Table S1: List of viral (green) and cellular (blue) proteins with their changes over time.

	log2 fold change				
Symbol	4hrs p.i.	8 hrs p.i.	10 hrs p.i.	12 hrs p.i.	Name
P03428	-1,39	0,52	1,74	2,01	PB2
P03431	-0,86	0,68	1,91	2,33	PB1
P03433	-0,60	1,37	2,48	2,72	PA
P03452	-1,32	2,21	3,73	4,10	HA
P03466	-1,47	2,86	4,37	4,83	NP
P03468	-1,80	0,70	2,38	3,07	NA
P03485	-1,96	2,37	4,33	4,88	M
P03496	-0,45	3,63	5,04	5,59	NS1
P03508	-0,27	0,75	2,48	2,38	NS2

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
LOC611024	611024	-2,14	-1,87	-1,99	-2,40	similar to 3-beta-hydroxysteroid-delta(8),delta(7)-isomerase (Cholestenol delta-isomerase) (Delta8-delta7 sterol isomerase) (D8-D7 sterol isomerase) (Emopamil-binding protein)
RPLP1	478356	-1,25	-0,90	-1,74	-1,50	ribosomal protein, large, P1
SFXN1	489109	-1,47	-1,40	-1,55	-1,67	sideroflexin 1
ELOVL1	482533	-1,29	-1,15	-1,49	-1,49	ELOVL fatty acid elongase 1
LOC478576	478576	-0,79	-0,71	-1,45	-1,22	similar to ribosomal protein S15a
PGRMC2	476084	-1,09	-0,93	-1,44	-2,05	progesterone receptor membrane component 2
RPL9	479109	-0,83	-0,53	-1,44	-1,06	ribosomal protein L9
LOC477944	477944	-0,81	-0,74	-1,44	-1,09	similar to ubiquinol-cytochrome c reductase binding protein
RPLP2	475991	-0,90	-0,59	-1,42	-0,99	ribosomal protein, large, P2
TIMM23	486776	-1,17	-0,87	-1,42	-1,40	translocase of inner mitochondrial membrane 23 homolog (yeast)
SSR1	403951	-1,22	-1,24	-1,42	-1,33	signal sequence receptor, alpha
LOC481543	481543	-0,82	-0,68	-1,40	-1,05	similar to ribosomal protein L31
RPS2	479886	-0,81	-0,65	-1,39	-1,17	ribosomal protein S2
ATP1B1	403966	-1,34	-1,17	-1,35	-1,55	ATPase, Na+/K+ transporting, beta 1 polypeptide
SQLE	608021	-0,95	-0,99	-1,35	-1,74	squalene epoxidase
FDFT1	477362	-1,29	-1,04	-1,33	-1,74	farnesyl-diphosphate farnesyltransferase 1
TMX1	610791	-1,17	-1,13	-1,33	-1,41	thioredoxin-related transmembrane protein 1
RPL30	480751	-0,62	-0,51	-1,29	-0,90	ribosomal protein L30
LOC479623	479623	-1,19	-1,14	-1,29	-1,42	similar to Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor (COX IV-1) (Cytochrome c oxidase polypeptide IV)
SPTLC1	484192	-1,12	-1,23	-1,28	-1,56	serine palmitoyltransferase, long chain base subunit 1
TRPV4	486308	-1,01	-0,77	-1,27	-1,64	transient receptor potential cation channel, subfamily V, member 4
LOC611134	611134	-1,12	-1,09	-1,25	-1,49	similar to cytochrome c oxidase, subunit 7a 3
LOC488258	488258	-1,14	-1,20	-1,25	-1,63	similar to Histone H1.2 (H1d)

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
LOC476758	476758	-1,37	-1,04	-1,25	-1,51	similar to basigin isoform 1
ATP5F1	479901	-1,04	-0,89	-1,24	-1,18	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1
VDAC1	474681	-1,03	-0,90	-1,24	-1,20	voltage-dependent anion channel 1
SLC25A4	475630	-0,91	-1,00	-1,24	-1,20	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4
GNAI2	442957	-0,92	-0,75	-1,24	-1,18	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
NOP2	611645	-0,98	-0,60	-1,23	-1,21	NOP2 nucleolar protein homolog (yeast)
VDAC2	479255	-1,05	-0,87	-1,23	-1,14	voltage-dependent anion channel 2
NDUFA5	475214	-0,94	-1,09	-1,22	-1,43	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
LOC610942	610942	-0,90	-0,87	-1,22	-1,23	similar to cytochrome b5 outer mitochondrial membrane precursor
FAF2	489102	-1,25	-1,05	-1,21	-1,14	Fas associated factor family member 2
RPS11	403684	-0,62	-0,64	-1,20	-1,06	ribosomal protein S11
STT3A	489300	-0,87	-0,53	-1,19	-1,09	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)
LOC477031	477031	-0,77	-0,58	-1,19	-1,06	similar to ribosomal protein L14
CANX	403908	-1,07	-0,99	-1,19	-1,30	calnexin
RPS5	476366	-0,83	-0,66	-1,19	-1,00	ribosomal protein S5
LARP1	612929	-0,68	-0,74	-1,18	-1,09	La ribonucleoprotein domain family, member 1
AGK	482764	-1,20	-1,05	-1,17	-1,36	acylglycerol kinase
TOMM40	611055	-1,13	-1,05	-1,17	-1,33	translocase of outer mitochondrial membrane 40 homolog (yeast)
RPS25	479412	-0,62	-0,53	-1,16	-0,86	ribosomal protein S25
SSR3	477124	-1,10	-0,77	-1,16	-1,32	signal sequence receptor, gamma (translocon-associated protein gamma)
LOC476637	476637	-0,55	-0,39	-1,16	-0,79	similar to ribosomal protein L18a
RPL6	403691	-0,65	-0,46	-1,16	-0,91	Ribosomal protein L6
CPT1A	403583	-1,16	-0,90	-1,15	-1,33	carnitine palmitoyltransferase 1A (liver)
AGPS	488421	-0,92	-0,92	-1,15	-1,01	alkylglycerone phosphate synthase
RPL15	477046	-0,60	-0,37	-1,14	-0,82	ribosomal protein L15
YBX1	479011	-0,56	-0,48	-1,14	-0,93	Y box binding protein 1
RPS8	475381	-0,63	-0,47	-1,14	-0,80	ribosomal protein S8
CISD2	610084	-1,02	-1,04	-1,14	-1,22	CDGSH iron sulfur domain 2
RPN1	476516	-1,07	-0,85	-1,13	-1,13	ribophorin I
RRP12	608725	-1,14	-0,57	-1,13	-1,27	ribosomal RNA processing 12 homolog (S. cerevisiae)
SLC3A2	483777	-1,03	-0,78	-1,12	-1,21	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2
UBTF	480503	-0,52	-0,34	-1,12	-1,34	upstream binding transcription factor, RNA polymerase I
LOC488273	488273	-0,81	-0,82	-1,12	-1,28	similar to Histone H1.5 (Histone H1a)
LOC489372	489372	-1,22	-1,07	-1,11	-1,20	similar to Histone H2A.x

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						(H2a/x)
GPD2	478755	-0,97	-0,86	-1,11	-1,22	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)
RPN2	477223	-1,10	-0,78	-1,11	-1,05	ribophorin II
SPTLC2	480403	-0,67	-0,86	-1,10	-1,18	serine palmitoyltransferase, long chain base subunit 2
RPS9	476387	-0,49	-0,35	-1,10	-0,74	ribosomal protein S9
RPL35A	478597	-0,57	-0,45	-1,09	-0,79	ribosomal protein L35a
RPL7	477912	-0,55	-0,40	-1,09	-0,80	ribosomal protein L7
CAV1	403980	-0,80	-1,05	-1,06	-1,35	caveolin 1, caveolae protein, 22kDa
TMEM43	484637	-0,75	-0,82	-1,06	-1,02	transmembrane protein 43
NDUFA10	608244	-1,08	-1,01	-1,06	-1,17	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10, 42kDa
RPL7A	403678	-0,57	-0,44	-1,05	-0,88	Ribosomal protein L7a
TIMM50	476461	-1,09	-1,04	-1,05	-1,25	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)
RPS4Y1	403893	-0,62	-0,47	-1,05	-0,82	ribosomal protein S4, Y-linked 1
IMMT	475764	-0,91	-0,78	-1,04	-1,10	inner membrane protein, mitochondrial
VDAC3	475462	-0,70	-0,70	-1,02	-0,94	voltage-dependent anion channel 3
CYP1B1	483038	-0,49	-0,60	-1,02	-1,30	cytochrome P450, family 1, subfamily B, polypeptide 1
LOC474504	474504	-0,47	-0,31	-1,02	-0,66	similar to 60S ribosomal protein L3 (L4)
ERLIN2	607518	-0,89	-0,81	-1,01	-1,05	ER lipid raft associated 2
FLT3LG	442938	-0,47	-0,38	-1,01	-0,65	fms-related tyrosine kinase 3 ligand
LOC475225	475225	-0,82	-0,81	-1,00	-1,15	similar to Cytochrome P450 51A1 (CYPLI) (P450LI) (Sterol 14-alpha demethylase) (Lanosterol 14-alpha demethylase) (LDM) (P450-14DM) (P45014DM)
RPS15	476753	-0,57	-0,44	-1,00	-0,89	ribosomal protein S15
OCIAD1	475140	-1,02	-1,03	-0,99	-1,26	OCIA domain containing 1
RPL8	475130	-0,51	-0,25	-0,99	-0,64	ribosomal protein L8
ITGB1	477956	-0,69	-0,62	-0,99	-0,99	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
SLC25A6	480830	-0,65	-0,73	-0,99	-0,88	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
LETM1	488807	-0,85	-0,86	-0,98	-0,83	leucine zipper-EF-hand containing transmembrane protein 1
ETFDH	475480	-0,81	-0,84	-0,98	-1,19	electron-transferring-flavoprotein dehydrogenase
SLC4A7	485637	-1,15	-0,80	-0,97	-1,07	solute carrier family 4, sodium bicarbonate cotransporter, member 7
PODXL	482252	-0,80	-0,89	-0,97	-1,21	podocalyxin-like
LOC474656	474656	-0,38	-0,25	-0,97	-0,65	similar to ribosomal protein L10a
LOC480235	480235	-0,47	-0,30	-0,97	-0,67	similar to ribosomal protein S13
LOC479261	479261	-0,64	-0,90	-0,97	-1,15	similar to R53.5
DPM1	477264	-0,69	-0,86	-0,97	-1,02	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit
ATP1A1	403992	-0,87	-0,70	-0,97	-0,95	ATPase, Na+/K+

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						transporting, alpha 1 polypeptide
DBT	479929	-0,48	-0,52	-0,96	-0,96	dihydrolipoamide branched chain transacylase E2
LOC479350	479350	-0,38	-0,50	-0,96	-0,85	similar to ribosomal protein L37
TMED5	479947	-0,66	-0,47	-0,96	-0,71	transmembrane emp24 protein transport domain containing 5
NDUFS3	475978	-0,73	-0,53	-0,96	-0,92	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
RPL22	479587	-0,46	-0,28	-0,96	-0,60	ribosomal protein L22
NDUFA9	477718	-0,57	-0,81	-0,96	-0,92	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa
ATP5C1	478009	-0,73	-0,78	-0,95	-0,92	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
RAB14	474818	-0,79	-0,88	-0,95	-0,86	RAB14, member RAS oncogene family
RPL27	403688	-0,57	-0,41	-0,95	-0,70	ribosomal protein L27
SLC1A5	484425	-1,91	-1,20	-0,94	-1,46	solute carrier family 1 (neutral amino acid transporter), member 5
ITGB3	403788	-0,54	-0,52	-0,93	-0,91	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
RPL12	476346	-0,49	-0,34	-0,93	-0,60	ribosomal protein L12
SLC25A3	475436	-0,71	-0,64	-0,93	-0,84	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
SLC25A24	611922	-0,74	-0,79	-0,93	-1,00	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24
YTHDF2	478161	-0,33	-0,08	-0,93	-0,72	YTH domain family, member 2
LOC476372	476372	-0,87	-0,84	-0,93	-0,98	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2
NOL10	482966	-0,93	-0,79	-0,92	-1,11	nucleolar protein 10
F11R	478974	-1,15	-1,23	-0,92	-1,27	F11 receptor
SLC25A1	608348	-0,61	-0,77	-0,91	-0,94	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
RPL36	476738	-0,37	-0,23	-0,90	-0,62	ribosomal protein L36
MCU	489042	-0,86	-0,78	-0,90	-1,02	mitochondrial calcium uniporter
LOC474433	474433	-0,88	-0,79	-0,90	-1,01	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a
LOC476525	476525	-0,42	-0,25	-0,90	-0,59	similar to 60S ribosomal protein L26 (Silica-induced gene 20 protein) (SIG-20)
SEC61G	404017	-0,69	-0,64	-0,89	-0,98	Sec61 gamma subunit
SLC25A13	610138	-0,93	-0,73	-0,89	-1,03	solute carrier family 25, member 13 (citrin)
ATP2A2	403878	-0,69	-0,77	-0,89	-0,89	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
PON2	403855	-0,67	0,06	-0,88	-0,63	paraoxonase 2
COX5B	474567	-0,74	-0,82	-0,87	-1,16	cytochrome c oxidase polypeptide Vb
MRPS35	477660	-0,59	-0,67	-0,87	-0,82	mitochondrial ribosomal protein S35
TRIM25	491103	-0,57	-0,76	-0,87	-0,95	tripartite motif containing 25

