

Table S1. Gene expression signatures underlying metabolism in human pluripotent stem cells

Gene Symbols	Description (Based on GeneCards and Entrez of NCBI)	Gene expression probes	RSeT vs primed (n = 6, Fold changes)	RN vs PN (n = 3, fold changes)	RH vs PH (n = 3, fold changes)
Metabolism gene expression (n = 93, ** indicates $P < 0.05$)					
AADAT	Aminoadipate Aminotransferase	A_23_P253484	0.61	0.59	0.63
AASS	Aminoadipate-Semialdehyde Synthase	A_23_P8754	0.63	0.83	0.48
ACACA	Acetyl-CoA Carboxylase Alpha	A_32_P215318	2.86*	2.95*	2.76*
ACLY	ATP Citrate Lyase	A_23_P66787	1.47*	1.31	1.65
ACO2	Aconitase 2	A_23_P103149	1.64*	1.51*	1.79*
AGMAT	Agmatinase	A_23_P103720	0.90	1.02	0.80
AHCY	Adenosylhomocysteinase	A_23_P17575	1.17*	1.21*	1.12
AHCYL2	Adenosylhomocysteinase Like 2	A_24_P72518	1.39*	1.34	1.45
ALDH1A1	Aldehyde Dehydrogenase 1 Family Member A1	A_23_P83098	0.51	0.26*	1.00
ALDH1B1	Aldehyde Dehydrogenase 1 Family Member B1	A_23_P135294	0.76*	0.63*	0.91
ALOX15B	Arachidonate 15-Lipoxygenase Type B	A_23_P60627	1.86	1.29	2.70
ALOX5	Arachidonate 5-Lipoxygenase	A_23_P104464	1.22	2.08	0.72
AOX1	Aldehyde Oxidase 1	A_23_P154037	0.69*	0.64	0.75
ASL	Argininosuccinate Lyase	A_23_P26223	0.95	0.80	1.11
ASS1	Argininosuccinate Synthase 1	A_23_P31921	1.03	0.88	1.19
ATP5E	ATP5F1E, ATP Synthase F1 Subunit Epsilon	A_23_P252322	0.62*	0.66*	0.57*
ATP5F1	ATP5PB, ATP Synthase Peripheral Stalk-Membrane Subunit B	A_23_P46275	1.55*	1.93	1.24*
ATP6	MT-ATP6, Mitochondrially Encoded ATP Synthase Membrane Subunit 6	A_23_P337726	1.04	0.99	1.10
BCAT1	Branched Chain Amino Acid Transaminase 1	A_24_P935986	0.62*	0.65*	0.60
BDH2	3-Hydroxybutyrate Dehydrogenase 2	A_23_P92490	0.93	0.94*	0.92
BHMT	Betaine--Homocysteine S-Methyltransferase	A_23_P81581	2.13*	2.71	1.67
COX6B2	Cytochrome C Oxidase Subunit 6B2	A_24_P267523	1.95	2.06	1.85
CPS1	Carbamoyl-Phosphate Synthase 1	A_23_P5300	1.98*	1.94	2.03
CS	Citrate Synthase	A_23_P47818	1.55*	1.25*	1.91*
CYP4F2	Cytochrome P450 Family 4 Subfamily F Member 2	A_24_P168494	0.83	0.83	0.83
