

Supporting Information

Systematic identification of characteristic genes of ovarian clear cell carcinoma compared with high-grade serous carcinoma based on RNA-sequencing

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Supplementary Table S1. Clinicopathological characteristics of 21 ovarian cancers and 6 normal tissues

Supplementary Table S2. Sequence of primers for qRT-PCR

Supplementary Table S3. Top 10 pathways enriched in clear cell carcinoma *versus* normal tissues

Supplementary Table S4. Top 10 pathways enriched in normal tissues *versus* clear cell carcinoma

Supplementary Table S5. Top 10 pathways enriched in high-grade serous carcinoma *versus* normal tissues

Supplementary Table S6. Top 10 pathways enriched in normal tissues *versus* high-grade serous carcinoma

Supplementary Table S7. Top 10 pathways enriched in clear cell carcinoma *versus* high-grade serous carcinoma

Supplementary Table S8. Top 10 pathways enriched in high-grade serous carcinoma *versus* clear cell carcinoma

Supplementary Figure S1. Pathway enrichment analysis using PC1-contributing genes in PCA.

Supplementary Figure S2. Gene expression levels of *CPNE8* and *BHLHE41* based on Oncomine.

Supplementary Figure S3. Up- and down-regulated pathway genes by siRNAs targeting *CPNE8* and *BHLHE41*.

Supplementary Table S1. Clinicopathological characteristics of 21 ovarian cancers and 6 normal tissues

Characteristics	Ovarian cancer subtype or normal tissue		
	Clear cell	High-grade serous	Normal tissue*
Total cases	6	15	6
Patient age			
Average	57.5	60.3	53.7
Median	59.5	61.0	53
Range	50-63	40-80	41-66
Menopause			
Premenopause	1	3	3
Menopause	5	12	3
FIGO Stage			
I, II	3	0	
III, IV	3	15	

* Among 6 normal tissues, 5 tissues were obtained from scrape biopsy of the contralateral unaffected ovary in patients with unilateral ovary tumor and one normal tissue was derived from ipsilateral oviduct of benign ovarian tumor (mucinous cyst adenoma).

Supplementary Table S2. Sequence of primers for qRT-PCR

Target Gene	Forward Primer	Reverse Primer
<i>EPHB6</i>	ATCCAGCTCCTTCAGCAACAC	GAGTCACGGGTATCGTCATTCTC
<i>MEIS1</i>	GCACACTGAGTCTTAGCGTTTCTG	CAACTGGGCTTGCGTTATT
<i>FRMD5</i>	GAGCTGTTACATCTCCATCATG	GAACGCACTGGTGTGGAATG
<i>EVPLL</i>	GAGGACTACAGCCGGATTCTGT	CCAGAAATCCCCTTCATGCA
<i>NOL4L</i>	GGCAAGAGCGTAGGTTCAATGT	AGGCCCAATGGACTTTAACAAC
<i>LGR6</i>	TGTGGTAGGTGCGATTGCA	GGGCATCGACTGAGGCTAGA
<i>WT1</i>	ACAGGGTACGAGAGCGATAACC	CCGTGCGTGTGTATTCTGTATTG
<i>HDAC7</i>	CAAGAGCAAGCGAAGTGCTGTA	TTCAGAATCACCTCCGCTAGCT
<i>PRSS1</i>	TTCTGTGTGGGCTTCCTTGAG	CACAGGGCCACCAGAATCA
<i>WT1-AS</i>	GAACCACCGATTGGCAAAGA	CCTCAGTTTCCTTCTCTGTAAAACG
<i>LYPD6</i>	TCTCAGTCACCAAACGCTGTGT	GAGTCTCTGCAGCCAGTGATA
<i>BHLHE41</i>	TAACCGCCTTAACCGAGCAA	TCAGAGATCGCTCCCCATTTC
<i>FBXO8</i>	CCATCTTGTCTACCTGAATGCA	TCGCAAGGTCCTGCCAAA
<i>RAPH1</i>	AGGGCAGGCTGTGTCAAAGT	GTTTGAATGGTGACAGGATGCA
<i>CEP44</i>	GGTGCTCCGCTTGCTAAATT	CTGCTGGGTCTCCCTTTATCAA
<i>HAVCR1P1</i>	CTGGAATAGAGGCGCACGTT	GGGTTCCATTGGTCCAGACA
<i>FUT4</i>	TGAGACGGAGTCTTGCACTGTAG	GAGGTTGCAGTGAGCCAAGAT
<i>KIAA0513</i>	TCTTAGGATGCAGCCGTCTCA	GACGCAGCTGGGAAAAAGTG
<i>CPNE8</i>	CAATATGGACAGCCGCTACAAC	GCGCTCAGCTGGTTCAAGTC
<i>ARSE</i>	AGGGAAGCTCACACACCTGATAC	CGAAAGGGCTGACCAGATGA
<i>CYP2B6</i>	ATGGAAACCGCTGGAAGGT	GCTTTCCCATCCCGAAGTC
<i>OPN5</i>	GTGAAAGCTGGCCTGAAAAGC	GAGTGTAGCTGCTCCAGTCAGAGA
<i>FAM155A</i>	GGCTCAGAAATGGCGACTGT	GTGATCAGAGAGCAGGACTGTGA
<i>RXFP1</i>	GCCTCAGCTCCTGCACTGTAA	TGTTGTCTCCACAGTTGTCCTCAT

Supplementary Table S3. Top 10 pathways enriched in clear cell carcinoma *versus* normal tissues

GO Term	Count	P value	Genes
Cell cycle phase	86	8.67E-33	<i>KIF23, E2F1, KIFC1, KIF22, XRCC2, PRC1, KNTC1, PKMYT1, TTK, AURKA, AURKB, PTTG1, CD2AP, GTSE1, FAM83D, CUL2, ACVR1B, KIF2C, CCNE1, CDCA8, CDKN2A, CDCA2, TUBG1, FANCA, CCNA2, CDCA5, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, KIF15, CCNF, TPX2, MND1, ESPL1, PBK, TACC3, NCAPD3, RAD51, MAD2L1, TIMELESS, SPAG5, FANCD2, ZWINT, BUB1B, USH1C, KPNA2, BLM, NEK2, USP9X, ANLN, CHEK1, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, OVOL1, BUB1, SKA3, SKA1, ERCC6L, TRIP13, EXO1, MKI67, KIF18A, NUF2, BRCA2, CENPF, CDC20, CENPE, NDC80, BIRC5, SIRT7, CDKN3, RAD54L, SMC4, CCNB1, CCNB2, PLK1, CKS2, RAD54B, CIT, DNM2</i>
M phase	76	4.02E-32	<i>KIF23, KIFC1, KIF22, XRCC2, PRC1, KNTC1, PKMYT1, TTK, AURKA, AURKB, PTTG1, CD2AP, FAM83D, KIF2C, CDCA8, CDCA2, TUBG1, FANCA, CCNA2, CDCA5, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF, KIF15, TPX2, MND1, ESPL1, PBK, TACC3, NCAPD3, RAD51, MAD2L1, TIMELESS, SPAG5, FANCD2, ZWINT, BUB1B, KPNA2, NEK2, USP9X, ANLN, CHEK1, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, OVOL1, BUB1, SKA3, SKA1, ERCC6L, TRIP13, EXO1, MKI67, KIF18A, NUF2, BRCA2, CENPF, CDC20, BIRC5, NDC80, CENPE, SIRT7, RAD54L, SMC4, CCNB1, CCNB2, PLK1, CKS2, RAD54B, CIT</i>
Cell cycle	118	9.59E-32	<i>KIFC1, XRCC2, PRC1, DTYMK, KNTC1, PKMYT1, TTK, AURKA, AURKB, PTTG1, CD2AP, CUL2, CDCA8, CDKN2A, CDCA2, TUBG1, CCNA2, CDCA5, ASPM, CDCA3, SGOL1, MND1, ESPL1, TACC3, NCAPD3, ESCO2, PPP1CA, UHRF1, KRT18, MAD2L1, TIMELESS, SPAG5, PSMA5, ZWINT, PSMA3, BLM, PKHD1, NEK2, CHEK1, ANLN, CALR, LLGL2, SPC25, NCAPG2, PSMB3, OVOL1, SKA3, SKA1, ERCC6L, CKAP2, MKI67, NUF2, BRCA2, CDC20, NDC80, RAD54L, BRCA1, PSMC4, PLK1, RAD54B, CHAF1A, KIF23, E2F1, KIF22, E2F7, GTSE1, CDT1, FAM83D, CCNE1, ACVR1B, KIF2C, FANCI, PSMD6, ARHGAP8, FANCA, PSMD8, CDK1, CDC6, KIF11, CCNF, KIF15, TPX2, PBK, CDK7, MCM2, CDK5, RAD51, FANCD2, USH1C, BUB1B, PSME3, KPNA2, USP9X, FOXM1, CEP55, NCAPH, NCAPG, HJURP, BUB1, TRIP13, EXO1, KIF18A, CENPF, BIRC5, CENPE, SIRT7, RACGAP1, CDKN3, GSG2, SMC4, CCNB1, PSMD14, CCNB2, PSMD12, PTP4A1, CKS2, CIT, DNM2</i>
Mitotic cell cycle	80	1.02E-31	<i>KIF23, E2F1, KIFC1, KIF22, PRC1, KNTC1, PKMYT1, TTK, AURKA, AURKB, PTTG1, CD2AP, GTSE1, FAM83D, CUL2, ACVR1B, KIF2C, CCNE1, CDCA8, CDKN2A, CDCA2, PSMD6, CDCA5, CCNA2, ASPM, PSMD8, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF,</i>

