High expression of *MAP7* predicts adverse prognosis in young patients with cytogenetically normal acute myeloid leukemia

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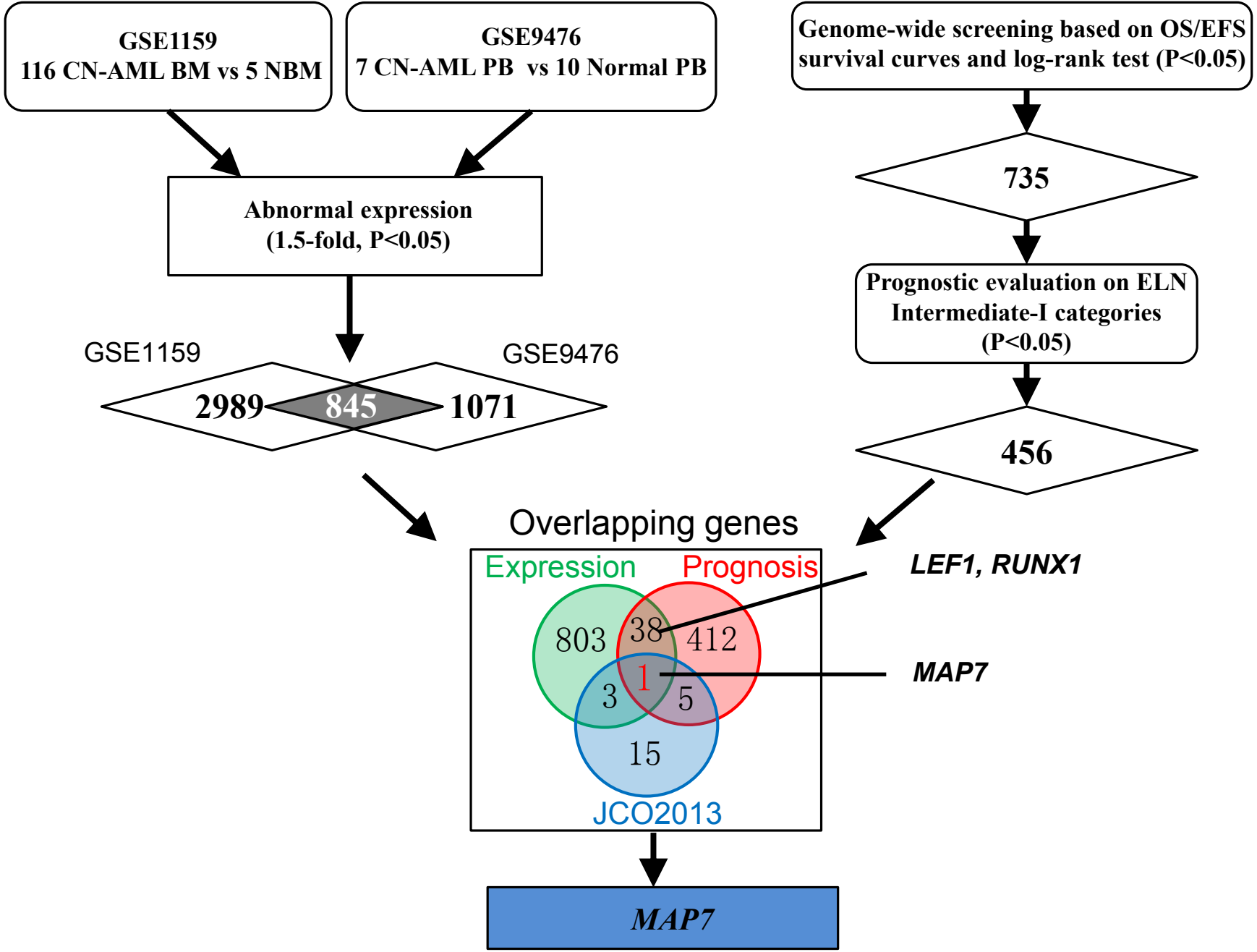
Table S1. Characteristics of the 88 CN-AML patients in the second independent cohort segregated based on *MAP7* expression level

