

Table SI. Clinicopathological parameters of patients with IDC.

Parameters	Breast cancer (n=25)
Age (years)	47.71±9.12
Height (m)	1.56±0.05
Weight (kg)	57.26±8.89
Body mass index (kg/m ²)	23.74±4.35
ER ⁺ , n (%)	19 (76)
ER ⁻ , n (%)	6 (24)
PR ⁺ , n (%)	18 (72)
PR ⁻ , n (%)	7 (28)
ER ⁺ /PR ⁺ , n (%)	13 (52)
ER ⁻ /PR ⁻ , n (%)	3 (12)
HER2 ⁺ , n (%)	5 (20)
HER2 ⁻ , n (%)	9 (36)
ER ⁺ /PR ⁺ , HER-2 ⁻ , n (%)	7 (28)
ER ⁺ /PR ⁺ , HER-2 ⁺ , n (%)	3 (12)
ER ⁻ /PR ⁻ , HER-2 ⁺ , n (%)	2 (8)
ER ⁻ /PR ⁻ , HER-2 ⁻ , n (%)	2 (8)
Lymphatic metastasis, n (%)	7 (28)
Tumor size (cm)	2.15±0.71
Stage 0, n (%)	2 (8)
Stage 1, n (%)	3 (12)
Stage 2, n (%)	5 (20)
Stage 3, n (%)	15 (60)

Values are presented as number (percentage) or mean ± SD. IDC, invasive ductal carcinoma; ER, estrogen receptor; PR, progesterone receptor; HER-2, human epidermal growth factor receptor 2.

Table SII. Serum FFA levels in patients with IDC and healthy controls.

No.	RT	FFAs ($\mu\text{g/ml}$)	Healthy control (n=19)	IDC (n=25)	P-value	Change	Mean fold
1	17.04	C12:0	34.5887879	37.96937501	0.6305	↑	1.10
2	19.76	C14:0	194.8496605	238.919325	0.0087 ^b	↑	1.23
3	21.5	C15:0	33.68282117	54.21263189	0.0008 ^c	↑	1.61
4	23.31	C16:1	59.90275083	90.10916183	0.1076	↑	1.50
5	23.8	C16:0	3545.346856	4376.244155	0.0191 ^a	↑	1.23
6	27.77	C18:2	2126.503947	3060.884378	0.0338 ^a	↑	1.44
7	27.89	C18:1	1479.430689	2515.951543	0.0017 ^b	↑	1.70
8	28.44	C18:0	2468.298307	2988.826595	0.0312 ^a	↑	1.21
9	31.31	C20:4	407.1559372	688.1518609	0.014 ^a	↑	1.69
10	31.68	C20:3	81.36529209	134.715364	0.0926	↑	1.66
11	32.17	C20:1	19.05303406	38.09160524	0.0343 ^a	↑	2.00
12	32.74	C20:0	29.94057555	42.44137519	0.0367 ^a	↑	1.42
13	36.18	C22:6	100.3944558	169.9744756	0.0236 ^a	↑	1.69
14	36.58	C22:4	23.85014306	42.36758227	0.043 ^a	↑	1.78
15	37.55	C22:1	38.33857879	43.77456635	0.3024	↑	1.14
16	38.15	C22:0	25.33922039	55.78587047	0.0077 ^b	↑	2.20

RT, retention time, Data are presented as means \pm SEM. ^aP<0.05, ^bP<0.01, ^cP<0.001 compared with healthy controls; mean fold is the ratio of mean FASN in IDC patients vs. healthy controls. FFA, free fatty acids; IDC, invasive ductal carcinoma; FASN, fatty acid synthase.

Table SIII. Levels of FFAs in patients with IDC exhibiting high and low FASN expression.

No.	RT	FFAs ($\mu\text{g/ml}$)	High FASN expression (n=12)	No/low FASN expression (n=13)	P-value	Change
1	23.8	C16:0	4982.76	3816.39	0.023	↑
2	27.89	C18:1	3175.37	1907.26	0.017	↑
3	28.44	C18:0	3397.54	2611.55	0.015	↑
4	31.31	C20:4	934.08	461.14	0.008	↑

RT, retention time, Data are presented as means \pm SEM. ^aP<0.05, ^bP<0.01 compared with healthy controls. FFA, free fatty acids; IDC, invasive ductal carcinoma; FASN, fatty acid synthase.

Table SIII. Top 20 of GO biological process enrichment analysis for differentially expressed genes (P<0.05).

