

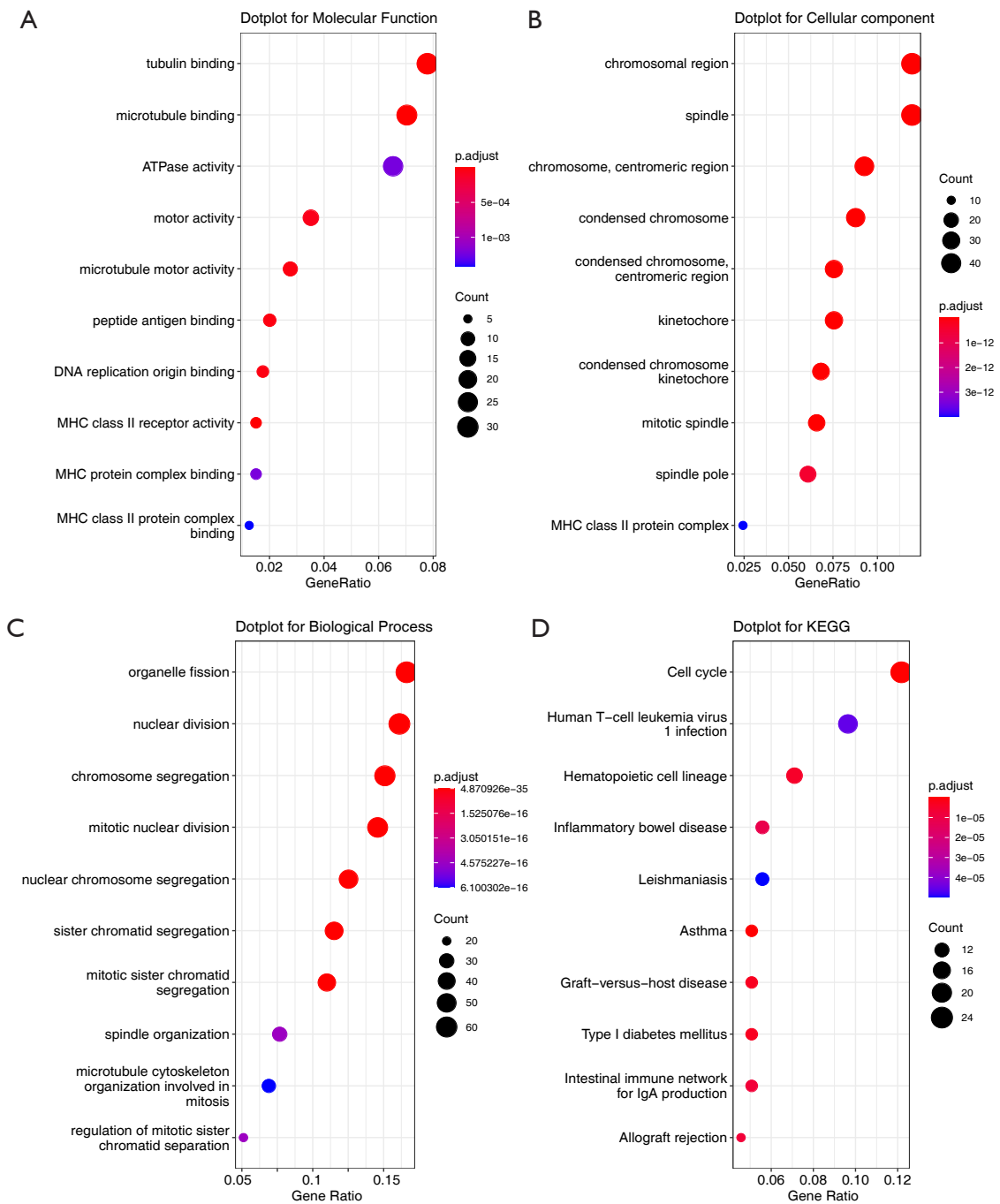
**Figure S1** Heatmap of the DEGs or methylation sites among the different subtypes in the training data set. (A) Correlations between the representative DEGs and clinical characteristics among different subtypes. (B) Correlations between the representative differential methylation sites and clinical characteristics among the different subtypes. Pathologic\_M: pathological metastasis; Pathologic\_T: primary pathological tumor; Pathologic\_N: pathological lymph node status. DEGs, differentially expressed genes.

