Figure S4. Associations of mutation sites of CHEK2:p.K373E or CHEK2:p.R406H and patients' prognosis. A and B, Longitudinal representation of CHEK2:p.K373E (A) and CHEK2:p.R406H (B) from all patients with a timepoint available. C and D, Survival analyses of combined somatic mutations of pre-CHEK2:p.K373E+pre-CHEK2:p.R406H (C, P = 0.8076) and post-CHEK2:p.K373E+post-CHEK2:p.R406H (D, P = 0.0048) in patients. E, Survival analysis of combined with CHEK2:p.K373E, CHEK2:p.R406H and MRE11A:p.K464R in post-treatment patients, P = 0.0011.