

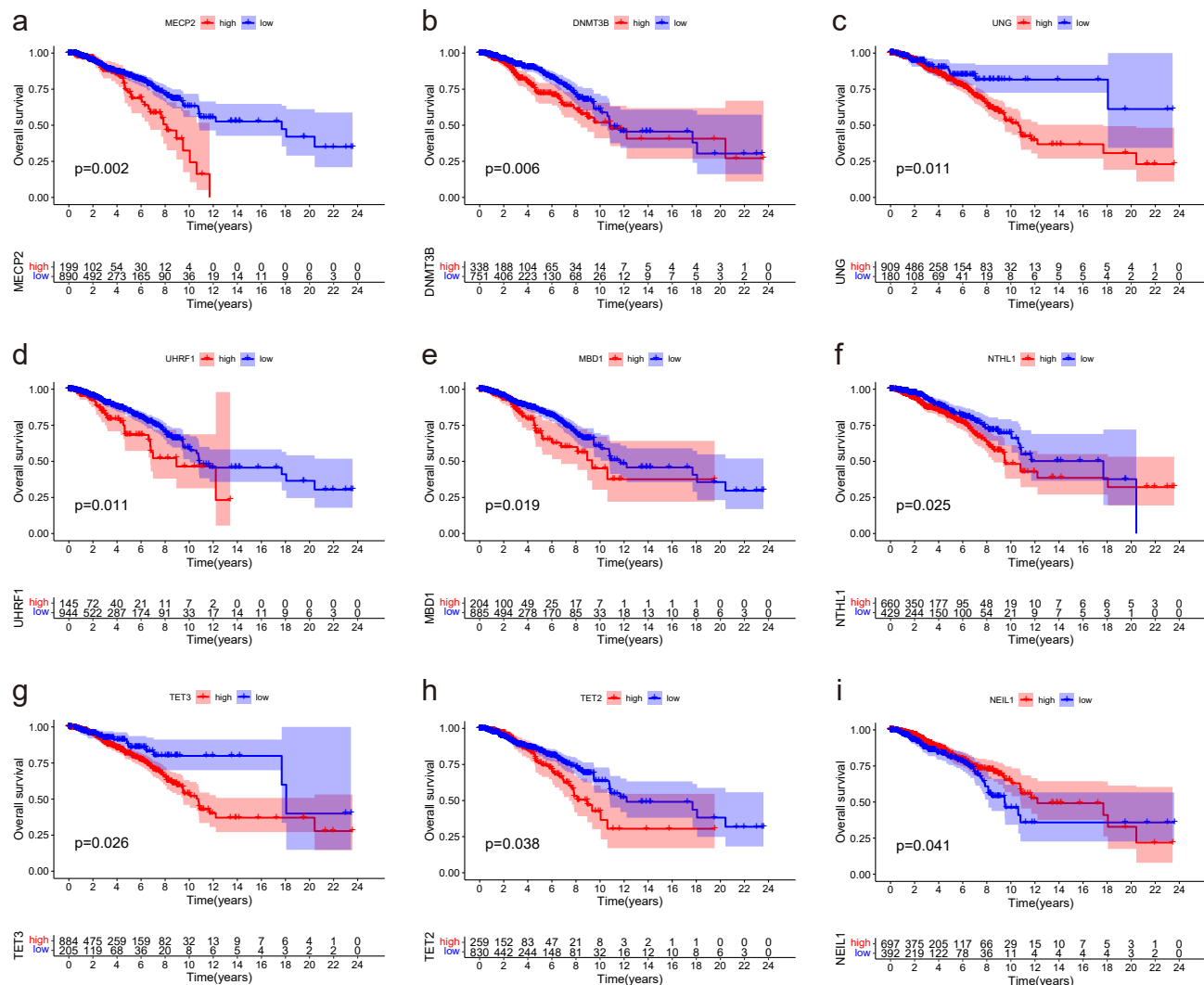


Figure S1. The prognostic role of m⁵C related regulatory genes in breast cancer (a) MECP2 ($p = 0.002$); (b) DNMT3B ($p = 0.006$); (c) UNG ($p = 0.011$); (d) UHRF1 ($p = 0.011$); (e) MBD1 ($p = 0.019$); (f) NTHL1 ($p = 0.025$); (g) TET3 ($p = 0.026$); (h) TET2 ($p = 0.038$); (i) NEIL1 ($p = 0.041$). Red, high expression; Blue, low expression.