			<i>KIF15, TPX2, ESPL1, PBK, NCAPD3, MAD2L1, TIMELESS, SPAG5, PSMA5, ZWINT, PSMA3, BUB1B, USH1C, PSME3, KPNA2, BLM, NEK2, USP9X, ANLN, CHEK1, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, PSMB3, BUB1, SKA3, SKA1, ERCC6L, KIF18A, NUF2, CENPF, CDC20, CENPE, BIRC5, NDC80, SIRT7, CDKN3, SMC4, CCNB1, PSMD14, CCNB2, PSMD12, PSMC4, PLK1, CIT, DNM2</i>
Cell cycle process	98	8.99E-31	<i>E2F1, KIF23, KIF22, KIFC1, XRCC2, PRC1, KNTC1, TTK, PKMYT1, AURKA, AURKB, PTTG1, CD2AP, GTSE1, FAM83D, KIF2C, ACVR1B, CCNE1, CUL2, CDCA8, CDKN2A, CDCA2, TUBG1, PSMD6, FANCA, CDCA5, CCNA2, ASPM, PSMD8, CDCA3, CDC6, CDK1 KIF11, SGOL1, KIF15, CCNF, TPX2, MND1, ESPL1, PBK, TACC3, NCAPD3, RAD51, MAD2L1, TIMELESS, SPAG5, FANCD2, PSMA5, ZWINT, PSMA3, USH1C, BUB1B, PSME3, KPNA2, BLM, NEK2, USP9X, CHEK1, ANLN, CEP55, CALR, SPC25, NCAPH, NCAPG2, NCAPG, PSMB3, OVOL1, BUB1, SKA3, SKA1, ERCC6L, TRIP13, EXO1, MKI67, KIF18A, NUF2, CENPF, BRCA2, CENPE, BIRC5, NDC80, CDC20, SIRT7, RACGAP1, CDKN3, RAD54L, BRCA1, SMC4, CCNB1, PSMD14, CCNB2, PSMC4, PSMD12, PLK1, CKS2, RAD54B, CIT, DNM2</i>
M phase of mitotic cell cycle	57	2.64E-26	<i>KIF23, KIF22, KIFC1, KNTC1, PKMYT1, AURKA, PTTG1, AURKB, CD2AP, FAM83D, KIF2C, CDCA8, CDCA2, CDCA5, CCNA2, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF, KIF15, TPX2, ESPL1, PBK, NCAPD3, MAD2L1, TIMELESS, SPAG5, ZWINT, BUB1B, NEK2, USP9X, ANLN, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, BUB1, SKA3, SKA1, ERCC6L, KIF18A, NUF2, CENPF, CDC20, BIRC5, NDC80, CENPE, SIRT7, SMC4, CCNB1, CCNB2, PLK1, CIT</i>
Nuclear division	56	7.49E-26	<i>KIF23, KIF22, KIFC1, KNTC1, PKMYT1, AURKA, PTTG1, AURKB, CD2AP, FAM83D, KIF2C, CDCA8, CDCA2, CDCA5, CCNA2, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF, KIF15, TPX2, ESPL1, PBK, NCAPD3, MAD2L1, TIMELESS, SPAG5, ZWINT, BUB1B, NEK2, USP9X, ANLN, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, BUB1, SKA3, SKA1, ERCC6L, KIF18A, NUF2, CENPF, BIRC5, NDC80, CENPE, CDC20, SMC4, CCNB1, CCNB2, PLK1, CIT</i>
Mitosis	56	7.49E-26	<i>KIF23, KIF22, KIFC1, KNTC1, PKMYT1, AURKA, PTTG1, AURKB, CD2AP, FAM83D, KIF2C, CDCA8, CDCA2, CDCA5, CCNA2, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF, KIF15, TPX2, ESPL1, PBK, NCAPD3, MAD2L1, TIMELESS, SPAG5, ZWINT, BUB1B, NEK2, USP9X, ANLN, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, BUB1, SKA3, SKA1, ERCC6L, KIF18A, NUF2, CENPF, BIRC5, NDC80, CENPE, CDC20, SMC4, CCNB1, CCNB2, PLK1, CIT</i>

Organelle fission	57	8.75E-26	<i>KIF23, KIF22, KIFC1, KNTC1, PKMYT1, AURKA, PTTG1, AURKB, CD2AP, FAM83D, KIF2C, CDCA8, CDCA2, CDCA5, CCNA2, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF, KIF15, TPX2, ESPL1, PBK, NCAPD3, MAD2L1, TIMELESS, SPAG5, ZWINT, BUB1B, NEK2, USP9X, ANLN, CEP55, SPC25, NCAPH, NCAPG, NCAPG2, BUB1, SKA3, SKA1, ERCC6L, KIF18A, NUF2, CENPF, CDC20, BIRC5, NDC80, CENPE, SMC4, CCNB1, CCNB2, PLK1, BAX, CIT</i>
Cell division	61	4.44E-23	<i>KIF23, KIFC1, PRC1, KNTC1, PTTG1, AURKB, CD2AP, FAM83D, TOP1, CCNE1, CDCA8, CDKN2A, CDCA2, CDCA5, CCNA2, ASPM, CDCA3, CDC6, CDK1, KIF11, SGOL1, CCNF, ESPL1, CDK7, CDK5, NCAPD3, PPP1CA, MAD2L1, TIMELESS, SPAG5, ZWINT, BUB1B, PKHD1, NEK2, USP9X, ANLN, CEP55, LLGL2, SPC25, NCAPH, NCAPG, NCAPG2, BUB1, SKA3, SKA1, ERCC6L, NUF2, CENPF, BRCA2, CDC20, BIRC5, NDC80, CENPE, RACGAP1, SMC4, CCNB1, CCNB2, PLK1, ANXA11, CKS2, CIT</i>

Supplementary Table S4. Top 10 pathways enriched in normal tissues *versus* clear cell carcinoma

GO Term	Count	P value	Genes
Transcription	181	4.42E-16	<p>MEF2C, THRA, TCEAL6, ZNF781, BBX, APOBEC3G, TCEAL7, TCEAL2, TCEAL1, TCEAL4, FOXO6, ZXDA, GTF2IRD2B, TCEAL3, HOXC6, PGR, ZFP92, EPC2, ZNF181, CRY2, CGGBP1, GATA6, ZFP90, PSIP1, ZNF442, ZNF397, ZNF395, RARA, ATOH8, SAP30L, FOXO3B, ZNF575, TWIST2, GABPB2, ZNF43, ZNF641, ZNF594, RCOR3, RXRA, ZHX1, MECP2, GTF2IRD2, HMG20A, ARID1B, TRERF1, PROX1, FOXN3, PRDM8, PTRF, ZNF197, PRDM5, ZNF383, PRDM2, TGFB1I1, ZIM2, CRT3, ZNF519, TSHZ3, EID1, TSHZ2, ZNF430, ZNF132, TADA3, ZNF514, WT1, ZNF512, NR2C2, ARNT, HTATSF1, TFDP2, TEF, ZNF425, ZNF599, MAML3, TCF4, ASF1A, ZNF70, ASXL3, ZNF529, TAF3, SMAD9, KLF12, SMAD5, TAF7, ZNF621, ZNF521, KLF15, MED13L, ZNF835, FOXP1, SALL2, CSRNP3, PHF1, DMTF1, EBF1, ATF7, ZIK1, KLF2, POU6F1, ZNF83, ZBTB33, BACH2, ELF2, ZNF532, EID2B, ZEB2, GLI2, GLI3, KCNIP3, MAX, ZNF738, HSF2, ANG, CCDC101, ZNF540, ZNF496, ZNF493, NR2F1, ZBTB22, SOX10, AR, ELP2, ZNF280D, FOXJ2, POLR1E, SPEN, ZFP28, ZNF333, ZNF688, NRIP2, PURA, ZMIZ1, ASH1L, ZNF711, ZFPM2, JMJD1C, ZNF33B, ZNF483, SUPT3H, ZNF275, NDN, SCML1, NFIX, ZBTB16, PRDM16, CALCOCO1, HIC1, ZNF660, NPAS3, TSPYL2, NR1D1, HAND2, NR1D2, ZNF708, ZNF286A, PER3, BAZ2B, CHD5, MAF, KAT2B, TBX3, AFF3, ZNF25, SNAI2, ZNF358, ZNF662, ATXN3, PHF19, BNC2, ZNF862, SP4, PHF21A, MAMLD1, DENND4A, ZBTB2, PBX1, PAPOLG, NFIC, APBB1, NFIA, NFIB</p>
Regulation of transcription	204	5.25E-14	<p>MEF2C, ZNF781, BBX, GTF2IRD2B, ZFP92, PGR, EPC2, CRY2, ZFP90, ZNF397, ZNF395, RARA, SAP30L,</p>

