

## Supplementary Material for

### Small-molecule inhibition of the acyl-lysine reader ENL as a strategy against acute myeloid leukemia

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Supplementary Table S17. Pol II S2P ChIP-seq normalized read counts at TSS + 300 bp to TES regions of different subsets of genes in MV4;11 cells treated with DMSO or TDI-11055 for 24 hours.

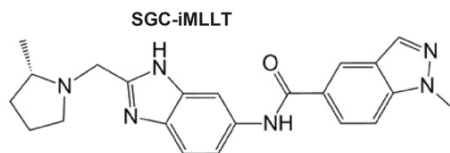
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Supplementary Table S20. Characterization of human primary patient samples used in this study.

Supplementary Table S21. Antibodies used in this study.

A



B

SGC-iMLLT Mouse PK	P.O., 30 mg/kg	P.O., 100 mg/kg
C <sub>max</sub> (nM, unbound)	727	13100
t <sub>max</sub> (h)	0.25	0.25
AUC <sub>inf</sub> (h.ng/mL)	1350	23131
t <sub>1/2</sub> (h)	0.84	0.83
F <sub>po</sub> (%)	41	210

C

Compound	TDI-11055	SGC-iMLLT
ENL, TR-FRET IC <sub>50</sub> (μM)	0.050*	0.121
AF9, TR-FRET IC <sub>50</sub> (μM)	0.066	0.218
GAS41, TR-FRET IC <sub>50</sub> (μM)	>100	>100
YEATS2, TR-FRET IC <sub>50</sub> (μM)	>100	N.A.

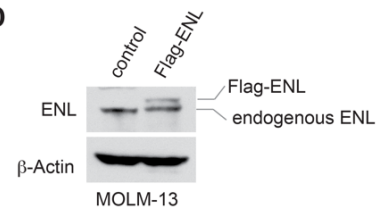
F

Parameter	TDI-11055
MW (g/mol)	388.5
LogD <sub>7.4</sub>	2.34
cpKa (strongest)	8.62 (basic)
Permeability (P <sub>app</sub> ) Caco-2 AB/BA/ER (10 <sup>-6</sup> cm/s)	6.1 / 14.3 / 2.4
Solubility PBS, pH7.4 (uM)	269
Solubility, FaSSIF (uM)	2500
Unbound fraction in plasma	0.31

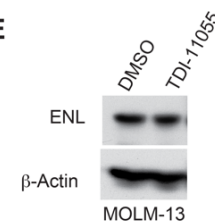
G

TDI-11055 Mouse PK	P.O., 30 mg/kg	P.O., 50 mg/kg	P.O., 100 mg/kg
t <sub>max</sub> (h)	0.5	0.5	0.5
C <sub>max</sub> (nM, unbound)	1181	1967	5596
AUC <sub>inf</sub> (h.ng/mL)	5512	9707	29151
AUC <sub>inf</sub> , unbound (h.ng/mL)	1709	3009	9037
t <sub>1/2</sub> (h)	2.7	2.8	5.0
F <sub>po</sub> (%)	109	116	173

