

Figure S1. Mixture models for all 30 MDGs in LUSC. Methylation state distributions in tumor samples are represented by the histograms, while the methylation state in normal samples is represented by a horizontal short black bar. MDG, methylation-driven gene; LUSC, lung squamous cell cancer.

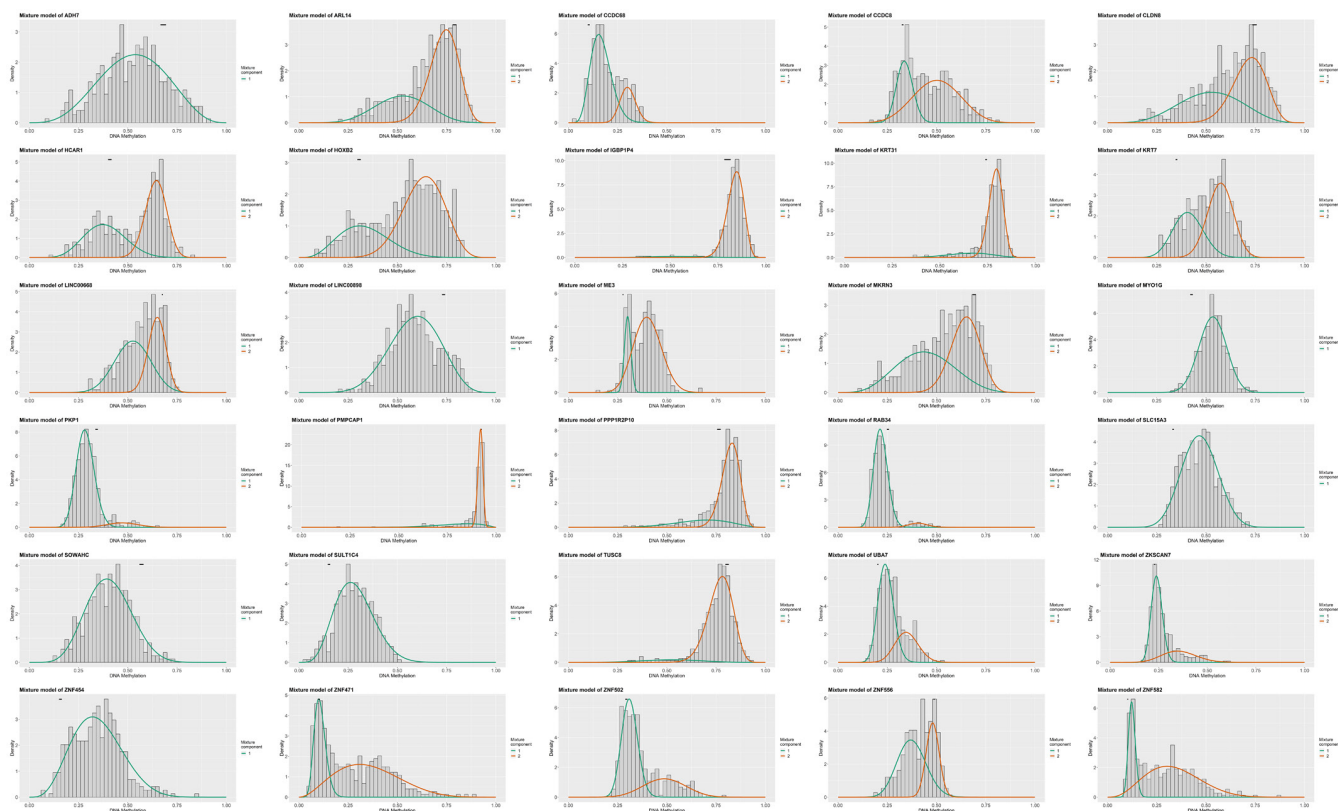


Figure S2. Correlation between DNA methylation state and expression of the 30 MDGs in LUSC. Strong inverse correlation was observed for all genes, with  $\text{Cor} < -0.5$ , and all correlations were statistically significant ( $P$ -value of  $\text{Cor} < 0.01$ ). MDG, methylation-driven gene; LUSC, lung squamous cell cancer; Cor, correlation coefficient.