FOXO3B, TIGD7, TWIST2, ZNF43, ZNF641, RCOR3,
 RXRA, ZHX1, MECP2, HMG20A, PROX1, PRDM8, PTRF,
 PRDM5, ZNF383, PRDM2, TGFB1I1, ZIM2, CRTC3,
 ZNF519, ZNF132, TADA3, AFAP1L2, ZNF514, ZNF512,
 JRK, HTATSF1, MAML3, TCF4, ZNF70, TCF23, BMP4,
 ASXL3, ZNF529, SMAD9, KLF12, ZNF621, SMAD5,
 ZNF521, KLF15, SFMBT2, CSRNP3, DMTF1, ZIK1, KLF2,
 ENG, ZBTB33, BACH2, ELF2, ZNF532, EID2B, ZEB2,
 GLI2, GLI3, KCNIP3, PBXIP1, ZNF738, HSF2, ZNF540,
 ZNF496, ZNF493, CSDC2, NR2F1, ZBTB22, AR, SPEN,
 ZNF333, ZNF688, ASH1L, ZNF33B, ZNF483, ZNF275,
 SCML1, ZBTB16, ZNF660, NR1D1, NR1D2, CSDE1,
 ZNF286A, PER3, BAZ2B, TBX3, ZNF25, AFF3, SNAI2,
 ZNF358, ZNF662, PKNOX2, PHF19, ZNF862, BNC2,
 PHF21A, ZBTB2, PBX1, APBB1, THRA, CCDC85B,
 TCEAL6, TCEAL7, TCEAL2, TCEAL1, TCEAL4, FOXO6,
 ZXDA, TCEAL3, HOXC6, ZNF181, GATA6, CGGBP1,
 PSIP1, ZNF442, ATOH8, ZNF575, GABPB2, ZNF594,
 SATB1, GTF2IRD2, ARID1B, TRERF1, FOXN3, KRBA2,
 ZNF197, EID1, TSHZ3, TSHZ2, ZNF430, NR2C2, WT1,
 ARNT, MEIS2, TEF, TFDP2, ZNF425, ZNF599, ASF1A,
 TAF3, RFX7, TAF7, LMCD1, MED13L, ZNF835, FOXP1,
 SALL2, PHF1, ATF7, EBF1, ABL1, POU6F1, ZNF83,
 PDCC4, MAX, CCDC101, SOX15, SOX10, ELP2, FOXJ2,
 ZNF280D, LDB1, ZFP28, NRIP2, PURA, ZMIZ1, ZNF711,
 ZFPM2, JMJD1C, MAPRE3, SUPT3H, NDN, NFIX,
 HCFC2, PRDM16, CALCOCO1, HIC1, TSC22D3, RGMB,
 TSPYL2, NPAS3, HAND2, ZNF708, CHD5, MAF, KAT2B,
 ATXN3, SP4, MAMLD1, DENND4A, JAK2, ID3, NFIC,
 NFIA, NFIB

DNA binding

179

4.65E-11

MEF2C, THRA, ZNF781, BBX, H1FX, RFXAP, TCEAL1,
 FOXO6, ZXDA, GTF2IRD2B, HOXC6, PGR, ZFP92,
 ZNF181, CGGBP1, GATA6, ZFP90, PSIP1, ZNF442,
 ZNF397, ZNF395, RARA, ATOH8, FOXO3B, ZNF575,

			<p> <i>TIGD7, TWIST2, ZNF43, SATB1, ZNF641, ZNF594, RCOR3, RXRA, ZHX1, MECP2, GTF2IRD2, HMG20A, ARID1B, TRERF1, PROX1, FOXN3, PRDM8, KRBA2, ZNF197, PRDM5, ZNF383, PRDM2, ZIM2, ZNF519, TSHZ3, TSHZ2, ZNF430, ZNF132, TADA3, CXXC4, ZNF514, WT1, ZNF512, NR2C2, ARNT, JRK, RPS27, MEIS2, TFDP2, TEF, ZNF425, ZNF599, TCF4, ZNF70, ZNF529, TAF3, SMAD9, SETDB2, SMG6, KLF12, RFX7, SMAD5, TAF7, ZNF621, ZNF521, KLF15, ZNF835, FOXP1, ATM, SALL2, CSRNP3, PHF1, DMTF1, EBF1, ATF7, ZIK1, KLF2, ABL1, PRKRIR, NYNRIN, POU6F1, ZNF83, ZBTB33, BACH2, ELF2, ZNF532, HP1BP3, ZEB2, GLI2, GLI3, KCNIP3, MAX, ZNF738, HSF2, ANG, SETMAR, ZNF540, SOX15, ZNF496, ZNF493, CSDC2, NR2F1, ZBTB22, SOX10, AR, ELP2, ZNF280D, FOXJ2, POLR1E, LDB1, SPEN, ZFP28, ZNF333, ZNF688, PURA, ASH1L, ZNF711, ZFPM2, ZNF33B, ZNF483, SUPT3H, ZNF275, NDN, SCML1, ABI2, NFIX, ZBTB16, PRDM16, HIC1, ZNF660, ZFP36L2, TSC22D3, NPAS3, TSPYL2, NR1D1, HAND2, NR1D2, SOS1, ZNF708, CSDE1, ZNF286A, BAZ2B, CHD5, MAF, PDS5B, TBX3, AFF3, ZNF25, SNAI2, ZNF358, ZNF662, TRIM21, PKNOX2, BNC2, SP4, ZRANB2, PHF21A, DENND4A, ZBTB2, PBX1, OGG1, NFIC, NFIA, NFIB</i> </p>
Regulation of transcription, DNA-dependent	142	4.35E-10	<p> <i>MEF2C, THRA, TCEAL1, FOXO6, PGR, ZFP92, HOXC6, ZNF181, GATA6, ZFP90, ZNF397, ZNF442, ZNF395, RARA, FOXO3B, TWIST2, ZNF43, ZNF641, SATB1, RXRA, ZHX1, MECP2, HMG20A, ARID1B, PROX1, TRERF1, FOXN3, KRBA2, ZNF197, ZNF383, PRDM2, TGFB1I1, ZIM2, ZNF519, TSHZ3, EID1, ZNF430, TSHZ2, ZNF132, TADA3, AFAP1L2, ZNF514, WT1, NR2C2, ARNT, MEIS2, HTATSF1, TFDP2, TEF, ZNF425, ZNF599, MAML3, TCF4, ASF1A, ZNF70, BMP4, ZNF529, SMAD9, KLF12, RFX7, SMAD5, TAF7, ZNF621, LMCD1, KLF15,</i> </p>

