Table S1. The summary of mapping results.

Sample name	EV-SUM159		FoxQ1-SUM159	
	Mean	SD	Mean	SD
Total reads	65198263	4386610	72027681	10214885
Total mapped	58914439 (90.38%)	3655237 (0.51%)	64895915 (90.17%)	8672753 (0.82%)
Multiple mapped	1147142 (1.76%)	81213 (0.01%)	1224173 (1.70%)*	154648 (0.03%)*
Uniquely mapped	57767297 (88.62%)	3574643 (0.52%)	63671741 (88.46%)	8518408 (0.80%)
Reads map to '+'	28883648 (44.31%)	1787322 (0.26%)	31835871 (44.23%)	4259204 (0.40%)
Reads map to '-'	28883648 (44.31%)	1787322 (0.26%)	31835871 (44.23%)	4259204 (0.40%)
Non-splice reads	32843918 (50.39%)	2036952 (0.30%)	36497716 (50.68%)	5119388 (0.56%)
Splice reads	24923378 (38.24%)	1546835 (0.33%)	27174025 (37.79%)	3464790 (1.14%)

*, Statistically significant by unpaired Student’s t test ($P < 0.05$).

Table S2. Correlation between *FoxQ1* and genes associated with "Cellular response to stress" category from TCGA-BrCa (n=1097) and RNA-seq results. Student *t* test was used for statistical analysis.

Correlation	*Genes*	TCGA-BrCa analysis		RNA-Seq data	
		Pearson r	*P* value	fold change (FoxQ1 *vs*. EV)	*P* value
Positive	*TUBB6*	0.4657	< 0.0001	+ 1.59	0.0032
	HMGA2	0.3699	< 0.0001	+ 1.56	0.0541
	CDK6	0.3684	< 0.0001	+ 1.29	0.0978
	MAP4K4	0.3093	< 0.0001	+ 1.65	0.0001
	SOD2	0.2869	< 0.0001	+ 2.18	< 0.0001
	IL8 (=CXCL8)	0.2812	< 0.0001	+ 2.42	0.0001
	IL1A	0.2779	< 0.0001	+ 23.04	0.0002
	ETS2	0.2657	< 0.0001	+ 1.53	0.0047
	C11orf73 (=HIKESHI)	0.2568	< 0.0001	+ 1.37	0.0512
	PHC2	0.2453	< 0.0001	+ 1.49	0.0001
	IGFBP7	0.2410	< 0.0001	+ 4.04	0.0015
	ETS1	0.2288	< 0.0001	+ 1.23	0.0341
	HMGA1	0.2181	< 0.0001	+ 1.22	0.0233
	JUN	0.1691	< 0.0001	+ 1.14	0.0265
	TFDP2	0.1550	< 0.0001	+ 1.74	0.0007
	AR	-0.2917	< 0.0001	– 9.71	< 0.0001
	MAP2K4	-0.1899	< 0.0001	– 1.56	0.0003
	BMI1	-0.1888	< 0.0001	– 1.24	0.0048
	DYNLL2	-0.1810	< 0.0001	– 1.32	0.0017
	HSPA1L	-0.1789	< 0.0001	– 3.45	0.0019
	ATP7A	-0.1738	< 0.0001	– 1.24	0.0500
	CBX4	-0.1715	< 0.0001	– 2.02	< 0.0001
	DYNC1LI1	-0.1714	< 0.0001	– 1.23	0.0025
	MAPK3	-0.1645	< 0.0001	– 1.79	0.0042
	UBN1	-0.1638	< 0.0001	– 1.14	0.0049
	GSR	-0.1506	< 0.0001	– 1.39	0.0095
Negative	*BAG2*	0.3692	< 0.0001	– 1.21	0.0004
	CA9	0.3279	< 0.0001	– 11.51	0.0119
	WTIP	0.3160	< 0.0001	– 2.46	0.0017
	CBX2	0.2512	< 0.0001	– 3.05	< 0.0001
	CCNE1	0.2497	< 0.0001	– 1.31	0.0304
	PSMB9	0.2361	< 0.0001	– 1.34	0.0600
	RPS6KA3	0.2278	< 0.0001	– 1.77	0.0004
	PSMB2	0.2273	< 0.0001	– 1.25	0.0431
	EGLN3	0.2229	< 0.0001	– 2.25	0.0010
	MAPK7	0.2111	< 0.0001	– 1.79	< 0.0001

TUBA1A	0.2091	< 0.0001	– 1.88	0.0015
E2F3	0.2000	< 0.0001	– 1.32	0.0109
UBE2D1	0.1940	< 0.0001	– 1.29	0.0022
PSMB10	0.1877	< 0.0001	– 1.79	0.0020
DNAJC2	0.1778	< 0.0001	– 1.27	0.0011
HIF1A	0.1683	< 0.0001	– 1.38	0.0018
PSMC1	0.1678	< 0.0001	– 1.49	0.0086
IL6	0.1650	< 0.0001	– 2.55	< 0.0001
TUBB2A	0.1633	< 0.0001	– 1.39	0.0089
UBE2C	0.1511	< 0.0001	– 1.32	0.0047
ERO1L (=ERO1A)	0.1509	< 0.0001	– 1.21	0.0711
DCTN4	-0.2692	< 0.0001	+ 1.15	0.0035
MDM2	-0.2195	< 0.0001	+ 1.26	0.0478
HIST4H4	-0.2000	< 0.0001	+ 3.34	0.0083
H2AFJ	-0.1580	< 0.0001	+ 2.30	0.0119
NUP210	-0.1561	< 0.0001	+ 14.72	< 0.0001
H2AFV	-0.1501	< 0.0001	+ 1.16	0.0022