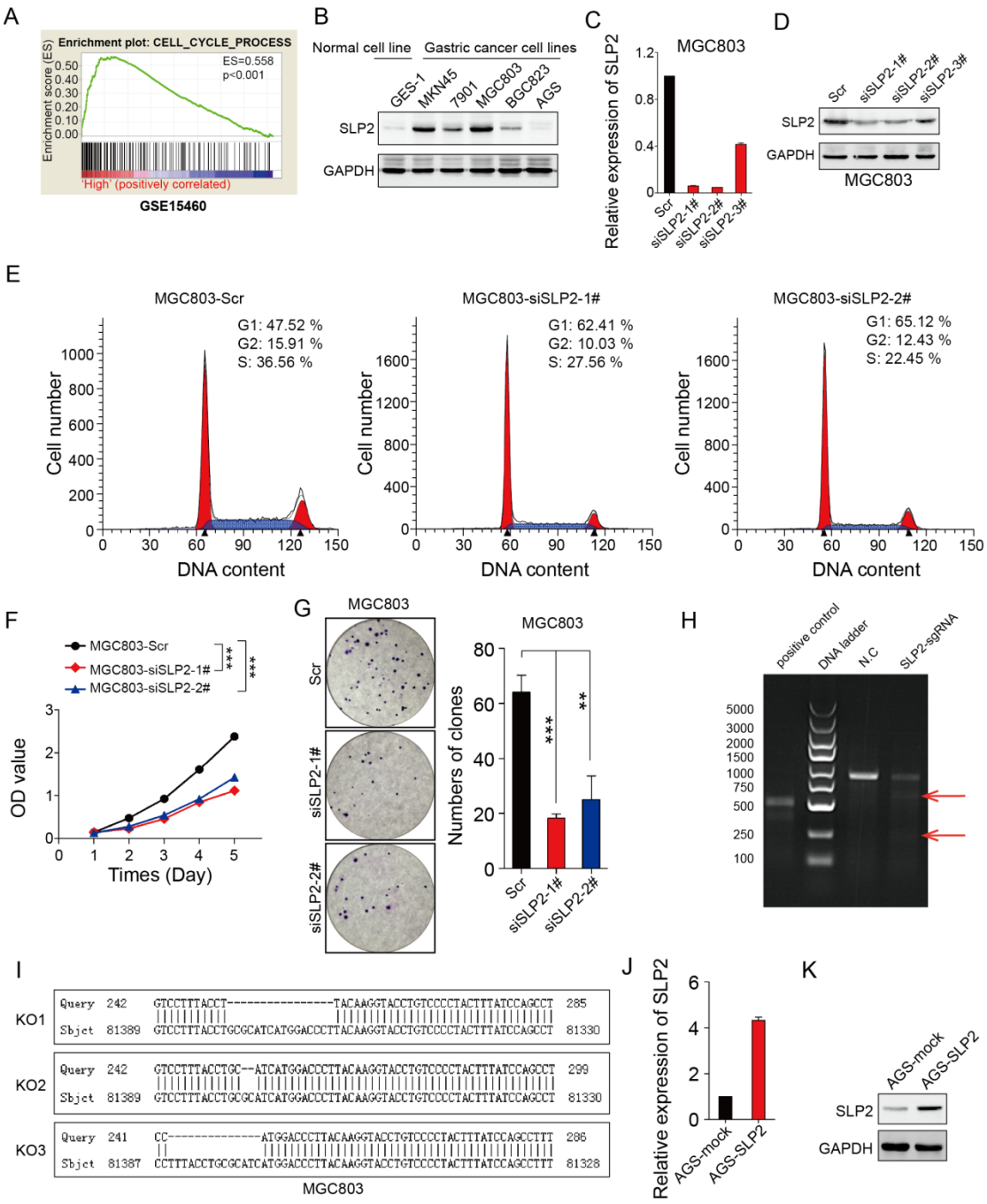
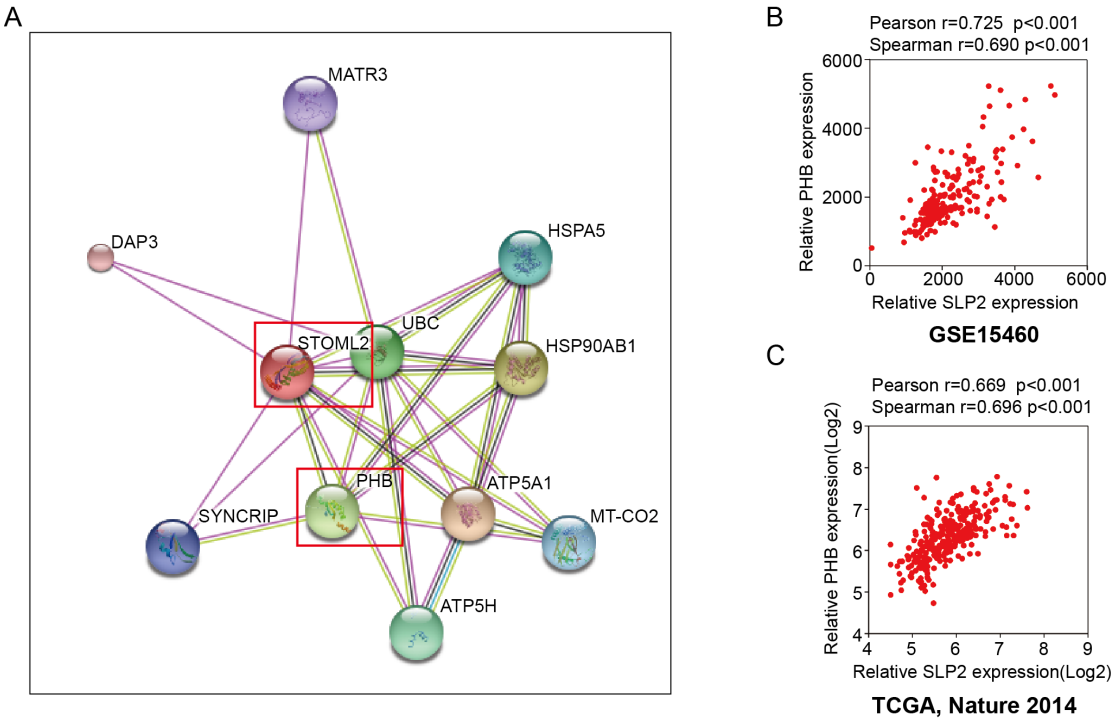
Supplementary table 1, primers for RT-Q-PCR and ChIP to detect indicated genes