			<p><i>MED13L, FOXP1, SALL2, CSRNP3, DMTF1, EBF1, ATF7, ZIK1, ABL1, ENG, POU6F1, ZNF83, BACH2, ELF2, ZEB2, GLI2, KCNIP3, ZNF738, HSF2, ZNF540, SOX15, ZNF496, ZNF493, NR2F1, CSDC2, SOX10, ELP2, AR, FOXJ2, LDB1, SPEN, ZFP28, ZNF333, ZNF688, NRIP2, PURA, ZMIZ1, ZFPM2, JMJD1C, ZNF33B, ZNF483, MAPRE3, SUPT3H, ZNF275, NDN, HCFC2, NFIX, ZBTB16, PRDM16, CALCOCO1, HIC1, TSC22D3, NPAS3, NR1D1, HAND2, NR1D2, ZNF708, CSDE1, ZNF286A, PER3, MAF, KAT2B, TBX3, ZNF25, SNAI2, ZNF662, PKNOX2, ZNF862, SP4, PHF21A, DENND4A, PBX1, ID3, NFIC, APBB1, NFIA, NFIB</i></p>
Regulation of RNA metabolic process	144	5.52E-10	<p><i>MEF2C, THRA, TCEAL1, FOXO6, PGR, ZFP92, HOXC6, ZNF181, GATA6, ZFP90, ZNF397, ZNF442, ZNF395, RARA, FOXO3B, TWIST2, ZNF43, ZNF641, SATB1, RXRA, ZHX1, MECP2, HMG20A, ARID1B, PROX1, TRERF1, FOXN3, KRBA2, CELF6, ZNF197, ZNF383, PRDM2, TGFB1I1, ZIM2, ZNF519, TSHZ3, EID1, ZNF430, TSHZ2, ZNF132, TADA3, AFAP1L2, ZNF514, WT1, NR2C2, ARNT, MEIS2, HTATSF1, TFDP2, TEF, ZNF425, ZNF599, MAML3, TCF4, ASF1A, ZNF70, BMP4, ZNF529, SMAD9, KLF12, RFX7, SMAD5, TAF7, ZNF621, LMCD1, KLF15, MED13L, FOXP1, SALL2, CSRNP3, DMTF1, EBF1, ATF7, ZIK1, ABL1, ENG, POU6F1, ZNF83, BACH2, ELF2, ZEB2, GLI2, KCNIP3, ZNF738, HSF2, ZNF540, SOX15, ZNF496, ZNF493, NR2F1, CSDC2, SOX10, ELP2, AR, FOXJ2, LDB1, SPEN, ZFP28, ZNF333, ZNF688, NRIP2, PURA, ZMIZ1, ZFPM2, JMJD1C, ZNF33B, ZNF483, MAPRE3, SUPT3H, ZNF275, NDN, HCFC2, NFIX, ZBTB16, PRDM16, CALCOCO1, HIC1, ZFP36L2, TSC22D3, NPAS3, NR1D1, HAND2, NR1D2, ZNF708, CSDE1, ZNF286A, PER3, MAF, KAT2B, TBX3, ZNF25, SNAI2, ZNF662, PKNOX2, ZNF862, SP4, PHF21A, DENND4A, PBX1, ID3, NFIC, APBB1, NFIA,</i></p>

NFIB			
Metal ion binding	271	2.05E-09	<p> <i>ADCY2, LTBP3, ATP1B2, SCN3B, LTBP4, SNCA, ZNF781, SYT9, GTF2IRD2B, FAH, ZFP92, PGR, ZFP90, CCBE1, ZNF397, RARA, ZNF395, SCD5, CDH23, ZNF43, MATN2, NUDT16, ZNF641, CGRRF1, RXRA, ZHX1, F8, NUDT10, NUDT11, LPCAT2, PRDM8, PGM5, PRDM5, ZNF383, RYR2, NEK9, PRDM2, TGFB1I1, ADAMTS3, ADD1, ZIM2, ZNF519, ZNF132, NEK1, CACNB2, CACNB3, ZNF514, ZNF512, RPS27, CDADC1, FAHD2B, ZNF70, TRPC1, ASXL3, ZC3H13, ZNF529, CYP46A1, KLF12, PCDH10, ZNF621, SMYD4, ZNF521, KLF15, PCDH19, PRPSAP2, PCDH18, KCNJ8, HEBP1, SYTL4, ZIK1, HEPH, KLF2, PRKRIR, ZBTB33, ZCCHC24, CACHD1, PCDHA3, ZNF532, SOBP, ZEB2, GLI2, KCNIP2, GLI3, VILL, KCNIP3, SLC23A2, ZNF540, ZNF496, MBLAC2, ZNF493, NR2F1, ZBTB22, AR, PCDH11X, PCDHB4, ZNF333, ZNF688, PJA2, ZDHHHC15, PJA1, NAALAD2, ZDHHHC17, MAST2, ASH1L, EGFL8, ZNF33B, ZNF483, PLA2G5, ZNF275, SCAPER, PCDHB15, ZBTB16, DCHS1, PLCL2, ZNF660, CYB561D2, ZFP36L2, PLCL1, NR1D1, MORC3, DGKD, NR1D2, FAT4, HAAO, SLC4A8, ZNF286A, BAZ2B, RASA4, DTNA, CCNB1IP1, RBM20, MEX3B, ZNF25, PDZRN3, SNAI2, TRIM23, ZNF662, ZNF358, TRIM21, LRP1, PHF19, PLSCR4, FYN, BNC2, SVIL, ZNF862, PHF21A, CHN2, ZBTB2, LRP4, THRA, ZAK, APOBEC3G, TRIM52, ZXDA, ZNF181, GATA6, RNF38, ZNF442, ZNF575, RNF146, NMNAT3, ZNF594, PCDHGA11, GTF2IRD2, CDO1, TRERF1, PLCE1, KCNT2, RASGRF2, ZNF197, MFAP4, DST, SLC40A1, PRPS1, ME1, TSHZ3, TSHZ2, ZNF430, CXXC4, EXTL2, ZC3H6, NR2C2, WT1, TRIM68, TTYH2, SRR, ZNF425, ZNF599, UNKL, CACNA2D1, SETDB2, TAF3, SMG6, SYT11, LMCD1, ZNF835, TRIM61, FOXP1, EPS15, SALL2, PHF2, PHF1, ATF7, EBF1, MTR, ANTXR2, RHBDL3, ABL1,</i> </p>

			<p>ZNF83, CLSTN2, PCDHGA8, ZCWPW2, PCDHGA7, ZCWPW1, PCDHGA6, PCDHGA5, PCDHGA3, PCDHGA2, PCDHGA1, TRIM4, OSR2, ANG, SETMAR, ATP8B2, ANO6, CDK15, ZNF280D, WBSCR17, PCDH9, PCDHGB6, PFKM, NRXN1, ZFP28, PCDHGB2, PCDHGB5, PCDHGB4, ZMIZ1, ZNF711, ZFPM2, JMJD1C, PRNP, PROS1, CYP2U1, LOC375196, FKBP7, PCDHGC5, PCDHGC4, PCDHGC3, PRDM16, NAALADL1, HIC1, CPZ, ANXA6, SMOC2, AGAP11, ZNF708, ZC3H12B, ZNF609, PLCD1, EHD2, CHD5, HRC, WDFY2, B3GALT2, CYP21A2, DTX3, FAM188A, MAN1C1, SP4, ZRANB2, BMPR1B, ATP8A1</p>
Ion binding	276	2.35E-09	<p>ADCY2, LTBP3, ATP1B2, SCN3B, LTBP4, SNCA, ZNF781, SYT9, GTF2IRD2B, FAH, ZFP92, PGR, ZFP90, CCBE1, ZNF397, RARA, ZNF395, SCD5, CDH23, ZNF43, MATN2, NUDT16, ZNF641, CGRRF1, RXRA, ZHX1, F8, NUDT10, NUDT11, LPCAT2, PRDM8, PGM5, PRDM5, RYR2, ZNF383, NEK9, PRDM2, TGFB1I1, ADAMTS3, ADD1, ZIM2, ZNF519, ZNF132, NEK1, CACNB2, CACNB3, ZNF514, ZNF512, RPS27, CDADC1, FAHD2B, ZNF70, TRPC1, ASXL3, ZC3H13, ZNF529, CYP46A1, KLF12, PCDH10, ZNF621, SMYD4, ZNF521, KLF15, PCDH19, PRPSAP2, PCDH18, KCNJ8, HEBP1, SYTL4, ZIK1, HEPH, KLF2, CLCN6, PRKRIR, ZBTB33, ZCCHC24, CACHD1, PCDHA3, ZNF532, SOBP, ZEB2, GLI2, KCNIP2, GLI3, VILL, KCNIP3, SLC23A2, ZNF540, ZNF496, MBLAC2, ZNF493, NR2F1, ZBTB22, AR, PCDH11X, PCDHB4, CLIC2, ZNF333, ZNF688, PJA2, ZDHHC15, PJA1, NAALAD2, ZDHHC17, MAST2, ASH1L, GLRA4, EGFL8, ZNF33B, ZNF483, PLA2G5, ZNF275, SCAPER, PCDHB15, ZBTB16, DCHS1, PLCL2, ZNF660, CYB561D2, ZFP36L2, PLCL1, NR1D1, MORC3, DGKD, NR1D2, FAT4, HAAO, SLC4A8, ZNF286A, BAZ2B, RASA4, DTNA, CCNB1IP1, RBM20, MEX3B, ZNF25, PDZRN3, SNAI2,</p>

