

Supplementary Table 5. Expression of genes in the mitochondrial electron transport chain 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	CMP		Log ₂ FC
			MDA-231	MDA-231 HM.LNm5	
Mitochondrial complex I					
NADH: ubiquinone oxidoreductase subunit (GO:006120) (HGNC family ID: 640, 645)					
<i>NDUF AF5</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 5	79133	10.1	18.0	1.16
<i>NDUF A10</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10	4705	61.4	101.5	0.73
<i>NDUF AF1</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 1	51103	13.0	16.4	0.71
<i>NDUF AF4</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4	29078	13.9	24.2	0.71
<i>NDUF AF6</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 6	137682	11.4	20.1	0.69
<i>NDUF VI</i>	NADH dehydrogenase (ubiquinone) flavoprotein 1	4723	155.6	196.7	0.63
<i>NDUF S8</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 8	4728	98.5	125.5	0.62
<i>NDUF</i>	NADH dehydrogenase (ubiquinone) 1,	4718	101.3	144.0	0.54

<i>C2</i>	subcomplex unknown, 2				
<i>NDUF</i> <i>B1</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1	4707	18.8	25.1	0.50
<i>NDUF</i> <i>B10</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	4716	44.8	69.4	0.48
<i>NDUF</i> <i>A9</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	4704	27.7	35.3	0.44
<i>NDUF</i> <i>S1</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 1	4719	95.8	130.3	0.44
<i>NDUF</i> <i>B8</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8	4714	73.6	81.7	0.41
<i>NDUF</i> <i>S7</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 7	374291	43.1	54.7	0.38
<i>NDUF</i> <i>B3</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3	4709	30.1	39.4	0.38
<i>NDUF</i> <i>A12</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	55967	63.0	69.9	0.35
<i>NDUF</i> <i>A13</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	51079	80.4	108.3	0.35
<i>NDUF</i> <i>B4</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4	4710	42.3	52.2	0.33
<i>NDUF</i> <i>B5</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	4711	38.9	50.3	0.28
<i>NDUF</i> <i>B9</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	4715	24.1	28.9	0.26

<i>NDUF</i> <i>S4</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 4	4724	32.3	42.2	0.26
<i>NDUF</i> <i>AB1</i>	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	4706	36.2	44.3	0.25
<i>NDUF</i> <i>S2</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 2	4720	85.6	89.5	0.22
<i>NDUF</i> <i>A7</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7	4701	17.9	17.7	0.18
<i>NDUF</i> <i>A3</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	4696	22.3	26.6	0.14
<i>NDUF</i> <i>A11</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11	126328	104.0	108.1	0.14
<i>NDUF</i> <i>AF2</i>	NADH dehydrogenase (ubiquinone) complex I, assembly factor 2	91942	14.4	15.2	0.07
<i>NDUF</i> <i>A2</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	4695	53.5	44.7	0.05
<i>ND5</i>	NADH dehydrogenase, subunit 5 (complex I)	4540	4311.5	4175.5	0.01
<i>NDUF</i> <i>B7</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	4713	57.3	58.5	-0.04
<i>ND6</i>	NADH dehydrogenase, subunit 6 (complex I)	4541	1844.6	1716.6	-0.08
<i>NDUF</i> <i>S5</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 5	4725	90.7	79.4	-0.09
<i>NDUF</i>	NADH dehydrogenase (ubiquinone)	25915	51.9	52.8	-0.13

<i>AF3</i>	complex I, assembly factor 3				
<i>NDUF C1</i>	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown	4717	21.5	19.1	-0.16
<i>NDUF A5</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	4698	28.7	34.1	-0.22
<i>NDUF AF7</i>	NADH dehydrogenase (ubiquinone) complex I, assembly	55471	14.6	12.5	-0.24
<i>NDUF B6</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	4712	52.2	42.1	-0.28
<i>ND4L</i>	NADH dehydrogenase, subunit 4L (complex I)	4539	592.3	468.6	-0.28
<i>NDUF A6</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6	4700	47.2	41.7	-0.36
<i>ND3</i>	NADH dehydrogenase, subunit 3 (complex I)	4537	755.2	661.9	-0.38
<i>ND4</i>	NADH dehydrogenase, subunit 4 (complex I)	4538	8843.6	6486.8	-0.44
<i>NDUF A1</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	4694	51.3	35.3	-0.45
<i>ND2</i>	Mitochondrially Encoded NADH:Ubiquinone Oxidoreductase Core Subunit 2	4536	2490.0	1875.6	-0.45
<i>NDUF A8</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	4702	55.2	36.7	-0.47
<i>ND1</i>	NADH dehydrogenase, subunit 1	4535	2585.1	2177.7	-0.58

