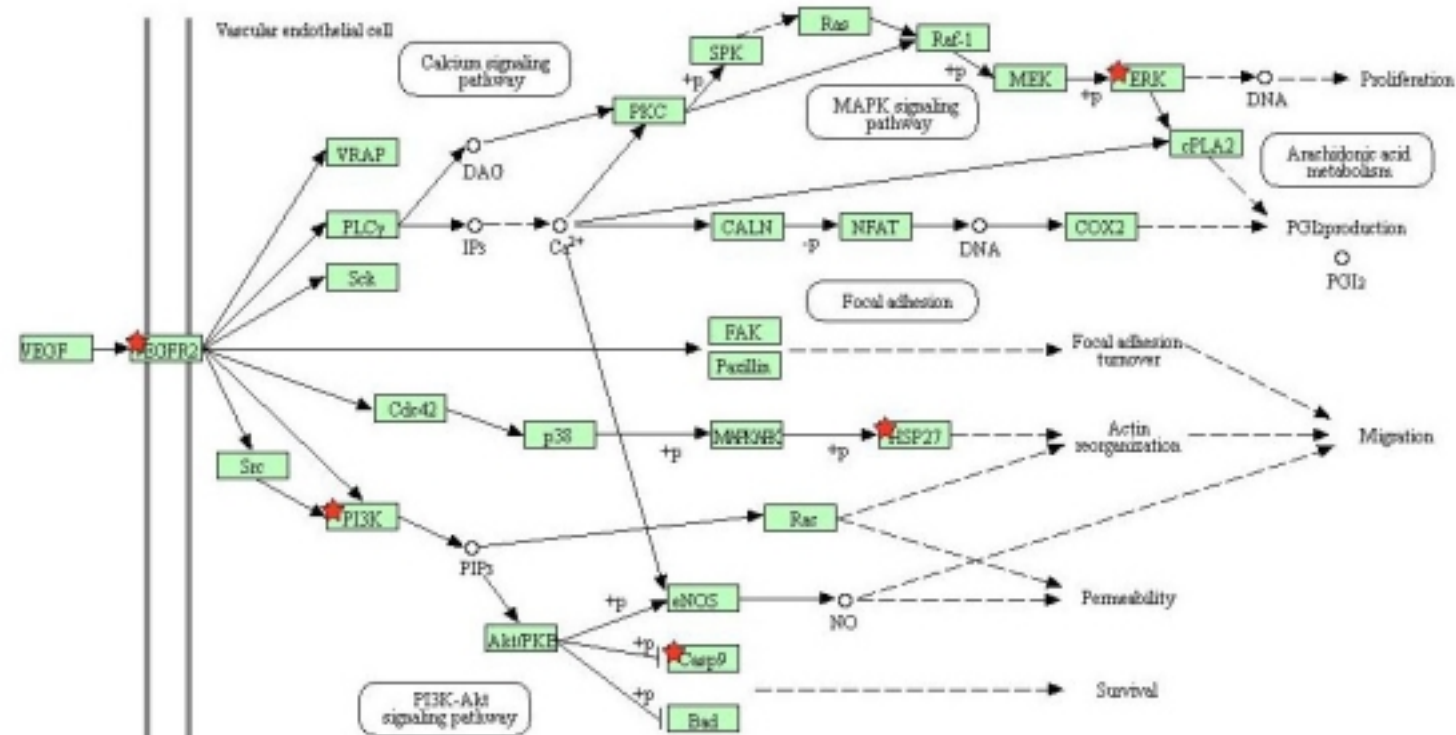


# VEGF SIGNALING PATHWAY



*No depression*      *Mild depression*      *Moderate / severe depression*

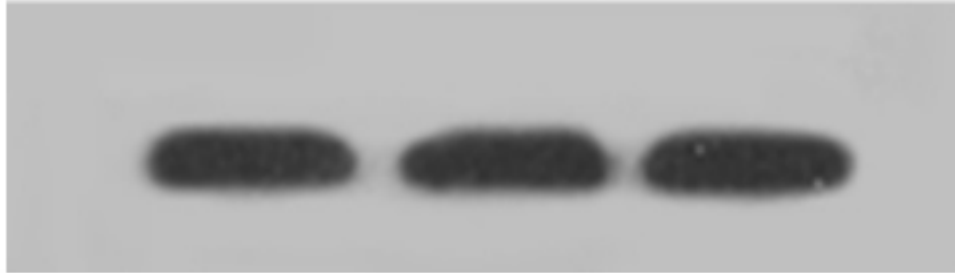
**HSPA8**



**HSP90AA1**



**β-action**



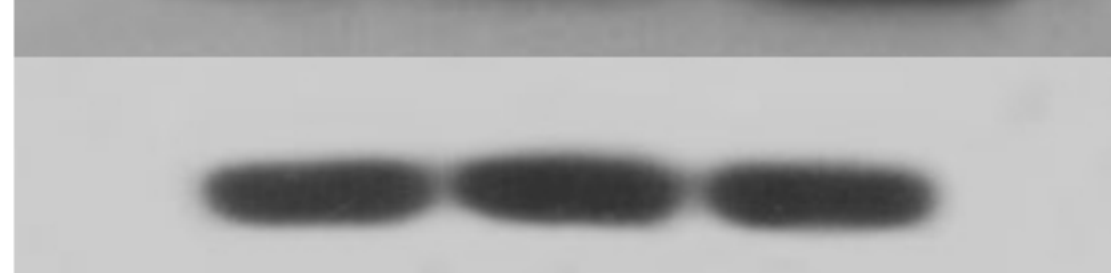
**HSPA8**



**HSP90AA1**



**β-action**



**Table S1.** Proteomic comparison of HCC tissues from patients with or without depression revealed 89 proteins that were up-regulated and 44 that were down-regulated in the presence of depression.

Accession ID	Protein name (gene name)	(95%) peptides	%COV	Gene locus	Log <sub>2</sub> (fold change)	-log <sub>10</sub> (P value)
<b>Up-regulated proteins</b>						
P 08238	HSP90AA1	7	41.26	14q32.3	2.64385619	4.924453039
P 07900	PDK1	8	47.68	10p15.1	1.056583528	4.882728704
P 11142	HSPA8	11	57.13	11q24.1	2.646162657	4.882728704
P 04792	HSPB1	6	58.54	7q11.23 *	1.895302621	4.832682665
P31939	PIK3CA	13	42.96	6p12**	2.482848283	4.790484985
Q96QV6	HSP90AB1	3	31.08	2q35	2.367371066	4.774690718
P10401	HSPA1A	9	29.77	6p22.2 *	2.263034406	4.76700389
P 19338	HSPA1B	5	23.01	6p22.1 *	1.992768431	4.679853714
P 62988	PIP2	4	38.45	2q37.1	1.89917563	4.665546249