SLP2-qPCR-F:	GGAAACGGGCCACAGTTCTA
SLP2-qPCR-R:	TCAGCTTTAGCCTTGGCCTT
PHB-qPCR-F:	TCTCGACCACGTAATGTGCC
PHB-qPCR-R:	TCTCAGTTGTGATGGACGGC
GAPDH-qPCR-F	ACAACTTTGGTATCGTGGAAGG
GAPDH-qPCR-R	GCCATCACGCCACAGTTTC
ChIP-SLP2-P1-F	GAGAGGGTGTGAAGGGGGA
ChIP-SLP2-P1-R	AAGGAGAAAAACCAGGCCCC
ChIP-SLP2-P2-F	CTACCAGAGAGGCAACAGGC
ChIP-SLP2-P2-R	CTTTACCCACCAACCCCTCC
ChIP-SLP2-P3-F	TCAGCCGTAGAAGCTGAACTC
ChIP-SLP2-P3-R	TGGTAGTCAAGAGACCTCCGT
ChIP-SLP2-P4-F	CGTTCGACCAAGTAACGCTGA
ChIP-SLP2-P4-R	CTCCCAGAAGCCTACCCGAG
ChIP-c-FOS -P-F	GAGCAGTTCCCGTCAATCC
ChIP-c-FOS -P-R	GCATTTCGCAGTTCCTGTCT
PCR-SLP2-KO-F	CTGAGGACCCATGACTCCTCTTTC
PCR-SLP2-KO-R	GGAAGTCTGGATCCTCCTGGTACT



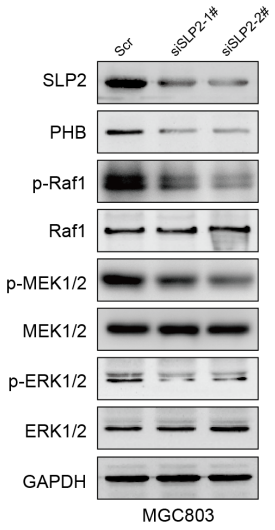
Supplementary Figure 1. A, biological progression was compared in SLP2 high-expressed tissues and lower ones by gene set enrichment analysis. **B**, immunoblot analysis of baseline expression of SLP2 in normal gastric cells and GC cells. **C** and **D**, immunoblot and RT-Q-PCR analysis of efficiencies of 3 small interference RNA targeting SLP2 in MGC803 cell. Data presented as means ± SEM from three independent experiments. **E**, indicated cells were stained with propidium iodide followed by DNA content analysis. **F**, proliferation rates of Scr or siRNAs targeting SLP2 transfected MGC803 cells measured by CCK8. 5000 indicated cells

