**Supplementary figure legends**

**Supplementary Figure 1.** A, Chemokine array using the SW837 cells engineered with stable *SMAD4*-knockdown (SW837-sh*SMAD4* #2) and scramble control. Comparison of a panel of chemokines was shown.B,qRT-PCR analysis using SW837 cells with or without 10ng/mL TGF-1 for 6 h. NT indicate nontreatment as control. \**P* < 0.05 by Student’s *t*-test. C, Luciferase reporter assay showing activities of SBE4-Luc, *CXCL1*-Luc and *CXCL8*-Luc. \**P* < 0.05 by Student’s *t*-test. D, Schematic representation of the *CXCL1* or *CXCL*8 gene. The sequence of this region was obtained by sequencing genomic DNA of SW837, and matches with that of database obtained from UCSC genome browser. Transcription start site (black arrow) was confirmed by 5’ rapid amplification of cDNA end. E,ChIP-PCR analysis for enrichment of SBE or TIE in the promotor region of CXCL1 or CXCL8.

**Supplementary Figure 2.** A, Screening with a series of kinase inhibitors treated for 24 hours. qRT-PCR analysis for *CXCL1* (top) and *CXCL8* (bottom). B, Chemotactic responses of neutrophils toward the human recombinant CXCL1 and CXCL8. Mean; *bars*, ± SD. \**P* < 0.05 by Student’s *t*-test. C, Neutrophils were isolated from peripheral blood and from CRC specimens of the same patients (n = 6) by FACS with CD45, CD66b, CD14, CD15, and CD16.