	(complex I)				
<i>NDUF</i> <i>S6</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 6	4726	66.3	47.3	-0.70
<i>NDUF</i> <i>S3</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 3	4722	39.4	33.8	-0.72
<i>NDUF</i> <i>B11</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	54539	44.0	26.2	-1.01
<i>NDUF</i> <i>B2</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	4708	73.4	36.7	-1.04
<i>NDUF</i> <i>V3</i>	NADH dehydrogenase (ubiquinone) flavoprotein 3	4731	37.8	19.9	-1.09
<i>NDUF</i> <i>V2</i>	NADH dehydrogenase (ubiquinone) flavoprotein 2	4729	18.2	11.1	-1.36
Mitochondrial complex II					
Succinate dehydrogenase subunits (SDH) (GO:006121) (HGNC family ID: 641, 645)					
<i>SDHAF</i> <i>2</i>	Succinate dehydrogenase complex assembly factor 2	54949	37.8	53.3	0.72
<i>SDHAF</i> <i>1</i>	Succinate dehydrogenase complex assembly factor 1	644096	8.1	13.8	0.55
<i>SDHAF</i> <i>3</i>	Succinate dehydrogenase complex assembly factor 3	57001	12.8	19.1	0.39
<i>SDHAF</i> <i>4</i>	Succinate dehydrogenase complex assembly factor 4	135154	8.2	7.9	0.31
<i>SDHC</i>	Succinate dehydrogenase complex, subunit C, integral membrane protein	6391	30.9	37.9	0.29

<i>SDHB</i>	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	6390	51.4	52.2	0.02
<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
Mitochondrial complex III					
Ubiquinol-cytochrome C reductase complex subunits (UQCR) (GO:0006122) (HGNC family ID: 642, 645)					
<i>BCSIL</i>	BC1 (ubiquinol-cytochrome C reductase) synthesis-like	617	23.3	55.2	1.71
<i>UQCR B</i>	Ubiquinol-cytochrome C reductase binding protein	7381	51.0	76.8	0.89
<i>UQCR FS1</i>	Ubiquinol-cytochrome C reductase, Rieske iron-sulfur polypeptide 1	7386	42.9	49.0	0.59
<i>UQCR C2</i>	Ubiquinol-cytochrome C reductase core protein II	7385	77.6	107.5	0.59
<i>UQCR 11</i>	Ubiquinol-cytochrome C reductase, complex III subunit XI	10975	83.6	96.0	0.38
<i>UQCC 3</i>	Ubiquinol-cytochrome C reductase complex assembly factor 3	790955	37.2	38.7	0.36
<i>UQCR Q</i>	Ubiquinol-cytochrome C reductase, complex III subunit VII	27089	76.5	83.6	0.23
<i>UQCR C1</i>	Ubiquinol-cytochrome C reductase core protein I	7384	138.4	166.5	0.19

<i>CYCI</i>	Cytochrome C-1	1537	142.6	151.5	0.10
<i>UQCR10</i>	Ubiquinol-cytochrome C reductase, complex III subunit X	29796	41.0	38.6	0.03
<i>UQCRH</i>	Ubiquinol-cytochrome C reductase hinge protein	7388	20.4	19.1	-0.12
<i>CYTB</i>	Cytochrome B	4519	2351.5	2287.9	-0.13
<i>UQCC1</i>	Ubiquinol-cytochrome C reductase complex assembly factor 1	55245	75.3	67.5	-0.16
<i>UQCC2</i>	Ubiquinol-cytochrome C reductase complex assembly factor 2	84300	39.9	36.8	-0.27
Mitochondrial complex IV					
Cytochrome C oxidase subunits (COX) (GO:0006123) (HGNC family ID: 643, 645)					
<i>SCO2</i>	SCO2 cytochrome C oxidase assembly protein	9997	2.4	3.2	0.78
<i>COX4I1</i>	Cytochrome C oxidase subunit IV isoform 1	1327	100.7	148.4	0.77
<i>COA4</i>	Cytochrome C oxidase assembly factor 4 homolog (<i>S. cerevisiae</i>)	51287	58.9	76.2	0.74
<i>COX7A1</i>	Cytochrome C oxidase subunit VIIa polypeptide 1 (muscle)	1346	2.4	4.3	0.70
<i>COX15</i>	Cytochrome C oxidase assembly homolog 15 (yeast)	1355	46.1	45.4	0.59
<i>COX7C</i>	Cytochrome C oxidase subunit VIIc	1350	54.0	73.2	0.57
<i>SCO1</i>	SCO1 cytochrome C oxidase assembly protein	6341	43.7	51.9	0.56

<i>COX18</i>	COX18 cytochrome C oxidase assembly factor	285521	25.3	40.5	0.49
<i>COA1</i>	Cytochrome C oxidase assembly factor 1 homolog (<i>S. cerevisiae</i>)	55744	40.5	49.5	0.44
<i>COX6A1</i>	Cytochrome C oxidase subunit VIa polypeptide 1	1337	68.5	86.2	0.36
<i>COX6B1</i>	Cytochrome C oxidase subunit VIb polypeptide 1 (ubiquitous)	1340	86.6	103.6	0.30
<i>COA7</i>	Cytochrome C oxidase assembly factor 7 (putative)	65260	31.3	32.7	0.26
<i>COX8A</i>	Cytochrome C oxidase subunit VIIIA (ubiquitous)	1351	171.0	167.9	0.21
<i>COX5A</i>	Cytochrome C oxidase subunit Va	9377	58.9	60.9	0.19
<i>COX10</i>	COX10 heme A:farnesyltransferase cytochrome C oxidase assembly factor	1352	20.4	21.2	0.18
<i>COX1</i>	Cytochrome C oxidase subunit I	4512	6763.3	7654.2	0.14
<i>COX3</i>	Cytochrome C oxidase III	4514	3407.6	3654.4	0.07
<i>COX6C</i>	Cytochrome C oxidase subunit VIc	1345	53.3	52.5	0.06
<i>COX2</i>	Cytochrome C oxidase subunit II	4513	3386.3	3056.4	-0.04
<i>COX5B</i>	Cytochrome C oxidase subunit Vb	1329	61.6	54.5	-0.10
<i>COX14</i>	COX14 cytochrome C oxidase assembly factor	84987	16.1	12.2	-0.12
<i>COA5</i>	Cytochrome C oxidase assembly factor 5	493753	19.9	19.3	-0.16

