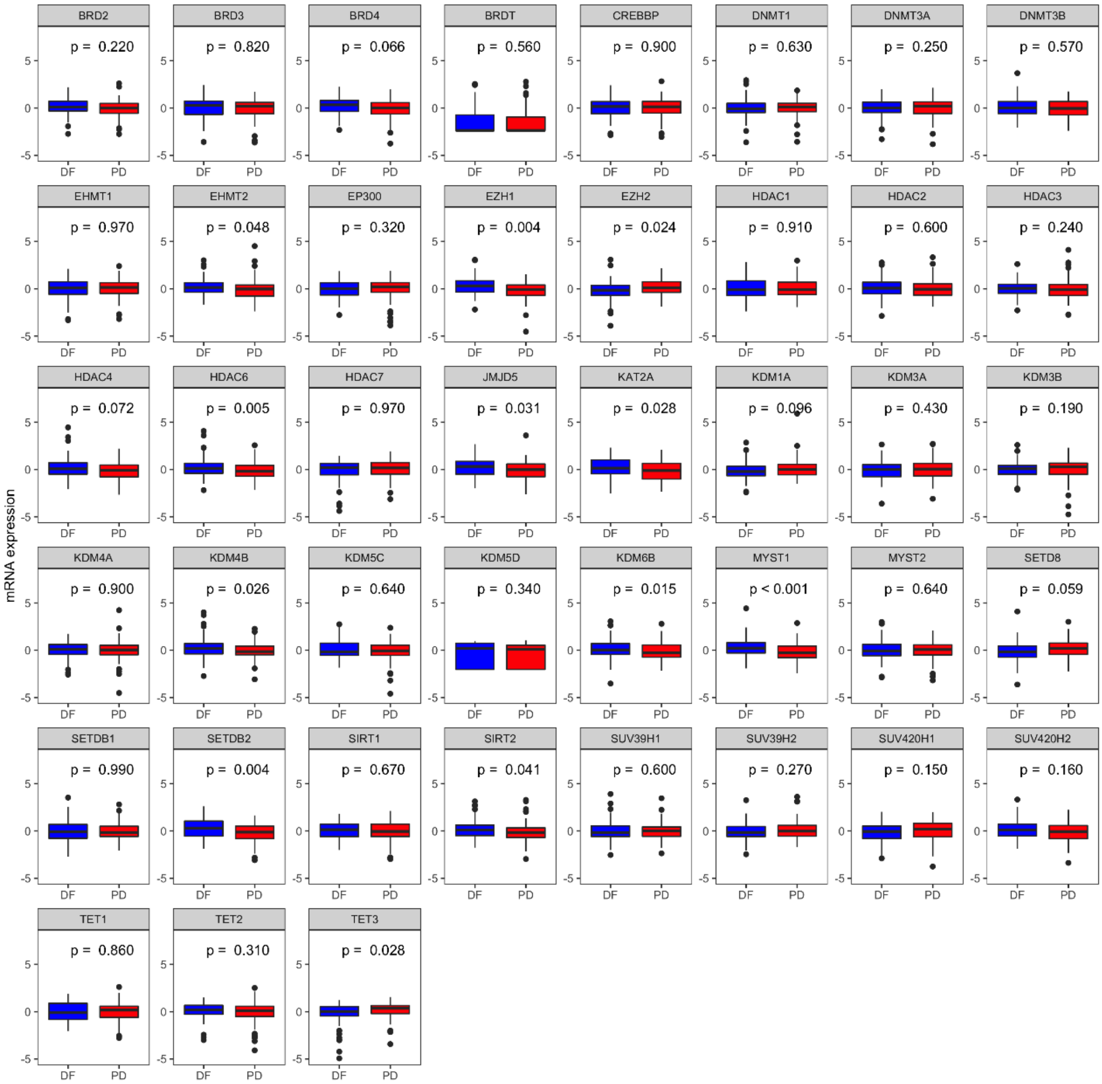
Supplementary Figure S1. Boxplot of RNA-seq expression for each of the candidate genes in the study population according to progression-free survival status. *P*-value is estimated using the Wilcoxon rank sum test. DF, disease-free. PD, progressed disease.

