Table 5. Gene ontology (GO) categories significantly up-regulated under starvation

Gene category (GO ID, GO system)	Entrez gene ID	Gene symbol	Gene title	x-fold over-expression 6 h	x-fold over-expression 24 h
Vesicular transport and membrane trafficking					
ARF guanyl-nucleotide ex-change factor activity (5086, MF)	26269	FBXO8	F-box only protein 8	2.1	4.0
	9267	PSCD1	Pleckstrin homology, Sec7 and coiled-coil domains 1	2.1	2.5
	9265	PSCD3	Pleckstrin homology, Sec7 and coiled-coil domains 3	2.6	2.6
Small GTPase mediated signal transduction (7264, BP)	399	ARHH	Ras homolog gene family, member H	1.4	2.1
	23433	ARHQ	Ras homolog gene family, member Q	2.6	3.7
	221079	ARL8	ADP-ribosylation factor-like 8	2.5	4.3
	55207	FLJ10702	Hypothetical protein FLJ10702	2.1	3.0
	2669	GEM	GTP binding protein overexpressed in skeletal muscle	3.5	8.0
	2889	GRF2	Guanine nucleotide-releasing factor 2	1.6	1.4
	3845	KRAS2	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	1.5	2.6
	51762	LOC51762	RAB-8b protein	1.7	2.0
	51735	PDZGEF2	PDZ domain containing guanine nucleotide exchange factor (GEF) 2	4.0	4.0
	5862	RAB2	RAB2, member RAS oncogene family	1.6	2.5
	84932	RAB2B	RAB2B, member RAS oncogene family	1.4	2.1
	5868	RAB5A	RAB5A, member RAS oncogene family	1.5	2.0
	9367	RAB9A	RAB9A, member RAS oncogene family	2.3	2.3
	10890	RAB10	RAB10, member RAS oncogene family	1.4	2.3
	51552	RAB14	RAB14, member RAS oncogene family	1.4	1.7
	23011	RAB21	RAB21, member RAS oncogene family	1.4	2.5
	57403	RAB22A	RAB22A, member RAS oncogene family	1.6	2.1
	5898	RALA	v-Ral simian leukemia viral oncogene homolog A	1.4	2.3
	57826	RAP2C	RAP2C, member of RAS oncogene family	1.6	2.1
	6009	RHEB	Ras homolog enriched in brain	1.6	1.5
	121268	RHEBL1	Ras homolog enriched in brain like 1	5.3	3.0
	6016	RIT1	Ras-like without CAAX 1	1.5	2.3
	64121	RRAGC	Ras-related GTP binding C	2.6	2.8
	22800	RRAS2	Related RAS viral (r-ras) oncogene homolog 2	1.5	1.9
	8036	SHOC2	Soc-2 suppressor of clear homolog (*C. elegans*)	1.7	2.1
	6478	SIAH2	Seven in absentia homolog 2 (*Drosophila*)	2.1	3.0
	7248	TSC1	Tuberous sclerosis 1	1.9	2.1
Amino acid transport and metabolism					
Amino acid transport (6865, BP)	6558	SLC12A2	Solute carrier family 12 (sodium/potassium/chloride transporters), member 2	1.4	3.0
Neutral amino acid transporter activity (15175, MF)	6509	SLC1A4	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.1	4.0
Amino acid permease activity (15359, MF)	6510	SLC1A5	Solute carrier family 1 (neutral amino acid transporter), member 5	1.4	3.0
	81539	SLC38A1	Solute carrier family 38, member 1	2.0	3.7
	54407	SLC38A2	Solute carrier family 38, member 2	4.3	4.9
	6520	SLC3A2	Solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	2.6	4.6
	6541	SLC7A1	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	2.8	3.7
	23657	SLC7A11	Solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	3.2	4.6
	8140	SLC7A5	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	3.0	4.9
Serine family amino acid biosynthesis (9070, BP)	1491	CTH	Cystathionase (cystathionine γ-lyase)	5.7	18.4
	26227	PHGDH	Phosphoglycerate dehydrogenase	2.6	6.1
	29968	PSAT1	Phosphoserine aminotransferase 1	3.7	9.8
