

Supplemental data

Table S1 the proteins detected by previous and our methods in the yeast pheromone signaling, filamentous growth and cell wall integrity pathways (the bold words denote the overlapped proteins in KEGG main chain pathway)

Pathway name	Scott's color-coding	Steffen's Netsearch	Zhao's ILP	Pathfinder	Our method
Pheromone signaling	STE3,STE4,STE18, CDC42, STE11, STE7,FUS3, DIG1,DIG2,STE12, AKR1,STE5, KSS1, CDC24, BEM1, FAR1,GPA1, STE50	STE3, STE18, STE4, STE11, STE7, DIG1, DIG2, STE12, STE5, FUS3, KSS1, AKR1 , CDC24,FAR1,BEM1, GPA1, SST2,MPT5, SPH1	STE3, STE4, STE18,CDC42, STE20, STE11, STE7, FUS3, DIG1, DIG2, STE12, CDC24, STE50, BEM1, CLA4, CDC28,STE5,FAR1, MPT5,AKR1,KSS1, CLN2, CLN1, IQG1, GCS1, ACT1, SWE1, BOI1, LAS17, RSR1, GIC1, BNI1, GIC2, SPA2 ($\lambda=0.5$)	STE3,STE4,STE20, STE11,STE7,FUS3, DIG1, DIG2, STE12, KSS1, STE5, BEM1,GPA1, CDC24, SST2, FAR1	STE3, STE4, STE18,CDC42, STE20, STE11, STE7, FUS3, DIG1, DIG2, STE12, AKR1, STE5, STE50, KSS1, ACO1, MPT5, IQG1, BNI4, CDC24, GPA1, BUD6, SPH1, KAP104, BOI2, BOB1
Filamentous growth	RAS2, STE11, STE7, KSS1,TEC1,CDC25, HSP82,STE5	RAS2, STE11, STE7,KSS1, TEC1,DIG1,DIG2, SRV2,ACT1 ,FUS1,F US3,	RAS2,STE11,STE7, KSS1,TEC1, DIG1, DIG2, STE20, FUS3, STE5,BEM1,BUD6,S RV2,ACT1,CYR1,	RAS2,CDC42, STE20, STE11, STE7, KSS1, DIG1, DIG2, TEC1, STE12, FUS1,	RAS2, CDC42, STE20, STE11, STE7, KSS1, DIG1, DIG2,TEC1, CDC25,HSP82,RTG3

STE12,CYR1,ABP1, LAS17, PFY1, BNI1, LAS17, CDH1, ,STE5,CDC48, BNI1,
 BEM1, BNI1,SPA2, STE20, GPA1, SPH1, CDC7, CDC28, SPH1, KAP104,
 STE5,CDC25,HSP82, AKR1, MCM1, SPA2, BEM1, GPA1, CLN2, ACO1,
 HSC82,BUD6 ARG81, SPA2, STE4, SSK1, SWE1, STE12,IRA1,
 SRV2, HSC82, ABP1 SSK2,NBP2, CLA4, CYR1,DBF2,
 ($\lambda= 0.5$) CDC24, STE5, PBS2, CDC15,ACT1,
 PTC1, HOG1, FUS3, BEM1
 FAR1, FLO8, BUD6

Cell wall integrity

MID2, RHO1, MID2,RHO1, MID2, RHO1, MID2, RHO1, MID2, RHO1,
PKC1, MKK1, PKC1 , BCK1, PKC1, MKK2, PKC1, BCK1,
SLT2, RLM1, MKK1, SLT2, MKK1, SLT2, MKK1, SLT2,
 ROM2, **RLM1,FKS1,RGA1, RLM1, ROM2, RLM1, ROM2,**
 RDI1, RDI1, BEM4, RGA1, SEC3, UBP15,
 BNI1,CDC42,GIC2, CDC42, BNI1, SPA2, NMA1, LYS14,
 ACT1, BUD6,SPA2, SWI6, SWI4, SKN7, OST1
 SPH1,MKK2, SMD3 MBP1 ($\lambda= 0.15$)

