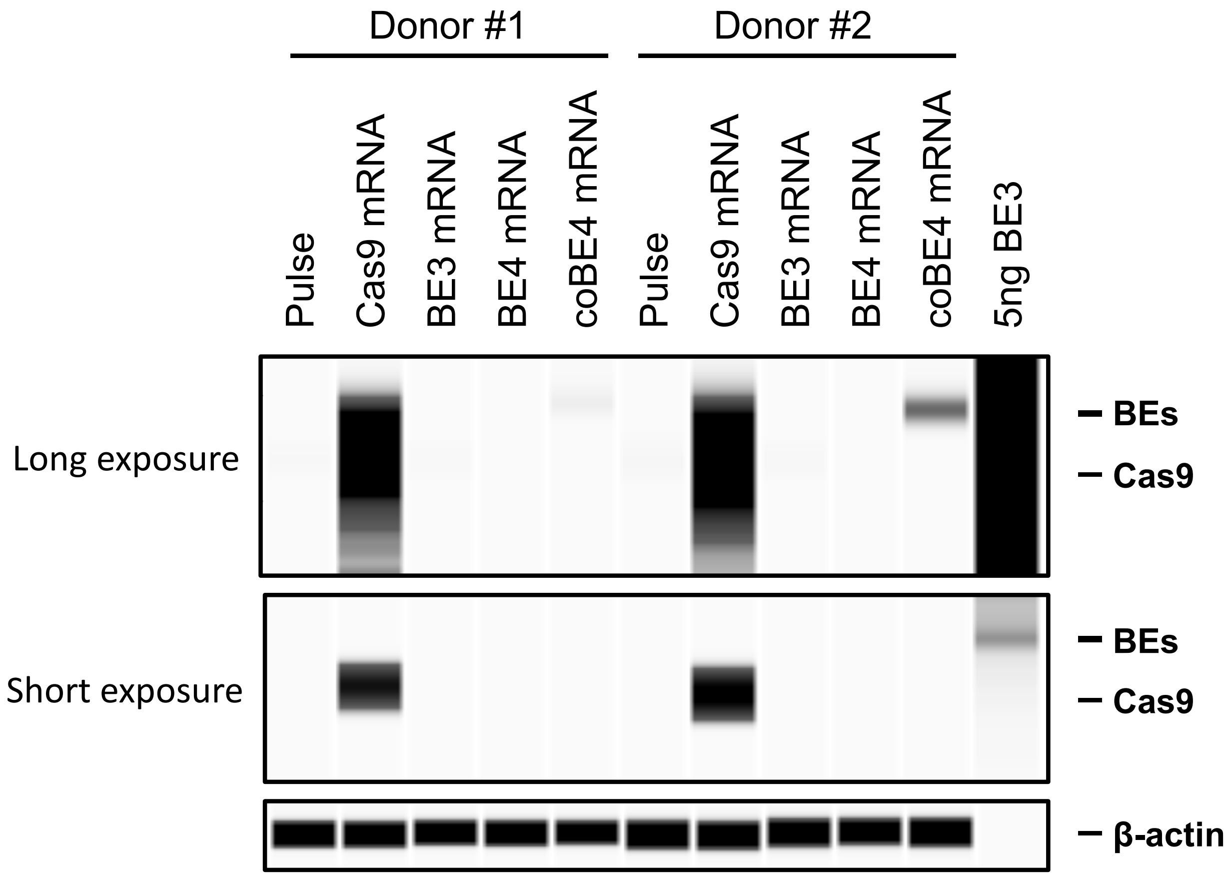
Supplementary Figure 2. Non-target editing for each sgRNA in figure 1. Data is analyzed from NGS. Height of stacked bars represents mean, with error bars ± 1 standard deviation. *n=3 independent donors.* Source data are provided as a Source Data file.



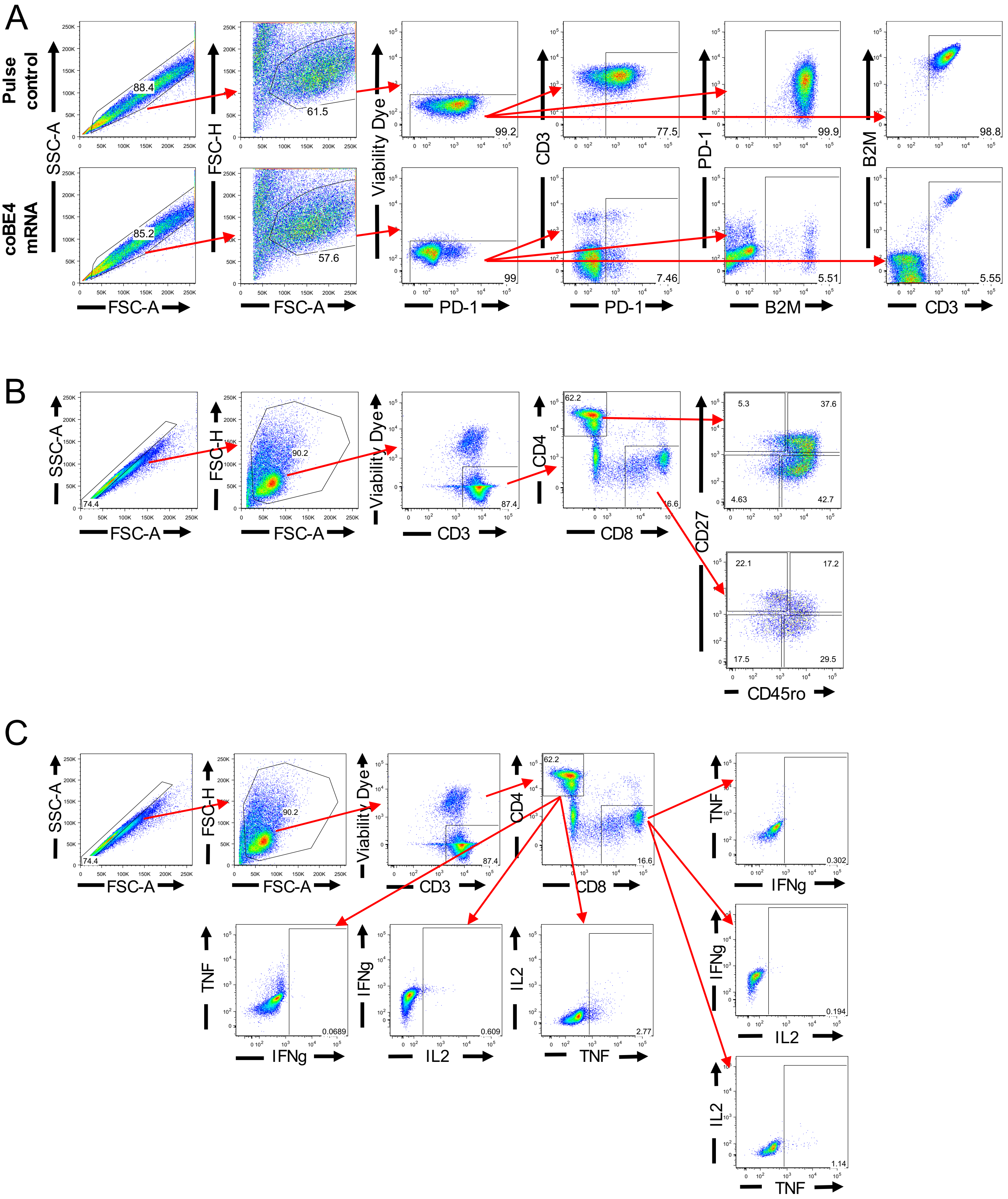
Supplementary Figure 3. Indels for all samples in Figure 1. Data is analyzed from NGS. Height of stacked bars represents mean, with error bars ± 1 standard deviation. *n=3 independent donors.* Source data are provided as a Source Data file.



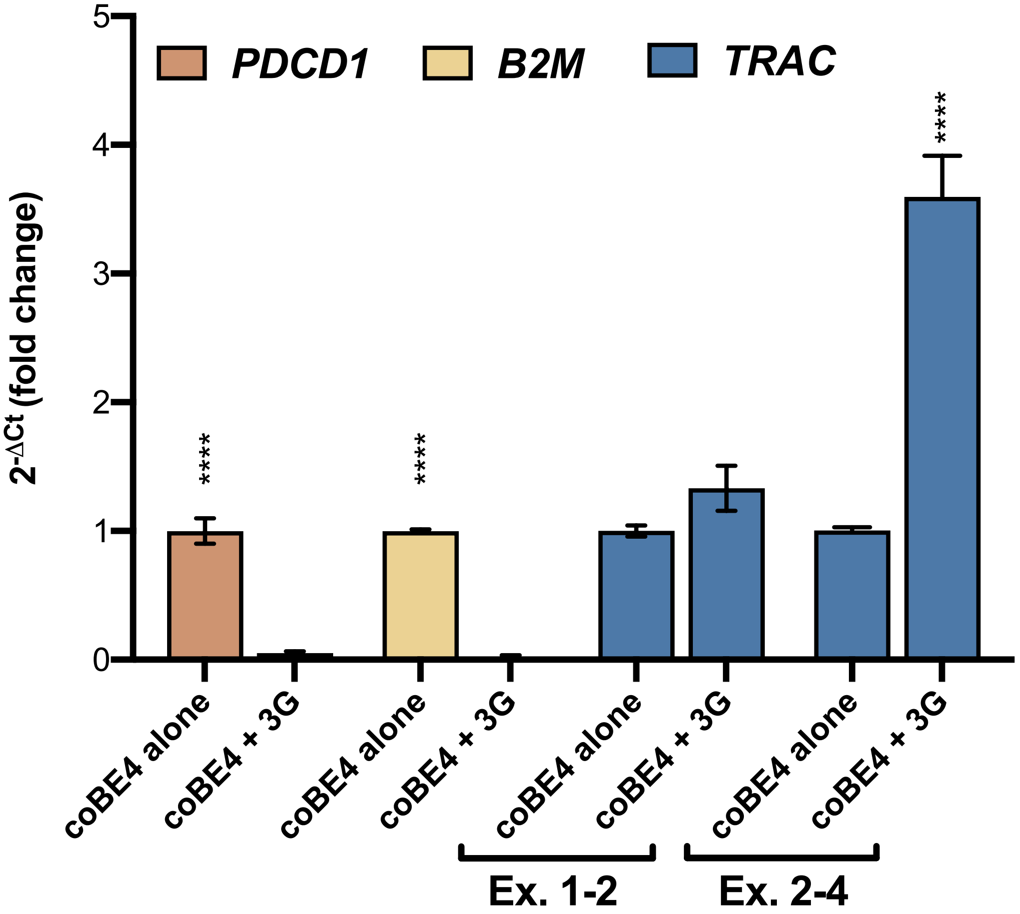
Supplementary Figure 4. Multiplex base editing of T cells using first-generation, low-dose (1.5 µg) BE3 or BE4 mRNA. Bar graph depicting base editor mediated knockout of TRAC, B2M and PD-1 at the protein level. Protein expression was assessed via flow cytometry as described in the methods section. *n = 2 independent donors.* Source data are provided as a Source Data file.