	5723	PSPH	Phosphoserine phosphatase	2.3	6.1
Effects on cell cycle					
Cell cycle arrest (7050, BP)	1026	CDKN1A	Cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.9	2.6
	1027	CDKN1B	Cyclin-dependent kinase inhibitor 1B (p27, Kip1)	1.5	3.2
	1647	GADD45A	Growth arrest and DNA-damage-inducible, alpha	2.8	3.5
	8522	GAS7	Growth arrest-specific 7	1.6	3.0
	283431	LOC283431	Hypothetical protein LOC283431	1.6	4.3
	5325	PLAGL1	Pleiomorphic adenoma gene-like 1	1.4	2.0
	23645	PPP1R15A	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	8.0	5.7
	83667	SESN2	Sestrin 2	4.3	12.1
Protein phosphatase type 2C activity (15071, MF)	5494	PPM1A	Protein phosphatase 1A (formerly 2C), magnesium-dependent, α isoform	2.3	2.6
	8493	PPM1D	Protein phosphatase 1D magnesium-dependent, δ isoform	2.1	4.6

Gene category **(GO ID, GO system)**	**Entrez gene ID**	**Gene symbol**	**Gene title**	**x-fold over-expression**	
				6 h	**24 h**
Apoptosis					
Apoptosis	64651	AXUD1	AXIN1 up-regulated 1	2.6	4.6
(6915, BP)	596	BCL2	B-cell CLL/lymphoma 2	1.6	4.9
	597	BCL2A1	BCL2-related protein A1	1.9	1.9
	598	BCL2L1	BCL2-like 1	1.4	1.9
	329	BIRC2	Baculoviral IAP repeat-containing 2	1.6	2.8
	331	BIRC4	Baculoviral IAP repeat-containing 4	1.5	1.5
	664	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	1.4	1.7
	665	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	2.1	2.6
	8837	CFLAR	CASP8 and FADD-like apoptosis regulator	1.7	1.5
	8087	FXR1	Fragile X mental retardation, autosomal homolog 1	1.5	1.6
	1647	GADD45A	Growth arrest and DNA-damage-inducible, α	2.8	3.5
	4616	GADD45B	Growth arrest and DNA-damage-inducible, β	2.6	4.6
	8870	IER3	Immediate early response 3	1.4	1.5
	51747	LUC7A	Cisplatin resistance-associated overexpressed protein	1.4	2.1
	4170	MCL1	Myeloid cell leukemia sequence 1 (BCL2-related)	2.1	1.7
	4790	NFKB1	Nuclear factor of κ light polypeptide gene enhancer in B-cells 1 (p105)	1.6	2.1
	7262	PHLDA2	Pleckstrin homology-like domain, family A, member 2	3.0	2.6
	23645	PPP1R15A	Protein phosphatase 1, regulatory (inhibitor) subunit 15A	8.0	5.7
	5885	RAD21	RAD21 homolog (*S. pombe*)	1.5	2.5
	8767	RIPK2	Receptor-interacting serine-threonine kinase 2	1.7	3.0
	64121	RRAGC	Ras-related GTP binding C	2.6	2.8
	6446	SGK	Serum/glucocorticoid regulated kinase	9.2	1.7
	23411	SIRT1	Sirtuin 1 (*S. cerevisiae*)	3.2	4.3
	9263	STK17A	Serine/threonine kinase 17a (apoptosis-inducing)	1.9	2.5
	9262	STK17B	Serine/threonine kinase 17b (apoptosis-inducing)	1.6	1.9
	7009	TEGT	Testis enhanced gene transcript (BAX inhibitor 1)	1.5	2.5
	7124	TNF	Tumor necrosis factor (TNF superfamily, member 2)	2.0	1.4
	7128	TNFAIP3	Tumor necrosis factor, α-induced protein 3	2.1	2.6
	8795	TNFRSF10B	Tumor necrosis factor receptor superfamily, member 10b	2.5	3.0
	8793	TNFRSF10D	Tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death domain	9.2	13.9
	958	TNFRSF5	Tumor necrosis factor receptor superfamily, member 5	1.9	1.4
	355	TNFRSF6	Tumor necrosis factor receptor superfamily, member 6	1.9	2.1
	3604	TNFRSF9	Tumor necrosis factor receptor superfamily, member 9	2.1	2.1
	970	TNFSF7	Tumor necrosis factor (ligand) superfamily, member 7	1.6	2.0
	8626	TP73L	Tumor protein p73-like	1.4	2.5