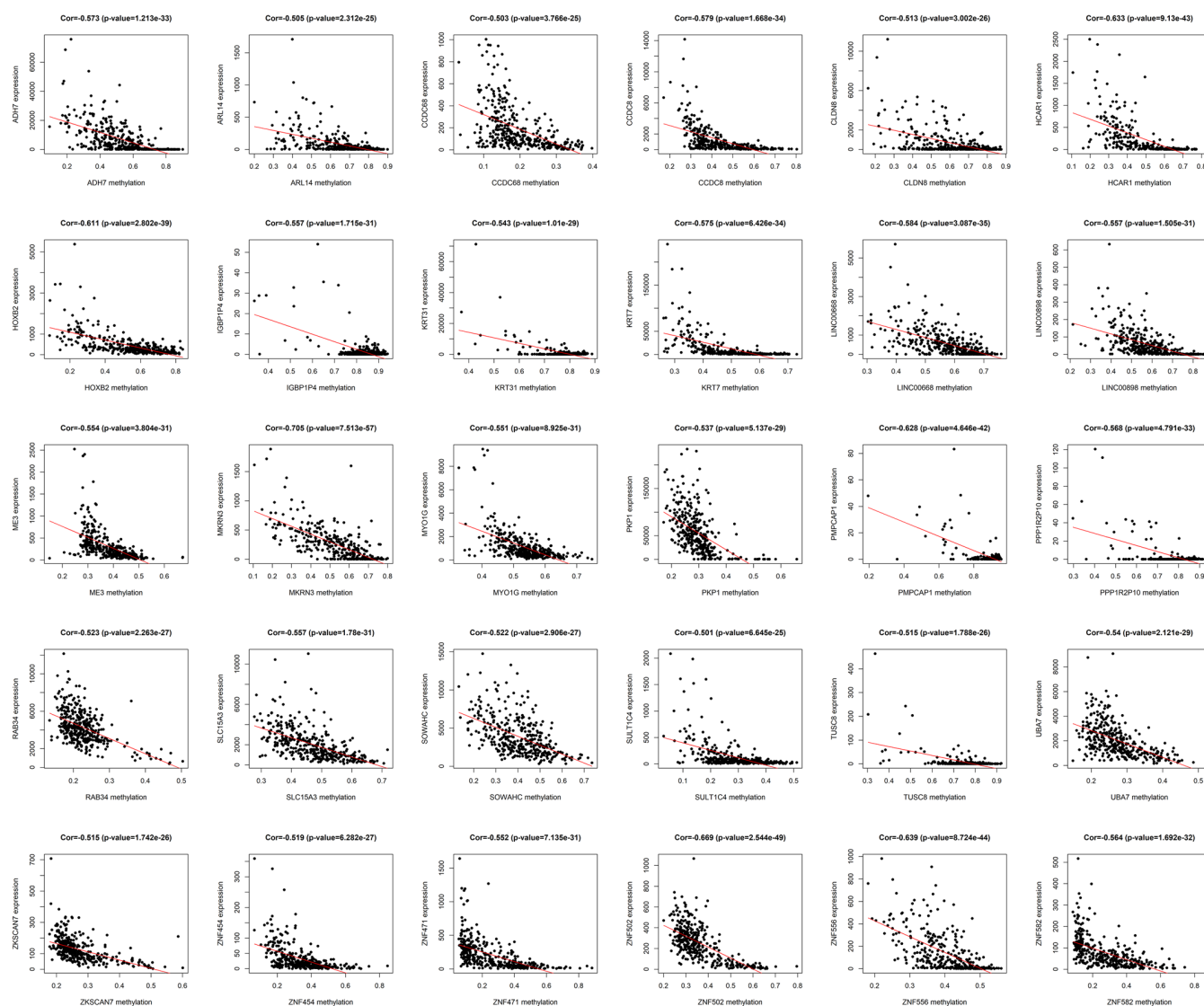


Figure S3. Kaplan-Meier survival analysis curves comparing overall survival between hypermethylation and hypomethylation of all 30 MDGs.  $P < 0.05$ . MDG, methylation-driven gene.

