

Supplementary Material

T-CAST: An optimized CAST-Seq pipeline for TALEN confirms superior safety and efficacy of obligate-heterodimeric scaffolds

Manuel Rhiel^{†1,2}, **Kerstin Geiger**^{†1,2,3}, **Geoffroy Andrieux**^{4,5,6}, **Julia Rositzka**^{1,2}, **Melanie Boerries**^{4,5,6,7}, **Toni Cathomen**^{1,2,6}, **Tatjana I Cornu**^{* 1,2,6}

¹ Institute for Transfusion Medicine and Gene Therapy, Medical Center-University of Freiburg, 79106 Freiburg, Germany.

² Center for Chronic Immunodeficiency (CCI), Medical Center-University of Freiburg, 79106 Freiburg, Germany.

³ Ph.D. Program, Faculty of Biology, University of Freiburg, 79104 Freiburg, Germany

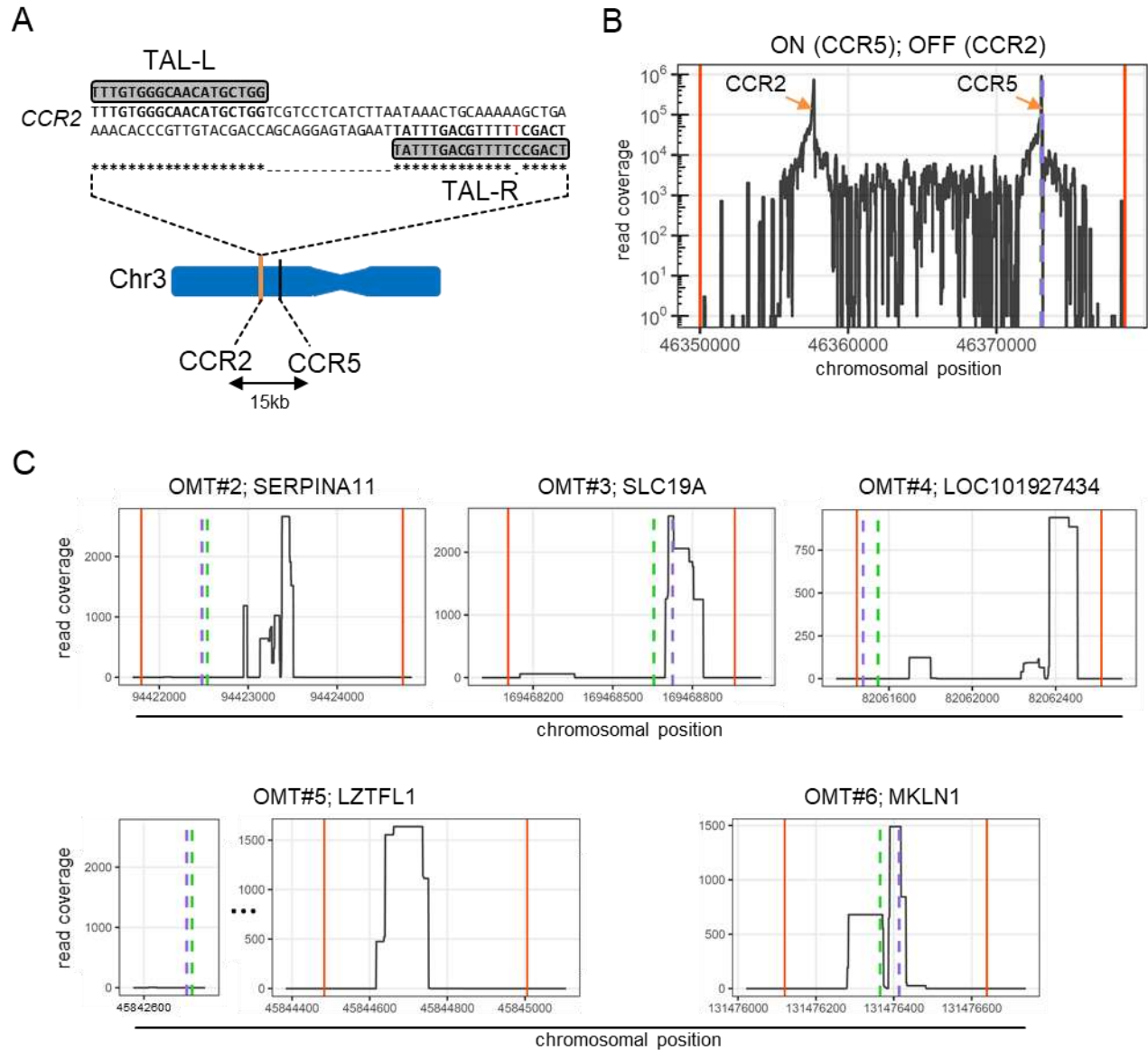
⁴ Institute of Medical Bioinformatics and Systems Medicine, Medical Center-University of Freiburg, Faculty of Medicine, University of Freiburg, Freiburg, Germany.

