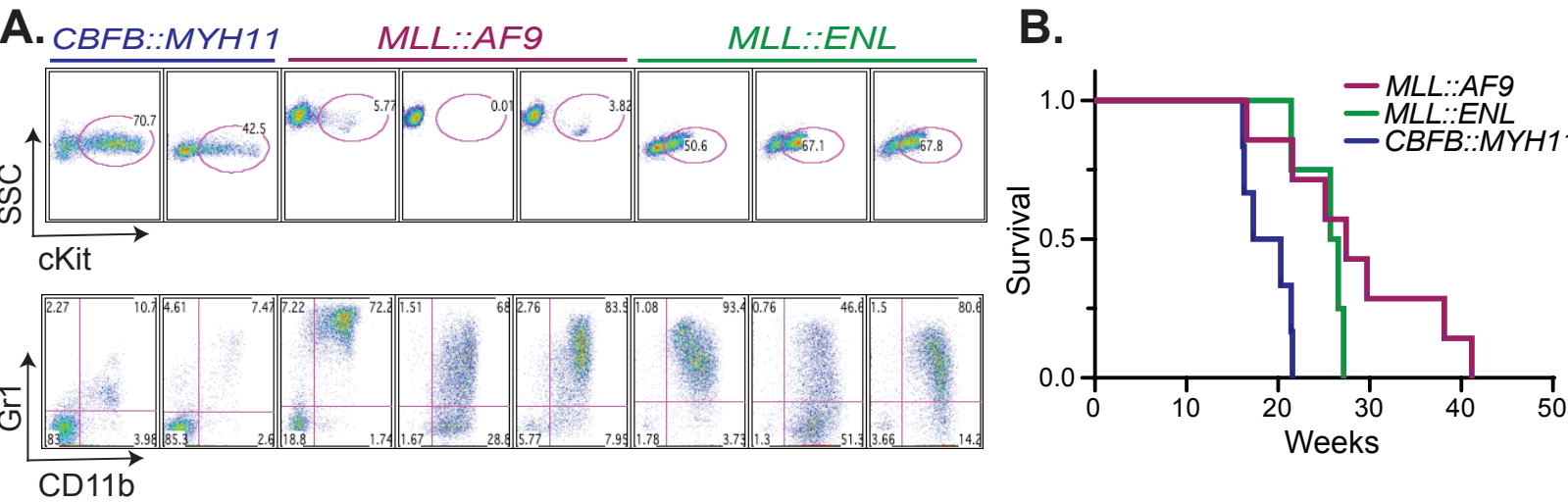
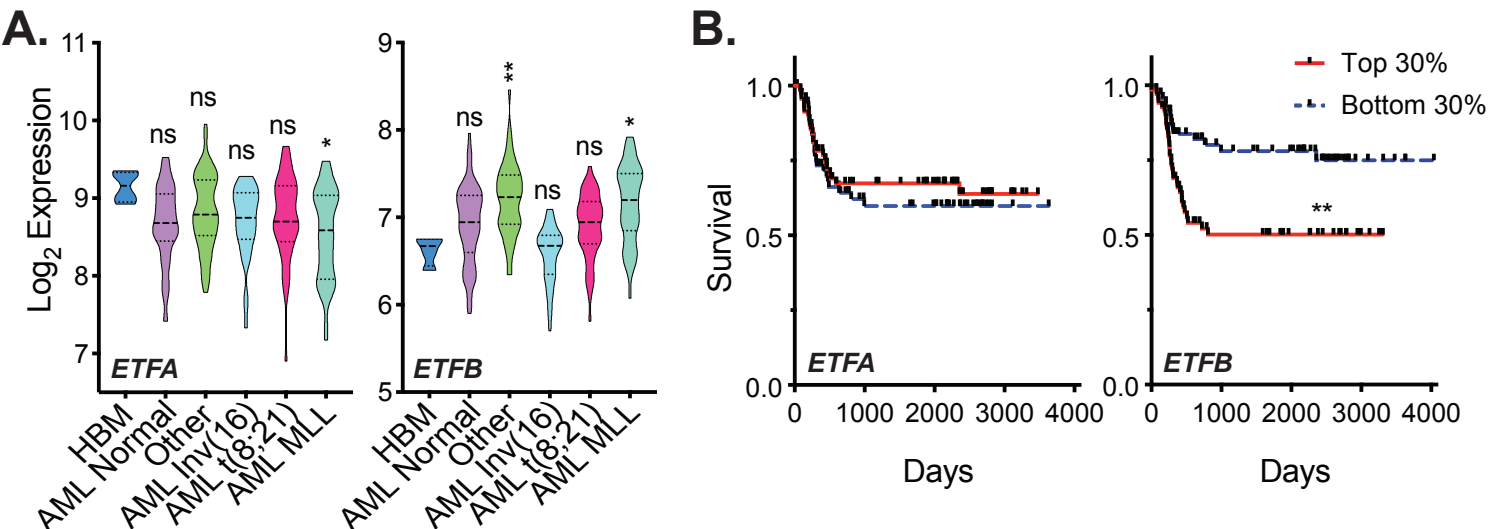


