






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.

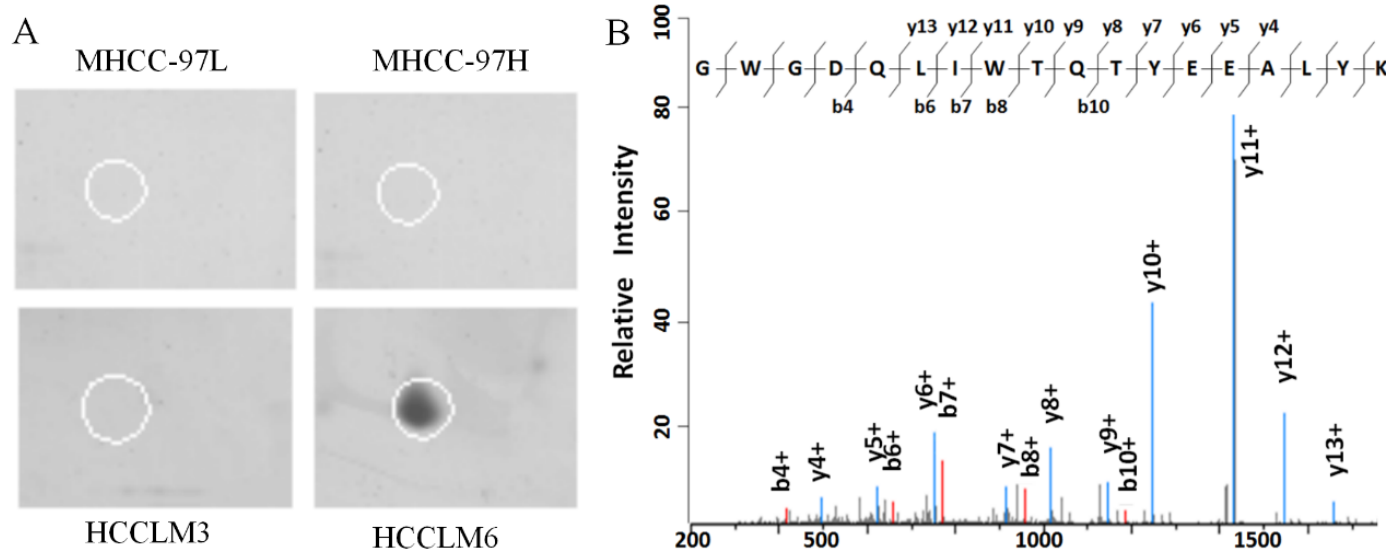
Supplementary Figure 3: Two examples of AGR2 interacting proteins identified by TAP and LC-MS/MS.

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%.

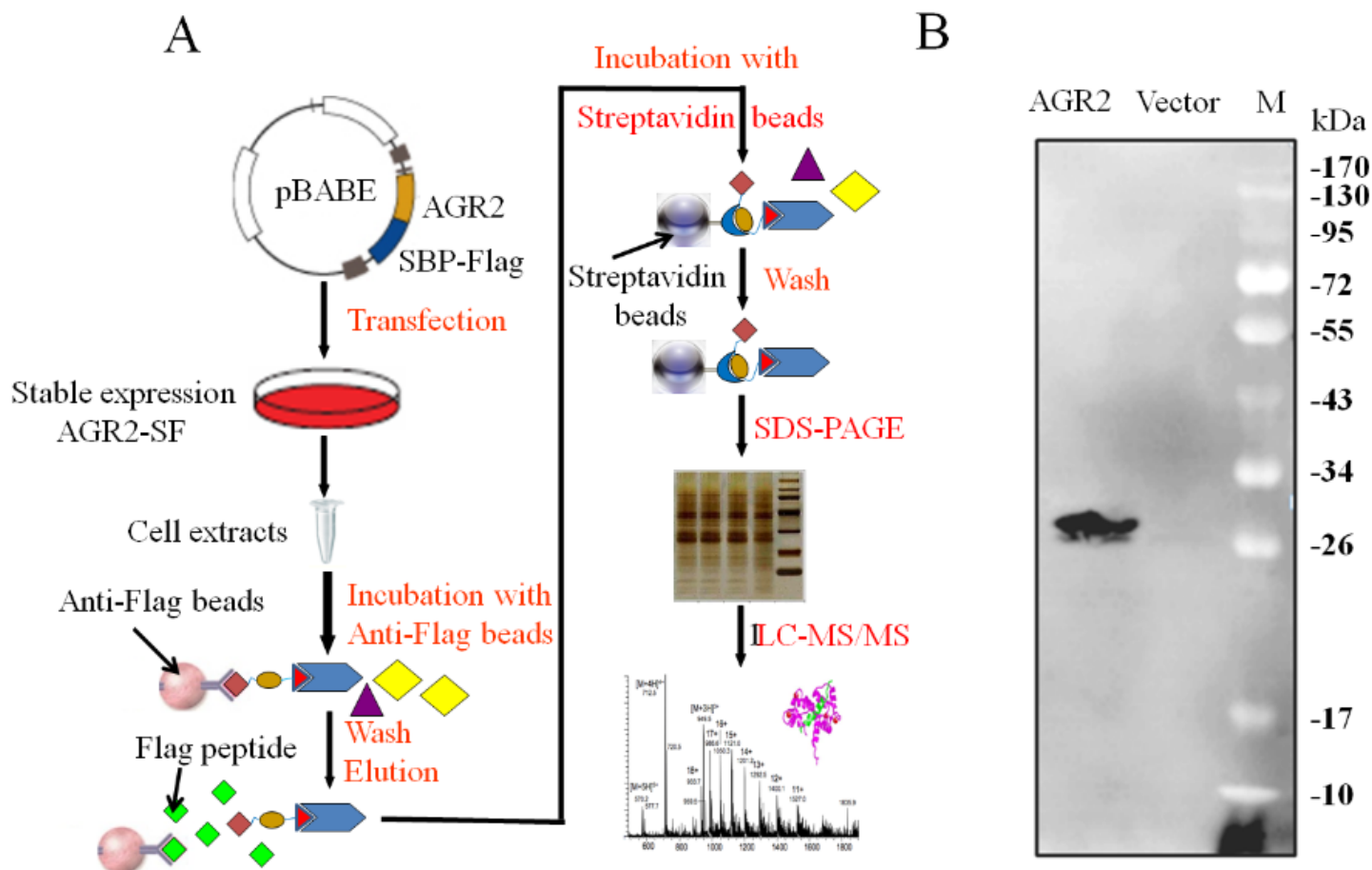
B: MS/MS Identification of STK4. Eight tryptic peptides (red) identified by LC-MS/MS assigned to the STK4, with total sequence coverage of 39.9%.