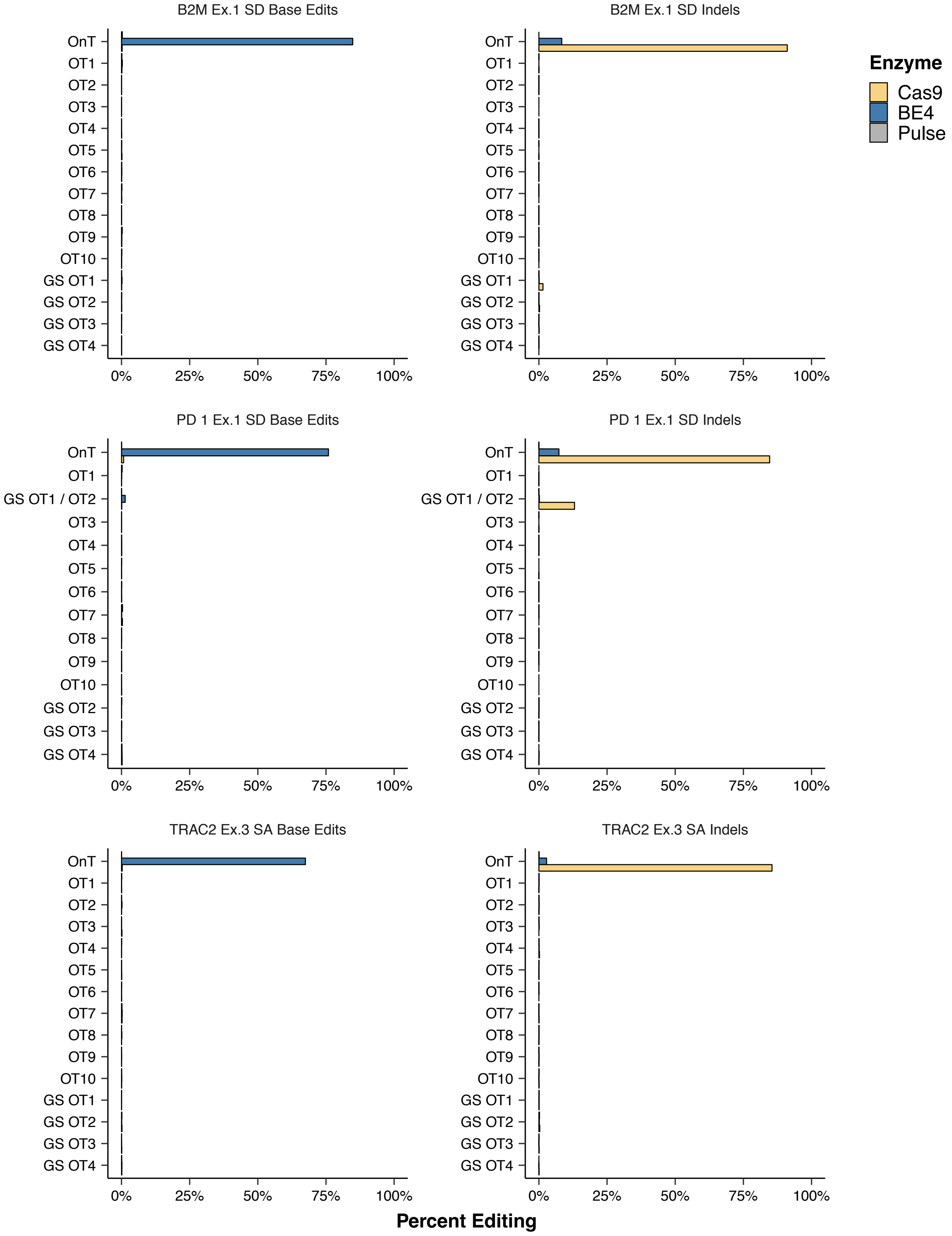
Supplementary Figure 5. Base editor protein levels following electroporation of T cells. Digital western blot results assessing the protein level achieved using mRNA encoding Cas9, BE3, BE4, and codon-optimized BE4 at 24 post electroporation of stimulated T cells in two independent donors. Purified BE3 protein was also used as a positive control for antibody detection of BE protein. Source data are provided as a Source Data file.



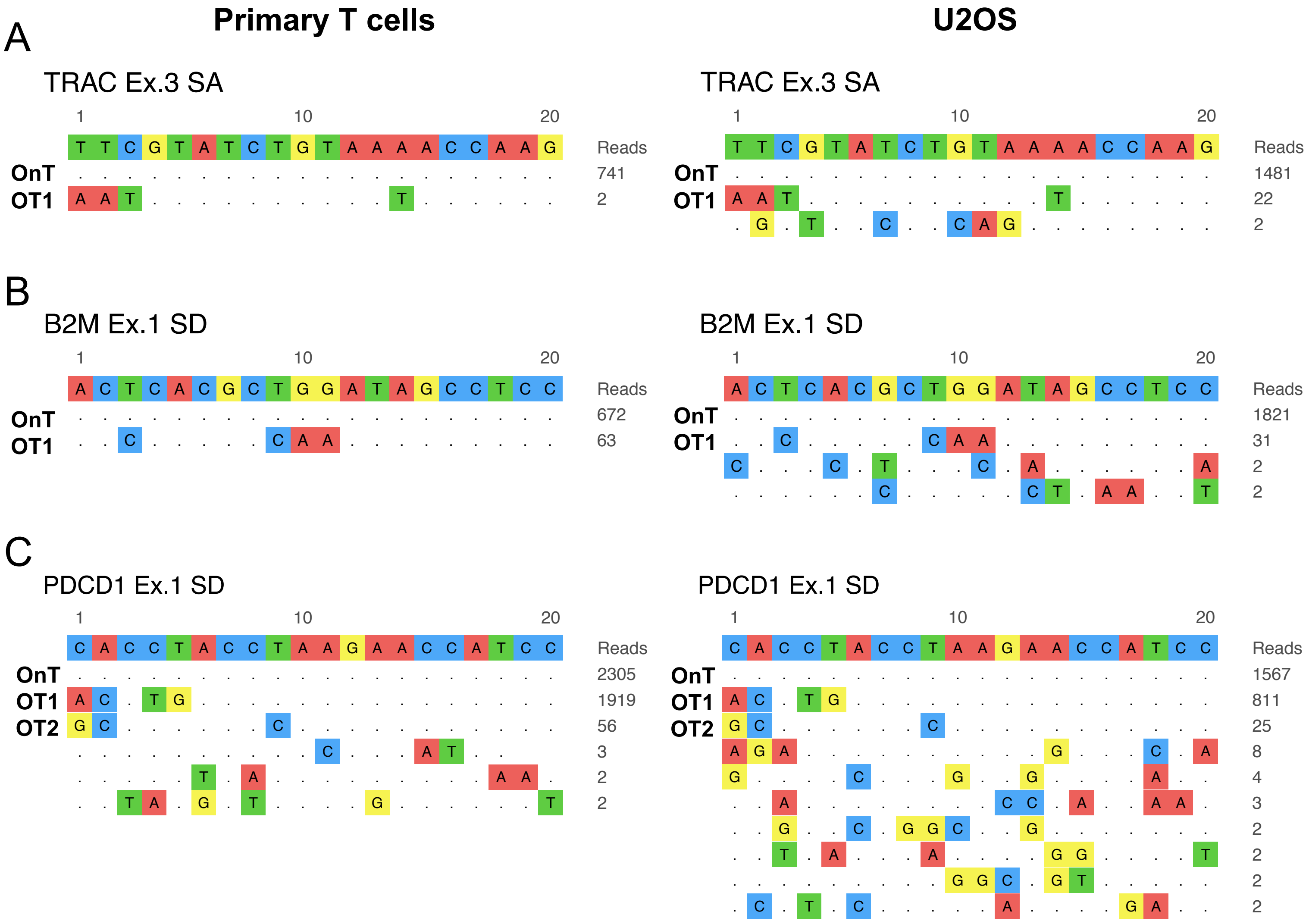
Supplementary Figure 6. Gating tree and representative flow plots for Figures 1, 2, 4a, 4b. (A) Gating tree for Figures 1 and 2. **(B)** Gating tree for Figure 4a. **(C)** Gating tree for Figure 4b.



