RNA-Binding Proteins of KHDRBS and IGF2BP families control

the Oncogenic Activity of MLL-AF4

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SUPPLEMENTARY INFORMATION

Supplementary Fig. 1. Virus production from the constructs of *MLL* **fusion genes. Related to Fig. 1.**

(a) Transduction of recombinant viruses into a murine pro-B cell line. Relative transduction units of retroviruses carrying various *MLL* fusion genes in murine Ba/F3 cells were determined using qPCR of the genomic DNA, as shown in Fig. 1f $(n=6)$.

(b) Transforming ability of MLL-AF4 with an excess virus titer. Transforming ability using a 6-fold concentrated pool of MLL-AF4 was examined using the myeloid progenitor transformation assay, as shown in Fig. 1a, along with a 10-fold diluted pool of the MLL-mAf4 virus (n=3).

(c) Protein expression of MLL-AF4 and MLL-mAf4 driven by various promoters. Western blot analysis was performed on the whole cell lysates of 293T cells transfected with the expression vectors by which MLL fusions are transcribed from the LTR (pMSCV) or pCMV promoters (pCMV5).

Data are presented as the mean \pm SD of indicated biologically independent replicates (a, b). P-value was calculated by one-way ANOVA followed by Tukey's test (a, b). Source data are provided as a Source Data file.

Supplementary Fig. 2. Post-transcriptional regulatory sequence affects AF4 protein expression. Related to Fig. 2.

(a) Schematic representation of various domain-swapping mutants of MLL-AF4 and MLL-mAf4. Domain swapping mutants are shown in blue (mouse) and white (human). The positions in the coding sequences are indicated on top.

(b) Protein expression of the domain-swapping mutants of MLL-AF4 and MLL-mAf4. Western blot analysis was performed on the whole cell lysates of 293T cells transfected with the MLL fusion expression vectors, as shown in Fig. 1d.

(c) Transforming ability of the domain-swapping mutants of MLL-AF4 and MLL-mAf4. The MLL fusion constructs shown in Supplementary Fig. 1A were examined for transformation of HSPCs under an ex vivo myeloid culture condition, as shown in Fig. 1a ($n=4$: Vector, MLL- Δ FP, MLL- Δ F4, MLLmAf4, MLL-AF4 m(S3-end), MLL-mAf4 h(S3-end), MLL-AF4 m(S5-end), MLL-mAf4 h(S5-end), MLL-AF4 m(S3-end), MLL-mAf4 h(S3-end); n=3: the others).

(d) Transforming ability of the domain-swapping mutants of murine/human MLL and murine/human AF4. Ex vivo myeloid progenitor transformation assays were performed as shown in Fig.1a (n=3).

(e) Transforming ability of AF4-MLL. Ex vivo myeloid progenitor transformation assays were performed as shown in Fig.1a (n=3).

(f) Protein expression of AF4-MLL. Western blot analysis was performed on the whole cell lysates of 293T cells transfected with AF4-MLL expression vectors, as shown in Fig. 1d.

(g) Transforming ability of MLL-AF4 in the presence of AF4-MLL. Two viruses were doubly transduced to HSPCs and their colony forming abilities were monitored as shown in Fig.1a (n=2).

Data are presented as the mean \pm SD of indicated biologically independent replicates (c, d, e, g). Pvalue was calculated by one-way ANOVA followed by Tukey's test (c, d). Source data are provided as a Source Data file.

(a) Surface marker expression of bone marrow cells from leukemic mice. Latency, antigen expression, and the weight of spleen of all leukemia cases are shown.

(b) Expression profiles of bone marrow cells harvested from MLL-AF4, MLL-mAf4 and MLL-ENL leukemic mice. Hierarchical clustering was performed by heatmap.2 function in r environment.

Supplementary Fig. 4. Three AU-rich sequences were the scaffold for association of various RBPs. Related to Fig. 4.

(a) Association of various RBPs with the PTRS. Immunoprecipitation-western blot analysis using the PTRS RNAs was performed on the lysates of 293T cells transiently expressing FLAG-tagged proteins

as shown in Fig. 4c.

(b) The RNA sites specifically recognized by various RBPs in the PTRS of human *AF4*. A result of CISBP-RNA database analysis is shown as in Fig. 4d for a broader region of the PTRS.

