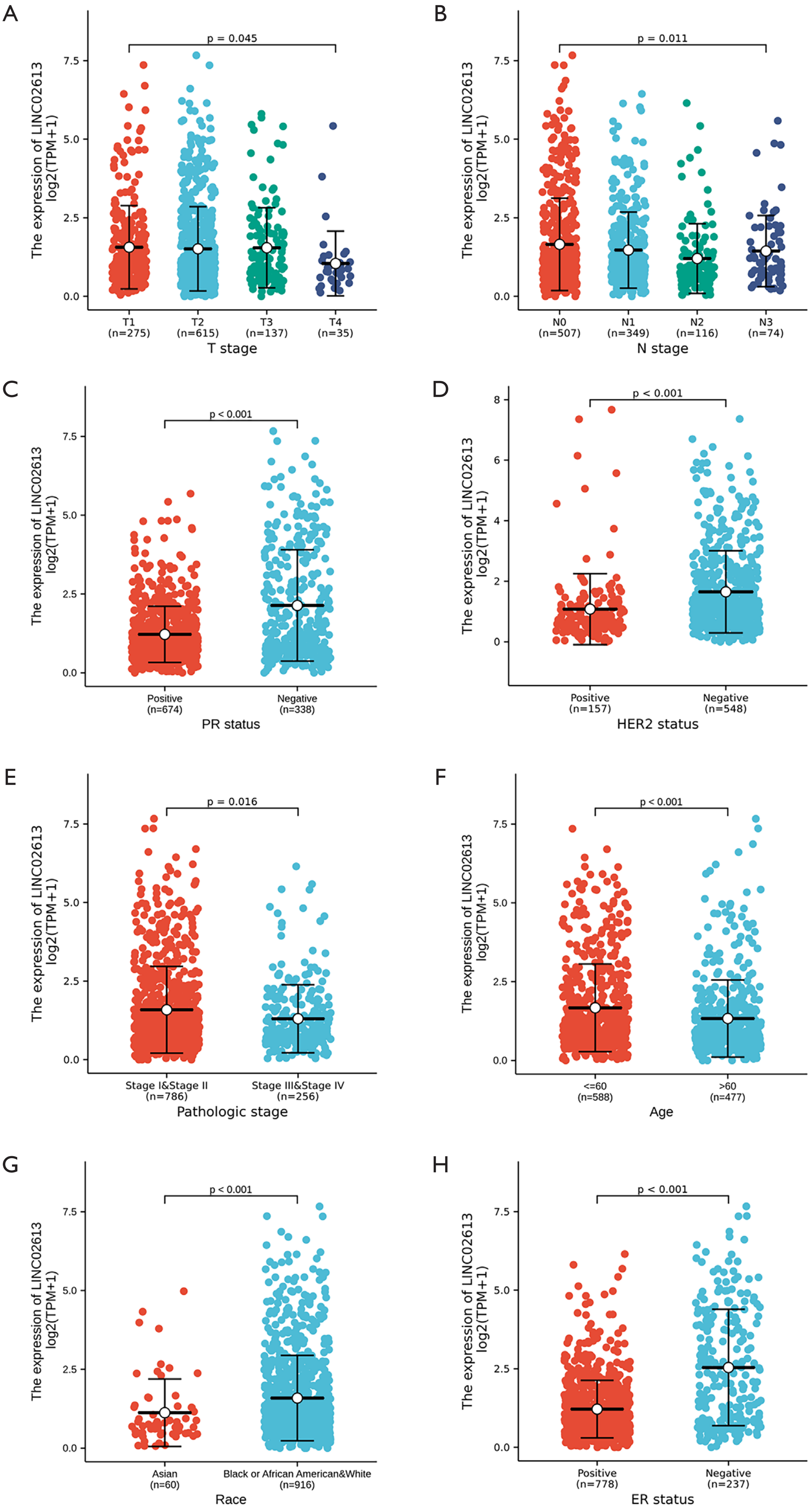

Figure S1 Relationships (A) between LINC02613 and T stage, (B) between LINC02613 and N stage, (C) between LINC02613 and PR status, (D) between LINC02613 and HER2 status, (E) between LINC02613 and pathological stage, (F) between LINC02613 and age, (G) between LINC02613 and race, (H) between LINC02613 and ER status.