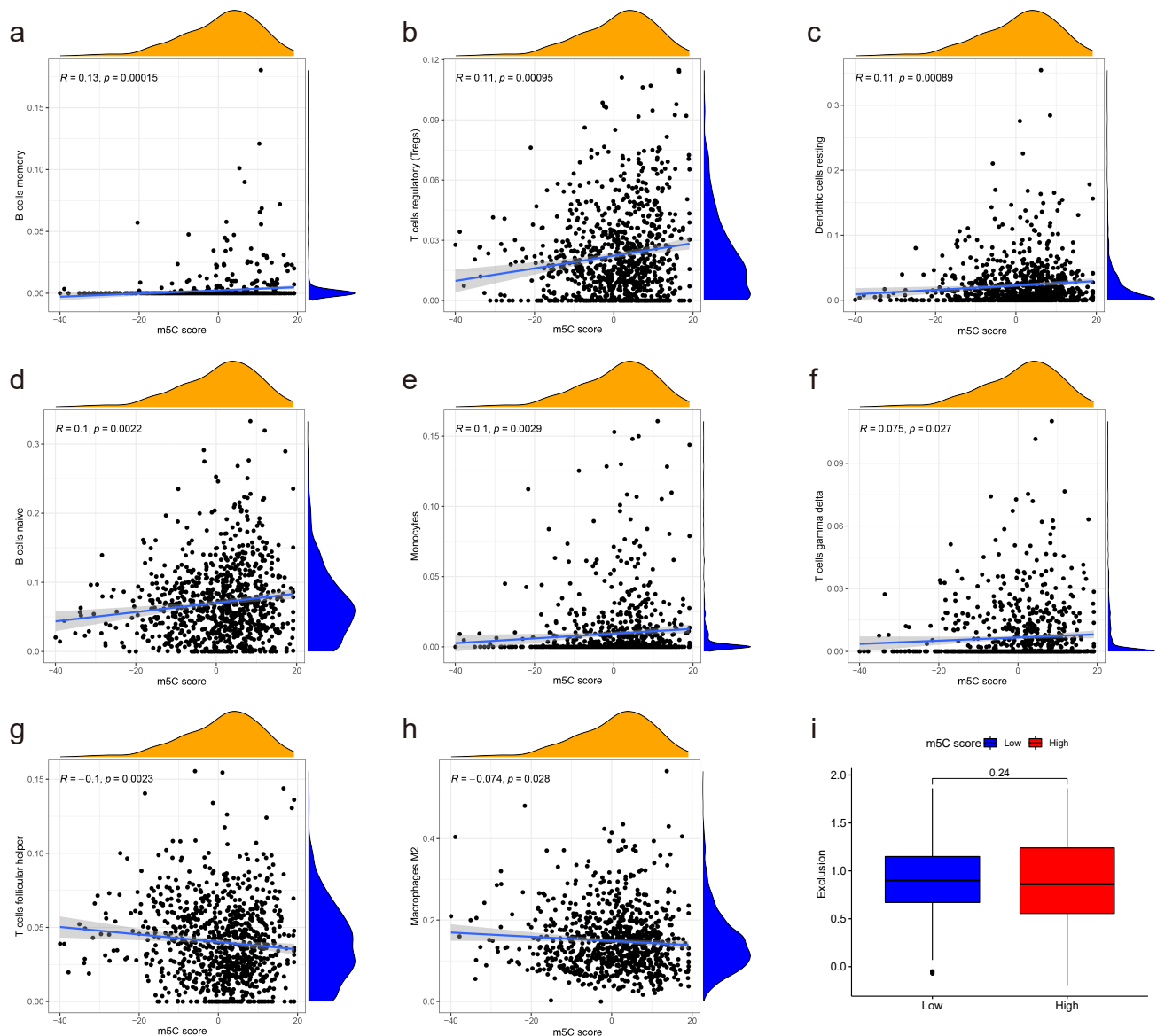


Figure S2. Correlation of the m⁵C score with the infiltration abundances of tumor-infiltrating immune cells and immune exclusion scores (a-h) m⁵C score with the tumor-infiltrating immune cell. (a) memory B cells ($R = 0.13, p = 0.00015$); (b) regulatory T cells ($R = 0.11, p = 0.00095$); (c) resting dendritic cells ($R = 0.11, p = 0.00089$); (d) naive B cells ($R = 0.1, p = 0.0022$); (e) Monocytes ($R = 0.1, p = 0.0029$); (f) gamma delta T cells ($R = 0.075, p = 0.027$); (g) follicular helper T cells ($R = -0.1, p = 0.0023$); (h) M2 macrophages ($R = -0.074, p = 0.028$). (i) The relative distribution of immune exclusion scores was compared between the low and high m⁵C score groups. The lines in the boxes represent the median value, the bottoms and tops of the boxes represent the interquartile range, and the dots represent outliers. Blue, low m⁵C score group; red, high m⁵C score group.

