Table 6. Gene ontology (GO) categories significantly down-regulated under starvation

Gene category (GO ID, GO system)	Entrez gene ID	Gene symbol	Gene title	x-fold over-expression	
				6 h	24 h
Vesicular transport					
Golgi stack (5795, CC)	23062	GGA2	Golgi associated, γ adaptin ear containing, ARF binding protein 2	-1.5	-1.7
	23163	GGA3	Golgi associated, γ adaptin ear containing, ARF binding protein 3	-1.6	-3.2
	2778	GNAS	GNAS complex locus	-1.5	-1.9
	4952	OCRL	Oculocerebrorenal syndrome of Lowe	-1.5	-2.3
	10040	TOM1L1	Target of myb1-like 1 (chicken)	-1.9	-1.6
DNA replication and repair					
DNA replication origin binding (3688, MF)	4999	ORC2L	Origin recognition complex, subunit 2-like (yeast)	-1.6	-1.6
	23595	ORC3L	Origin recognition complex, subunit 3-like (yeast)	-1.6	-1.5
	5001	ORC5L	Origin recognition complex, subunit 5-like (yeast)	-1.5	-2.0
Damaged DNA binding (3684, MF)	672	BRCA1	Breast cancer 1, early onset	-1.5	-2.3
	2237	FEN1	Flap structure-specific endonuclease 1	-1.6	-2.6
	2967	GTF2H3	General transcription factor IIH, polypeptide 3, 34kDa	-1.4	-1.6
	7965	JTV1	JTV1 gene	-1.5	-4.0
	5383	PMS2L5	Postmeiotic segregation increased 2-like 5	-1.7	-4.3
	5889	RAD51C	RAD51 homolog C (*S. cerevisiae*)	-1.7	-1.5
	5892	RAD51L3	RAD51-like 3 (*S. cerevisiae*)	-1.6	-1.7
	7508	XPC	Xeroderma pigmentosum, complementation group C	-1.4	-1.4
	7517	XRCC3	X-ray repair complementing defective repair in Chinese hamster cells 3	-1.4	-1.6
Ribosome formation					
Ribosome biogenesis and assembly (42254, BP)	10969	EBNA1BP2	EBNA1 binding protein 2	-1.6	-2.5
	23212	RRS1	Ribosome biogenesis regulator homolog (*S. cerevisiae*)	-2.5	-3.0
Nucleolus (5730, CC)	1663	DDX11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, *S. cerevisiae*)	-1.6	-2.6
	54606	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	-1.4	-4.0
	50628	GEMIN4	Gem (nuclear organelle) associated protein 4	-3.2	-10.6
	23567	JAZ	Double-stranded RNA-binding zinc finger protein JAZ	-1.4	-1.9
	84365	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	-1.7	-1.9
	10514	MYBBP1A	MYB binding protein (P160) 1a	-1.9	-3.5
	4809	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (*S. cerevisiae*)	-1.4	-1.6
	10528	NOL5A	Nucleolar protein 5A (56kDa with KKE/D repeat)	-1.4	-1.7
	9221	NOLC1	Nucleolar and coiled-body phosphoprotein 1	-1.4	-1.4
	54512	RRP41	Exosome complex exonuclease RRP41	-2.5	-18.4
	6949	TCOF1	Treacher Collins-Franceschetti syndrome 1	-1.6	-1.7
	7343	UBTF	Upstream binding transcription factor, RNA polymerase I	-2.5	-4.3
RNA synthesis and processing					
RNA cap binding (339, MF)	1973	EIF4A1	Eukaryotic translation initiation factor 4A, isoform 1	-1.7	-1.7
	9470	EIF4EL3	Eukaryotic translation initiation factor 4E-like 3	-4.3	-5.7
	4686	NCBP1	Nuclear cap binding protein subunit 1, 80 kDa	-1.5	-1.7
	22916	NCBP2	Nuclear cap binding protein subunit 2, 20 kDa	-1.4	-1.7