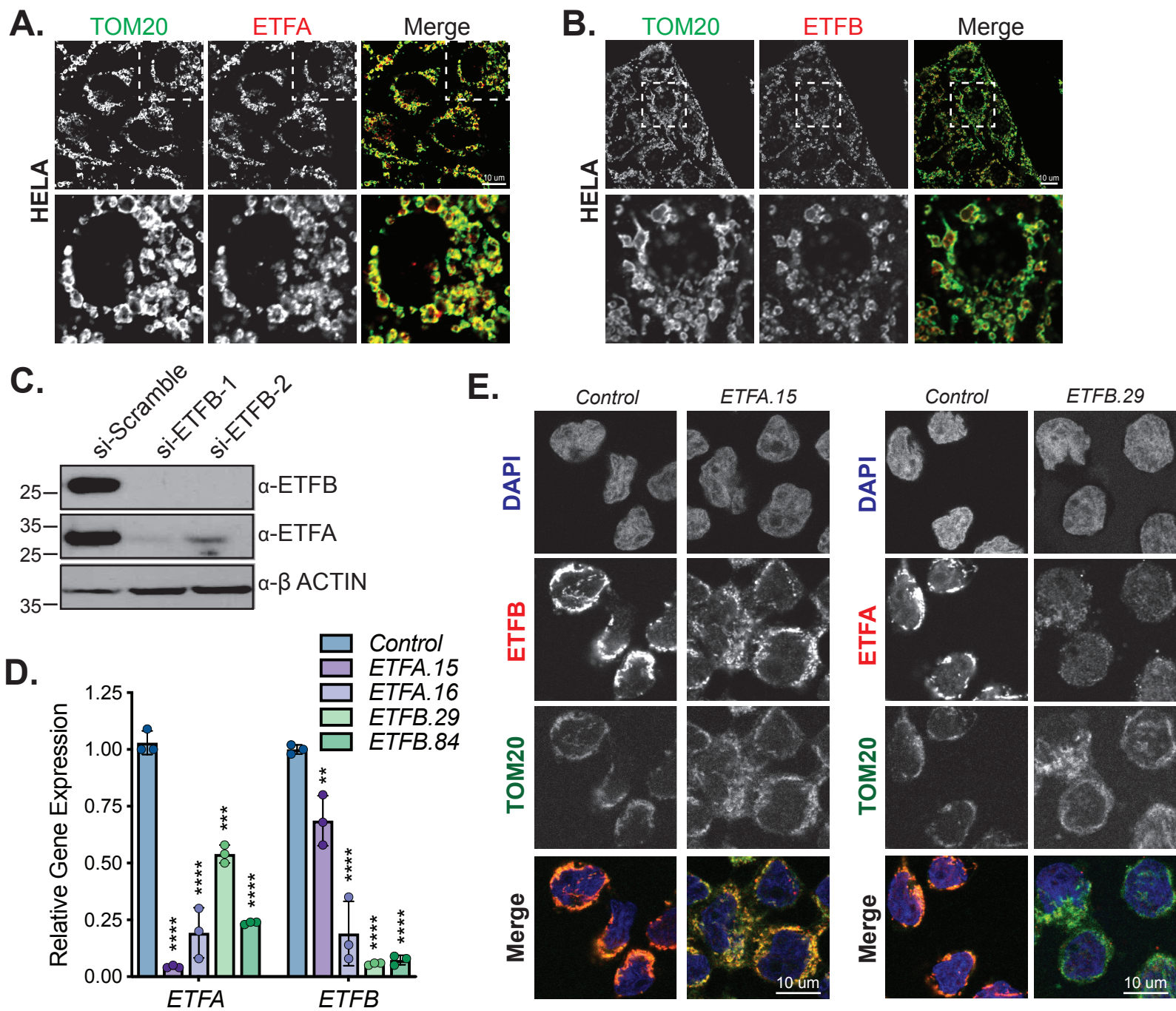
Caplan et al. Supplementary Figure 1



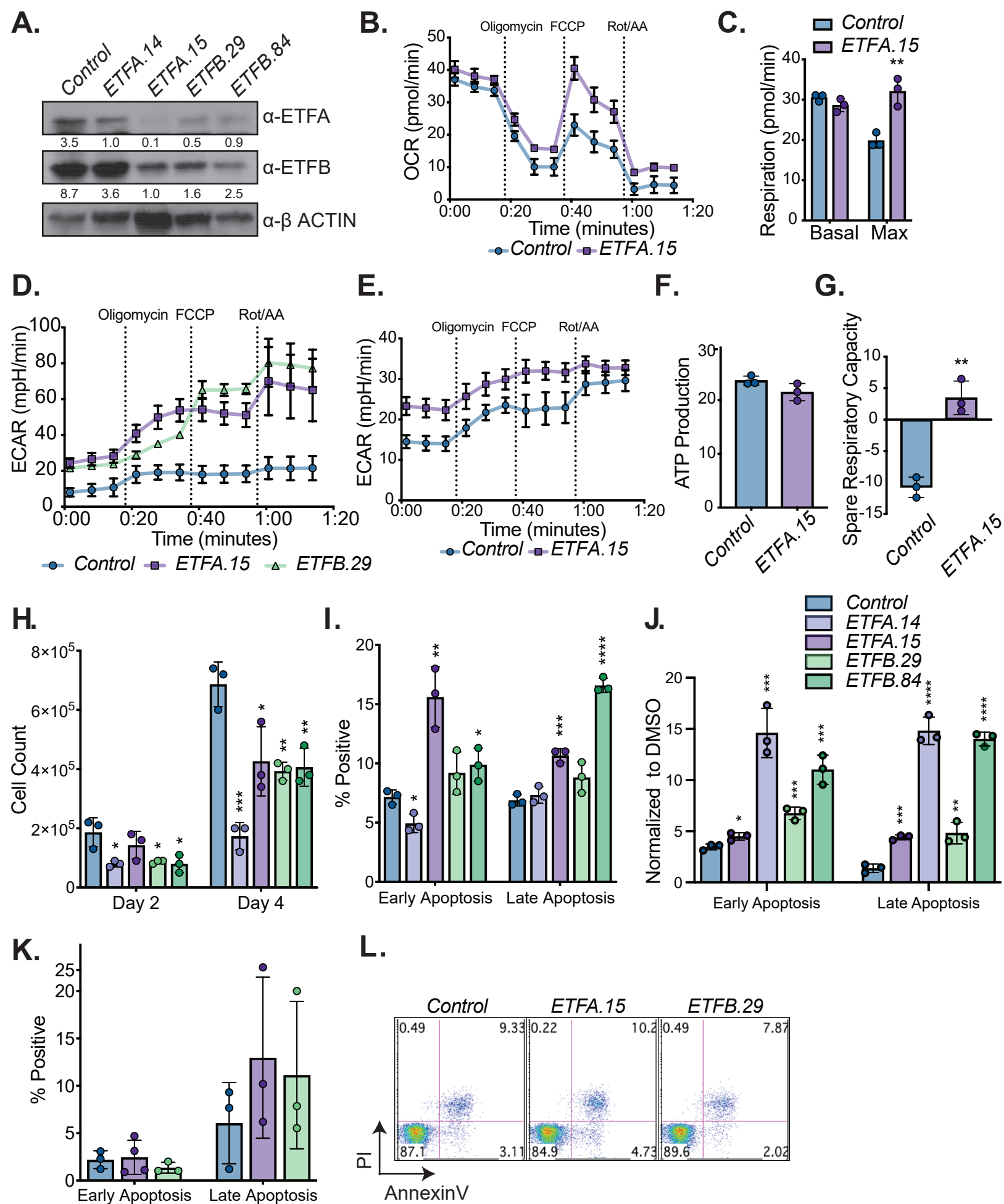
Caplan et al. Supplementary Figure 2



# Caplan et al. Supplementary Figure 3



# Caplan et al. Supplementary Figure 4





## SUPPLEMENTAL MATERIALS AND METHODS

**Supplementary Figure 1. Phenotype and expression differences in AML mouse models utilized for proteomic and transcriptomic analysis.** **A** Flow cytometry analysis of cKit, Gr1, and Mac1 (CD11b) cell surface markers on spleen tumor cells from each mouse sample. **B** Kaplan Meyer survival curve of mouse models. Weeks indicated from birth for *MLL::AF9*, from date of transplantation for *MLL::ENL*, and from first Poly:IC injection for *Cbfb::MYH11* (n = 8).

**Supplementary Figure 2. Electron transfer proteins ETFA and ETFB expression and survival in pediatric AML.** **A** *ETFA* and *ETFB* gene expression analysis of patient samples from the TARGET study. **B** Overall survival from TARGET pediatric AML patient dataset analyzing patients with the highest 30% and lowest 30% of *ETFA* and *ETFB* expression. (\*p < 0.05, \*\*p < 0.01, ns = non-significant).