GO biological process	GO	Count	P-value
Regulation of multicellular organismal process	GO:0051239	69	4.71x10 ⁻⁰⁷
Ossification	GO:0001503	15	1.06x10 ⁻⁰⁶
Skeletal system development	GO:0001501	21	1.27x10 ⁻⁰⁶
Extracellular matrix organization	GO:0030198	17	1.43x10 ⁻⁰⁶
Extracellular structure organization	GO:0043062	17	1.48x10 ⁻⁰⁶
Regulation of multicellular organismal development	GO:2000026	50	1.73x10 ⁻⁰⁶
Animal organ development	GO:0048513	67	3.56x10 ⁻⁰⁶
System development	GO:0048731	85	3.71x10 ⁻⁰⁶
Anatomical structure morphogenesis	GO:0009653	50	5.51x10 ⁻⁰⁶
Skeletal system morphogenesis	GO:0048705	13	1.16x10 ⁻⁰⁵
Regulation of developmental process	GO:0050793	56	1.19x10 ⁻⁰⁵
Animal organ morphogenesis	GO:0009887	29	1.32x10 ⁻⁰⁵
Multicellular organism development	GO:0007275	91	1.45x10 ⁻⁰⁵
Bone morphogenesis	GO:0060349	9	1.69x10 ⁻⁰⁵
Tube development	GO:0035295	26	1.79x10 ⁻⁰⁵
Multicellular organismal process	GO:0032501	115	3.75x10 ⁻⁰⁵
Collagen fibril organization	GO:0030199	6	4.11x10 ⁻⁰⁵
Bone development	GO:0060348	11	5.30x10 ⁻⁰⁵
Nucleic acid metabolic process	GO:0090304	9	5.33x10 ⁻⁰⁵
Mesenchyme development	GO:0060485	11	8.63x10 ⁻⁰⁵

GO, Gene Ontology.

Table SIV. Top 20 of GO molecular function enrichment analysis for differentially expressed genes (P<0.05).

GO molecular function	GO	Count	P-value
Glycosaminoglycan binding	GO:0005539	16	5.21x10 ⁻⁰⁸
Hemoglobin binding	GO:0030492	5	4.06x10 ⁻⁰⁷
Extracellular matrix structural constituent	GO:0005201	11	8.27x10 ⁻⁰⁶
Heparin binding	GO:0008201	11	1.26x10 ⁻⁰⁵
Sulfur compound binding	GO:1901681	12	8.52x10 ⁻⁰⁵
Serine-type endopeptidase activity	GO:0004252	9	3.26x10 ⁻⁰⁴
Signaling receptor binding	GO:0005102	36	6.44x10 ⁻⁰⁴
Serine-type peptidase activity	GO:0008236	9	7.44x10 ⁻⁰⁴
Organic cyclic compound binding	GO:0097159	50	7.87x10 ⁻⁰⁴
Hydrolase activity, acting on acid phosphorus-nitrogen bonds	GO:0016825	9	8.83x10 ⁻⁰⁴
Serine hydrolase activity	GO:0017171	9	8.83x10 ⁻⁰⁴
Growth factor activity	GO:0008083	8	1.04x10 ⁻⁰³
Receptor ligand activity	GO:0048018	15	1.05x10 ⁻⁰³
Structural molecule activity	GO:0005198	19	1.11x10 ⁻⁰³
Signaling receptor activator activity	GO:0030546	15	1.17x10 ⁻⁰³
Heterocyclic compound binding	GO:1901363	50	1.25x10 ⁻⁰³
Endopeptidase activity	GO:0004175	14	1.46x10 ⁻⁰³
Chloride transmembrane transporter activity	GO:0015108	6	1.63x10 ⁻⁰³
Metalloendopeptidase activity	GO:0004222	6	1.88x10 ⁻⁰³
Integrin binding	GO:0005178	7	1.93x10 ⁻⁰³

GO, Gene Ontology.

Table SV. Top 20 of GO cellular component enrichment analysis for differentially expressed genes (P<0.05).

GO cellular component	GO	Count	P-value
Extracellular region	GO:0005576	105	1.15x10 ⁻¹³
Extracellular space	GO:0005615	78	3.78x10 ⁻⁰⁹
Specific granule lumen	GO:0035580	10	1.28x10 ⁻⁰⁸
Extracellular matrix	GO:0031012	25	1.53x10 ⁻⁰⁸
Collagen-containing extracellular matrix	GO:0062023	21	4.96x10 ⁻⁰⁸
Specific granule	GO:0042581	12	1.04x10 ⁻⁰⁶
Nucleus	GO:0005634	60	6.35x10 ⁻⁰⁵
Phagocytic vesicle lumen	GO:0097013	3	8.81x10 ⁻⁰⁵
Secretory vesicle	GO:0099503	27	1.63x10 ⁻⁰⁴
Endocytic vesicle lumen	GO:0071682	4	1.70x10 ⁻⁰⁴
Secretory granule lumen	GO:0034774	13	1.83x10 ⁻⁰⁴
Cytoplasmic vesicle lumen	GO:0060205	13	2.05x10 ⁻⁰⁴
Vesicle lumen	GO:0031983	13	2.18x10 ⁻⁰⁴
Endocytic vesicle	GO:0030139	13	2.30x10 ⁻⁰⁴
Cellular anatomical entity	GO:0110165	240	2.49x10 ⁻⁰⁴
Extracellular exosome	GO:0070062	44	2.93x10 ⁻⁰⁴
Phagocytic vesicle	GO:0045335	8	3.12x10 ⁻⁰⁴
Secretory granule	GO:0030141	23	3.25x10 ⁻⁰⁴
Extracellular vesicle	GO:1903561	44	3.28x10 ⁻⁰⁴
Extracellular organelle	GO:0043230	44	3.38x10 ⁻⁰⁴

