

**Table S1**

Analysis of the evolution of the relative abundance of proteins identified by MS/MS spectrometry

The colour code is the same as that used in Figure 4:

only in D2, D2/D7 > 2, 2 > D2/D7 > 0.5, D2/D7 < 0.5, only in D7, non reproducible ratio

Identified protein	Gene	MW	mean ratio D2/D7	ratio D2/D7		
				Run 1	Run 2	Q-Star
<b>(1) Antigen presentation</b>						
MHC class I						
RT1.A1(F) protein (Fragment)	Q31257	39507	4,72	6,09	3,35	6,22
RT1.A(U) alpha chain (Fragment)	Q95571	39050	4,79	5,95	3,63	4,54
MHC class Ib RT1.S3 (Fragment)	Q7JJ65	40199	D2	D2	D2	D2
BM1 (Histocompatibility 2, T region locus 24)	Q4G002	42891	D2	D2	D2	
Beta-2-microglobulin	P07151	13720	D2	D2	D2	
<b>(2) Cell adhesion</b>						
Thrombospondin 1	Q71SA3	133579	0,50	0,30	0,70	
Thrombospondin-4 (Putative uncharacterized protein Thbs4)	D3ZFP9	110882	0,11	D7	0,22	D7
Putative uncharacterized protein Itga4 (integrin alpha 4)	D3ZMQ3	115592	D2	D2	D2	
integrin alpha 2b	D3ZAC0	114075	3,46	5,75	1,17	1,41
Integrin CD29 b1	ITB1	91686	3,22	D2	3,22	D2
Integrin beta	Q8R2H2	90066	1,89	2,67	1,12	1,13
Putative uncharacterized protein RGD1565416	D3ZA84	273795	D7	D7	D7	
Putative uncharacterized protein Icam4	D3ZP29	28809	D7	D7	D7	
<b>(3) Cell structure et motility</b>						
Stomatin	Q5XI04	31530	1,74	2,57	0,90	1,23
Adenylyl cyclase-associated protein 1	CAP1	51899	1,20	0,13	2,26	D2
Moesin	MOES	67867	3,57	3,57	D2	D2
Myosin-9	MYH9	227566	1,61	0,52	2,70	
Actin, cytoplasmic 2	ACTG	42108	0,63	0,99	0,89	1,53
Actin-related protein 2	ARP2	44990	0,89	0,40	1,38	
Actin-related protein 2/3 complex subunit 1A	ARC1A	42143	D7	D7	D7	D7
Actin-related protein 2/3 complex subunit 1B	ARC1B	41829	1,01	0,11	1,90	
Actin-related protein 2/3 complex subunit 2	ARPC2	34484	0,57	0,19	0,95	D7
Actin related protein 2/3 complex, subunit 3	B2GV73	20750	0,58	0,33	0,83	D7
Actin related protein 2/3 complex, subunit 4 (Predicted), isoform CRA_a	B2RZ72	19768	0,80	D7	0,80	
Actin-related protein 3	ARP3	47783	0,67	0,21	1,13	D7
ARP10 actin-related protein 10 homolog (S. cerevisiae)	Q5M9F7	46214	D7	D7	D7	
Tln1 protein	Q498D4	163473	0,47	0,18	0,76	
Calmodulin	CALM	16827	D2	D2	D2	D2
Coronin-1A	COR1A	51065	9,39	3,25	15,53	
Dynamamin-1-like protein	DNM1L	83908	0,14	D7	0,28	
Dynamamin-2	DYN2	98511	0,27	0,04	0,51	
Gelsolin	Q68FP1	86068	0,24	D7	0,47	
Vinculin	VINC	117112	4,61	D2	4,61	D2
Erythroid spectrin alpha	D3ZNU8	281212	0,14	0,03	0,25	D7
Erythroid spectrin beta	Q6XDA0	246974	0,03	D7	0,07	D7
Putative uncharacterized protein Epb4.1	D3ZHS9	D3ZHS9	0,14	0,15	0,13	
Erythrocyte protein band 4.2 (Predicted)	B5DF57	76740	0,29	0,40	0,18	
Galectin-5	LEG5	16414	0,65	0,57	0,73	
Centromere/kinetochore protein zw10 homolog	Q4V8C2	87967	D2	D2	D2	
Septin-2	Q91Y81	41793	0,13	0,07	0,19	
Microtubule-associated protein RP/EB family member 1	Q66HR2	30004	D7	D7	D7	
Microtubule-associated proteins 1A/1B light chain 3B	MLP3B	16441	D2	D2	D2 S3	
Putative uncharacterized protein Sirt2	D3ZME8	43626	0,23	0,13	0,33	
Calpain small subunit 1	Q64537	28570	D7	D7	D7	
Calpain-5	CAN5	74045	D2	D2	D2	
Kinesin-like protein KIF15	KIF15	159540	D7	D7	D7	
Kinesin-1 heavy chain	KINH	110204	D7	D7	D7	
Tubulin beta-2C chain	TBB2C	50225	1,07	0,60	1,55	0,38
Tubulin alpha-1B chain	TBA1B	50803	0,75	0,38	1,12	0,84
Filamin alpha	C0JPT7	283056	0,65	0,41	0,90	
Platelet-activating factor acetylhydrolase IB subunit alpha	LIS1	47210	0,25	D7	0,50	
Cofilin-1	COF1	18748	1,20	0,82	1,57	
Profilin-1	PROF1	15119	2,30	2,40	2,20	
<b>(4) Heat shock proteins and chaperonnes</b>						
DnaJ (Hsp40) homolog						