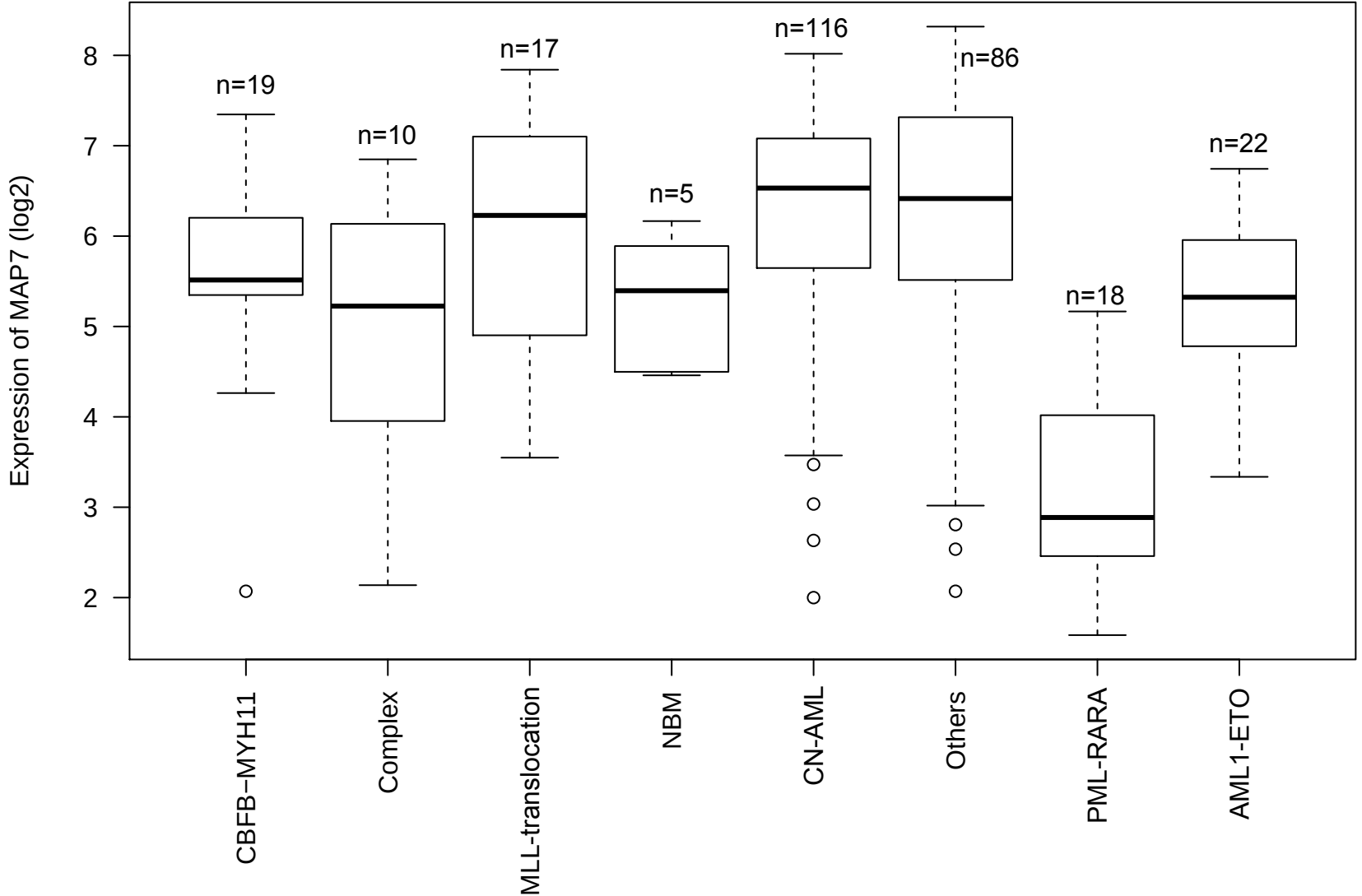
Variable	***MAP7*^{high}**, n=44	***MAP7*^{low}**,n=44	***P***
Median age. y (range)	46 (19-59)	47(17-59)	0.67
FAB subtype, no (%)			
M0	0 (0.0)	3 (6.8)	0.24
M1	13 (29.5)	7 (15.9)	0.21
M2	11 (25.0)	9 (20.5)	0.8
M4	16 (36.4)	12 (27.2)	0.49
M5	3 (6.8)	10 (22.7)	0.033
M6	1 (2.3)	3 (6.8)	0.62
High *ERG*, no (%)	31 (70.5)	13 (29.5)	<0.001
High *BAALC*, no (%)	21 (47.8)	23 (52.3)	0.83
High *LEF1*, no (%)	14 (31.8)	30 (68.2)	0.001
High *WT1*, no (%)	34 (77.3)	10 (22.7)	<0.001
High *DNMT3B*, no (%)	33 (75.0)	11 (25.0)	<0.001
High *DNMT3A*, no (%)	28 (63.6)	16 (36.4)	0.02
High *MAPKBP1*, no (%)	31 (70.5)	13 (29.5)	<0.001
High *ITPR2*, no (%)	37 (84.1)	7 (15.9)	<0.001
High *ATP1B1*, no (%)	33 (75.0)	11 (25.0)	<0.001

FAB, French-American-British classification.

