

Table SI. Differentially expressed genes between serous ovarian tumour and normal tissues.

ENTREZID	SYMBOL	Direction	ENTREZID	SYMBOL	Direction	ENTREZID	SYMBOL	Direction
55600	ITLN1	Down	253152	EPHX4	Up	55859	BEX1	Down
339896	GADL1	Down	100507218	RNF157-AS1	Up	503639	DUXAP10	Up
101928554	LOC101928554	Up	3075	CFH	Down	9055	PRC1	Up
646	BNC1	Down	2690	GHR	Down	132954	PDCL2	Up
4969	OGN	Down	9833	MELK	Up	4212	MEIS2	Down
590	BCHE	Down	6038	RNASE4	Down	81610	FAM83D	Up
10216	PRG4	Down	4674	NAP1L2	Down	94234	FOXQ1	Up
91851	CHRD1	Down	55765	INAVA	Up	3934	LCN2	Up
65055	REEP1	Down	125	ADH1B	Down	3039	HBA1	Down
56849	TCEAL7	Down	316	AOX1	Down	3040	HBA2	Down
84709	MGARP	Down	1825	DSC3	Down	100288637	LOC100288637	Up
4753	NELL2	Down	10332	CLEC4M	Down	89839	ARHGAP11B	Up
6695	SPOCK1	Down	5101	PCDH9	Down	10205	MPZL2	Up
3957	LGALS2	Down	1114	CHGB	Down	11065	UBE2C	Up
139221	MUM1L1	Down	167681	PRSS35	Down	54810	GIPC2	Down
400120	SERTM1	Down	3078	CFHR1	Down	23768	FLRT2	Down
4118	MAL	Up	27253	PCDH17	Down	216	ALDH1A1	Down
3047	HBG1	Down	116372	LYPD1	Up	6252	RTN1	Down
3048	HBG2	Down	7272	TTK	Up	1063	CENPF	Up
140597	TCEAL2	Down	4744	NEFH	Down	2823	GPM6A	Down
100133941	CD24	Up	4222	MEOX1	Up	6422	SFRP1	Down
55808	ST6GALNAC1	Up	4316	MMP7	Up	54845	ESRP1	Up
3294	HSD17B2	Down	701	BUB1B	Up	991	CDC20	Up
366	AQP9	Down	150051	LOC150051	Up	4223	MEOX2	Down
64321	SOX17	Up	389136	VGLL3	Down	152573	SHISA3	Down
653316	FAM153C	Down	4110	MAGEA11	Up	10635	RAD51AP1	Up
55026	TMEM255A	Down	2122	MECOM	Up	6279	S100A8	Down
150622	LINC01105	Down	6943	TCF21	Down	1999	ELF3	Up
344752	AADACL2	Down	192668	CYS1	Down	101060391	SNTG2-AS1	Up
5746	PTH2R	Up	2202	EFEMP1	Down	5653	KLK6	Up
3043	HBB	Down	4675	NAP1L3	Down	285987	DLX6-AS1	Up
1356	CP	Up	4246	SCGB2A1	Up	3832	KIF11	Up
9945	GFPT2	Down	91947	ARRDC4	Down	10647	SCGB1D2	Up
23532	PRAME	Up	10544	PROCR	Down	8412	BCAR3	Down
343450	KCNT2	Down	8685	MARCO	Down	100506621	LINC01279	Down
2731	GLDC	Up	283	ANG	Down	286097	MICU3	Down
6271	S100A1	Up	23414	ZFPM2	Down	101928513	CATIP-AS1	Up
93035	PKHD1L1	Down	5806	PTX3	Up	8707	B3GALT2	Down
2254	FGF9	Down	613266	LOC613266	Up	9077	DIRAS3	Down
93663	ARHGAP18	Down	116159	CYYR1	Up	3625	INHBB	Up
126	ADH1C	Down	440335	SMIM22	Up	5645	PRSS2	Up
8854	ALDH1A2	Down	3606	IL18	Down	9928	KIF14	Up
5918	RARRES1	Down	6860	SYT4	Down	113130	CDCA5	Up
51555	PEX5L	Down	4072	EPCAM	Up	9508	ADAMTS3	Down
79804	HAND2-AS1	Down	56892	TCIM	Up	9787	DLGAP5	Up
6273	S100A2	Up	1164	CKS2	Up	83463	MXD3	Up
2258	FGF13	Up	7103	TSPAN8	Down	11211	FZD10	Up
440712	RHEX	Up	2305	FOXM1	Up	139818	DOCK11	Down
9762	LZTS3	Up	283298	OLFML1	Down	3006	HIST1H1C	Up
6750	SST	Up	9037	SEMA5A	Down	1360	CPB1	Down
643911	CRNDE	Down	100507387	LOC100507387	Down	1365	CLDN3	Up
4692	NDN	Down	202134	FAM153B	Down	5311	PKD2	Down
794	CALB2	Down	5627	PROS1	Down	23767	FLRT3	Down
7980	TFPI2	Down	857	CAV1	Down	102659288	KCCAT333	Up
4332	MNDA	Down	9319	TRIP13	Up	6662	SOX9	Up
24137	KIF4A	Up	11082	ESM1	Up	1382	CRABP2	Up
5803	PTPRZ1	Down	25805	BAMBI	Down	8630	HSD17B6	Down
115749	C12orf56	Up	26022	TMEM98	Down	56992	KIF15	Up
1672	DEFB1	Up	57628	DPP10	Down	7474	WNT5A	Down
284654	RSPO1	Down	26577	PCOLCE2	Down	100526664	LY75-CD302	Down
4886	NPY1R	Down	55165	CEP55	Up	9936	CD302	Down
79589	RNF128	Down	157869	SBSPO1	Down	79977	GRHL2	Up
283383	ADGRD1	Down	375295	LINC01116	Down	130576	LYPD6B	Up
5577	PRKAR2B	Down	64105	CENPK	Up	23566	LPAR3	Up
10112	KIF20A	Up	8622	PDE8B	Down	9737	GPRASP1	Down
1687	GSDME	Down	100506834	GAS1RR	Down	4902	NRTN	Up

Table SII. Functional and pathway enrichment analyses of the genes in modules.

ID	Description	P-value	ENTREZID	Count
GO:0008017	Microtubule binding	<0.001	24137/10112/9055/81610/3832/9928/56992	7
GO:0003777	Microtubule motor activity	<0.001	24137/10112/3832/9928/56992	5
GO:0015631	Tubulin binding	<0.001	24137/10112/9055/81610/3832/9928/56992	7
GO:0003774	Motor activity	<0.001	24137/10112/3832/9928/56992	5
GO:0016887	ATPase activity	<0.001	24137/10112/3832/9928/56992	5
GO:0008574	ATP-dependent microtubule motor activity, plus-end-directed	0.001	3832/9928	2
GO:0019894	Kinesin binding	0.003	9055/81610	2
GO:1990939	ATP-dependent microtubule motor activity	0.003	3832/9928	2
hsa04110	Cell cycle	0.001	7272/701/991	3
hsa04120	Ubiquitin mediated proteolysis	0.016	11065/991	2

GO, Gene Ontology.