**Supplementary Figure 3. ETFA and ETFB are localized within the mitochondria.** **A-B** Immunofluorescence of ETFA, ETFB, and mitochondrial protein, TOM20 in HELA cells. **C** Western blot 48 hours post siRNA transfection in HELA cells. **D** MOLM-13 cells were lentivirally infected with shRNAs targeting *ETFA* and *ETFB* or non-targeting control, and analyzed 72 hours post puromycin selection. Changes in expression analyzed by qRT-PCR. **E** Immunofluorescence of ETFA, ETFB, and mitochondrial protein, TOM20 in MOLM-13 cells 96 hours post lentiviral infection with shRNAs targeting ETFA and ETFB, and 72 hours post puromycin selection.

**Supplementary Figure 4. Silencing of ETFA and ETFB leads to increased mitochondrial respiration and apoptosis.** HL-60 cells 96 hours post lentiviral infection with shRNAs targeting ETFA and ETFB 72 hours post puromycin selection. Analysis of changes following knockdown via **A** western blot, **B** oxygen consumption rate (OCR), **C** basal and maximum respiration rate, **D** ECAR, **E** ECAR in Molm-13, **F** ATP production, **G** spare respiratory capacity, **H** cell counts at day

2 and day 4, I and annexin V and PI staining by flow cytometry. J Flowcytometry analysis for annexin V and PI staining for percent apoptotic cells following 48 hrs with 5nM Venetoclax. K-L Human PB mobilized CD34<sup>+</sup> cells were infected with lentivirus expressing scramble control or shRNAs targeting *ETFA* and *ETFB* and analyzed 72 hours post puromycin selection for percent apoptotic by annexin V and PI flow cytometry staining. (\*p < 0.05, \*\*p < 0.01, \*\*\*p < 0.001, \*\*\*\*p < 0.0001).

#### Flow Cytometry Antibodies

| Antibody     | Fluorochrome | Clone   | Company   |
|--------------|--------------|---------|-----------|
| cKit         | BV421        | 2B8     | BioLegend |
| Gr-1         | APC          | RB6-8C5 | BioLegend |
| Mac1 (CD11b) | PE           | M1/70   | BioLegend |
| Annexin V    | APC          |         | BioLegend |
| CD34         | FITC         | 561     | BioLegend |
| CD45         | Pacific Blue | 2D1     | BioLegend |

#### Western Blot and Immunofluorescence Antibodies:

| Antibody    | Company     | Ref#       |
|-------------|-------------|------------|
| B-actin-HRP | Santa Cruz  | sc-47778   |
| ETFA        | Proteintech | 12262-1-AP |
| ETFB        | Proteintech | 17925-1-AP |
| TOM20       | Santa Cruz  | F-10       |

| qRT-PCR Primer  | Sequence                            |
|-----------------|-------------------------------------|
| <i>mGapdh F</i> | 5'– CAT GGC CTT CCG TGT TCC TA –3'  |
| <i>mGapdh R</i> | 5'– CTG GTC CTC AGT GTA GCC CAA –3' |
| <i>mEtfa F</i>  | 5'– TGC AGC AAC AAG TGG AGG TA –3'  |
| <i>mEtfa R</i>  | 5'– AAA GCC GGA CAA GTC TGG AG –3'  |
| <i>mEtfb F</i>  | 5'– AAA GCC GGA CAA GTC TGG AG –3'  |
| <i>mEtfb R</i>  | 5'– CAG TTC GGA TGG TCT CCT GG –3'  |
| <i>hGAPDH F</i> | 5'– CTT TTG CGT CGC CAG CCG AG –3'  |
| <i>hGAPDH R</i> | 5'– CCA GGC GCC CAA TAC GAC CA –3'  |
| <i>hETFA F</i>  | 5'– GCG GCC TCA TTG CTA CGA TT –3'  |
| <i>hETFA R</i>  | 5'– GTG CCA CCT TGT CAC ATT TGG –3' |
| <i>hETFB F</i>  | 5'– CAT CGA CTA CGC CGT GAA GA –3'  |
| <i>hETFB R</i>  | 5'– CGG TAC GAA TCG TCT CCT GG –3'  |

| <b>shRNA</b>             | <b>Target Sequence</b> |
|--------------------------|------------------------|
| <i>NonTarget Control</i> | CAACAAGATGAAGAGCACCAA  |
| <i>ETFA.64414</i>        | GAGAACTATTTATGCAGGAAA  |
| <i>ETFA.64415</i>        | GCTTGACCAGAAATTAACAAA  |
| <i>ETFA.64416</i>        | GCGGCCTCATTGCTACGATTT  |
| <i>ETFB.291084</i>       | CAAGGAGAAGAAGCTGGTGAA  |
| <i>ETFB.64429</i>        | GCCCAACATCATGAAAGCCAA  |