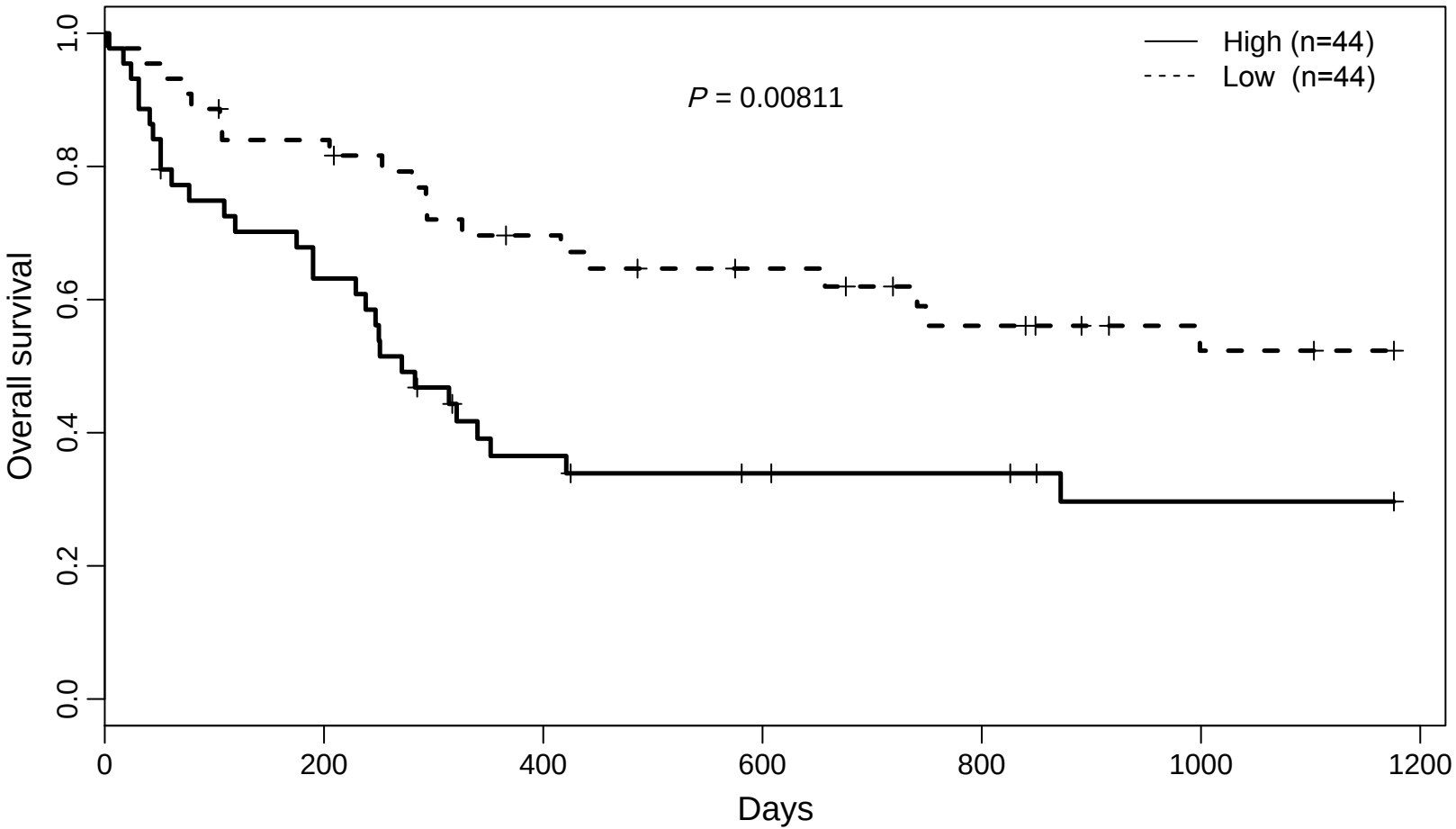
High *ERG*, *BAALC*, *LEF1*, *WT1*, *DNMT3B*, *DNMT3A*, *MAPKP1*, *ITPR2* and *ATP1B1* expression were defined as an expression level above the median of all samples, respectively.



