

TENT5C/FAM46C modulation *in vivo* reveals a trade-off between antibody secretion and tumor growth in multiple myeloma

Authors

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SUPPLEMENTARY TABLE

Antibody		
<i>mouse anti-β-Actin</i>	Sigma-Aldrich	A5441
<i>rabbit anti-Calreticulin</i>	GeneTex	GTX111627
<i>rabbit anti Calnexin</i>	Sigma-Aldrich	C4731
<i>rabbit anti-ERGIC53</i>	Sigma-Aldrich	E1031
<i>rabbit anti-CD68</i>	Cell Signaling	97778
<i>rabbit anti-lambda light chains</i>	Dako	A0194
<i>rabbit anti-H3</i>	Abcam	ab1791
<i>rabbit anti-PDI</i>	kindly provided by Dr. Ineke Braakman Lab	Utrecht, NL
<i>rabbit anti-PRDX4</i>	AbFrontier	PA0009
<i>rabbit anti-PRDX4</i>	Proteintech	10703-1-AP
<i>rabbit anti-TENT5C</i>	Proteintech	25038-1-AP
<i>Alexa Fluor 546 goat anti-mouse IgG</i>	Life Technologies	A11030
<i>Alexa Fluor 546 goat anti-rabbit IgG</i>	Life Technologies	A11010
<i>Alexa Fluor 647 goat anti-rabbit IgG</i>	Life Technologies	A21245
<i>Alexa Fluor 647 goat anti-mouse IgG</i>	Life Technologies	A21236
<i>Anti-rabbit IgG, HRP-linked</i>	Southern Biotech	4050-05
<i>Anti-mouse IgG, HRP-linked</i>	Southern Biotech	1031-05
<i>PE mouse IgG1 k isotype control</i>	Biologend	400112
<i>PE mouse IgG1 anti-human CD38</i>	Biologend	303506
<i>PE mouse IgG1 anti-calreticulin clone FMC75</i>	Abcam	Ab83220
<i>Goat anti-Human IgG (H+L) Secondary Antibody, HRP</i>	Thermo Scientific	A18805
Primers	FW	REV
<i>hCNX/CANX</i>	GTAGCCCTTCCTGTGTTCCCT	TGACAGTGCCACCATCTTCT
<i>hERGIC53/LMAN1</i>	TCCGCAACAAACCCTATCCT	CGGCTCTTTCCAGGTTTCAG
<i>hGAPDH</i>	CCACATCGCTCAGACACCAT	GTGACCAGGCGCCCAATAC
<i>hH3</i>	GTGAAGAAACCTCATCGTTA CAGGCCTGGT	CTGCAAAGCACCGATAGCT GCGCTCTGGAA
<i>hHSPA5/BiP</i>	TAGCGTATGGTGCTGCTGTC	TGACACCTCCCACAGTTTCA
<i>hIGLV6-57</i>	CTGGGCTCCACTACTTCTCA CC	ATGGAGCCAGAGAACCGAT CA

<i>hMZB1</i>	AAATCTGGCAAAGGCAGAG A	CTAAGTCCTGGGCCTGTGAG
<i>hPDI/P4HB</i>	TCACATCCTGCTGTTCTTGC	GTCGCTGTTCGATGAAGATGA
<i>hPRDX4</i>	AACAGCTGTGATCGATGGA G	TCAAGTCTGTTCGCCAAAAGC
<i>hTENT5C/FAM46C</i>	CAGGCATCAAAGTGCACGA C	AGCTTGTTACACCCTCTGG
<i>mCd206/Mrc1</i>	ATGCCAAGTGGGAAAATCT G	TGTAGCAGTGGCCTGCATAG
<i>mCd31/Pecam1</i>	AGGGGACCAGCTGCACATT AGG	AGGCCGCTTCTCTTGACCAC T
<i>mCd45/Ptprc</i>	GGAGACCAGGAAGTCTGTG C	GTTCTGGGCTCCTTCCTCTT
<i>mCd68</i>	CTGACAAGGGACACTTCGG G	AGGCCAATGATGAGAGGCA G
<i>mH3</i>	GTGAAGAAACCTCATCGTTA CAGGCCTGGT	CTGCAAAGCACCAATAGCT GCACTCTGGAA
<i>mTent5c</i>	TCACCTCCTCTTCCAACGCC	AGGTTGGAAAGTTGCCTCGC

Table S1: List of antibodies and primers used.