<i>COX19</i>	COX19 cytochrome C oxidase assembly factor	90639	18.2	17.5	-0.20
<i>COX11</i>	COX11 cytochrome C oxidase copper chaperone	1353	38.5	34.6	-0.26
<i>COX20</i>	COX20 cytochrome C oxidase assembly factor	116228	9.3	7.4	-0.33
<i>COX17</i>	COX17 cytochrome C oxidase copper chaperone	10063	6.5	7.7	-0.47
<i>COX7A</i> 2	Cytochrome C oxidase subunit VIIa polypeptide 2 (liver)	1347	38.3	26.1	-0.55
<i>COX7B</i>	Cytochrome C oxidase subunit VIIb	1349	45.7	32.4	-0.57
<i>COA3</i> 3	Cytochrome C oxidase assembly factor 3	28958	47.2	28.1	-0.87
<i>COA6</i> 6	Cytochrome C oxidase assembly factor 6	388753	16.8	9.2	-1.03
CPM < 1					
<i>COX6A</i> 2	Cytochrome C oxidase subunit VIa polypeptide 2	1339	0.0	0.0	0.00
<i>COX8C</i>	Cytochrome C oxidase subunit VIIC	341947	0.2	0.2	0.00
<i>COX6B</i> 2	Cytochrome C oxidase subunit VIb polypeptide 2 (testis)	125965	0.2	0.2	-0.95
<i>COX4I</i> 2	Cytochrome C oxidase subunit IV isoform 2 (lung)	84701	0.3	0.0	-3.18
<i>COX7B</i> 2	Cytochrome C oxidase subunit VIIb2	170712	0.6	0.0	-3.18

Mitochondrial complex V					
ATP synthase subunits (ATP5) (GO:0045259) (HGNC family ID:644, 645)					
<i>ATP5G</i> 2	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit C2 (subunit 9)	517	60.3	71.0	0.63
<i>ATP5S</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit s (factor B)	27109	12.8	16.9	0.59
<i>ATP5G</i> 3	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit C3 (subunit 9)	518	154.0	199.5	0.54
<i>ATP5E</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit	514	60.8	66.6	0.45
<i>ATP5D</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	513	65.1	90.4	0.39
<i>ATP5E</i> <i>P2</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, epsilon subunit pseudogene 2	432369	67.9	72.2	0.33
<i>ATP5A</i> <i>1</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	498	356.8	391.6	0.31
<i>ATP5F</i> <i>1</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit B1	515	82.5	109.2	0.31

<i>ATP5B</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide	506	434.2	499.4	0.21
<i>ATP5I</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit E	521	42.7	41.4	0.15
<i>ATP5C1</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	509	94.7	114.0	0.14
<i>ATP5J</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit F6	522	42.9	40.3	0.06
<i>ATPAF2</i>	ATP synthase mitochondrial F1 complex assembly factor 2	91647	15.2	12.3	0.00
<i>ATP5O</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit	539	75.0	69.6	-0.12
<i>ATPAF1</i>	ATP synthase mitochondrial F1 complex assembly factor 1	64756	36.6	35.1	-0.15
<i>ATP8</i>	ATP synthase F0 subunit 8	4509	584.3	540.2	-0.16
<i>ATP5L</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit G	10632	115.6	108.9	-0.20
<i>ATP5L2</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit G2	267020	9.7	9.6	-0.26
<i>ATP6</i>	ATP synthase F0 subunit 6	4508	4568.2	4171.6	-0.30
<i>ATP5H</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit d	10476	76.0	62.3	-0.41

<i>ATP5J</i> 2	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit F2	9551	97.0	58.0	-0.63
<i>ATP5G</i> 1	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit C1 (subunit 9)	516	43.2	30.4	-0.71

The parental cell line is used as the denominator when calculating fold change (\log_2FC). Gene lists extracted using the HUGO Gene Nomenclature Committee (HGNC) Gene family browser, under the gene family mitochondrial respiratory chain complexes (HGNC family ID: 639), which contains the 5 mitochondrial complexes subsets (HGNC family ID: 640, 641, 642, 643, 644). Genes in mitochondrial respiratory chain complex assembly factors (HGNC family ID: 645) are also incorporated in the gene lists. CPM: count per million; FC: fold change