

**SUPPLEMENTARY TABLE and TABLE LEGENDS:**

**Supplementary Table 1: Clinicopathological Correlation of AGR2 mRNA  
Expression in HCC (n =48)**

**Supplementary Table 2: Three top networks identified by IPA**

**Supplementary Table 1**

Clinicopathological Features	Number	AGR2 Overexpression	<i>P</i>
SEX			
Female	11	4(36.36%)	0.87
Male	37	17(45.95)	
AGE			
>50	34	13(38.23%)	0.661
≤50	14	8(57.14)	
AFP			
>400	11	6(54.54%)	0.498
≤400	37	15(40.54%)	
Tumor capsule			
Positive	21	6(28.57%)	0.002
Negative	27	15(55.56%)	
Tumor thrombi			
Present	19	11(57.89%)	0.094
Absent	29	10(34.48%)	
Metastasis			
Present	24	14(58.33%)	0.0006
Absent	24	7(29.17%)	
Number of tumors			
1	39	18(46.25%)	0.782
≥2	9	3(33.33%)	
Tumor size (cm) <sup>1</sup>			
>5	22	10(45.45%)	0.404
≤5	26	11(42.31%)	
TNM staging			
I	32	10(31.25%)	0.003
II-III	16	11(68.75%)	

1. Tumor size was measured by the length of the largest tumor nodule.

**Supplementary Table 2:** Three top networks identified by IPA

ID	Molecules in Network	Score	Focus Molecules	Top Functions
1	ATMIN, Caspase, EDARADD, EPS15, ERK, IKK (complex), Ikk (family), IL1, IL17RD, Jnk, KIR2DS2, MAP3K7, Map3k7-Map3k7ip1-Map3k7ip2, Mapk kinase, MAS1, NFkB (complex), P38 MAPK, PDCD6, Ras, RASSF5, SAV1, STK3, STK4, TAB1, TAB2, Tab1-Tak1, TAB2-TAK1, TIPRL, TRAF1-TRAF2-TRAF3, TRAF6-TAB2-TAK1, UBE2V1, Ubiquitin, UBR5, VRK2, WDR34	22	9	Embryonic Development, Tissue Development, Gene Expression
2	AASS, ADK, AGR2, ALDH18A1, ATAD3A, CDC42SE1, DHX15, ERBB2, ERLIN2, ESPL1, GYG1, HECTD1, LSR, MAP1B, MFAP1, MLXIP, MYC, MYO9A, NNMT, PRL2C3, PSME4, PXN, ROR1, RPL17, SF3B3, SLC25A5, SOLH, SPAG4, SPOCK1, SQRDL (includes EG:58472), SYCP3, TAX1BP3, TBC1D1, TGFB1, YWHAG	22	9	Cell Cycle, Hair and Skin Development and Function, Cell Morphology
3	FAF1, KLHL22, UBXN1, UBXN7	3	1	Protein Trafficking, Cell Signaling, Molecular Transport