**Table S1** The corresponding genes of methylation sites

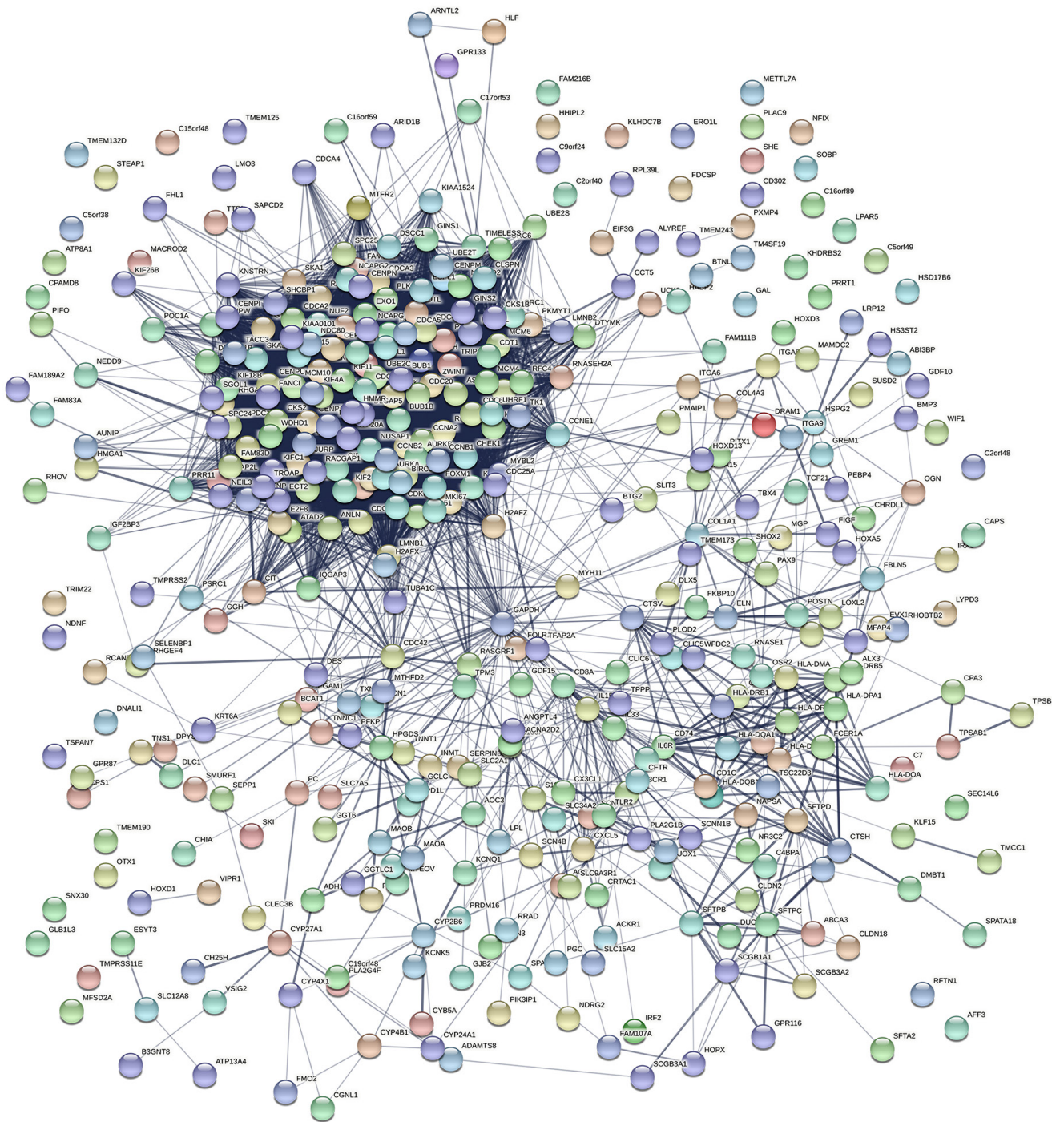
Methylation sites	Gene
cg23019935	<i>CDC42</i>
cg06679878	<i>TMEM132D</i>
cg04414975	<i>TMEM132D</i>
cg05384697	<i>TMEM132D</i>
cg22092126	<i>AFF3</i>
cg21037008	<i>PRRT1</i>
cg25138553	<i>HSPG2</i>
cg05726239	<i>SOBP</i>
cg02429905	<i>PRRT1</i>
cg12483545	<i>SKI</i>
cg05501617	<i>IRF2</i>
cg13035743	<i>PRRT1</i>
cg05445326	<i>TM4SF19</i>
cg05970721	<i>HS3ST2</i>
cg23149881	<i>IL1B</i>
cg17164954	<i>ARID1B</i>
cg17066349	<i>CIT</i>
cg11091914	<i>LRP12</i>
cg26165146	<i>ARNTL2</i>
cg01577755	<i>TRIP13</i>
cg01581084	<i>OSR2</i>
cg00640314	<i>SNORD87</i>
cg05634376	<i>PC</i>
cg11940177	<i>PGAM1</i>
cg26107890	<i>SLC12A8</i>
cg01044293	<i>ITGA6</i>
cg25136495	<i>LPAR5</i>
cg19050555	<i>TUBA1C</i>
cg17975443	<i>TBX4</i>
cg00277165	<i>TRIP13</i>
cg21031917	<i>KHDRBS2</i>
cg17495130	<i>HOXD13</i>
cg17510385	<i>TRIP13</i>
cg19643053	<i>HOXA5</i>