### **Mass Spectrometry**

Samples were loaded onto trap column Acclaim PepMap 100 75  $\mu$ m x 2 cm C18 LC Columns (Thermo Scientific™) at flow rate of 5  $\mu$ l/min then separated with a Thermo RSLC Ultimate 3000 (Thermo Scientific™) from 5-20% solvent B (0.1% FA in 80% ACN) from 10-98 minutes at 300 nL/min and 50 °C with a 120 minutes total run time for fractions one and two. For fractions three to six, solvent B was used at 5-45% for the same duration. Eluted peptides were analyzed by a Thermo Orbitrap Fusion Lumos Tribrid (Thermo Scientific™) mass spectrometer in a data dependent acquisition mode using synchronous precursor selection method. A survey full scan MS (from m/z 375-1500) was acquired in the Orbitrap with a resolution of 120,000. The AGC target for MS2 in iontrap was set as  $1 \times 10^4$  and ion filling time set as 150ms and fragmented using CID fragmentation with 35% normalized collision energy. The AGC target for MS3 in orbitrap was set as  $1 \times 10^5$  and ion filling time set as 200 ms with a scan range of 100-500 and fragmented using HCD with 65% normalized collision energy. Protein identification was performed using proteome discoverer software version 2.2 (Thermo Fisher Scientific) by searching MS/MS data against the UniProt mouse protein database. The search was set up for full tryptic peptides with a maximum of 2 missed cleavage sites. Oxidation, TMT6plex of the amino terminus, GG and GGQ ubiquitination, phosphorylation, and acetylation were included as variable modifications and

carbamidomethylation and TMT6plex of the amino terminus were set as fixed modifications. The precursor mass tolerance threshold was set at 10 ppm for a maximum fragment mass error of 0.6 Da with a minimum peptide length of 6 and a maximum peptide length of 144. The significance threshold of the ion score was calculated based on a false discovery rate calculated using the percolator node. Protein accessions were put into Ingenuity Pathway Analysis (QIAGEN Inc.) to identify gene symbols and localizations. Gene ontology pathway analysis was performed using DAVID Bioinformatics Database 6.8 using the functional annotation tool.

### siRNA transfection

HeLa cells were plated on 6 well plates and treated with human ETFA and ETFB siRNA oligonucleotides for 48 h at 37°C with Lipofectamine RNAiMAX (Thermo Fisher Scientific). The following siRNA oligonucleotides were used in this study: siRNA Universal Negative Control #1 (Sigma-Aldrich, catalog no. SIC001-1NMOL), siRNA ETFA (Sigma-Aldrich, product no. NM\_000126, siRNA ID SASI\_Hs01\_00216824 and SASI\_Hs01\_00216825), siRNA ETFB (Sigma-Aldrich, product no. NM\_001985, siRNA ID SASI\_Hs01\_00129106).

**Supplementary Table 1.** AML patient data characteristics.

| Sample | Sex | Age at Diagnosis | Stage FAB | Peripheral Blood Blast Count | Diagnosis | Karyotype |
|--------|-----|------------------|-----------|------------------------------|-----------|-----------|
| 1      | F   | 35               | M0        | 36%                          | De novo   | Unknown   |
| 2      | F   | 66               | M1        | 91%                          | De novo   | Unknown   |
| 3      | F   | 66               | M1        | 95%                          | De novo   | Unknown   |
| 4      | F   | 51               | M2        | 50%                          | De novo   | 46,XX     |

|   |   |    |    |     |         |         |
|---|---|----|----|-----|---------|---------|
| 5 | M | 65 | M4 | 94% | De novo | Unknown |
|---|---|----|----|-----|---------|---------|

**Supplementary Table 2.** A comprehensive list of overexpressed proteins identified from mass spectrometry reveals RNA and protein expression levels in subtypes *Cbfb-MYH11*, MLL-AF9, and MLL-ENL.