P 23284	PGK1	3	75.01	2p16	1.831877241	4.590066877
P14618	CASP9	2	51.39	15q21	1.580145484	4.54515514
P 07237	CDC37	7	46.89	15q22	1.565597176	4.494850022
P04843	P4HB	15	52.38	19q22	1.526068812	4.448550002
Q5VTEO	PKM	5	39.54	1p36.1	1.541019153	4.369572125
P 27797	ENO1	11	56.2	9q34.12	1.459431619	4.321481621
P 00558	COL1A1	5	33.57	19p13.3	1.350497247	4.306273051
43776	PPIB	3	55.64	Xq13.3**	1.049630768	4.295849483
Q 00839	ACSL1	1	12.77	18q21.3	1.286881148	4.290730039
P53999	CTSD	2	41.99	1q44**	1.207892852	4.124360063
P10155	HNRNPU	2	25.98	5p13.3**	1.084064265	4.111820506
P15104	TXN	2	20.45	1q31**	2.10433666	4.085656843
Q 15084	AKR1C2	4	25.47	1q31**	1.111031312	4.053547735
P00338	MAPK1	11	51.59	2p25.1	1.298658316	3.995678626
P07237	TYMP	3	47.59	11p15.4	1.5360529	3.869666232
14745	TKT	15	2.9	17q25**	1.077242999	3.823908741
Q05682	PDIA4	3	44.13	17q25.1 *	1.782408565	3.821023053
P 060218	SLC9A3R1	3	41.49	7q33**	3.204766751	3.728158393
Q 04828	PIP3	10	48.1	7q33.1**	2.56315813	3.671620397
P16435	TUBA1B	9	42.41	10p14	1.673556424	3.543633967
P 10809	SULT1A4	2	18.02	7q11.28 *	1.521050737	3.460923901
P 61604	IKBK	24	63.7	2q33.1	1.14404637	3.448550002