**Table S1** (*continued*)**Table S1** (*continued*)

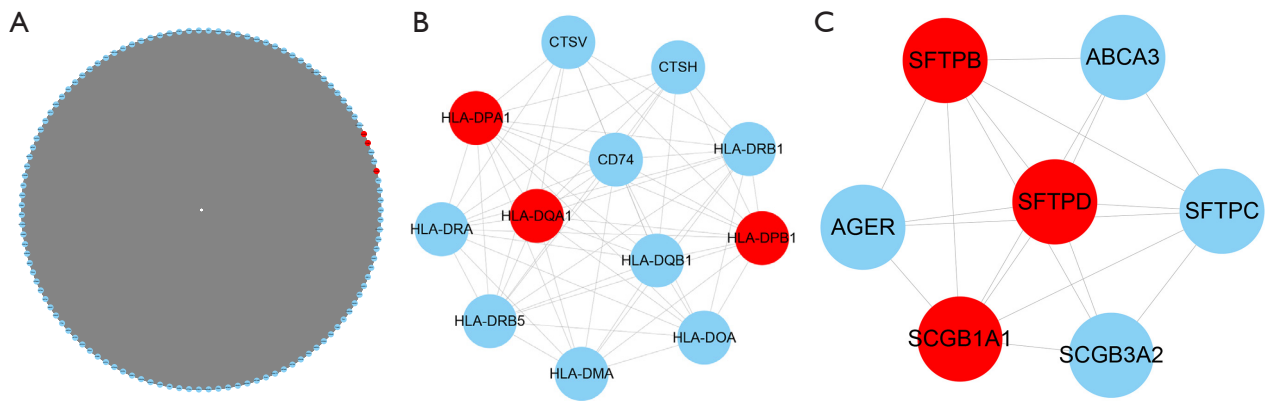
Methylation sites	Gene
cg09015973	<i>ARHGEF4</i>
cg04389897	<i>TFAP2A</i>
cg02466815	<i>HOXD1</i>
cg14499678	<i>TRIP13</i>
cg02409878	<i>OSR2</i>
cg19962750	<i>DLX5</i>
cg17432857	<i>HOXA5</i>
cg09803262	<i>DLX6AS</i>
cg19319037	<i>TTF2</i>
cg06389019	<i>SLC9A3R1</i>
cg03130248	<i>KIF26B</i>
cg19766988	<i>EIF3G</i>
cg21472506	<i>OTX1</i>
cg06890747	<i>LOC646999</i>
cg17582100	<i>GPR87</i>
cg09359114	<i>DLX5</i>
cg02531439	<i>SMURF1</i>
cg07974511	<i>OTX1</i>
cg09542210	<i>SHOX2</i>
cg10122865	<i>OTX1</i>
cg09181792	<i>CFTR</i>
cg17174023	<i>KLHDC7B</i>
cg13677149	<i>EVX1</i>
cg20399616	<i>BCAT1</i>
cg17916835	<i>DLX5</i>
cg23005797	<i>C2orf48</i>
cg07443717	<i>TMCC1</i>
cg12606911	<i>CD8A</i>
cg02773086	<i>HOXD3</i>
cg04415798	<i>PAX9</i>
cg27071152	<i>LOC646999</i>
cg11718162	<i>TPM3</i>
cg06809252	<i>ALX3</i>



