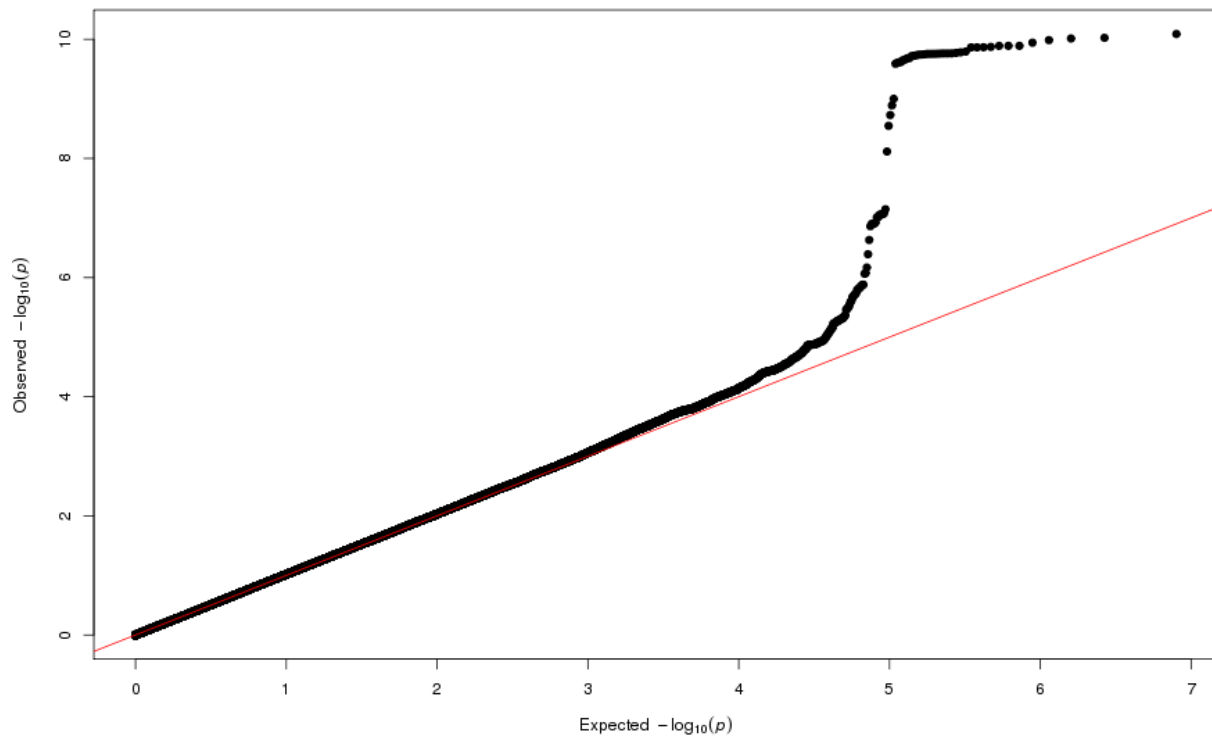


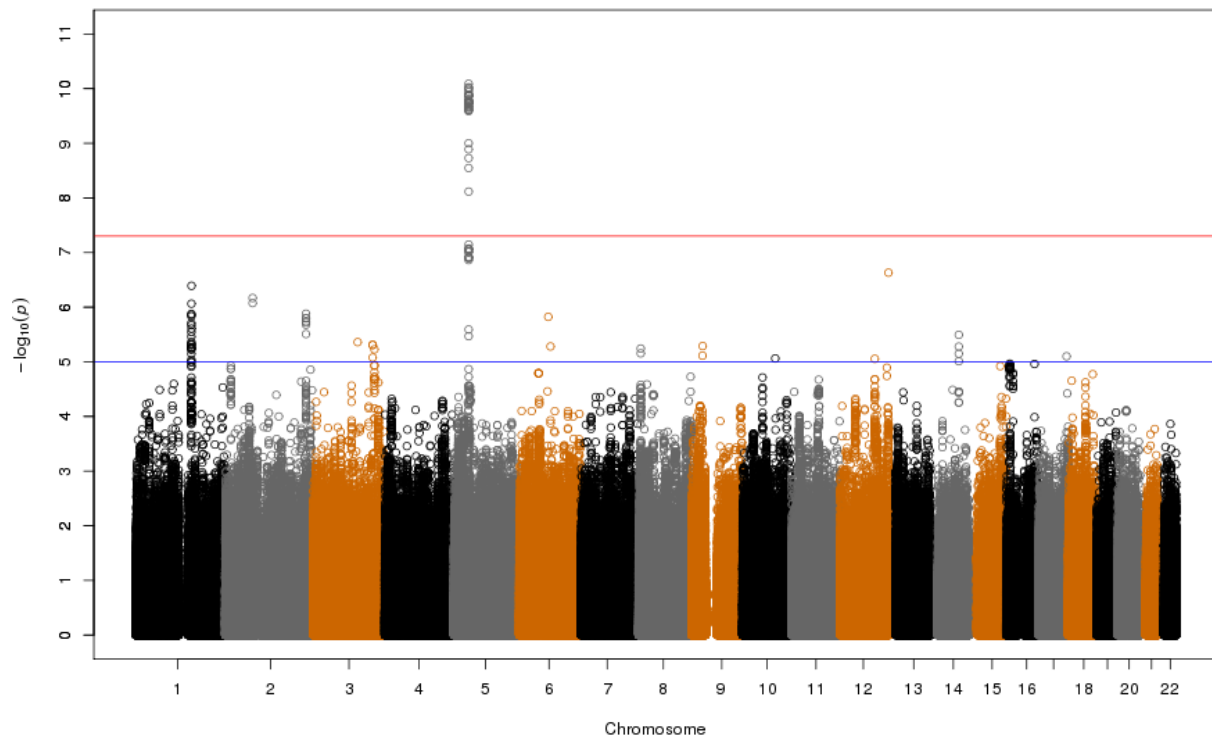
SUPPLEMENTAL MATERIALS

Identification of new susceptibility loci for gastric noncardia adenocarcinoma: Pooled results from two Chinese genome-wide association studies

Zhaoming Wang, Juncheng Dai, Nan Hu, Xiaoping Miao, Christian C. Abnet, Ming Yang, Neal D. Freedman, Jinfei Chen, Laurie Burdette, Xun Zhu, Charles C. Chung, Chuanli Ren, Sanford M Dawsey, Meilin Wang, Ti Ding, Jiangbo Du, Yu-Tang Gao, Rong Zhong , Carol Giffen, Wenting Pan, Woon-Puay Koh, Ningbing Dai, Linda M Liao, Caiwang Yan, You-Lin Qiao, Yue Jiang, Xiao-Ou Shu, Jiaping Chen, Chaoyu Wang, Hongxia Ma, Hua Su, Zhendong Zhang, Lemin Wang, Chen Wu, Yong-Bing Xiang , Zhibin Hu, Jian-Min Yuan, Lu Xie, Wei Zheng, Dongxin Lin, Stephen J. Chanock, Yongyong Shi, Alisa M. Goldstein, Guangfu Jin, Philip R. Taylor, Hongbing Shen



Supp. Figure 1 QQ Plot of the meta analysis p values for 3,996,998 SNPs after filtering out those with $P_{\text{het}} < 1.0 \times 10^{-4}$ or $I^2 > 75\%$. The genomic control lambda value is 1.02.



Supp Figure 2 Manhattan plot of the meta-analysis p values (stage1)