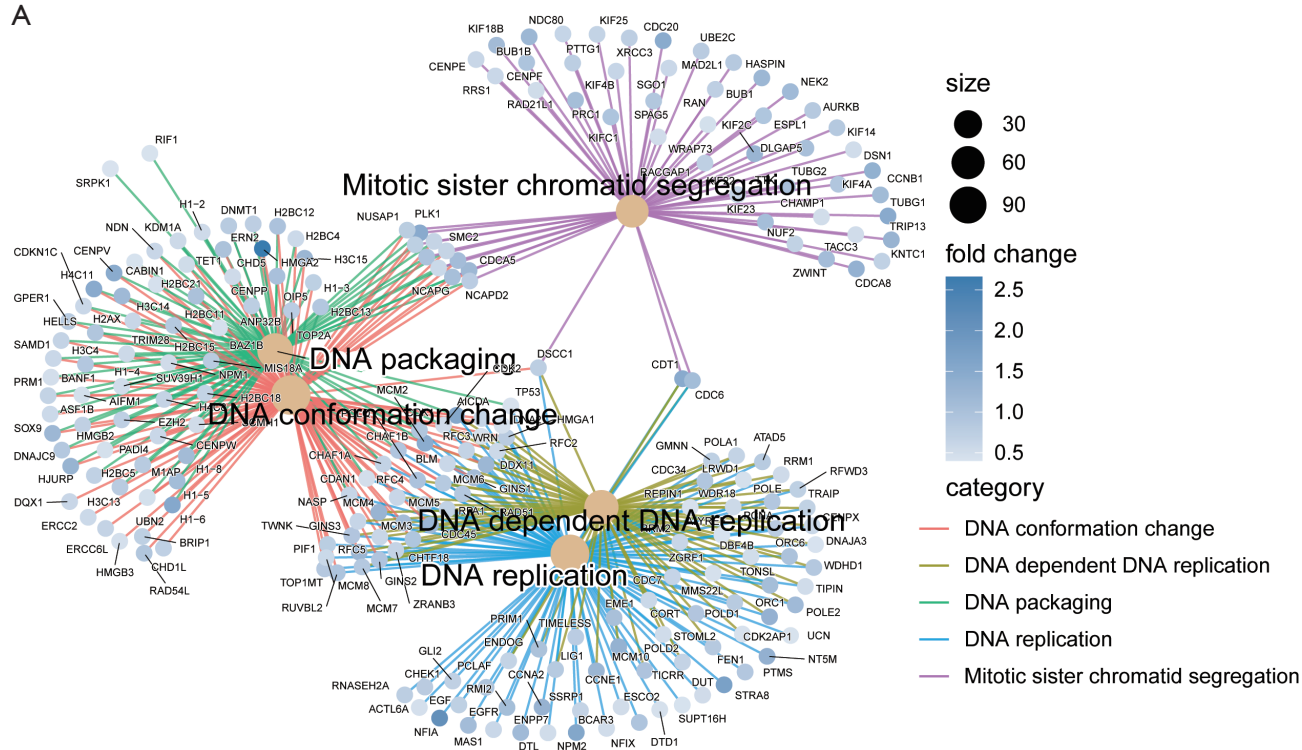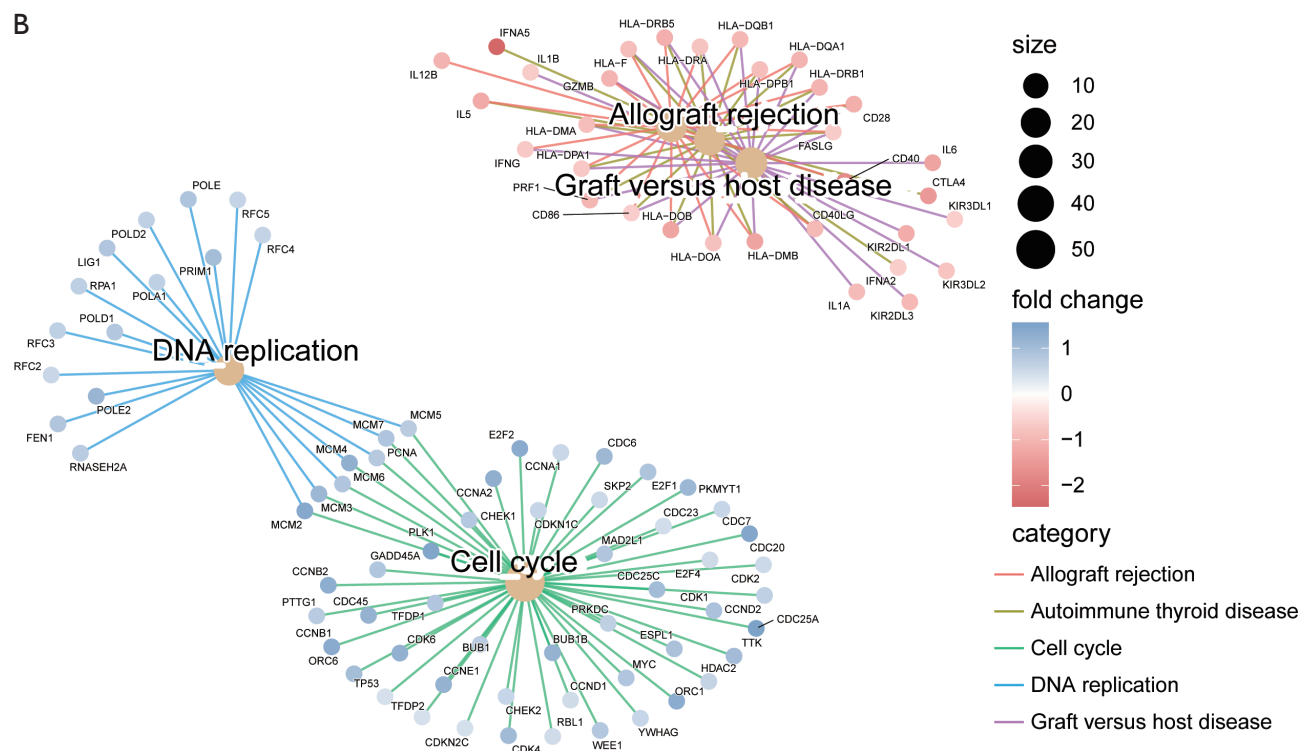Figure S1 Cnetplot of enriched pathways between *LIN28B*-positive and -negative subgroups. Blue dots represent up-regulated genes while red dots represent down-regulated genes. (A) GO-BP analysis. (B) KEGG analysis.