			<p> <i>TRIM23, ZNF662, ZNF358, TRIM21, LRP1, PHF19, PLSCR4, FYN, BNC2, SVIL, ZNF862, PHF21A, CHN2, ZBTB2, LRP4, THRA, ZAK, APOBEC3G, TRIM52, ZXDA, ZNF181, GATA6, RNF38, ZNF442, ZNF575, RNF146, NMNAT3, ZNF594, PCDHGA11, GTF2IRD2, CDO1, TRERF1, PLCE1, KCNT2, RASGRF2, ZNF197, MFAP4, DST, SLC40A1, PRPS1, ME1, FXYP1, TSHZ3, TSHZ2, ZNF430, CXXC4, HEXDC, EXTL2, ZC3H6, NR2C2, WT1, TRIM68, TTYH2, SRR, ZNF425, ZNF599, UNKL, CACNA2D1, SETDB2, TAF3, SMG6, SYT11, LMCD1, ZNF835, TRIM61, FOXP1, EPS15, SALL2, PHF2, PHF1, ATF7, EBF1, MTR, ANTXR2, RHBDL3, ABL1, ZNF83, CLSTN2, PCDHGA8, ZCWPW2, PCDHGA7, ZCWPW1, PCDHGA6, PCDHGA5, PCDHGA3, PCDHGA2, PCDHGA1, TRIM4, OSR2, ANG, SETMAR, ATP8B2, ANO6, CDK15, ZNF280D, WBSCR17, PCDH9, PCDHGB6, PFKM, NRXN1, ZFP28, PCDHGB2, PCDHGB5, PCDHGB4, ZMIZ1, ZNF711, ZFPM2, JMJD1C, PRNP, PROS1, CYP2U1, LOC375196, FKBP7, PCDHGC5, PCDHGC4, PCDHGC3, PRDM16, NAALADL1, HIC1, CPZ, ANXA6, SMOC2, AGAP11, ZNF708, ZC3H12B, ZNF609, PLCD1, EHD2, CHD5, HRC, WDFY2, B3GALT2, CYP21A2, DTX3, FAM188A, MAN1C1, SP4, ZRANB2, BMPR1B, ATP8A1</i> </p>
Homophilic cell adhesion	26	2.79E-09	<p> <i>CLSTN2, PCDHA3, PCDHGA8, PCDHB15, PCDHGC5, PCDHGA7, PCDHGC4, PCDHGA6, PCDHGA5, PCDHGC3, PCDHGA3, PCDHGA2, DCHS1, PCDHGA1, FAT4, ROBO1, CDH23, PCDHGA11, PCDH11X, PCDHB4, PCDH10, PCDH9, PCDHGB6, PCDHGB2, PCDH19, PCDHGB5, PCDH18, PCDHGB4</i> </p>
Cation binding	272	3.50E-09	<p> <i>ADCY2, LTBP3, ATP1B2, SCN3B, LTBP4, SNCA, ZNF781, SYT9, GTF2IRD2B, FAH, ZFP92, PGR, ZFP90, CCBE1, ZNF397, RARA, ZNF395, SCD5, CDH23, ZNF43, MATN2, NUDT16, ZNF641, CGRRF1, RXRA, ZHX1, F8,</i> </p>

NUDT10, NUDT11, LPCAT2, PRDM8, PGM5, PRDM5,
ZNF383, RYR2, NEK9, PRDM2, TGFB1I1, ADAMTS3,
ADD1, ZIM2, ZNF519, ZNF132, NEK1, CACNB2,
CACNB3, ZNF514, ZNF512, RPS27, CDADC1, FAHD2B,
ZNF70, TRPC1, ASXL3, ZC3H13, ZNF529, CYP46A1,
KLF12, PCDH10, ZNF621, SMYD4, ZNF521, KLF15,
PCDH19, PRPSAP2, PCDH18, KCNJ8, HEBP1, SYTL4,
ZIK1, HEPH, KLF2, PRKRIR, ZBTB33, ZCCHC24,
CACHD1, PCDHA3, ZNF532, SOBP, ZEB2, GLI2, KCNIP2,
GLI3, VILL, KCNIP3, SLC23A2, ZNF540, ZNF496,
MBLAC2, ZNF493, NR2F1, ZBTB22, AR, PCDH11X,
PCDHB4, ZNF333, ZNF688, PJA2, ZDHHC15, PJA1,
NAALAD2, ZDHHC17, MAST2, ASH1L, EGFL8, ZNF33B,
ZNF483, PLA2G5, ZNF275, SCAPER, PCDHB15, ZBTB16,
DCHS1, PLCL2, ZNF660, CYB561D2, ZFP36L2, PLCL1,
NR1D1, MORC3, DGKD, NR1D2, FAT4, HAAO, SLC4A8,
ZNF286A, BAZ2B, RASA4, DTNA, CCNB1IP1, RBM20,
MEX3B, ZNF25, PDZRN3, SNAI2, TRIM23, ZNF662,
ZNF358, TRIM21, LRP1, PHF19, PLSCR4, FYN, BNC2,
SVIL, ZNF862, PHF21A, CHN2, ZBTB2, LRP4, THRA,
ZAK, APOBEC3G, TRIM52, ZXDA, ZNF181, GATA6,
RNF38, ZNF442, ZNF575, RNF146, NMNAT3, ZNF594,
PCDHGA11, GTF2IRD2, CDO1, TRERF1, PLCE1, KCNT2,
RASGRF2, ZNF197, MFAP4, DST, SLC40A1, PRPS1,
ME1, TSHZ3, TSHZ2, ZNF430, CXXC4, HEXDC, EXTL2,
ZC3H6, NR2C2, WT1, TRIM68, TTYH2, SRR, ZNF425,
ZNF599, UNKL, CACNA2D1, SETDB2, TAF3, SMG6,
SYT11, LMCD1, ZNF835, TRIM61, FOXP1, EPS15,
SALL2, PHF2, PHF1, ATF7, EBF1, MTR, ANTXR2,
RHBDL3, ABL1, ZNF83, CLSTN2, PCDHGA8, ZCWPW2,
PCDHGA7, ZCWPW1, PCDHGA6, PCDHGA5, PCDHGA3,
PCDHGA2, PCDHGA1, TRIM4, OSR2, ANG, SETMAR,
ATP8B2, ANO6, CDK15, ZNF280D, WBSCR17, PCDH9,
PCDHGB6, PFKM, NRXN1, ZFP28, PCDHGB2,

			<i>PCDHGB5, PCDHGB4, ZMIZ1, ZNF711, ZFPM2, JMJD1C, PRNP, PROS1, CYP2U1, LOC375196, FKBP7, PCDHGC5, PCDHGC4, PCDHGC3, PRDM16, NAALADL1, HIC1, CPZ, ANXA6, SMOC2, AGAP11, ZNF708, ZC3H12B, ZNF609, PLCD1, EHD2, CHD5, HRC, WDFY2, B3GALT2, CYP21A2, DTX3, FAM188A, MAN1C1, SP4, ZNRANB2, BMPR1B, ATP8A1</i>
Transcription factor activity	85	1.30E-07	<i>MEF2C, POU6F1, ZNF83, BACH2, ELF2, THRA, ZEB2, GLI2, RFXAP, GLI3, TCEAL1, FOXO6, ZXDA, HOXC6, PGR, MAX, HSF2, GATA6, ZNF397, SOX15, RARA, FOXO3B, ZNF496, TWIST2, NR2F1, SOX10, SATB1, AR, FOXJ2, RXRA, ZHX1, HMG20A, SPEN, PROX1, TRERF1, FOXN3, PURA, ZNF197, PRDM2, ZNF33B, ZNF483, ZIM2, TSHZ3, TSHZ2, ZNF132, TADA3, SCML1, NFIX, ZBTB16, NR2C2, WT1, ARNT, HIC1, ZFP36L2, TSC22D3, MEIS2, NR1D1, NR1D2, HAND2, TFDP2, TEF, TCF4, ZNF70, MAF, SMAD9, TBX3, KLF12, SMAD5, TAF7, KLF15, FOXP1, PKNOX2, SALL2, CSRNP3, PHF1, DMTF1, ATF7, SP4, EBF1, ZNRANB2, PBX1, KLF2, NFIC, NFIA, NFIB</i>

Supplementary Table S5. Top 10 pathways enriched in high-grade serous carcinoma *versus* normal tissues