GO, Gene Ontology.

Table SVI. Top 20 of Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis for differentially expressed genes (P<0.05).

ID	Description	P-value	Count	GeneID
hsa05150	Staphylococcus aureus infection	0.00061	6	HLA-DRB5, DEFA4, HLA-DQB1, C4B, C4A, KRT17
hsa04151	PI3K-Akt signaling pathway	0.005105	10	KITLG, FGF18, THBS3, FGF7, ITGA11, GNG2, ITGB8, FGF9, CSH1, GH1
hsa05226	Gastric cancer	0.005705	6	FGF18, FGF7, FZD7, FGF9, JUP, FZD1
hsa05221	Acute myeloid leukemia	0.006083	4	CCNA1, CEBPE, MPO, JUP
hsa05133	Pertussis	0.009454	4	C4BPA, C4B, C4A, C4BPB
hsa04080	Neuroactive ligand-receptor interaction	0.011739	9	TRH, GABRD, EDN2, S1PR1, GABRP, TBXA2R, CSH1, GH1, INSL3
hsa04610	Complement and coagulation cascades	0.013857	4	C4BPA, C4B, C4A, C4BPB
hsa05322	Systemic lupus erythematosus	0.015075	5	HLA-DRB5, HLA-DQB1, C4B, C4A, ELANE
hsa04512	Extracellular matrix-receptor interaction	0.015571	4	DMP1, THBS3, ITGA11, ITGB8
hsa05202	Transcriptional misregulation in cancer	0.016012	6	CCNA1, CEBPE, MPO, ELANE, COMMD3-BMI1, JUP
hsa04727	GABAergic synapse	0.01617	4	ADCY1, GABRD, GNG2, GABRP
hsa05032	Morphine addiction	0.017413	4	ADCY1, GABRD, GNG2, GABRP
hsa04974	Protein digestion and absorption	0.020073	4	COL5A1, SLC7A8, COL3A1, COL5A2
hsa04514	Cell adhesion molecules	0.022259	5	HLA-DRB5, HLA-DQB1, VCAN, ITGB8, PTPRF
hsa05224	Breast cancer	0.022259	5	FGF18, FGF7, FZD7, FGF9, FZD1
hsa04916	Melanogenesis	0.024513	4	ADCY1, KITLG, FZD7, FZD1
hsa04145	Phagosome	0.025285	5	HLA-DRB5, HLA-DQB1, THBS3, MPO, COLEC12
hsa04015	Rap1 signaling pathway	0.027243	6	ADCY1, KITLG, FGF18, FGF7, EVL, FGF9
hsa04725	Cholinergic synapse	0.034091	4	ADCY1, GNG2, KCNJ12, KCNQ5
hsa04014	Ras signaling pathway	0.041318	6	PLA2G2A, KITLG, FGF18, FGF7, GNG2, FGF9

Table SVII. Top 20 of GO biological process enrichment analysis for differentially expressed genes in competing endogenous RNA network (P<0.05).

GO biological process	GO	Count	P-value
Animal organ morphogenesis	GO:0009887	16	6.11x10 ⁻⁰⁹
Anatomical structure morphogenesis	GO:0009653	22	2.59x10 ⁻⁰⁸
Extracellular matrix organization	GO:0030198	10	3.84x10 ⁻⁰⁸
Extracellular structure organization	GO:0043062	10	3.95x10 ⁻⁰⁸
Ossification	GO:0001503	9	4.89x10 ⁻⁰⁸
System development	GO:0048731	31	6.46x10 ⁻⁰⁸
Osteoblast differentiation	GO:0001649	7	7.48x10 ⁻⁰⁸
Multicellular organism development	GO:0007275	33	8.21x10 ⁻⁰⁸
Blood vessel development	GO:0001568	11	1.12x10 ⁻⁰⁷
Skeletal system development	GO:0001501	11	1.36x10 ⁻⁰⁷
Regulation of developmental process	GO:0050793	23	1.48x10 ⁻⁰⁷
Vasculature development	GO:0001944	11	1.71x10 ⁻⁰⁷
Blood vessel morphogenesis	GO:0048514	10	2.04x10 ⁻⁰⁷
Cardiovascular system development	GO:0072358	11	2.07x10 ⁻⁰⁷
Tube morphogenesis	GO:0035239	12	2.32x10 ⁻⁰⁷
Negative regulation of developmental process	GO:0051093	14	2.63x10 ⁻⁰⁷
Regulation of multicellular organismal development	GO:2000026	20	2.96x10 ⁻⁰⁷
Negative regulation of cell differentiation	GO:0045596	12	5.06x10 ⁻⁰⁷
tube development	GO:0035295	13	5.13x10 ⁻⁰⁷
Anatomical structure development	GO:0048856	33	5.75x10 ⁻⁰⁷