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
HSD17B12	475939	-0,72	-0,72	-0,86	-0,94	hydroxysteroid (17-beta) dehydrogenase 12
IGF2BP1	491064	-0,46	-0,48	-0,86	-0,75	insulin-like growth factor 2 mRNA binding protein 1
MRPL49	483747	-0,53	-0,71	-0,86	-1,02	mitochondrial ribosomal protein L49
RPS23	479159	-0,31	-0,27	-0,86	-0,56	ribosomal protein S23
LOC479257	479257	-0,28	-0,36	-0,86	-0,60	similar to ribosomal protein S24 isoform 3
SSR4	481082	-0,63	-0,48	-0,86	-0,63	signal sequence receptor, delta
RPS3A	403677	-0,25	-0,18	-0,86	-0,50	ribosomal protein S3A
STOML2	474755	-1,07	-0,89	-0,86	-1,12	stomatin (EPB72)-like 2
NDUFS1	478880	-0,79	-0,72	-0,85	-0,83	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)
LOC488264	488264	-0,44	-0,74	-0,85	-0,87	similar to Histone H1.2 (H1d)
ITGAV	488437	-0,72	-0,77	-0,85	-1,00	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
TSPAN8	474448	-0,53	-0,74	-0,84	-0,76	tetraspanin 8
AIFM1	481048	-0,86	-0,80	-0,84	-0,91	apoptosis-inducing factor, mitochondrion-associated, 1
ATL3	476044	-0,75	-0,54	-0,84	-0,84	atlastin GTPase 3
LOC474877	474877	-0,37	-0,36	-0,84	-0,58	similar to 40S ribosomal protein S10
CEACAM28	484473	-0,46	-0,92	-0,84	-0,90	carcinoembryonic antigen-related cell adhesion molecule 28
CYB5R3	474479	-0,75	-0,68	-0,84	-0,76	cytochrome b5 reductase 3
LOC475410	475410	-0,24	-0,22	-0,83	-0,53	similar to 60S ribosomal protein L32
ITGB4	483318	-0,55	-0,87	-0,83	-1,37	integrin, beta 4
RPS29	610596	-0,24	-0,31	-0,83	-0,52	ribosomal protein S29
MPDU1	489477	-0,87	-0,65	-0,83	-1,17	mannose-P-dolichol utilization defect 1
TMCO1	478992	-1,05	-1,01	-0,82	-1,07	transmembrane and coiled-coil domains 1
BCAP31	481080	-0,75	-0,69	-0,82	-0,98	B-cell receptor-associated protein 31
TSPO	474475	-1,09	-0,74	-0,82	-0,99	translocator protein (18kDa)
FKBP11	608951	-0,73	-0,56	-0,81	-0,66	FK506 binding protein 11, 19 kDa
NDUFA13	476659	-0,62	-0,60	-0,81	-0,89	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13
ACSL4	481018	-1,08	-0,94	-0,81	-1,18	acyl-CoA synthetase long-chain family member 4
HMGB3	481073	-0,47	-1,03	-0,80	-1,08	high mobility group box 3
NOMO2	489992	-0,73	-0,89	-0,80	-1,05	NODAL modulator 2
PABPC4	482464	-0,55	-0,50	-0,80	-0,70	poly(A) binding protein, cytoplasmic 4 (inducible form)
PHB	480547	-0,74	-0,68	-0,80	-0,90	prohibitin
SYNCRIP	474986	-0,48	-0,40	-0,80	-0,72	synaptotagmin binding, cytoplasmic RNA interacting protein
RALY	485845	-0,62	-0,34	-0,79	-0,41	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))
LOC483166	483166	-0,48	-0,56	-0,78	-0,72	similar to germinal histone H4 gene
DDOST	404012	-0,71	-0,65	-0,78	-0,76	dolichyl-diphosphooligosaccharide--protein glycosyltransferase
PTGS2	442942	-0,27	-0,37	-0,77	-0,52	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						cyclooxygenase)
RPL18	476422	-0,31	-0,18	-0,77	-0,49	ribosomal protein L18
HSD17B4	474630	-0,61	-0,55	-0,77	-0,82	hydroxysteroid (17-beta) dehydrogenase 4
CIRBP	476755	-0,27	-0,55	-0,77	-0,65	cold inducible RNA binding protein
H2AFY	481514	-0,66	-0,64	-0,77	-0,84	H2A histone family, member Y
NCL	608445	-0,40	-0,14	-0,77	-0,49	nucleolin
TMED10	610559	-0,77	-0,64	-0,76	-0,76	transmembrane emp24-like trafficking protein 10 (yeast)
LOC608089	608089	-1,14	0,33	-0,76	-1,08	similar to Adipocyte plasma membrane-associated protein (BSCv protein)
ATP5D	476756	-0,79	-0,82	-0,76	-0,85	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit
LOC491074	491074	-0,73	-0,88	-0,76	-0,67	similar to integrin alpha 3 isoform b, precursor
DLAT	489406	-0,68	-0,68	-0,76	-0,69	dihydrolipoamide S-acetyltransferase
RPS3	476804	-0,32	-0,21	-0,75	-0,57	ribosomal protein S3
ITGA2	489208	-0,28	-0,70	-0,75	-0,73	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
TOMM22	610117	-1,08	-0,90	-0,75	-1,23	translocase of outer mitochondrial membrane 22 homolog (yeast)
DDX21	476891	-0,61	-0,38	-0,74	-0,70	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21
LOC476842	476842	-0,12	-0,02	-0,74	-0,38	similar to ribosomal protein L27a
TFRC	403703	-0,35	-0,73	-0,74	-1,02	transferrin receptor (p90, CD71)
FIS1	479728	-0,66	-0,72	-0,74	-0,85	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)
HNRNPR	478192	-0,57	-0,49	-0,74	-0,75	heterogeneous nuclear ribonucleoprotein R
LOC483168	483168	-0,61	-0,77	-0,74	-0,82	similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615)
PGRMC1	481029	-0,64	-0,73	-0,73	-0,88	progesterone receptor membrane component 1
RPS17	403681	-0,19	-0,22	-0,73	-0,42	ribosomal protein S17
RAP1B	608981	-0,65	-0,67	-0,73	-0,68	RAP1B, member of RAS oncogene family
TMEM33	612937	-0,71	-0,58	-0,73	-0,68	transmembrane protein 33
GTPBP4	478021	-0,57	-0,23	-0,73	-0,66	GTP binding protein 4
LOC478370	478370	-0,68	-0,61	-0,73	-0,77	similar to Cytochrome c oxidase polypeptide Va, mitochondrial precursor
SLC25A5	492093	-0,27	-0,47	-0,73	-0,56	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
SUPT16H	612874	-0,67	-0,59	-0,72	-0,91	suppressor of Ty 16 homolog (S. cerevisiae)
LOC611089	611089	-0,51	-0,60	-0,72	-0,75	similar to H2B histone family, member F
LOC479778	479778	-0,42	-0,51	-0,71	-0,87	similar to fusion (involved in t(12;16) in malignant liposarcoma) (predicted)
ATP1B3	477098	-0,76	-0,69	-0,71	-0,81	ATPase, Na+/K+ transporting, beta 3 polypeptide
LOC476824	476824	-0,49	-0,40	-0,71	-0,55	similar to NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (Complex I-23KD) (CI-23KD) (TYKY subunit)
L1CAM	492244	-0,41	-0,59	-0,70	-0,83	L1 cell adhesion molecule

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
NDUFV2	480204	-0,69	-0,60	-0,70	-0,82	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
LOC483167	483167	-0,41	-0,50	-0,69	-0,71	similar to H3 histone, family 2 isoform 2
EIF2S3	480866	-0,37	-0,52	-0,69	-0,54	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
LRPPRC	474572	-0,58	-0,69	-0,69	-0,77	leucine-rich PPR-motif containing
CISD1	479212	-0,86	-0,85	-0,68	-0,66	CDGSH iron sulfur domain 1
PFDN2	488648	-0,47	-1,04	-0,68	-0,54	prefoldin subunit 2
UPF1	476664	-0,30	-0,49	-0,68	-1,00	UPF1 regulator of nonsense transcripts homolog (yeast)
PABPC1	612751	-0,25	-0,41	-0,67	-0,58	poly(A) binding protein, cytoplasmic 1
POR	489816	-1,00	-0,59	-0,67	-0,85	P450 (cytochrome) oxidoreductase
NDUFB10	479887	-0,43	-0,35	-0,67	-0,54	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
CTNND1	483489	-0,36	-0,53	-0,66	-0,72	catenin (cadherin-associated protein), delta 1
LOC475121	475121	-0,73	-0,55	-0,66	-0,69	similar to cytochrome c-1
LOC484627	484627	-0,25	-0,21	-0,66	-0,45	similar to H1 histone family, member X
REEP5	479137	-0,41	-0,76	-0,66	-0,69	receptor accessory protein 5
RPL35	480729	-0,15	-0,14	-0,66	-0,49	ribosomal protein L35
MYO1D	491153	-0,27	-0,47	-0,66	-0,81	myosin ID
DHX9	480032	-0,50	-0,44	-0,66	-0,67	DEAH (Asp-Glu-Ala-His) box polypeptide 9
ZMPSTE24	482460	-0,76	-0,86	-0,66	-0,70	zinc metallopeptidase (STE24 homolog, S. cerevisiae)
EPCAM	481360	-0,60	-0,31	-0,65	-0,45	epithelial cell adhesion molecule
PICALM	476780	-0,22	-0,37	-0,65	-0,58	phosphatidylinositol binding clathrin assembly protein
LOC478410	478410	-0,49	-0,51	-0,65	-0,69	similar to ATP synthase O subunit, mitochondrial precursor (Oligomycin sensitivity conferral protein) (OSCP)
CNP	607694	-0,49	-0,76	-0,65	-0,82	2',3'-cyclic nucleotide 3' phosphodiesterase
RTN4	474598	-0,78	-0,63	-0,65	-0,90	reticulon 4
LOC488289	488289	-0,53	-0,51	-0,63	-0,69	similar to Histone H2A.1
SYPL1	475889	-0,24	-0,51	-0,63	-0,72	synaptophysin-like 1
PDHX	475942	-0,49	0,16	-0,63	-0,98	pyruvate dehydrogenase complex, component X
STT3B	485628	-0,50	-0,26	-0,63	-0,55	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)
MRTO4	487406	-0,52	-0,49	-0,62	-0,65	mRNA turnover 4 homolog (S. cerevisiae)
YES1	490532	-0,51	-0,44	-0,62	-0,94	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1
MRPL12	608030	-0,44	-0,52	-0,62	-0,60	mitochondrial ribosomal protein L12
ARL6IP5	476559	-0,62	-0,73	-0,62	-0,77	ADP-ribosylation-like factor 6 interacting protein 5
SLC2A1	482437	-0,06	-0,18	-0,62	-0,43	solute carrier family 2 (facilitated glucose transporter), member 1
LOC612644	612644	-0,57	-0,79	-0,62	-0,90	similar to cytochrome c oxidase, subunit VIb polypeptide 1
STOM	612719	-0,51	-0,33	-0,61	-0,61	stomatin
ESYT1	474397	-0,66	-0,78	-0,61	-0,96	extended synaptotagmin-like protein 1

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
SRPK1	474887	-0,22	0,07	-0,61	-0,33	SRSF protein kinase 1
RAB2A	404009	-0,42	-0,56	-0,61	-0,63	RAB2A, member RAS oncogene family
ABCD3	479939	-0,49	-0,36	-0,61	-0,59	ATP-binding cassette, sub-family D (ALD), member 3
BMS1	477760	-0,25	-0,24	-0,61	-0,58	BMS1 homolog, ribosome assembly protein (yeast)
SRSF9	477510	-0,26	-0,42	-0,60	-0,66	serine/arginine-rich splicing factor 9
VAPA	480208	-0,43	-0,38	-0,60	-0,66	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa
PARP1	490385	-0,50	-0,61	-0,60	-0,60	poly (ADP-ribose) polymerase 1
ARL8B	612944	-0,44	-0,40	-0,59	-0,04	ADP-ribosylation factor-like 8B
PRPF4B	488199	-0,29	-0,65	-0,59	-0,39	PRP4 pre-mRNA processing factor 4 homolog B (yeast)
DDX55	486246	-0,28	-0,16	-0,59	-0,29	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55
LOC475524	475524	-0,73	-0,60	-0,59	-0,58	similar to single-stranded DNA binding protein 1 isoform 1
CSNK2A1	477185	-0,68	-0,88	-0,59	-0,68	casein kinase 2, alpha 1 polypeptide
PCYOX1	481418	-0,61	-0,64	-0,59	-0,65	prenylcysteine oxidase 1
ITPR3	481746	-0,43	-0,81	-0,58	-0,90	inositol 1,4,5-trisphosphate receptor, type 3
RPS27A	474599	0,05	-0,27	-0,58	-0,49	ribosomal protein S27a
LAMP2	481037	-0,28	-0,77	-0,58	-0,40	lysosomal-associated membrane protein 2
NPM3	477801	0,46	0,29	-0,57	-0,78	nucleophosmin/nucleoplasmin 3
LOC478509	478509	0,00	-0,12	-0,57	-0,33	similar to ribosomal protein L34
INTS2	610121	0,24	0,29	-0,57	0,14	integrator complex subunit 2
LOC475501	475501	-0,42	-0,52	-0,57	-0,41	similar to H2A histone family, member V isoform 5
PTBP1	485097	-0,24	-0,24	-0,56	-0,36	polypyrimidine tract binding protein 1
RAB1B	610762	-0,29	-0,27	-0,56	-0,34	RAB1B, member RAS oncogene family
RALA	475875	-0,25	-0,45	-0,56	-0,46	v-ral simian leukemia viral oncogene homolog A (ras related)
RPS18	403685	-0,01	0,04	-0,56	-0,30	ribosomal protein S18
MYBBP1A	489442	-0,52	-0,23	-0,56	-0,49	MYB binding protein (P160) 1a
MRPS26	477175	-1,02	-0,92	-0,56	-0,98	mitochondrial ribosomal protein S26
GNB1	403912	-0,41	-0,28	-0,55	-0,44	guanine nucleotide binding protein (G protein), beta polypeptide 1
RPL37A	478904	0,25	0,14	-0,55	-0,12	ribosomal protein L37a
RAB10	403958	-0,39	-0,32	-0,55	-0,42	RAB10, member RAS oncogene family
RAB7A	404007	-0,35	-0,51	-0,54	-0,59	RAB7A, member RAS oncogene family
WDR75	488443	-0,33	-0,30	-0,54	-0,66	WD repeat domain 75
HEATR1	479192	-0,46	-0,32	-0,54	-0,48	HEAT repeat containing 1
CLU	442971	-0,23	-0,21	-0,54	-0,52	clusterin
RSL1D1	479847	-0,45	-0,20	-0,53	-0,59	ribosomal L1 domain containing 1
CHCHD3	607574	-0,16	0,03	-0,53	-0,21	coiled-coil-helix-coiled-coil-helix domain containing 3
RBM4	610648	-0,33	-0,07	-0,53	-0,56	RNA binding motif protein 4
LOC490458	490458	-0,37	-0,64	-0,53	-0,81	similar to S100 calcium binding protein A16
LOC483175	483175	-0,31	-0,55	-0,53	-0,61	similar to histone H2A
NDUFV1	476004	-0,60	-0,58	-0,53	-0,62	NADH dehydrogenase (ubiquinone) flavoprotein 1,