	10073	RNUT1	RNA, U transporter 1	-1.4	-2.3
RNA elongation (6354, BP)	5438	POLR2I	Polymerase (RNA) II (DNA directed) polypeptide I	-1.5	-2.8
	51728	POLR3K	Polymerase (RNA) III (DNA directed) polypeptide K	-1.6	-2.5
	30834	ZNRD1	Zinc ribbon domain containing, 1	-1.6	-2.1

Gene category **(GO ID, GO system)**	**Entrez gene ID**	**Gene symbol**	**Gene title**	**x-fold over-expression**	
				6 h	**24 h**
Pre-mRNA splicing factor activity	9416	DDX23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	-1.9	-1.6
(8284, MF)	25929	GEMIN5	Gem (nuclear organelle) associated protein 5	-2.1	-6.1
	79833	GEMIN6	Gem (nuclear organelle) associated protein 6	-3.0	-4.6
	84967	LSM10	U7 snRNP-specific Sm-like protein LSM10	-1.5	-2.5
	57819	LSM2	LSM2 homolog, U6 small nuclear RNA associated (*S. cerevisiae*)	-1.5	-3.2
	23658	LSM5	LSM5 homolog, U6 small nuclear RNA associated (*S. cerevisiae*)	-1.4	-2.0
	51691	LSM8	LSM8 homolog, U6 small nuclear RNA associated (*S. cerevisiae*)	-1.7	-1.9
	8559	PRPF18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	-3.2	-4.3
	9128	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	-2.0	-5.3
	6426	SFRS1	Splicing factor, arginine/serine-rich 1 (splicing factor 2)	-1.6	-3.2
	9169	SFRS2IP	Splicing factor, arginine/serine-rich 2, interacting protein	-1.5	-2.1
	6432	SFRS7	Splicing factor, arginine/serine-rich 7, 35 kDa	-1.4	-3.7
	8487	SIP1	Survival of motor neuron protein interacting protein 1	-2.0	-4.3
RNA polymerase complex	5433	POLR2D	Polymerase (RNA) II (DNA directed) polypeptide D	-2.1	-3.2
(30880, CC)	5438	POLR2I	Polymerase (RNA) II (DNA directed) polypeptide I	-1.5	-2.8
	51728	POLR3K	Polymerase (RNA) III (DNA directed) polypeptide K	-1.6	-2.5
	10622	RPC32	Polymerase (RNA) III (DNA directed) (32 kDa)	-1.5	-2.6
	171568	RPC8	RNA polymerase III subunit RPC8	-1.9	-3.5
	9169	SFRS2IP	Splicing factor, arginine/serine-rich 2, interacting protein	-1.5	-2.1
	23528	ZNF281	Zinc finger protein 281	-1.5	-2.0
rRNA transcription	2971	GTF3A	General transcription factor IIIA	-1.7	-2.1
(9303, BP)	84365	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	-1.7	-1.9
rRNA processing	10436	C2F	C2f protein	-1.5	-3.7
(6364, BP)	54606	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	-1.4	-4.0
	29960	FTSJ2	FtsJ homolog 2 (*E. coli*)	-1.7	-2.3
	50628	GEMIN4	Gem (nuclear organelle) associated protein 4	-3.2	-10.6
	10528	NOL5A	Nucleolar protein 5A (56kDa with KKE/D repeat)	-1.4	-1.7
	9221	NOLC1	Nucleolar and coiled-body phosphoprotein 1	-1.4	-1.4
	22984	PDCD11	Programmed cell death 11	-1.5	-2.6
	23404	RRP4	Homolog of Yeast RRP4 (ribosomal RNA processing 4), 3'-5'-exoribonuclease	-1.9	-3.7
	51010	RRP40	Exosome component Rrp40	-2.1	-1.9
	54512	RRP41	Exosome complex exonuclease RRP41	-2.5	-18.4
Transcription from Pol III promoter	672	BRCA1	Breast cancer 1, early onset	-1.5	-2.3
	2971	GTF3A	General transcription factor IIIA	-1.7	-2.1