DBT	Dihydrolipoamide Branched Chain Transacylase E2	A_24_P28524	1.35*	1.38	1.31*
DHH	Desert Hedgehog Signaling Molecule	A_23_P162314	0.82	0.77	0.88
DLAT	Dihydrolipoamide S-Acetyltransferase	A_24_P372672	1.42*	1.28	1.58*
DLD	Dihydrolipoamide Dehydrogenase	A_23_P111835	1.28*	1.15	1.43*
ENO1	Enolase 1	A_24_P105501	0.98	0.87	1.11
ENO1-AS1	ENO1 Antisense RNA 1	A_32_P145447	0.90	0.84	0.97
ENO3	Enolase 3	A_23_P130149	1.19*	1.26	1.13
FA2H	Fatty Acid 2-Hydroxylase	A_23_P49448	6.12*	6.07*	6.18*
FAAH	Fatty Acid Amide Hydrolase	A_23_P103226	0.31*	0.25*	0.38*
FASN	Fatty Acid Synthase	A_23_P44132	2.48*	1.85	3.31
GAD1	Glutamate Decarboxylase 1	A_23_P209578	0.54	0.57	0.50
GLS	Glutaminase	A_23_P308800	0.50*	0.67	0.37
GLUD1	Glutamate Dehydrogenase 1	A_23_P138665	1.66*	1.64	1.69
GLUD2	Glutamate Dehydrogenase 2	A_23_P45361	1.62	1.30	2.01
GOT1	Glutamic-Oxaloacetic Transaminase 1	A_23_P63825	1.31*	1.24*	1.38
GOT2	Glutamic-Oxaloacetic Transaminase 2	A_23_P106575	0.96	0.83	1.12
GPDI	Glycerol-3-Phosphate Dehydrogenase 1	A_23_P413721	0.97	0.91	1.03
GPD1L	Glycerol-3-Phosphate Dehydrogenase 1 Like	A_23_P318284	0.42*	0.48	0.38*
GPT	Glutamic--Pyruvic Transaminase	A_23_P146339	1.07	1.23	0.93
GYS1	Glycogen Synthase 1	A_23_P208698	1.27	1.03	1.56
HAGHL	Hydroxyacylglutathione Hydrolase Like	A_24_P356373	0.86	0.74	1.00
HMGCS1	3-Hydroxy-3-Methylglutaryl-CoA Synthase 1	A_23_P133263	1.50*	1.51*	1.49*
IDH1	Isocitrate Dehydrogenase (NADP ⁺) 1	A_32_P45009	1.13	1.04	1.23
IDH1-AS1	IDH1 Antisense RNA 1	A_32_P16931	1.42	1.79	1.13
IDH3A	Isocitrate Dehydrogenase [NAD ⁺] 3 Catalytic Subunit Alpha	A_23_P140668	1.65	1.42	1.91
IDO1	Indoleamine 2,3-Dioxygenase 1	A_23_P112026	0.63*	0.69	0.57*
IL4I1	Interleukin 4 Induced 1	A_23_P502520	1.26	1.36	1.17
IMPA2	Inositol Monophosphatase 2	A_23_P50081	0.61*	0.60*	0.62*
LDHC*	Lactate Dehydrogenase C	A_23_P53039	1.17	1.34	1.03
Transcriptionally regulated in mESCs					
MAOA	Monoamine Oxidase A	A_23_P83857	0.56*	0.49	0.64
MAOB	Monoamine Oxidase B	A_23_P85008	1.05	1.09	1.00

