

Supplementary material

Table S1: List of 183 blue module genes identified through WGCNA, served as the input for subsequent differential gene expression (DEG) analysis

Table S1: Continued	
Blue module genes	
ABCF2	
ACBD7	
ADSL	
AEBP2	
AFG3L2	
AKIRIN2	
ANLN	
ATAD2	
ATAD5	
ATN1	
ATP11A	
B3GNT5	
BAK1	
BARD1	
BRIX1	
CAD	
CALCOCO1	
CCDC150	
CCT3	
CDC20	
CDC25A	
CDCA2	
CDCA3	
CDCA4	
CDK2	
CDKN2C	
CDT1	
CENPH	
CENPO	
CEP55	
CHAF1A	

(Continued)

Table S1: Continued

Blue module genes	
CKAP2L	
CKAP5	
COMMD2	
COP57A	
CORO1C	
CYB5B	
DDX47	
DHFR	
DHTKD1	
DIAPH3	
DNMT3A	
DTL	
EMG1	
EPCAM	
EXOSC2	
FAM47E	
FANCA	
FANCC	
FANCG	
FBXO45	
FGD4	
FOXN2	
GAS2L3	
GCNT2	
GDI2	
GIN54	
GNA13	
GPR161	
GPR180	
GTSE1	
HDGF	
HELLS	
HMGN3	
HSPA14	

(Continued)

Table S1: *Continued*

Blue module genes
<i>IARS</i>
<i>ILF2</i>
<i>IMPA2</i>
<i>JRKL</i>
<i>KIF20A</i>
<i>KIF2C</i>
<i>KPNA2</i>
<i>LBR</i>
<i>LMNB1</i>
<i>LMNB2</i>
<i>LRP8</i>
<i>LRRC42</i>
<i>LSM2</i>
<i>MCM6</i>
<i>MED21</i>
<i>MEX3A</i>
<i>MLLT10</i>
<i>MPHOSPH10</i>
<i>MRAS</i>
<i>MRPL37</i>
<i>MRPL51</i>
<i>MRPS22</i>
<i>MSH2</i>
<i>MTHFD1</i>
<i>MTHFD1L</i>
<i>MTHFD2</i>
<i>MYBL2</i>
<i>NAA15</i>
<i>NAE1</i>
<i>NCAPG2</i>
<i>NOL11</i>
<i>NOP2</i>
<i>NSUN2</i>
<i>PAPD7</i>
<i>PATL1</i>
<i>PDIA6</i>
<i>PK1</i>
<i>PFKP</i>
<i>PGAM5</i>
<i>PHB2</i>

(Continued)

Table S1: *Continued*

Blue module genes
<i>PHC1</i>
<i>PHF19</i>
<i>PIF1</i>
<i>PLCH1</i>
<i>PNO1</i>
<i>POLA2</i>
<i>POLR1B</i>
<i>POP1</i>
<i>PPP3R1</i>
<i>PPRC1</i>
<i>PRKAR1A</i>
<i>PSMD12</i>
<i>PSMD7</i>
<i>PUS7</i>
<i>RAD52</i>
<i>RAD54L</i>
<i>RANBP1</i>
<i>RCC2</i>
<i>RGMA</i>
<i>RHBDF2</i>
<i>RHEBL1</i>
<i>RNGTT</i>
<i>SASS6</i>
<i>SET</i>
<i>SKA3</i>
<i>SKP2</i>
<i>SLC25A13</i>
<i>SLC35F2</i>
<i>SLC5A6</i>
<i>SLC7A5</i>
<i>SMG5</i>
<i>SPAG5</i>
<i>SPC25</i>
<i>SPRYD3</i>
<i>SSB</i>
<i>SSRP1</i>
<i>SUOX</i>
<i>SUV39H2</i>
<i>SYNCRIP</i>
<i>TAF5</i>

(Continued)

Table S1: Continued

Blue module genes
TCF7L1
TDG
TFDP1
TIMELESS
TIPRL
TK2
TMC4
TMEM201
TPCN1
TPI1
TRIM65
TTC13
TTC8
TTK
TTL
TUBA1C
TUBB
UBASH3B
UBXN2A

(Continued)

