

A potential prognostic long non-coding RNA signature to predict metastasis-free survival of breast cancer patients

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Supplementary Table S1. Functional enrichment analysis of GO and KEGG pathway for mRNA positively correlated with prognostic lncRNAs

Function category	Function term	P value	Fold Enrichment
hsa04110:	Cell cycle	5.08E-03	3.33
hsa04114:	Oocyte meiosis	3.00E-02	2.94
hsa04115:	p53 signaling pathway	4.72E-02	3.4
GO:0031571	G1 DNA damage checkpoint	1.61E-02	15
GO:0005979	regulation of glycogen biosynthetic process	2.58E-02	11.78
GO:0032885	regulation of polysaccharide biosynthetic process	2.58E-02	11.78
GO:0010962	regulation of glucan biosynthetic process	2.58E-02	11.78
GO:0032881	regulation of polysaccharide metabolic process	2.94E-02	11
GO:0021545	cranial nerve development	4.56E-02	8.68
GO:0051184	cofactor transporter activity	2.14E-02	12.97
GO:0004033	aldo-keto reductase activity	2.82E-02	11.24
GO:0031575	G1/S transition checkpoint	3.31E-03	12.94
GO:0014032	neural crest cell development	2.15E-02	6.67
GO:0014033	neural crest cell differentiation	2.15E-02	6.67
GO:0009062	fatty acid catabolic process	2.70E-02	6.11
GO:0007051	spindle organization	4.77E-02	4.89
GO:0007093	mitotic cell cycle checkpoint	7.45E-03	6.39
GO:0000077	DNA damage checkpoint	1.09E-02	5.73
GO:0031570	DNA integrity checkpoint	1.44E-02	5.29
GO:0031329	regulation of cellular catabolic process	2.45E-02	4.51
GO:0009063	cellular amino acid catabolic process	3.47E-02	4.04
GO:0006986	response to unfolded protein	3.97E-02	3.87
GO:0042770	DNA damage response, signal transduction	1.50E-02	4.12
GO:0009894	regulation of catabolic process	3.02E-02	3.44
GO:0051789	response to protein stimulus	4.49E-02	3.08
GO:0001655	urogenital system development	4.96E-02	3
GO:0000075	cell cycle checkpoint	1.30E-03	4.83
GO:0040007	growth	4.90E-02	2.4
GO:0003774	motor activity	1.32E-02	3.17
GO:0046395	carboxylic acid catabolic process	9.17E-04	4.46
GO:0016054	organic acid catabolic process	9.17E-04	4.46
GO:0032269	negative regulation of cellular protein metabolic process	1.69E-02	2.75
GO:0051248	negative regulation of protein metabolic process	2.06E-02	2.65
GO:0006605	protein targeting	4.20E-02	2.3
GO:0050662	coenzyme binding	1.54E-02	2.79
GO:0003924	GTPase activity	3.46E-02	2.4
GO:0009055	electron carrier activity	4.35E-02	2.29
GO:0000226	microtubule cytoskeleton organization	1.43E-03	3.74
GO:0003006	reproductive developmental process	4.93E-02	2.1
GO:0003735	structural constituent of ribosome	3.06E-03	3.35
GO:0006414	translational elongation	1.43E-05	5.99

GO:0051301	cell division	1.89E-02	2.24
GO:0000280	nuclear division	6.78E-04	3.25
GO:0007067	mitosis	6.78E-04	3.25
GO:0048285	organelle fission	9.63E-04	3.12
GO:0000087	M phase of mitotic cell cycle	2.24E-04	3.44
GO:0007017	microtubule-based process	7.19E-04	3.04
GO:0051726	regulation of cell cycle	7.45E-03	2.33
GO:0000279	M phase	9.84E-04	2.67
GO:0006412	translation	1.05E-03	2.66
GO:0000278	mitotic cell cycle	4.20E-04	2.68
GO:0022403	cell cycle phase	1.95E-04	2.66
GO:0022402	cell cycle process	2.47E-04	2.34
GO:0007049	cell cycle	1.66E-04	2.13

Supplementary Table S2. Clinical and pathological characteristics of patients with breast cancer in our study.