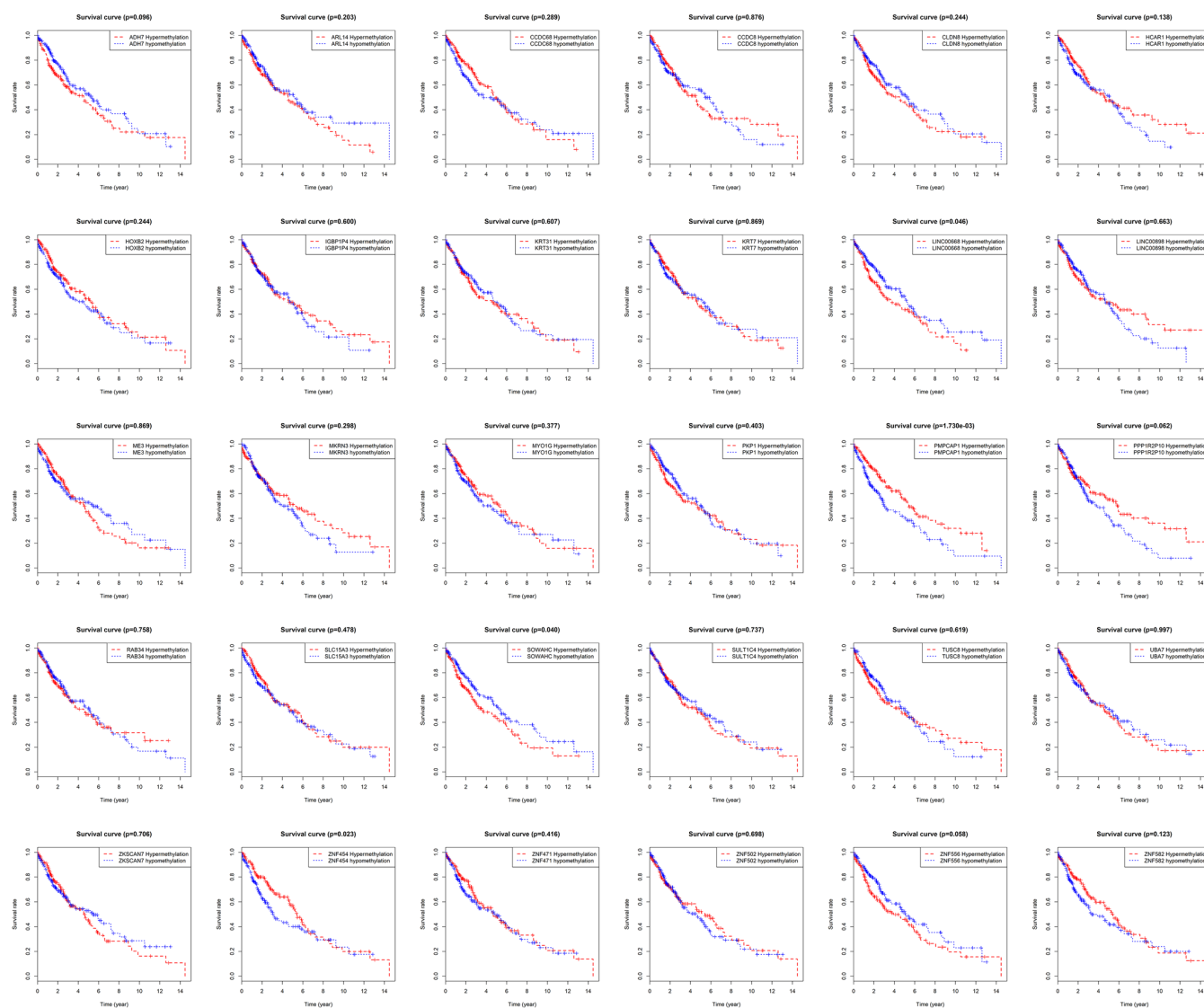


Figure S4. Joint survival analysis curves comparing overall survival between hypermethylation and low expression, and hypo-methylation and high expression of all 30 MDGs.  $P < 0.05$ . MDG, methylation-driven gene.