Supplementary Figure 7. mRNA expression level of target genes in base edited T cells. T cells were electroporated with coBE4 mRNA alone or with optimal sgRNAs targeting *PDCD1, B2M, and TRAC.* Five days post electroporation mRNA was collected and transcript levels were determined using RT-qPCR. Specific exon junction assayed is indicated for *TRAC.* Source data are provided as a Source Data file.



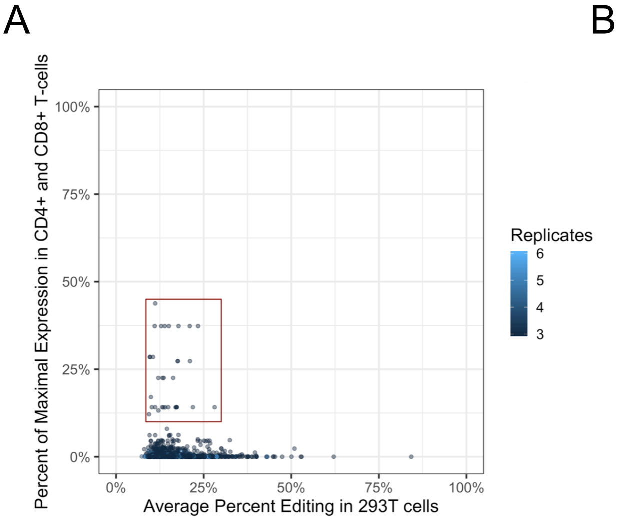
Supplementary Figure 8: Assessment of computationally predicted off-target base editing and indel formation. Base editing **(A)** and indel **(B)** frequency at on-target and top 10 computationally predicted off-target sgRNA binding sites, assessed using next generation sequencing, using optimal sgRNAs targeting *TRAC*, *B2M* or *PDCD1* combined with Cas9 or BE4 mRNA in T cells. Source data are provided as a Source Data file.



D

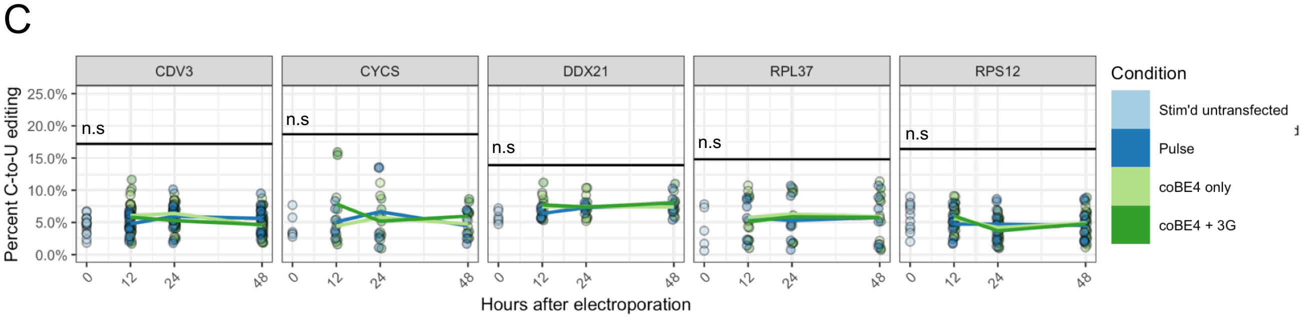
OT	Cas9 Indels	BE4 Indels	BE4 %C to T
TRAC Ex.3 SA GS_OT1	<0.1%	<0.1%	<0.1%
B2M Ex.1 SD GS_OT1	0.2%	<0.1%	<0.1%
PDCD1 Ex.1 SD GS_OT1*	13.1%	<0.1%	0.9%
PDCD1 Ex.1 SD GS_OT2	<0.1%	<0.1%	<0.1%

Supplementary Figure 9: GUIDE-seq assessment of off-target editing. GUIDE-seq (GS) analysis in primary human T cells and U2OS for **(A)** *TRAC* Ex.3 SA**, (B)** *B2M* Ex.1 SD, and **(C)** *PDCD1* Ex.1 SD. **(D)** Editing levels determined by NGS at OT sites identified in both primary T cells and U2OS**.** **PDCD1* GS-OT1 was also computationally identified as *PDCD1* OT2 in **Supplemental Data 8**.