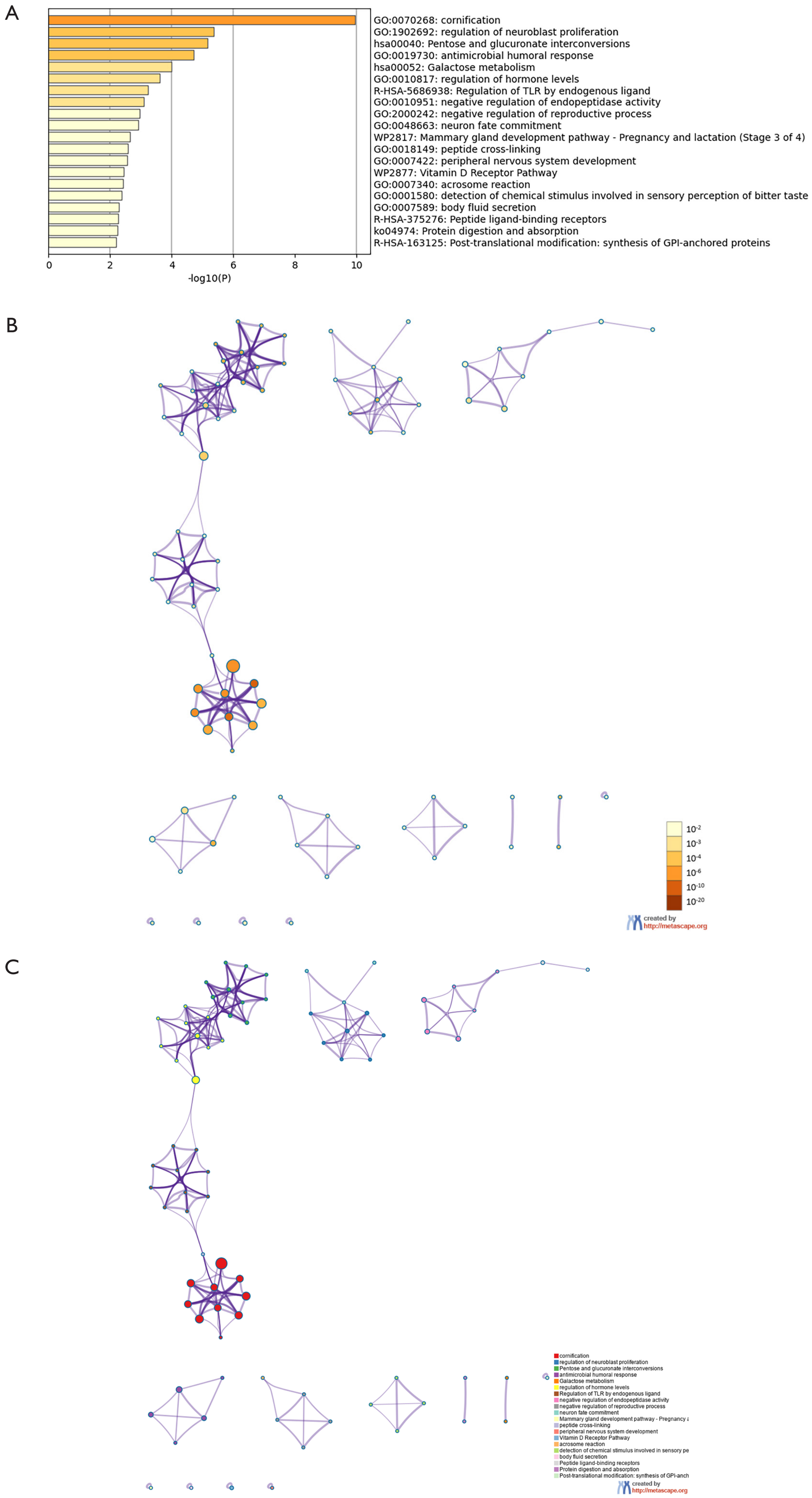

Figure S2 (A) GO analysis revealed that genes regulated by LINC02613 were mainly enriched in biological processes related to tissue development and energy metabolism, including cornification, regulation of neuroblast proliferation, pentose and glucuronate interconversions and galactose metabolism. (B) The network of interactions between LINC02613 and biological processes. (C) The network of interactions between LINC02613 and biological processes.