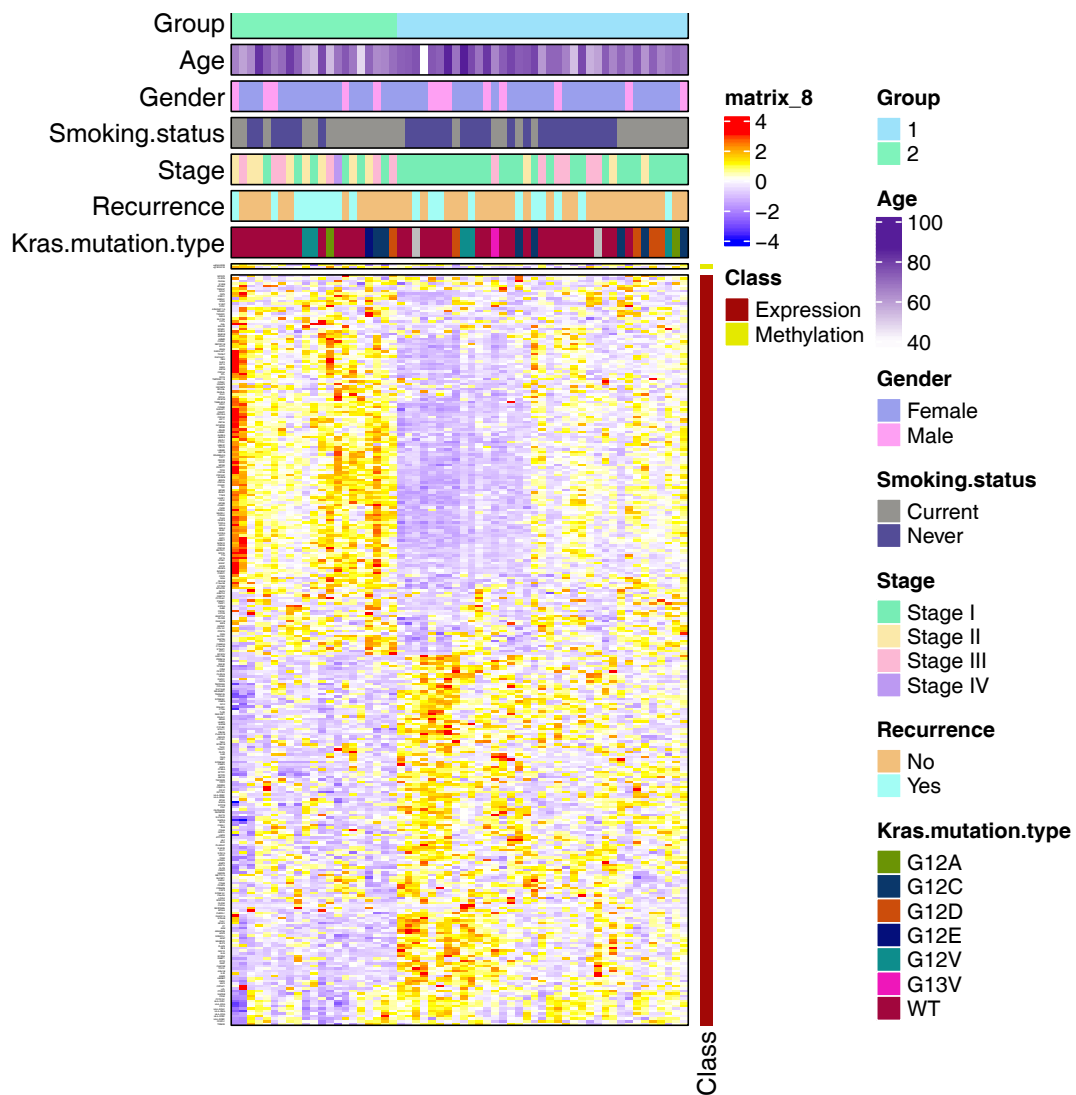
**Figure S2** MF analysis and pathway analysis of representative genes and the corresponding genes of the methylation sites. (A) MFs. (B) CCs. (C) BPs. (D) KEGG pathway analysis. BP, biological process; CC, cellular component; IgA, immunoglobulin A; KEGG, Kyoto Encyclopedia of Genes and Genomes; MF, molecular function; MHC, major histocompatibility complex.



**Figure S3** The PPI network of the representative genes and methylation sites and hub genes. The PPI networks were generated by STRING and then visualized with Cytoscape. Using the MCODE plug-in, 3 clusters were generated, and the degree value was used to define the hub gene. PPI, protein-protein interaction.



**Figure S4** The PPI network was generated by STRING. PPI, protein-protein interaction.



**Figure S5** Heatmap of the representative DEGs or genes corresponding to the methylation sites and immune cells among the different subtypes in the training data set. DEGs, differentially expressed genes; WT, wild type.