€ Predicted miRNA and lncRNA binding sites on the PTRSs. Results of miRbase and lncRNAdb database analyses are shown.

(d) Sequence of the mutated PTRSs. Mutations introduced in each mutant are highlighted in red.

(e) Association of endogenous RBPs to the PTRS of human *AF4* partially replaced by mouse sequences. Immunoprecipitation-western blot analysis using the PTRS RNAs shown in Fig. S4C was performed on the lysates of 293T cells, as shown in Fig. 4g. AU-rich sites of human PTRS were replaced by the corresponding mouse sequence.

(f) Protein expression of the MLL-mAF4 mutant with human AU-rich motifs in 293T cells. Protein level of the MLL-mAf4 mutant was analyzed as mentioned in Fig. 1d.

(g) Transforming ability of the MLL-mAf4 mutant, the AU-rich sites of which were replaced by human sequences. An MLL-mAf4 construct carrying human AU-rich sites was examined for transformation of HSPCs under ex vivo myeloid culture conditions, as shown in Fig. 1a (n=5). *Hoxa9* expression normalized to *Gapdh* is shown as the relative value of MLL-mAF4 (set to 100) (n=3). Data are presented as the mean \pm SD of indicated biologically independent replicates. P-value was calculated by two tailed T-test.

(h) Sequence alignment of the PTRS of various organisms. AU-rich sites are highlighted by red rectangles. Bases different from human AU-rich sites are shown in red letters.

(i) Expression of RNA-binding proteins in various leukemia cell lines. Western blotting of RBPs was performed using whole cell lysates of leukemia cell lines of various lineages.

Source data are provided as a Source Data file.

Supplementary Fig. 5. sgRNA screening of the transformation capabilities of the MLL-AF4 sAU13 mutant and protein expression of the mutant after depletion of IGF2BP3.

(a) Screening of RBPs responsible for post-transcriptional inactivation of MLL-AF4. The MLL-AF4 construct was examined for transformation of HSPCs under an ex vivo myeloid culture condition with co-transduction of various knockout constructs for RBPs, as shown in Fig. 5a $(n=3)$.

(b) Screening of RBPs responsible for post-transcriptional inactivation of MLL-AF4 sAU13. The MLL-AF4 construct carrying synonymous mutations at AU1 and 3 was examined for transformation of HSPCs under an ex vivo myeloid culture condition with co-transduction of various knockout constructs for RBPs, as shown in Fig. 5a. Data are shown as the mean \pm SD of three biological replicates (a, b) (n=3: MLL-AF4 sAU13 + sgHnrnpa0#1, MLL-AF4 sAU13 + sgHnrnpa0#2, MLL-AF4 sAU13 + sgHnrnpc#1, MLL-AF4 sAU13 + sgHnrnpc#2, MLL-AF4 sAU13 + sgHnrnpdl#1,

MLL-AF4 sAU13 + sgHnrnpdl#2, MLL-AF4 sAU13 + sgHnrnpl#1, MLL-AF4 sAU13 + sgHnrnpl#2, MLL-AF4 sAU13 + sgSyncrip#1, MLL-AF4 sAU13 + sgSyncrip#2; n=4: the others).

(c) Effects of knocking down *IGF2BP3* on protein expression of MLL-AF4. 293T cells were transduced with two different sh-RNA constructs for *IGF2BP3* and subsequently transfected with various MLL-AF4 expression vectors. Western blot analysis was performed on the whole cell lysate of transfected cells using anti-MLL antibody. Western blot analysis of TUBB and IGF2BP3 was also performed.

(d) Effects of Igf2bp3 knockout on various MLL fusion mediated transformation. MLL fusion constructs were doubly transduced with the CRISPR/Cas9 knockout construct for *Igf2bp3* into murine HSPCs and examined for their transforming abilities under ex vivo myeloid culture conditions, as shown in Fig. 5a (n=4: MLL-mAf4 + Vector, MLL-mAf4 + sgIgf2bp3, MLL-AF10 + Vector, MLL- $AF10 + sgIgf2bp3$; n=3: mMll-AF4 + Vector, mMll-AF4 + sgIgf2bp3, mMll-mAf4 + Vector, mMllmAf4 + sgIgf2bp3, MLL-ENL + Vector, MLL-ENL + sgIgf2bp3; n=2: MLL-AF4 + Vector, MLL-AF4 $+$ sgIgf2bp3).

