

Supplementary materials

Supplementary Table 1-4

Table S1. GO terms of DEGs that are enriched.

ID	Term	Count	GeneRatio (%)	adjusted P value
GO:0055114	oxidation-reduction process	57	12.47	2.47E-14
GO:0019373	epoxygenase P450 pathway	12	2.63	7.37E-11
GO:0008202	steroid metabolic process	15	3.28	1.10E-09
GO:0017144	drug metabolic process	11	2.41	3.13E-07
GO:0006805	xenobiotic metabolic process	15	3.28	3.20E-06
GO:0051301	cell division	27	5.91	2.83E-04
GO:0007067	mitotic nuclear division	22	4.81	3.38E-04
GO:0042493	response to drug	23	5.03	1.49E-03
GO:0007062	sister chromatid cohesion	13	2.84	1.49E-03
	cellular response to tumor necrosis			
	factor			
GO:0071356		13	2.84	2.77E-03
GO:0000082	G1/S transition of mitotic cell cycle	12	2.63	5.48E-03
GO:0006956	complement activation	11	2.41	6.59E-03
GO:0008152	metabolic process	15	3.28	8.43E-03
	anaphase-promoting complex-			
	dependent catabolic process			
GO:0031145		10	2.19	1.24E-02
GO:0000086	G2/M transition of mitotic cell cycle	12	2.63	4.38E-02
	negative regulation of protein kinase			
	activity			
GO:0006469		10	2.19	4.78E-02
GO:0070062	extracellular exosome	129	28.23	2.77E-11
GO:0031090	organelle membrane	18	3.94	3.32E-09
GO:0005615	extracellular space	70	15.32	1.51E-07
GO:0005576	extracellular region	78	17.07	2.47E-07
GO:0005829	cytosol	127	27.79	1.66E-06
GO:0072562	blood microparticle	17	3.72	3.89E-05
GO:0030496	midbody	15	3.28	1.13E-04
GO:0000777	condensed chromosome kinetochore	12	2.63	2.65E-04
GO:0005759	mitochondrial matrix	23	5.03	4.33E-04
GO:0005819	spindle	12	2.63	3.88E-03
GO:0000922	spindle pole	10	2.19	2.26E-02
GO:0005874	microtubule	18	3.94	2.50E-02
	oxidoreductase activity, acting on			
	paired donors, with incorporation or			
	reduction of molecular oxygen			
GO:0016705	arachidonic acid epoxygenase	16	3.50	4.37E-09
	activity			
GO:0008392		10	2.19	5.60E-09
GO:0019825	oxygen binding	14	3.06	1.93E-08
GO:0004497	monooxygenase activity	15	3.28	2.00E-08
GO:0016491	oxidoreductase activity	24	5.25	1.52E-07
GO:0020037	heme binding	20	4.38	1.52E-07
GO:0005506	iron ion binding	21	4.60	1.52E-07
GO:0009055	electron carrier activity	14	3.06	2.84E-05
GO:0003824	catalytic activity	19	4.16	8.51E-05
GO:0042803	protein homodimerization activity	36	7.88	7.44E-03

Table S2. Gene pairs selected by 10-folds cross validation Lasso regression

Gene pair	Coefficient
PLVAP SULT1E1	0.299272682
PSMD4 OAT	0.464321033
GPC3 HGFAC	0.187678869
GPC3 CLRN3	0.416983036
GPC3 CD5L	1.69954475
RGS5 FAHD2A	0.324198077
RGS5 CCL4	0.510061637
IRAK1 CXCL14	3.281257264
CXCL14 ECM1	-0.117015273
CXCL14 CFP	-1.108324041
CXCL14 CPED1	-0.649675769
CXCL14 SAMMD5	-0.257621447
LCAT SRD5A1	-0.018219001

Table S3. 10 hub genes assessed with highest connectivity degree.

