Supplementary

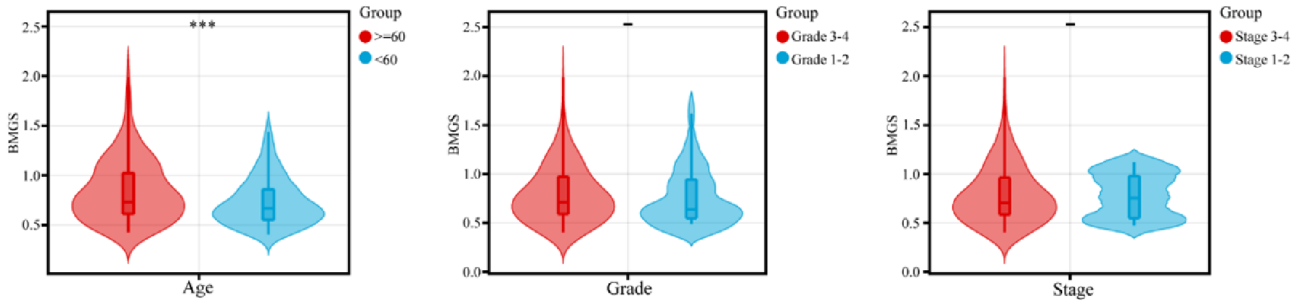

Figure S1 Box plot comparing BMGS risk scores across different clinical characteristics. BMGS, basement membrane gene signature. ***, P<0.001; -, not significant.