SUPPLEMENTARY FIGURES:

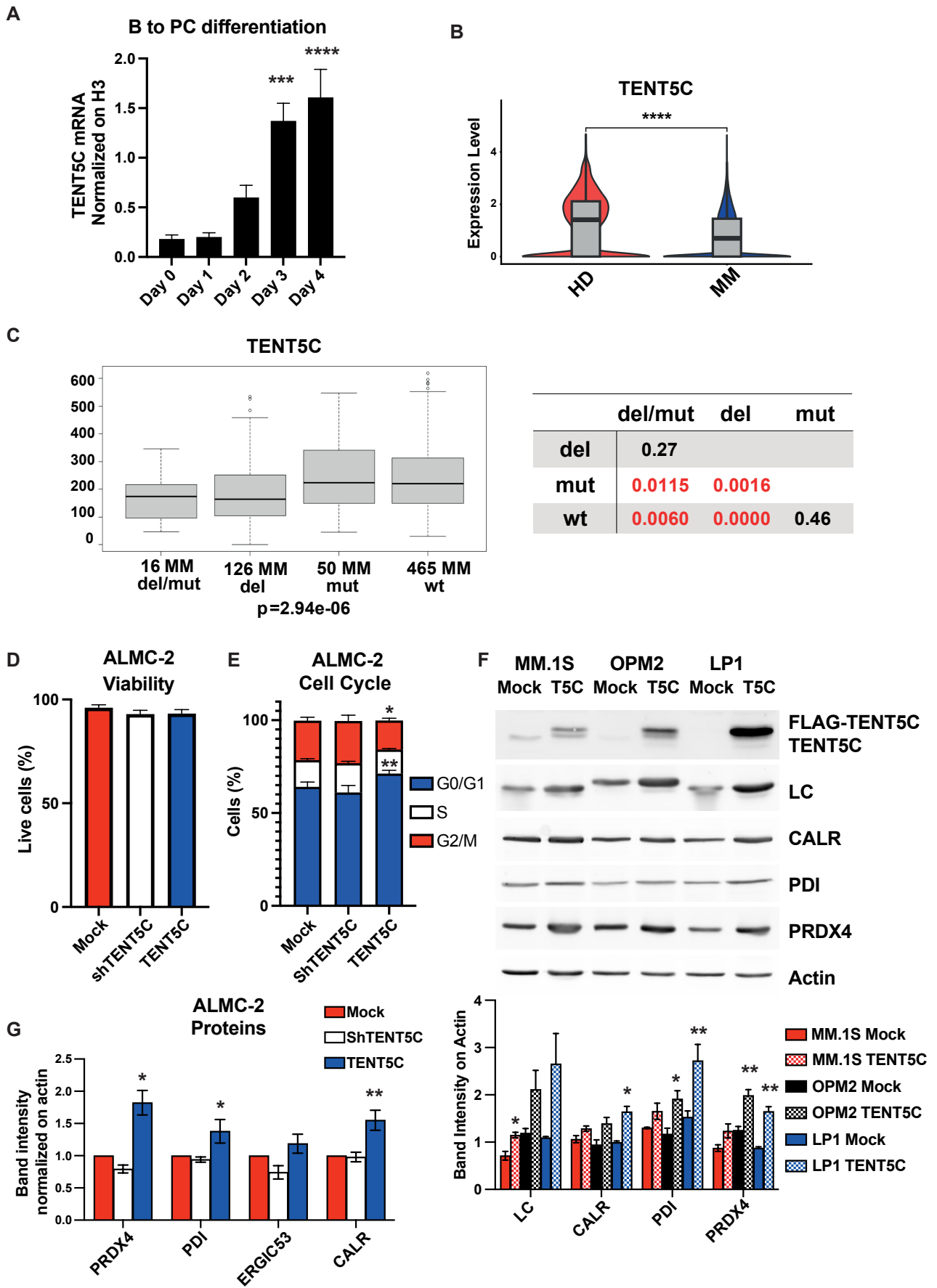


Figure S1 associated to Figure 1. (A) qRT-PCR analysis of TENT5C mRNA levels in LPS-activated murine splenic B cells, (mean \pm SEM normalized on H3 mRNA; n=6; ***p < 0.001; ****p < 0.0001; Ordinary One-way ANOVA with Dunnett's multiple comparison versus Day 0). Primary murine PCs were obtained by LPS-stimulation of purified splenic B cells from C57BL/6 wild-type mice (Charles River), as previously described in Pengo et al., Nat Immunol, 2013. **(B)** TENT5C expression levels in 6 healthy donors (5 derived from the public dataset GSE230705, Duan et al., Cell Reports, 2023) and 18 newly diagnosed multiple myeloma (MM) patients were measured by single cell RNA sequencing and have been integrated in a single Seurat object. Primary bone marrow samples were collected at the Hematology Department of Fondazione IRCCS Cà Granda, Ospedale Maggiore Policlinico-Milano (Italy). This study was approved by the local Ethics Committee (949/21), and all patients signed written consent in accordance with the Declaration of Helsinki. Briefly, purified PCs were counted and loaded into the Chromium Single Cell Chip G (PN-1000120) to yield a recovery of 9,000 single-cell transcriptomes. Subsequently, the libraries were pooled and sequenced on a NovaSeq6000 platform (Illumina) with a 150bp Paired End protocol. Raw sequences were preprocessed using Cell Ranger (version 5.0.0) pipelines using GRCh38 human reference transcriptome. Batch effect was corrected by Harmony (github.com/immunogenomics/harmony, v1.0) using "place" state as the variable on which compute the correction. Vlnplot was generated using "vlnplot" function by Seurat. Wilcoxon test was applied through "stat_compare_means" function: ****p < 0.0001. **(C)** Left, box plot of TENT5C expression level in 660 multiple myeloma cases freely accessible from MMRF CoMMpass Study (<https://research.themmr.org/>) retrieved from the Interim Analysis 15a. Transcript per Million (TPM) reads values of the TENT5C