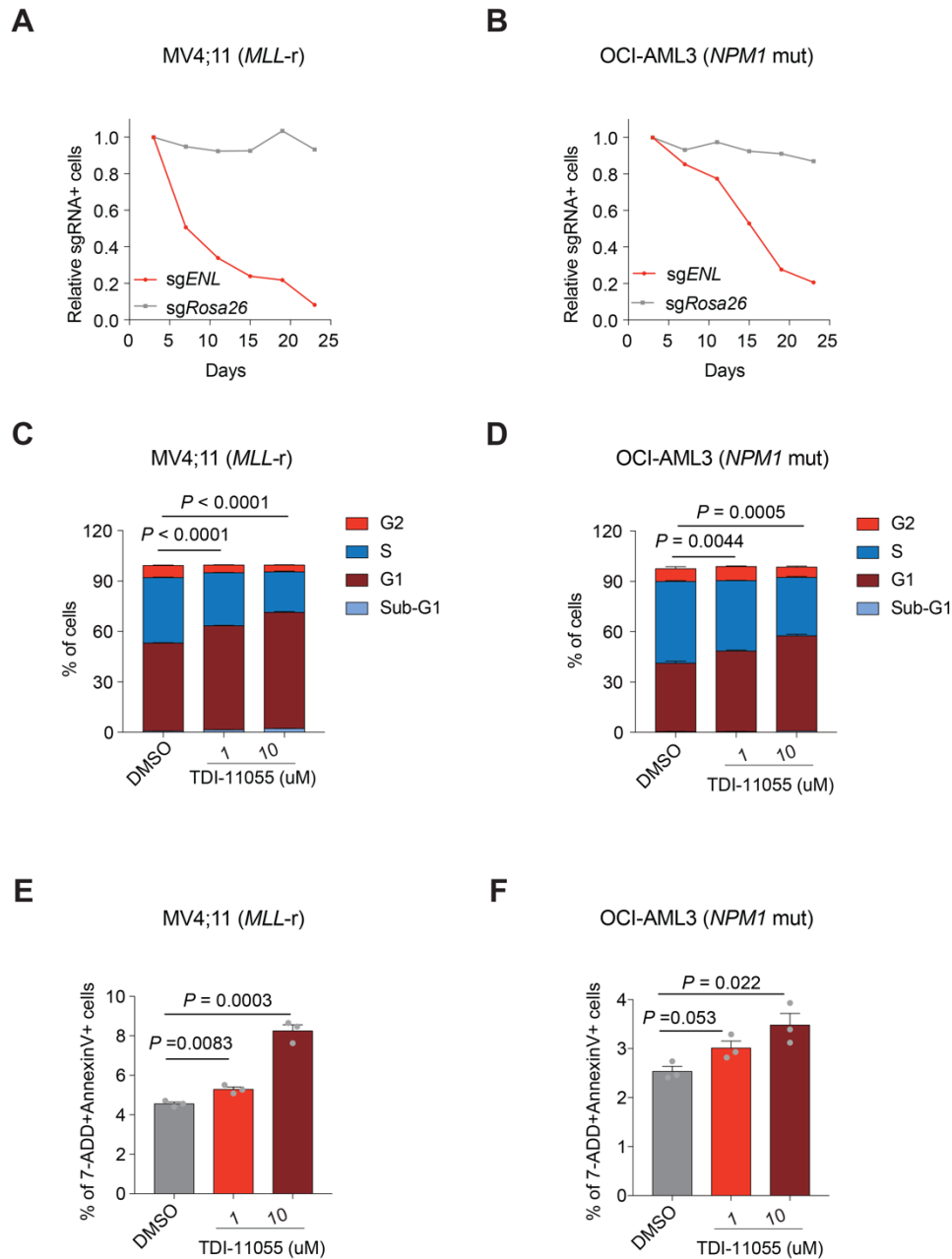
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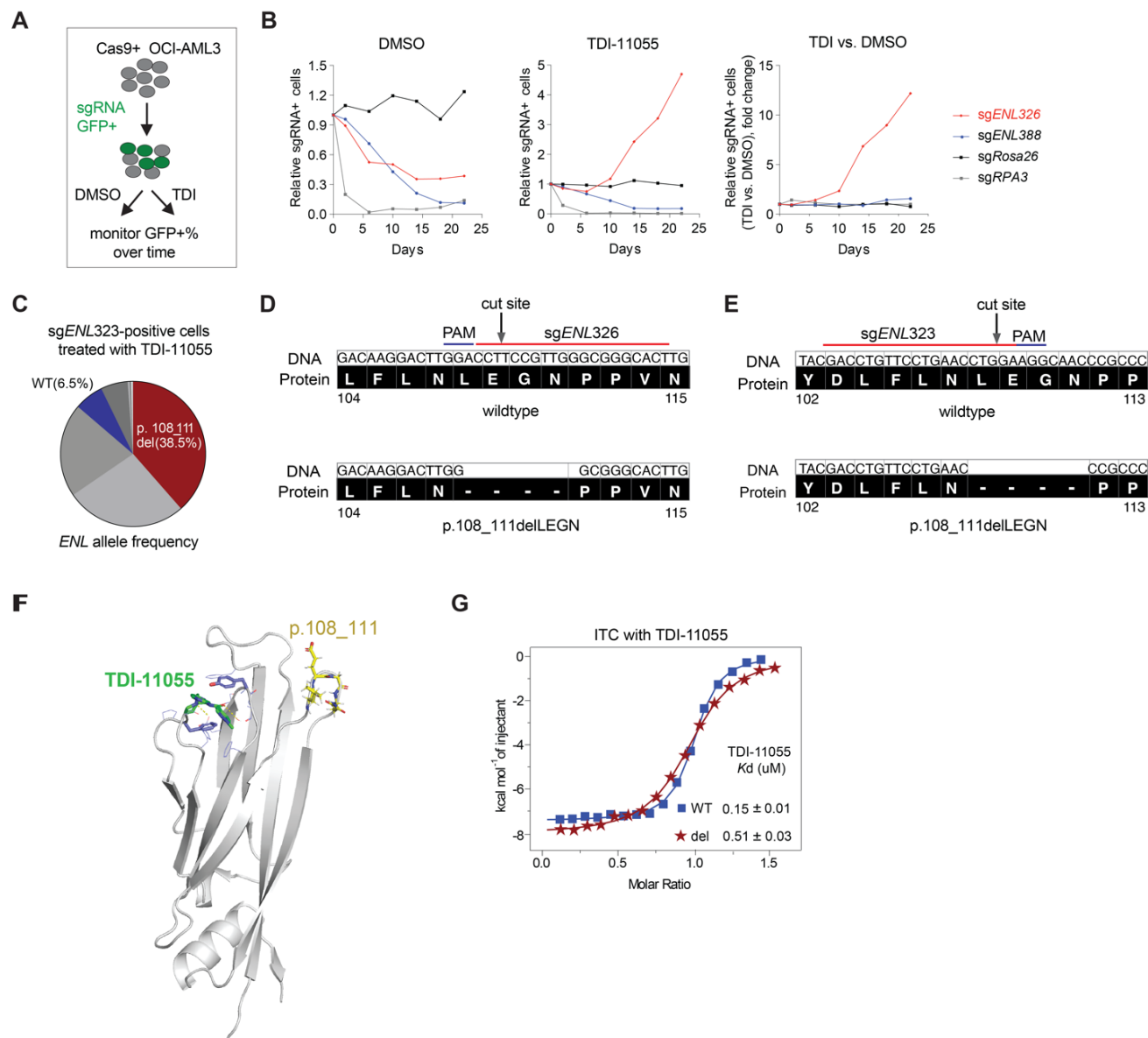
E



**Supplementary Figure S1. Development of a potent, selective, and orally bioavailable ENL/AF9 YEATS inhibitor.** **A**, Chemical structures of SGC-iMLLT. **B**, PK parameters for SGC-iMLLT upon oral administration at 30mg/kg and 100mg/kg doses to mice. Pharmacokinetic parameters: C<sub>max</sub> (maximum concentration achieved), *t*<sub>max</sub> (time at which the max concentration remained), AUC<sub>inf</sub> (area under the curve infinity), *t*<sup>1/2</sup> (time at which half of the max concentration remained), F<sub>po</sub> (oral bioavailability). P.O., (Per os), *n* = 3 mice / group. **C**, Table summarizing IC<sub>50</sub> concentrations for TDI-11055 and SGC-iMLLT obtained in TR-FRET (Time-resolved Fluorescence Resonance Energy Transfer) assays. Note (\*), as the ENL TR-FRET assays uses a protein concentration of 125 nM, its limit for potency measurements is approximately 62.5 nM. Therefore, the IC<sub>50</sub> of TDI-11055 may be lower than its reported value of 50 nM. **D**, Immunoblots showing levels of ectopically expressed Flag-ENL and endogenous ENL in MOLM-13 cells. β-Actin was used as loading control. **E**, Immunoblots showing levels of endogenous ENL proteins in MOLM-13 cells treated with DMSO or 5 μM TDI-11055 for 24 hours. β-Actin is used as loading control. **F**, Permeability parameters of TDI-11055 were measured in Caco2 cell monolayers. LogD<sub>7.4</sub> (partition coefficient between 1-octanol and aqueous buffer pH 7.4), cpKa (catalytic unit of protein kinase A), FaSSIF (Fasted State Simulated Intestinal Fluid). **G**, PK parameters for TDI-11055 upon oral administration at 30 mg/kg, 50 mg/kg, and 100 mg/kg to mice. Pharmacokinetic parameters: *t*<sub>max</sub> (time at which the max concentration was remained), C<sub>max</sub> (maximum concentration achieved), AUC<sub>inf</sub> (area under the curve infinity), *t*<sup>1/2</sup> (time at which half of the max concentration remained), F<sub>po</sub> (oral bioavailability). P.O. (Per os), *n* = 3 mice / group.