(e) Leukemogenic potential of MLL fusion-immortalized cells with or without Igf2bp3 knockout in vivo. MLL-AF10-immortalized cells with or without Igf2bp3 knockout and MLL-AF4 sAU13/Igf2bp3 knockout-immortalized cells established in Fig. 5a were transplanted into syngeneic mice. (MLL-AF4 sAU13 sgIgf2bp3, $n = 7$; MLL-AF10 vector, $n = 10$; MLL-AF10 sgIgf2bp3, $n = 11$). As for the transplantation experiment of MLL-AF4 sAU13/Igf2bp3 knockout-immortalized cells, two recipient mice died of unknown causes. Three recipient mice became sick with B-ALL, but the transgene expression was not detected by RT-PCR, therefore excluded as spontaneous leukemia cases. p-value (p=0.0377) was calculated by log-rank test (MLL-AF10 vector vs. MLL-AF10 sgIgf2bp3). Data are presented as the mean \pm SD of indicated biologically independent replicates (a, b, d). Source data are provided as a Source Data file.

Supplementary Fig. 6. Fluorescent reporter recapitulated post-transcriptional regulation of MLL-AF4 expression. Related to Fig. 6.

(a) Schematic representation of the self-cleaving GFP/RFP reporter system. Cleaving efficiency of the P2A sequence of the fluorescent reporter. 293T cells transfected with the reporter plasmid were analyzed using fluorescence microscopy and western blotting.

(b) mRNA stability of the reporter genes. The reporter plasmids were transfected into 293T cells and treated with actinomycin D for 24 h. The mRNAs were purified and quantified by RT-qPCR. The expression level was normalized by that of GAPDH. MYC gene was used as a positive control. Data are shown as the mean \pm SD of three biological replicates.

(c) Protein stability of the reporter proteins. The reporter plasmids were transfected into 293T cells and treated with cycloheximide for 24 h. The protein levels were visualized by western blotting. MYC protein was used as a positive control.

(d) Subcellular localization of fluorescence signals of various GFP-tagged PTRS reporters.

(e) Non-simultaneous binding of RBPs to hPTRS. Two-step IP analysis of IGF2BP3 and KHDRBS1 on the hPTRS RNA oligonucleotide was performed. The FLAG-tagged RBPs were transfected into 293T cells. Then the lysate was mixed with the hPTRS RNA oligonucleotide and subjected to subsequent pull down of FLAG-tagged proteins and the bait RNAs.

(f) Associated factors for the GFP-PTRS reporter proteins. Heatmap representation of the scores of the ribosomal proteins associated with PTRS reporters.

(g) scRNA-seq data of the murine embryonic HSPCs in the public database. The expression levels and percentages of the cells expressing Igf2bp3 during developmental stages were plotted. CPM: count per million, HSC: hematopoietic stem cell, HPC: hematopoietic progenitor cell. (Li et al., 2020¹⁸, GSE128761)

(h) Expression of RBPs in the human leukemia specimens. The log2 probe intensities in various subtypes of the leukemias were plotted (MILE stage 2^{19} , GSE13164). Data are shown as the boxplot. The center line indicates the median value. The box limits indicate the first and third quartiles. The bar limits indicate the maximum and minimum values. (mature B-ALL t(8;14): n=13, Pro-B-ALL t(11q23)/MLL: n=70, c-ALL/Pre-B-ALL t(9;22): n=122, T-ALL: n=174, ALL t(12;21): n=58, ALL t(1;19): n=36, ALL hyperdiploid: n=40, c-ALL/Pre-B-ALL w/o t(9;22): n=237, AML t(8;21): n=40, AML t(15;17): n=37, AML inv(16)/t(16;16): n=28, AML t(11q23)/MLL: n=38, AML normal karyotype: n=351, AML complex karyotype: n=48, CLL: n=448, CML: n=76, MDS: 206, Healthy bone: n=74) ALL: acute lymphoblastic leukemia, AML: acute myeloid leukemia, CLL: chronic lymphocytic leukemia, CML: chronic myeloid leukemia, MDS: myelodysplastic syndromes. Source data are provided as a Source Data file.