were plated in 96 well culture-plates. Data presented as means ± SEM from five independent experiments. ***p<0.001, two-way ANOVA test. **G**, colony formation of Scr or siRNAs targeting SLP2 transfected MGC803 cells. 200 indicated cells were plated in 6 well culture-plates. Data presented as means ± SEM from three independent experiments. **p<0.01, ***p<0.001, one-way ANOVA test. **H**, sgRNA targeting SLP2 or control sgRNA without target was transfected and DNA was extracted. PCR products were incubated with Cruiser™ Detecase and then subjected to southern blot. **I**, sgRNA transfected cell was cloned by limiting dilutions and clones were randomly picked. By PCR and DNA sequencing, 3 clones with frame shift mutation were selected for further studies. **J** and **K**, immunoblot and RT-Q-PCR analysis of efficiencies of SLP2 overexpression in AGS cells. Data presented as means ± SEM from three independent experiments.



Supplementary Figure 2. A, analysis of potential proteins interacted with SLP2 based on String database. **B** and **C**, analysis of correlation between SLP2 and PHB mRNA levels in GEO and TCGA database.

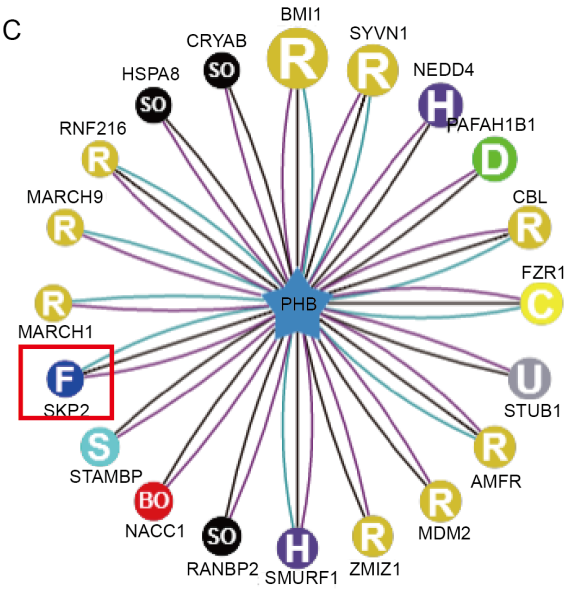
A



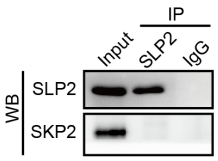
B

Pos	AA	Mod	Spectral Count
11	K	ace	5
83	K	ubi	5
114	Y	phos	2
128	K	ubi	6
186	K	ubi	7
186	K	ace	6
202	K	ubi	2
202	K	ace	2
219	K	ubi	1
240	K	ubi	2
240	K	ace	7
249	Y	phos	14
252	S	phos	1
254	S	phos	1
259	Y	phos	1