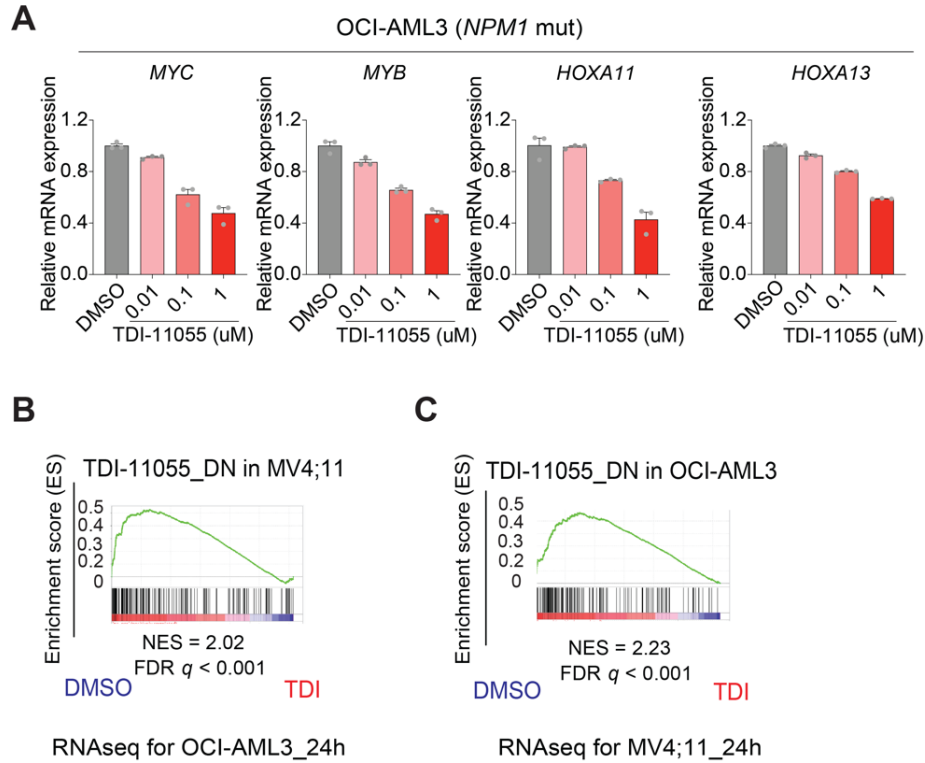
**Supplementary Figure S2. Inhibition of ENL suppresses cellular growth of *MLL-r* and *NPM1*-mutated leukemia cells.** **A, B**, A proliferation competition assay of MV4;11 (**A**), and OCI-AML3 (**B**) cells transduced with indicated sgRNAs. A sgRNA targeting Rosa26 (grey) serves as a negative control. **C, D**, Cell cycle analysis of MV4;11 (**C**) and OCI-AML3 (**D**) cells treated with DMSO or TDI-11055 (1 and 10  $\mu$ M) for 72 hours. Error bars represent mean  $\pm$  SEM ( $n = 3$ ).  $P$  value in G1 phase using unpaired two-tailed Student's  $t$ -test. **E, F**, Flow cytometric analysis showing the apoptosis percentage of MV4;11 (**E**) and OCI-AML3 (**F**) cells treat with DMSO or TDI-11055 (1 and 10  $\mu$ M) for 72 hours. Error bars represent mean  $\pm$  SEM ( $n = 3$ ).  $P$  value using unpaired two-tailed Student's  $t$ -test.



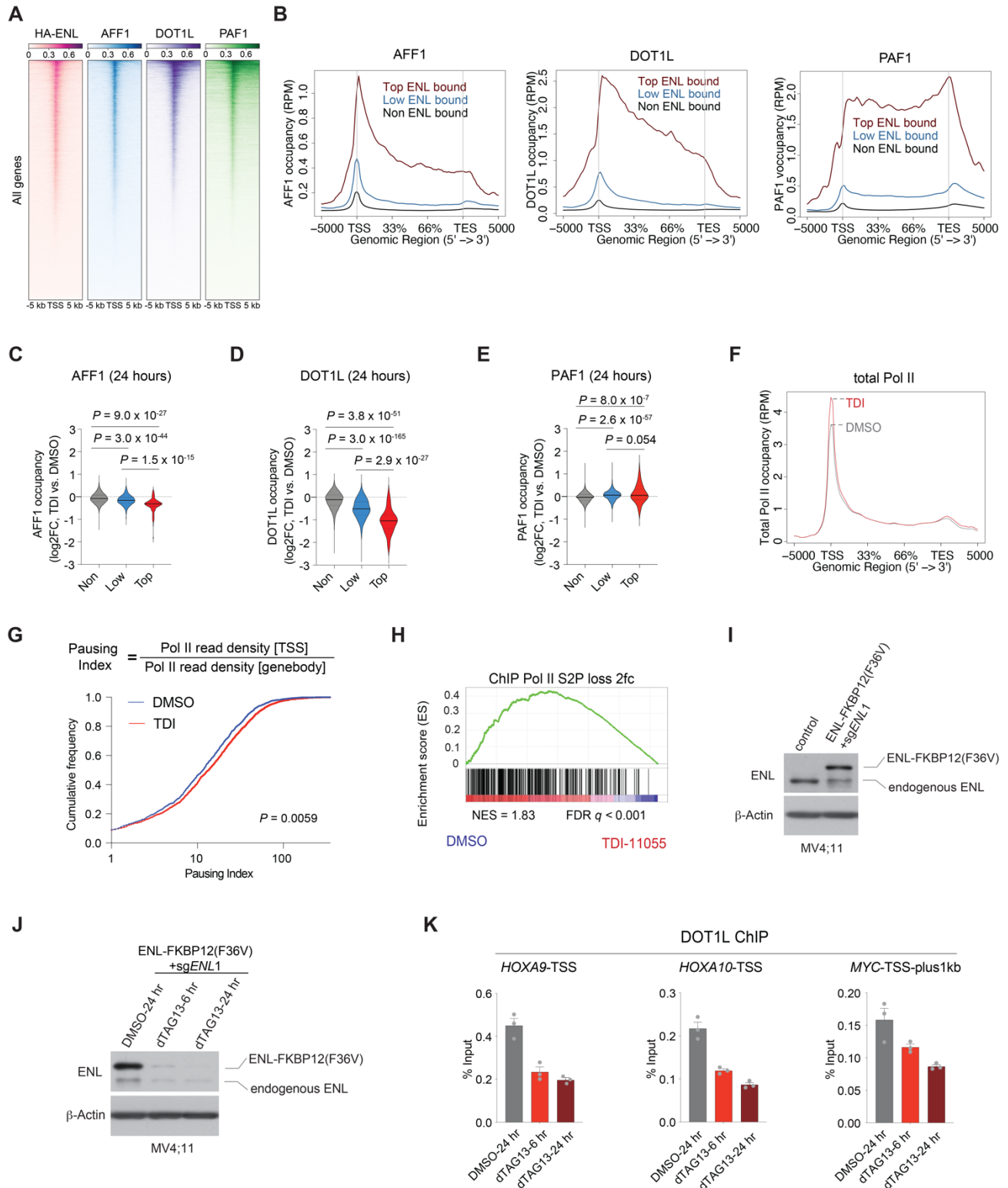
**Supplementary Figure S3. CRISPR-Cas9-mediated mutagenesis screen identifies a mutant, drug-resistant *ENL* allele.** **A**, Schematic for a proliferation competition assay used in **(B)**. **B**, Left and center: plots showing the relative fitness of indicated sgRNA<sup>+</sup> OCI-AML3 cells under DMSO (left) or TDI-11055 (5 $\mu$ M, center) treatment conditions; right, plots showing the fold-change enrichment (TDI-11055 vs. DMSO) of indicated sgRNA<sup>+</sup> cells. A sgRNA targeting *Rosa26* (black) or *RPA3* (grey) serves as a negative or positive control, respectively. *sgENL326* (red), but not *sgENL388* (blue), can induce mutation(s) in *ENL* that confers a growth advantage under TDI-11055 treatment condition. **C**, Pie chart of the relative abundance of *ENL* mutations induced by *sgENL323* in MV4;11 cells with long-term treatment of TDI-11055. Each slice represents the enrichment of a single mutant *ENL* allele. See Supplementary Table S5. **D**, **E**, DNA and protein sequence diagrams of the wildtype *ENL* and the drug-resistant, mutated *ENL* induced by *sgENL326* (**D**) or *sgENL323* (**E**) CRISPR mutagenesis under TDI-11055 treatment. **F**,



