

Supplementary Table 4. Expression of genes in tricarboxylic acid cycle in MDA-MB-231HM.LNm5 (MDA-231HM.LNm5) and parental MDA-MB-231 (MDA-231) cell lines, as detected by RNA-seq

TCA (GO:0006099)						
Gene symbol	Gene name	Entrez gene ID	CPM		Log₂FC	
			MDA-231	MDA-231 HM.LNm5		
<i>IDH1</i>	Isocitrate dehydrogenase 1 (NADP+), soluble	3417	43.7	69.7	0.93	
<i>IDH3B</i>	Isocitrate dehydrogenase 3 (NAD+) beta	3420	75.7	112.2	0.64	
<i>SUCLG2</i>	Succinate-CoA ligase, GDP-forming, beta subunit	8801	43.8	61.0	0.49	
<i>ACO2</i>	Aconitase 2, mitochondrial	50	55.9	68.3	0.39	
<i>DLST</i>	Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	1743	101.2	114.3	0.33	
<i>ACO1</i>	Aconitase 1, soluble	48	194.1	196.3	0.33	
<i>SUCLG1</i>	Succinate-CoA ligase, alpha subunit	8802	38.9	50.7	0.30	
<i>SDHC</i>	Succinate dehydrogenase complex, subunit C, integral membrane protein	6391	30.9	37.9	0.29	
<i>SUCLA2</i>	Succinate-CoA ligase, ADP-	8803	18.4	24.0	0.28	

	forming, beta subunit				
<i>PDHB</i>	Pyruvate dehydrogenase (lipoamide) beta	5162	104.2	101.2	0.05
<i>SDHB</i>	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	6390	51.4	52.2	0.02
<i>DHTKD1</i>	Dehydrogenase E1 and transketolase domain containing 1	55526	48.6	39.0	-0.17
<i>SDHA</i>	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	6389	162.1	145.1	-0.23
<i>SDHD</i>	Succinate dehydrogenase complex, subunit D, integral membrane protein	6392	38.9	31.9	-0.29
<i>FH</i>	Fumarate hydratase	2271	56.7	58.0	-0.29
<i>IDH3G</i>	Isocitrate dehydrogenase 3 (NAD+) gamma	3421	42.7	34.6	-0.31
<i>MDH2</i>	Malate dehydrogenase 2, NAD (mitochondrial)	4191	191.5	170.6	-0.34
<i>OGDH</i>	Oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	4967	204.7	177.9	-0.36
<i>CS</i>	Citrate synthase	1431	95.8	79.7	-0.40
<i>MDH1</i>	Malate dehydrogenase 1, NAD	4190	90.7	77.9	-0.41

	(soluble)				
<i>IDH3A</i>	Isocitrate dehydrogenase 3 (NAD+) alpha	3419	51.6	43.0	-0.43
<i>DLAT</i>	Dihydrolipoamide S- acetyltransferase	1737	104.6	79.4	-0.46
<i>NNT</i>	Nicotinamide nucleotide transhydrogenase	23530	130.1	95.2	-0.58
<i>DLD</i>	Dihydrolipoamide dehydrogenase	1738	120.0	87.7	-0.58
<i>PDHA1</i>	Pyruvate dehydrogenase (lipoamide) alpha 1	5160	102.1	70.4	-0.69
<i>IDH2</i>	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	3418	30.7	6.5	-2.39
CPM < 1					
<i>PDHA2</i>	Pyruvate dehydrogenase (lipoamide) alpha 2	5161	0.0	0.2	3.16
<i>MDH1B</i>	Malate dehydrogenase 1B, NAD (soluble)	130752	0.5	0.9	2.16
<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 extracted using the AmiGO browser from GO term tricarboxylic acid cycle (GO:0006099). CPM: count per million; FC: fold change; TCA: tricarboxylic acid