Supplementary Table 1, Materials

Target name	Target sequence
sgKhdrbs1#1	GAACCCACCACCGTCGCGTC
sgKhdrbs1#2	CGGGTCGAGCGAGTCCTTCT
sgKhdrbs3#1	AACGGCCGCCGAGCTCACCT
sgKhdrbs3#2	CGCTTCAGGGAATTGCCACG
sgIgf2bp1#1	TCATCGCCCAGTGCTCGTCG
sgIgf2bp1#2	ATAGCGCCTACATACTGCGT
sgIgf2bp2#1	CGCGCCATCGAGACCCTCTC
sgIgf2bp2#2	AGGTCGTCGGCGGTGACGGC
sgIgf2bp3#1	ACGCGTAGCCCGTCTTCACC
sgIgf2bp3#2	CTACGCGTTCGTGGACTGCC
sgElavl1#1	CTTATTCGGGATAAAGTAGC
sgElavl1#2	CGAAGTCTGTTCAGCAGCAT
sgHnrnpa0#1	TGTCGCGGGAGGATTCGGCG
sgHnrnpa0#2	TACGGGCCGATGAAGAGCGG
sgHnrnpab#1	GGCCTCGTGTCCGTTCTCGG
sgHnrnpab#2	GGACCACGACCGCACCGAGC
sgHnrnpc#1	ACACGGGAATTCATGGACCG
sgHnrnpc#2	GGACCGAGGATCTGTCTTGT
sgHnrnpd#1	GTCGGAGGAGCAGTTCGGAG
sgHnrnpd#2	GTTCTTACTGGCGTCGATCT
sgHnrnpdl#1	TAGCCGCCCCGCCCGCCAAT
sgHnrnpdl#2	GGAACAATGGCGGCGGCACA
sgHnrnpl#1	CTATTACGGCGGCGGCAACG
sgHnrnpl#2	GGCGGTGGTCGCTATTACGG
sgHnrnpr#1	TGCTTCATCGGGCCCTTTCG
sgHnrnpr#2	GCCCGATGAAGCAAAAATCA
sgSyncrip#1	TTTACTAGAGTCTGCTACTT
sgSyncrip#2	AAAGTAGCAGACTCTAGTAA
shIGF2BP3#1	TCTGCGGCTTGTAAGTCTATT
shIGF2BP3#2	TGTTGTAGTCTCACAGTATAA

Supplementary Table 2. Oligonucleotides for gene editing and shRNA-mediated knockdown.

Supplementary Table 3. Sequences of the custom TaqMan Probes.

Supplementary Table 4. Sequences of the primers for SYBR green qPCR.

Supplemental references

- 1. Morita, S., Kojima, T. & Kitamura, T. Plat-E: an efficient and stable system for transient packaging of retroviruses. *Gene Ther* **7**, 1063-1066 (2000).
- 2. Tkachuk, D.C., Kohler, S. & Cleary, M.L. Involvement of a homolog of Drosophila trithorax by 11q23 chromosomal translocations in acute leukemias. *Cell* **71**, 691-700 (1992).
- 3. Okuda, H., Kanai, A., Ito, S., Matsui, H. & Yokoyama, A. AF4 uses the SL1 components of RNAP1 machinery to initiate MLL fusion- and AEP-dependent transcription. *Nat Commun* **6**,

8869 (2015).

