

Supporting information

Identification of Epigenetic Regulators in Estrogen Signaling

Pathway via siRNA Screening

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Table of contents

1. Estrogen signaling regulators selected from siRNA screening (Table S1)
2. The topological parameters of genes in the PPI network (Table S2)
3. Expression of PcG genes according to breast cancer stages (Figure S1)
4. Kaplan-Meier analysis of relapse-free survival in breast cancer stratified by 10 PcG genes expression level (Figure S2)

Table S1. Estrogen signaling regulators selected from the siRNA screening

Gene symbols	Description	Fold change relative to siControl		
ZMYND8	zinc finger MYND-type containing 8	0.34	0.46	0.75
KAT6B	lysine acetyltransferase 6B	0.39	0.56	0.60
CBX6	chromobox 6	0.34	0.51	0.62
KAT7	lysine acetyltransferase	0.24	0.49	0.53
ZMYND1 1	zinc finger MYND-type containing 11	0.32	0.35	1.14
CDY2A	chromodomain Y-linked 2A	0.40	0.53	1.07
HMGN3	high mobility group nucleosomal binding domain 3	0.28	0.32	0.53
ATAD2	ATPase family AAA domain containing 2	0.35	0.35	1.18
DNMT3L	DNA methyltransferase 3 like	0.45	0.57	1.15
SMC3	structural maintenance of chromosomes 3	0.50	0.51	1.05
ZBTB4	zinc finger and BTB domain containing 4	0.19	0.34	0.48
KAT6A	lysine acetyltransferase 6A	0.27	0.46	0.87
KMT2D	lysine methyltransferase 2D	0.45	0.47	1.08
HMGA2	high mobility group AT-hook 2	0.33	0.51	0.64
NCOA3	nuclear receptor coactivator 3	0.11	0.27	0.31
SUV39H1	suppressor of variegation 3-9 homolog 1	0.34	0.59	1.34
CIITA	class II major histocompatibility complex transactivator	0.50	0.50	0.68
HMGB1	high mobility group box 1	0.21	0.47	0.50
HMGB2	high mobility group box 2	0.38	0.47	0.51
HMGB3	high mobility group box 3	0.19	0.30	0.98
HMGN1	high mobility group nucleosome binding domain 1	0.33	0.69	0.75
HMGA1	high mobility group AT-hook 1	0.18	0.30	0.85

MECP2	methyl-CpG binding protein 2	0.38	0.60	0.64
CHD6	chromodomain helicase DNA binding protein 6	0.47	0.64	1.25
EHMT1	euchromatic histone lysine methyltransferase 1	0.43	0.47	0.67
PCGF6	polycomb group ring finger 6	0.46	0.49	0.72
PCGF5	polycomb group ring finger 5	0.24	0.38	0.55
BRD3	bromodomain containing 3	0.44	0.53	0.57
BRD4	bromodomain containing 4	0.34	0.41	1.27
TRIM28	tripartite motif containing 28	0.15	0.26	0.64
KDM2B	lysine demethylase 2B	0.44	0.45	1.01
PCGF1	polycomb group ring finger 1	0.46	0.49	0.82
SMC1B	structural maintenance of chromosomes 1B	6.67	2.02	0.70
SUZ12	polycomb repressive complex 2 subunit	4.82	2.06	1.62
CBX1	chromobox 1	3.01	2.16	1.59
CHAF1A	chromatin assembly factor 1 subunit A	83.1	62.5	21.1
ELP3	elongator acetyltransferase complex subunit 3	6.66	2.87	2.43
CBX8	chromobox 8	3.41	3.33	2.09
EP400	E1A binding protein p400	3.09	2.72	1.23
CHAF1B	chromatin assembly factor 1 subunit B	25.0	4.31	0.83
RBBP7	RB binding protein 7	4.05	3.79	1.70
BMI1	BMI1 proto-oncogene, polycomb ring finger	2.87	2.84	0.82
ATF2	activating transcription factor 2	2.01	1.81	0.99
DNMT1	DNA methyltransferase 1	4.21	2.25	0.70
PHC3	polyhomeotic homolog 3	5.07	4.03	2.91
TAF1	TATA-box binding protein associated factor 1	4.08	2.72	1.29

TRIM33	tripartite motif containing 33	3.57	3.51	2.61
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Table S2. The topological parameters of genes in the PPI network

