Figure S1. Workflow of single cell RNA-sequencing used in the present study.



Figure S2. Amplification plots of predicted AML1-ETO positive single cells measured using a Mx3000P qPCR system and an ABI 7500 Real-Time PCR system. Results from the two platforms both suggest the existence of AML1-ETO gene fusion in (A and B) A\_C01, (C and D) A\_C19, (E and F) A\_C79, (G and H) A\_C80 and (I and J) A\_C94 cells. AML1-ETO, fusion protein acute myeloid leukemia 1 protein-protein ETO.



Figure S3. Distributions of sequencing data amounts of single cells from the two patients. Distribution patterns of the cells suggest the transcription difference of (A) patient A and (B) patient B.



Figure S4. Kaplan-Meier survival curves of patients with t(8;21) acute myeloid leukemia from the dataset GSE37642 (n=30). Overall survival curves using (A) *ACTG1*, (B) *EPC1*, (C) *JMJD1C*, (D) *RLIM*, (E) *ARGLU1* and (F) *HELLS* are presented. *ACTG1*, actin γ 1; *EPC1*, enhancer of polycomb homolog 1; *JMJD1C*, jumonji domain containing 1C; *RLIM*, ring finger protein, LIM domain interacting; *ARGLU1*, arginine and glutamate rich 1; *HELLS*, helicase, lymphoid specific.



Figure S5. Kaplan-Meier survival curves of patients with t(8;21) acute myeloid leukemia from the dataset GSE6891 (n=22). Overall survival curves using (A) *ATP5J*, (C) *BRCA1*, (D) *FANCD2*, (F) *LARP4B*, (H) *PTCD3*, (J) *RBM3*, (L) *SPCS2*, (N) *TUBA1B* and (P) *UBXN4*, and event-free survival curves using (B) *ATP5J*, (E) *FANCD2*, (G) *LARP4B*, (I) *PTCD3*, (K) *RBM3*, (M) *SPCS2*, (O) *TUBA1B* and (Q) *UBXN4* are presented. *ATP5J*, ATP synthase peripheral stalk subunit F6; *BRCA1*, BRCA1 DNA repair associated; *FANCD2*, FA complementation group D2; *LARP4B*, La ribonucleoprotein domain family member 4B; *PTCD3*, pentatricopeptide repeat domain 3; *RBM3*, RNA binding motif protein 3; *SPCS2*, signal peptidase complex subunit 2; *TUBA1B*, tubulin alpha 1b; *UBXN4*, UBX domain protein 4.

