Supplementary table 2: Energy metabolism related genes

Gene Symbol	**Gene title**	**Fold change GLT1+ vs. Thy1+**	**Regulation in GLT1+ cells**	**Corr. P-value**	**Probe Set ID**
Aco1	Aconitase 1	2.4	up	**0.0051**	1423644_at
Aco2	Aconitase 2, mitochondrial	2.0	up	**0.0119**	1451002_at
Aldoa	Aldolase 1, a isoform	1.5	up	**0.0428**	1434799_x_at
Aldoc	Aldolase 3, c isoform	118.7	up	**0.0001**	1424714_at
Bpgm	2,3-bisphosphoglycerate mutase	2.3	up	0.2119	1415864_at
Cs	Citrate synthase	2.2	up	**0.0091**	1422578_at
Dlst	Dihydrolipoamide s-succinyltransferase	1.0	up	0.9344	1423710_at
Eno1	Enolase 1, alpha non-neuron	50.2	up	**0.0107**	1419022_a_at
Eno2	Enolase 2, gamma neuronal	2.2	down	**0.0113**	1418829_a_at
Fh1	Fumarate hydratase 1	2.5	up	**0.0062**	1424828_a_at
G6pdx	Glucose-6-phosphate dehydrogenase x-linked	1.7	up	0.1096	1448354_at
Gad1	Glutamic acid decarboxylase 1	17.2	down	**0.0016**	1416561_at
Gls	Glutaminase	1.7	down	**0.0062**	1434657_at
Glud1	Glutamate dehydrogenase 1	4.3	up	**0.0023**	1448253_at
Glul	Glutamate-ammonia ligase (glutamine synthetase)	3.3	up	**0.0023**	1426235_a_at
Got1	Glutamate oxaloacetate transaminase 1, soluble	3.2	up	**0.0171**	1450970_at
Got2	Glutamate oxaloacetate transaminase 2, mitochondrial	1.5	down	0.2135	1430397_at
Gpd1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	1.7	down	0.0607	1416204_at
Gpd1l	Glycerol-3-phosphate dehydrogenase 1-like	1.7	up	0.0879	1438195_at
Gpd2	Glycerol phosphate dehydrogenase 2, mitochondrial	1.9	up	**0.0231**	1452741_s_at
Gpi1	Glucose phosphate isomerase 1	2.3	up	**0.0128**	1434814_x_at
Gys1	Glycogen synthase 1, muscle	4.4	up	**0.0187**	1450196_s_at
Hk1	Hexokinase 1	1.9	up	0.0541	1437974_a_at
Hk2	Hexokinase 2	3.6	up	0.1463	1422612_at
Idh3a	Isocitrate dehydrogenase 3 (nad+) alpha	1.5	up	**0.0262**	1432016_a_at
Idh3b	Isocitrate dehydrogenase 3 (nad+) beta	3.0	up	**0.0026**	1418886_s_at
Idh3g	Isocitrate dehydrogenase 3 (nad+), gamma	8.5	up	**0.0116**	1416789_at
Ldhb	Lactate dehydrogenase b	13.6	up	**0.0001**	1434499_a_at
Mdh1	Malate dehydrogenase 1, nad (soluble)	3.2	up	**0.0091**	1454925_x_at
Mdh2	Malate dehydrogenase 2, nad (mitochondrial)	2.0	up	0.0650	1416478_a_at

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Me2	Malic enzyme 2, nad(+)-dependent, mitochondrial	1.6	down	0.1410	1426573_at
Mod1	Malic enzyme, supernatant	5.6	up	**0.0046**	1416632_at
Ogdh	Oxoglutarate dehydrogenase (lipoamide)	1.7	up	0.0677	1451274_at
Pcx	Pyruvate carboxylase	2.4	up	**0.0016**	1416383_a_at
Pfkl	Phosphofructokinase, liver, b-type	1.3	up	0.1426	1450269_a_at
Pfkm	Phosphofructokinase, muscle	4.2	up	**0.0007**	1416780_at
Pfkp	Phosphofructokinase, platelet	2.9	up	**0.0091**	1416069_at
Pgam1	Phosphoglycerate mutase 1	1.4	up	**0.0210**	1426554_a_at
Pgk1	Phosphoglycerate kinase 1	1.5	up	0.1087	1417864_at
Pgm2	Phosphoglucomutase 2	8.7	up	**0.0015**	1451149_at
Pgm2l1	Phosphoglucomutase 2-like 1	3.2	down	**0.0062**	1452841_at
Pgm5	Phosphoglucomutase 5	44.9	down	**0.0023**	1437871_at
Pkm2	Pyruvate kinase, muscle	1.1	up	0.4985	1417308_at
Pygb	Brain glycogen phosphorylase	3.5	up	**0.0095**	1433504_at
Pygl	Liver glycogen phosphorylase	17.6	up	**0.0043**	1417741_at
Pygm	Muscle glycogen phosphorylase	3.6	up	**0.0099**	1448602_at
Sdha	Succinate dehydrogenase complex, subunit a, flavoprotein (fp)	1.3	up	0.1825	1426688_at
Sdhb	Succinate dehydrogenase complex, subunit b, iron sulfur (ip)	1.2	up	0.1967	1418005_at
Sdhc	Succinate dehydrogenase complex, subunit c, integral membrane protein	2.1	up	**0.0062**	1448630_a_at
Sdhd	Succinate dehydrogenase complex, subunit d, integral membrane protein	5.1	up	**0.0062**	1437489_x_at
Slc25a12	Solute carrier family 25 (mitochondrial carrier, aralar), member 12	2.5	up	0.1096	1428440_at
Sucla2	Succinate-coenzyme a ligase, adp-forming, beta subunit	1.4	up	0.0705	1452206_at
Suclg1	Succinate-coa ligase, gdp-forming, alpha subunit	4.6	up	**0.0001**	1415891_at
Suclg2	Succinate-coenzyme a ligase, gdp-forming, beta subunit	6.5	up	**0.0373**	1427441_a_at
Tpi1	Triosephosphate isomerase 1	4.8	up	**0.0048**	1452927_x_at

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Ugp2	UDP-glucose pyrophosphorylase 2	2.3	up	**0.0107**	1426461_at

Comparison between GLT1+ astrocytes (n = 6) and Thy1-YFP+ neurons (n = 3). Fold change indicates the ratio between GLT1+ astrocytes and Thy1-YFP+ neurons, and the direction of the fold change, either up or down, is indicated by the “Regulation in GLT1+ cells”. The P-values shown are FDR corrected and was calculated by a non-paired Student’s t-test using a Benjamini-Hochberg FDR correction. Probe set ID refers to the Affymetrix 430 2.0 chip probesets. If several probeset existed for one gene, the most significant probeset is shown here.