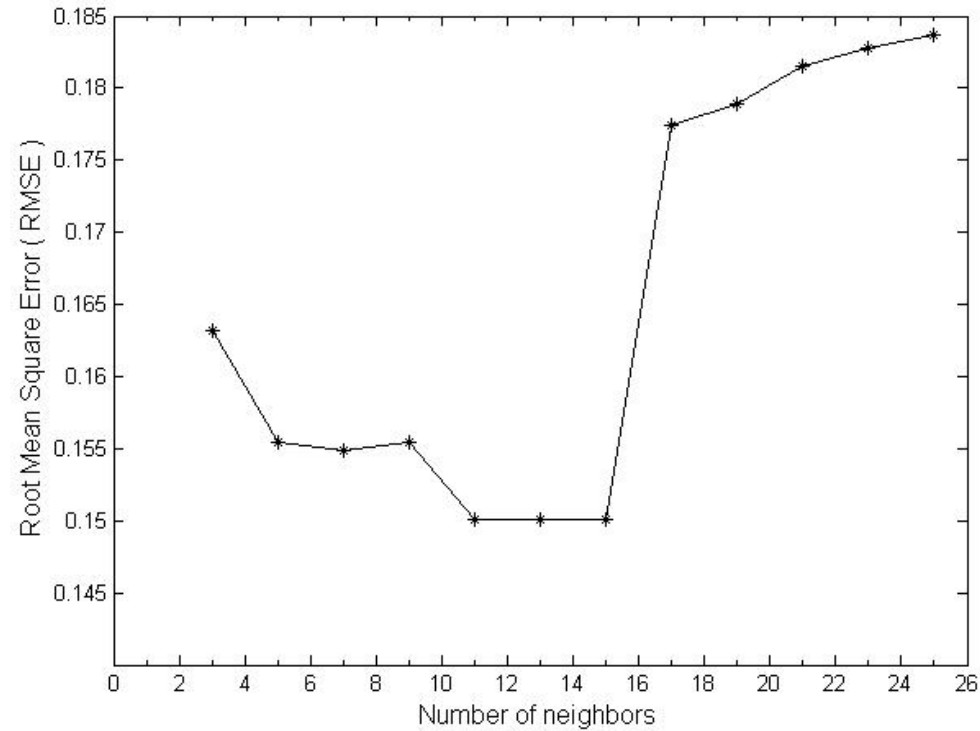


Figure S1 - effect of number of nearest neighbors used in KNN method for imputing missing values.

The accuracy of estimation values in the microarray data are calculated by Root Mean Squared error (RMSE) which denote the different values between imputed values and original values, divided by the number of missing value we computed. It shows that the estimated values with RMSE rates are under 0.185 while setting the 11-15 nearest neighbors in KNN method.

Table S2 - the evidences of the results we detected

We list the genes that extracted by our method and those results also confirmed by present biological evidence from the public literature.

Symbols	Gene name	Ref
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3	[42]
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1	[43]
FHL2	four and a half LIM domains 2	[44]
ABL1	c-abl oncogene 1, receptor tyrosine kinase	[45]
BRE	brain and reproductive organ-expressed	[46]
C11ORF30	chromosome 11 open reading frame 30	[47]
CBX5	chromobox homolog 5	[48]
XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	[49]
PCAF	K(lysine) acetyltransferase 2B	[50]
RNF14	ring finger protein 14	[51]
APEX1	APEX nuclease 1	[52]
HDAC1	histone deacetylase 1	[53]
HSPA8	heat shock 70kDa protein 8	[54]
SMAD3	SMAD family member 3	[55]
SP1	Sp1 transcription factor	[56]
CCND1	cyclin D1	[57]
LRPPRC	leucine-rich PPR-motif containing	[58]
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	[59]
GTF2B	general transcription factor IIB	[60]
PSMC2	proteasome 26S subunit, ATPase, 2	[61]

GTF2H1	general transcription factor IIIH	[62]
CDK7	cyclin-dependent kinase 7	[63]
NCOR2	nuclear receptor co-repressor 2	[64]
SET	SET nuclear oncogene	[65]
FANCD2	Fanconi anemia, complementation group D2	[66]
PPP2CA	protein phosphatase 2, catalytic subunit, alpha isoform	[67],[68]
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1	[69]
ANXA2	annexin A2	[70]
VCL	vinculin	[71]
PTPN11	protein tyrosine phosphatase, non-receptor type 11	[72]
STRN4	striatin, calmodulin binding protein 4	[73]
CALM1	calmodulin 1	[74]
BCR	breakpoint cluster region	[75]
JAK1	Janus kinase 1	[76]
STAT3	signal transducer and activator of transcription 3	[77]
DDX5	DEAD box polypeptide 5	[78]
H2AFX	H2A histone family, member X	[79]
PIAS1	protein inhibitor of activated STAT, 1	[80]
SP3	Sp3 transcription factor	[81]
GABPA	GA binding protein transcription factor, alpha subunit 60kDa	[82]
BAG1	BCL2-associated athanogene	[83]
UBE3A	ubiquitin protein ligase E3A	[84]