Gene symbol	MCC	Degree	Gene symbol	MCC	Degree
SUZ12	45976	18	NCOA3	16	9
PCGF6	45648	11	KAT6B	14	5
BMI1	45625	12	CHAF1A	12	4
PCGF1	45600	10	EP400	11	8
CBX6	45480	10	CHAF1B	11	6
CBX8	45480	10	ATAD2	9	5
PCGF5	45360	9	ELP3	8	4
RBBP7	40922	20	BRD3	8	4
PHC3	40440	9	HMGB1	7	5
KDM2B	5210	11	HMGA1	6	5
CBX1	618	17	SMC3	5	5
EHMT1	390	11	HMGA2	4	4
SUV39H1	372	11	HMGB2	4	3
DNMT1	372	11	SMC1B	4	3
MECP2	146	8	HMGB3	3	3
ATF2	122	7	HMGN1	3	3
KAT6A	64	12	KAT7	3	3
DNMT3L	54	6	CHD6	2	2
TRIM28	38	7	ZMYND11	2	2
TAF1	28	9	TRIM33	2	2
BRD4	28	9	ZBTB4	1	1
KMT2D	20	8			

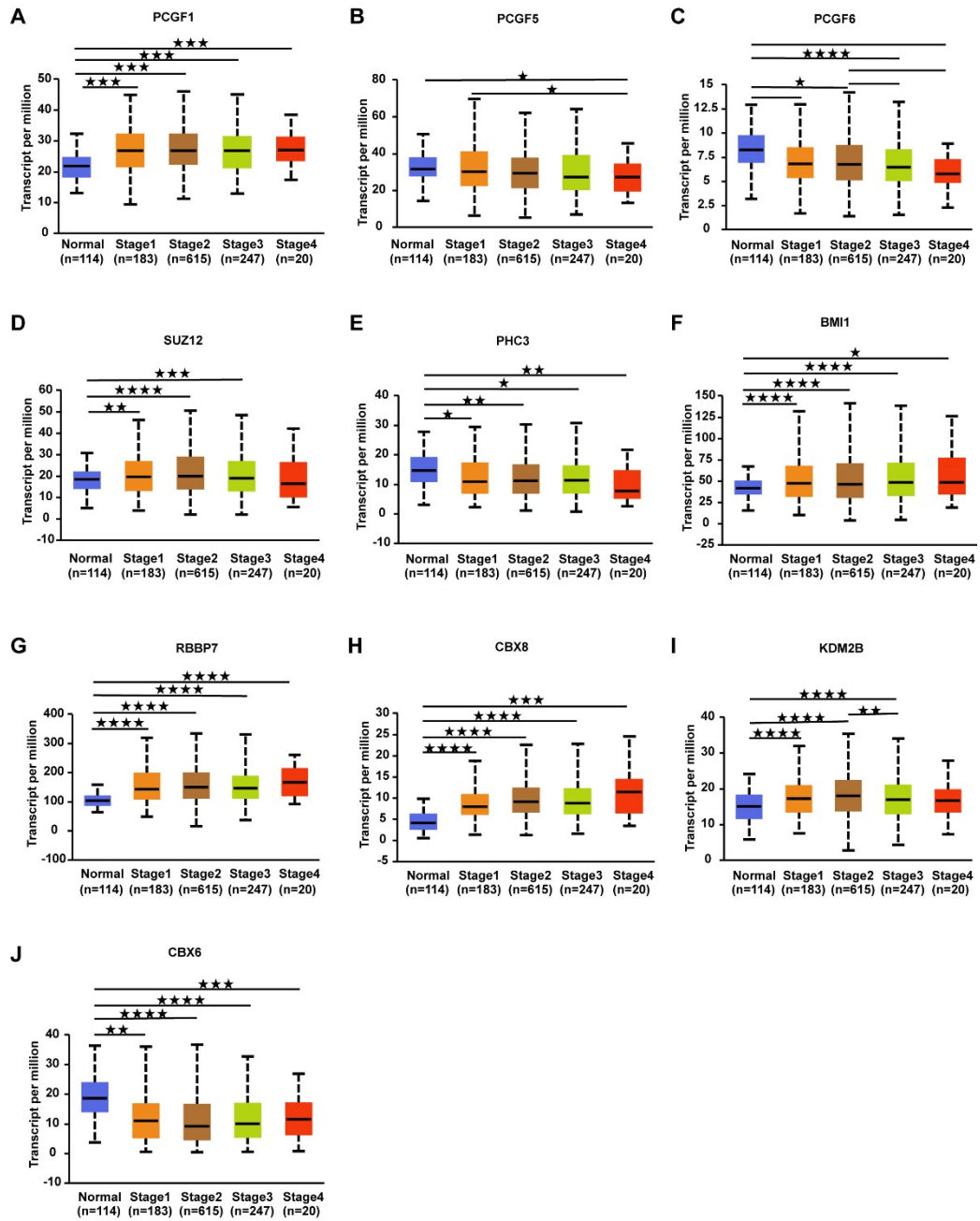


Figure S1. Expression of PcG genes according to breast cancer stages. (A)PCGF1, (B)PCGF5, (C)PCGF6, (D)SUZ12, (E)PHC3, (F)BMI1, (G)RBBP7, (H)CBX8, (I)KDM2B, (J)CBX6.

