

Supplementary Information for

Identification of CCNB2 as A Potential Non-Invasive Breast Cancer Biomarker in Peripheral Blood Mononuclear Cells Using The Systems Biology Approach

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Table S1: qPCR primers for assessing CCNB2 mRNA expression level using qRT-PCR

Primers	Primer sequence (5'-3')	
CCNB2	F: TTACTGCTCTTGGCTTC	
	R: TCTCGGATTTGGGAACTGGTATAAG	
GAPDH	F: ACATCAAGAAGGTGGTGAAGCAG	
	R: GCGTCAAAGGTGGAGGAGTG	

QRT-PCR; Quantitative reverse-transcription polymerase chain reaction.

Table S2: Power-law behavior of the node distribution of 187 cancer signature genes network, (10.9 KB docx)

Power-law distribution	Correlation coefficient of power-law fit (R)	R-squared of power-law fit*	R-squared of best line- fit
$y \approx 39.166x - 1.028$	0.961	0.82	0.413

^{*;} R-Squared is computed on logarithmized values.

Table S3: Central cancer signatures genes are conclusive set of Hub genes combined with betweenness centrality (13.9 KB docx)

No.	Betweenness centrality	Hub	Betweenness centrality + Hub
1	AURKA	AURKA	AURKA
2	PDIA6	PSMA7	PDIA6
3	CCT5	CCNB2	CCT5
4	NME1	NCL	NME1
5	PSMB8	NPM1	PSMB8
6	ACLY	PSMA4	ACLY
7	NCL		NCL
8	NPM1		NPM1
9	PSMA7		PSMA7
10	PSMB2		PSMB2
11	HNRNPK		HNRNPK
12	TUBA1B		TUBA1B
13	FKBP10		FKBP10
14	SNCA		SNCA
15	EIF2S2		EIF2S2
16	EIF2AK1		EIF2AK1
17	SPP1		SPP1
18	STAT1		STAT1
19	DTX3L		DTX3L
20	PSMA4		PSMA4
21	KDELR3		KDELR3
22	DNMT1		DNMTI
23	FBXO32		FBXO32
24	EPRS		EPRS
25	ALDH6A1		ALDH6A1
26	PLOD3		PLOD3
			CCNB2

The top 20% of genes with highest betweenness value were selected. Conclusive set of Hub genes combination with betweenness centrality was named central cancer signatures genes.