⁵ German Cancer Consortium (DKTK), Partner Site Freiburg, and German Cancer Research Center (DKFZ), Heidelberg, Germany.

⁶ Faculty of Medicine, University of Freiburg, 79106 Freiburg, Germany.

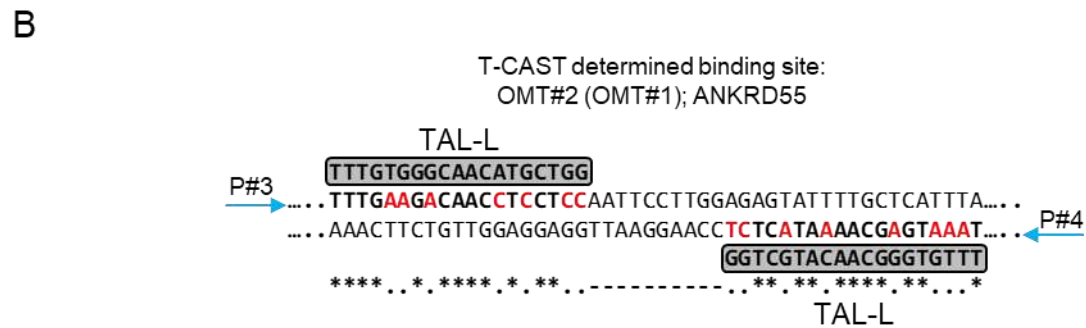
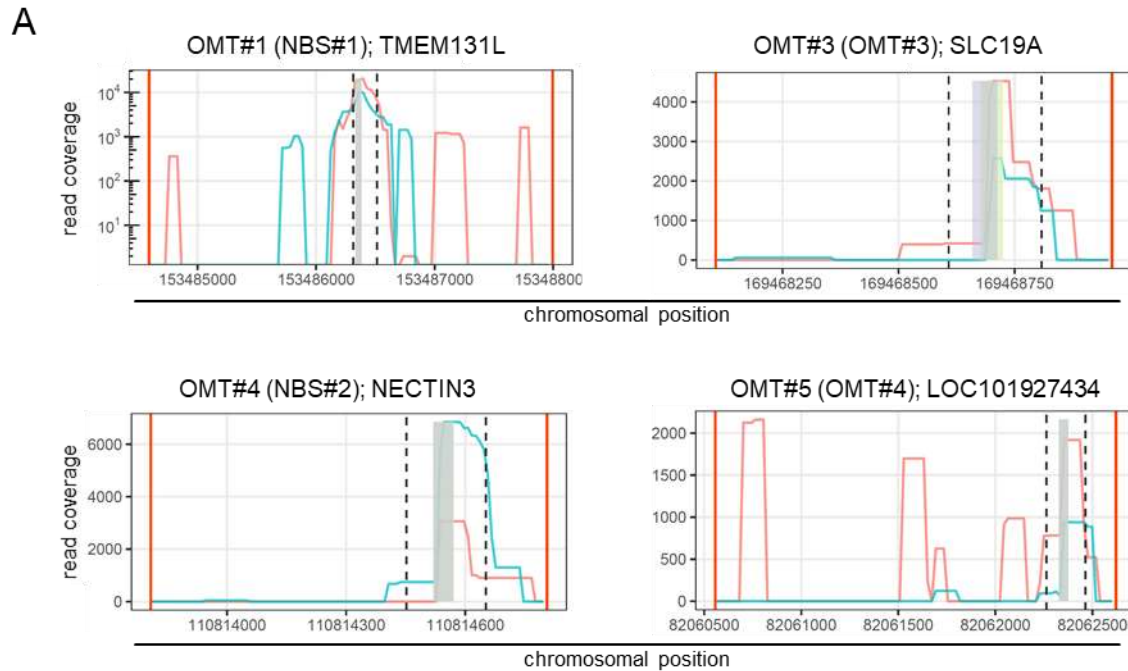
⁷ Comprehensive Cancer Center Freiburg (CCCF), Medical Center – University of Freiburg, 79106 Freiburg, Germany

Correspondence: Corresponding Author Tatjana.Cornu@uniklinik-freiburg.de



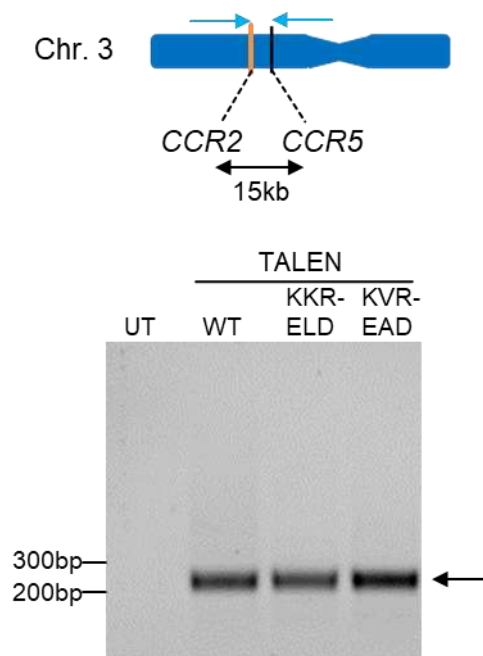
Supplementary Figure 1. CAST-Seq read coverage at on- and off-target sites of CCR5-targeting TALEN