transcript were retrieved using Salmon gene expression quantification data (MMRF_CoMMpass_IA15a_E74GTF_Salmon_V7.2_Filtered_Gene_TPM). Non-synonymous (NS) somatic mutation variants and counts data were obtained from whole exome sequencing (WES) analyses, and Copy Number Alteration (CNA) data were retrieved by means of NGS-based FISH (Miller et al., Blood, 2016). The presence of a specific CNA was considered when occurring in at least one of the investigated cytoband at a 20 percent cut-off for each considered chromosomal aberration (Todoerti et al., Haematologica. 2021). Patients were stratified based on the presence of both TENT5C deletions and mutations (16 MM del/mut); presence of TENT5C deletions (126 MM del); presence of TENT5C mutations (50 MM mut); absence of TENT5C deletions or mutations (465 MM wt). Right, the significant pairwise comparisons performed by the Dunn's test are marked red-bold in the table. **(D)** Equal numbers of mock, TENT5C-silenced or overexpressing ALMC-2 cells were seeded and counted with trypan blue staining after 2 days, (mean \pm SEM; n=6). **(E)** Cytofluorimetric analysis of cell cycle phase in

control, TENT5C-silenced and overexpressing ALMC-2 cells. After fixation in 70% ethanol, ALMC-2 cells were stained with propidium iodide (50 μ g/mL PI, 10 μ g/mL RNase in PBS) and analyzed with a BD FACSCanto II (mean \pm SEM; n=6; *p < 0.05; **p < 0.01; Repeated measure one-way ANOVA with Dunnett's multiple comparison versus Mock). **(F)** Immunoblots of selected endoplasmic reticulum (ER)-resident proteins and IgG λ in TENT5C control or overexpressing MM cells. Top, representative images; bottom, quantification of band intensities of 3 independent experiments normalized on actin (mean \pm SEM; *p < 0.05; **p < 0.01; unpaired t test). **(G)** Quantification of band intensities of at least 5 independent experiments normalized on actin represented in **Figure 1E** (mean \pm SEM; *p < 0.05; **p < 0.01; Kruskal-Wallis one-way test with Dunn's multiple comparison versus Mock).