Characteristics		Training dataset n=254	Testing dataset n=254	GSE25066 dataset n=508	GSE4922 dataset n=289	GSE1456 dataset n=159
Age, no (%)	(0, 40]	46 (18%)	51 (20%)	97 (19%)	19 (7%)	
	(40, 50]	103 (40%)	77 (30%)	180 (35%)	35 (12%)	
	(50, 60]	58 (23%)	77 (30%)	135 (27%)	52 (18%)	
	(60, 70]	37 (15%)	44 (17%)	81 (16%)	65 (22%)	
	(70, 99)	10 (4%)	5 (2%)	15 (3%)	78 (27%)	
	NA				40 (14%)	
ER, no (%)	P	140 (55%)	157 (62%)	297 (58%)	211 (73%)	
	N	110 (43%)	95 (37%)	205 (40%)	34 (12%)	
	I	2 (1%)	2 (1%)	4 (1%)	0	
	NA	2 (1%)	0	2 (1%)	44 (15%)	
ESR1, no (%)	P	145 (57%)	146 (57%)	291 (57%)		
	N	109 (43%)	108 (43%)	217 (43%)		
ERBB2, no (%)	P	14 (5%)	16 (6%)	29 (6%)		
	N	241 (95%)	238 (94%)	479 (94%)		
Tumor size, no (%)	(0, 3]				211 (73%)	
	(3, 5]				32 (11%)	
	(5, 13]				6 (2%)	
	NA				40 (14%)	
Metastasis event	Yes(1)	62 (24%)	49 (19%)	111 (22%)	89 (31%)	40 (25%)
	NO(0)	192 (76%)	205 (81%)	397 (78%)	160 (55%)	119 (75%)
	NA	0	0	0	40 (14%)	

Supplementary Table S3. The detailed information of probe sets and their corresponding lncRNAs in the Affymetrix HG-U133A platform used in our study

lncRNA ID	Probe
ENSG00000093100.13	212715_s_at
ENSG00000116652.6	215629_s_at
ENSG00000126005.13	213171_s_at
ENSG00000130600.13	217723_x_at
ENSG00000152931.7	"205834_s_at,215972_at"
ENSG00000157306.12	"207699_at,214341_at,218540_at"
ENSG00000173867.8	215919_s_at
ENSG00000175147.9	213752_at
ENSG00000176868.2	212069_s_at
ENSG00000177133.8	207890_s_at
ENSG00000177699.4	215688_at
ENSG00000182109.5	220204_s_at
ENSG00000182873.5	220846_s_at
ENSG00000183562.3	220514_at
ENSG00000186056.7	215053_at
ENSG00000187621.12	219840_s_at
ENSG00000189223.11	"209552_at,213917_at"
ENSG00000197670.5	215861_at
ENSG00000203325.3	214185_at
ENSG00000203386.4	"208725_at,209297_at,209298_s_at,216628_at"
ENSG00000203605.3	206250_x_at
ENSG00000203876.7	222072_at
ENSG00000204929.9	217012_at
ENSG00000204971.3	204437_s_at
ENSG00000205054.4	"207999_s_at,209578_s_at,212421_at,217118_s_at"
ENSG00000205861.9	222277_at
ENSG00000211683.3	221108_at
ENSG00000213904.6	"206576_s_at,206676_at,209498_at"
ENSG00000214184.3	202832_at
ENSG00000215866.5	213739_at
ENSG00000215908.6	221988_at
ENSG00000221819.4	207615_s_at
ENSG00000223442.1	209349_at
ENSG00000223479.3	214276_at
ENSG00000223563.1	219935_at
ENSG00000223647.1	210052_s_at
ENSG00000223653.3	"206837_at,209094_at"
ENSG00000223745.5	201798_s_at
ENSG00000223774.3	211562_s_at
ENSG00000223797.3	206191_at
ENSG00000223799.1	204786_s_at

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ENSG00000223907.1 212758_s_at
ENSG00000223910.1 209538_at
ENSG00000223947.1 "205459_s_at,213462_at,39549_at"
ENSG00000223949.4 "201716_at,213364_s_at,216357_at"
ENSG00000224063.3 "213258_at,214378_at"
ENSG00000224066.1 219585_at
ENSG00000224078.10 "211575_s_at,213128_s_at,213291_s_at,221001_at,221974_at"
ENSG00000224081.5 "208468_at,215103_at,216739_at"
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ENSG00000224149.1 212352_s_at
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ENSG00000224459.1 208520_at
ENSG00000224505.2 202815_s_at
ENSG00000224597.7 202565_s_at
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ENSG00000237298.6 208195_at
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ENSG00000237413.3 206360_s_at
ENSG00000237416.4 216058_s_at
ENSG00000237435.6 206643_at
ENSG00000237491.6 "208954_s_at,218725_at,218993_at,220806_x_at"
ENSG00000237505.4 213063_at
ENSG00000237517.6 215003_at
ENSG00000237667.3 216505_x_at
ENSG00000237781.3 220578_at
ENSG00000237836.3 209439_s_at
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