(6383, BP)	10625	IVNS1ABP	Influenza virus NS1A binding protein	-1.7	-5.7
	51728	POLR3K	Polymerase (RNA) III (DNA directed) polypeptide K	-1.6	-2.5
	10622	RPC32	Polymerase (RNA) III (DNA directed) (32 kDa)	-1.5	-2.6
	171568	RPC8	RNA polymerase III subunit RPC8	-1.9	-3.5
	6619	SNAPC3	Small nuclear RNA activating complex, polypeptide 3	-1.4	-2.0
	10302	SNAPC5	Small nuclear RNA activating complex, polypeptide 5	-1.6	-1.7
tRNA processing	81627	C1orf25	Chromosome 1 open reading frame 25	-2.1	-3.2
(8033, BP)	83480	FKSG32	Hypothetical protein FKSG32	-1.4	-2.1
	79042	LENG5	Leukocyte receptor cluster (LRC) member 5	-1.4	-2.1
	80746	MGC2776	Hypothetical protein MGC2776	-2.0	-3.0
	10940	POP1	Processing of precursors 1	-1.7	-3.2
	80324	PUS1	Pseudouridylate synthase 1	-1.5	-2.0
	11102	RPP14	Ribonuclease P (14kD)	-1.6	-1.4
	10248	RPP20	POP7 (processing of precursor, *S. cerevisiae*) homolog	-1.6	-3.2
	10557	RPP38	Ribonuclease P (38kD)	-1.6	-1.7
	51095	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	-1.6	-2.5
	10785	WDR4	WD repeat domain 4	-1.6	-2.1
tRNA-specific ribonuclease activity	79042	LENG5	Leukocyte receptor cluster (LRC) member 5	-1.4	-2.1
(4549, MF)	80746	MGC2776	Hypothetical protein MGC2776	-2.0	-3.0
	10940	POP1	Processing of precursors 1	-1.7	-3.2
	11102	RPP14	Ribonuclease P (14 kDa)	-1.6	-1.4
	10248	RPP20	POP7 (processing of precursor, *S. cerevisiae*) homolog	-1.6	-3.2
	10557	RPP38	Ribonuclease P (38 kDa)	-1.6	-1.7

Gene category (GO ID, GO system)	Entrez gene ID	Gene symbol	Gene title	x-fold over-expression 6 h	24 h
Mitochondrial metabolism					
Protein-mitochondrial targeting (6626, BP)	26515	FXC1	Fracture callus 1 homolog (rat)	-1.7	-2.6
	80273	GRPEL1	GrpE-like 1, mitochondrial (*E. coli*)	-1.4	-2.0
	3329	HSPD1	Heat shock 60-kDa protein 1 (chaperonin)	-1.7	-4.0
	1678	TIMM8A	Translocase of inner mitochondrial membrane 8 homolog A	-2.6	-3.7
	26521	TIMM8B	Translocase of inner mitochondrial membrane 8 homolog B	-1.5	-2.0
	26520	TIMM9	Translocase of inner mitochondrial membrane 9 homolog	-1.4	-1.6
	51095	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	-1.6	-2.5
Protein translocase activity (15450, MF)	51300	C3orf1	Chromosome 3 open reading frame 1	-1.5	-2.0
	26515	FXC1	Fracture callus 1 homolog (rat)	-1.7	-2.6
	55176	SEC61A2	Sec61 α 2 subunit (*S. cerevisiae*)	-1.4	-1.5
	1678	TIMM8A	Translocase of inner mitochondrial membrane 8 homolog A	-2.6	-3.7
	26521	TIMM8B	Translocase of inner mitochondrial membrane 8 homolog B	-1.5	-2.0
	26520	TIMM9	Translocase of inner mitochondrial membrane 9 homolog	-1.4	-1.6
Carnitine O-acyltransferase activity (16406, MF)	1375	CPT1B	Carnitine palmitoyltransferase 1B (muscle)	-1.7	-1.9
	1376	CPT2	Carnitine palmitoyltransferase II	-2.0	-7.0
	54677	CROT	Carnitine O-octanoyltransferase	-1.7	-1.7

Genes fulfilling the down-regulation requirements are shown (-2 means 50% 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).