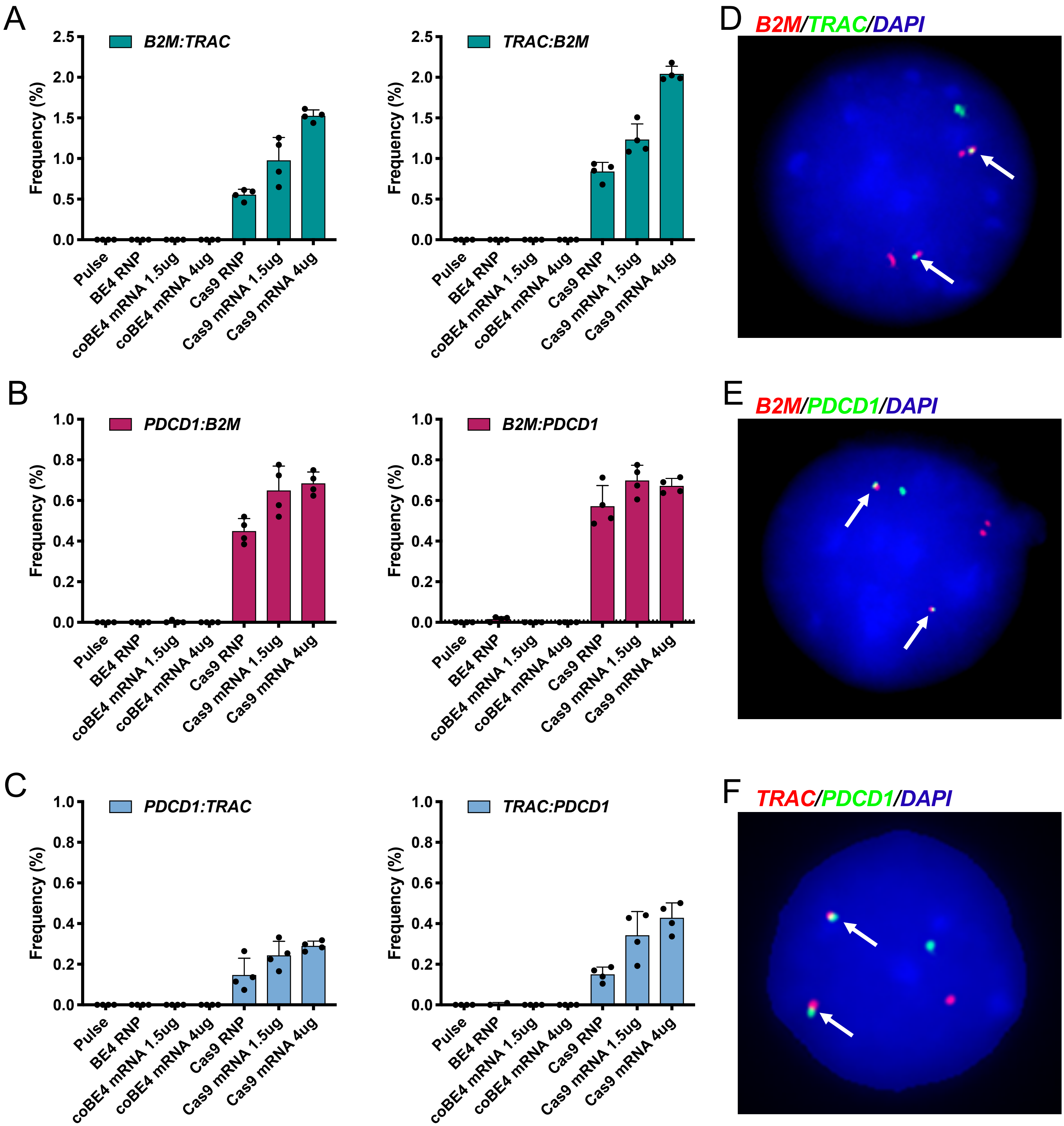


B

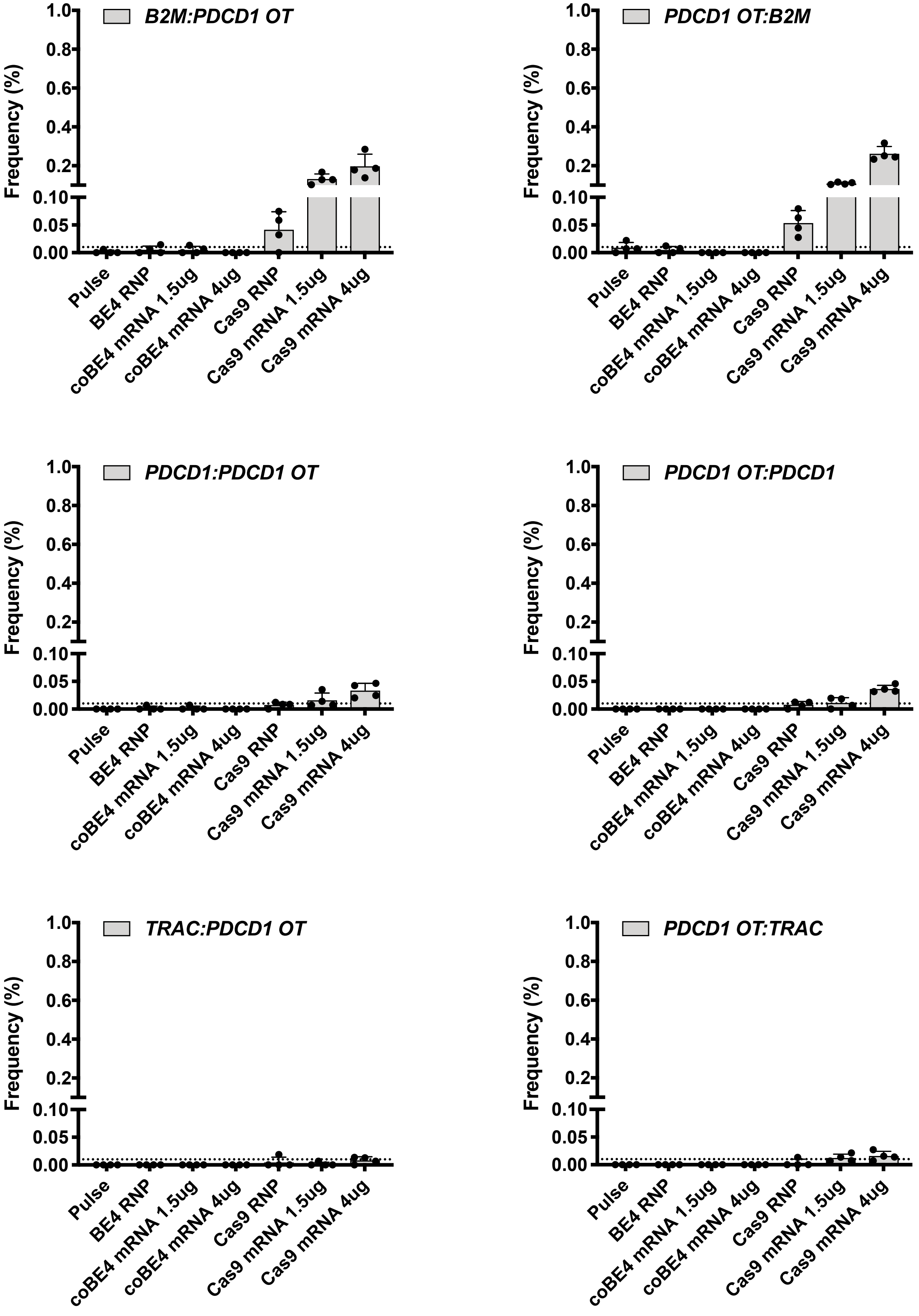
Gene	Edits	Average % Edit	SD % Edit	Transcript Length (bp)	CD4+ Reads	CD8+ Reads
CDV3	9	16.8	5.56	1161	1981.57	1876.55
RPS12	7	16.43	4.5	2749	2776.58	3531.95
DDX21	4	13.79	1.78	876	2780.54	2128.8
CYCS	3	18.74	2.02	236	3221.52	2228.1
RPL37	3	14.83	1.87	1043	1740.31	2131.52



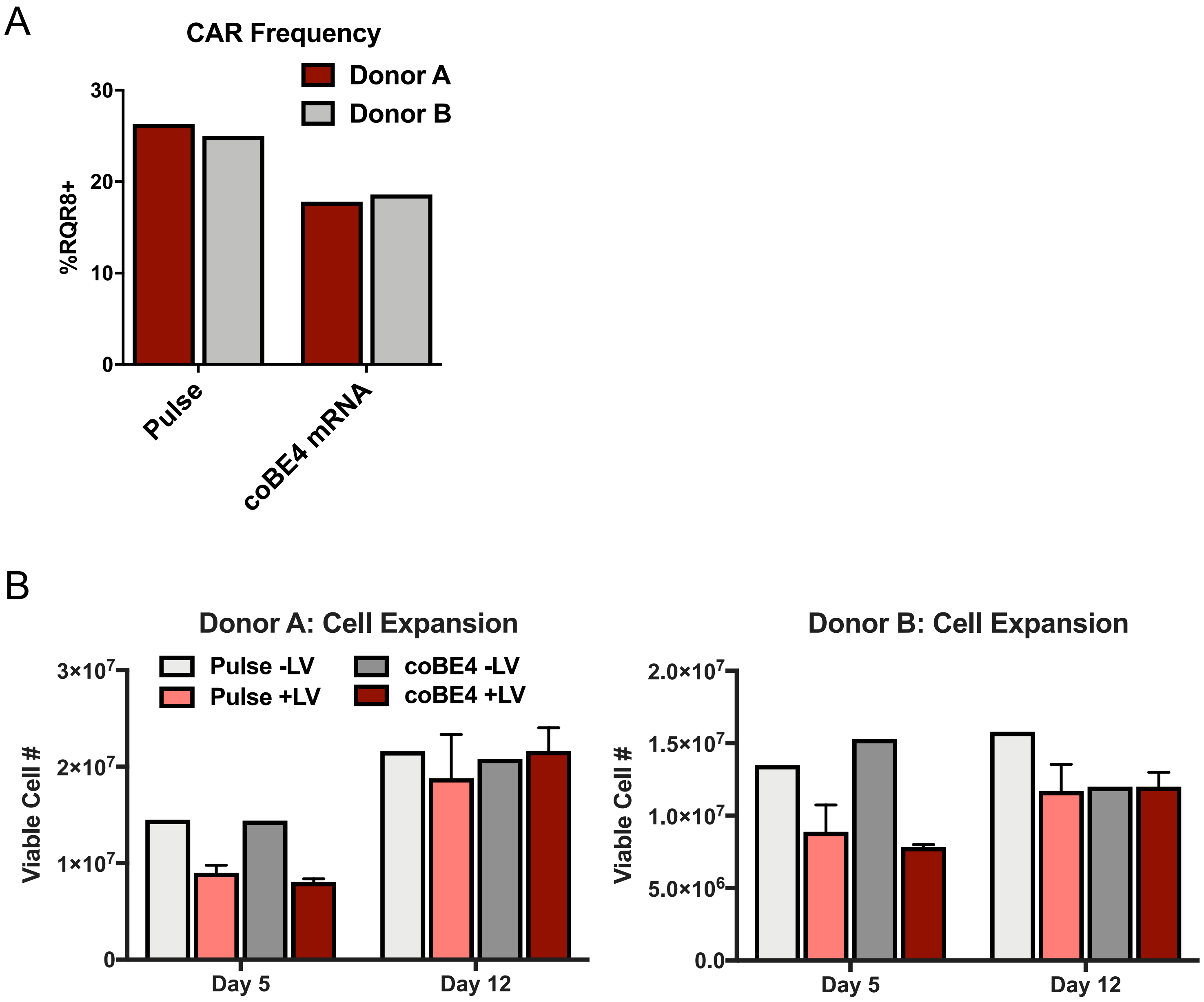
Supplementary Figure 10: Off-target RNA editing analysis. (A) Percent maximal gene expression in CD4$^+$-CD8$^+$ T cells plotted against multiplicate RNA editing observed in previous reports in HEK 293T cells. Red box indicates transcripts selected based on observed editing in HEK 293T and high expression in T cells. **(B)** Summary of gene transcripts analyzed for off-target RNA editing. **(C)** Line plots of the measured C-to-U editing across each treatment condition over indicated time points. Black horizontal line represents % editing previously observed in HEK 293T cells. Differences in measured % T fluorescence are not significant with respect to condition, time points, and donor across all genes tested (One way repeated measures ANOVA, *P* > 0.10, N = 26). Source data are provided as a Source Data file.



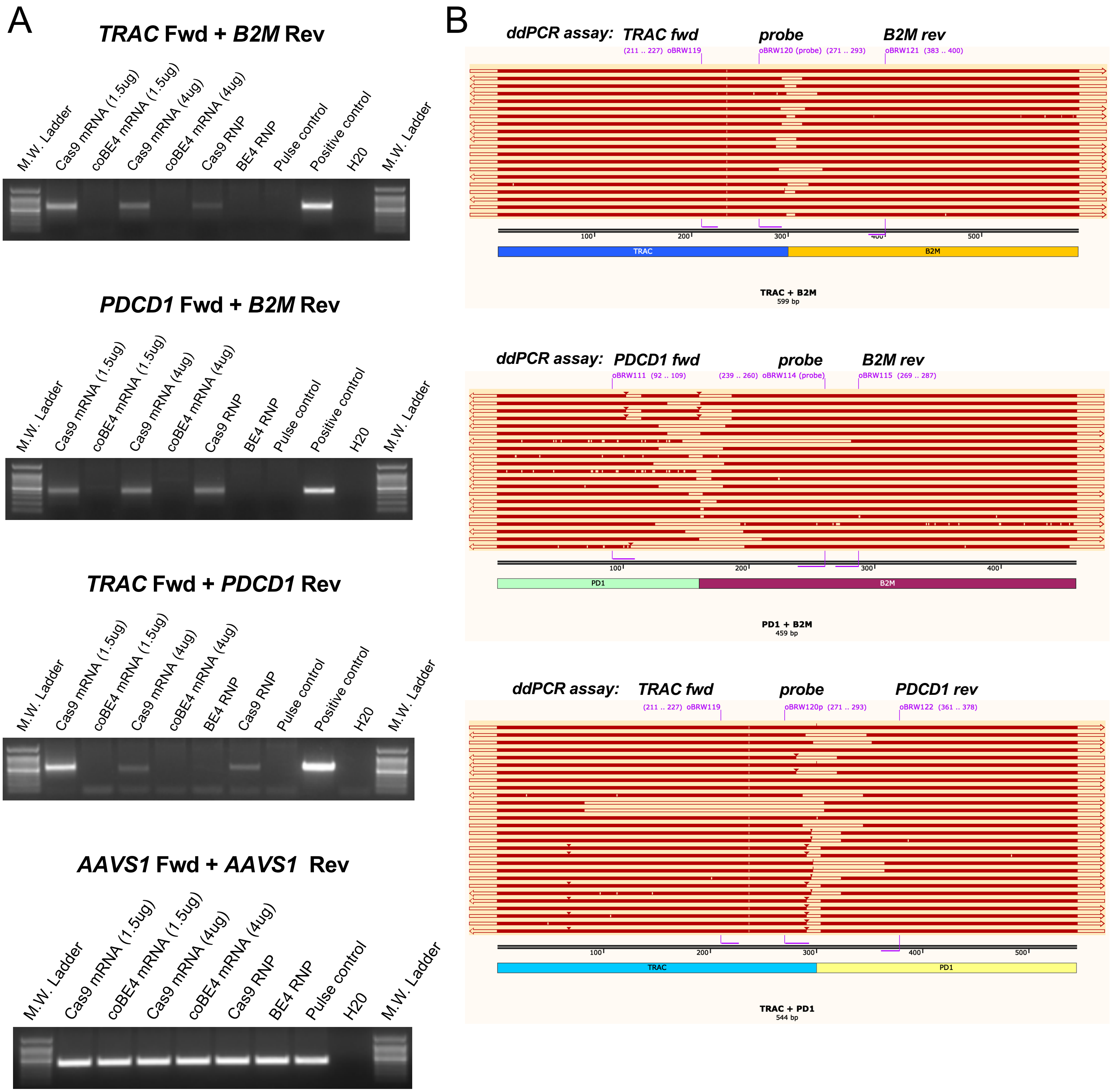
Supplementary Figure 11: Translocation frequency between *TRAC, B2M, and PDCD1* target loci. Droplet digital PCR (ddPCR) quantification of translocation frequency between *TRAC and B2M* **(A)**, *B2M and PDCD1* **(B)**, and *PDCD1 and TRAC* **(C)** following delivery of *TRAC, B2M,* and *PDCD1* sgRNA plus spCas9 protein, spCas9 mRNA, BE4 protein, or coBE4 mRNA at indicated doses. **(D, E, F)** Fluorescence *in situ* hybridization (FISH) verification of translocation event in multiplex Cas9 nuclease engineered T cells. *n=2 independent T cell donors assayed in duplicate.* Source data are provided as a Source Data file.