subfamily B, member 1	B0K030	38294	3,69	4,44	2,94	
subfamily B, member 4	Q5XIP0	37969	6,00	6,00	Abs	
subfamily B member 6	DNJB6	39012	2,00	D2	2,00	
subfamily C member 5	P60905	22885	D2	D2	D2	
Putative uncharacterized protein Dnajc13	D3ZNI6	209275	0,27	D7	0,53	
Hsc70-interacting protein	P50503	41424	12,25	D2	12,50	
Heat Shock cognate 71 kDa protein (Hsc 70)	HSP7C	71055	2,26	2,45	2,06	2,05
BAG family molecular chaperone regulator 5	Q5QJC9	51030	D2	D2	D2	
Heat shock 70 kDa protein 1A/1B	HSP71	70427	1,17	D2	1,17	
Heat shock 70 kDa protein 4	HSP74	94057	0,18	0,05	0,32	
Endoplasmin	ENPL	92998	0,69	0,71	0,67	
Stress-induced-phosphoprotein 1	STIP1	63157	5,57	4,00	7,14	
78 kDa glucose-regulated protein, HSPa5	GRP78	72473	2,05	2,35	1,76	D2
HSP 90 alpha	HS90A	85160	0,38	0,26	0,51	D7
HSP 90 beta	HS90B	83571	0,22	D7	0,44	D7
T-complex protein 1						
alpha	TCPA	60834	0,47	0,22	0,71	D7
beta	TCPB	57764	0,54	0,23	0,85	0,11
delta	TCPD	58775	0,55	0,25	0,86	0,15
epsilon	TCPE	59954	0,49	0,20	0,78	D7
gamma	TCPG	61178	0,38	0,12	0,64	D7
Chaperonin subunit 6a (Zeta)	Q3MHS9	58437	0,50	0,21	0,78	0,15
eta (RCG55994, isoform CRA_c)	D4AC23	60133	0,53	0,26	0,81	
<b>(5) Metabolic enzymes</b>						
Peroxisomal multifunctional enzyme type 2	P97852	79428	3,47	D2	3,47	
Peroxiredoxin-1	PRDX2	22109	0,17	D7	0,35	
Pyridoxal phosphate phosphatase	PLPP	33115	D7	D7	D7	
Transketolase	TKT	68342	1,74	0,08	3,40	
α-enolase (ENO-1)	ENOA	47440	0,93	0,39	1,48	0,50
Enoyl-CoA hydratase domain-containing protein 1	Q6AYG5	32631	D7	D7	D7	
Glyceraldehyde-3-phosphate dehydrogenase	G3P	36090	0,69	0,54	0,83	0,44
Phosphoglycerate Kinase 1	PGK1	44909	0,89	0,30	1,48	0,70
Phosphoglycerate mutase	Q6P6G4	30229	0,25	0,20	0,30	D7
Triosephosphate isomerase	TPIS	27345	0,43	0,23	0,63	
6-phosphofructokinase, liver type	K6PL	86083	0,16	0,04	0,44	D7
6-phosphofructo-1-kinase, M-type	Q52KS1	85343	D7	D7	D7	
6-phosphogluconolactonase	P85971	27234	D7	D7	D7	
Pyruvate Kinase M2	Q6P7S0	53472	12,58	D2	12,58	D2
Pyruvate Kinase isoenzyme L/R	KPYR	62503	0,08	D7	0,16	D7
Ribose-phosphate pyrophosphokinase 1	PRPS1	35325	0,11	0,13	0,20	D7
Hexokinase-1	HXK1	103540	0,38	D7	0,76	1,00
Galactokinase 1	Q5RKH2	42806	0,10	D7	0,21	
Glucose-6-phosphate 1-dehydrogenase	G6PD	59794	0,66	0,09	1,24	D7