| Protein Symbol | Gene Name                                                                     | Fold Increase protein |         |         | Fold Increase RNA |         |         |
|----------------|-------------------------------------------------------------------------------|-----------------------|---------|---------|-------------------|---------|---------|
|                |                                                                               | Cbfb-MYH11            | MLL-AF9 | MLL-ENL | Cbfb-MYH11        | MLL-AF9 | MLL-ENL |
| AFG3L2         | AFG3 like matrix AAA peptidase subunit 2                                      | 2.31                  | 1.58    | 1.55    | 2.43              | 1.13    | 1.09    |
| ALG1           | ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase                   | 1.79                  | 1.61    | 2.31    | 2.07              | 2.15    | 2.61    |
| Chtop          | chromatin target of PRMT1                                                     | 1.93                  | 1.81    | 1.78    | 1.44              | 1.39    | 1.46    |
| CISD2          | CDGSH iron sulfur domain 2                                                    | 1.75                  | 1.71    | 2.09    | 2.07              | 1.66    | 1.68    |
| DHODH          | dihydroorotate dehydrogenase (quinone)                                        | 2.34                  | 1.57    | 2.01    | 2.85              | 1.52    | 2.42    |
| ETFA           | electron transfer flavoprotein subunit alpha                                  | 1.99                  | 1.86    | 1.85    | 1.67              | 1.34    | 1.36    |
| ETFB           | electron transfer flavoprotein subunit beta                                   | 1.86                  | 1.71    | 1.75    | 1.37              | 0.88    | 1.7     |
| FDXR           | ferredoxin reductase                                                          | 2.40                  | 1.56    | 1.51    | 3.51              | 1.91    | 2.1     |
| GATD3A/GATD3B  | glutamine amidotransferase like class 1 domain containing 3A                  | 1.84                  | 1.85    | 1.82    |                   |         |         |
| HADH           | hydroxyacyl-CoA dehydrogenase                                                 | 2.53                  | 1.62    | 1.61    | 2.83              | 1.29    | 1.35    |
| HADHA          | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha | 2.32                  | 1.63    | 1.80    | 2.17              | 1.41    | 1.46    |
| HADHB          | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta  | 2.36                  | 1.62    | 1.78    | 1.97              | 1.05    | 1.01    |
| ILVBL          | ilvB acetolactate synthase like                                               | 1.93                  | 1.61    | 2.12    | 2.25              | 1.28    | 1.9     |
| ITPR1          | inositol 1,4,5-trisphosphate receptor type 1                                  | 2.03                  | 1.73    | 1.55    | 9.7               | 10.13   | 5.83    |
| MAN2A1         | mannosidase alpha class 2A member 1                                           | 1.53                  | 1.59    | 1.78    | 3.24              | 4       | 3.48    |
| MARC2          | mitochondrial amidoxime reducing component 2                                  | 2.01                  | 1.78    | 2.43    | 1.47              | 0.99    | 1.34    |
| MAU2           | MAU2 sister chromatid cohesion factor                                         | 1.69                  | 1.73    | 1.86    | 2.24              | 2.33    | 2.08    |
| MRPL10         | mitochondrial ribosomal protein L10                                           | 2.13                  | 1.54    | 1.74    | 1.21              | 1.49    | 1.52    |
| MRPS23         | mitochondrial ribosomal protein S23                                           | 1.75                  | 1.54    | 1.79    | 1.47              | 1.09    | 1.34    |
| MVP            | major vault protein                                                           | 1.63                  | 1.62    | 1.55    | 2.23              | 2.4     | 1.73    |
| OTULINL        | OTU deubiquitinase with linear linkage specificity like                       | 2.99                  | 2.10    | 1.75    |                   |         |         |
| PMPCA          | peptidase, mitochondrial processing alpha subunit                             | 1.78                  | 1.50    | 1.72    | 2.27              | 1.29    | 1.35    |
| PTRH2          | peptidyl-tRNA hydrolase 2                                                     | 2.61                  | 1.52    | 1.73    | 1.72              | 0.83    | 1.04    |
| RAB10          | RAB10, member RAS oncogene family                                             | 1.78                  | 1.68    | 1.69    | 1.87              | 1.36    | 0.99    |
| SHMT2          | serine hydroxymethyltransferase 2                                             | 3.77                  | 1.75    | 2.16    | 4.1               | 1.4     | 1.68    |
| SLC25A11       | solute carrier family 25 member 11                                            | 2.19                  | 1.95    | 2.06    | 2.02              | 1.55    | 1.54    |
| SLC25A3        | solute carrier family 25 member 3                                             | 2.03                  | 1.60    | 1.72    | 1.67              | 1.09    | 1.08    |
| SLC25A5        | solute carrier family 25 member 5                                             | 2.23                  | 1.71    | 1.86    | 1.48              | 1.05    | 1.08    |
| SNRPA1         | small nuclear ribonucleoprotein polypeptide A'                                | 1.83                  | 1.53    | 1.85    | 1.57              | 1.15    | 1.38    |
| SNRPD1         | small nuclear ribonucleoprotein D1 polypeptide                                | 1.76                  | 1.62    | 1.97    | 1.3               | 0.99    | 1.44    |



|        |                                                |      |      |      |      |      |      |
|--------|------------------------------------------------|------|------|------|------|------|------|
| TOMM22 | translocase of outer mitochondrial membrane 22 | 2.20 | 1.80 | 2.12 | 1.18 | 1    | 1.12 |
| TXNL4A | thioredoxin like 4A                            | 1.95 | 1.59 | 1.82 | 1.56 | 0.72 | 0.52 |
| U2AF2  | U2 small nuclear RNA auxiliary factor 2        | 1.65 | 1.50 | 1.67 | 2.17 | 1.74 | 1.66 |
| VDAC3  | voltage dependent anion channel 3              | 1.97 | 1.67 | 1.89 | 1.43 | 0.8  | 0.96 |