Supplementary Figure S2. Boxplot of RNA-seq expression for each of the candidate genes in the study population according to overall survival status. *P*-value is estimated using the Wilcoxon rank sum test. DF, disease-free. PD, progressed disease.

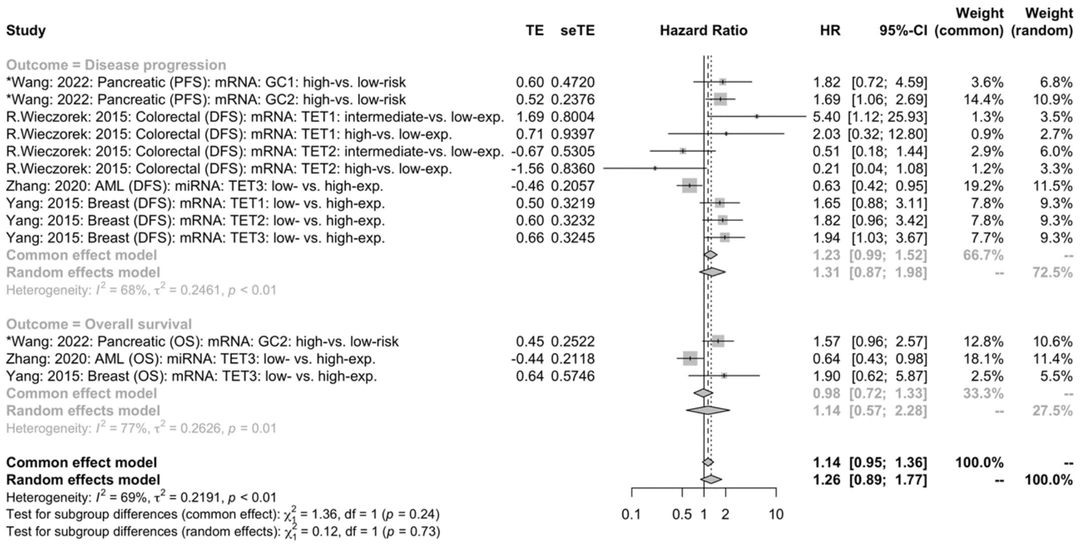
Supplementary Figure S3. Forest plot for risk estimation based on gene expression associated with chromatin remodeling. *Results from the current study. GC: gene cluster, exp.: expression, AML: acute myeloid leukemia, TE: effect size, SE: standard error, HR: hazard ratio, CI: confidence interval, PFS: progression-free survival, DFS: disease-free survival, OS: overall survival.

sFigure 1.


mRNA expression
DF
PD
5
0
-5
BRD2 p = 0.220
BRD3 p = 0.820
BRD4 p = 0.066
BRDT p = 0.560
CREBBP p = 0.900
DNMT1 p = 0.630
DNMT3A p = 0.250
DNMT3B p = 0.570
EHMT1 p = 0.970
EHMT2 p = 0.048
EP300 p = 0.320
EZH1 p = 0.004
EZH2 p = 0.024
HDAC1 p = 0.910
HDAC2 p = 0.600
HDAC3 p = 0.240
HDAC4 p = 0.072
HDAC6 p = 0.005
HDAC7 p = 0.970
JMJD5 p = 0.031
KAT2A p = 0.028
KDM1A p = 0.096
KDM3A p = 0.430
KDM3B p = 0.190
KDM4A p = 0.900
KDM4B p = 0.026
KDM5C p = 0.640
KDM5D p = 0.340
KDM6B p = 0.015
MYST1 p < 0.001
MYST2 p = 0.640
SETD8 p = 0.059
SETDB1 p = 0.990
SETDB2 p = 0.004
SIRT1 p = 0.670
SIRT2 p = 0.041
SUV39H1 p = 0.600
SUV39H2 p = 0.270
SUV420H1 p = 0.150
SUV420H2 p = 0.160
TET1 p = 0.860
TET2 p = 0.310
TET3 p = 0.028

sFigure 2.

sFigure 3.


