SUPPLEMENTARY FIGURES and FIGURE LEGENDS:

Supplementary Figure 1: Overexpressed AGR2 is associated with HCC metastasis in HCC cell lines. A, 2DE images of proteins expressed in the four human hepatocarcinoma syngeneic-alike cell lines. High expression AGR2 was detected in HCCLM6 with high metastasis potential. B, A typical MS/MS spectra for representative peptides of AGR2.

Supplementary Figure 2: Proteome-wide identification of binding partners to AGR2. A, Flowchart of the SF-TAP procedure. Symbol: for FLAG, for SBP, for AGR2, for binding partner to AGR2, and for non-interacting proteins. B, Western blot analysis of AGR2 immunoprecipitates from mock-transfected or SF-tagged AGR2-overexpressing HEK293T cells resolved by anti-FLAG antibody.

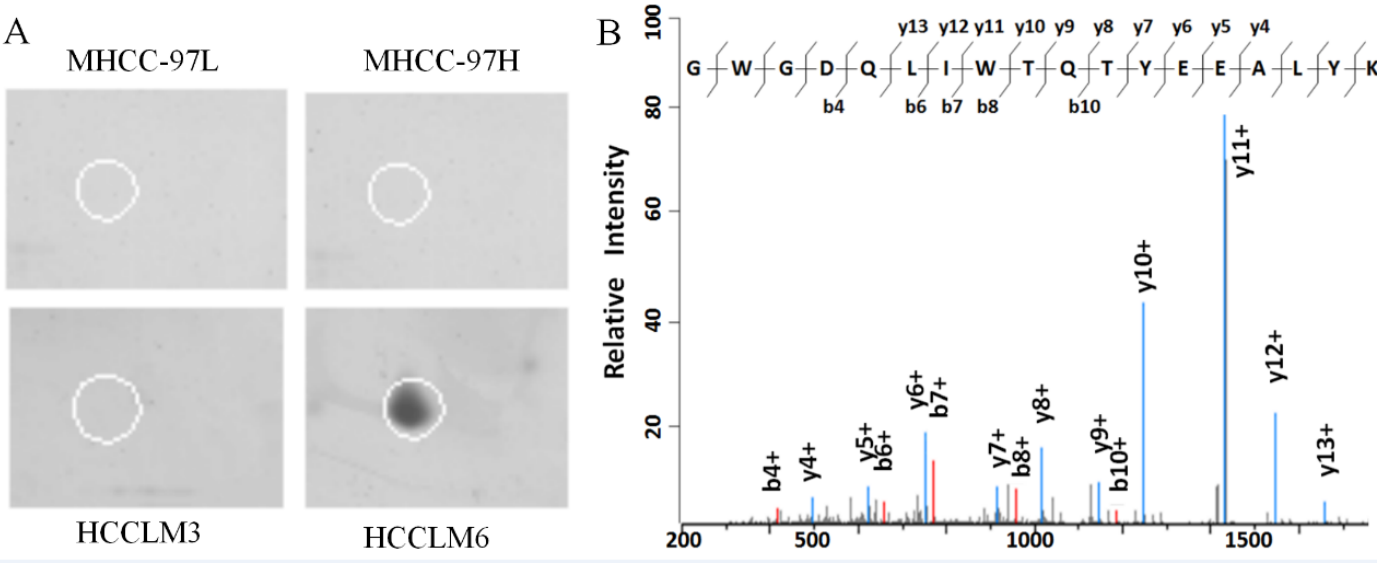
Supplementary Figure 3: Two examples of AGR2 interacting proteins identified by TAP and LC-MS/MS.

A: MS/MS Identification of TAK1. Eight tryptic peptides (red) identified by LC-MS/MS assigned to the TAK1, with total sequence coverage of 10.1%.