<i>MAT1A</i>	Methionine Adenosyltransferase 1A	A_23_P23996	0.26*	0.25	0.27
<i>NAT8L</i>	N-Acetyltransferase 8 Like	A_24_P91991	0.50*	0.61*	0.41
<i>NMRK1</i>	Nicotinamide Riboside Kinase 1	A_23_P32036	0.79*	0.78	0.80*
<i>NOS1AP</i>	Nitric Oxide Synthase 1 Adaptor Protein	A_23_P74309	2.19*	1.93	2.48
<i>NOS2</i>	Nitric Oxide Synthase 2	A_23_P502464	1.16	2.09	0.64
<i>NT5C2</i>	5'-Nucleotidase, Cytosolic II	A_23_P97906	0.47*	0.54*	0.40*
<i>ODC1</i>	Ornithine Decarboxylase 1	A_23_P165840	1.59	1.44	1.74
<i>OGDH</i>	Oxoglutarate Dehydrogenase	A_23_P123133	1.66	1.64	1.68
<i>PC</i>	Pyruvate Carboxylase	A_23_P161647	1.00	1.07	0.94
<i>PDHA1</i>	Pyruvate Dehydrogenase E1 Subunit Alpha 1	A_23_P251095	1.57*	1.51*	1.63*
<i>PDHB</i>	Pyruvate Dehydrogenase E1 Subunit Beta	A_23_P20932	0.85	0.75*	0.97
<i>PKD1</i>	Pyruvate Dehydrogenase Kinase 1	A_23_P10614	1.59*	1.69	1.49*
<i>PKD2</i>	Pyruvate Dehydrogenase Kinase 2	A_23_P207517	0.94	0.72*	1.23
<i>PKD3</i>	Pyruvate Dehydrogenase Kinase 3	A_32_P214503	1.04	1.13*	0.95
PDXDC1	Pyridoxal Dependent Decarboxylase Domain Containing 1 Transcriptionally regulated in mESCs, high in Tesar data	A_23_P391583	0.63*	0.53*	0.74*
<i>PFKL</i>	Phosphofructokinase, Liver Type	A_23_P29079	2.18	1.94	2.44
<i>PGK1</i>	Phosphoglycerate Kinase 1	A_24_P254532	1.58	1.87	1.33
PLA2G10	Phospholipase A2 Group X; Transcriptionally regulated in mESCs, high in Tesar data	A_23_P88767	2.87*	2.73	3.02
<i>PPARGC1B</i>	PPARG Coactivator 1 Beta (Known as PGC-1-Beta)	A_24_P560519	2.23*	2.05*	2.44
<i>PRKACA</i>	Protein Kinase cAMP-Activated Catalytic Subunit Alpha	A_24_P399630	1.58	1.27	1.98
<i>PRODH</i>	Proline Dehydrogenase 1	A_23_P68786	5.65*	3.38*	9.45*
<i>PYCR1</i>	Pyrroline-5-Carboxylate Reductase 1	A_23_P130194	0.49*	0.48	0.50*
<i>PYCR2</i>	Pyrroline-5-Carboxylate Reductase 2	A_24_P165259	0.48*	0.63	0.37
PYGL	Glycogen Phosphorylase L Transcriptionally regulated with naïve protocols, low in naïve mESCs	A_23_P48676	0.65	0.67	0.64
<i>PYGM</i>	Glycogen Phosphorylase, Muscle Associated	A_23_P52657	1.24	1.32	1.17
<i>RRM2B</i>	Ribonucleotide Reductase Regulatory TP53 Inducible Subunit M2B	A_23_P20225	0.56*	0.76*	0.42*
<i>SC5D</i>	Sterol-C5-Desaturase	A_23_P98446	0.83	0.73	0.94
<i>SCO2</i>	Synthesis of Cytochrome C Oxidase 2	A_23_P132388	0.77*	0.80	0.73
<i>SDHB</i>	Succinate Dehydrogenase Complex Iron Sulfur Subunit B	A_23_P149649	1.09	0.99	1.20
<i>SDS</i>	Serine Dehydratase	A_24_P304439	0.52*	0.45	0.60
SLC16A2	Monocarboxylate Transporter; Transcriptionally regulated in mESCs, high in Tesar data	A_23_P137097	3.04*	2.55*	3.62*
<i>SLC29A1</i>	Solute Carrier Family 29 Member 1 (Augustine Blood Group)	A_23_P133694	0.76*	0.67*	0.86
<i>SMS</i>	Spermine Synthase	A_32_P50452	1.02	1.08	0.96
<i>SQLE</i>	Squalene Epoxidase	A_23_P146284	1.41*	1.35*	1.48
<i>TDH</i>	L-Threonine Dehydrogenase (Pseudogene)	A_23_P337778	4.47*	3.59*	5.56*
<i>TK2</i>	Thymidine Kinase 2	A_23_P351679	1.15	1.36	0.97
<i>TYMP</i>	Thymidine Phosphorylase	A_23_P91802	0.56*	0.63	0.69

FOOTNOTES

*Transcriptionally regulated genes are indicated in bold gene symbols, with up-regulated gene in red and down-regulated gene in blue colors.

** Indicates *P* values < 0.05 with two-tailed Student *t*-test, for fold changes of gene expression in microarray.

Abbreviations: mESCs, naive mouse embryonic stem cells; PN and PH, primed hESCs under normoxic and hypoxic growth conditions respectively; RN and RH, RSeT hESCs under normoxic and hypoxic growth conditions respectively; Tesar data: data published by Tesar et al., Nature 2007 (PMID: 17597760).