

Supplementary Table 3. Expression of genes regulating the processes glycolysis in MDA-MB-231HM.LNm5 (MDA-231HM.LNm5) and parental MDA-MB-231 (MDA-231) cell lines, as detected by RNA-seq

Gene symbol	Gene name	Entrez gene ID	CPM		Log ₂ F C
			MDA-231	MDA-231 HM.LNm5	
Positive regulator of glycolytic process (GO: 0045821)					
<i>ENTPD5</i>	Ectonucleoside triphosphate diphosphohydrolase 5	957	12.7	19.4	0.84
<i>HIF1A</i>	Hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	3091	421.2	471.3	0.68
<i>PRKAA2</i>	Protein kinase, AMP-activated, alpha 2 catalytic subunit	5563	29.3	31.8	-0.16
<i>PRKAA1</i>	Protein kinase, AMP-activated, alpha 1 catalytic subunit	5562	97.4	92.0	-0.27
<i>ARNT</i>	Aryl hydrocarbon receptor nuclear translocator	405	54.6	37.0	-0.65
<i>INSR</i>	Insulin receptor	3643	65.5	34.9	-1.06
<i>MLXIPL</i>	MLX interacting protein-like	51085	3.8	0.5	-6.73
CPM < 1					
<i>HTR2A</i>	5-hydroxytryptamine (serotonin)	3356	0.0	0.0	0.00

	receptor 2A, G protein-coupled				
<i>INS</i>	Insulin	3630	0.0	0.0	0.00
<i>P2RX7</i>	Purinergic receptor P2X, ligand gated ion channel, 7	5027	0.2	0.2	-3.18
<i>IGF1</i>	Insulin-like growth factor 1 (somatomedin C)	3479	0.3	0.2	4.07
<i>GPD1</i>	Glycerol-3-phosphate dehydrogenase 1 (soluble)	2819	0.5	0.6	1.16
Negative regulator of glycolytic process (GO: 0045820)					
<i>PPARG</i>	Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	10891	7.8	10.0	0.93
<i>C12orf5</i>	Chromosome 12 open reading frame 5	57103	11.6	14.5	0.40
<i>SIRT6</i>	Sirtuin 6	51548	34.8	42.4	0.24
<i>HDAC4</i>	Histone deacetylase 4	9759	30.9	36.8	-0.02
<i>ACTN3</i>	Actinin, alpha 3 (gene/pseudogene)	89	1.3	2.2	-0.03
<i>STAT3</i>	Signal transducer and activator of transcription 3 (acute-phase response factor)	6774	191.1	140.5	-0.57
<i>DDIT4</i>	DNA-damage-inducible transcript 4	54541	255.2	128.2	-0.90
<i>PPARA</i>	Peroxisome proliferator-activated receptor alpha	5465	45.3	17.7	-1.02
<i>IER3</i>	Immediate early response 3	8870	590.1	278.6	-1.48
<i>FBP1</i>	Fructose-1,6-bisphosphatase 1	2203	29.1	2.4	-5.36

CPM < 1					
<i>MYOG</i>	Myogenin (myogenic factor 4)	4656	0.2	0.0	-3.18
<i>CBFA2T3</i>	Core-binding factor, runt domain, alpha subunit 2; translocated to, 3	863	0.3	0.5	-0.03
Regulation of glycolytic process (GO: 0006110)					
<i>ECD</i>	Ecdysoneless homolog (Drosophila)	11319	30.7	42.1	0.46
<i>PRKAG1</i>	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit	5571	38.0	37.6	-0.11
<i>OGT</i>	O-linked N-acetylglucosamine (GlcNAc) transferase	8473	256.8	244.6	-0.23
<i>PRKAG2</i>	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	51422	71.4	32.7	-1.95

The parental is used as the denominator when calculating fold change (\log_2FC). Gene lists were extracted using the AmiGO browser from GO term: “positive regulator of glycolytic process” (GO:0045821); “negative regulator of glycolytic process” (GO:0045820) and “regulation of glycolytic process” (GO:0006110). CPM: count per million; FC: fold change