Rank	Name	Score
1	CDK1	69
2	CDC20	68
3	MAD2L1	64
4	CCNB2	63
4	CCNA2	63
6	UBE2C	62
7	BUB1B	61
8	CCNB1	60
9	AURKA	59
10	NDC80	58

Table S4. Gene pairs with prognostic value by

univariate Cox regression

ID	Hazard Ratio (HR)	Pvalue			
NUSAP1 BIRC5	0.2065	0.0009	SFN F9	5.2265	0.0010
COL15A1 OLFML2B	0.1178	0.0002	SHCBP1 UROC1	4.8166	0.0010
PRC1 UROC1	5.7263	0.0009	RAB3B IGFALS	5.1590	0.0006
HMMR PALM3	6.6523	0.0001	CTHRC1 UROC1	5.8758	0.0008
HMMR UROC1	6.5218	0.0004	SIPA1L2 UROC1	8.2737	0.0008
HMMR XDH	7.3917	0.0000	PRKAA2 PALM3	5.8611	0.0003
ECT2 OIT3	6.0887	0.0002	PRKAA2 FXYD1	5.7363	0.0005
FLVCR1 UROC1	8.2466	0.0002	PRKAA2 AKR1D1	5.7784	0.0002
RFX5 PGLYRP2	6.7409	0.0001	C12orf75 PROZ	6.8740	0.0001
PODXL STK39	0.1834	0.0005	C12orf75 OGDHL	4.9295	0.0008
KPNA2 ATF5	4.7936	0.0010	B3GNT5 IGFALS	5.1922	0.0007
CCNB1 PGLYRP2	5.0821	0.0008	STK39 PALM3	5.2867	0.0009
PBK UROC1	6.1977	0.0005	STK39 AKR1D1	7.5497	0.0001
CENPU IGFALS	8.2198	0.0009	SPP1 ANG	5.5002	0.0005
CCDC34 OIT3	8.7479	0.0006	SPP1 HPD	5.4783	0.0004
CCDC34 PALM3	6.5617	0.0004	SPP1 FABP1	7.0485	0.0000
CCDC34 UROC1	5.6872	0.0010	SPP1 SULT2A1	5.5690	0.0004
CCDC34 CFHR3	5.1804	0.0007	IGFALS LYVE1	0.1926	0.0005
ESM1 AKR1D1	6.3705	0.0005	IGFALS SLC17A3	0.1202	0.0008
TRIP13 XDH	5.2518	0.0005	FAHD2A UROC1	8.1390	0.0009
PRIM1 UROC1	6.9095	0.0007	FAHD2A AKR1D1	5.8473	0.0008
PRIM1 AKR1D1	5.3344	0.0008	LYVE1 GRAMD1C	9.8981	0.0003
CENPK IGFALS	5.3844	0.0004	FOS PGLYRP2	5.1193	0.0006
KIF20A UROC1	6.5218	0.0004	UROC1 SLC19A3	0.1276	0.0001
NDC80 IGFALS	8.5221	0.0007	UROC1 ACSM3	0.1747	0.0009
NDC80 AKR1D1	4.8645	0.0009	UROC1 HBB	0.1203	0.0008
CCNB2 UROC1	6.0553	0.0006	UROC1 CD163	0.1518	0.0009
ZNF623 PRKAA2	0.1928	0.0005	SLC19A3 AKR1D1	5.2189	0.0005
NCAPG PALM3	5.0857	0.0006	SLC17A3 AKR1D1	4.9775	0.0010
NCAPG UROC1	5.4037	0.0008	SLC17A3 SLC22A1	4.8408	0.0009
TOMM40L PGLYRP2	5.4916	0.0007	DEPDC7 PGLYRP2	5.0600	0.0008
OTUD6B OIT3	5.0532	0.0008	GPT2 CYP2C9	5.0250	0.0007
OTUD6B UROC1	7.4423	0.0004	PGLYRP2 SLC41A2	0.1783	0.0004
OTUD6B ANO1	5.4902	0.0007	PGLYRP2 SOCS3	0.2005	0.0008
NUF2 OIT3	5.4716	0.0005	PGLYRP2 CDA	0.1905	0.0006
CDC20 MASP1	6.8162	0.0008	PGLYRP2 HSD17B2	0.1899	0.0006
GMNN SLC22A7	4.8318	0.0009	PGLYRP2 SRD5A1	0.2072	0.0009
FOXM1 UROC1	6.9095	0.0007	DHRS1 SPP2	4.9483	0.0009
CDC6 UROC1	5.8792	0.0008	SLC22A7 SLC13A5	0.1396	0.0001
CEP55 UROC1	5.0170	0.0007			
CDKN2B OIT3	4.8348	0.0009			
SPC25 IGFALS	6.5786	0.0009			
SPC25 AKR1D1	5.0484	0.0006			
OLFML2B UROC1	6.1538	0.0006			