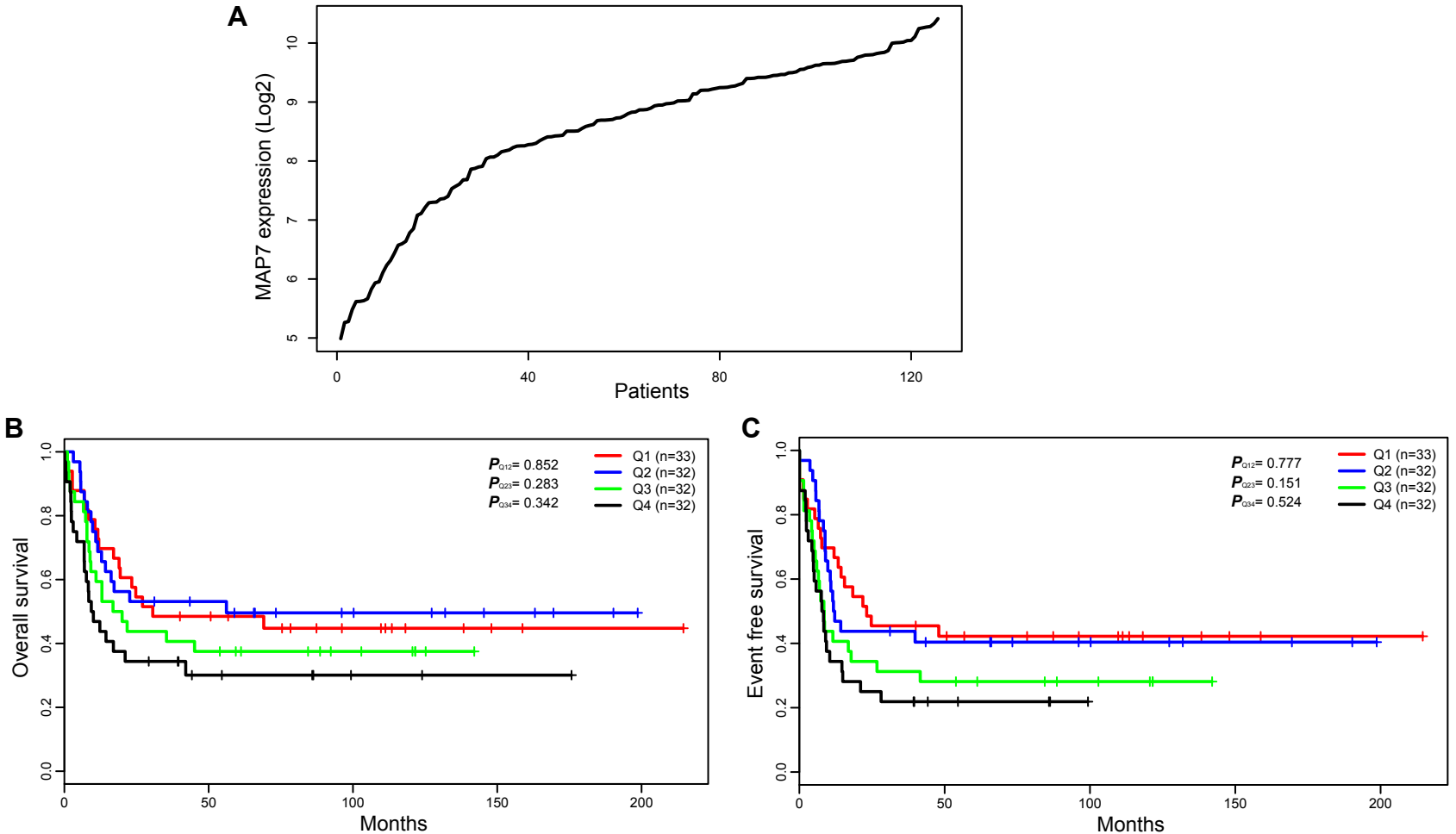
Supplementary Figure 1. A schematic diagram of the systematic strategies for uncovering the prognostic significance of *MAP7* in CN-AML patients.



Supplementary Figure 2. *MAP7* levels in various different subgroups of AML patients.



Supplementary Figure 3. OS of CN-AML patients in the second independent



Supplementary Figure 4. Median value of *MAP7* expression as the cut-off. (A) *MAP7* expression is normally distributed. (B) OS and (C) EFS AML patients were subdivided into four quartiles based on the quartile of *MAP7* expression.