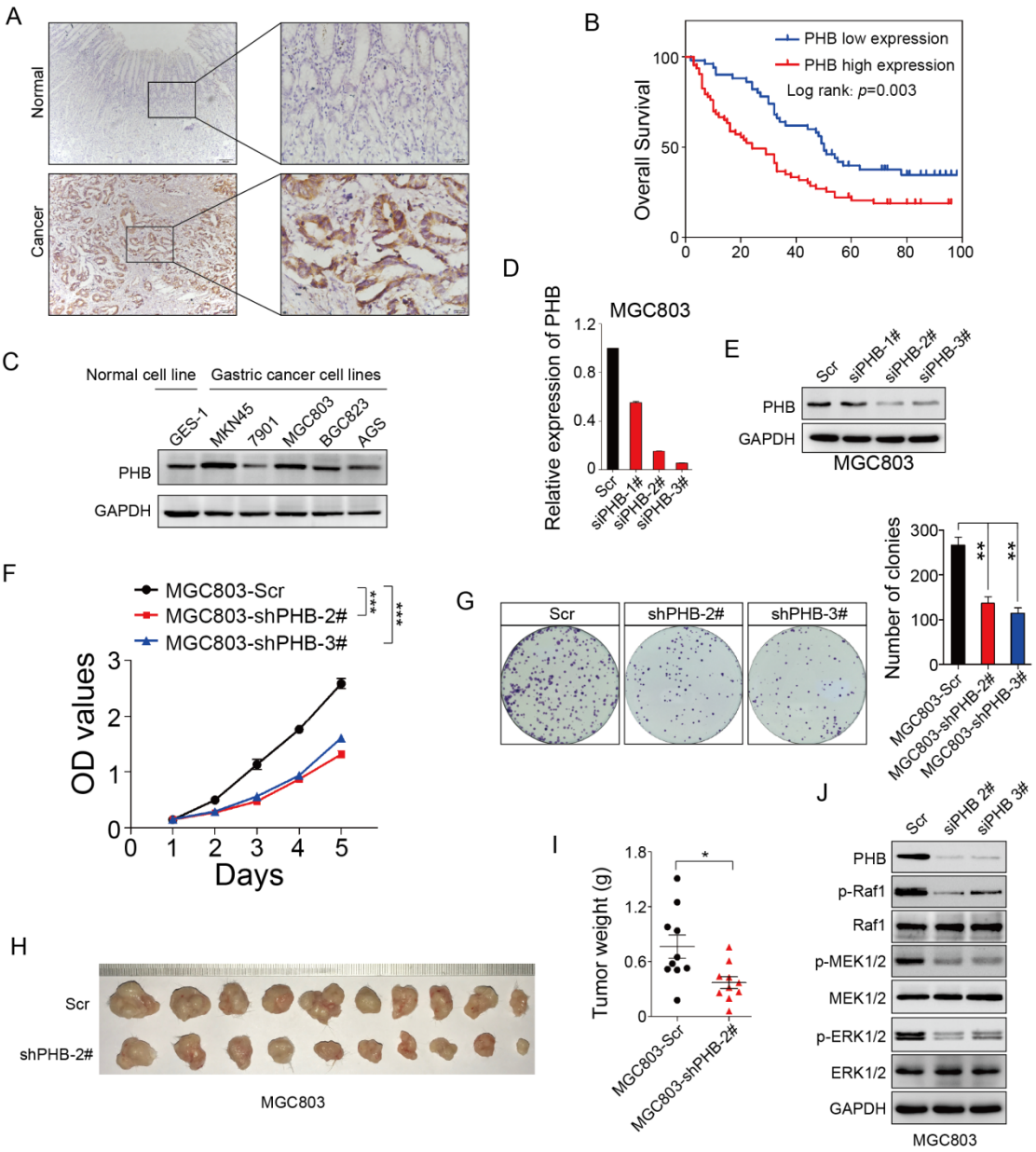
C



D

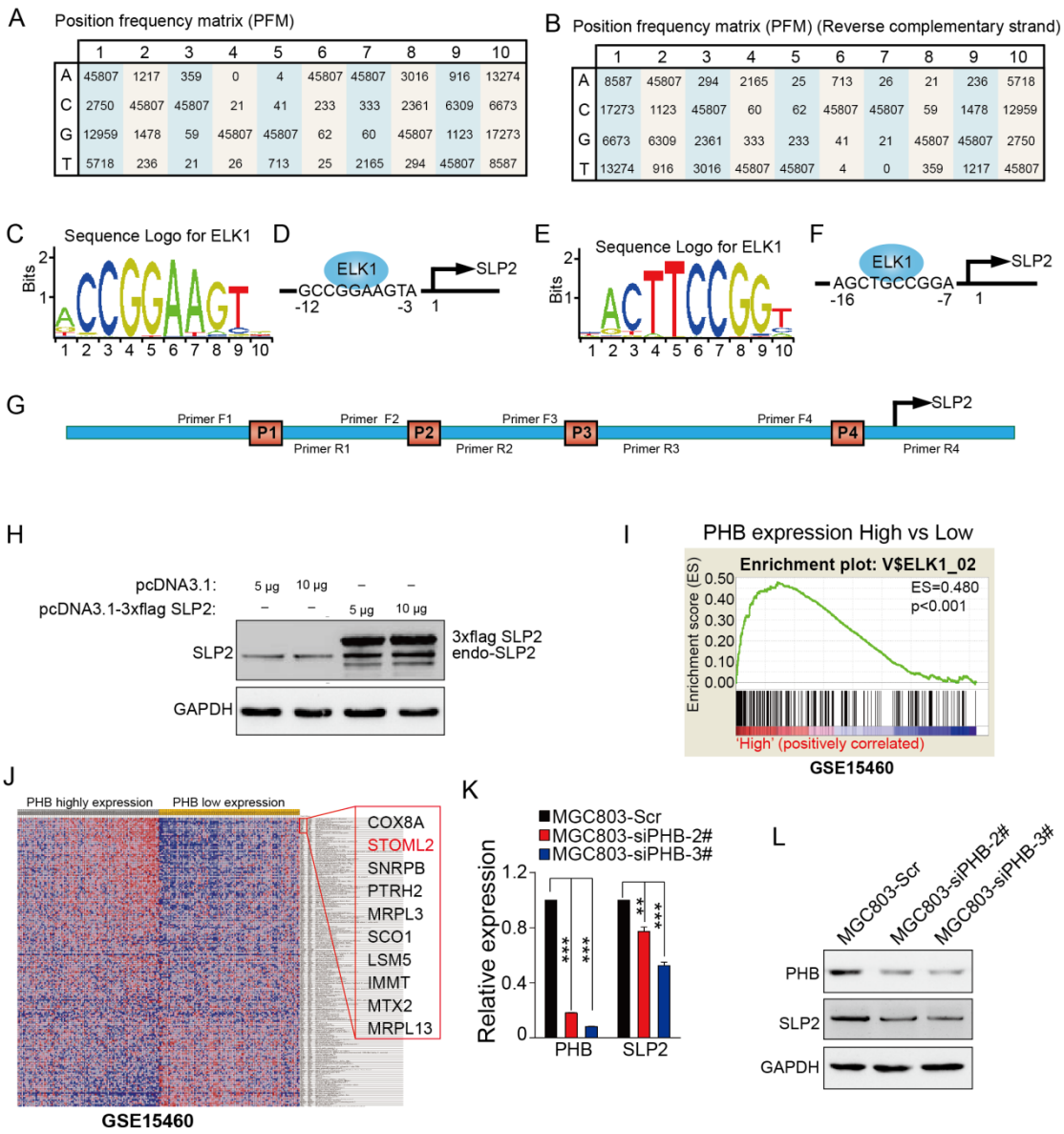


Supplementary Figure 3. A, immunoblot ananlysis of indicated protein in SLP2 knocked-down cells. **B**, analysis of potential posttranscriptional modification sites of PHB in PTMfunc database. **C**, analysis of potential E3 ubiquitin ligases binding to PHB. **D**, total cell lysates from MGC803 cell were precipitated with anti-SLP2 and subjected to immunoblot with anti-SLP2 and anti-SKP2 antibody.



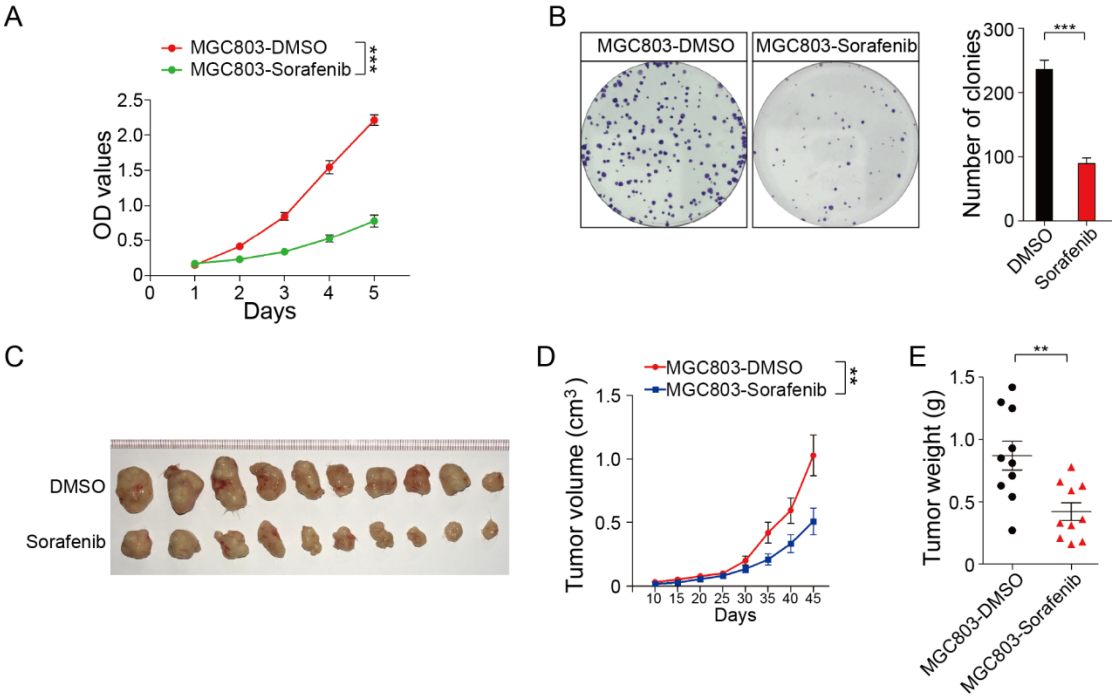
Supplementary Figure 4. A, representative images of PHB staining in GC and paired normal tissues. **B**, Kaplan-Meier tumor-free survival curves for GC patients with different PHB expression. **C**, immunoblot analysis of baseline expression of SLP2 in normal gastric cells and GC cells. and **D**, RT-Q-PCR analysis of efficiencies of 3 small interference RNA targeting PHB in MGC803 cells. Data presented as means ± SEM from three independent experiments. **E**, immunonlot analysis of efficiencies of 3 siRNAs targeting PHB in MGC803 cells. **F**, proliferation rates of Scr or siRNAs targeting PHB transfected MGC803 cells measured by CCK8. 5000 indicated cells were plated in 96 well culture-plates. Data presented as means ± SEM from five independent experiments. ***p<0.001, two-way ANOVA test. **G**, colony formation of