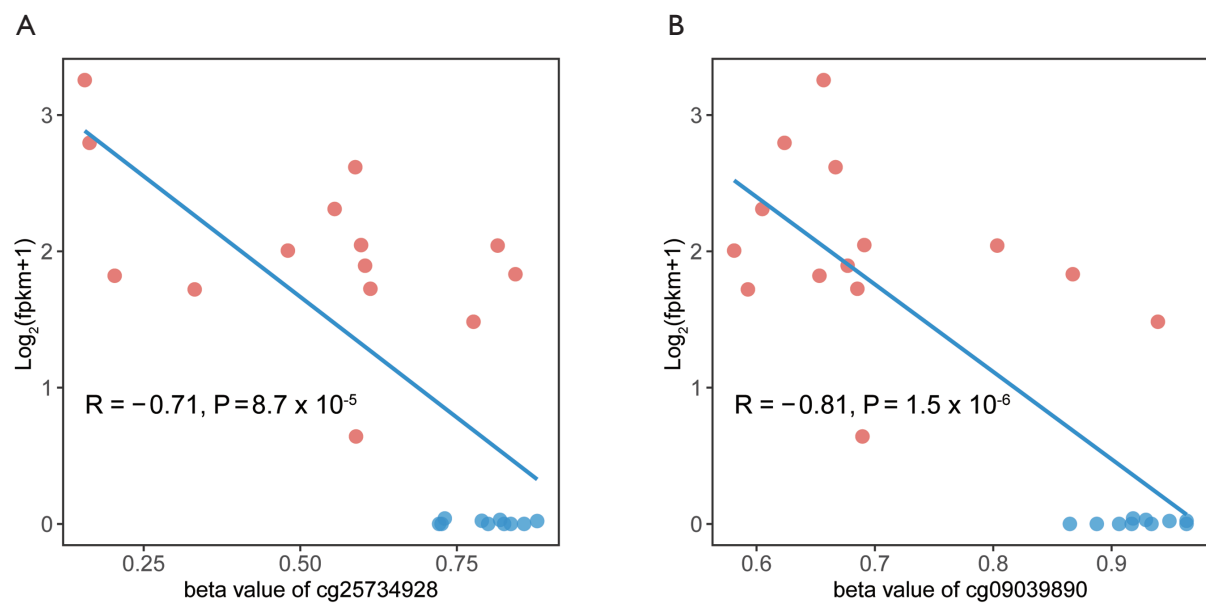
Figure S2 Correlation plot of methylation status and *LIN28B* expression. Red dots: JMML patients in *LIN28B*-positive subgroup; blue dots: JMML patients in *LIN28B*-negative subgroup. (A) Methylation of probe cg25734928. (B) Methylation of probe cg09039890.
