

Supplementary Table S4.

Downregulated gene profile in human breast cancer MDA-MB-231 cells with fucoxanthinol (FxOH) treatment.^a

No.	Gene symbol	Description	Fold ^b	p-Value ^c
1	<i>HIST1H2BM</i>	Histone cluster 1, H2bm	-104.5	4.0 × 10 ⁻¹¹
2	<i>TNFSF10</i>	Tumor necrosis factor (ligand) superfamily, member 10	-37.0	3.7 × 10 ⁻⁷
3	<i>CEMIP</i>	Cell migration inducing protein, hyaluronan binding	-25.1	2.1 × 10 ⁻⁶
4	<i>SPRY1</i>	Sprouty RTK signaling antagonist 1	-14.1	4.8 × 10 ⁻⁹
5	<i>TMEM19</i>	Transmembrane protein 19	-12.3	2.1 × 10 ⁻⁹
6	<i>CDH11</i>	Cadherin 11, type 2, OB-cadherin (osteoblast)	-12.3	9.7 × 10 ⁻⁹
7	<i>HIST1H2AG</i>	Histone cluster 1, H2ag	-12.2	2.5 × 10 ⁻¹⁰
8	<i>FAM111B</i>	Family with sequence similarity 111, member B	-11.8	5.7 × 10 ⁻⁹
9	<i>COL13A1</i>	Collagen, type XIII, alpha 1	-11.2	5.5 × 10 ⁻⁸
10	<i>PLAU</i>	Plasminogen activator, urokinase	-11.1	9.6 × 10 ⁻¹⁰
11	<i>POLE2</i>	Polymerase (DNA directed), epsilon 2, accessory subunit	-10.2	4.9 × 10 ⁻⁸
12	<i>SERTAD4</i>	SERTA domain containing 4	-9.8	2.0 × 10 ⁻⁸
13	<i>CDK1</i>	Cyclin-dependent kinase 1	-9.5	2.7 × 10 ⁻⁹
14	<i>HIST1H2AM</i>	Histone cluster 1, H2am; histone cluster 1, H3j	-9.2	6.3 × 10 ⁻⁹
15	<i>SCARA3</i>	Scavenger receptor class A, member 3	-9.0	5.1 × 10 ⁻⁸
16	<i>E2F1</i>	E2F transcription factor 1	-9.0	1.5 × 10 ⁻⁸
17	<i>UNG</i>	Uracil DNA glycosylase	-8.8	4.9 × 10 ⁻⁹
18	<i>TBC1D2</i>	TBC1 domain family, member 2	-8.7	8.8 × 10 ⁻⁹
19	<i>ESCO2</i>	Establishment of sister chromatid cohesion N-acetyltransferase 2	-8.6	1.3 × 10 ⁻⁹
20	<i>VIPR1</i>	Vasoactive intestinal peptide receptor 1	-8.6	9.4 × 10 ⁻⁹
21	<i>HIST2H3A</i>	Histone cluster 2, H3a	-8.5	7.9 × 10 ⁻⁹
22	<i>CHAF1B</i>	Chromatin assembly factor 1, subunit B (p60)	-8.5	2.6 × 10 ⁻⁹
23	<i>MCM5</i>	Minichromosome maintenance complex component 5	-8.5	2.7 × 10 ⁻⁸
24	<i>SAA2</i>	Serum amyloid A2	-8.4	2.6 × 10 ⁻⁶
25	<i>FBXO5</i>	F-box protein 5	-8.3	2.5 × 10 ⁻⁹
26	<i>LAMB1^d</i>	Laminin, beta 1	-8.3	1.7 × 10 ⁻⁹
27	<i>SLCO4A1</i>	Solute carrier organic anion transporter family, member 4A1	-8.0	5.4 × 10 ⁻⁸
28	<i>HIST1H2BJ</i>	Histone cluster 1, H2bj	-7.9	1.3 × 10 ⁻⁸
29	<i>E2F8</i>	E2F transcription factor 8	-7.9	1.9 × 10 ⁻⁸
30	<i>TOP2A</i>	Topoisomerase (DNA) II alpha	-7.8	6.0 × 10 ⁻⁹
31	<i>ADGRF5</i>	Adhesion G protein-coupled receptor F5	-7.8	1.9 × 10 ⁻⁷
32	<i>RIN2</i>	Ras and Rab interactor 2	-7.8	3.8 × 10 ⁻⁷
33	<i>THBS1^d</i>	Thrombospondin 1	-7.8	5.8 × 10 ⁻⁹
34	<i>LMNB1</i>	Lamin B1	-7.8	2.8 × 10 ⁻⁸
35	<i>KCNN4</i>	Potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 4	-7.7	2.5 × 10 ⁻⁷
36	<i>EFEMP1</i>	EGF containing fibulin-like extracellular matrix protein 1	-7.7	3.7 × 10 ⁻⁹
37	<i>HIST2H3A</i>	Histone cluster 2, H3a; histone cluster 2, H3c	-7.7	8.4 × 10 ⁻⁹
38	<i>MCM6</i>	Minichromosome maintenance complex component 6	-7.5	4.7 × 10 ⁻⁸
39	<i>SDC3^d</i>	Syndecan 3	-7.4	6.9 × 10 ⁻⁹