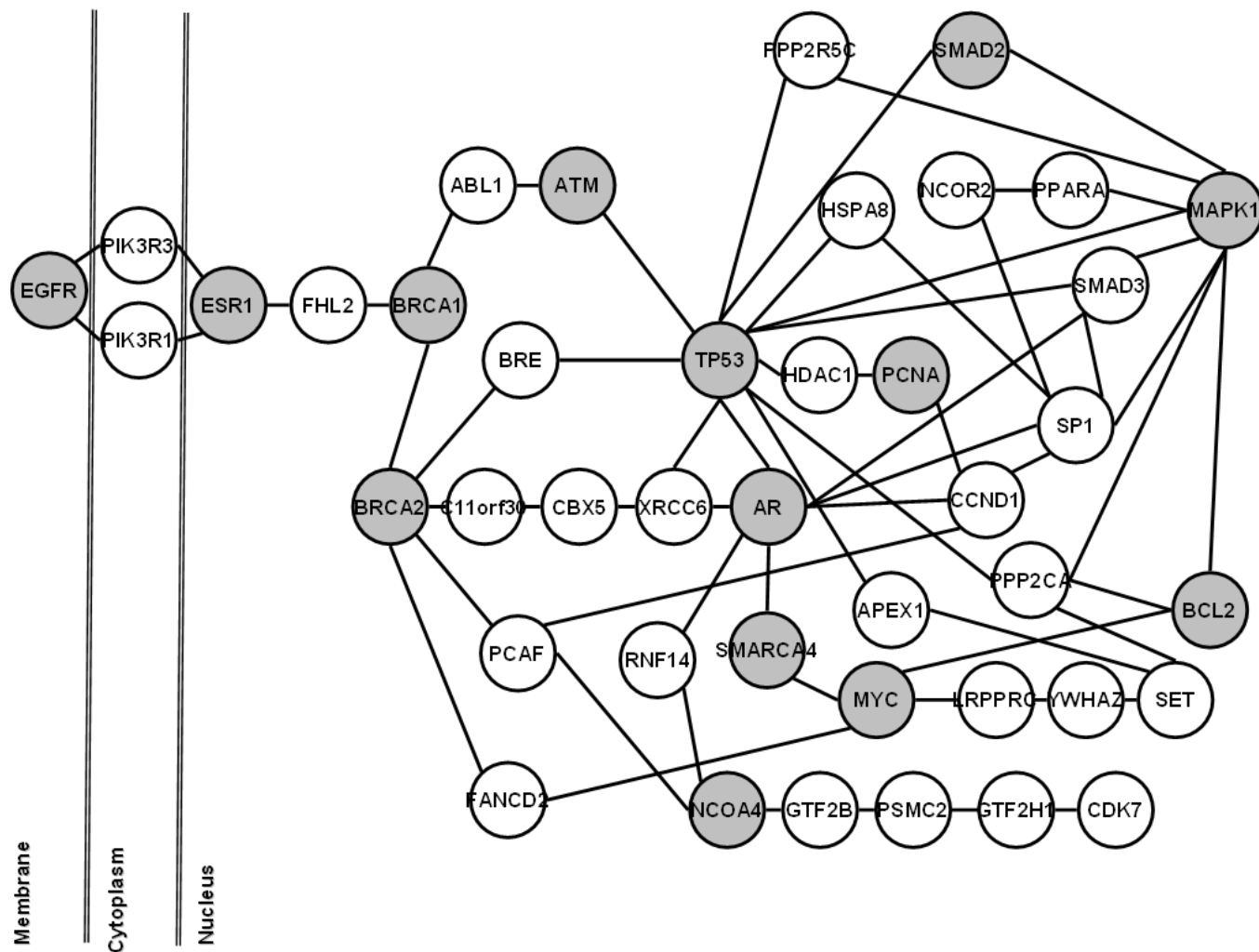


Figure S2 - the part of networks of human prostate cancer from EGFR to BCL2; The nodes with grey color denote the disease-related genes

