FAS rs2234767 and rs1800682 polymorphisms jointly contributed to risk of colorectal cancer by affecting SP1/STAT1 complex recruitment to chromatin Shizhi Wang, Shenshen Wu, Qingtao Meng, Xiaobo Li, Rui Chen, Meilin Wang

Figure legends.

Fig. S1. *FAS* rs2234767A and rs1800682G alleles affect coupled SP1 and STAT1 recruitment to chromatin. (A) Chromatin immunoprecipitation (ChIP) of the *FAS* promoter with three different genotypes (rs2234767GG/rs1800682AA, rs2234767GA/rs1800682AG and rs2234767AA/rs1800682GG) using antibody for SP1 and STAT1(single pool generated from triplicate biological samples/manipulation; triplicate measurements/pool; mean \pm SE). (B) Sequential ChIP of the *FAS* promoter containing SP1 motif immunoprecipitated first using antibody for SP1 followed by antibody for STAT1 (upper) or first using antibody for STAT1 followed by antibody for SP1 (lower). (C) Sequential ChIP of the *FAS* promoter containing STAT1 motif immunoprecipitated first using antibody for STAT1 (upper) or first using antibody for SP1 followed by antibody for STAT1 (upper) or first using antibody for SP1 followed by antibody for STAT1 antif immunoprecipitated first using antibody for SP1 (lower). For all combined genotypes in the figure, left genotype arises from the rs2234767 and right from the rs1800682 polymorphism.