Study TE seTE Hazard Ratio HR 95%-CI Weight (common) Weight (random)
Outcome = Disease progression
*Wang: 2022: Pancreatic (PFS): mRNA: GC1: high-vs. low-risk 0.60 0.4720 1.82 [0.72; 4.59] 3.6% 6.8%
*Wang: 2022: Pancreatic (PFS): mRNA: GC2: high-vs. low-risk 0.52 0.2376 1.69 [1.06; 2.69] 14.4% 10.9%
R.Wieczorek: 2015: Colorectal (DFS): mRNA: TET1: intermediate-vs. low-exp. 1.69 0.8004 5.40 [1.12; 25.93] 1.3% 3.5%
R.Wieczorek: 2015: Colorectal (DFS): mRNA: TET1: high-vs. low-exp. 0.71 0.9397 2.03 [0.32; 12.80] 0.9% 2.7%
R.Wieczorek: 2015: Colorectal (DFS): mRNA: TET2: intermediate-vs. low-exp. -0.67 0.5305 0.51 [0.18; 1.44] 2.9% 6.0%
R.Wieczorek: 2015: Colorectal (DFS): mRNA: TET2: high-vs. low-exp. -1.56 0.8360 0.21 [0.04; 1.08] 1.2% 3.3%
Zhang: 2020: AML (DFS): miRNA: TET3: low- vs. high-exp. -0.46 0.2057 0.63 [0.42; 0.95] 19.2% 11.5%
Yang: 2015: Breast (DFS): mRNA: TET1: low- vs. high-exp. 0.50 0.3219 1.65 [0.88; 3.11] 7.8% 9.3%
Yang: 2015: Breast (DFS): mRNA: TET2: low- vs. high-exp. 0.60 0.3232 1.82 [0.96; 3.42] 7.8% 9.3%
Yang: 2015: Breast (DFS): mRNA: TET3: low- vs. high-exp. 0.66 0.3245 1.94 [1.03; 3.67] 7.7% 9.3%
Common effect model 1.23 [0.99; 1.52] 66.7% --
Random effects model 1.31 [0.87; 1.98] -- 72.5%
Heterogeneity: $I^2 = 68\%$, $\tau^2 = 0.2461$, $p < 0.01$
Outcome = Overall survival
*Wang: 2022: Pancreatic (OS): mRNA: GC2: high-vs. low-risk 0.45 0.2522 1.57 [0.96; 2.57] 12.8% 10.6%
Zhang: 2020: AML (OS): miRNA: TET3: low- vs. high-exp. -0.44 0.2118 0.64 [0.43; 0.98] 18.1% 11.4%
Yang: 2015: Breast (OS): mRNA: TET3: low- vs. high-exp. 0.64 0.5746 1.90 [0.62; 5.87] 2.5% 5.5%
Common effect model 0.98 [0.72; 1.33] 33.3% --
Random effects model 1.14 [0.57; 2.28] -- 27.5%
Heterogeneity: $I^2 = 77\%$, $\tau^2 = 0.2626$, $p = 0.01$
Common effect model 1.14 [0.95; 1.36] 100.0% --
Random effects model 1.26 [0.89; 1.77] -- 100.0%
Heterogeneity: $I^2 = 69\%$, $\tau^2 = 0.2191$, $p < 0.01$
Test for subgroup differences (common effect): $\chi^2_1 = 1.36$, df = 1 ($p = 0.24$)
Test for subgroup differences (random effects): $\chi^2_1 = 0.12$, df = 1 ($p = 0.73$)
0.1
0.5
1
2
10