Docking structural view of ENL YEATS (grey ribbon): TDI-11055 (green stick) showing the amino acids LEGN (yellow stick) which is deleted in the drug-resistant ENL mutant. **G**, ITC experiment demonstrating TDI-11055 binds weaker to ENL (delLEGN) YEATS domain than to the ENL (WT).

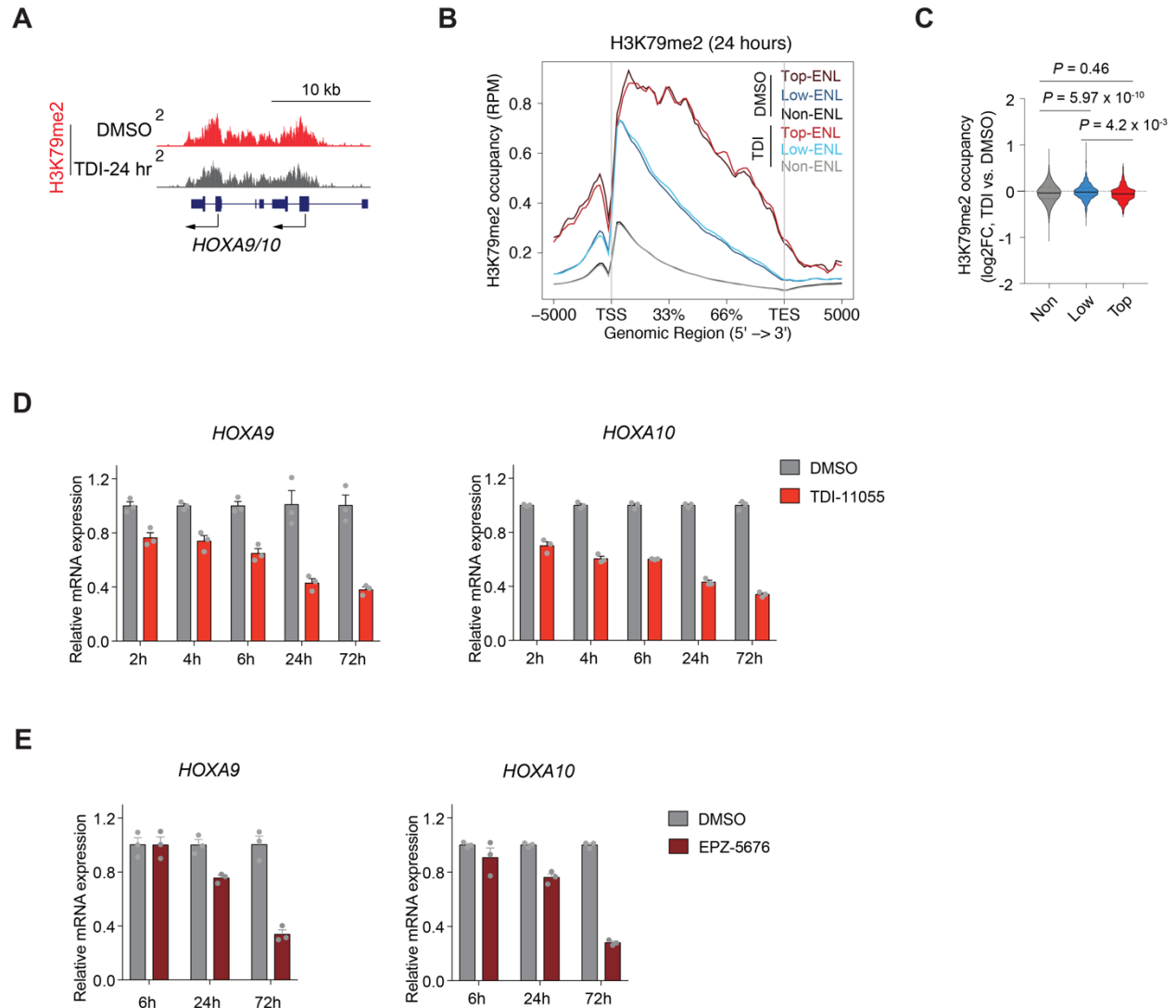


**Supplementary Figure S4. Gene expression changes induced by TDI-11055 in OCI-AML3 cells.** **A**, RT-qPCR analysis showing mRNA expression levels (normalized to *B2M*) of selected genes in OCI-AML3 cells upon treatment with increasing dosages of TDI-11055 for 72 hours. Error bars represent mean  $\pm$  SEM ( $n = 3$ ). **B**, GSEA plot evaluating gene expression changes in OCI-AML3 cells treated with TDI-11055 (1  $\mu$ M for 24 hours) with genes downregulated in MV4;11 cells upon TDI-11055 treatment (5  $\mu$ M for 24 hours). FDR, false discovery rate; NES, normalized enrichment score. **C**, GSEA plot evaluating gene expression changes in MV4;11 cells treated with TDI-11055 (5  $\mu$ M for 24 hours) with genes downregulated in OCI-AML3 cells upon TDI-11055 treatment (1  $\mu$ M for 24 hours). FDR, false discovery rate; NES, normalized enrichment score.