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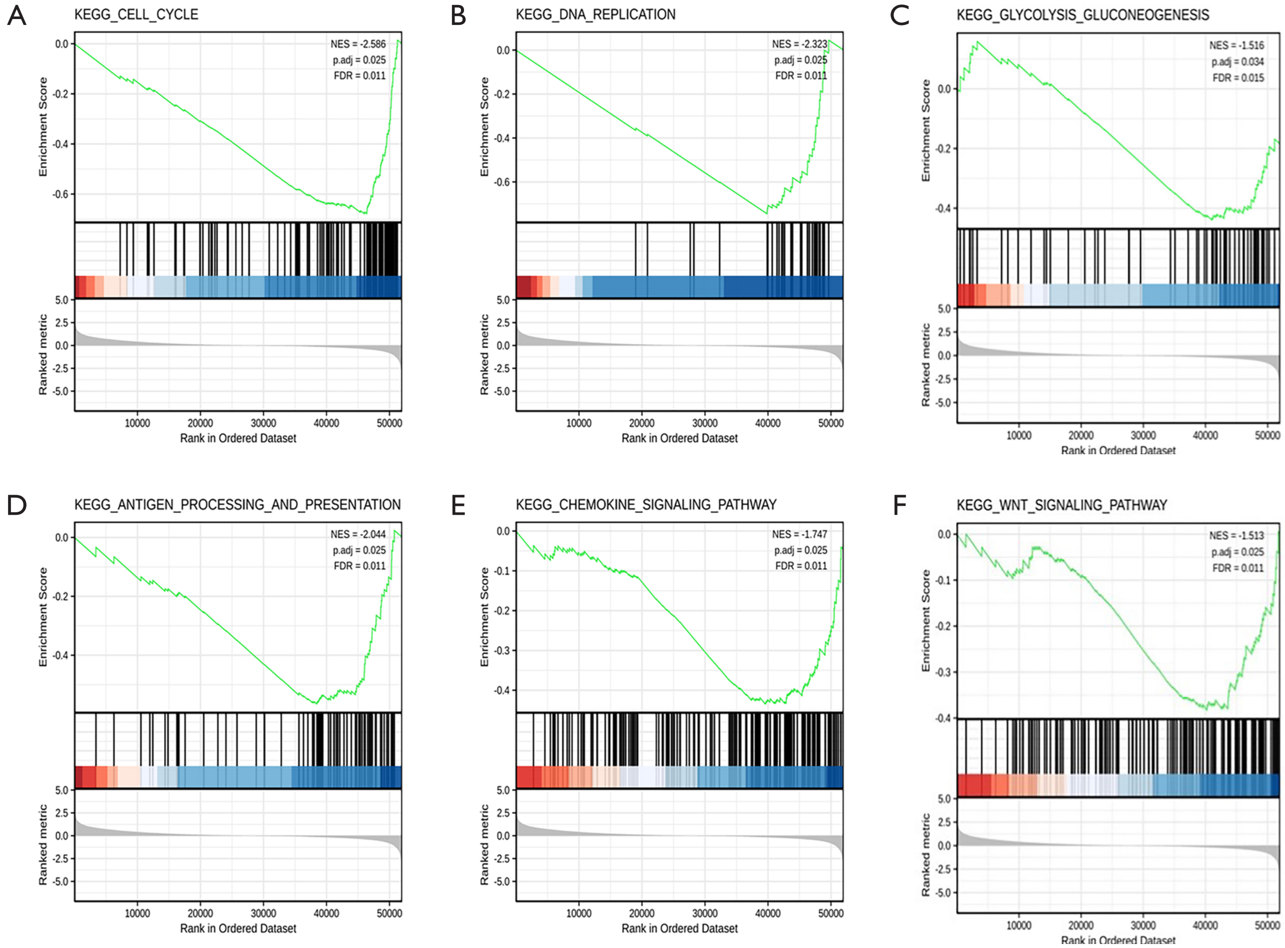

Figure S3 (A) GSEA showed that the cell cycle dataset was significantly enriched in the LINC02613 low expression group. (B) GSEA showed that the DNA replication dataset was significantly enriched in the LINC02613 low expression group. (C) GSEA showed that the glycolysis gluconeogenesis dataset was significantly enriched in the LINC02613 low expression group. (D) GSEA showed that the antigen processing and presentation dataset was significantly enriched in the LINC02613 low expression group. (E) GSEA showed that the chemokine signaling pathway dataset was significantly enriched in the LINC02613 low expression group. (F) GSEA showed that the WNT signaling pathway dataset was significantly enriched in the LINC02613 low expression group.