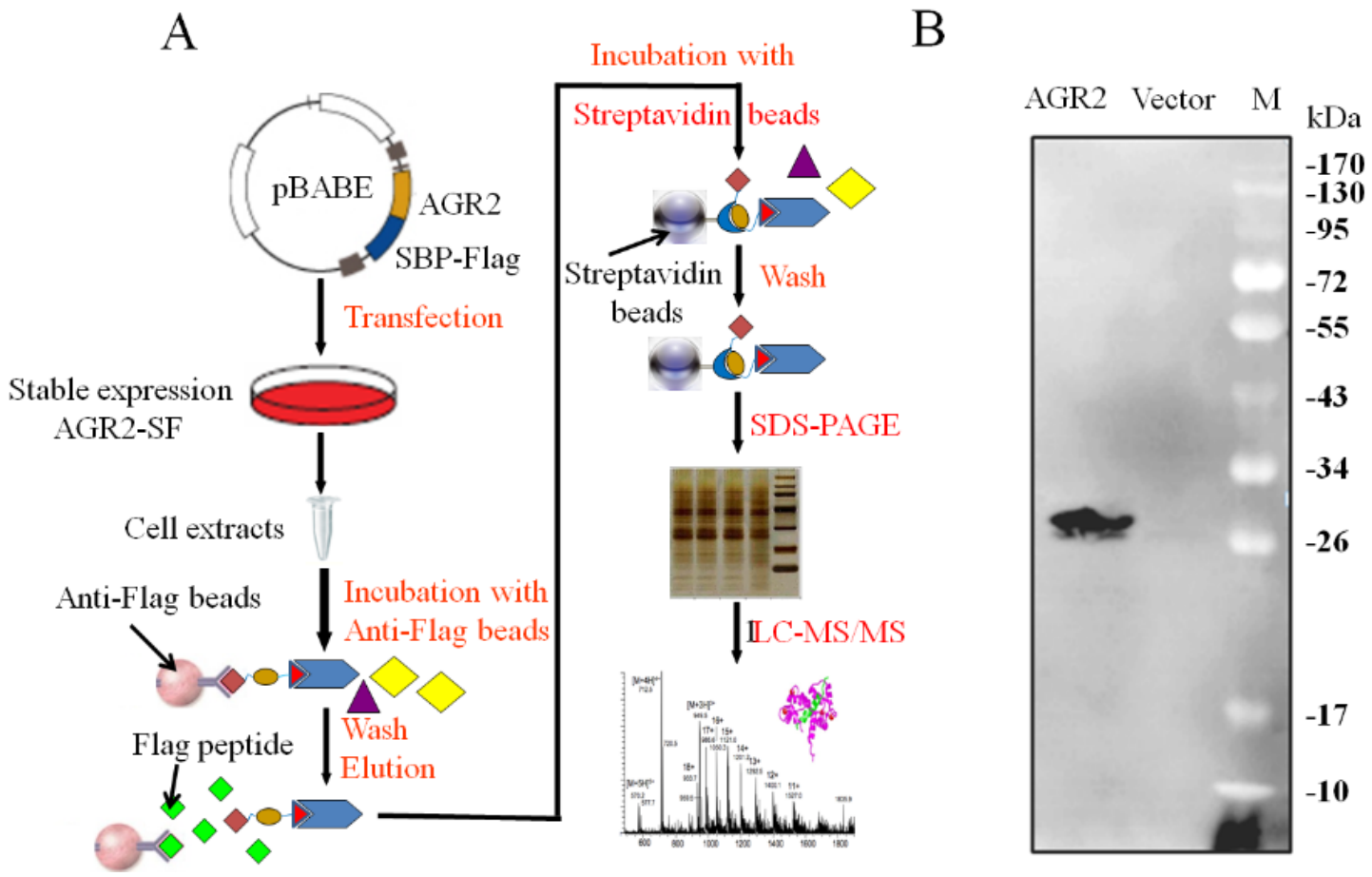
B: MS/MS Identification of STK4. Eight tryptic peptides (red) identified by LC-MS/MS assigned to the STK4,with total sequence coverage of 39.9%.

Representative MS/MS spectra for two peptides derived fromTAK1 and STK4 are shown on the right respectively.

Supplementary Figure 1

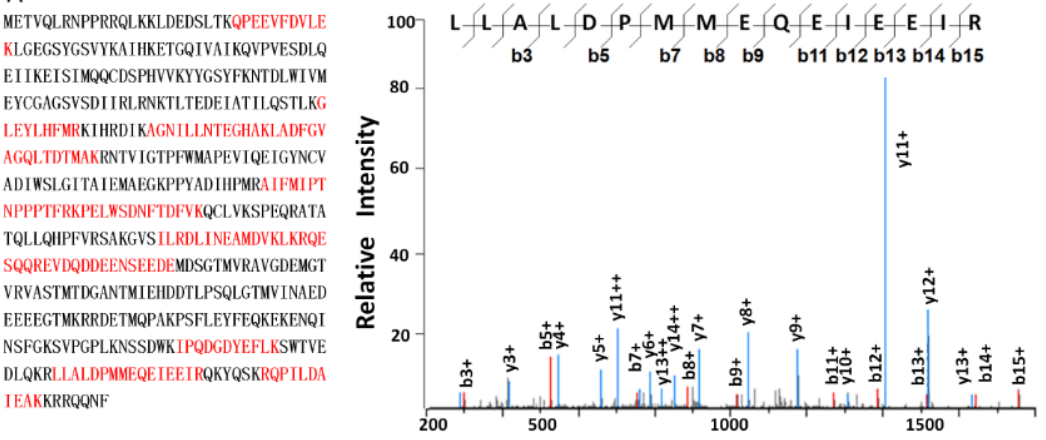


Supplementary Figure 2



Supplementary Figure 3

A



B