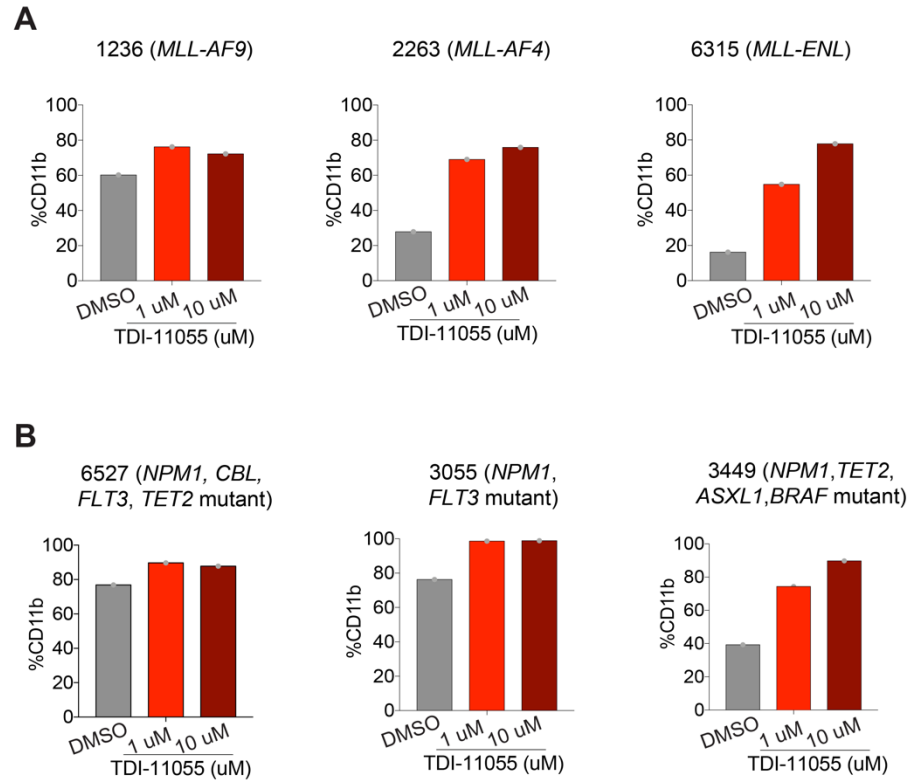


**Supplementary Figure S5. Chromatin changes induced by TDI-11055.** **A**, HA-ENL, AFF1, DOT1L, and PAF1 ChIP-seq data in MV4;11 cells were plotted as heatmap plots across genes in the genome at transcription start site (TSS)  $\pm$  5 kb. **B**, Average occupancies of AFF1, DOT1L,