https://dx.doi.org/10.21037/tcr-2026-1-0227

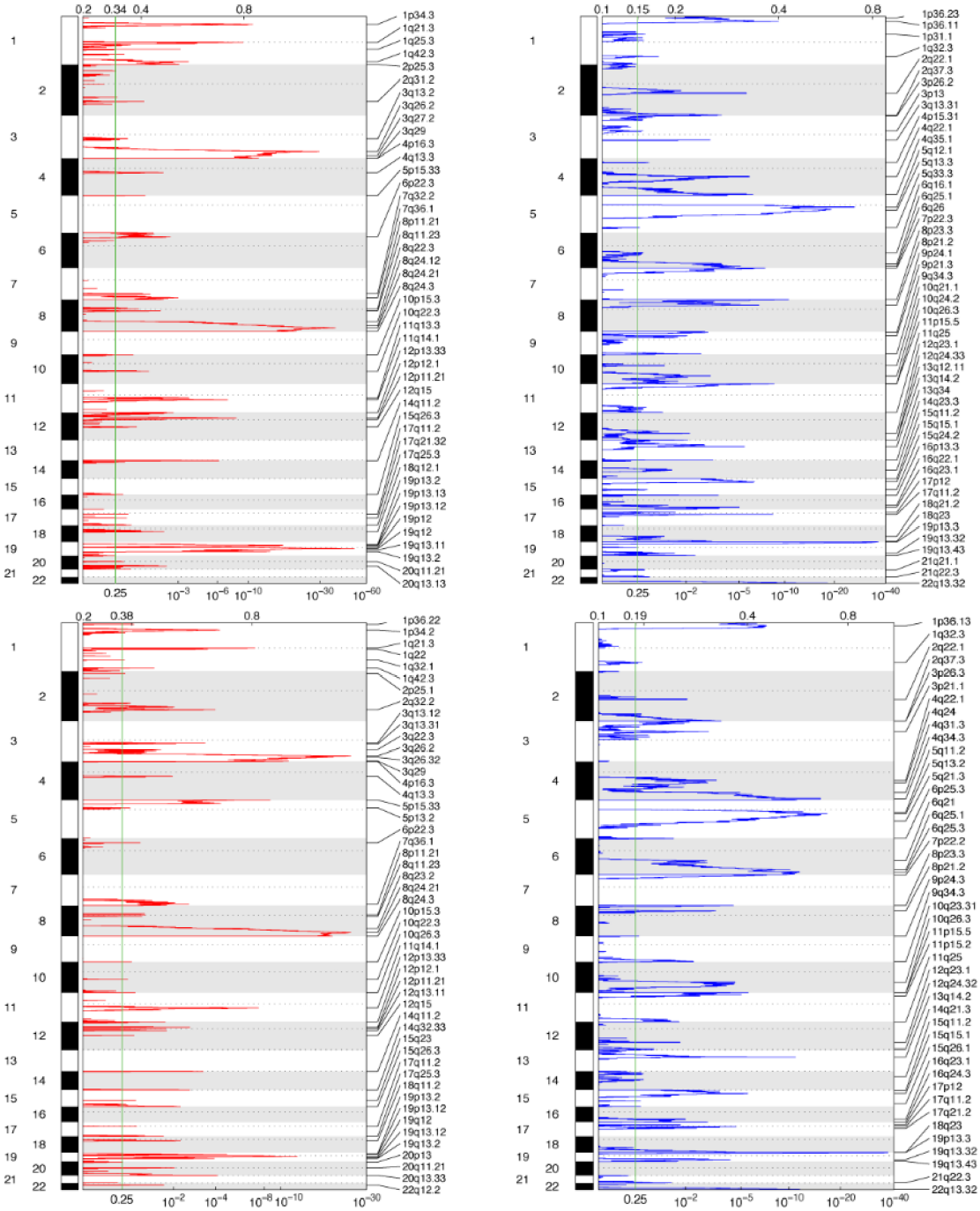

Figure S2 Copy number analysis of the high- and low-risk groups in TCGA-OV (top: high-risk group; bottom: low-risk group; red amplification; blue: loss). OV, ovarian cancer; TCGA, The Cancer Genome Atlas.

https://dx.doi.org/10.21037/tcr-2026-1-0227

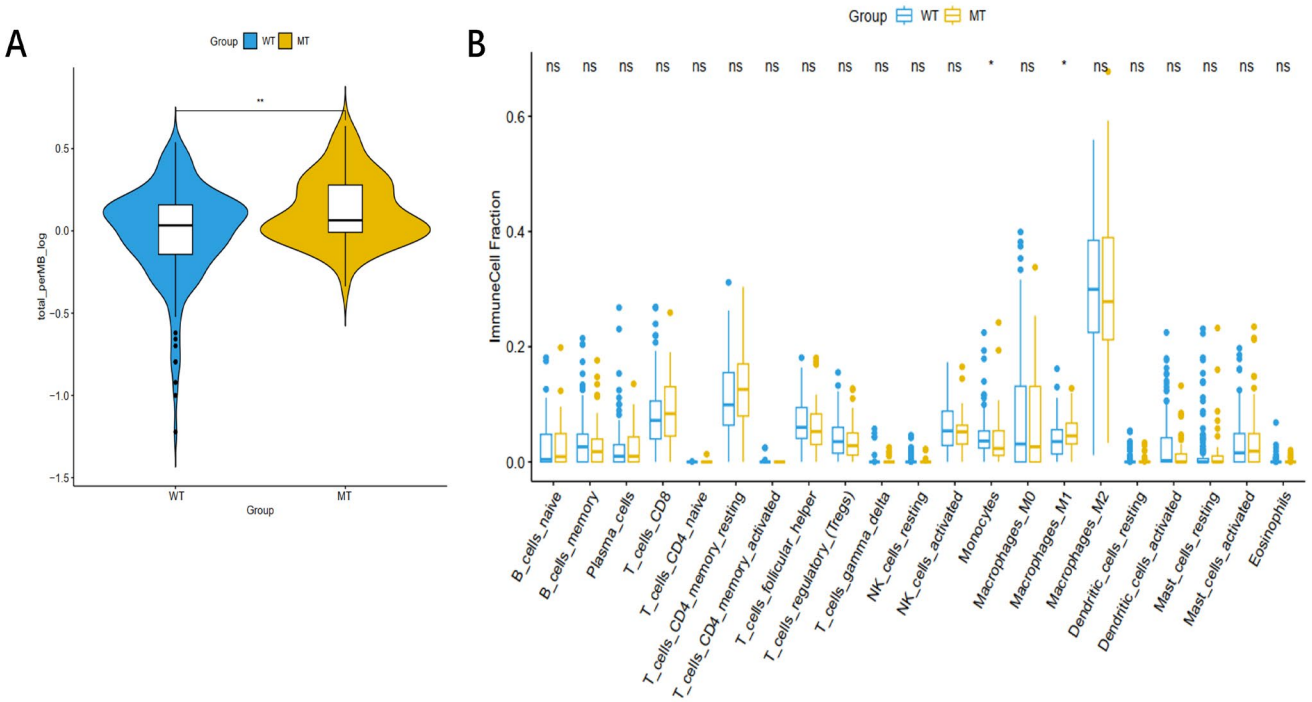

Figure S3 The correlation between *TTN* mutations and TMB, immune infiltration. (A) The comparison of TMB values between *TTN* versus wild-type in the TCGA-OV cohort. (B) Immune cell infiltration between *TTN*-mutant and *TTN*-wild-type ovarian cancer samples. *, 0.01≤P≤0.05; ns, not significant. MT, mutant type; OV, ovarian cancer; TCGA, The Cancer Genome Atlas; TMB, tumor mutation burden; WT, wild-type.