GO Term	Count	P value	Genes
M phase	50	1.10E-46	<i>KIF23, KIF22, KIFC1, XRCC2, PRC1, NEK2, TTK, AURKA, PTTG1, AURKB, CEP55, FAM83D, KIF2C, SPC25, NCAPH, CDCA8, DDX11, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, TRIP13, CDK1, KIF11, MKI67, SGOL1, KIF15, CCNF, TPX2, NUF2, KIF18A, CDC20, BIRC5, NDC80, ESPL1, TACC3, RAD54L, NCAPD2, RAD51, MAD2L1, CCNB2, PLK1, CKS2, BUB1B, CIT, KPNA2</i>
Cell cycle phase	52	2.08E-44	<i>KIF23, KIFC1, KIF22, XRCC2, PRC1, TTK, AURKA, AURKB, PTTG1, GTSE1, FAM83D, KIF2C, CDCA8, DDX11, CDCA5, ASPM, CDCA3, CDK1, KIF11, CCNF, KIF15, SGOL1, TPX2, ESPL1, TACC3, RAD51, NCAPD2, MAD2L1, BUB1B, KPNA2, BLM, NEK2, CEP55, SPC25, NCAPH, NCAPG, BUB1, SKA3, SKA1, TRIP13, ERCC6L, MKI67, KIF18A, NUF2, NDC80, BIRC5, CDC20, RAD54L, CCNB2, PLK1, CKS2, CIT</i>
Cell cycle	63	1.84E-43	<i>KIF23, KIF22, KIFC1, E2F3, XRCC2, PRC1, E2F7, TTK, AURKA, PTTG1, AURKB, GTSE1, FAM83D, KIF2C, CDCA8, DDX11, FANCI, CDCA5, ASPM, CDCA3, CDK1, KIF11, SGOL1, CCNF, KIF15, TPX2, ESPL1, TACC3, NCAPD2, RAD51, KRT18, MAD2L1, BUB1B, KPNA2, CKS1B, BLM, NEK2, FOXM1, CEP55, LLGL2, SPC25, NCAPH, NCAPG, HJURP, BUB1, SKA3, SKA1, ERCC6L, TRIP13, PARD6B, MKI67, PSRC1, KIF18A, NUF2, CDC20, BIRC5, NDC80, RACGAP1, RAD54L, CCNB2, PLK1, CKS2, CIT</i>
Mitosis	40	8.58E-40	<i>KIF23, KIF22, KIFC1, NEK2, AURKA, PTTG1, CEP55, AURKB, FAM83D, KIF2C, SPC25, NCAPH, CDCA8, DDX11, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, CDK1, KIF11, SGOL1, KIF15, CCNF, TPX2, NUF2, KIF18A, CDC20, BIRC5, NDC80, ESPL1,</i>

			<i>NCAPD2, MAD2L1, CCNB2, PLK1, BUB1B, CIT</i>
Nuclear division	40	8.58E-40	<i>KIF23, KIF22, KIFC1, NEK2, AURKA, PTTG1, CEP55, AURKB, FAM83D, KIF2C, SPC25, NCAPH, CDCA8, DDX11, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, CDK1, KIF11, SGOL1, KIF15, CCNF, TPX2, NUF2, KIF18A, CDC20, BIRC5, NDC80, ESPL1, NCAPD2, MAD2L1, CCNB2, PLK1, BUB1B, CIT</i>
M phase of mitotic cell cycle	40	1.81E-39	<i>KIF23, KIF22, KIFC1, NEK2, AURKA, PTTG1, CEP55, AURKB, FAM83D, KIF2C, SPC25, NCAPH, CDCA8, DDX11, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, CDK1, KIF11, SGOL1, KIF15, CCNF, TPX2, NUF2, KIF18A, CDC20, BIRC5, NDC80, ESPL1, NCAPD2, MAD2L1, CCNB2, PLK1, BUB1B, CIT</i>
Organelle fission	40	4.49E-39	<i>KIF23, KIF22, KIFC1, NEK2, AURKA, PTTG1, CEP55, AURKB, FAM83D, KIF2C, SPC25, NCAPH, CDCA8, DDX11, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, CDK1, KIF11, SGOL1, KIF15, CCNF, TPX2, NUF2, KIF18A, CDC20, BIRC5, NDC80, ESPL1, NCAPD2, MAD2L1, CCNB2, PLK1, BUB1B, CIT</i>
Cell cycle process	53	9.36E-39	<i>KIF23, KIFC1, KIF22, XRCC2, PRC1, TTK, AURKA, AURKB, PTTG1, GTSE1, FAM83D, KIF2C, CDCA8, DDX11, CDCA5, ASPM, CDCA3, CDK1, KIF11, CCNF, KIF15, SGOL1, TPX2, ESPL1, TACC3, RAD51, NCAPD2, MAD2L1, BUB1B, KPNA2, BLM, NEK2, CEP55, SPC25, NCAPH, NCAPG, BUB1, SKA3, SKA1, TRIP13, ERCC6L, MKI67, KIF18A, NUF2, NDC80, BIRC5, CDC20, RACGAP1, RAD54L, CCNB2, PLK1, CKS2, CIT</i>
Mitotic cell cycle	45	3.16E-37	<i>KIF23, KIF22, KIFC1, PRC1, BLM, NEK2, TTK, AURKA, PTTG1, CEP55, AURKB, GTSE1, FAM83D, KIF2C, SPC25, NCAPH, CDCA8, DDX11, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, CDK1, KIF11, SGOL1, KIF15, CCNF, TPX2, NUF2, KIF18A, CDC20, BIRC5, NDC80, ESPL1, NCAPD2, MAD2L1,</i>

			<i>CCNB2, PLK1, BUB1B, CIT, KPNA2</i>
Cell division	39	2.87E-33	<i>KIF23, CKS1B, KIFC1, PRC1, NEK2, PTTG1, CEP55, AURKB, LLGL2, FAM83D, SPC25, NCAPH, CDCA8, NCAPG, BUB1, SKA3, SKA1, CDCA5, ASPM, ERCC6L, CDCA3, PARD6B, CDK1, KIF11, SGOL1, CCNF, NUF2, CDC20, BIRC5, NDC80, ESPL1, RACGAP1, NCAPD2, MAD2L1, CCNB2, PLK1, CKS2, BUB1B, CIT</i>

Supplementary Table S6. Top 10 pathways enriched in normal tissues *versus* high-grade serous carcinoma

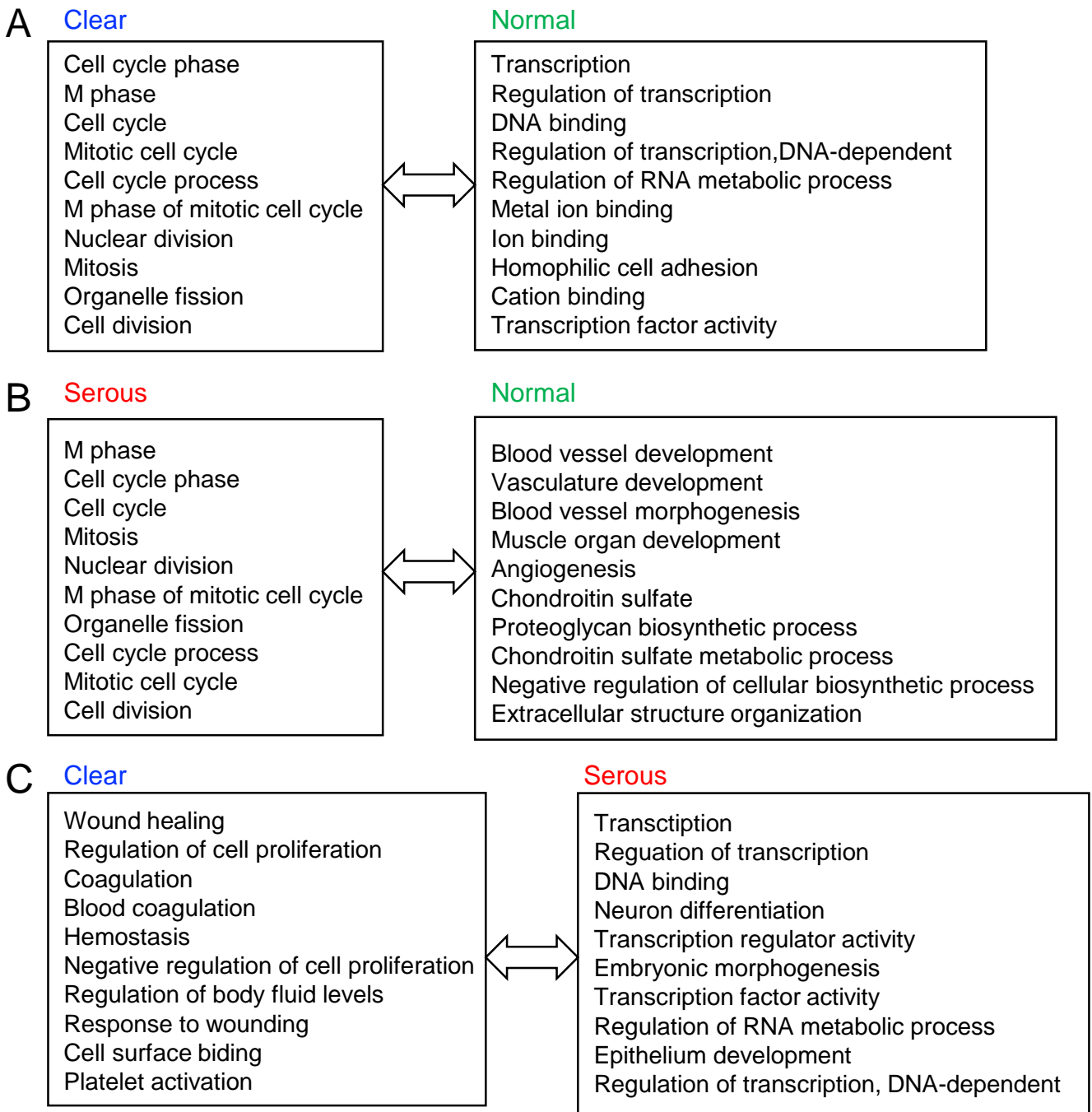
GO Term	Count	P value	Genes
Blood vessel development	10	4.25E-05	<i>RECK, CAV1, ANG, HAND2, LEPR, CCBE1, RHOB, NR2F2,</i>
Vasculature development	10	5.13E-05	<i>RECK, CAV1, ANG, HAND2, LEPR, CCBE1, RHOB, NR2F2,</i>
Blood vessel morphogenesis	9	9.29E-05	<i>CAV1, ANG, HAND2, LEPR, CCBE1, RHOB, NR2F2, FGF2,</i>
Muscle organ development	9	9.29E-05	<i>LAMA2, POU6F1, CAV1, SVIL, MRAS, CACNA1H, CACNB</i>
Angiogenesis	7	5.10E-04	<i>ANG, HAND2, LEPR, CCBE1, RHOB, FGF2, ENG</i>
Chondroitin sulfate biosynthetic process	3	1.25E-03	<i>CSGALNACT1, CHST7, CHST3</i>
Chondroitin sulfate proteoglycan biosynthetic process	3	2.42E-03	<i>CSGALNACT1, CHST7, CHST3</i>
Chondroitin sulfate metabolic process	3	3.95E-03	<i>CSGALNACT1, CHST7, CHST3</i>
Negative regulation of cellular biosynthetic process	11	4.72E-03	<i>CAV1, TSPYL2, ANG, PPARG, ZEB2, NR2F2, FGF2, ENG,</i>
Extracellular structure organization	6	5.06E-03	<i>CSGALNACT1, RECK, PDGFRA, CACNB2, ECM2, ENG</i>

