

Table S3. Differentially expressed genes for OXPHOS and glycolysis gene sets between Cluster I and II

Gene		Log Fold	p-	False
symbol	Gene title	change	value	discovery rates
<u>OXPHOS gene set</u>				
<i>Overexpressed in Cluster II vs Cluster I</i>				
NDUFA4	NDUFA4, mitochondrial complex associated	0.531	0.000	0.018
COX7B	cytochrome c oxidase subunit 7B	0.657	0.000	0.018
NDUFA3	NADH:ubiquinone oxidoreductase subunit A3	0.624	0.001	0.018
NDUFB7	NADH:ubiquinone oxidoreductase subunit B7	0.630	0.001	0.018
COX5B	cytochrome c oxidase subunit 5B	0.789	0.001	0.019
UQCRC2	ubiquinol-cytochrome c reductase core protein II	0.524	0.001	0.019
NDUFA9	NADH:ubiquinone oxidoreductase subunit A9	0.528	0.003	0.055
NDUFS7	NADH:ubiquinone oxidoreductase core subunit S7	0.320	0.003	0.055
COX6B1	cytochrome c oxidase subunit 6B1	0.476	0.004	0.055
NDUFS1	NADH:ubiquinone oxidoreductase core subunit S1	0.603	0.004	0.055
COX5A	cytochrome c oxidase subunit 5A	0.463	0.005	0.057
NDUFA8	NADH:ubiquinone oxidoreductase subunit A8	0.55	0.006	0.065
NDUFB3	NADH:ubiquinone oxidoreductase subunit B3	0.650	0.006	0.065
COX11	COX11, cytochrome c oxidase copper chaperone	0.437	0.007	0.065
NDUFA11	NADH:ubiquinone oxidoreductase subunit A11	0.340	0.007	0.065
SDHC	succinate dehydrogenase complex subunit C	0.362	0.008	0.068
COX7A2L	cytochrome c oxidase subunit 7A2 like	0.699	0.008	0.070
NDUFA1	NADH:ubiquinone oxidoreductase subunit A1	0.278	0.010	0.075
NDUFA7	NADH:ubiquinone oxidoreductase subunit A7	0.341	0.011	0.079
ATP6V0E1	ATPase H ⁺ transporting V0 subunit e1	0.433	0.013	0.089
UQCRQ	ubiquinol-cytochrome c reductase complex III subunit VII	0.483	0.015	0.090
NDUFAB1	NADH:ubiquinone oxidoreductase subunit AB1	0.373	0.016	0.090
COX4I2	cytochrome c oxidase subunit 4I2	0.366	0.016	0.090
COX7A1	cytochrome c oxidase subunit 7A1	0.731	0.016	0.090
NDUFB5	NADH:ubiquinone oxidoreductase subunit B5	0.397	0.020	0.104
UQCRFS1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0.378	0.022	0.106
ATP6V1E2	ATPase H ⁺ transporting V1 subunit E2	0.468	0.025	0.114
SDHB	succinate dehydrogenase complex iron sulfur subunit B	0.314	0.027	0.114
CYC1	cytochrome c1	0.547	0.027	0.114
NDUFS2	NADH:ubiquinone oxidoreductase core subunit S2	0.393	0.034	0.132
COX6A1	cytochrome c oxidase subunit 6A1	0.231	0.036	0.134
UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI	0.265	0.038	0.134
COX7C	cytochrome c oxidase subunit 7C	0.455	0.038	0.134
COX4I1	cytochrome c oxidase subunit 4I1	0.245	0.038	0.134
SDHA	succinate dehydrogenase complex flavoprotein subunit A	0.455	0.040	0.137
COX15	COX15, cytochrome c oxidase assembly homolog	0.290	0.041	0.137
NDUFV2	NADH:ubiquinone oxidoreductase core subunit V2	0.492	0.041	0.137
UQCRC1	ubiquinol-cytochrome c reductase core protein I	0.349	0.046	0.145
NDUFV1	NADH:ubiquinone oxidoreductase core subunit V1	0.245	0.059	0.175
COX7B2	cytochrome c oxidase subunit 7B2	0.179	0.059	0.175
NDUFA2	NADH:ubiquinone oxidoreductase subunit A2	0.287	0.062	0.175
COX6A2	cytochrome c oxidase subunit 6A2	0.399	0.062	0.175