Q9NS69	KDR	3	66.67	2q33.1	1.201633861	3.35261703
P61981	PDIA6	1	27.46	22q12	1.367371066	3.222573178
P 06733	SULT1A2	2	53.04	7q11.25 *	1.117695043	3.216096421
P 0C7M2	PPIAP22	19	56.91	1p36.2	1.765534746	3.211124884
P 62937	TUBAP2	3	56.56	12q13.1	1.124328135	3.016373713
P 38646	AKR1C1	9	81.72	7p13	1.244887059	3.009217308
P52758	ENO1-IT1	16	54.05	5q31.1	1.416839742	2.991399828
P 11021	MDH2	2	70.8	8q22 <sup>*</sup>	1.070389328	2.978810701
P 07339	PIK3R1	14	50.76	9q33.3	1.807354922	2.974694135
P30837	AKR7A2	9	48.3	11p15.5	1.14404637	2.954677021
P 13667	CALR	4	34.43	9p11.1	1.286881148	2.931814138
P 40926	CFL1	5	33.38	7q35 <sup>*</sup>	1.500802053	2.910094889
Q99471	APOE	8	56.51	7q22 <sup>*</sup>	1.084064265	2.906578315
P 02649	ESPL1	1	46.75	12q12	1.49057013	2.896196279
P 08107	NCL	5	71.61	19q13.2	1.286881148	2.826813732
Q05682	CALD1	10	45.09	6p21.3 <sup>*</sup>	1.007195501	2.826813732
P23528	CKAP4	3	41.49	7q33 <sup>*</sup>	1.992768431	2.795880017
P20700	LONP2	3	42.17	11q13	1.875780063	2.793174124
Q07065	RNU6-29P	3	38.23	5q23.2	1.448900951	2.790484985
P06899	AKR1C4	3	33.89	12q23.3	2.070389328	2.653647026
P19971	FTCD	14	72.22	6p22.1 *	1.220329955	2.642065153
P62805	BGN	3	26,56	22q13.3	2.364572432	2.567030709
P61978	SHMT1	5	74.76	6p22.1 <sup>*</sup>	2.046141782	2.559090918
P27824	HADH	4	41.9	9q21.3	1.963474124	2.543633967
P55072	UGP2	4	22.8	5q35	1.739848103	2.514278574
P68363	TGM2	3	41.81	9p13.3	1.244887059	2.512861625
P10599	ATIC	10	44.35	12q13.1	1.510961919	2.474955193
Q14749	ABAT	3	58.1	9q31	1.97819563	2.446116973
P69905	FLNA	2	34.92	16p12 <sup>*</sup>	1.275007047	2.437707136
P 11586	MYH10	18	56.34	16p13.3 <sup>*</sup>	1.608809243	2.436518915
P 68871	CPT2	8	40	14q24 <sup>*</sup>	1.765534746	2.37161107
P23786	HRSP12	57	89.8	11p15.5	2.097610797	2.364516253
P18206	NARS	2	27.66	1p32 <sup>*</sup>	1.700439718	2.354577731
P35580	ALDOB	4	36.07	10q22.2 <sup>*</sup>	1.007195501	2.347753659
Q9Y2S2	PGS1	6	31.73	17p13 <sup>*</sup>	1.195347598	2.258848401
P 05181	HBG2	3	21.63	13q12.1 <sup>*</sup>	1.275007047	2.229147988
P07099	SUB1	2	24.34	10q24.3 <sup>*</sup>	1.560714954	2.158015195
Q16696	GRHPR	3	33.19	1q42.1	1.510961919	2.153662888
P28332	CARHSP1	2	14.37	19q13.2 <sup>*</sup>	1.176322773	2.139063379
P 21980	TROVE2	1	9.23	4q23 <sup>*</sup>	1.344828497	2.128427064