Table S1: Continued

Blue module genes
UGP2
UHRF1
UNG
UPF2
USP39
USP5
VPS39
VPS72
WDR53
WRNIP1
XPO1
XPO5
YES1
ZC3H18
ZDHHC18
ZFP91
ZNF367
ZNF384
ZNF695

Table S2: A summary of ontology of blue module genes obtained through Metascape Enrichment Analysis

GO	Category	Description	Count	%	Log10(P)	Log10(q)
R-HSA-69278	Reactome Gene Sets	Cell Cycle, Mitotic	29.00	15.85	-18.07	-13.73
GO:0000278	GO Biological Processes	mitotic cell cycle	27.00	14.75	-15.44	-11.57
GO:0010564	GO Biological Processes	regulation of cell cycle process	28.00	15.30	-13.83	-10.18
GO:0006259	GO Biological Processes	DNA metabolic process	26.00	14.21	-12.36	-8.79
WP2446	WikiPathways	Retinoblastoma gene in cancer	11.00	6.01	-11.16	-7.82
GO:0006260	GO Biological Processes	DNA replication	14.00	7.65	-10.64	-7.34
R-HSA-453279	Reactome Gene Sets	Mitotic G1 phase and G1/S transition	12.00	6.56	-9.90	-6.71
GO:0051052	GO Biological Processes	regulation of DNA metabolic process	18.00	9.84	-8.66	-5.66
R-HSA-8953854	Reactome Gene Sets	Metabolism of RNA	20.00	10.93	-7.72	-4.81
GO:0006338	GO Biological Processes	chromatin remodeling	18.00	9.84	-6.72	-3.97
GO:0034504	GO Biological Processes	protein localization to nucleus	10.00	5.46	-6.56	-3.87
GO:1901989	GO Biological Processes	positive regulation of cell cycle phase transition	8.00	4.37	-6.15	-3.57
WP241	WikiPathways	One carbon metabolism	5.00	2.73	-6.10	-3.55
M258	Canonical Pathways	PID BARD1 PATHWAY	5.00	2.73	-6.10	-3.55
WP4352	WikiPathways	Ciliary landscape	10.00	5.46	-6.07	-3.55
GO:0065004	GO Biological Processes	protein-DNA complex assembly	10.00	5.46	-5.84	-3.34
R-HSA-6790901	Reactome Gene Sets	rRNA modification in the nucleus and cytosol	6.00	3.28	-5.73	-3.24
GO:0006310	GO Biological Processes	DNA recombination	10.00	5.46	-5.55	-3.10
GO:0051983	GO Biological Processes	regulation of chromosome segregation	7.00	3.83	-4.79	-2.43
WP2363	WikiPathways	Gastric cancer network 2	4.00	2.19	-4.45	-2.17

Table S3: A summary of processes and corresponding *p*-value scores for genes within the four major networks associated with ER-linked Wnt genes, as identified through Metascape enrichment analysis

Color	MCODE	GO	Description	Log10(P)
red	MCODE_1	GO:0006260	DNA replication	-6.70
red	MCODE_1	R-HSA-1640170	Cell Cycle	-6.60
red	MCODE_1	R-HSA-8953854	Metabolism of RNA	-6.40
blue	MCODE_2	GO:0034504	protein localization to nucleus	-6.70
blue	MCODE_2	R-HSA-68886	M Phase	-5.40
blue	MCODE_2	hsa04210	Apoptosis	-5.10
green	MCODE_3	GO:0140694	non-membrane-bounded organelle assembly	-4.10
purple	MCODE_4	R-HSA-8951664	Neddylation	-6.30

Table S4: Gene components included in each signature

ER-associated multigene signature components linked to Overall Survival	ER-associated multigene signature components linked to Disease Free Survival	Multigene signature components for tumor-normal classification linked to Overall Survival	Multigene signature components for tumor-normal classification linked to Disease Free Survival
<i>TTC8, SLC5A7, PLCH1</i>	<i>ZNF695, SLC7A5, PLCH1</i>	<i>SPC25, ANLN, KPNA2, SLC7A5</i>	<i>SPC25, KIF20A, SKA3, DTL, CDCA3, ANLN, TTK, RAD54L, MYBL2, ZNF695, SLC7A5</i>