

Supplementary Table 2. Expression of genes in glycolytic process in MDA-MB-231HM.LNm5 (MDA-231HM.LNm5) and parental MDA-MB-231 (MDA-231) cell lines, as detected by RNA-seq

Canonical glycolysis (GO:0061621); glycolytic process (GO: 0006096)					
Gene symbol	Gene name	Entrez gene ID	CPM		Log₂F C
			MDA-231	MDA-231 HM.LNm5	
<i>ENO3</i>	Enolase 3 (beta, muscle)	2027	12.8	31.9	2.08
<i>ALDO C</i>	Aldolase C, fructose-bisphosphate	230	10.6	16.4	0.93
<i>PFKM</i>	Phosphofructokinase, muscle	5213	83.1	111.3	0.52
<i>ALDO A</i>	Aldolase A, fructose-bisphosphate	226	1176.9	1502.2	0.49
<i>PGAM 4</i>	Phosphoglycerate mutase family member 4	441531	7.4	8.2	0.29
<i>PGAM 1</i>	Phosphoglycerate mutase 1 (brain)	5223	140.1	157.1	0.24
<i>GAPD H</i>	Glyceraldehyde-3-phosphate dehydrogenase	2597	1713.2	1923.8	0.19
<i>HK2</i>	Hexokinase 2	3099	140.4	170.1	0.16
<i>GPI</i>	Glucose-6-phosphate isomerase	2821	566.5	589.8	0.14
<i>TPI1</i>	Triosephosphate isomerase 1	7167	362.3	334.2	-0.03
<i>ADPG</i>	ADP-dependent glucokinase	83440	45.9	49.5	-0.04

<i>K</i>					
<i>PFKFB3</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	5209	321.8	343.5	-0.13
<i>DHTKDI</i>	Dehydrogenase E1 and transketolase domain containing 1	55526	48.6	39.0	-0.17
<i>PKM</i>	Pyruvate kinase, muscle	5315	1963.0	1967.0	-0.19
<i>HK1</i>	Hexokinase 1	3098	317.2	265.3	-0.23
<i>GAPDHS</i>	Glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	26330	1.3	1.4	-0.29
<i>PFKFB4</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	5210	57.6	47.1	-0.32
<i>PFKP</i>	Phosphofructokinase, platelet	5214	547.2	522.3	-0.34
<i>PFKFB2</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	5208	33.6	28.5	-0.34
<i>OGDH</i>	Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	4967	204.7	177.9	-0.36
<i>PGM1</i>	Phosphoglucomutase 1	5236	195.8	135.0	-0.47
<i>PGK2</i>	Phosphoglycerate kinase 2	5232	3.0	2.7	-0.65
<i>PGAM2</i>	Phosphoglycerate mutase 2 (muscle)	5224	3.8	2.1	-0.67
<i>ENO4</i>	Enolase family member 4	387712	2.8	1.3	-0.72
<i>ENO1</i>	Enolase 1, (alpha)	2023	2139.4	1623.1	-0.74
<i>LDHA</i>	Lactate dehydrogenase A	3939	1356.0	1012.9	-0.76
<i>PKLR</i>	Pyruvate kinase, liver and RBC	5313	1.3	1.7	-0.82

<i>BPGM</i>	2,3-bisphosphoglycerate mutase	669	18.5	9.5	-1.01
<i>ENO2</i>	Enolase 2 (gamma, neuronal)	2026	204.2	115.1	-1.01
<i>PGK1</i>	Phosphoglycerate kinase 1	5230	804.8	408.4	-1.07
<i>PFKL</i>	Phosphofructokinase, liver	5211	255.6	117.1	-1.29
<i>PPP2R5D</i>	Protein phosphatase 2, regulatory subunit B', delta	5528	214.5	88.7	-1.35
<i>HKDC1</i>	Hexokinase domain containing 1	80201	19.5	3.2	-6.64
CPM < 1					
<i>GCK</i>	Glucokinase (hexokinase 4)	2645	0.2	0.2	3.16
<i>PFKFB1</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	5207	0.2	0.3	0.93
<i>HK3</i>	Hexokinase 3 (white cell)	3101	0.2	0.0	-3.18
<i>ALDOB</i>	Aldolase B, fructose-bisphosphate	229	0.2	0.2	-3.18
<i>OGDHL</i>	Oxoglutarate dehydrogenase-like	55753	0.9	0.3	-5.37

The parental is used as the denominator when calculating fold change (log₂FC). Gene lists were extracted using the AmiGO browser from GO term: “canonical glycolysis” (GO:0061621) and “glycolytic process” (GO:006096). CPM: count per million; FC: fold change