Scr or siRNAs targeting PHB transfected MGC803 cells. 500 indicated cells were plated in 6 well culture-plates. Data presented as means ± SEM from three independent experiments. $^{**}p<0.01$, one-way ANOVA test. **H**, tumors derived from hind limbs of NCG mice 50 days after subcutaneous injection of indicated cells. **I**, tumor weight was determined 50 days after transplantation. Data are presented as means ± SEM; n = 10 for each group. $^{*}p<0.001$, Mann-Whitney test. **J**, immunoblot analysis of indicated proteins in Scr or siRNAs targeting PHB transfected MGC803 cells.



Supplementary Figure 5. A and **B**, position frequency matrix (PFM) analysis of ELK1 binding sites. **C**, sequence logo for ELK1 binding sites in plus strand derived from Jaspar database. **D**, potential binding site of ELK1 in plus strand of SLP2 promoter predicted in Jaspar database. **E**, sequence logo for ELK1 binding sites in reverse complementary strand derived from Jaspar database. **F**, potential binding site of ELK1 in reverse complementary strand of SLP2 promoter predicted in Jaspar database. **G**, diagrammatic sketch of sites for SLP2 promoter amplification primers. **H**, an expression vector for triple flag-tagged SLP2 were transfected into AGS cells and total cell lysates were subjected to immunoblot to detect exogenous and endogenous SLP2 levels. **I** and **J**, enrichment of potential genes regulated by ELK1 in PHB highly

expressed tissues. **K**, mRNA levels of SLP2 and PHB measured by RT-Q-PCR in indicated cells. Data presented as means ± SEM from three independent experiments. $^{**}p<0.01$, $^{***}p<0.001$, one-way ANOVA test. **L**, protein expression levels of SLP2 and PHB measured by immunoblot in indicated cells.



Supplementary Figure 6. A, proliferation rates of DMSO and Sorafenib (10μM) treated MGC803 cells measured by CCK8 assay, 5000 indicated cells were plated in 96 culture-plates. Data are presented as means ± SEM from five independent experiments. The *p* values were determined using a two-way ANOVA test. ***$p<0.001$, **B**, 500 indicated cells were plated in 6 well culture-plates and the colonies were stained with giemsa for quantification. Data presented as means ± SEM from three independent experiments. ***$p<0.001$, one-way ANOVA test. **C**, tumors derived from hind limbs of NCG mice 50 days after subcutaneous injection of MGC803 cells treated with or without Sorafenib. **D**, MGC803 cells (1×10^6) were transplanted into NCG mice, and tumor growth was monitored after the indicated times. Data are presented as means ± SEM; n = 10 tumors for each group. **$p<0.001$, two-way ANOVA test. **E**, tumor weight was determined 45 days after transplantation. Data are presented as means ± SEM; n = 10 for each group. **$p<0.001$, Mann-Whitney test.