

Figure S4. The correlation between GABPA and TGFBR2 mRNA expression in ccRCC tumors from GSE73731 and E-MTAB-1980 cohorts. GSE73731 cohort contains 265 ccRCC tumors analyzed using theAffymetrix Microarrays (A), while RNA sequencing was performed on 101 ccRCC tumors in E-MTAB-1980(B). For RNA seq, mRNA levels were expressed as Log2(RSEM) (RNA-Seq by Expectation-Maximization).mRNA levels assessed using Affymetrix were expressed as log2(probevalue).