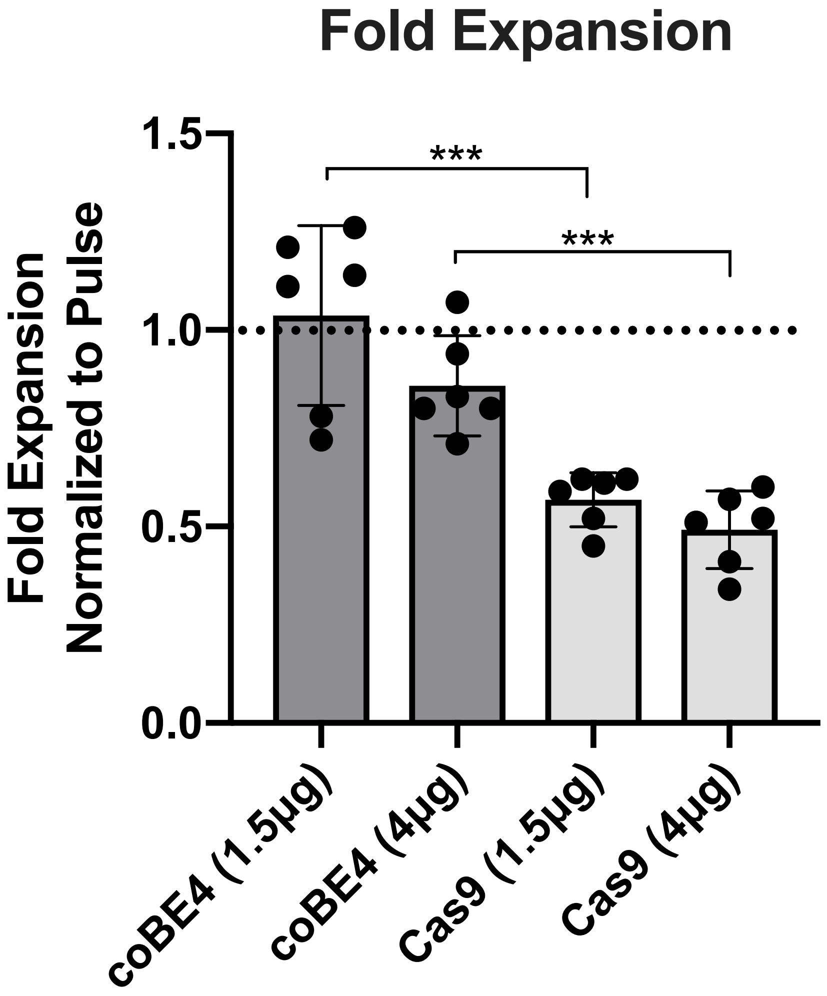
Supplementary Figure 12: Translocation frequency between target loci and PDCD1 off-target site. Droplet digital PCR quantification of translocation frequency between *PDCD1* OT site and *TRAC, B2M,* and *PDCD1* after delivery of three sgRNA and spCas9 protein, spCas9 mRNA, BE4 protein, or coBE4 mRNA. Dashed line indicates 0.01% limit of detection (LOD). *n=2 independent T cell donors assayed in duplicate.* Source data are provided as a Source Data file.



Supplementary Figure 13: CAR transduction and T cell expansion efficiency. A. Bar graph depicting the frequency of transduced T cells using the MND-CD19 CAR-RQR8 lentiviral vectors, MOI of 20, via staining for RQR8 in two independent donors. RQR8 is a hybrid molecule containing domains for staining with CD34 and CD20 specific antibody and serves as a surrogate for determining CAR positive T cell frequency. **B.** Bar graphs depicting the number of viable cells at day 5 and 12 post electroporation and transduction. *n=2 independent donors.* Source data are provided as a Source Data file.



Supplementary Figure 14: Sequencing of sub-cloned PCR products spanning translocation junctions. A. Results of translocation PCR performed between the noted target genes using Cas9 or BE mRNA or protein, as noted. An AAVS1 control PCR was also performed to confirm gDNA quality and functionality for PCR**. B.** PCR products from (A) were TA cloned into TOPO plasmids and subsequently analyzed via Sanger sequencing. Resultant chromatograms were then aligned to a hypothetical 'perfect' junction sequence between the noted target gene gRNA cut sites and aligned. Also depicted are ddPCR probes used to generate the data presented in main Figure 3. Source data are provided as a Source Data file.



Supplementary Figure 15: Expansion of multiplex edited T cells. T cells were electroporated with nothing (pulse) or the indicated dose of coBE4 or spCas9 nuclease mRNA plus *PDCD1, B2M, and TRAC* sgRNAs. Electroporated T cells were immediately transferred to one well of a G-Rex 24-well culture vessel and allowed to expand for 12 days, at which point viable cells were quantified. Fold expansion was determined for each condition and normalized to the pulse control. *n=3 independent T cell donors assayed in duplicate.* Source data are provided as a Source Data file.

Supplemental Table 1. Guide RNA sequences and associated information.

Gene	gRNA Name	5' - gRNA Sequence - 3'	Orientation	Target base(s)	Predicted Outcome
PDCD1	Ex. 1 SD	CACCTA**C**CTAAGAACCATCC	Antisense	C7	Splice donor disruption: **G**T → **A**T
PDCD1	Ex. 2 SA	GGAGT**C**TGAGAGATGGAGAG	Antisense	C6	Splice acceptor disruption: A**G** → A**A**
PDCD1	Ex. 3 SA	TTCTCT**C**TGGAAGGGCACAA	Antisense	C7	Splice acceptor disruption: A**G** → A**A**
PDCD1	Ex. 3 SD	GACGTTA**C**CTCGTGCGGCCC	Antisense	C8	Splice donor disruption: **G**T → **A**T
PDCD1	Ex. 4 SA	C**C**TGCAGAGAAACACACTTG	Antisense	C2	Splice acceptor disruption: A**G** → A**A**
PDCD1	Ex. 2 pmSTOP	GGGGTT**CC**AGGGCCTGTCTG	Antisense	C7, C8	pmSTOP induction: T**GG** (Trp) → T**A**G, TG**A**, T**AA**
PDCD1	Ex. 3 pmSTOP_1	CAGTTC**C**AAACCCTGGTGGT	Sense	C7	pmSTOP induction: **C**AA (Gln) → **T**AA
PDCD1	Ex. 3 pmSTOP_2	GGAC**CC**AGACTAGCAGCACC	Antisense	C5, C6	pmSTOP induction: T**GG** (Trp) → T**A**G, TG**A**, T**AA**
TRAC	Ex. 1 SD	CTTA**C**CTGGGCTGGGGAAGA	Antisense	C5	Splice donor disruption: **G**T → **A**T
TRAC	Ex. 3 SA	TTCGTAT**C**TGTAAAACCAAG	Antisense	C8	Splice acceptor disruption: A**G** → A**A**
TRAC	Ex. 3 pmSTOP_1	TTT**C**AAAACCTGTCAGTGAT	Sense	C4	pmSTOP induction: **C**AA (Gln) → **T**AA
TRAC	Ex. 3 pmSTOP_2	TT**C**AAAACCTGTCAGTGATT	Sense	C3	pmSTOP induction: **C**AA (Gln) → **T**AA
B2M	Ex. 1 SD	ACTCA**C**GCTGGATAGCCTCC	Antisense	C6	Splice donor disruption: **G**T → **A**T
B2M	Ex. 3 SA	TCGAT**C**TATGAAAAAGACAG	Antisense	C6	Splice acceptor disruption: A**G** → A**A**
B2M	Ex. 2 pmSTOP	CTTACC**CC**ACTTAACTATCT	Antisense	C7, C8	pmSTOP induction: T**GG** (Trp) → T**A**G, TG**A**, T**AA**

Supplemental Table 2. OT NGS primer sequences.

