

Figure S1 The frequency of CDK12 genetic alterations across multiple tumor types based on TCGA datasets.

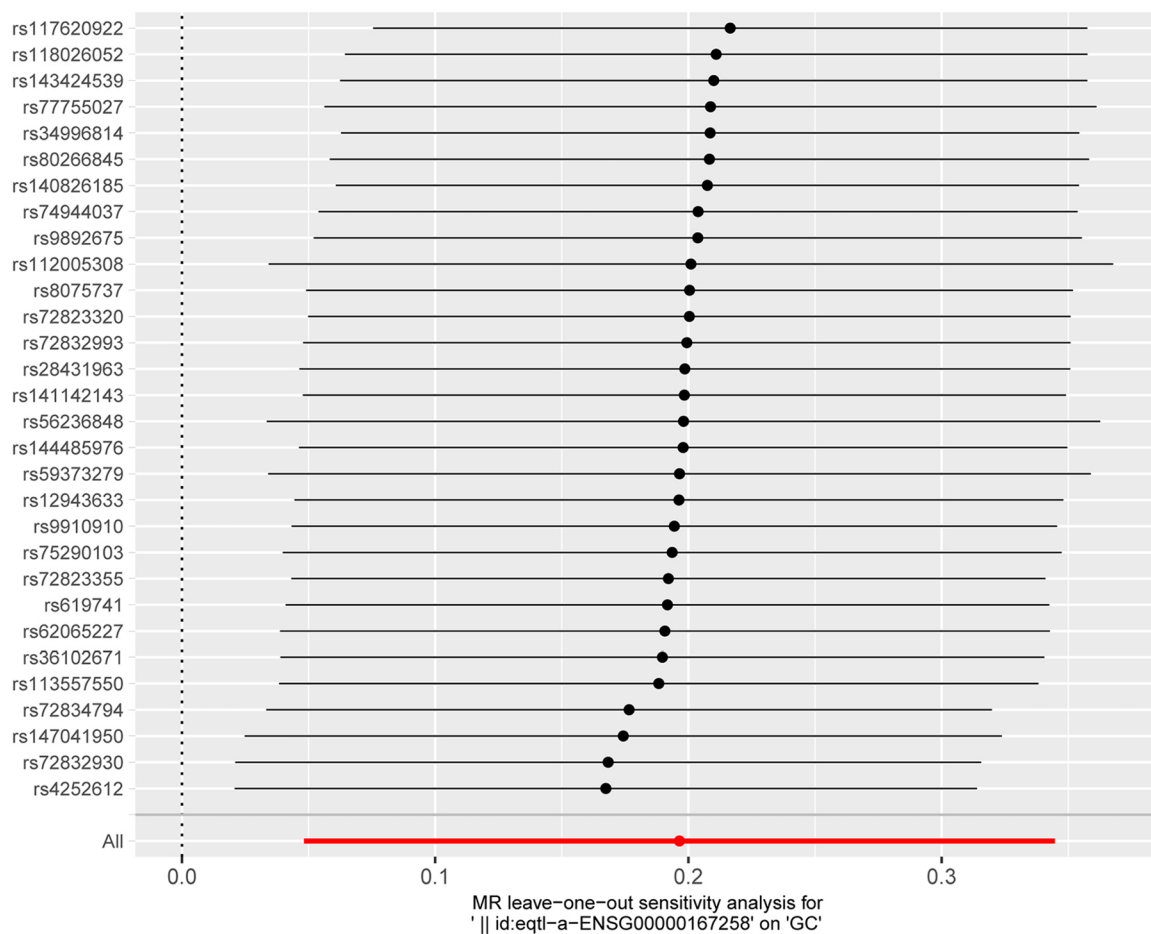


Figure S2 Leave-one-out sensitivity analysis for CDK12 expression and gastric cancer.

Table S1 CDK12 pleiotropy analysis on GC

ID.exposure	ID.outcome	Outcome	Exposure	Egger_intercept	SE	Pval
eqtl-a-ENSG00000167258	finn-b-C3_STOMACH	GC	id: eqtl-a-ENSG00000167258	-0.039248133	0.045660894	0.397333156

Table S2 CDK12 heterogeneity analysis on GC

ID.exposure	ID.outcome	Outcome	Exposure	Method	Q	Q_df	Q_pval
eqtl-a-ENSG00000167258	finn-b-C3_STOMACH	GC	id: eqtl-a-ENSG00000167258	MR Egger	34.58914	28	0.182145
eqtl-a-ENSG00000167258	finn-b-C3_STOMACH	GC	id: eqtl-a-ENSG00000167258	Inverse variance weighted	35.50185	29	0.188532