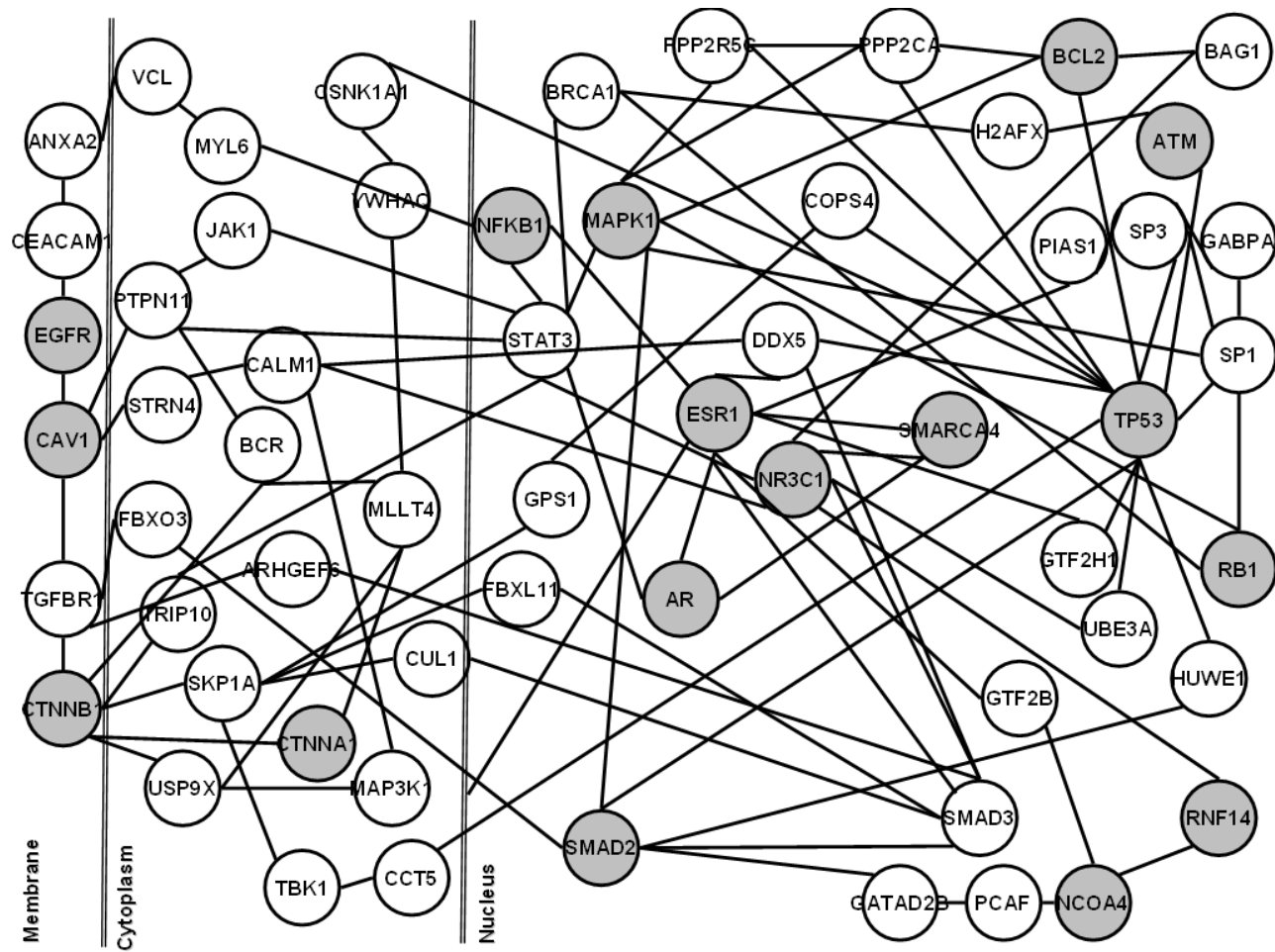


Figure S3- the part of networks of human prostate cancer from EGFR to BCL2; The nodes with grey color denote the disease-related genes
 In Figure S2 and S3, we search the significant paths from membrane protein EGFR to BCL2 with path length 15 and assembled the paths to human prostate cancer network.

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