	7187	TRAF3	TNF receptor-associated factor 3	1.6	1.6
	8565	YARS	Tyrosyl-tRNA synthetase	2.1	1.7
Anti-apoptosis	596	BCL2	B-cell CLL/lymphoma 2	1.6	4.9
(6916, BP)	597	BCL2A1	BCL2-related protein A1	1.9	1.9
Apoptosis inhibitor activity	598	BCL2L1	BCL2-like 1	1.4	1.9
(8189, MF)	329	BIRC2	Baculoviral IAP repeat-containing 2	1.6	2.8
	331	BIRC4	Baculoviral IAP repeat-containing 4	1.5	1.5
	664	BNIP3	BCL2/adenovirus E1B 19-kDa interacting protein 3	1.4	1.7
	673	BRAF	v-Raf murine sarcoma viral oncogene homolog B1	1.4	3.7
	8837	CFLAR	CASP8 and FADD-like apoptosis regulator	1.7	1.5
	25816	GG2-1	TNF-induced protein	1.9	2.6
	8870	IER3	Immediate early response 3	1.4	1.5
	4790	NFKB1	Nuclear factor of κ light polypeptide gene enhancer in B-cells 1 (p105)	1.6	2.1
	5663	PSEN1	Presenilin 1 (Alzheimer disease 3)	1.7	2.8
	5055	SERPINB2	Serine (or cysteine) proteinase inhibitor, clade B, member 2	1.9	3.7
	8887	TAX1BP1	Tax1 binding protein 1	1.4	2.0
	7124	TNF	Tumor necrosis factor (TNF superfamily, member 2)	2.0	1.4
	7128	TNFAIP3	Tumor necrosis factor, α-induced protein 3	2.1	2.6
	355	TNFRSF6	Tumor necrosis factor receptor superfamily, member 6	1.9	2.1
Sphingoid and ceramide metabolism					
Sphingoid metabolism	427	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	1.4	2.6
(46519, BP) *Ceramide metabolism*	8439	NSMAF	Neutral sphingomyelinase (N-SMase) activation associated factor	2.5	1.7
(6672, BP)	5515	PPP2CA	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	1.4	1.5
	7357	UGCG	UDP-glucose ceramide glucosyltransferase	3.2	3.2

Gene category **(GO ID, GO system)**	**Entrez gene ID**	**Gene symbol**	**Gene title**	**x-fold over-expression**	
				6 h	**24 h**
Regulation of transcription					
Transcription corepressor activity (3714, MF)	467	ATF3	Activating transcription factor 3	6.5	8.0
	22809	ATF5	Activating transcription factor 5	1.4	1.5
	1810	DR1	Down-regulator of transcription 1, TBP-binding	1.4	2.3
	3726	JUNB	Jun B proto-oncogene	1.7	2.0
	11278	KLF12	Kruppel-like factor 12	1.9	2.5
	4601	MXI1	MAX interacting protein 1	1.9	2.5
	23522	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	1.9	1.7
	8554	PIAS1	Protein inhibitor of activated STAT, 1	1.7	1.4
	5971	RELB	v-Rel reticuloendotheliosis viral oncogene homolog B	1.5	1.4
	6478	SIAH2	Seven in absentia homolog 2 (*Drosophila*)	2.1	3.0
	22797	TFEC	Transcription factor EC	1.4	5.3
	7528	YY1	YY1 transcription factor	2.0	2.5
Histone acetyltransferase activity (4402, MF)	1387	CREBBP	CREB binding protein (Rubinstein-Taybi syndrome)	1.6	1.9
	2033	EP300	E1A binding protein p300	1.6	2.0
	23522	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	1.9	1.7
	8202	NCOA3	Nuclear receptor coactivator 3	1.7	2.0
Nuclear membrane					
Nuclear inner membrane (5637, CC)	4000	LMNA	Lamin A/C	3.5	2.3
	23592	MAN1	Integral inner nuclear membrane protein	1.6	2.1
	5663	PSEN1	Presenilin 1 (Alzheimer disease 3)	1.7	2.8

Genes fulfilling the up-regulation requirements are shown (2 means 200% of mRNA was detected in starved compared with control cells). The first column indicates the GO category together with the GO ID and the GO system (BP, biological process; CC, cellular component; MF, molecular function).