<i>NDUFA10</i>	NADH:ubiquinone oxidoreductase subunit A10	0.163	0.063	0.175
<i>SDHD</i>	succinate dehydrogenase complex subunit D	0.238	0.076	0.190
<i>NDUFB10</i>	NADH:ubiquinone oxidoreductase subunit B10	0.249	0.077	0.190
<i>NDUFA6</i>	NADH:ubiquinone oxidoreductase subunit A6	0.407	0.085	0.205
<i>NDUFV3</i>	NADH:ubiquinone oxidoreductase subunit V3	0.307	0.093	0.215
<i>NDUFB2</i>	NADH:ubiquinone oxidoreductase subunit B2	0.264	0.094	0.215
<i>ATP6AP1</i>	ATPase H+ transporting accessory protein 1	0.239	0.108	0.238
<i>NDUFB9</i>	NADH:ubiquinone oxidoreductase subunit B9	0.348	0.134	0.282
<i>NDUFB6</i>	NADH:ubiquinone oxidoreductase subunit B6	0.225	0.140	0.291
<i>UQCRB</i>	ubiquinol-cytochrome c reductase binding protein	0.415	0.144	0.296
<i>COX8A</i>	cytochrome c oxidase subunit 8A	0.289	0.148	0.300
<i>NDUFC1</i>	NADH:ubiquinone oxidoreductase subunit C1	0.238	0.153	0.306
<i>ATP6V1C1</i>	ATPase H+ transporting V1 subunit C1	0.313	0.179	0.345
<i>ATP6V0B</i>	ATPase H+ transporting V0 subunit b	0.298	0.212	0.384
<i>ATP6V1G1</i>	ATPase H+ transporting V1 subunit G1	0.270	0.214	0.384
<i>NDUFS3</i>	NADH:ubiquinone oxidoreductase core subunit S3	0.296	0.234	0.409
<i>COX6C</i>	cytochrome c oxidase subunit 6C	0.148	0.287	0.467
<i>ATP6V0A4</i>	ATPase H+ transporting V0 subunit a4	0.066	0.426	0.646
<i>ATP6V1A</i>	ATPase H+ transporting V1 subunit A	0.126	0.436	0.653
<i>PPA1</i>	pyrophosphatase (inorganic) 1	0.210	0.456	0.659
<i>ATP6V0E2</i>	ATPase H+ transporting V0 subunit e2	0.265	0.458	0.659
<i>COX6B2</i>	cytochrome c oxidase subunit 6B2	0.073	0.465	0.659
<i>COX7A2</i>	cytochrome c oxidase subunit 7A2	0.156	0.511	0.699
<i>ATP6V1D</i>	ATPase H+ transporting V1 subunit D	0.092	0.575	0.741
<i>NDUFS4</i>	NADH:ubiquinone oxidoreductase subunit S4	0.075	0.647	0.783
<i>NDUFA4L2</i>	NDUFA4, mitochondrial complex associated like 2	0.083	0.706	0.841
<i>ATP4A</i>	ATPase H+/K+ transporting alpha subunit	0.038	0.775	0.896
<i>NDUFS6</i>	NADH:ubiquinone oxidoreductase subunit S6	0.042	0.843	0.946
<i>UQCR10</i>	ubiquinol-cytochrome c reductase, complex III subunit X	0.027	0.892	0.967
<i>COX10</i>	COX10, heme A:farnesyltransferase cytochrome c oxidase assembly factor	0.015	0.905	0.967
<i>PPA2</i>	pyrophosphatase (inorganic) 2	0.013	0.933	0.990
<i>ATP6V1G3</i>	ATPase H+ transporting V1 subunit G3	0.005	0.959	0.992
<i>ATP6V1G2</i>	ATPase H+ transporting V1 subunit G2	0.016	0.969	0.992
<i>NDUFB8</i>	NADH:ubiquinone oxidoreductase subunit B8	0.004	0.971	0.992
<i>ATP4B</i>	ATPase H+/K+ transporting beta subunit	0.001	0.993	0.995