GO, Gene Ontology.

Table SVIII. Top 20 of GO molecular function enrichment analysis for differentially expressed genes in competing endogenous RNA network (P<0.05).

GO molecular function	GO	Count	P-value
Glycosaminoglycan binding	GO:0005539	8	3.17x10 ⁻⁰⁷
Extracellular matrix structural constituent	GO:0030492	6	7.50x10 ⁻⁰⁶
Heparin binding	GO:0005201	6	9.74x10 ⁻⁰⁶
Integrin binding	GO:0008201	5	5.10x10 ⁻⁰⁵
Sulfur compound binding	GO:1901681	6	8.08x10 ⁻⁰⁵
Extracellular matrix structural constituent conferring tensile strength	GO:0004252	3	2.42x10 ⁻⁰⁴
Cell adhesion molecule binding	GO:0005102	7	4.63x10 ⁻⁰⁴
Platelet-derived growth factor binding	GO:0008236	2	6.64x10 ⁻⁰⁴
Growth factor binding	GO:0097159	4	6.86x10 ⁻⁰⁴
Binding	GO:0016825	53	9.13x10 ⁻⁰⁴
SMAD binding	GO:0017171	3	1.35x10 ⁻⁰³
Wnt-activated receptor activity	GO:0008083	2	1.37x10 ⁻⁰³
Molecular_function	GO:0048018	57	1.50x10 ⁻⁰³
	GO:0005198		
Signaling receptor binding	GO:0030546	12	1.88x10 ⁻⁰³
Protein binding	GO:1901363	45	2.00x10 ⁻⁰³
Fibronectin binding	GO:0004175	2	3.09x10 ⁻⁰³
Structural molecule activity	GO:0015108	7	3.15x10 ⁻⁰³
Protein-containing complex binding	GO:0004222	9	4.17x10 ⁻⁰³
Wnt-protein binding	GO:0005178	2	4.42x10 ⁻⁰³

GO, Gene Ontology.

Table SIX. Top 20 of GO cellular component enrichment analysis for differentially expressed genes in competing endogenous RNA network (P<0.05).

GO cellular component	GO	Count	P-value
Extracellular matrix	GO:0031012	10	1.95x10 ⁻⁰⁶
Fibrillar collagen trimer	GO:0005583	3	8.54x10 ⁻⁰⁶
Banded collagen fibril	GO:0098643	3	8.54x10 ⁻⁰⁶
Collagen-containing extracellular matrix	GO:0062023	8	1.65x10 ⁻⁰⁵
Extracellular region	GO:0005576	26	3.03x10 ⁻⁰⁵
Complex of collagen trimers	GO:0098644	3	3.73x10 ⁻⁰⁵
Collagen type V trimer	GO:0005588	2	7.26x10 ⁻⁰⁵
Integrin complex	GO:0008305	3	1.18x10 ⁻⁰⁴
Collagen trimer	GO:0005581	4	1.26x10 ⁻⁰⁴
Extracellular space	GO:0005615	21	1.65x10 ⁻⁰⁴
Basement membrane	GO:0005604	4	1.73x10 ⁻⁰⁴
Protein complex involved in cell adhesion	GO:0098636	3	1.77x10 ⁻⁰⁴
Endoplasmic reticulum lumen	GO:0005788	6	2.19x10 ⁻⁰⁴
Interstitial matrix	GO:0005614	2	6.51x10 ⁻⁰⁴
Integral component of membrane	GO:0016021	28	8.94x10 ⁻⁰⁴
Focal adhesion	GO:0005925	6	9.57x10 ⁻⁰⁴
Cell-substrate junction	GO:0030055	6	1.04x10 ⁻⁰³
Intrinsic component of membrane	GO:0031224	28	1.05x10 ⁻⁰³
Plasma membrane	GO:0005886	27	1.59x10 ⁻⁰³
Cell periphery	GO:0071944	27	2.78x10 ⁻⁰³

GO, Gene Ontology.