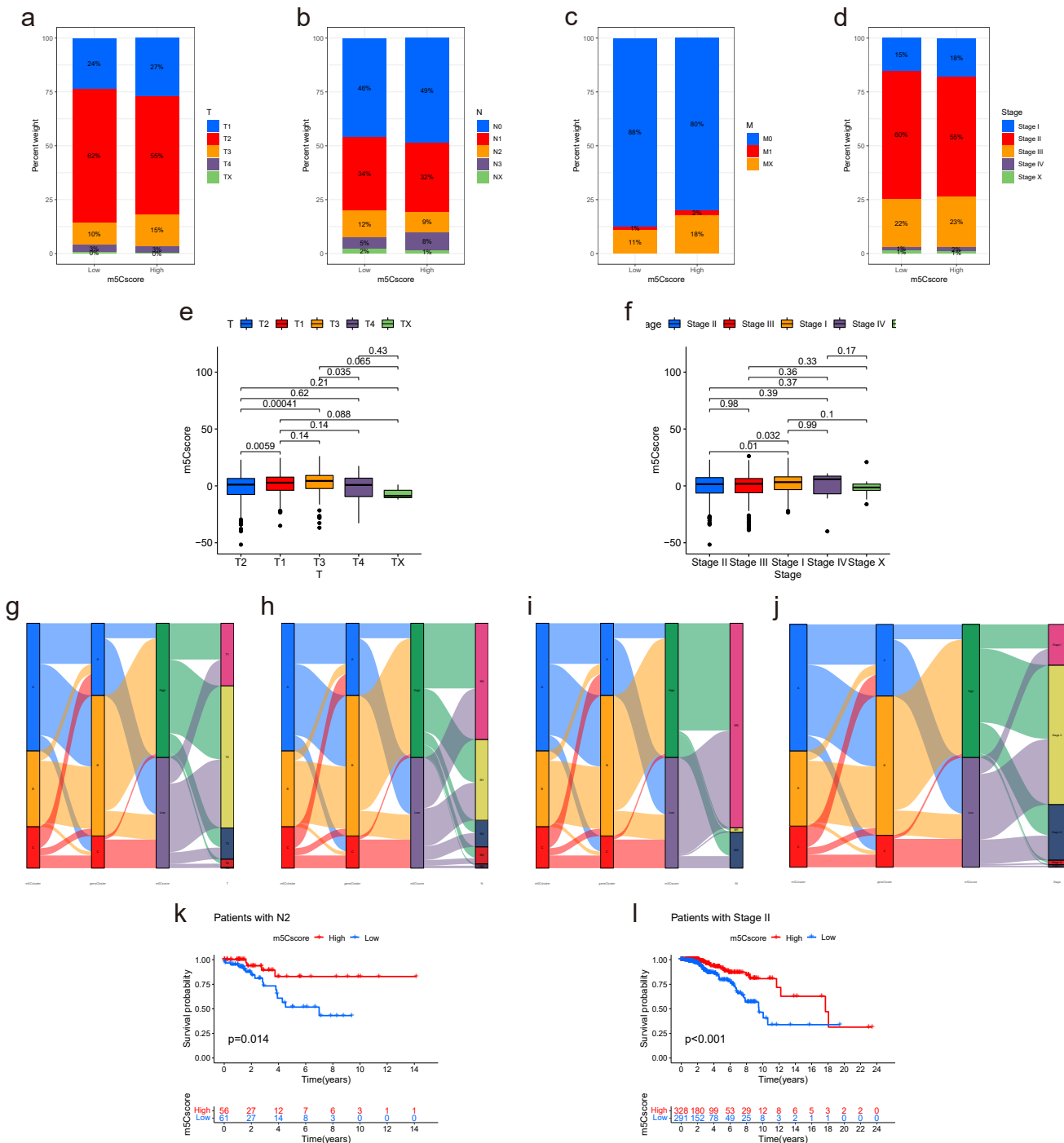


Figure S3. Correlation between clinicopathological characteristics and the m⁵Cscore (a) The T stage in the low and high m⁵Cscore groups. Blue, T1 stage group; red, T2 stage group; yellow, T3 stage group; purple, T4 stage group; green, Tx stage group. (b) The N stage in the low and high m⁵Cscore groups. Blue, N0 stage group; red, N1 stage group; yellow, N2 stage group; purple, N3 stage group; green, Nx stage group. (c) The M stage in the low and high m⁵Cscore groups. Blue, M0 stage group; red, M1 stage group; yellow, Mx stage group. (d) The clinical stage in the low and high m⁵Cscore groups. Blue, stage I group; red, stage II group; yellow, stage III group; purple, stage IV group; green, stage X group. (e) The m⁵Cscore based on T stage. Blue, T2 stage group; red, T1 stage group; yellow, T3 stage group; purple, T4 stage group; green, Tx stage group. (f) The m⁵Cscore based on clinical stage. Blue, stage II group; red, stage III group; yellow, stage I group; purple, stage IV group; green, stage X group. (g-j) The Sankey diagram showing the changes of m⁵C cluster, m⁵C gene cluster, m⁵Cscore and (g) T stage, (h) N stage, (i) M stage and (j) cancer stage. (k-l) Kaplan–Meier survival analysis based on the m⁵Cscore in subgroups with different clinical characteristics. Red, high m⁵Cscore group; blue, low m⁵Cscore group. (k) Patients with N2 disease; (l) patients with stage II disease.