Representative MS/MS spectra for two peptides derived from TAK1 and STK4 are shown on the right respectively.

Supplementary Figure 1



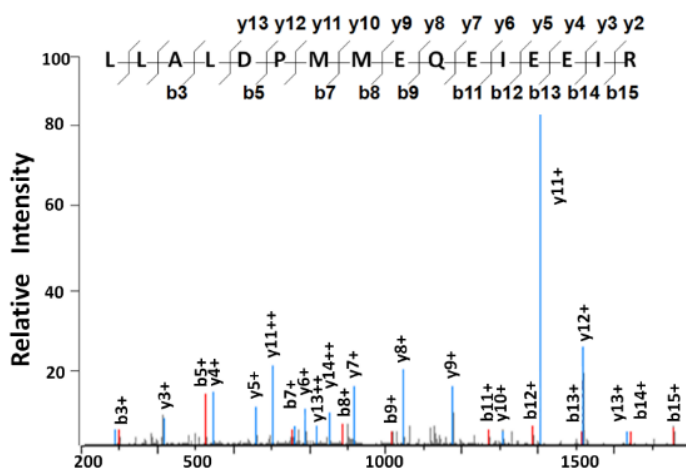
Supplementary Figure 2



Supplementary Figure 3

A

METVQLRNPPRRQLKLLDEDSLTK**QPEEVFDVLE**
 KLGGESYGSVYKAIHKETGQIVAIKQVPVESDLQ
 EIIKEISTMQCCDSPHVVKYYSYFKNTDLWIVM
 EYCGAGSVSDIIRLRNKTLEDEIATILQSTLKG
LEYLHFMRKITHRDIKAGNILLNTEGHAKLADFGV
AGQLTDTMAKRNTVIGTPFWMAPEVIQEIGYNCV
 ADIWSLGITATEMAEGKPPYADIIHPMRA**IFMIP**
NPPPTFRKPELWSDNFTDFVKQCLVKSPEQRATA
 TQLLQHPFVRSAGVSLRDLIN**EAMDVKLKRQE**
SQQREVDQDDEENSEEDEMDSGTMVRAVGDEMG
 VRVASTMTDGANTMEHDDTLPSQLGTMVINAED
 EEEEGTMKRREDETMQPAKPSFLEYFEQKEKENQI
 NSFSGSVPGPLKNSSDW**KIPQDGDYEF**LKSWTVE
 DLQKRLLALD**PMMEQEIEE**TRKQYQSKR**QPILDA**
TEAKRRRQQNF



B

MSTASAASSSSSSAGEMTEAPSQVLNFEEIDYKE
 IEVEEVYGRGAFGVVCKAKWRADVAIRQIESESE
RKAFIVELRQLSRVNHPIVKLYGACLNPCLVME
 YAEGGSLYNVLHGAEPYPYTAHAMSWCLQCSQG
 VAYLHSMQPKAL**IHRDLKPPNLLVAGGT**VLKICD
 FGTACDIQTHMTNNGSAAMMAPEVFEQSNSYSEK
 DVFSWGIIILWEVITRRKPFDEIGGPAFRIM**WAVHN**
GTRPPLIKNLPKPIESLMTRCWSKDPSPQPSMEEI
 VKIMTHLMRYFPGADEPLQYPCQYSDEGQNSATS
 TGSFMDIASTNTSNKSDT**NMEQVPATNDTI**KRLES
 KLLKNQAKQSESGRLSLGASRGSSVESLPPTSEG
 KRMSADMSEIEARIAATTAYSKPKRGHRK6**TASFG**
NILDVPEIIVISGNGQPRRSIQDLTYVTGTEPGQVS
SRSSSPSVRMITTSSGPTSEKPTRSHPWTPDDSDT
 NGSDNSIPMAYLTL**DHQL**PLAPCNSKESMAVFE
 QHCKMAQEMKVQTEIALL**QRKQELVAELDQDEK**
 DQQNTSRLVQEHKLLDENKSLSTYY**QCKKQLEV**
IRSQQKRQGTS