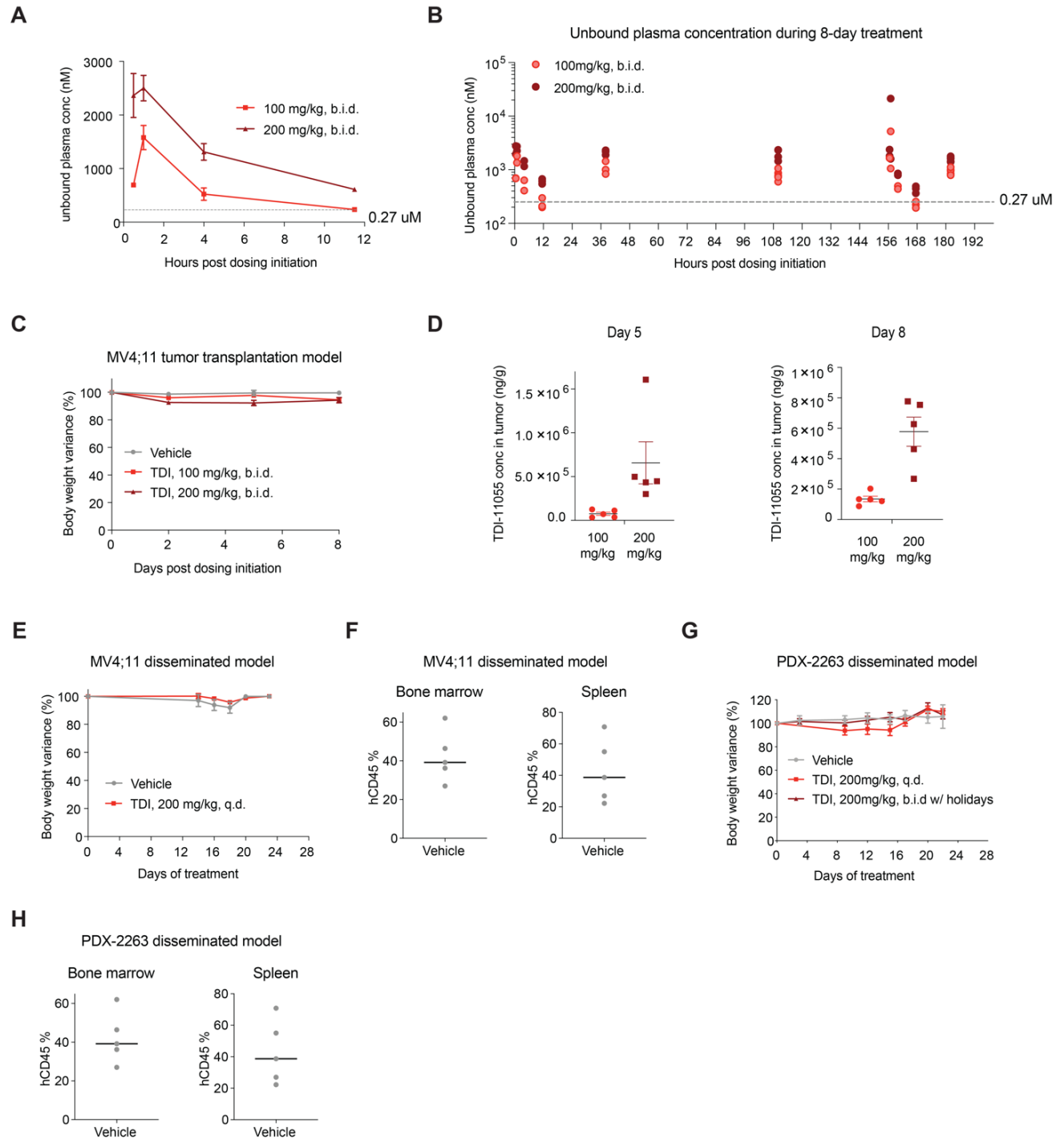
and PAF1 at top, low, and non-ENL-bound genes along the transcription unit. TSS, transcription start site; TES, transcription end site. See Supplementary Tables S11-S13. **C-E**, Quantification of AFF1 (**C**), DOT1L (**D**), and PAF1 (**E**) on top, low, and non-ENL-bound genes along the transcription unit in DMSO and TDI-11055 (5  $\mu$ M for 24 hours) treatment conditions. Black solid lines denote median and black dash lines denote quartiles. *P* values by Welch's two-tailed *t*-test. See Supplementary Tables S11-S13. **F**, Average occupancies of total Pol II at ENL-bound genes along the transcription unit in DMSO (grey) and TDI-11055 (red, 5  $\mu$ M for 24 hours) treatment conditions. See Supplementary Table S18. **G**, Top, illustration of the pausing index calculation based on the ratio of Pol II density around the TSS (TSS +/- 300 bp) to Pol II density in the gene body (TSS + 300bp to TES). Bottom, empirical cumulative density function (ECDF) plots of Pol II pausing index in DMSO (grey) and TDI-11055 (red, 5  $\mu$ M for 24 hours) treatment conditions at ENL-bound genes in MV4;11 cells. *P* value was calculated using Kolmogorov-Smirnov test. **H**, GSEA plot evaluating transcriptional changes in MV4;11 cells upon TDI-11055 treatment (5  $\mu$ M for 24 hours) for genes whose Pol II S2P occupancy is decreased by TDI-11055. FDR, false discovery rate; NES, normalized enrichment score. **I**, Immunoblots showing protein levels of ectopically expressed ENL-FKBP12(F36V) and endogenous ENL in Cas9-positive MV4;11 cells expressing a sgRNA targeting only the endogenous *ENL* gene.  $\beta$ -Actin was used as loading control. **J**, Immunoblots showing a decrease in ENL-FKBP12(F36V) proteins upon dTAG13 (500 nM, 6 and 24 hours).  $\beta$ -Actin was used as loading control. **K**, ChIP-qPCR analysis of DOT1L at select ENL target genes (*HOXA9/10*, *MYC*) in MV4;11 cells expressing sg*ENL1* and ENL-FKBP12(F36V) and treated with DMSO or 500 nM dTAG-13 (6 and 24 hours). TSS, transcription start site; Error bars represent mean  $\pm$  SEM (*n* = 3).



**Supplementary Figure S6. Rapid transcriptional changes induced by TDI-11055 treatment at early time points are not attributed to loss of DOT1L-mediated H3K79 methylation.** **A**, The genome browser view of H3K79me2 ChIP-seq signal at *HOXA9/10* genes under DMSO and TDI-11055 (5  $\mu$ M for 24 hours) treatment conditions in MV4;11 cells. **B**, **C**, Average occupancies (**B**) and quantification of H3K79me2 (**C**) on top, low, and non-ENL-bound genes along the transcription unit in DMSO and TDI-11055 (5  $\mu$ M for 24 hours) treatment conditions. TSS, transcription start site; TES, transcription end site. In (**C**), black solid lines denote median, and black dash lines denote quartiles. See Supplementary Table S19. **D**, RT-qPCR analysis showing mRNA expression levels (normalized to *B2M*) of *HOXA9* (left) and *HOXA10* (right) in MV4;11 cells upon treatment with TDI-11055 (1  $\mu$ M) for the indicated time. Error bars represent mean  $\pm$  SEM ( $n = 3$ ). **E**, RT-qPCR analysis showing mRNA expression levels (normalized to *B2M*) of *HOXA9* (left) and *HOXA10* (right) in MV4;11 cells upon treatment with the DOT1L inhibitor EPZ-5676 (1  $\mu$ M) for the indicated time. Error bars represent mean  $\pm$  SEM ( $n = 3$ ).



