**Supplementary figure legend**

Supplementary figure 1. The forest plot of the comparison on virus prevalence between gastric cancer and any controls before excluding subjects with known Hp and EBV positive (A) The forest plot for HBV; (B) The forest plot for HCMV: Jin[1-5]: different sequences of HCMV genome were detected, Zhang[1-2]:IgG or IgM was detected; (C)The forest plot for HPV: Kamangar[1-3]:different subtypes of HPV were investigated, Ma[1-2]:different test methods were used; (D)The forest plot for HTLV-1; (E)The forest plot for JCV: Jang[1-2]: different test methods were used, Murai[1-3]: different sequences of JCVgenome were detected by southern blot, Murai[4]: T-Ag were detected by immunohistochemistry, Shin[1-3]: different sequences of JCV genome were detected.

Supplementary figure 2. Begg’s funnel plot, Egger’s regression plot, L’Abbé plot, and Galbraith plot of the all-included meta-analysis refer to HBV

Supplementary figure 3. Begg’s funnel plot, Egger’s regression plot, L’Abbé plot, and Galbraith plot of the all-included meta-analysis refer to HCMV

Supplementary figure 4. Begg’s funnel plot, Egger’s regression plot, L’Abbé plot, and Galbraith plot of the all-included meta-analysis refer to HPV

Supplementary figure 5. Begg’s funnel plot, Egger’s regression plot, L’Abbé plot, and Galbraith plot of the all-included meta-analysis refer JCV