**Supplementary Table 3.** A comprehensive list of overexpressed proteins identified from mass spectrometry reveals cellular localization, related pathways, and associated roles in leukemia.

| Protein Symbol | Gene Name                                                                     | Localization                        | Pathway                        | Role in Leukemia                                                            |
|----------------|-------------------------------------------------------------------------------|-------------------------------------|--------------------------------|-----------------------------------------------------------------------------|
| AFG3L2         | AFG3 like matrix AAA peptidase subunit 2                                      | Mitochondria                        | Proteolysis                    | N/A                                                                         |
| ALG1           | ALG1, chitobiosyldiphosphodolichol beta-mannosyltransferase                   | Endoplasmic reticulum               | Protein glycosylation          | Autophagy protects myeloid cells from oxidative stress, apoptotic signaling |
| Chtop          | chromatin target of PRMT1                                                     | Nucleus                             | mRNA transport/processing      | N/A                                                                         |
| CISD2          | CDGSH iron sulfur domain 2                                                    | Endoplasmic reticulum, mitochondria | Energy metabolism              | N/A                                                                         |
| DHODH          | dihydroorotate dehydrogenase (quinone)                                        | Mitochondria                        | UMP biosynthesis               | Inhibitor of DHODH allows for differentiation in MLL AML                    |
| ETFA           | electron transfer flavoprotein subunit alpha                                  | Mitochondria                        | Respiratory electron transport | N/A                                                                         |
| ETFB           | electron transfer flavoprotein subunit beta                                   | Mitochondria                        | Respiratory electron transport | N/A                                                                         |
| FDXR           | ferredoxin reductase                                                          | Mitochondria                        | Metabolism                     | N/A                                                                         |
| GATD3A/GATD3B  | glutamine amidotransferase like class 1 domain containing 3A                  | Mitochondria                        | N/A                            | N/A                                                                         |
| HADH           | hydroxyacyl-CoA dehydrogenase                                                 | Mitochondria                        | Beta oxidation                 | Contributes to embryonic stem cell-like proliferation in MLL-AF9 AML        |
| HADHA          | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha | Mitochondria                        | Beta oxidation                 | Overexpressed in tumor-infiltrating myeloid-derived suppressor cells        |
| HADHB          | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta  | Mitochondria, endoplasmic reticulum | Beta oxidation                 | N/A                                                                         |
| ILVBL          | ilvB acetolactate synthase like                                               | Membrane                            | Ion binding                    | N/A                                                                         |
| ITPR1          | inositol 1,4,5-trisphosphate receptor type 1                                  | Membrane, endoplasmic reticulum     | Signaling                      | N/A                                                                         |
| MAN2A1         | mannosidase alpha class 2A member 1                                           | Golgi                               | Biosynthesis/transport         | SNP identified in acute lymphoblastic leukemia and associated with risk     |
| MARC2          | mitochondrial amidoxime reducing component 2                                  | Mitochondria, peroxisome            | Functionalization of compounds | N/A                                                                         |