Underexpressed in Cluster II vs Cluster I

<i>ATP6V0A1</i>	ATPase H+ transporting V0 subunit a1	-0.657	0.005	0.057
<i>ATP6V1H</i>	ATPase H+ transporting V1 subunit H	-0.387	0.027	0.114
<i>ATP12A</i>	ATPase H+/K+ transporting non-gastric alpha2 subunit	-0.204	0.045	0.145
<i>ATP6V0D2</i>	ATPase H+ transporting V0 subunit d2	-0.200	0.064	0.175
<i>ATP6V1B2</i>	ATPase H+ transporting V1 subunit B2	-0.419	0.118	0.256
<i>NDUFB4</i>	NADH:ubiquinone oxidoreductase subunit B4	-0.112	0.217	0.384
<i>COX8C</i>	cytochrome c oxidase subunit 8C	-0.088	0.243	0.416
<i>COX17</i>	COX17, cytochrome c oxidase copper chaperone	-0.144	0.392	0.599
<i>LHPP</i>	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	-0.162	0.475	0.665
<i>ATP6V0D1</i>	ATPase H+ transporting V0 subunit d1	-0.116	0.534	0.713
<i>NDUFB1</i>	NADH:ubiquinone oxidoreductase subunit B1	-0.110	0.535	0.713
<i>NDUFA5</i>	NADH:ubiquinone oxidoreductase subunit A5	-0.051	0.638	0.783

<i>ATP6V1E1</i>	ATPase H ⁺ transporting V1 subunit E1	-0.130	0.641	0.783
<i>TCIRG1</i>	T-cell immune regulator 1, ATPase H ⁺ transporting V0 subunit a3	-0.161	0.642	0.783
<i>ATP6V1C2</i>	ATPase H ⁺ transporting V1 subunit C2	-0.019	0.825	0.939
<i>ATP6V0A2</i>	ATPase H ⁺ transporting V0 subunit a2	-0.029	0.840	0.946
<i>ATP6V1B1</i>	ATPase H ⁺ transporting V1 subunit B1	-0.015	0.890	0.967
<i>ATP6V0C</i>	ATPase H ⁺ transporting V0 subunit c	-0.001	0.995	0.995

Glycolysis gene set

Overexpressed in Cluster II vs Cluster I

<i>ALDH1B1</i>	aldehyde dehydrogenase 1 family member B1	0.590	0.001	0.018
<i>PDHB</i>	pyruvate dehydrogenase (lipoamide) beta	0.546	0.011	0.080
<i>PGK1</i>	phosphoglycerate kinase 1	0.592	0.014	0.090
<i>DLAT</i>	dihydrolipoamide S-acetyltransferase	0.618	0.018	0.098
<i>PGK2</i>	phosphoglycerate kinase 2	0.213	0.021	0.106
<i>ALDOA</i>	aldolase, fructose-bisphosphate A	0.415	0.024	0.114
<i>BPGM</i>	bisphosphoglycerate mutase	0.697	0.029	0.117
<i>GPI</i>	glucose-6-phosphate isomerase	0.523	0.054	0.170
<i>LDHB</i>	lactate dehydrogenase B	0.363	0.062	0.175
<i>DLD</i>	dihydrolipoamide dehydrogenase	0.424	0.067	0.177
<i>GCK</i>	glucokinase	0.522	0.073	0.190
<i>PGAM1</i>	phosphoglycerate mutase 1	0.348	0.078	0.190
<i>ALDH2</i>	aldehyde dehydrogenase 2 family (mitochondrial)	0.457	0.108	0.238
<i>LDHC</i>	lactate dehydrogenase C	0.346	0.167	0.330
<i>LDHAL6A</i>	lactate dehydrogenase A like 6A	0.271	0.173	0.337
<i>PGM1</i>	phosphoglucomutase 1	0.272	0.182	0.347
<i>PDHA2</i>	pyruvate dehydrogenase (lipoamide) alpha 2	0.125	0.191	0.359
<i>ENO1</i>	enolase 1	0.342	0.208	0.381
<i>FBP2</i>	fructose-bisphosphatase 2	0.115	0.253	0.428
<i>PDHA1</i>	pyruvate dehydrogenase (lipoamide) alpha 1	0.233	0.255	0.428
<i>GALM</i>	galactose mutarotase	0.162	0.282	0.467
<i>HK2</i>	hexokinase 2	0.226	0.285	0.467
<i>LDHA</i>	lactate dehydrogenase A	0.295	0.300	0.483
<i>ADH5</i>	alcohol dehydrogenase 5 (class III), chi polypeptide	0.201	0.310	0.494
<i>ALDOC</i>	aldolase, fructose-bisphosphate C	0.343	0.342	0.529
<i>TPI1</i>	triosephosphate isomerase 1	0.179	0.449	0.659
<i>PKLR</i>	pyruvate kinase, liver and RBC	0.062	0.463	0.659
<i>HK3</i>	hexokinase 3	0.102	0.545	0.720
<i>ENO2</i>	enolase 2	0.418	0.567	0.741
<i>PKM</i>	pyruvate kinase, muscle	0.127	0.594	0.759
<i>PFKM</i>	phosphofructokinase, muscle	0.129	0.604	0.766
<i>ALDH3A1</i>	aldehyde dehydrogenase 3 family member A1	0.045	0.615	0.773
<i>PFKP</i>	phosphofructokinase, platelet	0.115	0.647	0.783
<i>ADH1C</i>	alcohol dehydrogenase 1C (class I), gamma polypeptide	0.207	0.740	0.875
<i>ADH1A</i>	alcohol dehydrogenase 1A (class I), alpha polypeptide	0.046	0.746	0.875
<i>ALDH3A2</i>	aldehyde dehydrogenase 3 family member A2	0.048	0.809	0.928
<i>GAPDH</i>	glyceraldehyde-3-phosphate dehydrogenase	0.039	0.865	0.960
<i>PCK2</i>	phosphoenolpyruvate carboxykinase 2, mitochondrial	0.038	0.868	0.960
<i>PGAM2</i>	phosphoglycerate mutase 2	0.054	0.902	0.967
<i>ENO3</i>	enolase 3	0.006	0.964	0.992