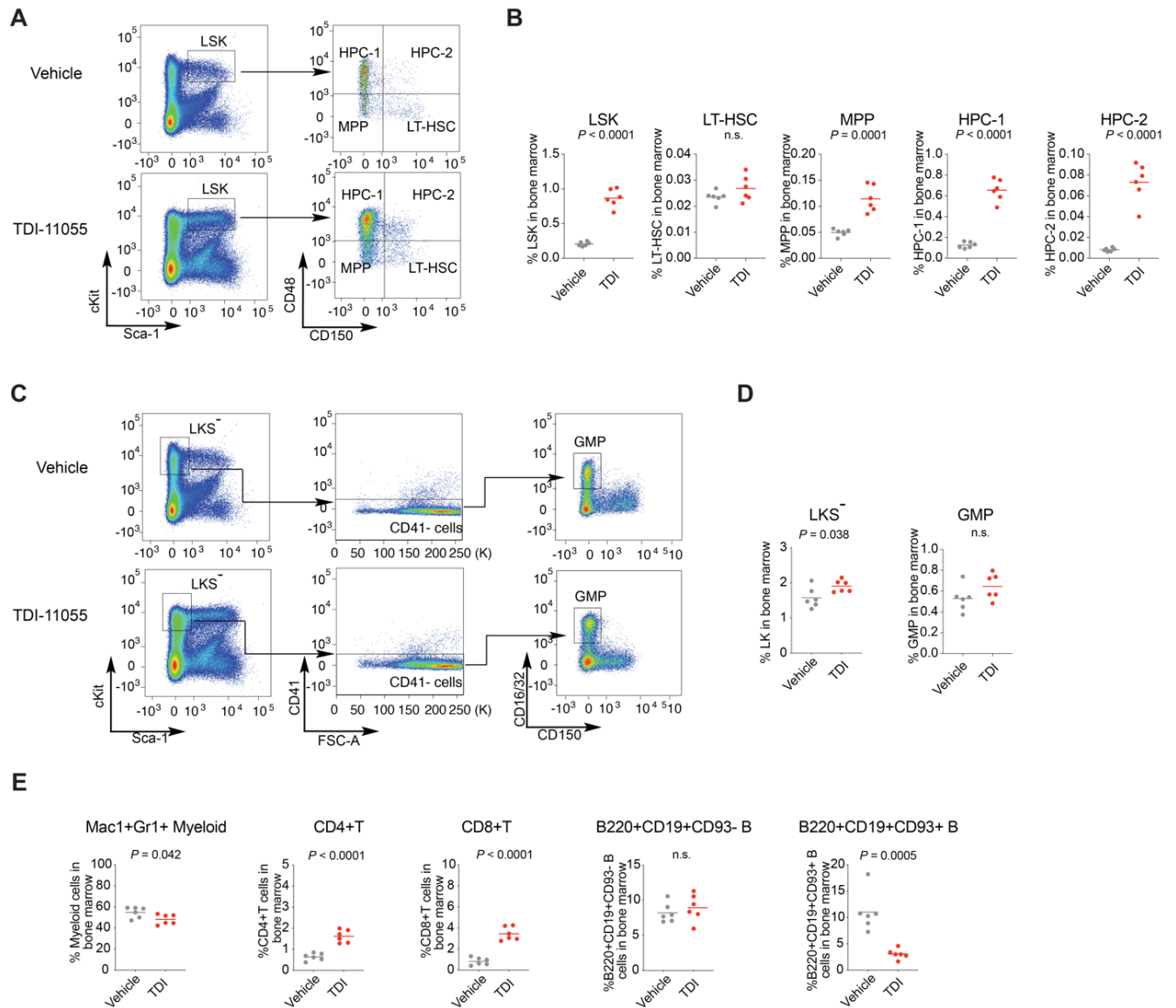
**Supplementary Figure S7. TDI-11055 induces differentiation of *MLL-r* and *NPM1*-mutated primary AML samples. A, B,** Flow cytometric analysis of CD11b expression levels in three different *MLL-r* (**A**) and three different *NPM1*-mutated (**B**) primary AML samples under DMSO or TDI-11055 (1 and 10  $\mu$ M) treatment conditions. See Supplementary Table S20 for more information about the primary patient samples.



**Supplementary Figure S8. *In vivo* effect of TDI-11055 in xenograft models of *MLL-r* and *NPM1*-mutated leukemia.** **A**, Pharmacokinetic profile in tumor bearing mice demonstrating unbound plasma concentrations of TDI-11055 after oral administration at 100 and 200 mg/kg within the first 12 hours were maintained above the *in vitro* IC50 (0.27  $\mu$ M, dash line) for MV4;11 cell proliferation. Error bars represent mean  $\pm$  SEM (for 0.5, 1, 4 hours,  $n = 2$ ; for 11.5

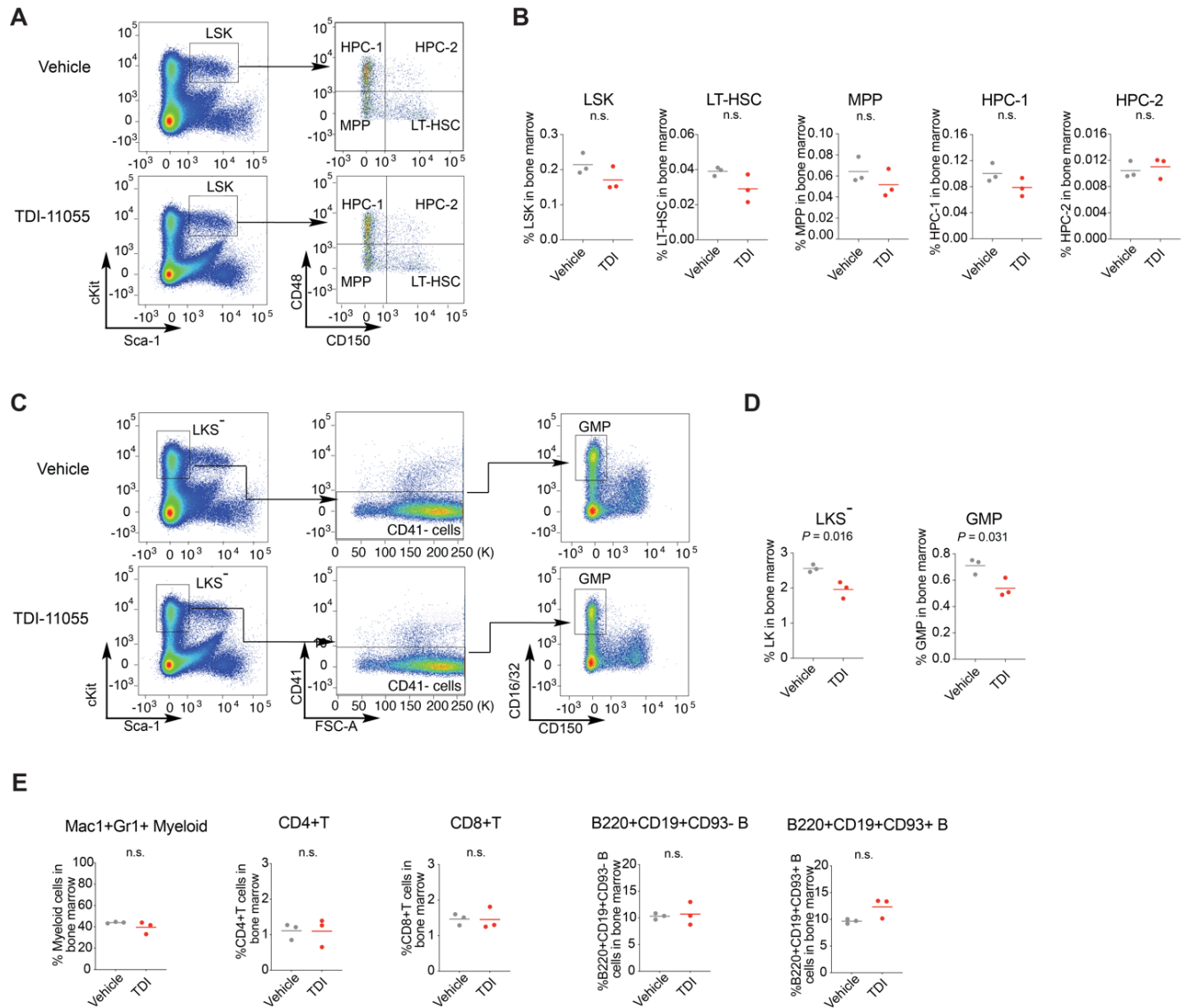
hours,  $n = 3$ ). b.i.d, twice daily. **B**, Pharmacokinetic profile in tumor bearing mice demonstrating unbound plasma concentrations of TDI-11055 after oral administration at 100 and 200 mg/kg over 8 days were maintained above the *in vitro* IC50 for MV4;11. **C**, Body weight variance overtime in BALB/c nude mice subcutaneously transplanted with MV4;11 cells and treated with the indicated doses of TDI-11055 (100 or 200 mg/kg, p.o., b.i.d). Error bars represent mean  $\pm$  SEM ( $n = 5$ ). **D**, Pharmacokinetic profile in mice demonstrating concentration of TDI-11055 in tumors after oral administration of TDI-11055 (b.i.d) at 100 and 200 mg/kg for 5 days (left) or 8 days (right). Error bars represent mean  $\pm$  SEM ( $n = 5$ ). **E**, Body weight variance overtime in NSG mice transplanted with MV4;11 cells and treated with vehicle or TDI-11055 (200mg/kg, p.o., q.d.). Error bars represent mean  $\pm$  SEM ( $n = 5$ ). **F**, % of human CD45<sup>+</sup> cells in the bone marrow (left) and the spleen (right) at necropsy from NSG mice transplanted with MV4;11 cells and treated with vehicle. Bars represent the median ( $n = 5$ ). **G**, Body weight variance over time in NSG mice transplanted with *MLL-r* PDX (2263) cells and treated with vehicle or TDI-11055 (200mg/kg, p.o., q.d.; or 200 mg/kg, p.o., b.i.d., with 5 days on and 2 days off). Error bars represent mean  $\pm$  SEM ( $n = 7$ ). **H**, % of human CD45<sup>+</sup> cells in the bone marrow (left) and the spleen (right) at necropsy from NSG mice transplanted with PDX (2263) cells and treated with vehicle. Bars represent the median ( $n = 5$ ).