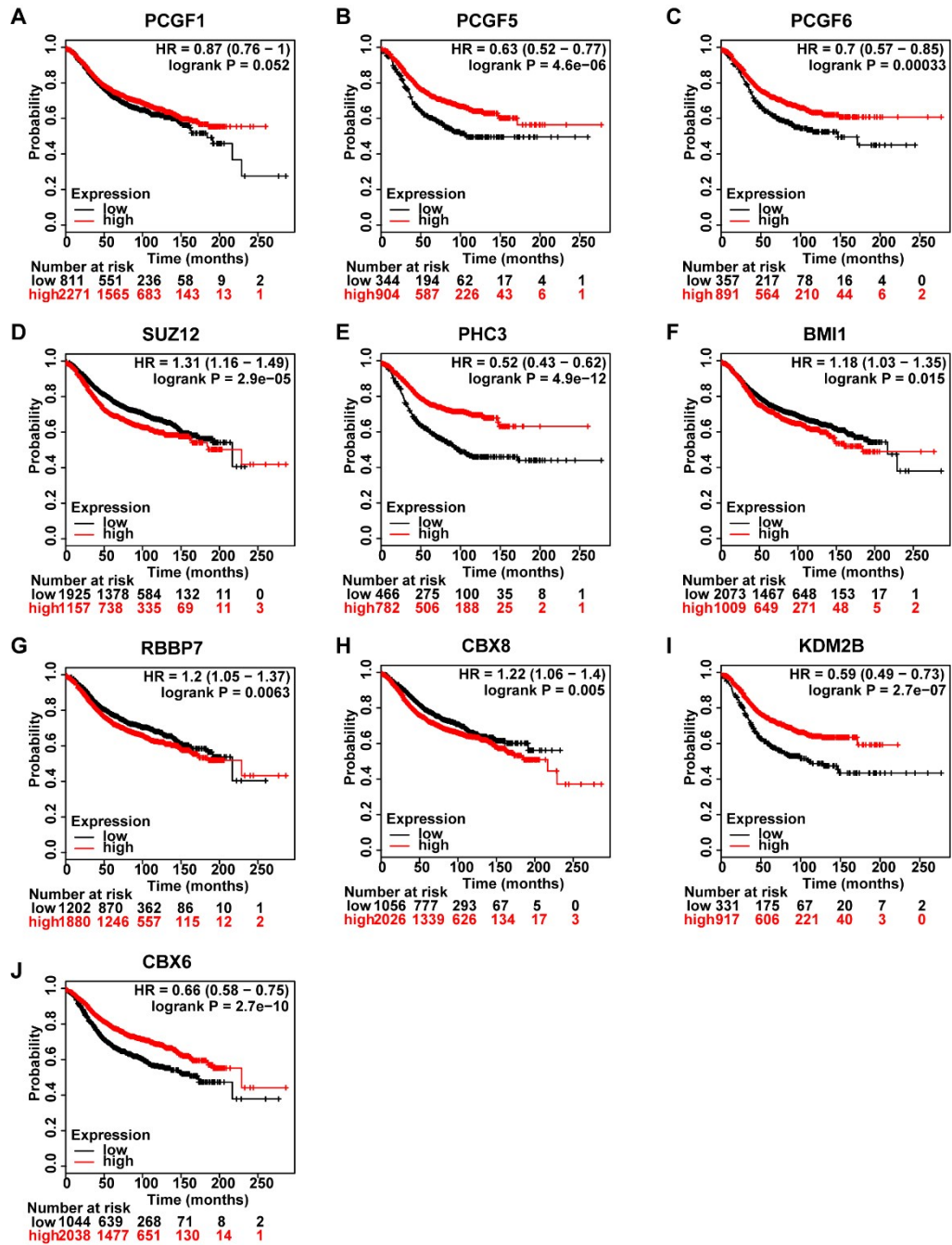


Figure S2. Kaplan-Meier analysis of relapse-free survival in breast cancer stratified by gene expression level. (A) PCGF1, (B) PCGF5, (C) PCGF6, (D) SUZ12, (E) PHC3, (F) BMI1, (G) RBBP7, (H) CBX8, (I) KDM2B, (J) CBX6.