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						51kDa
HMGB2	486068	-0,04	-0,52	-0,52	-0,70	high mobility group box 2
UQCRC2	479815	-0,47	-0,49	-0,52	-0,68	ubiquinol-cytochrome c reductase core protein II
ENTPD3	485604	-0,31	-0,74	-0,52	-0,76	ectonucleoside triphosphate diphosphohydrolase 3
FKBP10	490975	-0,59	-1,11	-0,52	-0,96	FK506 binding protein 10, 65 kDa
CSDE1	475807	-0,11	-0,24	-0,52	-0,42	cold shock domain containing E1, RNA-binding
MYO1C	480646	-0,53	-0,51	-0,52	-0,63	myosin IC
WDR43	475713	-0,42	-0,95	-0,52	-0,75	WD repeat domain 43
SEC61B	404018	-0,32	-0,61	-0,52	-0,21	Sec61 beta subunit
ATP5B	403669	-0,58	-0,59	-0,52	-0,57	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
LOC481774	481774	-0,12	-0,25	-0,52	-0,49	similar to U1 small nuclear ribonucleoprotein C (U1 snRNP protein C) (U1C protein) (U1-C)
COPA	478973	-0,19	-0,36	-0,51	-0,52	coatomer protein complex, subunit alpha
ATAD3B	479568	-0,46	-0,35	-0,51	-0,43	ATPase family, AAA domain containing 3B
RAB1A	403774	-0,43	-0,36	-0,51	-0,48	RAB1A, member RAS oncogene family
ILF3	484950	-0,28	-0,30	-0,51	-0,52	interleukin enhancer binding factor 3, 90kDa
EPHA2	487421	-0,28	-0,74	-0,51	-0,36	EPH receptor A2
RRS1	486978	-0,60	-0,39	-0,50	-0,62	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
BCKDHB	474978	-0,40	-0,54	-0,50	-0,71	branched chain keto acid dehydrogenase E1, beta polypeptide
TRA2B	478663	-0,29	-0,37	-0,50	-0,56	transformer 2 beta homolog (Drosophila)
RAB6A	608330	-0,35	-0,34	-0,50	-0,46	RAB6A, member RAS oncogene family
AFG3L2	490560	-0,40	0,37	-0,50	-0,37	AFG3 ATPase family gene 3-like 2 (S. cerevisiae)
SDHB	478217	-0,47	-0,55	-0,50	-0,67	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
CELF1	475979	-0,13	-0,52	-0,49	-0,80	CUGBP, Elav-like family member 1
LOC478348	478348	-0,06	-0,02	-0,49	-0,20	similar to ribosomal protein L4
ERP29	477482	-0,45	-0,83	-0,48	-0,79	endoplasmic reticulum protein 29
LOC474698	474698	-0,21	-0,27	-0,47	-0,43	similar to catenin (cadherin-associated protein), alpha 1, 102kDa
SUCLA2	485448	-0,35	-0,43	-0,47	-0,50	succinate-CoA ligase, ADP-forming, beta subunit
NDUFS2	478981	-0,26	-0,14	-0,47	-0,60	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase)
RPS19	476450	0,11	-0,03	-0,47	-0,22	ribosomal protein S19
GNA11	403914	-0,36	-0,23	-0,47	-0,19	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
CTNNB1	477032	-0,28	-0,43	-0,47	-0,56	catenin (cadherin-associated protein), beta 1, 88kDa
HNRNPH1	481455	-0,32	-0,32	-0,46	-0,55	heterogeneous nuclear ribonucleoprotein H1 (H)
RPS16	476463	0,11	0,07	-0,46	-0,18	ribosomal protein S16
UBXN4	476130	-0,39	-0,52	-0,45	-0,61	UBX domain protein 4
LOC491080	491080	-0,42	-0,41	-0,45	-0,47	similar to CG3408-PA

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
SRPR	489293	-0,26	-0,78	-0,45	-0,58	signal recognition particle receptor (docking protein)
RBM28	475203	-0,33	0,06	-0,45	-0,51	RNA binding motif protein 28
CAT	403474	-0,51	-0,70	-0,45	-0,68	catalase
ZONAB	403728	-0,46	-0,55	-0,45	-0,71	Y-box protein ZONAB-A
HNRNPD	478450	-0,06	-0,23	-0,45	-0,32	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
RTN3	476043	-0,42	-0,47	-0,44	-0,43	reticulon 3
UQCRC1	608455	-0,09	-0,36	-0,44	-0,38	ubiquinol-cytochrome c reductase core protein I
RAB8A	403773	-0,37	-0,59	-0,44	-0,52	RAB8A, member RAS oncogene family
PPIB	478337	-0,25	-0,37	-0,44	-0,35	peptidylprolyl isomerase B (cyclophilin B)
DRAP1	476018	-0,05	-0,48	-0,43	-0,34	DR1-associated protein 1 (negative cofactor 2 alpha)
POGLUT1	487993	-0,17	-0,57	-0,43	-0,71	protein O-glucosyltransferase 1
LOC480971	480971	-0,44	-0,85	-0,43	-0,29	similar to Ewing sarcoma breakpoint region 1 isoform EWS
RPL10	481085	0,09	0,09	-0,42	-0,05	ribosomal protein L10
HK1	479234	-0,36	-0,19	-0,42	-0,17	hexokinase 1
PRRC1	481489	-0,34	-0,78	-0,41	-0,86	proline-rich coiled-coil 1
DDX18	476120	-0,20	-0,10	-0,41	-0,38	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18
NOP10	607299	-0,37	-0,32	-0,41	-0,58	NOP10 ribonucleoprotein homolog (yeast)
ACSS1	477002	-0,34	-0,53	-0,41	-0,22	acyl-CoA synthetase short-chain family member 1
EIF6	477210	-0,40	-0,42	-0,41	-0,49	eukaryotic translation initiation factor 6
NMT1	480494	-0,03	-0,14	-0,41	-0,29	N-myristoyltransferase 1
PRDX4	491776	-0,15	-0,48	-0,41	-0,45	peroxiredoxin 4
IGF2BP2	478662	0,01	-0,18	-0,41	-0,64	insulin-like growth factor 2 mRNA binding protein 2
NLE1	491142	-0,31	-0,61	-0,40	-0,37	notchless homolog 1 (Drosophila)
HNRNPA3	608074	-0,26	-0,23	-0,40	-0,34	heterogeneous nuclear ribonucleoprotein A3
BAX	403523	-0,24	-0,68	-0,40	0,02	BCL2-associated X protein
RPL17	475077	0,14	0,10	-0,40	-0,11	ribosomal protein L17
UGGT1	476101	-0,37	-0,61	-0,39	-0,57	UDP-glucose glycoprotein glucosyltransferase 1
TM9SF3	612786	-0,50	-0,31	-0,39	-0,38	transmembrane 9 superfamily member 3
FAU	483748	0,06	-0,22	-0,39	-0,17	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed
EIF2S1	480361	0,04	-0,09	-0,39	-0,18	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
COPB2	477088	-0,20	-0,42	-0,38	-0,40	coatomer protein complex, subunit beta 2 (beta prime)
HADHA	475687	-0,38	-0,48	-0,38	-0,47	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
LOC608656	608656	-0,47	-0,48	-0,37	-0,58	similar to oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1 precursor
MTX1	480130	-0,19	-0,44	-0,37	-0,31	metaxin 1
NDUFAB1	479805	-0,21	-0,48	-0,37	-0,51	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
ACAD9	476519	-0,15	-0,36	-0,36	-0,38	acyl-CoA dehydrogenase

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						family, member 9
DAO	486317	-0,19	-0,41	-0,36	-0,33	D-amino-acid oxidase
ACADVL	489463	-0,37	-0,50	-0,36	-0,47	acyl-CoA dehydrogenase, very long chain
SRSF1	609693	-0,27	-0,36	-0,36	-0,53	serine/arginine-rich splicing factor 1
MANF	608421	0,00	-0,40	-0,36	-0,34	mesencephalic astrocyte-derived neurotrophic factor
LOC477839	477839	-0,29	-0,63	-0,36	-0,47	similar to Thioredoxin-dependent peroxide reductase, mitochondrial precursor (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein homolog) (HBC189) (PRX III)
EIF4A3	475922	-0,12	-0,21	-0,36	-0,29	eukaryotic translation initiation factor 4A3
LOC479283	479283	0,01	-0,19	-0,36	-0,32	similar to Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (p14)
NCAPD2	477715	-0,06	-0,49	-0,35	-0,45	non-SMC condensin I complex, subunit D2
RPS28	485010	0,17	0,08	-0,35	-0,12	ribosomal protein S28
HIBADH	479610	-0,28	-0,65	-0,35	-0,31	3-hydroxyisobutyrate dehydrogenase
RBM47	403423	-0,50	-0,34	-0,35	-0,58	RNA binding motif protein 47
RPL24	478547	0,14	0,10	-0,35	-0,14	ribosomal protein L24
P4HB	483369	-0,19	-0,61	-0,34	-0,42	prolyl 4-hydroxylase, beta polypeptide
LOC477695	477695	-0,18	-0,40	-0,34	-0,34	similar to mago-nashi homolog
F3	490153	-0,18	-0,32	-0,34	-0,50	coagulation factor III (thromboplastin, tissue factor)
SERPINH1	485187	-0,24	-0,37	-0,34	-0,43	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
HMGB1	403170	0,13	-0,48	-0,33	-0,52	high mobility group box 1
LMNB2	485070	-0,01	-0,26	-0,33	-0,69	lamin B2
ATP5A1	480149	-0,27	-0,38	-0,33	-0,34	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
DNAJB11	478664	-0,19	-0,10	-0,33	-0,25	DnaJ (Hsp40) homolog, subfamily B, member 11
SF3B1	488456	-0,29	-0,45	-0,31	-0,43	splicing factor 3b, subunit 1, 155kDa
SHMT2	607458	-0,23	-0,33	-0,31	-0,42	serine hydroxymethyltransferase 2 (mitochondrial)
MAK16	475593	-0,37	-0,21	-0,31	-0,14	MAK16 homolog (S. cerevisiae)
GANAB	483784	-0,19	-0,58	-0,31	-0,48	glucosidase, alpha; neutral AB
ACOT9	480864	0,05	-0,28	-0,31	-0,17	acyl-CoA thioesterase 9
PNN	403907	-0,01	-0,41	-0,31	-0,37	pinin, desmosome associated protein
AP1M2	611211	0,01	-0,37	-0,31	-0,36	adaptor-related protein complex 1, mu 2 subunit
SRSF2	612817	-0,21	-0,19	-0,29	-0,38	serine/arginine-rich splicing factor 2
HYOU1	479410	-0,24	-0,44	-0,29	-0,32	hypoxia up-regulated 1
NOP16	479282	0,11	0,14	-0,29	0,44	NOP16 nucleolar protein homolog (yeast)
MYO6	481884	-0,01	-0,40	-0,29	-0,36	myosin VI
HNRPDL	476976	0,03	-0,17	-0,28	-0,12	heterogeneous nuclear ribonucleoprotein D-like
LOC480466	480466	-0,02	-0,17	-0,28	-0,21	similar to ELAV-like protein 1 (Hu-antigen R) (HuR)

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
HSPA9	474697	-0,24	-0,34	-0,28	-0,30	heat shock 70kDa protein 9 (mortalin)
LOC476328	476328	0,20	0,00	-0,28	-0,22	similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP)
BLMH	480635	-0,21	-1,33	-0,27	-0,96	bleomycin hydrolase
BANF1	611961	-0,31	-0,45	-0,27	-0,65	barrier to autointegration factor 1
RPL13	479612	0,20	0,08	-0,27	0,03	ribosomal protein L13
SOD2	476258	-0,09	-0,50	-0,26	-0,30	superoxide dismutase 2, mitochondrial
IARS2	478963	-0,42	-0,75	-0,26	-0,52	isoleucyl-tRNA synthetase 2, mitochondrial
HSPA5	480726	-0,21	-0,55	-0,26	-0,28	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
SRSF3	403687	-0,29	-0,35	-0,26	-0,50	serine/arginine-rich splicing factor 3
SUCLG2	476562	-0,02	-0,37	-0,25	-0,25	succinate-CoA ligase, GDP-forming, beta subunit
AIMP2	479752	-0,03	-0,41	-0,25	-0,08	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2
LOC490572	490572	0,10	-0,09	-0,25	-0,15	similar to myosin, light polypeptide 6, alkali, smooth muscle and non-muscle
HNRNPL	476466	-0,09	-0,04	-0,25	-0,19	heterogeneous nuclear ribonucleoprotein L
EIF2S2	477197	0,09	-0,17	-0,25	-0,02	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa
LOC490810	490810	-0,27	-0,57	-0,25	-0,60	similar to CG33071-PC, isoform C
UTRN	442965	-0,25	-0,72	-0,25	-0,52	utrophin
PYCR2	480112	-0,13	-0,70	-0,25	-0,44	pyrroline-5-carboxylate reductase family, member 2
ILF2	480139	-0,03	-0,05	-0,24	-0,25	interleukin enhancer binding factor 2, 45kDa
P4HA2	474672	0,00	-0,20	-0,23	-0,23	prolyl 4-hydroxylase, alpha polypeptide II
RPL28	476378	0,32	0,22	-0,23	0,05	ribosomal protein L28
SDHA	478634	-0,18	-0,44	-0,23	-0,37	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
NOP56	612871	-0,16	-0,11	-0,22	-0,27	NOP56 ribonucleoprotein homolog (yeast)
PNPT1	481376	-0,21	-0,52	-0,22	-0,89	polyribonucleotide nucleotidyltransferase 1
NUP155	479360	-0,12	-0,10	-0,22	-0,31	nucleoporin 155kDa
PITRM1	478018	-0,15	-0,10	-0,22	-0,29	pitrilysin metallopeptidase 1
HSP90B1	404019	-0,10	-0,52	-0,21	-0,31	heat shock protein 90kDa beta (Grp94), member 1
OXCT1	479347	0,17	-0,15	-0,21	-0,17	3-oxoacid CoA transferase 1
HADH	478506	-0,20	-0,56	-0,21	-0,35	hydroxyacyl-CoA dehydrogenase
TAS1R2	478213	0,07	-0,11	-0,21	0,05	taste receptor, type 1, member 2
ETFA	610134	-0,17	-0,24	-0,21	-0,15	electron-transfer-flavoprotein, alpha polypeptide
ESRP2	489745	0,19	0,01	-0,20	-0,24	epithelial splicing regulatory protein 2
LOC488888	488888	0,25	-0,38	-0,20	-0,06	hypothetical LOC488888
DLST	480388	-0,08	-0,17	-0,20	-0,25	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)
ERO1L	490691	-0,11	-0,51	-0,20	-0,33	ERO1-like (S. cerevisiae)
LOC478864	478864	0,21	0,12	-0,20	0,01	similar to 60S ribosomal protein L21
RPL19	403682	0,31	0,23	-0,20	0,09	ribosomal protein L19