P 42765	COMT	3	38.14	20q12	1.269033146	2.111259039
P00480	HBA1	11	47.86	18q21.1	1.3950628	2.067526235
P 02671	FGB	4	22.88	Xp21.1	1.416839742	2.048662481
P 08670	LMNB1	9	28.98	4q28 <sup>*</sup>	1.046141782	2.037157319
P29401	TFG	26	69.31	10p13	1.007195501	2.026872146
P21549	HBB	5	23.27	3p14.3	1.070389328	1.970616222
P 12111	AKR1B10	5	42.09	2q37 <sup>*</sup>	1.646162657	1.966576245
Q06520	ASS1	7	27.7	2q37 <sup>*</sup>	1.124328135	1.943095149
Q9Y2V2	FGA	3	39.65	19q13.3 <sup>*</sup>	1.364572432	1.931814138
P00441	HNRNPK	2	31.97	16p13.2 <sup>*</sup>	1.117695043	1.88941029
Q7Z4W1	SLC27A5	3	50.65	21q22.1 <sup>*</sup>	1.232660757	1.886056648
P34913	AOX1	5	69.26	17q25.3	1.03562391	1.835647144
Q02318	ADH4	2	28.29	8p21.2 <sup>*</sup>	1.883620816	1.815308569
Q06278	ACY1	2	8.28	2q33 <sup>*</sup>	1.275007047	1.806875402
P35579	PHGDH	3	26.01	2q33 <sup>*</sup>	1.269033146	1.795880017
Q92734	ARG1	19	10.36	22q13.1 <sup>*</sup>	1.275007047	1.777283529
P 02675	ACAT2	3	17.25	2q12.2 <sup>*</sup>	1.819668183	1.769551079
P10799	IGHA1	2	27.9	4q28 <sup>*</sup>	1.327687364	1.761953897
<b>Down-regulated proteins</b>						
P 08319	DAK	7	60	4q22 <sup>*</sup>	-3.058893689	4.829738285
Q03154	PCK2	7	35.29	3p21.1	-1.556393349	4.821023053
Q9NY33	SORD	3	27	11q12	-3.836501268	4.694648631
O43175	PGM1	4	31.89	1p12	-2.120294234	4.410050399
P05089	GSTA1	5	56.21	6q23 <sup>*</sup>	-1.888968688	4.317854924
Q9BWD1	ALDH1L1	5	34.51	6q25.3 <sup>*</sup>	-1.089267338	4.268411235
P01876	GOT2	3	42.21	14q32.3 <sup>*</sup>	-1.120294234	4.193820026
P36776	CES1	2	22.31	19p13.2 <sup>*</sup>	-1.395928676	3.935542011
P36776	PYGL	1	22.31	16q12.1 <sup>*</sup>	-1.395928676	3.829738285
P02765	ADH1C	2	17.71	3q27	-1.836501268	3.823908741
P36269	SULT1A1	1	7.58	22q11.2 <sup>*</sup>	-2.120294234	3.801342913
Q3LXA3	ADH1A	8	48	11q12.2	-1.217591435	3.540607512
Q16822	BHMT	13	51.41	14q11.2 <sup>*</sup>	-1.556393349	3.360513511
P 05062	PBLD	26	56.59	9q21.3	-1.434402824	3.179798541
Q00796	ECHS1	5	47.34	15q15.3	-1.434402824	3.119186408
Q16851	MTHFD1	3	45.47	2p14	-1.358453971	2.954677021
P 36871	VCL	8	43.95	1p31 <sup>*</sup>	-1.286304185	2.910094889
P 08263	CRYL1	2	43.24	6p12.1	-1.286304185	2.684029655
P 21333	EPHX1	12	29.4	Xq28	-2.556393349	2.628932138
95954	CYP2A13	10	65.43	21q22.3 <sup>*</sup>	-1.836501268	2.600326279
P 00966	ADH6	3	34.47	9q34.1	-1.736965594	2.591760035
75891	ACAA2	3	30.93	3q21.3	-1.120294234	2.591760035
P 00505	OTC	4	50	16q21 <sup>*</sup>	-1.152003093	2.455931956