https://dx.doi.org/10.21037/tcr-2026-1-0227

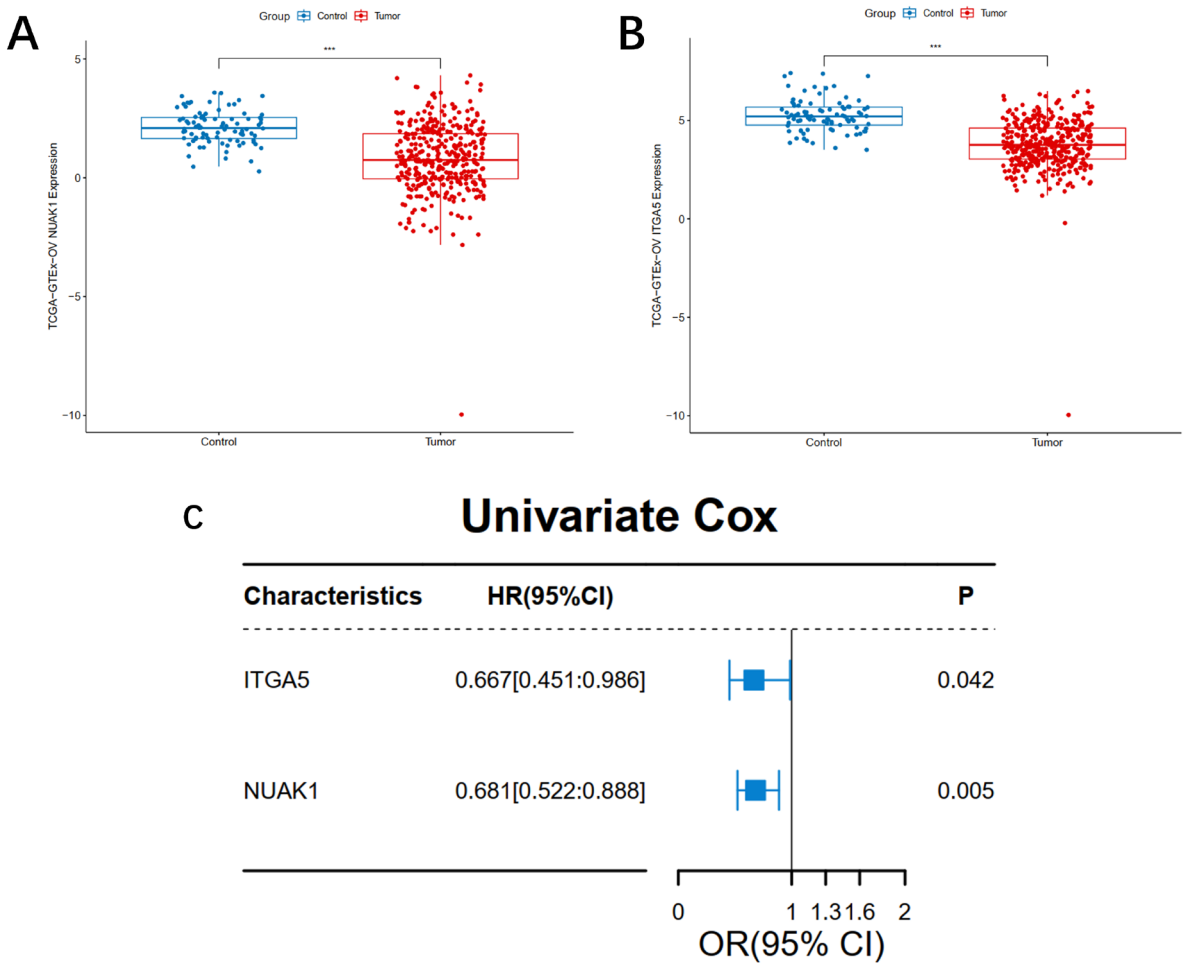

Figure S4 The verification of the expression of *ITGA5* and *NUAK1* in ovarian cancer tissues and their independent association with prognosis. (A,B) The box plots showing differential expression levels of *NUAK1* (A) and *ITGA5* (B) between ovarian cancer tissues and normal ovarian tissues using the combined data from the TCGA-OV and GTEx databases. (C) Univariate Cox regression analyses for *ITGA5* and *NUAK1* as independent prognostic factors for patients with ovarian cancer. ***, P<0.001. CI, confidence interval; GTEx, Genotype-Tissue Expression; HR, hazard ratio; OR, odds ratio; OV, ovarian cancer; TCGA, The Cancer Genome Atlas.

https://dx.doi.org/10.21037/tcr-2026-1-0227