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
STAT3	490967	0,37	-0,18	-0,19	-0,45	signal transducer and activator of transcription 3 (acute-phase response factor)
CALR	476694	-0,09	-0,58	-0,19	-0,29	calreticulin
CNPY2	607115	-0,21	-0,58	-0,19	-0,26	canopy 2 homolog (zebrafish)
RAB11B	611619	-0,06	-0,15	-0,19	-0,20	RAB11B, member RAS oncogene family
ASNA1	476699	-0,24	-0,86	-0,19	-0,57	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
PDIA3	478279	-0,06	-0,36	-0,19	-0,12	protein disulfide isomerase family A, member 3
PRKCSH	484941	-0,23	-0,53	-0,19	-0,52	protein kinase C substrate 80K-H
ACAA1	477023	-0,25	-0,72	-0,19	-0,29	acetyl-CoA acyltransferase 1
SNRPF	482609	0,01	-0,33	-0,18	-0,38	small nuclear ribonucleoprotein polypeptide F
SCP2	479564	0,02	-0,40	-0,18	-0,45	sterol carrier protein 2
IDH2	479043	0,08	-0,22	-0,18	-0,01	isocitrate dehydrogenase 2 (NADP+), mitochondrial
MTHFD1L	476245	-0,16	-0,47	-0,18	-0,36	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like
CAPRIN1	607420	0,17	0,11	-0,18	-0,05	cell cycle associated protein 1
TBL3	490064	0,03	0,04	-0,17	-0,10	transducin (beta)-like 3
CDC42	403934	-0,40	-0,64	-0,17	-0,85	cell division cycle 42 (GTP binding protein, 25kDa)
TUBA1C	608138	0,23	0,07	-0,17	-0,24	tubulin, alpha 1c
PCK2	480255	0,02	-0,18	-0,16	-0,28	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
PDHB	476574	-0,25	-0,41	-0,16	-0,32	pyruvate dehydrogenase (lipoamide) beta
BCAS2	475805	0,11	0,15	-0,16	-0,07	breast carcinoma amplified sequence 2
LOC474524	474524	0,09	0,02	-0,16	-0,11	similar to CG9987-PA
ME2	476198	-0,17	-0,57	-0,15	-0,44	malic enzyme 2, NAD(+)-dependent, mitochondrial
HNRNPA0	481524	0,11	-0,16	-0,15	-0,04	heterogeneous nuclear ribonucleoprotein A0
LOC475044	475044	0,03	-0,07	-0,15	-0,01	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP)
STXBP2	403880	-0,35	-0,61	-0,14	-0,65	syntaxin binding protein 2
ALDH18A1	477781	-0,10	-0,29	-0,14	-0,28	aldehyde dehydrogenase 18 family, member A1
PA2G4	474396	0,25	0,08	-0,14	0,05	proliferation-associated 2G4, 38kDa
PTPN11	477488	-0,03	-1,09	-0,14	-0,24	protein tyrosine phosphatase, non-receptor type 11
PRPF8	480651	-0,15	-0,21	-0,14	-0,34	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)
TUBB6	480213	0,25	0,07	-0,13	-0,08	tubulin, beta 6
GNB2	479733	0,41	0,33	-0,13	0,24	guanine nucleotide binding protein (G protein), beta polypeptide 2
TIMM44	485005	-0,18	-0,51	-0,13	-0,50	translocase of inner mitochondrial membrane 44 homolog (yeast)
LOC607081	607081	-0,03	0,00	-0,12	-0,16	similar to non-POU domain containing, octamer-binding
ATP6V0D1	479685	-0,33	-0,35	-0,12	-0,05	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						d1
LOC478855	478855	-0,03	-0,29	-0,12	-0,19	similar to heat shock 10kDa protein 1 (chaperonin 10)
M6PR	477700	-0,10	-0,16	-0,12	-0,11	mannose-6-phosphate receptor (cation dependent)
ZNF326	612406	-0,15	-0,10	-0,12	-0,13	zinc finger protein 326
ANXA13	403935	-0,08	-0,12	-0,11	-0,04	annexin A13
AP1G1	479666	0,20	-0,07	-0,11	-0,14	adaptor-related protein complex 1, gamma 1 subunit
HSPD1	478854	-0,11	-0,29	-0,11	-0,14	heat shock 60kDa protein 1 (chaperonin)
EIF1	403674	0,17	-0,24	-0,11	-0,14	eukaryotic translation initiation factor 1
PSPC1	477347	-0,07	-0,09	-0,11	-0,27	paraspeckle component 1
RNPS1	479880	-0,13	-0,32	-0,11	-0,23	RNA binding protein S1, serine-rich domain
HNRNPCL1	474964	0,14	-0,05	-0,10	0,00	heterogeneous nuclear ribonucleoprotein C-like 1
TUBB	474830	0,19	0,03	-0,10	-0,24	tubulin, beta
PRKCDBP	476831	0,35	-0,24	-0,10	-0,10	protein kinase C, delta binding protein
NOP58	607667	0,01	0,02	-0,10	-0,11	NOP58 ribonucleoprotein homolog (yeast)
TIAL1	477841	-0,04	-0,12	-0,10	-0,32	TIA1 cytotoxic granule-associated RNA binding protein-like 1
RDX	479446	0,03	-0,30	-0,10	-0,06	radixin
RPL23	403683	0,26	0,12	-0,09	0,06	ribosomal protein L23
PDIA6	475668	0,05	-0,37	-0,09	-0,14	protein disulfide isomerase family A, member 6
GLS	488448	0,00	-0,04	-0,08	0,08	glutaminase
SNRNP70	484388	-0,08	-0,28	-0,08	-0,27	small nuclear ribonucleoprotein 70kDa (U1)
HSD17B10	480930	-0,24	-0,37	-0,08	-0,21	hydroxysteroid (17-beta) dehydrogenase 10
DHX15	488856	0,25	0,36	-0,07	0,14	DEAH (Asp-Glu-Ala-His) box polypeptide 15
AKR7A2	478210	0,32	-0,13	-0,07	-0,41	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)
MRPS31	477294	-0,04	-0,30	-0,07	-0,31	mitochondrial ribosomal protein S31
TOM1	608746	-0,38	-0,73	-0,07	-0,36	target of myb1 (chicken)
SNRPD1	480178	-0,29	-0,41	-0,07	-0,35	small nuclear ribonucleoprotein D1 polypeptide 16kDa
SNRNP200	475742	0,09	-0,05	-0,07	-0,14	small nuclear ribonucleoprotein 200kDa (U5)
GPNMB	482355	0,02	-0,18	-0,07	-0,01	glycoprotein (transmembrane) nmb
LOC474696	474696	0,31	0,07	-0,06	0,03	similar to eukaryotic translation termination factor 1 (predicted)
CS	474403	0,05	-0,25	-0,06	-0,17	citrate synthase
ABCF1	474826	0,28	0,02	-0,06	-0,19	ATP-binding cassette, sub-family F (GCN20), member 1
STX7	483987	-0,25	0,10	-0,06	-0,06	syntaxin 7
LOC610135	610135	0,09	-0,17	-0,06	-0,12	similar to small nuclear ribonucleoprotein polypeptide G
LONP1	611425	0,16	-0,08	-0,06	-0,07	lon peptidase 1, mitochondrial
JUP	480522	0,22	-0,01	-0,05	-0,03	junction plakoglobin
TUBB2A	478701	0,10	0,03	-0,05	-0,19	tubulin, beta 2A
CALU	475201	-0,03	-0,41	-0,05	-0,08	calumenin
SUCLG1	475775	0,15	-0,10	-0,05	-0,09	succinate-CoA ligase, alpha subunit
LOC477554	477554	0,03	-0,20	-0,05	-0,11	similar to small nuclear

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						ribonucleoprotein D3
PFDN5	477597	-0,08	-0,85	-0,05	-0,27	prefoldin subunit 5
MYOF	607472	-0,46	-0,20	-0,04	-0,53	myoferlin
FECH	610360	-0,19	-0,66	-0,04	-0,15	ferrochelatase
FH	480092	-0,01	-0,40	-0,03	-0,22	fumarate hydratase
CAPZA2	503863	0,09	-0,47	-0,03	-0,10	capping protein (actin filament) muscle Z-line, alpha 2
PDHA1	480858	0,12	-0,15	-0,03	0,06	pyruvate dehydrogenase (lipoamide) alpha 1
RAB5C	403941	0,02	-0,32	-0,03	-0,03	RAB5C, member RAS oncogene family
ACAT1	489421	0,07	-0,14	-0,03	0,00	acetyl-CoA acetyltransferase 1
DLD	403978	0,10	-0,19	-0,03	-0,12	dihydrolipoamide dehydrogenase
MYH9	481280	0,46	0,26	-0,03	0,10	myosin, heavy chain 9, non-muscle
SF3B3	479659	0,02	-0,16	-0,02	-0,17	splicing factor 3b, subunit 3, 130kDa
EIF5A	489468	0,45	0,19	-0,02	0,01	eukaryotic translation initiation factor 5A
DSG2	490500	-0,28	-0,61	-0,02	-0,07	desmoglein 2
MYL12B	480193	0,43	0,31	-0,02	0,19	myosin, light chain 12B, regulatory
RPL23A	476799	0,52	0,35	-0,01	0,17	ribosomal protein L23a
NAPA	612960	-0,03	-0,29	-0,01	-0,20	N-ethylmaleimide-sensitive factor attachment protein, alpha
ACO1	481576	0,09	-0,53	-0,01	-0,27	aconitase 1, soluble
AP2B1	480605	0,15	-0,24	-0,01	-0,11	adaptor-related protein complex 2, beta 1 subunit
POLR2E	611859	0,02	-0,43	0,00	-0,17	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa
C1QBP	489450	0,12	0,14	0,00	0,18	complement component 1, q subcomponent binding protein
LMNB1	474663	0,27	0,19	0,00	-0,03	lamin B1
SRSF5	490754	0,16	0,07	0,00	0,08	serine/arginine-rich splicing factor 5
ALDH5A1	488246	0,16	-0,25	0,01	-0,34	aldehyde dehydrogenase 5 family, member A1
EPS8	477686	0,06	-0,47	0,01	-0,20	epidermal growth factor receptor pathway substrate 8
TUFM	479796	-0,11	-0,33	0,01	-0,19	Tu translation elongation factor, mitochondrial
SRSF7	475730	-0,05	-0,26	0,01	-0,22	serine/arginine-rich splicing factor 7
NUCB1	484391	-0,16	-0,13	0,01	-0,17	nucleobindin 1
MATR3	474700	0,03	-0,05	0,02	-0,08	matrin 3
MCM4	477871	0,52	-0,03	0,02	0,40	minichromosome maintenance complex component 4
MKI67IP	476111	0,06	0,05	0,03	0,01	MKI67 (FHA domain) interacting nucleolar phosphoprotein
NOL6	481582	-0,30	-0,25	0,03	-0,25	nucleolar protein family 6 (RNA-associated)
NOB1	489733	0,28	0,33	0,03	0,25	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)
EFTUD2	490935	0,00	-0,11	0,03	-0,29	elongation factor Tu GTP binding domain containing 2
TUBB2C	491231	0,25	0,14	0,04	-0,11	tubulin, beta 2C
CCAR1	479230	0,19	-0,04	0,04	-0,06	cell division cycle and apoptosis regulator 1
RBM3	609457	0,04	-0,01	0,04	-0,01	RNA binding motif (RNP1, RRM) protein 3
SNRPE	478934	0,06	-0,25	0,04	-0,15	small nuclear ribonucleoprotein

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						polypeptide E
PMPCA	480677	-0,11	-0,37	0,04	-0,19	peptidase (mitochondrial processing) alpha
NXF1	483780	0,09	-0,22	0,04	-0,15	nuclear RNA export factor 1
UBAP2L	480135	0,20	-0,28	0,04	-0,02	ubiquitin associated protein 2-like
ACO2	474487	0,07	-0,20	0,04	-0,05	aconitase 2, mitochondrial
TRIM28	403689	0,29	-0,21	0,05	-0,13	tripartite motif containing 28
LOC479969	479969	0,30	0,25	0,05	0,19	similar to Protein C14orf166
SAR1A	479237	0,31	0,05	0,05	0,11	SAR1 homolog A (S. cerevisiae)
VAPB	477274	0,16	0,01	0,05	0,00	VAMP (vesicle-associated membrane protein)-associated protein B and C
CPSF7	476066	0,01	-0,17	0,06	-0,05	cleavage and polyadenylation specific factor 7, 59kDa
CHD4	477714	0,29	0,11	0,06	0,20	chromodomain helicase DNA binding protein 4
ALB	403550	-8,44	-7,87	0,06	-7,76	albumin
TMPO	482618	-0,11	-0,10	0,06	-0,19	thymopoietin
PRKAG1	486559	0,34	-0,28	0,06	0,07	protein kinase, AMP-activated, gamma 1 non-catalytic subunit
TOP2A	480525	0,19	-0,37	0,07	-0,04	topoisomerase (DNA) II alpha 170kDa
SND1	475204	0,42	0,18	0,07	0,04	staphylococcal nuclease and tudor domain containing 1
PTRF	490966	0,41	0,01	0,07	0,06	polymerase I and transcript release factor
LOC474576	474576	0,12	0,12	0,07	-0,04	similar to DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein 4) (DnaJ protein homolog 2) (HSJ-2) (HSDJ)
RPS14	403690	0,41	0,31	0,08	0,28	ribosomal protein S14
GOT2	478103	0,08	-0,16	0,08	-0,01	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
ASAH1	482897	0,03	-0,54	0,08	0,04	N-acylsphingosine amidohydrolase (acid ceramidase) 1
LOC482601	482601	-0,02	-0,25	0,08	0,00	similar to malate dehydrogenase 2, NAD (mitochondrial)
MSN	491924	0,29	-0,34	0,09	-0,15	moesin
TRAP1	490032	0,04	-0,29	0,09	-0,07	TNF receptor-associated protein 1
SMU1	474740	0,35	0,18	0,09	-0,13	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)
CAMK2D	610764	0,51	-0,10	0,09	-0,02	calcium/calmodulin-dependent protein kinase II delta
METAP2	475429	0,33	0,05	0,09	0,09	methionyl aminopeptidase 2
NAA15	483817	0,20	-0,19	0,09	0,04	N(alpha)-acetyltransferase 15, NatA auxiliary subunit
OGDH	475499	0,05	-0,33	0,09	-0,04	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)
LOC609251	609251	0,24	-0,36	0,09	-0,05	similar to niban protein
SNX4	478595	0,22	-0,60	0,10	-0,12	sorting nexin 4
GRSF1	475170	0,13	-0,05	0,10	-0,01	G-rich RNA sequence binding factor 1
OAT	477858	-0,11	-0,14	0,10	0,09	ornithine aminotransferase
ARF6	490679	0,21	-0,43	0,10	-0,29	ADP-ribosylation factor 6
GRPEL1	488784	0,20	-0,15	0,10	0,03	GrpE-like 1, mitochondrial (E. coli)
YARS	478148	0,18	-0,28	0,11	0,22	tyrosyl-tRNA synthetase