P23141	VIM	11	50.44	16q22.2 <sup>*</sup>	-1.152003093	2.431798276
P 05091	COL6A3	11	59.38	12q24.2	-1.029146346	2.420216403
P06737	SULT2A1	1	24.44	14q21 <sup>*</sup>	-1.152003093	2.408935393
P 00326	SOD1	4	38.13	4q23 <sup>*</sup>	-4.321928095	2.399027104
P 21810	DCXR	3	26.63	17q25.3	-2.473931188	2.375717904
Q16836	EPHX2	2	33.76	4q22 <sup>*</sup>	-1.251538767	2.344861565
Q9Y2P5	CYP27A1	2	15.07	19q13.4 <sup>*</sup>	-1.395928676	2.269217724
P 33121	MYH9	5	36.82	4q35 <sup>*</sup>	-2.321928095	2.134896025
P50225	PKM2	2	36.61	16p21.2 <sup>*</sup>	-1.358453971	2.049148541
P 80404	PDIA1	3	30.6	16p13.2 <sup>*</sup>	-1.217591435	1.920818754
P02452	GLUL	3	50.82	17q21.3	-2.120294234	1.913640169
P43488	LDHA	3	34.82	1p36.1 <sup>*</sup>	-3.184424571	1.896196279
Q9UBQ7	PRO	3	24.7	9q12	-1.089267338	1.696803943
P21810	TOMM22	3	15.22	Xq28 <sup>*</sup>	-2.473931188	1.576754126
P07327	YWHAG	4	32	4q23 <sup>*</sup>	-2.473931188	1.496209317
P69892	PPIA	5	48.33	11p15.5	-1.434402824	1.465973894
Q93088	GRP75	8	49.75	5q13.3	-1.59946207	1.335358024
P21964	GRP78)	1	12.92	22q11.2 <sup>*</sup>	-1.089267338	1.701146924
P34896	ALDH1B1	2	18.43	17p12 <sup>*</sup>	-2.395928676	1.688246139
P30039	PFDN5	2	27.78	10q21.3 <sup>*</sup>	-1.434402824	1.688246139
P30084	CANX	6	23.79	10q26.2 <sup>*</sup>	-2.395928676	1.679853714

**Table S2.** Analysis of gene ontology (molecular function, biological process and cellular component) and pathway enrichment based on proteins up-regulated in HCC patients in the presence of depression.

Cellular component	No. genes	Fold enrichment	P value (Hypergeometric test)	Bonferroni method	BH method	Q-value (Storey-Tibshirani method)	Genes
Cytosol	28	5.37865422	6.21E-14	4.87E-11	9.88E-12	6.21432E-11	HSP90AA1; HSPA8; PIK3CA; HSP90AB1; HSPA1A; CASP9; PKM; PPIB; ACSL1; TXN; AKR1C2; MAPK1; TKT; TUBA1B; SULT1A4; IKBKG; AKR1C1; PIK3R1; CALR; CFL1; AKR1C4; SHMT1; FLNA; NARS; COMT; ASS1; ACY1; PHGDH;
Cytoplasm	63	2.50763395	2.49E-17	1.95E-14	6.51E-15	4.09501E-14	HSP90AA1; HSPA8; HSPB1; HSP90AB1; HSPA1A; HSPA1B; PGK1; CASP9; CDC37; P4HB; PKM; ENO1; PPIB; CTSD; HNRNPU; TXN; MAPK1; TYMP; TKT; SLC9A3R1; TUBA1B; SULT1A4; IKBKG; SULT1A2; AKR1C1; PIK3R1; AKR7A2; CALR; CFL1; APOE; NCL; CALD1; CKAP4; AKR1C4; FTCD; SHMT1; HADH; UGP2; TGM2; ATIC; FLNA; MYH10; HRSP12; NARS; ALDOB; SUB1; GRHPR; CARHSP1; TROVE2; COMT; HBA1; FGB; LMNB1; TFG; HBB; FGA; HNRNPK; AOX1; ADH4; ACY1; ARG1; ACAT2; AHSG;
Exosomes	53	5.86944187	1.08E-30	8.49E-28	8.49E-28	5.3407E-27	HSP90AA1; HSPA8; HSPB1; HSP90AB1; HSPA1A; HSPA1B; PGK1; CASP9; CDC37; P4HB;