40	<i>MYH10</i>	Myosin, heavy chain 10, non-muscle	-7.4	7.1×10^{-8}
41	<i>PLAT</i>	Plasminogen activator, tissue	-7.3	6.0×10^{-9}
42	<i>TGOLN2</i>	Trans-golgi network protein 2	-7.3	1.5×10^{-8}
43	<i>CDCA7</i>	Cell division cycle associated 7	-7.3	2.5×10^{-6}
44	<i>MCM3</i>	Minichromosome maintenance complex component 3	-7.2	4.2×10^{-9}
45	<i>DDX12P</i>	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 12, pseudogene	-7.2	1.8×10^{-8}
46	<i>SKP2</i>	S-Phase kinase-associated protein 2, E3 ubiquitin protein ligase	-7.2	2.7×10^{-8}
47	<i>HIST1H2AB</i>	Histone cluster 1, H2ab	-7.2	6.5×10^{-9}
48	<i>CTDSP1</i>	CTD small phosphatase like	-7.2	9.4×10^{-9}
49	<i>NCAPH</i>	Non-SMC condensin I complex subunit H	-7.1	7.5×10^{-9}
50	<i>LAMA5^d</i>	Laminin, alpha 5	-7.1	5.6×10^{-8}
ECM receptor interaction signal				
	<i>COL6A3</i>	Collagen, type VI, alpha3	-6.4	8.9×10^{-7}
	<i>LAMA5</i>	Laminin, alpha 5	-7.1	5.6×10^{-8}
	<i>LAMB1</i>	Laminin, beta 1	-8.3	1.7×10^{-9}
	<i>SDC3</i>	Syndecan 3	-7.4	6.9×10^{-9}
	<i>COL5A1</i>	Collagen, type V, alpha 1	-5.5	8.3×10^{-9}
	<i>ITGB4</i>	Integrin beta 4	-5.2	9.1×10^{-8}
	<i>ITGB5</i>	Integrin beta 5	-6.2	3.8×10^{-9}
	<i>SDC1</i>	Syndecan 1	-4.6	1.6×10^{-6}
	<i>ITGA6</i>	Integrin alpha 6	-6.3	1.9×10^{-9}
	<i>LAMA3</i>	Laminin, alpha 3	-3.2	1.3×10^{-7}
	<i>THBS1</i>	Thrombospondin 1	-7.8	5.8×10^{-9}
	<i>ITGB8</i>	Integrin beta 8	-2.0	0.0003
	<i>DAG1</i>	Dystroglycan 1	-4.5	1.3×10^{-8}
	<i>COL4A1</i>	Collagen, type IV, alpha 1	-2.2	0.0002
	<i>AGRN</i>	Agrin	-2.2	3.1×10^{-6}
	<i>FN1</i>	Fibronectin 1	-2.7	1.1×10^{-5}
	<i>CD44</i>	CD44 molecule	-2.5	4.8×10^{-5}
	<i>ITGAV</i>	Integrin alpha V	-2.7	5.0×10^{-6}
	<i>LAMC2</i>	Laminin, gamma 2	-2.9	1.2×10^{-5}
	<i>COL6A1</i>	Collagen, type VI, alpha 1	-2.6	3.8×10^{-5}
	<i>LAMB3</i>	Laminin, beta 3	-2.7	7.7×10^{-7}
	<i>CD47</i>	CD47 molecule	-2.3	3.1×10^{-6}
	<i>ITGA3</i>	Integrin alpha 3	-2.8	4.1×10^{-7}
	<i>ITGB1</i>	Integrin beta 1	-2.7	7.3×10^{-7}

^a Among all 1,702 downregulated genes with significant alterations, the top 50 genes (fold) with 24 genes belonging to ECM receptor interaction signal were shown. ^b Fold change of gene expression in MDA-MB-231 cells with FxOH treatment, compared

with that of control cells. ^c Significant difference between MDA-MB-231 cells with and without FxOH treatment using one-way ANOVA ($n=3$). ^d The genes were overlapped with the genes list of ECM receptor interaction signal