

Table S1, Supplemental Digital Content. Gene ontology analysis of DEGs in breast cancer.

	Category	Term	Count	%	PValue
Up-regulated	GOTERM_BP_DIRECT	GO:0007018~microtubule-based movement	10	16.7	7.9E-12
	GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	10	16.7	7.1E-11
	GOTERM_BP_DIRECT	GO:0007080~mitotic metaphase plate congression	6	10.0	1.7E-07
	GOTERM_BP_DIRECT	GO:0031145~anaphase-promoting complex-dependent catabolic process	7	11.7	3.0E-07
	GOTERM_BP_DIRECT	GO:0006890~retrograde vesicle-mediated transport, Golgi to ER	7	11.7	3.7E-07
	GOTERM_BP_DIRECT	GO:0000086~G2/M transition of mitotic cell cycle	8	13.3	4.4E-07
	GOTERM_BP_DIRECT	GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	7	11.7	7.4E-07
	GOTERM_BP_DIRECT	GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process	7	11.7	1.4E-05
	GOTERM_CC_DIRECT	GO:0005871~kinesin complex	9	15.0	5.1E-12
	GOTERM_CC_DIRECT	GO:0000776~kinetochore	9	15.0	1.7E-10
	GOTERM_CC_DIRECT	GO:0005874~microtubule	13	21.7	2.2E-10
	GOTERM_CC_DIRECT	GO:0072686~mitotic spindle	6	10.0	1.9E-07
	GOTERM_CC_DIRECT	GO:0000777~condensed chromosome kinetochore	6	10.0	8.3E-06
	GOTERM_CC_DIRECT	GO:0005876~spindle microtubule	5	8.3	1.1E-05
	GOTERM_CC_DIRECT	GO:0097149~centralspindlin complex	3	5.0	3.0E-05
	GOTERM_CC_DIRECT	GO:0000784~nuclear chromosome, telomeric region	3	5.0	6.4E-02
	GOTERM_MF_DIRECT	GO:0003777~microtubule motor activity	9	15.0	3.2E-10
	GOTERM_MF_DIRECT	GO:0008017~microtubule binding	10	16.7	4.1E-08
	GOTERM_MF_DIRECT	GO:0008574~ATP-dependent microtubule motor activity, plus-end-directed	4	6.7	2.7E-05
	GOTERM_MF_DIRECT	GO:0016887~ATPase activity	7	11.7	4.2E-05
	GOTERM_MF_DIRECT	GO:0004672~protein kinase activity	6	10.0	8.3E-03
	GOTERM_MF_DIRECT	GO:0004674~protein serine/threonine kinase activity	6	10.0	1.0E-02
	GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	3	5.0	2.3E-02
	GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	3	5.0	2.7E-01
Down	GOTERM_BP_DIRECT	GO:0032355~response to estradiol	7	8.2	5.0E-06

GOTERM_BP_DIRECT	GO:0044849~estrous cycle	3	3.5	3.0E-03
GOTERM_BP_DIRECT	GO:0042493~response to drug	7	8.2	3.5E-03
GOTERM_BP_DIRECT	GO:0045926~negative regulation of growth	3	3.5	3.7E-03
GOTERM_BP_DIRECT	GO:0071294~cellular response to zinc ion	3	3.5	3.7E-03
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	4	4.7	4.9E-03
GOTERM_BP_DIRECT	GO:0008544~epidermis development	4	4.7	8.0E-03
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	4	4.7	1.6E-02
GOTERM_CC_DIRECT	GO:0005882~intermediate filament	4	4.7	1.4E-02
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	5	5.9	3.3E-02
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	6	7.1	1.5E-01
GOTERM_MF_DIRECT	GO:0008201~heparin binding	5	5.9	7.0E-03
GOTERM_MF_DIRECT	GO:0005200~structural constituent of cytoskeleton	4	4.7	1.5E-02
GOTERM_MF_DIRECT	GO:0005198~structural molecule activity	5	5.9	3.0E-02
GOTERM_MF_DIRECT	GO:0003690~double-stranded DNA binding	3	3.5	5.7E-02
GOTERM_MF_DIRECT	GO:0043565~sequence-specific DNA binding	5	5.9	2.3E-01
GOTERM_MF_DIRECT	GO:0003700~transcription factor activity, sequence-specific DNA binding	7	8.2	3.0E-01
GOTERM_MF_DIRECT	GO:0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	3	3.5	3.1E-01
GOTERM_MF_DIRECT	GO:0003677~DNA binding	6	7.1	9.1E-01

DEGs = differentially expressed genes.