							PKM; ENO1; PPIB; CTSD; TXN; TKT; PDIA4; SLC9A3R1; TUBA1B; PDIA6; MDH2; AKR7A2; CALR; CFL1; APOE; NCL; CKAP4; FTCD; BGN; SHMT1; UGP2; TGM2; ATIC; FLNA; MYH10; HRSP12; NARS; ALDOB; SUB1; GRHPR; COMT; HBA1; FGB; HBB; AKR1B10; ASS1; FGA; HNRNPK; AOX1; ACY1; PHGDH; ACAT2; AHS;G
Lysosome	38	5.30749591	4.04E-19	3.17E-16	1.58E-16	9.96102E-16	HSP90AA1; HSPA8; HSPB1; HSPA1A; HSPA1B; PGK1; P4HB; PKM; ENO1; PPIB; CTSD; TYMP; TKT; PDIA6; MDH2; AKR7A2; CALR; CFL1; CKAP4; HADH; UGP2; TGM2; ATIC; FLNA; MYH10; CPT2; HBG2; GRHPR; COMT; HBA1; HBB; ASS1; FGA; HNRNPK; ARG1; LONP1; AHS;G; GGT5;
Centrosome	22	7.58960331	6.3E-14	4.94E-11	9.88E-12	6.21432E-11	HSP90AA1; PDK1; HSPA8; HSP90AB1; PGK1; ENO1; HNRNPU; TXN; MAPK1; TKT; TUBA1B; CFL1; ESPL1; NCL; HADH; ATIC; MYH10; SUB1; CARHSP1; LMNB1; HNRNPK; PHGDH;
<b>Molecular function</b>	<b>No. genes</b>	<b>Fold enrichment</b>	<b>P value (Hypergeometric test)</b>	<b>Bonferroni method</b>	<b>BH method</b>	<b>Q-value (Storey-Tibshirani method)</b>	<b>Genes</b>
Ligase activity	3	6.07881872	0.013443	1	0.563856	1	ACSL1; NARS; ASS1;
Transaminase activity	2	19.7600907	0.004599	1	0.343409	1	TGM2; ABAT;
Catalytic activity	16	6.80739624	1.27E-09	2.85E-07	2.85E-07	1.62763E-06	PDK1; PGK1; PKM; ENO1;



							TXN; AKR1C1; MDH2; AKR7A2; AKR1C4; PGS1; GRHPR; AKR1B10; ASS1; AOX1; ADH4; PHGDH;
Chaperone activity	9	16.1744407	4.52E-09	1.01E-06	5.06E-07	2.88795E-06	HSP90AA1; HSPB1; HSP90AB1; HSPA1A; HSPA1B; CDC37; PPIB; PDIA4; CALR;
Transferase activity, transferring aldehyde or ketonic groups	1	75.9039492	0.013203	1	0.563856	1	TKT;
<b>Biological process</b>	<b>No. genes</b>	<b>Fold enrichment</b>	<b>P value (Hypergeomet ric test)</b>	<b>Bonferroni method</b>	<b>BH method</b>	<b>Q-value (Storey-Tibshir ani method)</b>	<b>Genes</b>
Protein metabolism	19	3.25033769	3.88E-06	0.000691	0.00023	0.001521699	HSP90AA1; HSPA8; HSPB1; HSPA1A; HSPA1B; CDC37; P4HB; PPIB; CTSD; PDIA4; PDIA6; CALR; ESPL1; LONP2; HRSP12; NARS; FGB; FGA; LONP1;
Metabolism	33	4.43678436	4.01E-14	7.14E-12	3.57E-12	2.35774E-11	PDK1; PGK1; PKM; ENO1; ACSL1; TXN; AKR1C2; TKT; AKR1C1; MDH2; AKR7A2; AKR1C4; FTCD; SHMT1; UGP2; TGM2; ATIC; ABAT; CPT2; ALDOB; PGS1; GRHPR; COMT; AKR1B10; ASS1; SLC27A5; AOX1; ADH4; ACY1; PHGDH; ARG1; ACAT2; GGT5;
Energy pathways	33	4.57263119	1.69E-14	3.02E-12	3.02E-12	1.9909E-11	PDK1; PGK1; PKM; ENO1; ACSL1; TXN; TKT; SULT1A2; AKR1C1; MDH2; AKR7A2; AKR1C4; FTCD; SHMT1; UGP2; TGM2; ATIC; ABAT; CPT2; ALDOB; PGS1; GRHPR; COMT; AKR1B10; ASS1; SLC27A5; AOX1; ADH4;