Supplementary Table S7. Top 10 pathways enriched in clear cell carcinoma *versus* high-grade serous carcinoma

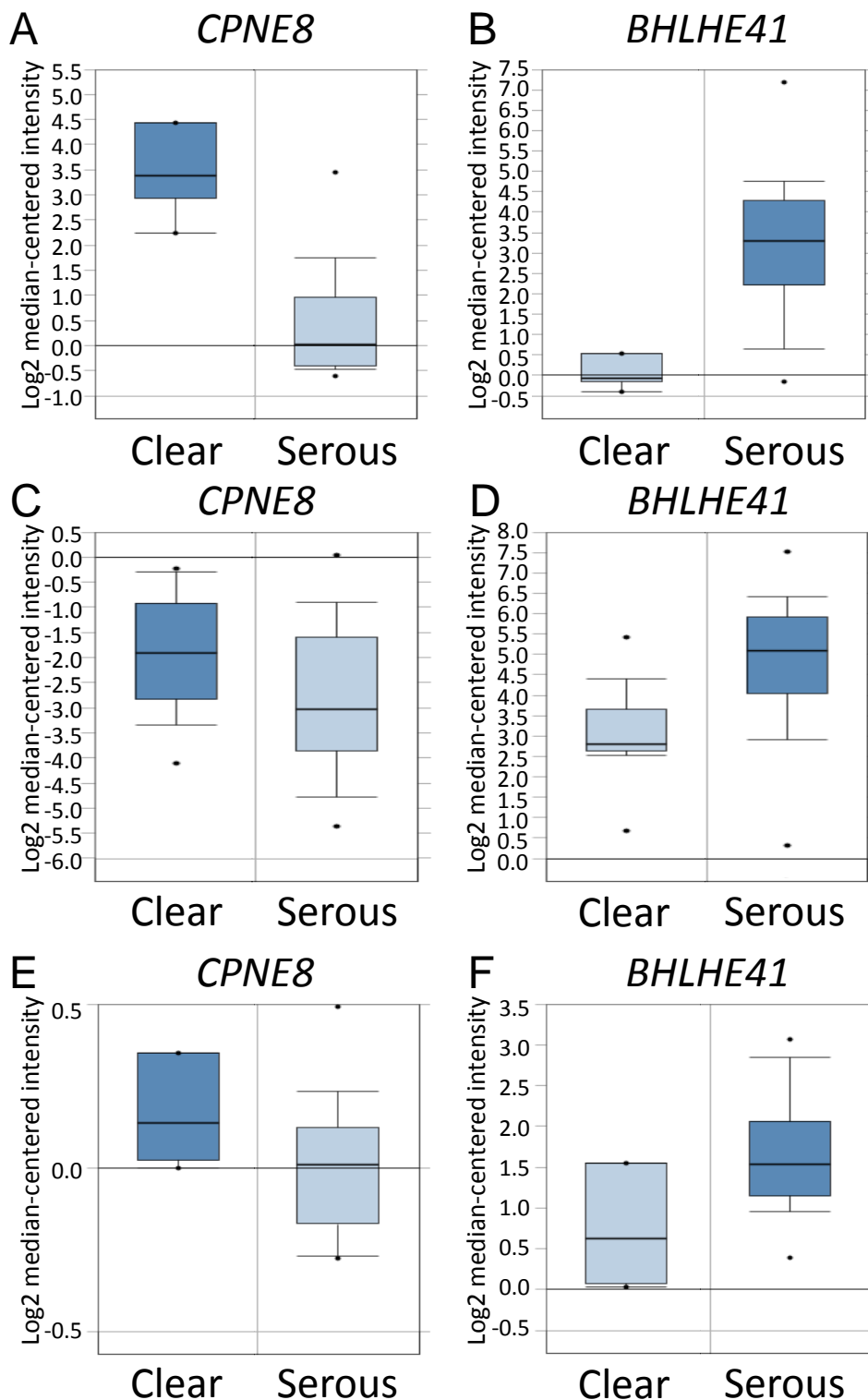
GO Term	Count	P value	Genes
Wound healing	14	1.51E-06	<i>KNG1, B4GALT1, GNA13, NOG, ITGA2, FGG, HIF1A, HNF4A, FGA, FGB, F3, F2, IGFBP1, PAPSS2</i>
Regulation of cell proliferation	29	1.53E-06	<i>RBP4, NOG, FGFR4, IGFBP7, MITF, PNP, ITCH, ASPH, LAMB1, THPO, B4GALT1, HYAL1, COL4A3, TESC, HCLS1, ITGA2, GJB6, PTHLH, CDKN1A, CTH, HIF1A, HNF4A, COG8, SSTR1, DLX5, F3, SCIN, LAMC1, TOB2</i>
Coagulation	10	8.10E-06	<i>GNA13, KNG1, FGG, HNF4A, FGA, FGB, F3, F2, ITGA2, PAPSS2</i>
Blood coagulation	10	8.10E-06	<i>GNA13, KNG1, FGG, HNF4A, FGA, FGB, F3, F2, ITGA2, PAPSS2</i>
Hemostasis	10	1.29E-05	<i>GNA13, KNG1, FGG, HNF4A, FGA, FGB, F3, F2, ITGA2, PAPSS2</i>
Negative regulation of cell proliferation	17	2.43E-05	<i>B4GALT1, RBP4, COL4A3, HYAL1, TESC, NOG, IGFBP7, GJB6, PTHLH, CTH, CDKN1A, HNF4A, SSTR1, SCIN, ASPH, ITCH, TOB2</i>
Regulation of body fluid levels	10	1.06E-04	<i>GNA13, KNG1, FGG, HNF4A, FGA, FGB, F3, F2, ITGA2, PAPSS2</i>
Response to wounding	19	2.34E-04	<i>B4GALT1, GNA13, KNG1, NOG, ITGA2, FGG, HIF1A, FGA, HNF4A, FGB, F3, F2, MGLL, RTN4RL2, LBP, IGFBP1, ITCH, PAPSS2, BLNK</i>
Cell surface binding	5	6.47E-04	<i>FGG, FGA, FGB, F3, LBP</i>
Platelet activation	5	7.98E-04	<i>GNA13, FGG, FGA, FGB, F2</i>

Supplementary Table S8. Top 10 pathways enriched in high-grade serous carcinoma *versus* clear cell carcinoma