- 4. Dull, T. *et al.* A third-generation lentivirus vector with a conditional packaging system. *J Virol* **72**, 8463-8471 (1998).
- 5. Yokoyama, A. & Cleary, M.L. Menin critically links MLL proteins with LEDGF on cancerassociated target genes. *Cancer cell* **14**, 36-46 (2008).
- 6. DiMartino, J.F. *et al.* The AF10 leucine zipper is required for leukemic transformation of myeloid progenitors by MLL-AF10. *Blood* **99**, 3780-3785 (2002).
- 7. Tzelepis, K. *et al.* A CRISPR Dropout Screen Identifies Genetic Vulnerabilities and Therapeutic Targets in Acute Myeloid Leukemia. *Cell Rep* **17**, 1193-1205 (2016).
- 8. Cong, L. *et al.* Multiplex genome engineering using CRISPR/Cas systems. *Science* **339**, 819- 823 (2013).
- 9. Labun, K. *et al.* CHOPCHOP v3: expanding the CRISPR web toolbox beyond genome editing. *Nucleic Acids Res* **47**, W171-W174 (2019).
- 10. Ray, D. *et al.* A compendium of RNA-binding motifs for decoding gene regulation. *Nature* **499**, 172-177 (2013).
- 11. Kozomara, A., Birgaoanu, M. & Griffiths-Jones, S. miRBase: from microRNA sequences to function. *Nucleic Acids Res* **47**, D155-D162 (2019).
- 12. Amaral, P.P., Clark, M.B., Gascoigne, D.K., Dinger, M.E. & Mattick, J.S. lncRNAdb: a reference database for long noncoding RNAs. *Nucleic Acids Res* **39**, D146-151 (2011).
- 13. Schneider, C.A., Rasband, W.S. & Eliceiri, K.W. NIH Image to ImageJ: 25 years of image analysis. *Nat Methods* **9**, 671-675 (2012).
- 14. Dobin, A. *et al.* STAR: ultrafast universal RNA-seq aligner. *Bioinformatics* **29**, 15-21 (2013).
- 15. Li, B. & Dewey, C.N. RSEM: accurate transcript quantification from RNA-Seq data with or

without a reference genome. *BMC Bioinformatics* **12**, 323 (2011).

- 16. Robinson, M.D., McCarthy, D.J. & Smyth, G.K. edgeR: a Bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics* **26**, 139-140 (2010).
- 17. Hao, Y. *et al.* Integrated analysis of multimodal single-cell data. *Cell* **184**, 3573-3587 e3529 (2021).
- 18. Li, Y. *et al.* Single-Cell Analysis of Neonatal HSC Ontogeny Reveals Gradual and Uncoordinated Transcriptional Reprogramming that Begins before Birth. *Cell Stem Cell* **27**, 732-747 e737 (2020).
- 19. Haferlach, T. *et al.* Clinical utility of microarray-based gene expression profiling in the diagnosis and subclassification of leukemia: report from the International Microarray Innovations in Leukemia Study Group. *J Clin Oncol* **28**, 2529-2537 (2010).

Uncropped scans of western blotting data in this supplementary information

MLL Antibody (CST, #14689, 1/1000 dilution)

TUBB Antibody (Thermo, #PA5-25050, 0.5 µg/ml)

Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

Supplementary Figure 2f

AF4 Antibody (Bethyl laboratories, #A302-344A, 1 µg/ml) Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

TUBB Antibody (Thermo, #PA5-25050, 0.5 µg/ml)

FLAG Antibody (Sigma, #F3165, 1 µg/ml)

Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

Supplementary Figure 4a

Supplementary Figure 4e

Top: IGF2BP3 Antibody
(Bethyl laboratories, #A303-426A, 1 µg/ml)

Bottom: HNRNPAB Antibody
(SantaCruz, #sc-376411, 1 µg/ml)

Supplementary Figure 4f

MLL Antibody (CST, #14689, 1/1000 dilution)

Upper: TUBB Antibody (Thermo, #PA5-25050, 0.5 µg/ml) Lower: NPTII Antibody (Millipore, #06-747, 1 µg/ml)

Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

Lower : HNRNPAB Antibody
(SantaCruz, #sc-376411, 1 µg/ml)

Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

Supplementary Figure 5c

■
Right : IGF2BP3 Antibody
(Bethyl laboratories, #A303-426A, 1 µg/ml)

Supplementary Figure 6a

Upper: FLAG Antibody (Sigma, #F3165, 1 µg/ml) Lower: HA Antibody (Roche, #11867423001, 1 µg/ml)

Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)

Supplementary Figure 6c

Supplementary Figure 6e

KHDRBS1 Antibody
KHDRBS1 Antibody
(Bethyl laboratories, #A302-110A, 1 µg/ml) IGF2BP3 Antibody
(Bethyl laboratories, #A303-426A, 1 µg/ml) Protein ladder: PageRuler™ Plus Prestained Protein Ladder, 10 to 250 kDa (Thermo, #26620)