Site Name	Off-Target Sequence	Primer Name	Primer Sequence
B2M_Ex1_SD_OnT.1	ACTCACGCTGGATAGCCTCC	B2M_Ex1_SD_OnT Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCCAGCCCTGGACTAGC
B2M_Ex1_SD_OnT.1	ACTCACGCTGGATAGCCTCC	B2M_Ex1_SD_OnT Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTCTCTCTAACCTGGCACTG
B2M_Ex1_SD_OnT.1	ACTCACGCTGGATAGCCTCC	B2M_Ex1_SD_OnT Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATCCAGCCCTGGACTAGC
B2M_Ex1_SD_OnT.1	ACTCACGCTGGATAGCCTCC	B2M_Ex1_SD_OnT Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCCTCTCTCTAACCTGGCACT
B2M_Ex1_SD_OT1.1	TCTGCCCCTGGATAGCCTCC	B2M_Ex1_SD_OT1 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCCAGACATGAGAAGGTTAT
B2M_Ex1_SD_OT1.1	TCTGCCCCTGGATAGCCTCC	B2M_Ex1_SD_OT1 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTTACAGGCTCCCCTTC
B2M_Ex1_SD_OT1.1	TCTGCCCCTGGATAGCCTCC	B2M_Ex1_SD_OT1 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCCAGACATGAGAAGGTTAT
B2M_Ex1_SD_OT1.1	TCTGCCCCTGGATAGCCTCC	B2M_Ex1_SD_OT1 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTCTAGGCGTCCTCATCAC
B2M_Ex1_SD_OT2.1	ACTCACCTTCCATAGCCTCC	B2M_Ex1_SD_OT2 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGATGTTCTTTGGTGTTTGT
B2M_Ex1_SD_OT2.1	ACTCACCTTCCATAGCCTCC	B2M_Ex1_SD_OT2 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTCCGTCTCTGAACACTC
B2M_Ex1_SD_OT2.1	ACTCACCTTCCATAGCCTCC	B2M_Ex1_SD_OT2 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAATGTTGGGATGTTCTTTG
B2M_Ex1_SD_OT2.1	ACTCACCTTCCATAGCCTCC	B2M_Ex1_SD_OT2 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTCCGTCTCTGAACACTC
B2M_Ex1_SD_OT3.1	GCTCCTGCTGCATAGCCTCC	B2M_Ex1_SD_OT3 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATAGTTGCCATTTCTGCTTG
B2M_Ex1_SD_OT3.1	GCTCCTGCTGCATAGCCTCC	B2M_Ex1_SD_OT3 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGGGTGAAAGACTGAAAAA
B2M_Ex1_SD_OT3.1	GCTCCTGCTGCATAGCCTCC	B2M_Ex1_SD_OT3 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAATAGTTGCCATTTCTGCTT
B2M_Ex1_SD_OT3.1	GCTCCTGCTGCATAGCCTCC	B2M_Ex1_SD_OT3 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAGGGTGAAAGACTGAAAAA
B2M_Ex1_SD_OT4.1	TCTCACTGTGGTTAGCCTCC	B2M_Ex1_SD_OT4 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTTTTTGTGAAGGCTTTTC
B2M_Ex1_SD_OT4.1	TCTCACTGTGGTTAGCCTCC	B2M_Ex1_SD_OT4 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTGTCACCAGCTGATTGTA
B2M_Ex1_SD_OT4.1	TCTCACTGTGGTTAGCCTCC	B2M_Ex1_SD_OT4 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTTTTTGTGAAGGCTTTTC
B2M_Ex1_SD_OT4.1	TCTCACTGTGGTTAGCCTCC	B2M_Ex1_SD_OT4 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGTCACCAGCTGATTGTAGA
B2M_Ex1_SD_OT5.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT5 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCAAGAGCAAGAAACCAGT
B2M_Ex1_SD_OT5.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT5 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGACTTTGAAATACCAGCA

B2M_Ex1_SD_OT5.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT5 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGAGTCAGCAGCTCAAGA
B2M_Ex1_SD_OT5.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT5 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGACTTTGAAATACCAGCA
B2M_Ex1_SD_OT6.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT6 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCAAGAGCAAGAAACCAGT
B2M_Ex1_SD_OT6.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT6 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGACTTTGAAATACCAGCA
B2M_Ex1_SD_OT6.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT6 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGAGTCAGCAGCTCAAGA
B2M_Ex1_SD_OT6.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT6 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGACTTTGAAATACCAGCA
B2M_Ex1_SD_OT7.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT7 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTCAAGAGCAAGAAACCAGT
B2M_Ex1_SD_OT7.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT7 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGACTTTGAAATACCAGCA
B2M_Ex1_SD_OT7.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT7 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGAGTCAGCAGCTCAAGA
B2M_Ex1_SD_OT7.1	TCTCTCACTGGATAGCCTAC	B2M_Ex1_SD_OT7 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGGACTTTGAAATACCAGCA
B2M_Ex1_SD_OT8.1	AGCCACCCTGGAGAGCCTCC	B2M_Ex1_SD_OT8 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCTCAGCTTGCTCCACT
B2M_Ex1_SD_OT8.1	AGCCACCCTGGAGAGCCTCC	B2M_Ex1_SD_OT8 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTTCTTGAGGCTGTTCA
B2M_Ex1_SD_OT8.1	AGCCACCCTGGAGAGCCTCC	B2M_Ex1_SD_OT8 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCTCAGCTTGCTCCACT
B2M_Ex1_SD_OT8.1	AGCCACCCTGGAGAGCCTCC	B2M_Ex1_SD_OT8 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTCTTGAGGCTGTTCAGG
B2M_Ex1_SD_OT9.1	ACTCCCGCTGGAAAGCCTGC	B2M_Ex1_SD_OT9 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTTCGCCAGCTCAAAAA
B2M_Ex1_SD_OT9.1	ACTCCCGCTGGAAAGCCTGC	B2M_Ex1_SD_OT9 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCAGCGAGCTCTACTGGTG
B2M_Ex1_SD_OT9.1	ACTCCCGCTGGAAAGCCTGC	B2M_Ex1_SD_OT9 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTTTCGCCAGCTCAAAAA
B2M_Ex1_SD_OT9.1	ACTCCCGCTGGAAAGCCTGC	B2M_Ex1_SD_OT9 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCGAGCTCTACTGGTGCTG
B2M_Ex1_SD_OT10.1	CCTCCCGCTGTGTAGCCTCC	B2M_Ex1_SD_OT10 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGTGGATTACAATGGAAACA
B2M_Ex1_SD_OT10.1	CCTCCCGCTGTGTAGCCTCC	B2M_Ex1_SD_OT10 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCATGAAAGGGGGTTATACAT
B2M_Ex1_SD_OT10.1	CCTCCCGCTGTGTAGCCTCC	B2M_Ex1_SD_OT10 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGATTACAATGGAAACATCAA
B2M_Ex1_SD_OT10.1	CCTCCCGCTGTGTAGCCTCC	B2M_Ex1_SD_OT10 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCATGAAAGGGGGTTATACAT
PD-1_Ex.1_SD_OnT.1	CACCTACCTAAGAACCATCC	PD-1_Ex.1_SD_OnT Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGCCAGGGACTGAGAGT
PD-1_Ex.1_SD_OnT.1	CACCTACCTAAGAACCATCC	PD-1_Ex.1_SD_OnT Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGTGGATGTGGAGGAAGAG

PD-1_Ex.1_SD_OnT.1	CACCTACCTAAGAACCATCC	PD-1_Ex.1_SD_OnT Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCTGCCAGGGACTGAGAGT
PD-1_Ex.1_SD_OnT.1	CACCTACCTAAGAACCATCC	PD-1_Ex.1_SD_OnT Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACGTGGATGTGGAGGAAG
PD-1_Ex.1_SD_OT1.1	CGGCCACCTGAGAACCATCC	PD-1_Ex.1_SD_OT1 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTCACTTCTATCCCACACC
PD-1_Ex.1_SD_OT1.1	CGGCCACCTGAGAACCATCC	PD-1_Ex.1_SD_OT1 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAGTTCTCTGGTTCCTGTG
PD-1_Ex.1_SD_OT1.1	CGGCCACCTGAGAACCATCC	PD-1_Ex.1_SD_OT1 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTCACTTCTATCCCACACC
PD-1_Ex.1_SD_OT1.1	CGGCCACCTGAGAACCATCC	PD-1_Ex.1_SD_OT1 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAAAAGTTCTCTGGTTCCTG
PD-1_Ex.1_SD_OT2.1	ACCTGACCTAAGAACCATCC	PD-1_Ex.1_SD_OT2 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGGCCACTTGTGCTAGAG
PD-1_Ex.1_SD_OT2.1	ACCTGACCTAAGAACCATCC	PD-1_Ex.1_SD_OT2 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGACTAGTGCCCATGATAGCAG
PD-1_Ex.1_SD_OT2.1	ACCTGACCTAAGAACCATCC	PD-1_Ex.1_SD_OT2 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCATGTACACGTCTGACCACT
PD-1_Ex.1_SD_OT2.1	ACCTGACCTAAGAACCATCC	PD-1_Ex.1_SD_OT2 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAATTTACTAGTGCCCATGAT
PD-1_Ex.1_SD_OT3.1	CTTCTATCTCAGAACCATCC	PD-1_Ex.1_SD_OT3 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACACTAACGATTGCTGATGA
PD-1_Ex.1_SD_OT3.1	CTTCTATCTCAGAACCATCC	PD-1_Ex.1_SD_OT3 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTCTCACTCGCTCTTTCTC
PD-1_Ex.1_SD_OT3.1	CTTCTATCTCAGAACCATCC	PD-1_Ex.1_SD_OT3 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCACTAACGATTGCTGATGAC
PD-1_Ex.1_SD_OT3.1	CTTCTATCTCAGAACCATCC	PD-1_Ex.1_SD_OT3 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTCTCACTCGCTCTTTCTC
PD-1_Ex.1_SD_OT4.1	TACCCAGCTCAGAACCATCC	PD-1_Ex.1_SD_OT4 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTCTAGCTTCTGCCTTCTC
PD-1_Ex.1_SD_OT4.1	TACCCAGCTCAGAACCATCC	PD-1_Ex.1_SD_OT4 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCTTTTCAGAATTGATGTG
PD-1_Ex.1_SD_OT4.1	TACCCAGCTCAGAACCATCC	PD-1_Ex.1_SD_OT4 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATTTCTAGCTTCTGCCTTCTC
PD-1_Ex.1_SD_OT4.1	TACCCAGCTCAGAACCATCC	PD-1_Ex.1_SD_OT4 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCTTTTCAGAATTGATGTG
PD-1_Ex.1_SD_OT5.1	CACTCACTTAAGTACCATCC	PD-1_Ex.1_SD_OT5 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGTAGTTCAGGGCTGTTAGG
PD-1_Ex.1_SD_OT5.1	CACTCACTTAAGTACCATCC	PD-1_Ex.1_SD_OT5 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTCAAAACTAACCAATCTGC
PD-1_Ex.1_SD_OT5.1	CACTCACTTAAGTACCATCC	PD-1_Ex.1_SD_OT5 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCTGTTAGGGAGACTGAGAA
PD-1_Ex.1_SD_OT5.1	CACTCACTTAAGTACCATCC	PD-1_Ex.1_SD_OT5 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTCAAAACTAACCAATCTGC
PD-1_Ex.1_SD_OT6.1	CACAAACCTGAGAACCATCG	PD-1_Ex.1_SD_OT6 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTGAGGAGGCATCCGAGT
PD-1_Ex.1_SD_OT6.1	CACAAACCTGAGAACCATCG	PD-1_Ex.1_SD_OT6 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCAAATTAAAGAATCTCTGAAAA