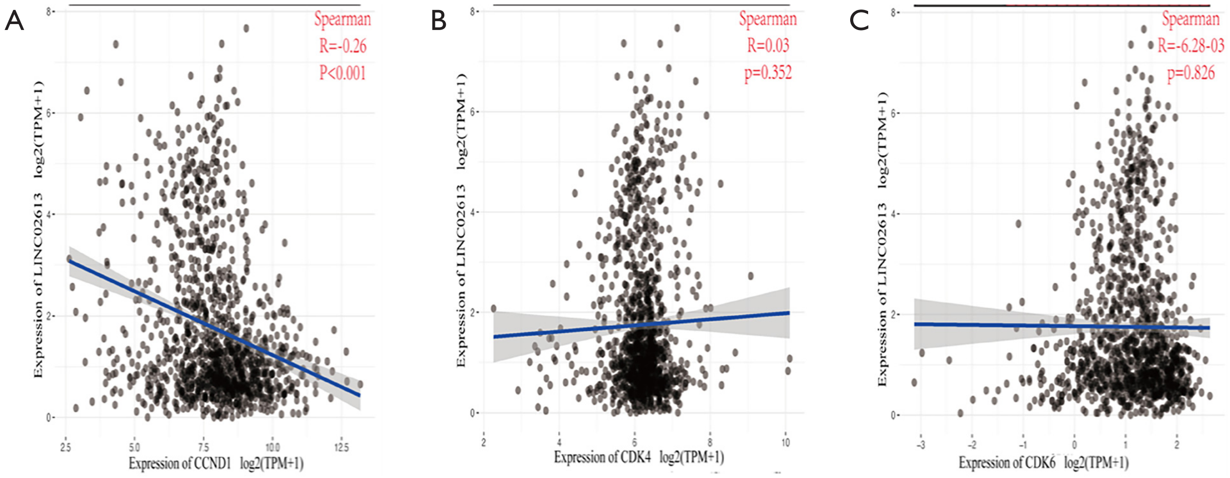

Figure S4 (A) The expression of CCND1 was negatively related to LINC02613. (B) The expression of CDK4 was unrelated to LINC02613. (C) The expression of CDK6 was unrelated to LINC02613.

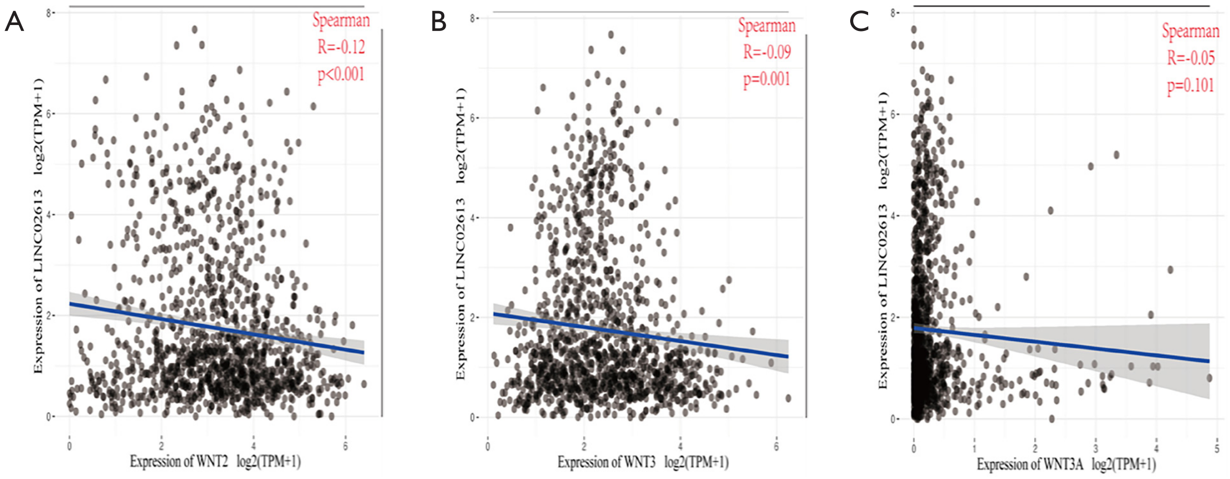

Figure S5 (A) The expression of Wnt2 was negatively related to LINC02613. (B) The expression of Wnt3 was negatively related to LINC02613. (C) The expression of Wnt3A was unrelated to LINC02613.