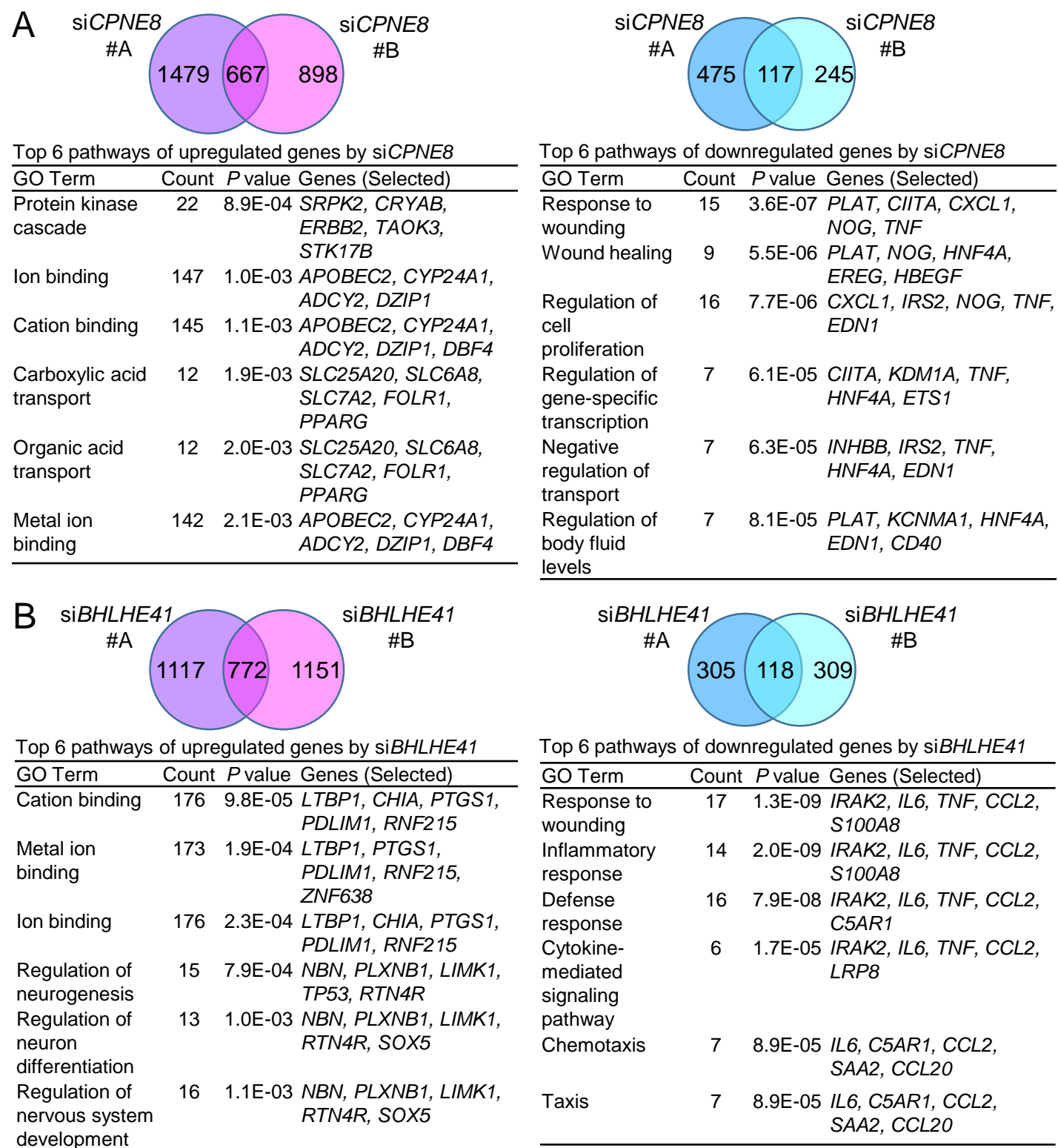
GO Term	Count	P value	Genes
Transcription	27	9.17E-04	<i>ZNF519, ZNF827, CTCFL, NFIX, MEIS1, TCF7L2, FOXO6, WT1, ZNF512, ZFP92, NPAS3, PPP1R1B, PER3, BHLHE41, BAZ2B, PHOX2A, SSBP3, KLF12, ESR1, SPEN, ZNF334, EYA2, CDCA7L, PBX1, ZNF99, HDAC7, NFIB</i>
Regulation of transcription	31	1.05E-03	<i>ZNF519, CRABP2, ZNF827, CTCFL, NFIX, MEIS1, TCF7L2, WT1, ZNF512, FOXO6, ZFP92, NPAS3, PER3, BAZ2B, BHLHE41, PHOX2A, SSBP3, KLF12, EMX2, ESR1, SPEN, ABCG4, ZNF334, PRKCQ, EYA2, CDCA7L, PBX1, LRCH4, ZNF99, HDAC7, NFIB</i>
DNA binding	26	1.83E-03	<i>ZNF519, ZNF827, ABI2, CTCFL, NFIX, MEIS1, TCF7L2, WT1, ZNF512, FOXO6, ZFP92, NPAS3, BHLHE41, BAZ2B, PHOX2A, SSBP3, KLF12, CBL, EMX2, ESR1, SPEN, ZNF334, H2AFY2, PBX1, ZNF99, NFIB</i>
Neuron differentiation	10	2.50E-03	<i>PHOX2A, PRKCQ, GPC2, RET, DRD2, CLIC5, EMX2, NTNG1, ABI2, IGSF9</i>
Transcription regulator activity	19	3.17E-03	<i>PHOX2A, CUTA, SSBP3, KLF12, CBL, EMX2, ESR1, CTCFL, NFIX, SPEN, MEIS1, TCF7L2, FOXO6, WT1, NPAS3, PBX1, LRCH4, BHLHE41, NFIB</i>
Embryonic morphogenesis	8	4.34E-03	<i>RET, EYA2, CLIC5, VANGL2, CRABP2, AMOT, PBX1, TCF7L2</i>
Transcription factor activity	14	5.08E-03	<i>PHOX2A, KLF12, EMX2, CBL, ESR1, NFIX, SPEN, TCF7L2, MEIS1, FOXO6, WT1, PBX1, BHLHE41, NFIB</i>
Regulation of RNA metabolic process	21	1.45E-02	<i>PHOX2A, ZNF519, KLF12, CRABP2, EMX2, ESR1, NFIX, SPEN, MEIS1, TCF7L2, FOXO6, WT1, ZNF334, ZFP92, NPAS3, RBM38, PBX1, PER3, BHLHE41, ZNF99, NFIB</i>
Epithelium development	6	1.77E-02	<i>RET, VANGL2, TGM1, PBX1, CDSN, WT1</i>
Regulation of transcription, DNA-dependent	20	2.28E-02	<i>PHOX2A, ZNF519, KLF12, CRABP2, EMX2, ESR1, NFIX, SPEN, MEIS1, TCF7L2, FOXO6, WT1, ZNF334, ZFP92, NPAS3, PBX1, PER3, BHLHE41, ZNF99, NFIB</i>



Supplementary Figure S1. Pathway enrichment analysis using PC1-contributing genes in PCA. Principal component analysis (PCA) was performed based on the expression level represented by log2RPKM value for each RefSeq CCC, HGSC, and normal tissues. DAVID Bioinformatics Resources 6.7 showed differentially expressed genes in pathways and clusters of functionally related genes in clear cell carcinoma compared to normal tissues (A), in serous carcinoma compared to normal tissues (B), and in clear cell carcinoma compared to serous carcinoma (C).



Supplementary Figure S2. Gene expression levels of *CPNE8* and *BHLHE41* based on Oncomine. (A) *CPNE8* was expressed higher in clear cell carcinoma ($n = 6$) than in serous carcinoma ($n = 71$) among Meyniel Ovarian Statistics ($n = 140$). (B) *BHLHE41* was expressed higher in serous carcinoma than in clear cell carcinoma among the same dataset with (A). (C) *CPNE8* was expressed higher in clear cell carcinoma ($n = 13$) than in serous carcinoma ($n = 79$) among Bittner Ovarian Statistics ($n = 241$). (D) *BHLHE41* was expressed higher in serous carcinoma than in clear cell carcinoma among the same dataset with (C). (E) *CPNE8* was expressed higher in clear cell carcinoma ($n = 7$) than in serous carcinoma ($n = 20$) among Lu Ovarian Statistics ($n = 50$). (F) *BHLHE41* was expressed higher in serous carcinoma than in clear cell carcinoma among the same dataset with (E).



Supplementary Figure S3. Up- and down-regulated pathway genes by siRNAs targeting *CPNE8* and *BHLHE41*. (A) Venn diagram showing the number of overlapping upregulated (>1.5-fold, left panel) and downregulated (<0.66-fold, right panel) microarray probes in RMG1 cells after treatment of si*CPNE8* #A and #B compared with siControl. Pathway analysis using the overlapping genes shows high enrichment of ion-related and neuron-related pathways in upregulated genes, whereas high enrichment of cytokines and inflammatory pathways in downregulated genes. (B) Similar microarray analysis was performed as in (A) except that OVCAR3 cells and si*BHLHE41* #A and #B were used. Pathway analysis shows high enrichment of protein kinase and ion-related pathways in upregulated genes, whereas high enrichment of wound response and cell proliferation pathways in downregulated genes.