(A) Alignment. Illustrated is the CAST-Seq alignment for *CCR2* to both TALEN arms. Mismatched bases are highlighted in red letters, the relative location with respect to the *CCR5* target site is illustrated on the bottom. (B) Coverage plot for the *CCR5-CCR2* region. Plot shows chromosomal position vs. number of reads. (C) Coverage plots for off-target regions. Green and purple dotted lines indicate the putative TALEN binding sites predicted by CAST-Seq.



Supplementary Figure 2. Coverage plot-based nomination of off-target sites by T-CAST

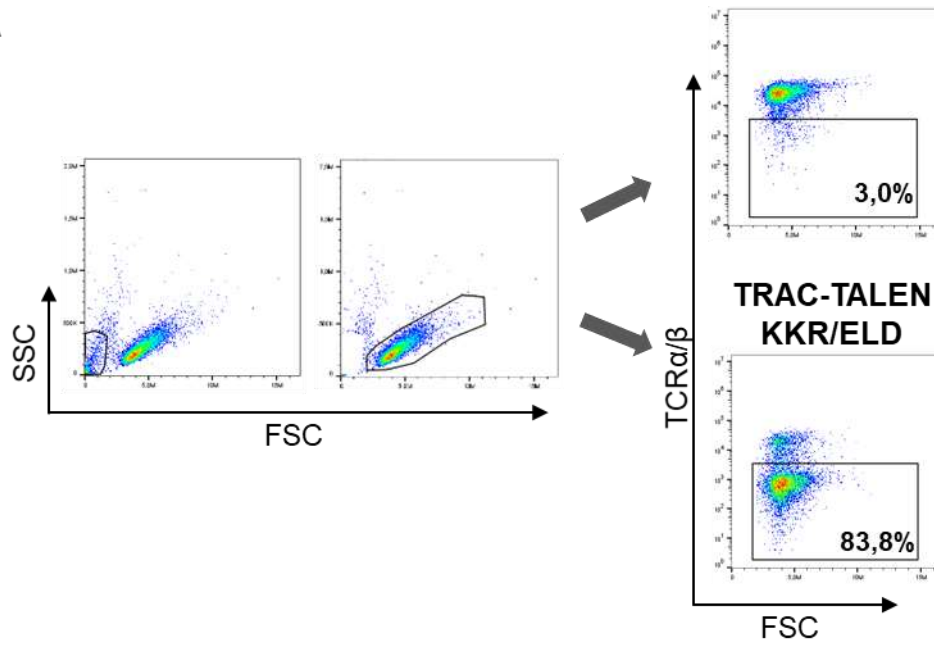
(A) Coverage plots for off-target regions. Black dotted lines indicate the region (± 100 bp) flanking the bin with highest coverage (grey). Plots show coverage of two replicates (turquoise, light red) at indicated OMTs. The former nomination based on the CAST-Seq is given in brackets. Red vertical lines denote boundary of entire region. (B) Alignment. Illustrated is T-CAST based alignment for ANKRD55 (OMT#2) to two left TALEN arms. Mismatched bases are denoted by dots, primer binding sites used for validation (P#3/P#4) are indicated by arrows.



Supplementary Figure 3. Large deletion between *CCR5* and *CCR2*

Schematic specifying the PCR primer positions (blue arrows) used to amplify the *CCR2-CCR5* junction is shown on top. PCR products were analyzed by agarose gel electrophoresis. The positions of the expected PCR amplicon (arrow) and size markers are indicated.

A



Supplementary Figure 4. TALEN-mediated *TRAC* knockout

(A) Gating strategy. Shown is a representative flow cytometry analysis to assess the reduction in TCRα/β surface expression after disruption of *TRAC*. Debris was excluded through gating, and TCRα/β expression was assessed in living cells.

Supplementary Tables

S1: Target sites and RVDs of CCR5 and TRAC TALEN

S2: Prognos analysis of CCR5 TALEN

S3: Prognos analysis of TRAC TALEN

S4: CAST-Seq output analysis of CCR5 WT TALEN

S5: T-CAST output file of CCR5 WT TALEN

S6: T-CAST output file of CCR5 KKR-ELD TALEN

S7: T-CAST output file of CCR5 KVR-EAD TALEN

S8: T-CAST output file of TRAC WT TALEN

S9: T-CAST output file of TRAC KKR-ELD TALEN

S10: T-CAST output file of TRAC KVR-EAD TALEN

S11: Oligonucleotides used in this study

S12: T-CAST substitution matrix