							ACY1; PHGDH; ARG1; ACAT2; GGT5;
Amino acid and derivative metabolism	1	56.9752835	0.017565	1	0.781651	1	FTCD;
Xenobiotic metabolism	1	38.0151226	0.026233	1	0.933898	1	SULT1A4;
<b>KEGG pathway</b>	<b>No. genes</b>	<b>Fold enrichment</b>	<b>P value (Hypergeometric test)</b>	<b>Bonferroni method</b>	<b>BH method</b>	<b>Q-value (Storey-Tibshirani method)</b>	<b>Genes</b>
Syndecan-1-mediated signaling events	26	4.53634965	2.94E-11	4.9E-08	8.28E-09	4.1273E-08	HSP90AA1; HSPA8; HSPB1; PIK3CA; HSPA1A; HSPA1B; PGK1; CASP9; PKM; ENO1; COL1A1; PIIB; CTSD; TXN; MAPK1; SLC9A3R1; IKBKG; KDR; PIK3R1; NCL; SHMT1; HBG2; FGB; FGA; ARG1; AHSG;
Signaling events mediated by VEGFR1 and VEGFR2	26	4.55038311	2.74E-11	4.58E-08	8.28E-09	4.1273E-08	HSP90AA1; HSPA8; HSPB1; PIK3CA; HSP90AB1; HSPA1A; HSPA1B; PGK1; CASP9; PKM; ENO1; COL1A1; CTSD; TXN; MAPK1; SLC9A3R1; IKBKG; KDR; PIK3R1; NCL; SHMT1; HBG2; FGB; FGA; ARG1; AHSG;
VEGF and VEGFR signaling network	26	4.52240249	3.15E-11	5.25E-08	8.28E-09	4.1273E-08	HSP90AA1; HSPA8; HSPB1; PIK3CA; HSP90AB1; HSPA1A; HSPA1B; PGK1; CASP9; PKM; ENO1; COL1A1; CTSD; TXN; MAPK1; SLC9A3R1; IKBKG; KDR; PIK3R1; NCL; SHMT1; HBG2; FGB; FGA; ARG1; AHSG;
Alpha9 beta1 integrin signaling	26	4.51892909	3.2E-11	5.34E-08	8.28E-09	4.1273E-08	HSP90AA1; HSPA8; HSPB1; PIK3CA; HSPA1A;

events							HSPA1B; PGK1; CASP9; PKM; ENO1; COL1A1; CTSD; TXN; MAPK1; SLC9A3R1; IKBKG; KDR; PIK3R1; NCL; SHMT1; TGM2; HBG2; FGB; FGA; ARG1; AHSG;
Proteoglycan syndecan-mediated signaling events	27	4.55279742	9.97E-12	1.66E-08	8.28E-09	4.1273E-08	HSP90AA1; HSPA8; HSPB1; PIK3CA; HSPA1A; HSPA1B; PGK1; CASP9; PKM; ENO1; COL1A1; PIIB; CTSD; TXN; MAPK1; SLC9A3R1; IKBKG; KDR; PIK3R1; NCL; SHMT1; FLNA; HBG2; FGB; FGA; ARG1; AHSG;
LKB1 signaling events	26	4.50854082	3.37E-11	5.62E-08	8.28E-09	4.1273E-08	HSP90AA1; HSPA8; HSPB1; PIK3CA; HSPA1A; HSPA1B; PGK1; CASP9; CDC37; PKM; ENO1; COL1A1; CTSD; TXN; MAPK1; SLC9A3R1; IKBKG; KDR; PIK3R1; NCL; SHMT1; HBG2; FGB; FGA; ARG1; AHSG;

**Table S3.** Analysis of gene ontology (molecular function, biological process and cellular component) and pathway enrichment based on proteins down-regulated in HCC patients in the presence of depression.

Cellular component	No. genes	Fold enrichment	P value (Hypergeometric test)	Bonferroni method	BH method	Q-value (Storey-Tibshirani method)	Genes
Mitochondrion	16	6.43344797	5.83E-10	4.57E-07	2.29E-07	1.49477E-06	PCK2; GOT2; ECHS1; MTHFD1; ACAA2; OTC; VIM; SOD1; DCXR; CYP27A1; MYH9; GLUL; TOMM22; PPIA; ALDH1B1; CANX;
Cytosol	13	5.58740253	2.05E-07	0.000161	4.03E-05	0.000263169	PCK2; PGM1; MTHFD1; VCL; VIM; SULT2A1; SOD1; EPHX2; MYH9; GLUL; LDHA; YWHAG; PPIA;
Exosomes	25	6.19333882	5.4E-16	4.24E-13	4.24E-13	2.7686E-12	SORD; PGM1; GSTA1; ALDH1L1; GOT2; PYGL; BHMT; PBLD; MTHFD1; VCL; CRYL1; ADH6; ACAA2; VIM; COL6A3; SOD1; DCXR; EPHX2; MYH9; GLUL; LDHA; TOMM22; YWHAG; PPIA; CANX;
Lysosome	15	4.68753623	1.72E-07	0.000135	4.03E-05	0.000263169	PGM1; GOT2; ECHS1; MTHFD1; VCL; EPHX1; COL6A3; SOD1; DCXR; MYH9; LDHA; TOMM22; YWHAG; PPIA; CANX;
Mitochondrial matrix	5	32.0802175	4.65E-07	0.000364	7.28E-05	0.000476063	GOT2; ECHS1; OTC; SOD1; CYP27A1;
Molecular function	No. genes	Fold enrichment	P value (Hypergeometric test)	Bonferroni method	BH method	Q-value (Storey-Tibshirani method)	Genes
Transaminase activity	2	44.1937729	0.000937	0.209914	0.069971	0.443756146	GOT2; GLUL;
Catalytic activity	10	9.51910073	5.68E-08	1.27E-05	1.27E-05	8.07559E-05	PCK2; SORD; PGM1; ALDH1L1; ADH1C; ECHS1; MTHFD1; ADH6; LDHA; ALDH1B1;
Oxidoreductase	5	15.7422395	1.55E-05	0.003476	0.001738	0.011023622	ADH1A; CRYL1;