PD-1_Ex.1_SD_OT6.1	CACAAACCTGAGAACCATCG	PD-1_Ex.1_SD_OT6 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAGGAGGGGGTGAGGAG
PD-1_Ex.1_SD_OT6.1	CACAAACCTGAGAACCATCG	PD-1_Ex.1_SD_OT6 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAAGTAAAGCATTTCTGAATCC
PD-1_Ex.1_SD_OT7.1	CACCTCCATTTGAACCATCC	PD-1_Ex.1_SD_OT7 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACCCTGCACAGAACCTATAA
PD-1_Ex.1_SD_OT7.1	CACCTCCATTTGAACCATCC	PD-1_Ex.1_SD_OT7 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAGGACTTGGCTTGTCTTCT
PD-1_Ex.1_SD_OT7.1	CACCTCCATTTGAACCATCC	PD-1_Ex.1_SD_OT7 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACCCTGCACAGAACCTATAA
PD-1_Ex.1_SD_OT7.1	CACCTCCATTTGAACCATCC	PD-1_Ex.1_SD_OT7 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGACTTGGCTTGTCTTCTGAT
PD-1_Ex.1_SD_OT8.1	CACCCACCTAAGCACCATCT	PD-1_Ex.1_SD_OT8 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTATTTCATATTGGGTGGA
PD-1_Ex.1_SD_OT8.1	CACCCACCTAAGCACCATCT	PD-1_Ex.1_SD_OT8 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCAAAACACAGGGAAAACT
PD-1_Ex.1_SD_OT8.1	CACCCACCTAAGCACCATCT	PD-1_Ex.1_SD_OT8 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTCATATTGGGTGGATTGT
PD-1_Ex.1_SD_OT8.1	CACCCACCTAAGCACCATCT	PD-1_Ex.1_SD_OT8 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTCAAAACACAGGGAAAACT
PD-1_Ex.1_SD_OT9.1	CACCTTCATCAGAACCATCT	PD-1_Ex.1_SD_OT9 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAGCATCACCTGTGTAAC
PD-1_Ex.1_SD_OT9.1	CACCTTCATCAGAACCATCT	PD-1_Ex.1_SD_OT9 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAAGTAAAAAGCAGAGGAAGC
PD-1_Ex.1_SD_OT9.1	CACCTTCATCAGAACCATCT	PD-1_Ex.1_SD_OT9 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGCAGCATCACCTGTGTAA
PD-1_Ex.1_SD_OT9.1	CACCTTCATCAGAACCATCT	PD-1_Ex.1_SD_OT9 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAAGTAAAAAGCAGAGGAAGC
PD-1_Ex.1_SD_OT10.1	CAGCTATCTCAGAACCTTCC	PD-1_Ex.1_SD_OT10 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTACATGTTTTCTATATGAGGCATT
PD-1_Ex.1_SD_OT10.1	CAGCTATCTCAGAACCTTCC	PD-1_Ex.1_SD_OT10 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTCCTCTAAGTCTCAGCTCAT
PD-1_Ex.1_SD_OT10.1	CAGCTATCTCAGAACCTTCC	PD-1_Ex.1_SD_OT10 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTTTCTATTTTTCCATACTTTTTAG
PD-1_Ex.1_SD_OT10.1	CAGCTATCTCAGAACCTTCC	PD-1_Ex.1_SD_OT10 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGCCTTTCAGATTAGTCAGG
TRAC2_Ex.3_SA_OnT.1	TTCGTATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OnT Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTCAGAGCTTAGGATGCAC
TRAC2_Ex.3_SA_OnT.1	TTCGTATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OnT Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTTGAAACACAATACTGTTGG
TRAC2_Ex.3_SA_OnT.1	TTCGTATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OnT Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTCAGAGCTTAGGATGCAC
TRAC2_Ex.3_SA_OnT.1	TTCGTATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OnT Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTGAAACACAATACTGTTGG
TRAC2_Ex.3_SA_OT1.1	TTGGGATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT1 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACATACATTGCCTTACTTTGC
TRAC2_Ex.3_SA_OT1.1	TTGGGATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT1 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTTTGACTGCCAGAAGGT

TRAC2_Ex.3_SA_OT1.1	TTGGGATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT1 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGACATACATTGCCTTACTTTGC
TRAC2_Ex.3_SA_OT1.1	TTGGGATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT1 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGAAGCCAAAAGTTATACATGA
TRAC2_Ex.3_SA_OT2.1	TGAGCATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT2 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAGTTTGGCATCTTCTTTACCT
TRAC2_Ex.3_SA_OT2.1	TGAGCATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT2 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGTGGGGCTTCTCATCAC
TRAC2_Ex.3_SA_OT2.1	TGAGCATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT2 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAGTTTGGCATCTTCTTTACC
TRAC2_Ex.3_SA_OT2.1	TGAGCATCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT2 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGTGGGGCTTCTCATCAC
TRAC2_Ex.3_SA_OT3.1	TTCTAATCTCTAAAACCAAG	TRAC2_Ex.3_SA_OT3 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAATGATAGATCCCAGCTGAA
TRAC2_Ex.3_SA_OT3.1	TTCTAATCTCTAAAACCAAG	TRAC2_Ex.3_SA_OT3 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGCTTTCCTCCTTGCATGTATT
TRAC2_Ex.3_SA_OT3.1	TTCTAATCTCTAAAACCAAG	TRAC2_Ex.3_SA_OT3 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGGAGCCACAGATTAAATGAT
TRAC2_Ex.3_SA_OT3.1	TTCTAATCTCTAAAACCAAG	TRAC2_Ex.3_SA_OT3 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTCTTTCCTCCTTGCATGTAT
TRAC2_Ex.3_SA_OT4.1	GTGGTATCTGCAAAACCAAG	TRAC2_Ex.3_SA_OT4 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCATGAATGGTGACTCAGAA
TRAC2_Ex.3_SA_OT4.1	GTGGTATCTGCAAAACCAAG	TRAC2_Ex.3_SA_OT4 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAATGCCAGCCACTTTTT
TRAC2_Ex.3_SA_OT4.1	GTGGTATCTGCAAAACCAAG	TRAC2_Ex.3_SA_OT4 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAATCATGAATGGTGACTCAG
TRAC2_Ex.3_SA_OT4.1	GTGGTATCTGCAAAACCAAG	TRAC2_Ex.3_SA_OT4 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAAATGCCAGCCACTTTTT
TRAC2_Ex.3_SA_OT5.1	TCCTCATGTGTAAAACCAAG	TRAC2_Ex.3_SA_OT5 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCAAACCATATTAGCAAAC
TRAC2_Ex.3_SA_OT5.1	TCCTCATGTGTAAAACCAAG	TRAC2_Ex.3_SA_OT5 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTGAGTTCATGAGAATCGTG
TRAC2_Ex.3_SA_OT5.1	TCCTCATGTGTAAAACCAAG	TRAC2_Ex.3_SA_OT5 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCCAAACCATATTAGCAAAC
TRAC2_Ex.3_SA_OT5.1	TCCTCATGTGTAAAACCAAG	TRAC2_Ex.3_SA_OT5 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATTGAGTTCATGAGAATCGTG
TRAC2_Ex.3_SA_OT6.1	TCTGCATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT6 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAAACGTACACTGTAATGC
TRAC2_Ex.3_SA_OT6.1	TCTGCATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT6 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTTTGCTGAGACCATAGAT
TRAC2_Ex.3_SA_OT6.1	TCTGCATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT6 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGCAAACGTACACTGTAATGC
TRAC2_Ex.3_SA_OT6.1	TCTGCATCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT6 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGATGCTTTGCTGAGACCATAG
TRAC2_Ex.3_SA_OT7.1	TTTGTATCTTTAAAACCATG	TRAC2_Ex.3_SA_OT7 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAAAGTGCTGGGATTACAGA
TRAC2_Ex.3_SA_OT7.1	TTTGTATCTTTAAAACCATG	TRAC2_Ex.3_SA_OT7 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTGCAAAGTTTTATGTAGTTTAAGTG