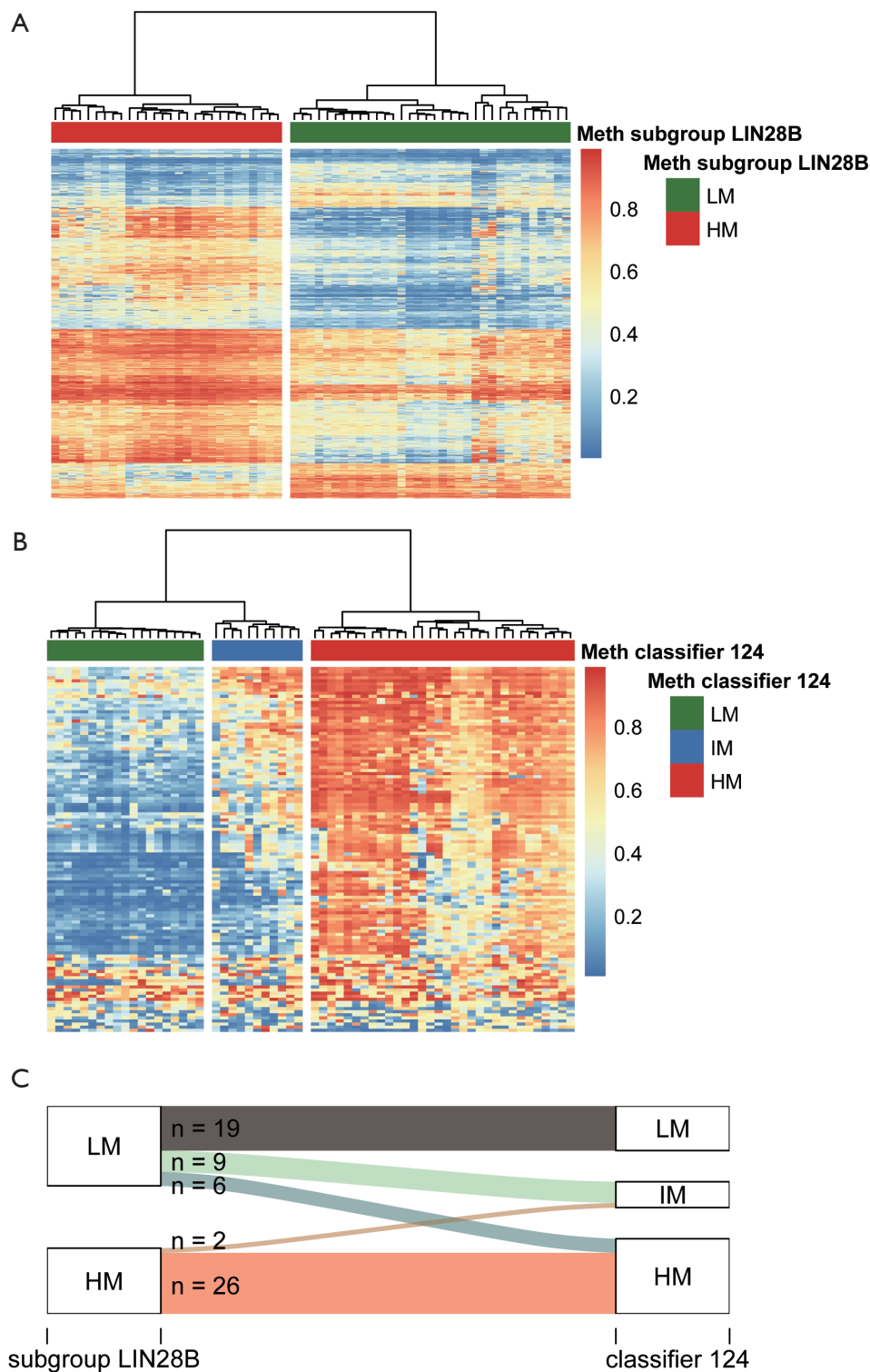
Figure S3 Methylation subgroups of 62 JMML patients. (A) Pheatmap of 62 validation JMML samples identified by top 1,000 DMPs (subgroup LIN28B). (B) Pheatmap of 62 validation JMML samples identified by JMML DNA methylation classifier (classifier 124). (C) Alluvial plot of the JMML subgroups between top 1,000 DMPs and the JMML methylation classifier. The colors of flows represent different changes in the methylation groups.

Table S1 Comparison of clinical features between the 24 JMML cohort and 62 JMML cohort

Index	Total (n=86)	JMML cohort (n=24)	JMML cohort (n=62)	P
Sex				
Male	54 (62.8)	15 (62.5)	39 (62.9)	>0.99
Female	32 (37.2)	9 (37.5)	23 (37.1)	
Age (years)				
Median (range)	2.48 (0.20, 15.20)	3.13 (0.18, 9.13)	2.24 (0.20, 15.20)	0.58
<2 years	38 (44.2)	9 (37.5)	29 (46.8)	0.48
≥2 years	48 (55.8)	15 (62.5)	33 (53.2)	
Mutations				
PTPN11	46 (53.5)	17 (70.8)	29 (46.8)	0.056
NF1	18 (20.9)	3 (12.5)	15 (24.2)	0.38
KRAS	9 (10.5)	3 (12.5)	6 (9.7)	0.71
NRAS	17 (19.8)	5 (20.8)	12 (19.4)	>0.99
CBL	8 (9.3)	3 (12.5)	5 (8.1)	0.68
MONO7				
Positive	10 (15.9)	1 (5.6)	9 (20.0)	0.28
Negative	53 (84.1)	17 (94.4)	36 (80.0)	
HbF				
Elevated	49 (86.0)	18 (85.7)	31 (86.1)	>0.99
Normal	8 (14.0)	3 (14.3)	5 (13.9)	

Note: Data are presented as n (%), unless otherwise specified.