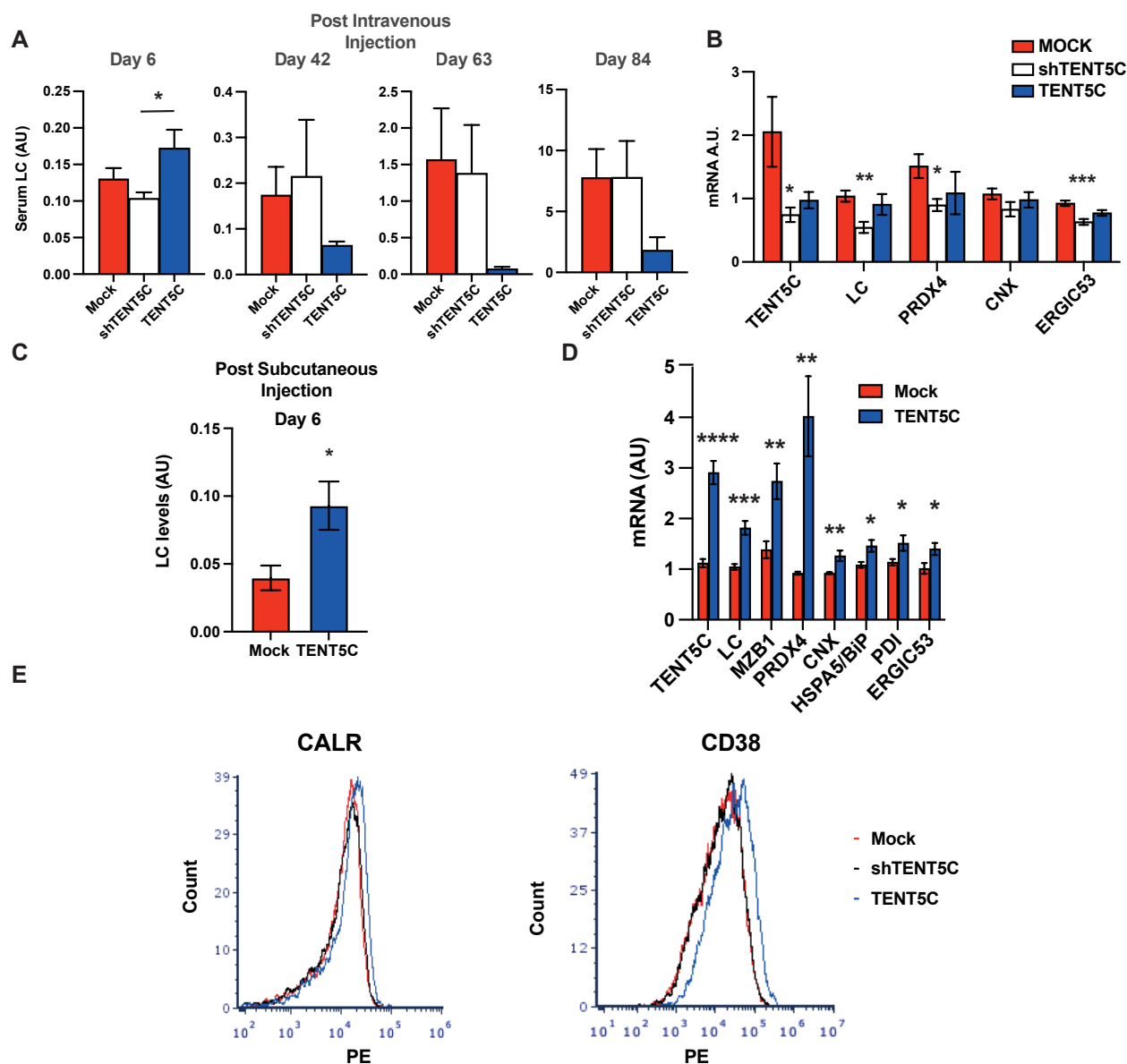


Figure S2 associated to Figure 2 and 3. (A) Quantifications of immunoblot analyses for the Ig λ LC in 1 μ l of serum collected at the indicated timepoints from mice intravenously injected with control, TENT5C-silenced or overexpressing ALMC-2 cells, (mean \pm SEM; n=8 per group; *p < 0.05; Ordinary one-way ANOVA). **(B)** qRT-PCR analysis of TENT5C, IGLV6-57 and selected ER-targeted mRNAs in excised plasmacytomas (mean \pm SEM normalized on GAPDH mRNA; n=6 Mock, 7 shTENT5C and 4 TENT5C; *p < 0.05; **p < 0.01; ***p < 0.001; Ordinary One-way ANOVA with Dunnett's multiple comparison versus Mock). Total RNA was extracted from tumor biopsies by homogenization in TriFAST (Euroclone, EMR507100). 1000 ng of RNA were retro-transcribed with PrimeScriptTM RT reagent Kit with gDNA Eraser (Takara, RR047A). qPCRs were performed using iTaq SYBR Green Supermix (Bio-Rad, 1725122) on Bio-Rad CFX96 PCR. **(C)** Quantifications of immunoblot analyses for the Ig λ LC in 1 μ l of serum collected from the retro-orbital vein at the indicated timepoint from mice subcutaneously injected with control or

TENT5C-overexpressing ALMC-2 cells (mean \pm SEM; n=7 per group, *p < 0.05; unpaired t test). (D) qRT-PCR analysis of IGLV6-57 and selected ER-targeted mRNAs in excised subcutaneous tumors (mean \pm SEM normalized on GAPDH mRNA; n=7 Mock, 6 TENT5C; *p < 0.05; **p < 0.01; ***p < 0.001; ****p < 0.0001; unpaired t test). (E) Representative cytofluorimetry histograms of CALR and CD38 surface expression in control, TENT5C-overexpressing and silenced ALMC-2 cells.