**Supplementary Figure S9. The impact of TDI-11055 on normal hematopoiesis after 28 days of treatment.** **A, B**, Representative flow cytometric gating plots (**A**) and the percentage (**B**) of LSK (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>), LT-HSC (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>+</sup>CD48<sup>-</sup>), MPP (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>-</sup>CD48<sup>-</sup>), HPC-1 (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>-</sup>CD48<sup>+</sup>), and HPC-2 (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>+</sup>CD48<sup>+</sup>) populations in bone marrow samples harvested from mice at the end of 28-day treatment with vehicle or TDI-11055 (200 mg/kg, p.o., q.d.). Bars represent the median ( $n = 6$ ).  $P$  values by unpaired two-tailed Student's  $t$ -test. **C, D**, Representative flow cytometric gating plots (**C**) and the percentage (**D**) of LKS<sup>-</sup> (Lin<sup>-</sup>c-Kit<sup>+</sup> Sca-1<sup>-</sup>), GMP (Lin<sup>-</sup>Sca-1<sup>-</sup>c-Kit<sup>+</sup>CD41<sup>-</sup>CD150<sup>-</sup>CD16/32<sup>+</sup>) populations in bone marrow samples harvested from mice at the end of 28-day treatment with vehicle or TDI-11055. Bars represent the median ( $n = 6$ ).  $P$  values by unpaired two-tailed Student's  $t$ -test. **E**, Percentage of myeloid cell (Mac1<sup>+</sup>Gr1<sup>+</sup>), CD8<sup>+</sup> T (TCRb<sup>+</sup>CD8<sup>+</sup>), CD4<sup>+</sup> T (TCRb<sup>+</sup>CD4<sup>+</sup>), mature recirculating B (B220<sup>+</sup>CD19<sup>+</sup>CD93<sup>-</sup>), and

developing B (B220<sup>+</sup>CD19<sup>+</sup>CD93<sup>+</sup>) cell populations in bone marrow samples harvested from mice at the end of 28-day treatment with vehicle or TDI-11055. Bars represent the median ( $n = 6$ ).  $P$  values by unpaired two-tailed Student's  $t$ -test.



**Supplementary Figure S10. TDI-11055-induced changes in normal hematopoiesis are reversible after cessation of treatment.** **A, B**, Representative flow cytometric gating plots (**A**) and the percentage (**B**) of LSK (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>), LT-HSC (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>+</sup>CD48<sup>-</sup>), MPP (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>-</sup>CD48<sup>-</sup>), HPC-1 (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>+</sup>CD48<sup>+</sup>), and HPC-2 (Lin<sup>-</sup>Sca-1<sup>+</sup>c-Kit<sup>+</sup>CD150<sup>+</sup>CD48<sup>+</sup>) populations in bone marrow samples harvested from mice 80 days after completing treatment with vehicle or TDI-11055 (200 mg/kg, p.o., q.d.). Bars represent the median ( $n = 3$ ).  $P$  values by unpaired two-tailed Student's  $t$ -test. **C, D**, Representative flow cytometric gating plots (**C**) and the percentage (**D**) of LKS<sup>-</sup> (Lin<sup>-</sup>c-Kit<sup>+</sup> Sca-1<sup>-</sup>), GMP (Lin<sup>-</sup>Sca-1<sup>-</sup>c-Kit<sup>+</sup>CD41<sup>-</sup>CD150<sup>-</sup>CD16/32<sup>+</sup>) populations in bone marrow samples harvested from mice 80 days after completing treatment with vehicle or TDI-11055. Bars represent the median ( $n = 3$ ).  $P$  values by unpaired two-tailed Student's  $t$ -test. **E**, Percentage of myeloid cell (Mac1<sup>+</sup>Gr1<sup>+</sup>), CD8<sup>+</sup> T (TCRb<sup>+</sup>CD8<sup>+</sup>), CD4<sup>+</sup> T (TCRb<sup>+</sup>CD4<sup>+</sup>), mature recirculating

B (B220<sup>+</sup>CD19<sup>+</sup>CD93<sup>-</sup>), and developing B (B220<sup>+</sup>CD19<sup>+</sup>CD93<sup>+</sup>) cell populations in bone marrow samples harvested from mice 80 days after completing treatment with vehicle or TDI-11055. Bars represent the median ( $n = 3$ ).  $P$  values by unpaired two-tailed Student's  $t$ -test.