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
COL17A1	403739	0,39	-0,39	0,11	-0,38	collagen, type XVII, alpha 1
NARS	607631	0,41	0,02	0,11	0,32	asparaginyl-tRNA synthetase
MNDA	488622	-0,07	-0,49	0,11	0,34	myeloid cell nuclear differentiation antigen
SRP68	403952	0,30	0,26	0,11	0,01	signal recognition particle 68kDa
LOC479071	479071	0,35	0,33	0,11	0,20	similar to Probable ATP-dependent RNA helicase DDX6 (DEAD-box protein 6) (ATP-dependent RNA helicase p54) (Oncogene RCK)
PRPF40A	476152	0,07	-0,12	0,11	-0,16	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
HNRNPF	477757	0,14	0,11	0,11	0,03	heterogeneous nuclear ribonucleoprotein F
SEC22B	475816	0,24	0,08	0,11	0,09	SEC22 vesicle trafficking protein homolog B (S. cerevisiae) (gene/pseudogene)
IQGAP1	479050	0,14	-0,19	0,12	0,29	IQ motif containing GTPase activating protein 1
HNRNPH3	479227	0,09	0,00	0,12	0,02	heterogeneous nuclear ribonucleoprotein H3 (2H9)
HIBCH	607040	-0,11	-0,42	0,12	-0,21	3-hydroxyisobutyryl-CoA hydrolase
LOC478254	478254	0,24	0,20	0,12	0,25	similar to CG5913-PA
IDH3B	477177	0,06	-0,05	0,12	0,23	isocitrate dehydrogenase 3 (NAD+) beta
LOC475374	475374	0,22	-1,01	0,13	-0,48	similar to Alcohol dehydrogenase [NADP+] (Aldehyde reductase) (Aldo-keto reductase family 1 member A1)
RPS20	477887	0,45	0,33	0,13	0,30	ribosomal protein S20
PSIP1	474712	0,15	-0,35	0,13	-0,05	PC4 and SFRS1 interacting protein 1
VAT1	490953	0,27	-0,33	0,13	-0,04	vesicle amine transport protein 1 homolog (T. californica)
PRMT5	480242	0,31	-0,18	0,13	0,32	protein arginine methyltransferase 5
LOC607058	607058	0,00	-0,30	0,14	-0,05	similar to SVH protein
LOC477550	477550	0,28	-0,22	0,14	0,00	similar to poly(rC) binding protein 2 (predicted)
ATPIF1	478165	0,36	0,20	0,14	0,34	ATPase inhibitory factor 1
RPS7	475649	0,66	0,53	0,14	0,39	ribosomal protein S7
ALDH6A1	490779	0,14	-0,26	0,14	0,07	aldehyde dehydrogenase 6 family, member A1
DDX17	474508	0,36	0,17	0,14	0,13	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
LOC476337	476337	0,19	-0,66	0,15	0,05	similar to D19Bwg1357e protein
RPL36AL	480311	0,70	0,42	0,15	0,45	ribosomal protein L36a-like
GOLPH3L	475838	0,32	0,00	0,15	-0,10	golgi phosphoprotein 3-like
POLR1C	474912	0,17	-0,08	0,15	0,16	polymerase (RNA) I polypeptide C, 30kDa
HNRNPUL2	476053	0,33	0,07	0,15	0,09	heterogeneous nuclear ribonucleoprotein U-like 2
HNRNPA2B1	475260	0,20	0,10	0,15	0,21	heterogeneous nuclear ribonucleoprotein A2/B1
FARSA	476695	0,38	-0,09	0,15	0,07	phenylalanyl-tRNA synthetase, alpha subunit
ECHS1	480828	0,06	-0,25	0,16	-0,10	enoyl CoA hydratase, short chain, 1, mitochondrial
LMNA	480124	0,42	0,36	0,16	0,21	lamin A/C
EIF1AX	611715	0,73	0,39	0,17	0,22	eukaryotic translation initiation factor 1A, X-linked
BUB3	477857	0,51	0,13	0,17	0,30	budding uninhibited by

		log2 fold change				
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						benzimidazoles 3 homolog (yeast)
COPE	476663	0,29	0,12	0,17	0,07	coatomer protein complex, subunit epsilon
RPS27	490449	0,47	0,34	0,17	0,23	ribosomal protein S27
DDX1	475671	0,33	0,43	0,18	0,22	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1
SEC13	607653	0,90	0,41	0,18	0,69	SEC13 homolog (S. cerevisiae)
RPS6	474722	0,65	0,59	0,19	0,47	ribosomal protein S6
CHADL	481234	0,68	-0,17	0,20	-0,50	chondroadherin-like
SNRPB	485806	0,51	0,18	0,20	0,24	small nuclear ribonucleoprotein polypeptides B and B1
VAMP8	609784	0,36	0,10	0,20	0,18	vesicle-associated membrane protein 8 (endobrevin)
RAE1	485942	0,11	-0,03	0,21	0,05	RAE1 RNA export 1 homolog (S. pombe)
WDR61	479068	0,21	-0,08	0,21	0,47	WD repeat domain 61
CARS	475998	0,32	-0,33	0,21	0,05	cysteinyl-tRNA synthetase
IFIT5	486788	0,67	0,02	0,21	0,62	interferon-induced protein with tetratricopeptide repeats 5
GRWD1	612058	0,35	0,21	0,21	0,16	glutamate-rich WD repeat containing 1
ABCE1	475454	0,37	-0,01	0,22	0,13	ATP-binding cassette, sub-family E (OABP), member 1
CDK1	488997	0,27	-0,17	0,22	-0,20	cyclin-dependent kinase 1
LOC475682	475682	0,46	0,49	0,22	0,40	similar to splicing factor 3B, 14 kDa subunit
NACA	474408	0,62	0,13	0,22	0,12	nascent polypeptide-associated complex alpha subunit
IVD	478259	-0,15	-0,34	0,22	-0,13	isovaleryl-CoA dehydrogenase
MCM5	610519	0,47	0,15	0,22	0,10	minichromosome maintenance complex component 5
ALDH7A1	481486	0,26	-0,44	0,23	-0,17	aldehyde dehydrogenase 7 family, member A1
RAB5B	474394	0,30	-0,05	0,23	0,17	RAB5B, member RAS oncogene family
PRPF19	611552	0,22	0,08	0,23	0,11	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)
KTN1	480332	0,32	0,17	0,23	0,25	kinectin 1 (kinesin receptor)
PSAP	479240	0,38	-0,21	0,24	0,23	prosaposin
PPL	490021	0,38	-0,10	0,24	-0,01	periplakin
PRKCI	478686	0,25	-0,37	0,24	-0,03	protein kinase C, iota
CDK11A	489591	0,57	0,08	0,24	0,08	cyclin-dependent kinase 11A
TARS	479370	0,48	-0,35	0,24	0,16	threonyl-tRNA synthetase
LOC487948	487948	0,41	-0,06	0,24	0,22	similar to coproporphyrinogen oxidase
IDH3A	479066	0,19	-0,06	0,25	0,16	isocitrate dehydrogenase 3 (NAD+) alpha
RHOA	403954	0,29	-0,26	0,25	-0,03	ras homolog gene family, member A
TUBA3C	610636	0,51	0,32	0,25	0,14	tubulin, alpha 3c
USP39	475767	0,12	0,14	0,25	0,18	ubiquitin specific peptidase 39
PSMA8	490508	0,50	-0,23	0,26	0,35	proteasome (prosome, macropain) subunit, alpha type, 8
KIF5B	477968	0,44	0,29	0,26	0,32	kinesin family member 5B
SRRT	479731	0,25	-0,14	0,26	0,20	serrate RNA effector molecule homolog (Arabidopsis)
AARS	479656	0,38	-0,56	0,26	0,03	alanyl-tRNA synthetase

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
FBL	476460	0,46	0,46	0,26	0,34	fibrillarin
SF3B4	483177	0,18	0,00	0,26	-0,06	splicing factor 3b, subunit 4, 49kDa
FKBP3	480306	0,44	0,13	0,26	0,10	FK506 binding protein 3, 25kDa
CLTA	474765	0,43	0,05	0,26	-0,06	clathrin, light chain A
DDX5	480472	0,38	0,21	0,26	0,20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
TROVE2	478957	0,47	0,02	0,27	0,25	TROVE domain family, member 2
EIF5B	474556	0,48	0,32	0,27	0,33	eukaryotic translation initiation factor 5B
DSP	488207	0,49	0,23	0,28	0,18	desmoplakin
LOC474513	474513	0,42	-0,04	0,29	0,35	similar to eukaryotic translation initiation factor 3 subunit 6 interacting protein
PIP5K1A	475846	0,24	-0,28	0,29	0,16	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha
NSUN2	478625	0,19	-0,13	0,29	0,02	NOP2/Sun domain family, member 2
ACADM	490207	0,16	-0,07	0,30	-0,28	acyl-CoA dehydrogenase, C-4 to C-12 straight chain
LOC610939	610939	0,03	-0,61	0,30	-0,09	similar to LSM5 homolog, U6 small nuclear RNA associated
RARS	609803	0,33	-0,38	0,30	0,47	arginyl-tRNA synthetase
NUDT21	478123	0,28	-0,19	0,30	0,16	nudix (nucleoside diphosphate linked moiety X)-type motif 21
TJP2	403854	0,00	-1,01	0,31	-0,17	tight junction protein 2 (zona occludens 2)
WARS	480435	0,37	-0,44	0,31	0,15	tryptophanyl-tRNA synthetase
LOC488269	488269	-0,06	-0,42	0,31	-0,52	similar to Histone H1.4 (Histone H1b)
RRBP1	403809	0,37	0,05	0,31	0,30	ribosome binding protein 1 homolog 180kDa (dog)
STRAP	486663	0,54	0,31	0,31	0,37	serine/threonine kinase receptor associated protein
LYPLA2	487374	0,42	-0,30	0,31	-0,24	lysophospholipase II
LGALS3BP	483345	0,70	-0,24	0,31	0,20	lectin, galactoside-binding, soluble, 3 binding protein
EIF3H	475081	0,31	-0,19	0,31	0,33	eukaryotic translation initiation factor 3, subunit H
HDLBP	477431	0,63	0,25	0,31	0,30	high density lipoprotein binding protein
POLR2H	478656	0,35	-0,22	0,32	-0,16	polymerase (RNA) II (DNA directed) polypeptide H
CTSD	483662	0,22	0,00	0,32	0,25	cathepsin D
LOC474484	474484	0,42	-0,04	0,32	0,12	similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1) ([U4/U6.U5] tri-snRNP 15.5 kDa protein) (Sperm specific antigen 1) (Fertilization antigen 1) (FA-1)
PSMB6	607466	-0,15	-0,65	0,32	0,00	proteasome (prosome, macropain) subunit, beta type, 6
GNB2L1	480818	0,85	0,55	0,33	0,35	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
LOC480437	480437	0,40	0,08	0,33	0,31	similar to dynein, cytoplasmic, heavy polypeptide 1
SNRPA1	607102	0,42	0,21	0,33	0,45	small nuclear ribonucleoprotein polypeptide A'
ACLY	607852	0,70	0,28	0,35	0,15	ATP citrate lyase
LOC489167	489167	0,55	0,16	0,35	0,44	similar to CG9590-PA

		log2 fold change				
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MCM3	481839	0,58	0,16	0,35	0,31	minichromosome maintenance complex component 3
LOC607948	607948	0,55	0,44	0,36	0,46	similar to THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Transcriptional coactivator Aly/REF) (bZIP enhancing factor BEF)
CTNNBL1	477224	0,66	0,19	0,36	0,37	catenin, beta like 1
TIMM10	475968	0,69	0,17	0,36	0,66	translocase of inner mitochondrial membrane 10 homolog (yeast)
SEPT2	487886	0,56	-0,02	0,36	0,39	septin 2
HDGF	612089	0,30	-0,36	0,36	0,19	hepatoma-derived growth factor
SCPEP1	480566	0,27	-0,41	0,36	0,08	serine carboxypeptidase 1
KPNA4	478680	0,50	0,13	0,37	0,33	karyopherin alpha 4 (importin alpha 3)
ACTR1A	403791	0,56	0,04	0,37	0,33	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)
DPY30	475715	0,20	0,08	0,37	0,31	dpy-30 homolog (C. elegans)
S100A10	475851	0,60	0,24	0,37	0,16	S100 calcium binding protein A10
ETFB	476400	0,55	0,13	0,37	0,32	electron-transfer-flavoprotein, beta polypeptide
KARS	479644	0,43	0,10	0,38	0,57	lysyl-tRNA synthetase
SSB	478787	0,47	0,07	0,38	0,44	Sjogren syndrome antigen B (autoantigen La)
ARG2	480364	0,15	-0,33	0,38	0,22	arginase, type II
HK2	475781	0,38	-0,35	0,38	0,32	hexokinase 2
TMOD3	487554	0,55	0,26	0,38	0,39	tropomodulin 3 (ubiquitous)
RBMX	481063	0,38	0,15	0,38	0,29	RNA binding motif protein, X-linked
RCC2	487412	0,39	0,00	0,38	0,03	regulator of chromosome condensation 2
OXSR1	607809	0,47	-0,24	0,38	0,12	oxidative-stress responsive 1
MSH2	494002	0,21	-0,13	0,38	0,11	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)
LOC607254	607254	0,53	-0,16	0,38	0,15	similar to EF hand domain containing 2
PAK2	612814	0,25	-0,73	0,39	-0,30	p21 protein (Cdc42/Rac)-activated kinase 2
RPSA	477029	0,79	0,55	0,39	0,57	ribosomal protein SA
TK1	483343	0,60	-0,56	0,39	0,23	thymidine kinase 1, soluble
LOC476840	476840	0,51	0,02	0,40	0,39	similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa
DDX39B	474839	0,49	0,09	0,40	0,29	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B
SLC9A3R1	483299	0,42	-0,01	0,40	0,23	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
VPS4B	607306	0,50	-0,35	0,40	0,37	vacuolar protein sorting 4 homolog B (S. cerevisiae)
DDX19A	479658	0,48	-0,04	0,40	0,15	DEAD (Asp-Glu-Ala-As) box polypeptide 19A
TNPO1	478093	0,65	0,08	0,40	0,20	transportin 1
SAFB	485028	0,73	0,41	0,41	0,69	scaffold attachment factor B
CIRH1A	489738	0,51	0,34	0,41	0,35	cirrhosis, autosomal recessive 1A (cirhin)
MCM2	484622	0,69	0,22	0,41	0,40	minichromosome maintenance complex component 2
FARSB	478926	0,70	0,15	0,42	0,50	phenylalanyl-tRNA synthetase, beta subunit