<i>ALDOB</i>	aldolase, fructose-bisphosphate B	0.002	0.973	0.992
<i>ALDH9A1</i>	aldehyde dehydrogenase 9 family member A1	0.003	0.987	0.995

Underexpressed in Cluster II vs Cluster I

<i>PFKL</i>	phosphofructokinase, liver type	-0.706	0.031	0.126
<i>ALDH1A3</i>	aldehyde dehydrogenase 1 family member A3	-0.981	0.065	0.176
<i>ALDH3B1</i>	aldehyde dehydrogenase 3 family member B1	-0.169	0.076	0.190
<i>G6PC2</i>	glucose-6-phosphatase catalytic subunit 2	-0.218	0.091	0.215
<i>ACSS1</i>	acyl-CoA synthetase short-chain family member 1	-0.169	0.105	0.238
<i>ADH1B</i>	alcohol dehydrogenase 1B (class I), beta polypeptide	-0.690	0.127	0.271
<i>ACSS2</i>	acyl-CoA synthetase short-chain family member 2	-0.154	0.195	0.362
<i>LDHAL6B</i>	lactate dehydrogenase A like 6B	-0.099	0.240	0.416
<i>HK1</i>	hexokinase 1	-0.267	0.329	0.519
<i>G6PC</i>	glucose-6-phosphatase catalytic subunit	-0.126	0.340	0.529
<i>ALDH3B2</i>	aldehyde dehydrogenase 3 family member B2	-0.053	0.442	0.657
<i>PGM2</i>	phosphoglucomutase 2	-0.120	0.477	0.665
<i>PCK1</i>	phosphoenolpyruvate carboxykinase 1	-0.160	0.491	0.678
<i>FBP1</i>	fructose-bisphosphatase 1	-0.226	0.518	0.703
<i>ADH6</i>	alcohol dehydrogenase 6 (class V)	-0.044	0.570	0.741
<i>ALDH7A1</i>	aldehyde dehydrogenase 7 family member A1	-0.068	0.682	0.818
<i>AKR1A1</i>	aldo-keto reductase family 1 member A1	-0.051	0.752	0.876
<i>ADH7</i>	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	-0.009	0.899	0.967
<i>ADH4</i>	alcohol dehydrogenase 4 (class II), pi polypeptide	-0.006	0.940	0.991

Differentially expressed genes (false discovery rate <0.2) used for clustering analysis are indicated in bold