|          |                                                         |                                         |                                      |                                                                      |
|----------|---------------------------------------------------------|-----------------------------------------|--------------------------------------|----------------------------------------------------------------------|
| MAU2     | MAU2 sister chromatid cohesion factor                   | Nucleus                                 | Cohesin loading onto chromatin       | Cohesin complex partners mutated in AML                              |
| MRPL10   | mitochondrial ribosomal protein L10                     | Mitochondria                            | Mitochondrial translation initiation | N/A                                                                  |
| MRPS23   | mitochondrial ribosomal protein S23                     | Mitochondria                            | Mitochondrial translation initiation | N/A                                                                  |
| MVP      | major vault protein                                     | Nucleus                                 | Protein transport                    | Correlated with resistance of AML drugs                              |
| OTULINL  | OTU deubiquitinase with linear linkage specificity like | Nucleus, endoplasmic reticulum          | Inactive deubiquitinase              | N/A                                                                  |
| PMPCA    | peptidase, mitochondrial processing alpha subunit       | Mitochondria                            | Protein metabolism                   | Downregulated in chronic lymphocytic leukemia                        |
| PTRH2    | peptidyl-tRNA hydrolase 2                               | Mitochondria                            | Apoptosis/protein modification       | Deletions at locus identified in myeloid malignancies                |
| RAB10    | RAB10, member RAS oncogene family                       | Golgi, cytoplasm, endoplasmic reticulum | Transport                            | Upregulated by TUG1 in AML cells                                     |
| SHMT2    | serine hydroxymethyltransferase 2                       | Mitochondria                            | Metabolism                           | Identified as Crenolanib target in treatment of AML                  |
| SLC25A11 | solute carrier family 25 member 11                      | Mitochondria                            | Gluconeogenesis                      | Identified as Crenolanib target in treatment of AML                  |
| SLC25A3  | solute carrier family 25 member 3                       | Mitochondria                            | Transport                            | Potential biomarker for chronic myeloid leukemia                     |
| SLC25A5  | solute carrier family 25 member 5                       | Mitochondria                            | Transport                            | N/A                                                                  |
| SNRPA1   | small nuclear ribonucleoprotein polypeptide A'          | Nucleus                                 | mRNA splicing                        | More abundant in human pluripotent stem cells, interacts with SNRPD1 |
| SNRPD1   | small nuclear ribonucleoprotein D1 polypeptide          | Nucleus, cytosol                        | mRNA splicing                        | More abundant in human pluripotent stem cells, interacts with SNRPA1 |
| TOMM22   | translocase of outer mitochondrial membrane 22          | Mitochondria                            | mitochondrial protein import         | N/A                                                                  |
| TXNL4A   | thioredoxin like 4A                                     | Mitochondria                            | mRNA splicing                        | N/A                                                                  |
| U2AF2    | U2 small nuclear RNA auxiliary factor 2                 | Nucleus                                 | mRNA splicing                        | Mutations common in myeloid malignancies                             |
| VDAC3    | voltage dependent anion channel 3                       | Mitochondria                            | Transport                            | N/A                                                                  |

**Supplementary Table 4.** Corresponding references for identified proteins associated with leukemia.

| Protein Symbol | References                                                                                                                |
|----------------|---------------------------------------------------------------------------------------------------------------------------|
| AFG3L2         |                                                                                                                           |
| ALG1           | <a href="https://www.ncbi.nlm.nih.gov/pubmed/30859901">https://www.ncbi.nlm.nih.gov/pubmed/30859901</a>                   |
| Chtop          |                                                                                                                           |
| CISD2          | -                                                                                                                         |
| DHODH          | <a href="https://www.ncbi.nlm.nih.gov/pubmed/31253180">https://www.ncbi.nlm.nih.gov/pubmed/31253180</a>                   |
| ETFA           |                                                                                                                           |
| ETFB           |                                                                                                                           |
| FDXR           |                                                                                                                           |
| GATD3A/GATD3B  |                                                                                                                           |
| HADH           | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6080909/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6080909/</a> |
| HADHA          | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4636942/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4636942/</a> |
| HADHB          |                                                                                                                           |
| ILVBL          |                                                                                                                           |
| ITPR1          |                                                                                                                           |
| MAN2A1         | <a href="https://pubmed.ncbi.nlm.nih.gov/20189245">https://pubmed.ncbi.nlm.nih.gov/20189245</a>                           |
| MARC2          |                                                                                                                           |
| MAU2           | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4980180/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4980180/</a> |
| MRPL10         |                                                                                                                           |
| MRPS23         |                                                                                                                           |
| MVP            | <a href="https://www.ncbi.nlm.nih.gov/pubmed/10025900">https://www.ncbi.nlm.nih.gov/pubmed/10025900</a>                   |
| OTULINL        |                                                                                                                           |
| PMPCA          | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3496725/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3496725/</a> |
| PTRH2          | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3636093/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3636093/</a> |
| RAB10          | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7025684/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7025684/</a> |
| SHMT2          | <a href="https://pubmed.ncbi.nlm.nih.gov/30942519/">https://pubmed.ncbi.nlm.nih.gov/30942519/</a>                         |
| SLC25A11       | <a href="https://pubmed.ncbi.nlm.nih.gov/30942519/">https://pubmed.ncbi.nlm.nih.gov/30942519/</a>                         |
| SLC25A3        | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2759651/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2759651/</a> |
| SLC25A5        | -                                                                                                                         |
| SNRPA1         | <a href="https://www.ncbi.nlm.nih.gov/pubmed/28595116">https://www.ncbi.nlm.nih.gov/pubmed/28595116</a>                   |
| SNRPD1         | <a href="https://www.ncbi.nlm.nih.gov/pubmed/28595116">https://www.ncbi.nlm.nih.gov/pubmed/28595116</a>                   |
| TOMM22         |                                                                                                                           |
| TXNL4A         |                                                                                                                           |
| U2AF2          | <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6005654/">https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6005654/</a> |
| VDAC3          |                                                                                                                           |