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
RPS12	476206	0,63	0,39	0,42	0,52	ribosomal protein S12
DNPEP	478922	0,49	-0,08	0,42	0,38	aspartyl aminopeptidase
RRM2	482963	0,67	0,20	0,42	0,17	ribonucleotide reductase M2
XPO1	474609	0,43	-0,16	0,42	0,19	exportin 1 (CRM1 homolog, yeast)
CCT6B	491146	0,57	0,20	0,42	0,43	chaperonin containing TCP1, subunit 6B (zeta 2)
HNRNPM	476725	0,55	0,31	0,42	0,57	heterogeneous nuclear ribonucleoprotein M
OSBP	483448	0,35	-0,07	0,42	0,18	oxysterol binding protein
MCM6	476131	0,56	-0,09	0,42	0,35	minichromosome maintenance complex component 6
TES	475293	0,67	-0,39	0,42	0,16	testis derived transcript (3 LIM domains)
PLCD1	485586	0,64	0,39	0,43	0,26	phospholipase C, delta 1
RBM39	477216	0,54	0,17	0,43	0,37	RNA binding motif protein 39
MAP4	484781	0,38	-0,42	0,43	0,22	microtubule-associated protein 4
ACTC1	478250	0,43	-0,18	0,43	0,28	actin, alpha, cardiac muscle 1
RPL5	479949	0,82	0,45	0,43	0,59	ribosomal protein L5
ARPC1B	479744	0,57	-0,19	0,44	0,18	actin related protein 2/3 complex, subunit 1B, 41kDa
EIF3J	487532	0,38	-0,16	0,44	0,74	eukaryotic translation initiation factor 3, subunit J
GTF2I	479714	-0,70	-1,10	0,44	-0,40	general transcription factor IIi
PPP2R2A	477374	0,62	-0,02	0,44	0,25	protein phosphatase 2, regulatory subunit B, alpha
LOC475156	475156	0,20	-0,34	0,44	0,23	similar to peroxiredoxin 1
SCFD1	480281	0,36	-0,13	0,45	0,37	sec1 family domain containing 1
LTA4H	482611	0,46	-0,32	0,45	-0,02	leukotriene A4 hydrolase
PAFAH1B3	476449	0,41	-0,55	0,45	-0,01	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)
USO1	478430	0,48	0,06	0,45	0,34	USO1 vesicle docking protein homolog (yeast)
LOC479165	479165	0,21	-0,80	0,45	0,01	similar to Dihydrofolate reductase
BCLAF1	483999	0,46	0,17	0,46	0,39	BCL2-associated transcription factor 1
GLO1	474894	0,67	-0,60	0,46	0,08	glyoxalase I
SEPT7	475284	0,44	-0,07	0,46	0,21	septin 7
LOC475721	475721	0,72	0,67	0,46	1,37	similar to CG5913-PA
ACP6	475822	0,03	-0,16	0,46	0,10	acid phosphatase 6, lysophosphatidic
GORASP2	488395	0,17	-0,43	0,47	0,05	golgi reassembly stacking protein 2, 55kDa
HNRNPH2	480989	0,12	0,04	0,47	0,30	heterogeneous nuclear ribonucleoprotein H2 (H')
CBR1	610164	0,41	-0,52	0,47	0,06	carbonyl reductase 1
USP7	479854	0,43	-0,21	0,47	0,19	ubiquitin specific peptidase 7 (herpes virus-associated)
LOC481459	481459	-0,22	-0,12	0,48	0,20	similar to sequestosome 1
TCEA1	477879	0,59	3,33	0,48	0,97	transcription elongation factor A (SII), 1
LOC475722	475722	0,63	0,62	0,49	0,72	similar to nucleophosmin 1
EIF5	480442	0,71	0,30	0,49	0,46	eukaryotic translation initiation factor 5
BZW2	475250	0,68	0,04	0,49	0,51	basic leucine zipper and W2 domains 2
SRP72	403944	0,66	0,51	0,49	0,34	signal recognition particle 72kDa
KPNA6	487314	0,72	0,49	0,49	0,43	karyopherin alpha 6 (importin alpha 7)
LAP3	479081	0,27	-0,46	0,49	0,13	leucine aminopeptidase 3
EPRS	478962	0,55	0,02	0,50	0,60	glutamyl-prolyl-tRNA synthetase

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
CAPNS1	611746	0,68	-0,16	0,50	0,25	calpain, small subunit 1
EIF3E	475070	0,58	0,13	0,51	0,38	eukaryotic translation initiation factor 3, subunit E
SERBP1	479535	0,93	0,71	0,51	0,83	SERPINE1 mRNA binding protein 1
PIR	480846	0,28	-0,70	0,51	-0,18	pirin (iron-binding nuclear protein)
NUDT5	478006	0,46	-0,66	0,51	0,25	nudix (nucleoside diphosphate linked moiety X)-type motif 5
VARS	481716	0,25	-0,21	0,51	0,41	valyl-tRNA synthetase
CAD	483009	0,76	0,43	0,51	0,56	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase
CTSB	486077	0,48	-0,21	0,52	0,35	cathepsin B
PPP2R1B	479444	0,41	-0,13	0,52	0,23	protein phosphatase 2, regulatory subunit A, beta
EML4	483048	0,45	0,02	0,52	0,49	echinoderm microtubule associated protein like 4
CAST	479148	0,46	0,18	0,52	0,72	calpastatin
MCM7	479737	0,47	-0,06	0,52	0,36	minichromosome maintenance complex component 7
COPG	476517	0,51	0,00	0,53	0,36	coatomer protein complex, subunit gamma
PDCD6IP	477015	0,53	-0,22	0,53	0,28	programmed cell death 6 interacting protein
UBE2V1	477262	0,42	-0,71	0,53	0,08	ubiquitin-conjugating enzyme E2 variant 1
CAPZB	478209	0,67	0,12	0,54	0,51	capping protein (actin filament) muscle Z-line, beta
ARPC2	478907	0,68	-0,07	0,54	0,33	actin related protein 2/3 complex, subunit 2, 34kDa
QARS	476628	0,52	-0,02	0,54	0,52	glutaminyl-tRNA synthetase
ADK	479253	0,57	-0,51	0,55	0,20	adenosine kinase
IPO7	485383	0,61	-0,12	0,55	0,45	importin 7
EIF4G2	476854	0,72	0,10	0,55	0,53	eukaryotic translation initiation factor 4 gamma, 2
TLN1	474759	0,42	-0,17	0,55	0,29	talin 1
PCBP1	481417	0,73	0,23	0,55	0,39	poly(rC) binding protein 1
EIF3M	475950	0,74	0,11	0,55	0,59	eukaryotic translation initiation factor 3, subunit M
ARF1	474591	0,61	0,02	0,55	0,27	ADP-ribosylation factor 1
KPNA2	480469	0,48	0,08	0,56	0,25	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
KPNA3	476909	0,71	0,20	0,56	0,42	karyopherin alpha 3 (importin alpha 4)
NAP1L4	483670	0,59	0,15	0,56	0,45	nucleosome assembly protein 1-like 4
PGM1	479545	0,37	-0,62	0,56	0,06	phosphoglucomutase 1
NAMPT	483267	0,49	-0,04	0,56	0,17	nicotinamide phosphoribosyltransferase
COPS2	478295	0,20	-0,25	0,56	0,31	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)
EZR	484056	0,69	-0,23	0,56	0,23	ezrin
PSAT1	476318	0,99	-0,19	0,56	0,25	phosphoserine aminotransferase 1
CLTC	480578	0,63	0,43	0,57	0,53	clathrin, heavy chain (Hc)
MTPN	403487	0,63	-0,49	0,57	-0,22	myotrophin
SAE1	476425	-0,03	-0,89	0,57	0,04	SUMO1 activating enzyme subunit 1
HSP70	403612	0,41	0,09	0,58	0,47	heat shock protein 70
API5	483413	0,62	0,13	0,58	0,53	apoptosis inhibitor 5
TCP1	484064	0,60	0,14	0,58	0,56	t-complex 1
TSTA3	475116	0,82	-0,40	0,58	-0,09	tissue specific transplantation antigen P35B
ARF4	607073	0,56	-0,08	0,58	0,39	ADP-ribosylation factor 4

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
DDX3X	480886	0,79	0,45	0,58	0,50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
AP1B1	486344	0,05	0,01	0,58	0,13	adaptor-related protein complex 1, beta 1 subunit
LOC606787	606787	0,75	0,34	0,58	0,54	similar to T-complex protein 1, zeta subunit (TCP-1-zeta) (CCT-zeta) (CCT-zeta-1)
ACTN4	484526	0,70	0,04	0,58	0,38	actinin, alpha 4
HSBP1	609752	0,64	-0,15	0,59	0,36	heat shock factor binding protein 1
DARS	476132	0,72	0,07	0,59	0,78	aspartyl-tRNA synthetase
AATF	480595	0,62	0,28	0,59	0,67	apoptosis antagonizing transcription factor
FLNA	481084	0,69	-0,12	0,60	0,48	filamin A, alpha
TNNT2	403532	0,66	-0,43	0,60	0,24	troponin T type 2 (cardiac)
LOC475208	475208	0,84	0,16	0,61	0,43	similar to Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)
TXNRD1	474536	0,17	-0,59	0,61	0,77	thioredoxin reductase 1
HNRNPU	480100	0,79	0,49	0,61	0,65	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
FXR1	478642	0,69	0,45	0,61	0,49	fragile X mental retardation, autosomal homolog 1
SMARCC1	476640	0,70	0,12	0,61	0,81	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
PRKAR2A	484774	0,41	-0,09	0,62	0,51	protein kinase, cAMP-dependent, regulatory, type II, alpha
TAX1BP3	491221	0,52	-0,45	0,62	0,38	Tax1 (human T-cell leukemia virus type I) binding protein 3
VPS35	475346	0,66	0,01	0,62	0,44	vacuolar protein sorting 35 homolog (S. cerevisiae)
VPS26A	479233	0,66	-0,17	0,62	0,38	vacuolar protein sorting 26 homolog A (S. pombe)
EIF3A	486914	0,62	0,06	0,62	0,53	eukaryotic translation initiation factor 3, subunit A
CCT4	482271	0,68	0,27	0,62	0,60	chaperonin containing TCP1, subunit 4 (delta)
SEPT9	483339	0,79	0,06	0,62	0,51	septin 9
EIF3I	478152	0,64	0,20	0,62	0,57	eukaryotic translation initiation factor 3, subunit I
OLA1	478803	0,59	-0,28	0,62	0,28	Obg-like ATPase 1
EEF1E1	478717	0,57	-0,05	0,63	0,68	eukaryotic translation elongation factor 1 epsilon 1
LOC608479	608479	0,66	-0,05	0,63	0,62	similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
LOC477309	477309	0,82	0,34	0,63	0,38	similar to Transcription factor BTF3 homolog 3
UCK2	608979	0,69	-0,11	0,63	0,59	uridine-cytidine kinase 2
UCHL5	478958	0,64	-0,23	0,63	0,47	ubiquitin carboxyl-terminal hydrolase L5
DDX39A	476689	0,52	0,01	0,63	0,33	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A
UBE2L3	477572	0,65	-0,25	0,64	-0,05	ubiquitin-conjugating enzyme E2L 3
MARS	474414	0,43	-0,12	0,64	0,54	methionyl-tRNA synthetase
EDF1	480674	0,87	0,32	0,64	0,32	endothelial differentiation-related factor 1
RBM14	610639	0,67	0,14	0,64	0,58	RNA binding motif protein 14
ANXA7	479246	0,58	-0,42	0,64	0,16	annexin A7
EIF3B	479766	0,75	0,28	0,65	0,64	eukaryotic translation initiation factor 3, subunit B
WDR1	611070	0,78	-0,03	0,65	0,42	WD repeat domain 1
LOC491969	491969	0,68	-0,10	0,65	0,43	similar to CG7519-PA

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
IDH1	478889	0,74	-0,36	0,65	0,46	isocitrate dehydrogenase 1 (NADP+), soluble
ACACA	491130	0,74	0,14	0,65	0,48	acetyl-CoA carboxylase alpha
IPO4	480260	0,44	-0,33	0,66	0,34	importin 4
ARCN1	479415	0,66	0,07	0,66	0,57	archain 1
MAPK1	477575	0,65	0,34	0,66	0,60	mitogen-activated protein kinase 1
HRSP12	475043	0,63	-0,24	0,66	0,43	heat-responsive protein 12
EIF3K	476468	0,67	0,06	0,66	0,60	eukaryotic translation initiation factor 3, subunit K
YWHAG	489818	0,55	-0,01	0,66	0,55	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
PPP1R7	477430	0,66	-0,34	0,66	0,62	protein phosphatase 1, regulatory (inhibitor) subunit 7
SERPINB5	476177	0,40	-0,88	0,67	-0,16	serpin peptidase inhibitor, clade B (ovalbumin), member 5
CAPZA1	475857	0,64	-0,02	0,67	0,55	capping protein (actin filament) muscle Z-line, alpha 1
GLOD4	480640	0,61	-0,61	0,67	0,29	glyoxalase domain containing 4
CSE1L	477257	0,49	-0,06	0,67	0,42	CSE1 chromosome segregation 1-like (yeast)
PSMD14	478765	0,55	0,05	0,67	0,63	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14
NSF	490921	0,64	-0,02	0,67	0,86	N-ethylmaleimide-sensitive factor
GARS	475268	0,70	-0,11	0,67	0,55	glycyl-tRNA synthetase
PSME3	480512	0,78	0,06	0,67	0,50	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
EIF3D	608665	0,85	0,40	0,67	0,71	eukaryotic translation initiation factor 3, subunit D
PEA15	610113	0,85	-0,76	0,67	0,15	phosphoprotein enriched in astrocytes 15
PSMD11	480610	0,64	0,02	0,68	0,63	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11
PSME1	480256	0,88	-0,16	0,68	0,45	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
PSMC5	480478	0,48	-0,18	0,68	0,45	proteasome (prosome, macropain) 26S subunit, ATPase, 5
COPB1	476866	0,60	0,16	0,68	0,43	coatomer protein complex, subunit beta 1
RRM1	476823	0,54	-0,09	0,68	0,30	ribonucleotide reductase M1
TUBA4A	478918	0,75	0,54	0,68	0,39	tubulin, alpha 4a
PMPCB	475897	0,19	-0,23	0,68	-0,08	peptidase (mitochondrial processing) beta
LOC476790	476790	0,79	0,45	0,69	0,68	similar to chaperonin containing TCP1, subunit 3 isoform c
PSMC4	476459	0,51	-0,24	0,69	0,66	proteasome (prosome, macropain) 26S subunit, ATPase, 4
ACTR2	481396	0,69	-0,07	0,69	0,31	ARP2 actin-related protein 2 homolog (yeast)
ACTN1	480369	0,81	0,09	0,69	0,47	actinin, alpha 1
KRT7	477602	1,08	0,91	0,69	0,75	keratin 7
MAPK1IP1L	480329	0,51	-0,14	0,69	0,79	mitogen-activated protein kinase 1 interacting protein 1-like
NUP85	475913	0,48	-0,04	0,69	0,37	nucleoporin 85kDa
DDX46	474685	0,70	-0,10	0,69	0,61	DEAD (Asp-Glu-Ala-Asp)