activity							CYP2A13; DCXR; CYP27A1;
Carboxyl- and carbamoyltransferase activity	1	254.218386	0.003948	0.884432	0.22029	1	OTC;
Sulfotransferase activity	2	19.1831487	0.004917	1	0.22029	1	SULT1A1; SULT2A1;
<b>Biological process</b>	<b>No. genes</b>	<b>Fold enrichment</b>	<b>P value (Hypergeometric test)</b>	<b>Bonferroni method</b>	<b>BH method</b>	<b>Q-value (Storey-Tibshirani method)</b>	<b>Genes</b>
Metabolism	28	8.4199217	3.86E-22	6.87E-20	6.87E-20	4.63479E-19	PCK2; SORD; PGM1; GSTA1; ALDH1L1; GOT2; CES1; PYGL; ADH1C; SULT1A1; ADH1A; BHMT; ECHS1; MTHFD1; CRYL1; EPHX1; CYP2A13; ADH6; ACAA2; OTC; SULT2A1; SOD1; DCXR; EPHX2; CYP27A1; GLUL; LDHA; ALDH1B1;
Energy pathways	27	8.36791732	4.74E-21	8.44E-19	4.22E-19	2.84643E-18	PCK2; SORD; PGM1; GSTA1; ALDH1L1; GOT2; PYGL; ADH1C; SULT1A1; ADH1A; BHMT; ECHS1; MTHFD1; CRYL1; EPHX1; CYP2A13; ADH6; ACAA2; OTC; SULT2A1; SOD1; DCXR; EPHX2; CYP27A1; GLUL; LDHA; ALDH1B1;
Cell growth and/or maintenance	4	1.80330684	0.180257	1	1	1	VCL; VIM; COL6A3; MYH9;
Protein folding	2	63.5164718	0.000448	0.079811	0.026604	0.179376121	PPIA; CANX;
Peptide metabolism	1	127.426173	0.007882	1	0.350728	1	PPIA;
<b>KEGG pathway</b>	<b>No. genes</b>	<b>Fold enrichment</b>	<b>P value (Hypergeometric test)</b>	<b>Bonferroni method</b>	<b>BH method</b>	<b>Q-value (Storey-Tibshirani method)</b>	<b>Genes</b>
Platelet degranulation	3	54.3669572	2.25E-05	0.037595	0.010235	0.061849128	VCL; SOD1; PPIA;

Response to elevated platelet cytosolic Ca <sup>2+</sup>	3	39.0366181	6.19E-05	0.103317	0.01476	0.089189143	VCL; SOD1; PPIA;
Metabolism	9	5.53861681	2.45E-05	0.040941	0.010235	0.061849128	GSTA1; GOT2; SULT1A1; MTHFD1; CYP2A13; OTC; SULT2A1; CYP27A1; GLUL;
Phase II conjugation	3	39.0366181	6.19E-05	0.103317	0.01476	0.089189143	GSTA1; SULT1A1; SULT2A1;
Biological oxidations	5	25.8612181	1.36E-06	0.002272	0.002272	0.013731392	GSTA1; SULT1A1; CYP2A13; SULT2A1; CYP27A1;
Glucose metabolism	3	42.2887662	4.86E-05	0.081049	0.01476	0.089189143	PCK2; GOT2; PYGL;