TRAC2_Ex.3_SA_OT7.1	TTTGTATCTTTAAAACCATG	TRAC2_Ex.3_SA_OT7 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCAAAGTGCTGGGATTACAGA
TRAC2_Ex.3_SA_OT7.1	TTTGTATCTTTAAAACCATG	TRAC2_Ex.3_SA_OT7 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAATTTGCAAAGTTTTATGTAGTTT
TRAC2_Ex.3_SA_OT8.1	TTCTTATGTGTGAAACCAAG	TRAC2_Ex.3_SA_OT8 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTGGGACTCTTGGTTCTGTAT
TRAC2_Ex.3_SA_OT8.1	TTCTTATGTGTGAAACCAAG	TRAC2_Ex.3_SA_OT8 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTTTGTTGTTGTTTTACTTGAA
TRAC2_Ex.3_SA_OT8.1	TTCTTATGTGTGAAACCAAG	TRAC2_Ex.3_SA_OT8 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTTGGGACTCTTGGTTCTGTA
TRAC2_Ex.3_SA_OT8.1	TTCTTATGTGTGAAACCAAG	TRAC2_Ex.3_SA_OT8 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGTTTTTGTTGTTGTTTTACTTGAA
TRAC2_Ex.3_SA_OT9.1	CTCTCTTCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT9 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGAAATTCTTCTTGGGCTCAG
TRAC2_Ex.3_SA_OT9.1	CTCTCTTCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT9 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTCATTACTGGGTTAAGCA
TRAC2_Ex.3_SA_OT9.1	CTCTCTTCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT9 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGAAATTCTTCTTGGGCTCAG
TRAC2_Ex.3_SA_OT9.1	CTCTCTTCTGTAAAACCAAG	TRAC2_Ex.3_SA_OT9 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGCTCATTACTGGGTTAAGCA
TRAC2_Ex.3_SA_OT10.1	TGGGTTTCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT10 Fwd 1	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGTCTAGGCTCTTGACACCATC
TRAC2_Ex.3_SA_OT10.1	TGGGTTTCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT10 Rev 1	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAACAACTAGACCCAATGTGA
TRAC2_Ex.3_SA_OT10.1	TGGGTTTCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT10 Fwd 2	TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGGTCTAGGCTCTTGACACCAT
TRAC2_Ex.3_SA_OT10.1	TGGGTTTCTTTAAAACCAAG	TRAC2_Ex.3_SA_OT10 Rev 2	GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGAACAACTAGACCCAATGTGA

Supplemental Table 3. Primer and probe sequences used for ddPCR analysis.

Translocation	Forward Primer	Probe	Reverse Primer
B2M Exon 3 Reference	GGTTTCATCCATCCGACATTGAAGTTGAC	GACCAGTCCTTGCTGAAAGACAAGTCTG	GGGTGAATTCAGTGTAGTACAAGAGATAG
PDCD1:B2M	GGCATGCAGATCCCACAG	AAGTCACGGAGCGAGAGAGCAC	GGCCACCAAGGAGAACTTG
PDCD1:TRAC	GGCATGCAGATCCCACAG	CCTGTCAGTGATTGGGTTCCGAATCCTCCTCC	CATGAGCAGATTAAACCCGGCCAC
B2M:TRAC	ATGTCTCGCTCCGTGGCCTTAG	CCTGTCAGTGATTGGGTTCCGAATCCTCCTCC	CATGAGCAGATTAAACCCGGCCAC
B2M:PDCD1	GGGCATTCCTGAAGCTGAC	CCTTAGCTGTGCTCGCGCTACT	AGGGACTGAGGGTGGAAG
TRAC:B2M	CAGCCTGCTCTGCCTTG	CATGCAAGCCCATAACCGCTGTG	AAGTCACGGAGCGAGAGA
TRAC:PDCD1	CAGCCTGCTCTGCCTTG	CATGCAAGCCCATAACCGCTGTG	AGGGACTGAGGGTGGAAG
TRAC:PD1 OT2.1	CAGCCTGCTCTGCCTTG	CATGCAAGCCCATAACCGCTGTG	GTTGGCTAAGAATCTGAGAAGGG
B2M:PD1 OT2.1	GGGCATTCCTGAAGCTGAC	CCTTAGCTGTGCTCGCGCTACT	GTTGGCTAAGAATCTGAGAAGGG
PD1:PD1 OT2.1	GGCATGCAGATCCCACAG	TCTGGGCGGTGCTACAACTGG	TCTGGGCGGTGCTACAACTGG
PD1 OT2.1:TRAC	AGAGAGAGAGACGCATGGTCAACC	CCTGTCAGTGATTGGGTTCCGAATCCTCCTCC	CATGAGCAGATTAAACCCGGCCAC
PD1 OT2.1:B2M	CCACTGTTTTACTTCTAGCCAGTC	AAGTCACGGAGCGAGAGAGCAC	GGCCACCAAGGAGAACTTG
PD1 OT2.1:PD1	CCACTGTTTTACTTCTAGCCAGTC	CAGGGACTGAGGGTGGAAGGTC	CAGGGACTGAGAGTGAAAGGTC

Supplemental Table 4. Primers used for Sanger sequencing and EditR analysis.

Target Site	Primer Name	Primer Sequence
PDCD1 Ex1 SD	PD1 Ex1 SD Fwd	ACCCTCCCTTCAACCTGAC
	PD1 Ex1 SD Rev	AAGCCACACAGCTCAGGGTA
PDCD1 Ex2	PD1 Ex2 Fwd	GCCTCACGTAGAAGGAAGAGG
	PD1 Ex2 Rev	CAGTTGTGTGACACGGAAGC
PDCD1 Ex3	PD1 Ex3 Fwd	ACCGGCATCTCTGTCCTCTA
	PD1 Ex3 Rev	CTTAGTCCAGGGGCCTTCAT
PDCD1 Ex4	PD1 Ex4 Fwd	AAACCCTGGTGGTTGGTGTCG
	PD1 Ex4 Rev	GGTCCTGGCTATAATAGAATGTGAGTCC
TRAC Ex1	TRAC Ex1 Fwd	TCACGAGCAGCTGGTTTCTA
	TRAC Ex1 Rev	CCATTCCTGAAGCAAGGAAA
TRAC Ex3	TRAC Ex3 Fwd	GGACCCGAGGTATTGTGATG
	TRAC Ex3 Rev	TTAGGATGCACCCAGAGACC
B2M Ex1	B2M Ex1 Fwd	TTGGAGACAGGTGACGGTCC
	B2M Ex1 Rev	TTATCGACGCCCTAAACTTTGTCC
B2M Ex2	B2M Ex2 Fwd	GGTGCCTGATATAGCTTGACACC
	B2M Ex2 Rev	GACTCATTCAGGGTAGTATGGCC
B2M Ex3	B2M Ex3 Fwd	GTTTGTAAGTCCTGCTGTCCTAGC
	B2M Ex3 Rev	CCTGTAGGATTCTTCTTTCCCTGC

Supplemental Table 5. Primer sequences used for OT RNA editing analysis.

Primer	Sequence	Product Size
CDV3 cDNA Ex.5 Fwd 1	AGCCTTTTGGTGTGTCTTTA	525
CDV3 cDNA Ex.5 Rev 1	GCTCAGTTACTCACCCAAAT	
CDV3 cDNA Ex.5 Fwd 2	AGCGTTTTCAGATAGGAGTTT	522
CDV3 cDNA Ex.5 Rev 2	GTACAATGGACAGCCTCATC	
CYCS cDNA Ex.3 Fwd	GGTATCACTGTTTACCCCTTT	510
CYCS cDNA Ex.3 Rev	TGGCTGTTTAAAGACAATCC	
DDX21 cDNA Ex.15 Fwd	CTCAAAAGTGTCCCTTAATAGTG	553
DDX21 cDNA Ex.15 Rev	TCTTGAGCAATGCTAATCTG	
RPL37 cDNA Ex.4 Fwd 1	CTTGACCTGACCCATGTATT	420
RPL37 cDNA Ex.4 Rev 1	CAAGGATAACTACCCAGCAG	
RPL37 cDNA Ex.4 Fwd 2	ACCCCTTCTGTATCCTTGAT	384
RPL37 cDNA Ex.4 Rev 2	GCCTTTCTCCTGTACTGTTTT	
RPS12 cDNA Fwd	TGCGTTCAAGATTCAACTTC	458
RPS12 cDNA Rev	TGTGAGCCAAAGATTTATTTC	

Supplemental Note: Amino Acid Sequence of coBE4.

```
MSSETGPVAVDPTLRRRIEPHEFEVFFDPRELRKETCLLYEINWGGRHSIWRHTSQNT
NKHVEVNFIEKFTTERYFCPNTRCSITWFLSWSPCGECSRAITEFLSRYPHVTLFIYIAR
LYHHADPRNRQGLRDLISSGVTIQIMTEQESGYCWRNFVNYSPSNEAHWPRYPHLWV
RLYVLELYCIILGLPPCLNILRRKQPQLTFFTIALQSCHYQRLPPHILWATGLKSGGSSG
GSSGSETPGTSESATPESSGGSSGGSDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFK
VLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKV
DDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRL
IYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSA
RLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDD
DLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTL
LKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLN
REDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPL
ARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHS
LLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKI
ECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIE
ERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR
NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKV
MGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQN
EKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGK
SDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVET
RQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHA
HDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIM
NFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTG
GFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVK
ELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQK
GNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVIL
ADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEV
LDATLIHQSITGLYETRIDLSQLGGDSGGSGGSGGSTNLSDIIEKETGKQLVIQESILMLP
EEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLS
GGSGGSGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTD
ENVMLLTSDAPEYKPWALVIQDSNGENKIKMLSGGSKRTADGSEFESPKKKRKVE*
```