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						box polypeptide 46
AIMP1	487893	0,44	-0,24	0,69	0,69	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1
PSMC2	475896	0,35	-0,37	0,69	0,46	proteasome (prosome, macropain) 26S subunit, ATPase, 2
RPS21	485959	1,01	0,86	0,69	0,87	ribosomal protein S21
HPRT1	442945	0,86	-0,18	0,70	0,35	hypoxanthine phosphoribosyltransferase 1
FLNB	484713	0,78	-0,09	0,70	0,55	filamin B, beta
CAND1	474437	0,66	-0,02	0,70	0,48	cullin-associated and neddylation-dissociated 1
PSMA5	490123	0,74	0,01	0,70	0,63	proteasome (prosome, macropain) subunit, alpha type, 5
PSMD5	474703	0,45	-0,22	0,70	0,30	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5
DNM1L	477649	0,58	-0,35	0,70	0,57	dynamin 1-like
LOC475101	475101	0,76	-0,17	0,71	0,31	similar to L-lactate dehydrogenase B chain (LDH-B) (LDH heart subunit) (LDH-H)
MAP2K3	489547	0,71	-0,10	0,71	0,43	mitogen-activated protein kinase kinase 3
MAT2A	475770	0,89	0,24	0,71	0,47	methionine adenosyltransferase II, alpha
COMMD9	608575	0,89	0,37	0,71	0,49	COMM domain containing 9
APEX1	482558	0,81	0,26	0,71	0,71	APEX nuclease (multifunctional DNA repair enzyme) 1
EIF3C	479795	0,74	0,20	0,71	0,71	eukaryotic translation initiation factor 3, subunit C
ASNS	475240	0,90	0,28	0,71	0,59	asparagine synthetase (glutamine-hydrolyzing)
HSPA8	479406	0,73	0,29	0,71	0,64	heat shock 70kDa protein 8
HDAC2	475035	0,64	0,29	0,72	0,67	histone deacetylase 2
PABPN1	490611	0,74	0,57	0,72	0,82	poly(A) binding protein, nuclear 1
PTGR1	474802	0,65	-0,21	0,72	0,41	prostaglandin reductase 1
PDCD6	609549	0,87	-0,14	0,72	0,14	programmed cell death 6
G3BP1	479322	0,91	0,62	0,73	0,79	GTPase activating protein (SH3 domain) binding protein 1
CALM2	474584	0,89	0,35	0,73	0,66	calmodulin 2 (phosphorylase kinase, delta)
DIABLO	477463	0,68	0,21	0,73	0,84	diablo, IAP-binding mitochondrial protein
U2AF1	478422	0,44	0,42	0,73	0,52	U2 small nuclear RNA auxiliary factor 1
BZW1	478865	0,99	0,18	0,73	0,62	basic leucine zipper and W2 domains 1
TNPO3	482263	0,57	0,12	0,73	0,40	transportin 3
UGDH	479107	0,37	-0,22	0,73	0,57	UDP-glucose 6-dehydrogenase
HSPH1	477322	0,70	0,05	0,73	0,63	heat shock 105kDa/110kDa protein 1
G3BP2	478429	0,81	0,42	0,73	0,76	GTPase activating protein (SH3 domain) binding protein 2
LOC486736	486736	0,68	-0,29	0,73	0,13	similar to chromosome 12 open reading frame 5
KHDRBS1	487316	0,59	-0,05	0,74	0,55	KH domain containing, RNA binding, signal transduction associated 1
SF3A1	477538	0,49	-0,27	0,74	0,41	splicing factor 3a, subunit 1, 120kDa
VPS29	477477	0,45	-0,13	0,74	0,61	vacuolar protein sorting 29 homolog (S. cerevisiae)
SPR	483118	0,67	-0,45	0,74	0,27	sepiapterin reductase (7,8-

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						dihydrobiopterin:NADP+ oxidoreductase)
GSPT1	479846	0,94	0,08	0,74	0,63	G1 to S phase transition 1
CASP8	488473	1,01	-0,05	0,74	0,65	caspase 8, apoptosis-related cysteine peptidase
PSMD2	478654	0,64	-0,20	0,74	0,44	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
CCT2	474445	0,79	0,27	0,74	0,77	chaperonin containing TCP1, subunit 2 (beta)
PSMD8	476470	0,46	-0,51	0,74	0,49	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8
PFKP	478019	0,83	0,25	0,74	0,68	phosphofructokinase, platelet
ARPC5L	612856	0,89	0,43	0,75	0,66	actin related protein 2/3 complex, subunit 5-like
ALDH1L1	476506	0,43	-0,14	0,75	0,57	aldehyde dehydrogenase 1 family, member L1
RUVBL1	476512	0,67	0,29	0,75	0,57	RuvB-like 1 (E. coli)
TWF1	486600	0,81	0,06	0,75	0,52	twinfilin, actin-binding protein, homolog 1 (Drosophila)
PGM3	474981	0,70	-0,31	0,75	0,15	phosphoglucomutase 3
ZW10	479433	0,86	0,52	0,75	0,89	ZW10, kinetochore associated, homolog (Drosophila)
CSTF2	492015	0,40	-0,25	0,75	0,38	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa
NUTF2	479681	0,55	-0,34	0,75	0,40	nuclear transport factor 2
PLA2G4A	480048	0,78	-0,03	0,75	0,53	phospholipase A2, group IVA (cytosolic, calcium-dependent)
SHMT1	489536	0,47	-0,17	0,75	0,08	serine hydroxymethyltransferase 1 (soluble)
CCT5	606873	0,86	0,28	0,76	0,70	chaperonin containing TCP1, subunit 5 (epsilon)
DDX42	480479	0,60	0,29	0,76	0,56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42
NUP93	478119	0,59	0,03	0,76	0,50	nucleoporin 93kDa
RSU1	477993	0,53	-0,23	0,76	0,39	Ras suppressor protein 1
PSME2	480258	0,86	0,04	0,76	0,64	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
CLIC1	474847	0,69	-0,25	0,76	0,22	chloride intracellular channel 1
SUMO2	474963	0,68	-0,40	0,76	0,48	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)
ACTR3	403702	0,91	0,16	0,77	0,64	ARP3 actin-related protein 3 homolog (yeast)
EIF4A2	488118	0,89	0,13	0,77	0,44	eukaryotic translation initiation factor 4A2
UTP14A	492128	0,85	-0,39	0,77	0,89	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)
SPTAN1	403484	0,83	0,34	0,77	0,71	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)
CTH	479991	0,66	-0,37	0,77	0,38	cystathionase (cystathionine gamma-lyase)
ACTB	403580	0,82	0,15	0,78	0,60	actin, beta
ARPC3	477474	0,77	-0,03	0,78	0,52	actin related protein 2/3 complex, subunit 3, 21kDa
TPR	480045	0,58	-0,06	0,78	0,55	translocated promoter region (to activated MET oncogene)
RUVBL2	476418	0,79	0,34	0,78	0,73	RuvB-like 2 (E. coli)
PSMC1	478703	0,58	0,14	0,78	0,72	proteasome (prosome, macropain) 26S subunit, ATPase, 1
UPP1	480772	1,02	-0,21	0,78	0,48	uridine phosphorylase 1

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
DUT	609526	0,36	-0,50	0,78	0,44	deoxyuridine triphosphatase
ANXA4	606756	0,89	-0,11	0,78	0,33	annexin A4
EEF1B2	478881	0,95	0,41	0,79	0,83	eukaryotic translation elongation factor 1 beta 2
cOR2W9	488336	0,89	0,02	0,79	0,54	cOR2W9 olfactory receptor family 2 subfamily W-like
FDPS	480129	0,76	-0,26	0,79	0,42	farnesyl diphosphate synthase
DPYSL2	486107	0,67	-0,23	0,79	0,66	dihydropyrimidinase-like 2
ARPC4	476540	0,94	0,18	0,79	0,61	actin related protein 2/3 complex, subunit 4, 20kDa
CACYBP	480062	0,82	-0,05	0,80	0,59	calcyclin binding protein
UFM1	477297	0,73	-0,09	0,80	0,28	ubiquitin-fold modifier 1
HSPA4	474680	0,75	0,06	0,80	0,69	heat shock 70kDa protein 4
CNDP2	476166	0,99	0,04	0,80	0,73	CNDP dipeptidase 2 (metallopeptidase M20 family)
PSMC6	478522	0,72	0,05	0,81	0,62	proteasome (prosome, macropain) 26S subunit, ATPase, 6
PSMD12	480465	0,77	0,11	0,81	0,74	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
PARK7	479595	0,63	-0,36	0,81	0,17	parkinson protein 7
ANXA2	403435	1,11	0,69	0,81	0,72	annexin A2
NPEPPS	480538	0,79	-0,19	0,81	0,43	aminopeptidase puromycin sensitive
LOC489680	489680	1,09	-0,29	0,81	0,48	similar to coactosin-like 1
RBBP7	480854	0,85	0,33	0,82	0,83	retinoblastoma binding protein 7
CFL2	490649	0,50	-0,35	0,83	0,48	cofilin 2 (muscle)
LOC609233	609233	1,10	0,43	0,83	0,75	similar to dynein, cytoplasmic, light peptide
IPO5	485528	0,82	0,12	0,83	0,71	importin 5
PSMA6	480290	0,84	0,07	0,83	0,77	proteasome (prosome, macropain) subunit, alpha type, 6
UBA2	476490	0,56	-0,21	0,83	0,68	ubiquitin-like modifier activating enzyme 2
MBNL1	477116	0,75	0,28	0,83	0,97	muscleblind-like (Drosophila)
KRT17	490977	1,22	0,24	0,84	0,48	keratin 17
SNRPA	476454	0,79	0,16	0,84	0,45	small nuclear ribonucleoprotein polypeptide A
ATP6V1B2	486137	0,67	0,11	0,84	0,64	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2
PRPS2	476855	1,08	0,68	0,84	0,88	phosphoribosyl pyrophosphate synthetase 2
VIM	477991	0,84	0,55	0,85	0,60	vimentin
PCNA	477166	0,95	0,24	0,85	0,72	proliferating cell nuclear antigen
RANBP1	477563	0,71	-0,11	0,85	0,46	RAN binding protein 1
PCMT1	476242	0,60	-0,21	0,85	0,51	protein-L-isoaspartate (D-aspartate) O-methyltransferase
HNRNPK	476309	0,90	0,31	0,85	0,85	heterogeneous nuclear ribonucleoprotein K
KHSRP	485022	0,91	0,36	0,85	0,75	KH-type splicing regulatory protein
CNN3	479937	0,61	-0,39	0,86	0,38	calponin 3, acidic
MTHFD1	480352	0,87	-0,02	0,86	0,57	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase
ARHGAP1	483631	0,86	-0,42	0,86	0,29	Rho GTPase activating

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						protein 1
TPI1	477711	0,90	-0,09	0,86	0,60	triosephosphate isomerase 1
ATIC	488513	0,92	-0,09	0,86	0,60	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
ERH	480371	0,97	0,55	0,86	0,84	enhancer of rudimentary homolog (Drosophila)
PRDX5	476032	0,75	-0,28	0,86	0,36	peroxiredoxin 5
EEF1A1	403506	0,99	0,36	0,86	0,70	eukaryotic translation elongation factor 1 alpha 1
CBX3	482015	0,89	0,39	0,86	0,76	chromobox homolog 3
CAP1	475317	0,87	0,07	0,87	0,79	CAP, adenylate cyclase-associated protein 1 (yeast)
PSMA4	475132	0,77	-0,14	0,87	0,77	proteasome (prosome, macropain) subunit, alpha type, 4
BLVRB	476456	0,56	-0,41	0,87	0,12	biliverdin reductase B (flavin reductase (NADPH))
SARS	490124	0,58	-0,39	0,87	0,60	seryl-tRNA synthetase
KATNAL2	490465	0,46	-0,23	0,87	0,51	katanin p60 subunit A-like 2
MDH1	474614	1,04	0,09	0,87	0,63	malate dehydrogenase 1, NAD (soluble)
COPS4	478455	0,35	-0,42	0,88	0,48	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)
GLRX3	477869	0,91	0,03	0,88	0,44	glutaredoxin 3
PSMB5	480246	0,93	0,09	0,88	0,83	proteasome (prosome, macropain) subunit, beta type, 5
FASN	483378	0,90	0,07	0,88	0,59	fatty acid synthase
FUBP1	490201	0,73	0,02	0,88	0,48	far upstream element (FUSE) binding protein 1
CCT8	478399	0,91	0,35	0,88	0,86	chaperonin containing TCP1, subunit 8 (theta)
OTUB1	476039	0,96	-0,01	0,88	0,51	OTU domain, ubiquitin aldehyde binding 1
HSPB1	403979	0,37	-0,35	0,88	0,43	heat shock 27kDa protein 1
ADSL	474499	0,88	-0,03	0,89	0,59	adenylosuccinate lyase
KRT8	486513	1,25	0,97	0,89	0,96	keratin 8
DDB1	476067	0,73	-0,04	0,89	0,68	damage-specific DNA binding protein 1, 127kDa
PRMT1	476411	0,97	0,67	0,89	0,79	protein arginine methyltransferase 1
S100A6	480143	1,01	-0,25	0,89	0,47	S100 calcium binding protein A6
PDAP1	489861	1,10	0,29	0,89	1,04	PDGFA associated protein 1
DDT	607589	0,93	-0,29	0,89	0,51	D-dopachrome tautomerase
PTGES3	612760	0,92	-0,14	0,89	0,71	prostaglandin E synthase 3 (cytosolic)
DCTN2	474415	0,72	0,11	0,89	0,97	dynactin 2 (p50)
NME2	480559	1,04	0,24	0,90	0,68	non-metastatic cells 2, protein (NM23B) expressed in
LOC607890	607890	1,15	0,36	0,90	0,86	similar to D-3-phosphoglycerate dehydrogenase (3-PGDH)
NUDC	487349	0,68	-0,25	0,90	0,60	nuclear distribution gene C homolog (A. nidulans)
CDC37	484955	0,74	-0,02	0,90	0,90	cell division cycle 37 homolog (S. cerevisiae)
ANXA3	478447	1,11	0,16	0,90	0,66	annexin A3
LDHA	476882	1,03	0,22	0,90	0,73	lactate dehydrogenase A
PSMD6	484700	0,83	0,21	0,90	0,77	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6
PSMC3	475980	0,68	0,06	0,90	0,60	proteasome (prosome, macropain) 26S subunit, ATPase, 3

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
PSMA1	476867	0,87	-0,05	0,91	0,82	proteasome (prosome, macropain) subunit, alpha type, 1
PAICS	475150	0,76	-0,12	0,91	0,67	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
PUF60	607245	0,61	-0,08	0,91	0,49	poly-U binding splicing factor 60KDa
CAPN2	480118	1,11	0,04	0,91	0,81	calpain 2, (m/II) large subunit
PPM1G	475703	0,60	-0,06	0,91	0,72	protein phosphatase, Mg2+/Mn2+ dependent, 1G
PSMA7	404305	0,81	0,09	0,91	0,69	proteasome (prosome, macropain) subunit, alpha type, 7
NASP	475373	0,79	0,23	0,91	0,90	nuclear autoantigenic sperm protein (histone-binding)
PSMA2	475870	0,82	0,12	0,92	0,87	proteasome (prosome, macropain) subunit, alpha type, 2
NDRG1	482049	1,03	-0,02	0,92	0,35	N-myc downstream regulated 1
PDLIM5	478482	0,84	-0,03	0,92	0,27	PDZ and LIM domain 5
KRT18	477601	1,29	1,06	0,92	1,06	keratin 18
PLEC	482083	1,17	0,68	0,92	0,79	plectin
RNMT	476200	0,77	0,22	0,92	0,75	RNA (guanine-7-) methyltransferase
PGD	478236	0,77	-0,07	0,92	0,59	phosphogluconate dehydrogenase
KPNB1	491042	0,88	0,25	0,93	0,82	karyopherin (importin) beta 1
HMGA1	442946	0,77	0,33	0,93	0,38	high mobility group AT-hook 1
TSNAX	479203	0,60	-0,19	0,93	0,56	translin-associated factor X
PPP1CA	403609	0,92	0,48	0,93	0,81	protein phosphatase 1, catalytic subunit, alpha isozyme
SF3B2	476015	0,72	0,18	0,94	0,60	splicing factor 3b, subunit 2, 145kDa
G6PD	481088	0,71	-0,18	0,94	0,47	glucose-6-phosphate dehydrogenase
GART	487740	0,82	0,05	0,94	0,66	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase
PPA1	479238	0,80	-0,28	0,94	0,72	pyrophosphatase (inorganic) 1
LOC474798	474798	0,95	3.81332562604872e-05	0,95	0,26	similar to Thioredoxin (ATL-derived factor) (ADF) (Surface associated sulphydryl protein) (SASP)
THRAP3	482476	0,95	0,43	0,95	0,86	thyroid hormone receptor associated protein 3
ACOT7	479589	0,84	-0,30	0,95	0,36	acyl-CoA thioesterase 7
LOC475852	475852	1,10	0,01	0,95	0,56	similar to Calgizzarin (S100 calcium-binding protein A11) (S100C protein) (MLN 70)
NQO1	610935	0,90	-0,27	0,95	0,43	NAD(P)H dehydrogenase, quinone 1
USP5	486718	0,68	-0,40	0,95	0,56	ubiquitin specific peptidase 5 (isopeptidase T)
CPNE1	477213	0,80	-0,21	0,96	0,57	copine I
ALDH1A1	476323	1,16	0,11	0,96	0,84	aldehyde dehydrogenase 1 family, member A1
SF3A3	475326	0,93	0,27	0,96	0,85	splicing factor 3a, subunit 3, 60kDa
TALDO1	475937	1,20	0,08	0,96	0,83	transaldolase 1
LOC476570	476570	1,01	0,45	0,96	0,93	similar to Elongation factor 1-gamma (EF-1-gamma)

