

## Identification of ovarian cancer subtype-specific network modules and candidate drivers through an integrative genomics approach

### Supplementary Materials

Supplementary Table S1: 8 modules identified in ovarian cancer subtype 1 network

Module label	Number of genes	Genes
RHOA	16	RHPN1(1) RHPN2(1) SNTB1(1) RHOA*(10) DNM2(1) PLD1(2) DGKQ(1) PKN1(3) MAPK12(2) PTK2(3) IL27RA(1) MAPK11(1) TYK2(2) S1PR2(1) PTP4A3(1) PIK3CA(4)
SMARCA4	11	DNAJB1(1) FGFR3(1) RPL8(2) HSF1(2) CTBP1(2) CCNE1(1) MYC(3) ACTL6A(2) EEF1D(2) PARP10(1) SMARCA4(3)
NDRG1	11	AKAP8L(1) GAK(1) TUBGCP6(1) AP1M2(3) ILF3(1) SLC2A2(1) AP2M1(2) PRKACA(5) NDRG1(6) PSMD2(1) LDLR(1)
DLST	23	ATP5O*(18) ATP5D*(18) ATP5H*(18) ATP5L*(18) IDH3G*(11) NDUFB5(19) ATP5G1*(18) NDUFB9(19) IDH3B*(11) ATP5J*(18) DLST*(13) ATP5B*(18) CYC1(19) ATP5F1*(18) IDH3A*(11) CYP11B2(16) MCCC1(15) ATP5A1*(18) UQCERS1(19) ATP5E*(18) NDUFB7(19) CYP11B1(16) ATP5I(18)
POLR2H	3	CPSF1(1) POLR2H(2) WHSC2(1)
ABCF3	2	ABCF3(1) SLC35E1(1)
LY6H	3	LY6H(2) DVL3(1) PPP1R16A(1)
ZHX1	2	ZHX1(2) ZHX2(1)

\*Linker gene is not altered in ovarian cancer, but is statistically enriched for connections to ovarian cancer altered genes. The number in brackets is the degree of gene.

**Supplementary Table S2: 14 modules identified in ovarian cancer subtype 2 network**

Module label	Number of genes	Genes
PDX1	3	SLC2A2(1) MAFA(1) PDX1(2)
ZHX1	2	ZHX2(1) ZHX1(2)
DLST	14	IDH3B*(12) CYC1(10) MCCC1(5) IDH3A*(12) CYP11B2(6) COX6C(8) NDUFB5(9) CYP11B1(6) NDUFB9(9) UQCRFS1(10) ATP5A1*(10) IDH3G*(12) DLST*(15) UQCRB(10)
RB1	5	MYC(3) ACTL6A(1) RB1(2) PARP10(1) CCNE1(1)
EEF1D	3	EEF1D(2) RPL8(2) RPL30(2)
CPSF1	5	NFKBIB(1) HNRNPL(3) CPSF1(3) POLR2K(3) POLR2H(4)
MAPK12	4	DLG2(2) SNTB1(1) MAPK12(2) FZD4(1)
PRSS23	4	PRSS23(3) FXR1(1) RECQL4(1) MAPK8IP2(1)
TNFSF10	2	TNFSF10(1) TNFRSF11B(1)
NDRG1	8	EIF3H(4) PABPC1(5) AP2M1(1) EIF3K(4) PSMD2(1) EIF4G1(4) EIF3E(4) NDRG1(4)
PIK3CA	5	SDC2(1) MAPK11(1) PTK2(1) PIK3CA(4) ANGPT1(1)
LY6H	3	DVL3(1) PPP1R16A(1) LY6H(2)
POP1	2	POP4(1) POP1(1)
YWHAZ	4	KCNK9(1) PAK4(2) YWHAZ(4) PRKCI(1)

\*Linker gene is not altered in ovarian cancer, but is statistically enriched for connections to ovarian cancer altered genes. The number in brackets is the degree of gene.

**Supplementary Table S3: Pathways associated with ovarian cancer subtype****(A) Subtype 1**

Annotation source	Term	Count	Raw <i>P</i> -value	Benjamini-Hochberg adjusted <i>P</i> -value
PANTHER_PATHWAY	P00005:Angiogenesis	8	0.000349139	0.01902272
PANTHER_PATHWAY	P04398:p53 pathway feedback loops 2	5	0.000610762	0.016660739
PANTHER_PATHWAY	P04393:Ras Pathway	5	0.002483911	0.044571194

Note: Count represents the number of annotated genes in each pathway term.

**(B) Subtype 2**

Annotation source	Term	Count	Raw <i>P</i> -value	Benjamini-Hochberg adjusted <i>P</i> -value
PANTHER_PATHWAY	P04398:p53 pathway feedback loops 2	6	0.0000376	0.002068051
PANTHER_PATHWAY	P00005:Angiogenesis	8	0.000349	0.009557028
PANTHER_PATHWAY	P00056:VEGF signaling pathway	5	0.001459193	0.026416224
PANTHER_PATHWAY	P00010:B cell activation	5	0.002010594	0.02729409

Note: Count represents the number of annotated genes in each pathway term.