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						(eEF-1B gamma)
TCEB1	477914	0,73	0,09	0,96	0,89	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)
CA2	477928	0,83	0,12	0,96	0,76	carbonic anhydrase II
UMPS	478593	0,95	0,07	0,96	0,85	uridine monophosphate synthetase
USP10	479625	0,95	0,32	0,96	0,79	ubiquitin specific peptidase 10
GMPS	477123	0,70	0,00	0,97	0,73	guanine monphosphate synthetase
TCEB2	479873	1,15	0,29	0,97	0,81	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
IMPDH2	476630	0,88	0,58	0,97	1,04	IMP (inosine 5'-monophosphate) dehydrogenase 2
SEC31A	478453	0,51	-0,18	0,97	0,72	SEC31 homolog A (S. cerevisiae)
PSMD13	475934	0,83	0,23	0,97	0,85	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
SKP1	474682	0,90	0,32	0,97	0,62	S-phase kinase-associated protein 1
CAB39	477403	1,04	-0,02	0,98	0,64	calcium binding protein 39
CD2AP	474928	0,67	-0,32	0,98	0,47	CD2-associated protein
RBM25	610314	0,22	-0,22	0,98	0,39	RNA binding motif protein 25
SEPHS1	477999	0,91	0,24	0,98	0,84	selenophosphate synthetase 1
AK2	478145	0,58	0,07	0,99	0,76	adenylate kinase 2
CFL1	476022	1,02	-0,20	0,99	0,40	cofilin 1 (non-muscle)
PSMB4	475848	0,83	0,18	0,99	1,07	proteasome (prosome, macropain) subunit, beta type, 4
LOC483608	483608	1,07	0,33	0,99	0,90	similar to heat shock 70kD protein binding protein
PGK1	480964	1,02	0,10	1,00	0,71	phosphoglycerate kinase 1
PSMD7	479671	0,82	0,06	1,00	0,80	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7
ME1	403709	0,61	-0,07	1,01	0,60	malic enzyme 1, NADP(+)-dependent, cytosolic
ANXA5	476094	1,16	-0,25	1,01	0,54	annexin A5
COPS3	479528	0,88	0,03	1,01	0,78	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)
PPID	475481	1,01	-0,09	1,01	0,67	peptidylprolyl isomerase D
PRDX6	480069	0,99	-0,24	1,01	0,51	peroxiredoxin 6
LUC7L2	475529	1,12	0,43	1,01	0,90	LUC7-like 2 (S. cerevisiae)
FKBP4	477726	0,93	0,04	1,02	0,84	FK506 binding protein 4, 59kDa
MAP2K1	478347	0,79	0,13	1,02	0,61	mitogen-activated protein kinase kinase 1
UBA1	480896	1,10	0,07	1,02	0,85	ubiquitin-like modifier activating enzyme 1
EEF1D	475115	1,17	0,57	1,02	1,00	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
CPSF6	474441	0,77	0,46	1,02	0,81	cleavage and polyadenylation specific factor 6, 68kDa
LOC474987	474987	1,02	0,33	1,02	1,13	similar to Proteasome subunit beta type 3 (Proteasome theta chain) (Proteasome chain 13) (Proteasome component C10-II)
FABP3	478156	0,73	-0,74	1,02	-0,07	fatty acid binding protein 3, muscle and heart

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
						(mammary-derived growth inhibitor)
SEC23A	480295	0,66	0,24	1,02	0,44	Sec23 homolog A (S. cerevisiae)
ENO1	479597	1,06	0,08	1,02	0,73	enolase 1, (alpha)
ATP6V1G2	474840	1,08	0,46	1,02	1,03	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2
ATP6V1A	487981	0,89	0,17	1,03	0,83	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
PSMD3	491018	0,76	0,02	1,03	0,71	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
ACAT2	484063	0,98	-0,19	1,03	0,54	acetyl-CoA acetyltransferase 2
YWHAE	480645	1,08	0,40	1,04	0,87	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
LOC477951	477951	0,91	-0,04	1,04	0,66	similar to suppressor of G2 allele of SKP1
SPTBN1	403743	1,05	0,55	1,04	0,95	spectrin, beta, non-erythrocytic 1
LOC478521	478521	1,23	0,46	1,04	0,96	similar to 14-3-3 protein theta (14-3-3 protein tau)
ANXA11	479259	1,09	0,01	1,04	0,67	annexin A11
PSMB2	475338	0,99	0,21	1,05	1,03	proteasome (prosome, macropain) subunit, beta type, 2
DCXR	475926	0,88	-0,02	1,05	0,62	dicarbonyl/L-xylulose reductase
GDI2	403818	1,00	0,08	1,05	0,74	GDP dissociation inhibitor 2
PSMA3	480338	1,03	0,32	1,05	1,03	proteasome (prosome, macropain) subunit, alpha type, 3
RNH1	483402	0,93	-0,13	1,05	0,68	ribonuclease/angiogenin inhibitor 1
SRRM2	609638	0,70	0,02	1,06	0,81	serine/arginine repetitive matrix 2
EIF4B	477600	1,23	0,77	1,06	1,06	eukaryotic translation initiation factor 4B
CTTN	610283	1,10	0,33	1,06	0,86	cortactin
PSMB1	475040	0,97	0,18	1,06	1,08	proteasome (prosome, macropain) subunit, beta type, 1
AK1	480712	0,69	-0,46	1,06	0,24	adenylate kinase 1
ESD	607116	0,52	-0,60	1,06	0,42	esterase D
HSP90AB1	474919	0,98	0,21	1,07	0,92	heat shock protein 90kDa alpha (cytosolic), class B member 1
TXNL1	483970	0,96	-0,15	1,07	0,65	thioredoxin-like 1
ATOX1	403713	1,13	-0,30	1,07	0,02	ATX1 antioxidant protein 1 homolog (yeast)
SRI	475220	1,27	0,08	1,07	0,87	sorcin
PKM2	403874	1,08	0,26	1,07	1,01	pyruvate kinase, muscle
TIMM8A	480986	1,01	0,85	1,07	1,07	translocase of inner mitochondrial membrane 8 homolog A (yeast)
EEF2	476744	1,15	0,31	1,08	0,84	eukaryotic translation elongation factor 2
CDK6	609920	0,74	-0,15	1,08	0,01	cyclin-dependent kinase 6
NME1	476767	0,99	0,12	1,08	0,69	non-metastatic cells 1, protein (NM23A) expressed in
STIP1	474837	1,09	0,32	1,08	1,03	stress-induced-phosphoprotein 1
TTLL12	474474	0,90	-0,01	1,08	0,78	tubulin tyrosine ligase-like family, member 12
CRYAB	479441	0,85	0,19	1,08	0,91	crystallin, alpha B

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
LOC486122	486122	0,67	0,19	1,09	0,62	similar to p30 DBC protein
YWHAB	477237	1,09	0,44	1,09	0,99	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
LOC480151	480151	0,87	0,27	1,09	0,89	similar to CG14299-PA, isoform A
RAN	442976	1,04	0,14	1,09	0,89	RAN, member RAS oncogene family
BCAT1	486633	1,03	-0,03	1,10	0,71	branched chain amino-acid transaminase 1, cytosolic
ATP6V1E1	477740	0,75	-0,06	1,11	0,77	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1
LOC607013	607013	1,00	0,29	1,11	1,04	similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP)
CAPG	483082	1,29	0,00	1,11	0,71	capping protein (actin filament), gelsolin-like
IPO9	480004	0,97	0,08	1,12	0,93	importin 9
LASP1	608624	1,15	0,09	1,12	0,76	LIM and SH3 protein 1
ANXA8	479270	1,11	-0,10	1,13	0,57	annexin A8
VCP	481590	0,86	0,34	1,13	0,99	valosin containing protein
EIF3G	612971	1,15	0,44	1,13	0,95	eukaryotic translation initiation factor 3, subunit G
GSPT2	480921	0,71	-0,07	1,13	0,84	G1 to S phase transition 2
TBCA	479173	0,80	-0,46	1,13	0,44	tubulin folding cofactor A
DGKA	474393	0,98	-0,03	1,13	0,93	diacylglycerol kinase, alpha 80kDa
S100A4	403787	1,05	-0,79	1,13	0,09	S100 calcium binding protein A4
PGLS	610090	0,67	-0,47	1,13	0,20	6-phosphogluconolactonase
UBQLN1	476312	0,99	0,04	1,14	0,88	ubiquilin 1
PPP2CA	403608	1,02	0,39	1,14	0,89	protein phosphatase 2, catalytic subunit, alpha isozyme
PEBP1	477501	0,96	-0,22	1,14	0,37	phosphatidylethanolamine binding protein 1
PNP	475393	1,33	0,15	1,14	0,88	purine nucleoside phosphorylase
GDI1	403819	1,09	-0,03	1,14	0,78	GDP dissociation inhibitor 1
ISG15	479575	1,32	0,10	1,14	1,53	ISG15 ubiquitin-like modifier
LOC476784	476784	1,00	0,07	1,15	0,62	similar to ubiquitin-conjugating enzyme E2N
ANXA1	476322	1,34	0,10	1,15	0,73	annexin A1
EIF4H	607749	1,28	0,56	1,15	0,98	eukaryotic translation initiation factor 4H
PRDX2	484926	1,11	0,33	1,16	0,97	peroxiredoxin 2
HMGCS1	479344	1,15	0,51	1,16	0,68	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)
CORO1B	476007	1,13	0,32	1,16	0,88	coronin, actin binding protein, 1B
VASP	403936	1,13	0,08	1,16	0,89	vasodilator-stimulated phosphoprotein
PRKAR1A	480459	1,01	0,07	1,16	0,81	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
BPNT1	608525	0,97	0,03	1,17	0,72	3'(2'), 5'-bisphosphate nucleotidase 1
USP14	480182	0,99	0,24	1,17	0,86	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)
TPT1	476924	1,34	0,31	1,17	0,91	tumor protein, translationally-controlled 1
EIF4A1	479485	1,23	0,60	1,18	0,98	eukaryotic translation initiation factor 4A1
PDCD5	476499	0,89	-0,24	1,18	0,90	programmed cell death 5
CSTB	478424	1,33	0,01	1,19	0,61	cystatin B (stefin B)

		log2 fold change				
Symbol	**Entrez Id**	**4hrs p.i.**	**8 hrs p.i.**	**10 hrs p.i.**	**12 hrs p.i.**	**Name**
TKT	476588	1,22	0,30	1,20	1,02	transketolase
UBXN1	476055	0,91	-0,12	1,21	0,84	UBX domain protein 1
AHSA1	480402	0,67	-0,02	1,22	0,98	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)
SF1	476031	0,74	0,50	1,22	0,85	splicing factor 1
ALDOC	480622	0,75	-0,11	1,22	0,82	aldolase C, fructose-bisphosphate
YWHAZ	475864	1,27	0,50	1,23	1,03	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
HINT1	474667	1,17	0,07	1,23	0,83	histidine triad nucleotide binding protein 1
PGAM1	477786	1,04	-0,04	1,24	0,71	phosphoglycerate mutase 1 (brain)
GSTO1	477813	1,29	-0,08	1,24	0,75	glutathione S-transferase omega 1
DBNL	607412	0,87	0,15	1,24	0,88	drebrin-like
PREP	481945	0,89	-0,18	1,25	0,78	prolyl endopeptidase
TFG	487954	1,05	-0,13	1,25	1,13	TRK-fused gene
LOC475191	475191	1,20	-0,07	1,26	0,74	similar to Glutathione S-transferase P (GST 7-7) (Chain 7) (GST class-pi)
EML2	476434	0,65	-0,31	1,28	0,40	echinoderm microtubule associated protein like 2
NOLC1	609496	1,04	0,32	1,29	1,05	nucleolar and coiled-body phosphoprotein 1
TAGLN2	610210	1,37	0,20	1,29	0,93	transgelin 2
TPM1	478332	1,53	0,65	1,33	1,33	tropomyosin 1 (alpha)
STMN1	478175	1,46	-0,10	1,34	0,87	stathmin 1
ARHGDIA	475924	1,21	0,23	1,35	0,84	Rho GDP dissociation inhibitor (GDI) alpha
SERPINB9	488192	1,36	0,35	1,37	1,56	serpin peptidase inhibitor, clade B (ovalbumin), member 9
LOC476719	476719	1,21	0,25	1,38	1,09	similar to Fructose-bisphosphate aldolase A (Muscle-type aldolase) (Lung cancer antigen NY-LU-1)
SFN	487351	1,42	0,43	1,39	1,07	stratifin
NDUFA8	480741	-0,76	-0,64	1,39	-0,64	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
DBI	476115	1,61	0,17	1,43	0,76	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)
HNRNPK	480979	1,53	0,98	1,45	1,56	heterogeneous nuclear ribonucleoprotein K
PPIA	403581	1,70	0,63	1,45	1,10	peptidylprolyl isomerase A (cyclophilin A)
GLTP	612989	1,41	0,52	1,46	0,75	glycolipid transfer protein
SRRM1	478185	1,40	0,40	1,46	1,15	serine/arginine repetitive matrix 1
LOC613005	613005	1,60	0,59	1,48	1,00	similar to thymosin, beta 10
TPM4	609879	1,60	0,44	1,48	1,33	tropomyosin 4
SF3A2	612188	0,98	0,41	1,50	1,14	splicing factor 3a, subunit 2, 66kDa
AHCY	477198	1,08	-0,02	1,51	1,12	adenosylhomocysteinase
LGALS3	404021	1,71	0,74	1,52	1,00	lectin, galactoside-binding, soluble, 3
PAFAH1B2	479425	1,41	0,23	1,54	1,06	platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)
APRT	479615	1,24	-0,25	1,56	0,84	adenine phosphoribosyltransferase
ANP32A	403534	1,67	0,74	1,68	1,68	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
PKP3	483399	0,27	-0,01	-	-0,27	plakophilin 3

		log2 fold change				
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				3.48646191479722e-05		