L-lactate dehydrogenase A chain	LDHA	36712	1,16	1,16	1,15	
L-lactate dehydrogenase B chain	LDHB	36612	D7	D7	D7	
6-phosphogluconate dehydrogenase, decarboxylating	6PGD	53715	0,66	0,16	1,15	
Malate dehydrogenase, cytoplasmic	MDHC	36631	0,32	0,29	0,35	D7
Aldehyde dehydrogenase family 16 member A1	A16A1	86159	0,21	D7	0,42	D7
Aldose reductase	ALDR	35797	D7	D7	D7	
Fructose-bisphosphate aldolase A	ALDOA	39783	0,86	0,73	1,00	
Alcohol dehydrogenase [NADP+]	AK1A1	36711	0,05	0,11	D7	
Alcohol dehydrogenase class-3	ADHX	40348	D7	D7	D7	
4-trimethylaminobutyraldehyde dehydrogenase	AL9A1	54530	0,27	D7	0,53	
Aflatoxin B1 aldehyde reductase member 2	ARK72	41105	0,25	0,14	0,36	D7
Aflatoxin B1 aldehyde reductase member 3	ARK73	37122	0,30	0,07	0,53	D7
Adenosine kinase	ADK	40450	D7	D7	D7	
Protein phosphatase 2A activator, regulatory subunit 4	B2RYQ2	36879	D7	D7	D7	D7
Protein phosphatase 2 (Formerly 2A), regulatory subunit A (PR 65), alpha isoform, isoform CRA_a	Q5XI34	65323	0,26	0,06	0,45	
Low molecular weight phosphotyrosine protein phosphatase	PPAC	18596	0,26	0,33	0,18	D7
Guanine deaminase	Q9JKB7	51554	0,44	0,32	0,57	D7
Aminopeptidase B	AMPB	72620	1,59	D7	3,17	
Ppa1 protein (Fragment)	Q499R7	38223	0,02	0,04	D7	D7
Acylamino-acid-releasing enzyme	P13676	82415	0,03	D7	0,07	D7
Putative uncharacterized protein Mphosph8	D4A5B4	138708	D7	D7	D7	
NAD(P)(+)-arg ADP-ribosyltransferase (Frgmt)	Q6LAL6	20247	1,88	2,00	1,75	3,00
Glutathione peroxidase 1	GPX1	22463	0,42	0,27	0,58	0,22
S-formylglutathione hydrolase	ESTD	31971	0,20	0,14	0,26	D7
Bis(5'-nucleosyl)-tetrakisphosphate [asymmetrical]	AP4A	17090	0,20	D7	0,40	
Glutamate--cysteine ligase catalytic subunit	GSH1	73371	D7	D7	D7	
3-mercaptopyruvate sulfurtransferase	THTM	33205	0,50	0,28	0,72	0,15
Hypoxanthine-guanine phosphoribosyltransferase	HPRT	24690	0,29	0,27	0,31	D7
Glutathione S-transferase Mu 5	GSTM5	27067	D7	D7	D7	
Adenylosuccinate lyase (Predicted)	D3ZW08	54852	D7	D7	D7	

Cad protein	D4A8A0	245824	0,56	0,31	0,81	
Phosphoribosyl pyrophosphate synthetase-associated protein 1	Q63468	39753	D7	D7	D7	
Carbonyl reductase [NADPH] 1	CBR1	30844	D7	D7	D7	
Arachidonate 12-lipoxygenase, leukocyte-type	LX12L	76369	0,59	0,64	0,53	0,26
Asparagine synthetase [glutamine-hydrolyzing]	ASNS	64776	0,40	0,10	0,71	D7
D-3-phosphoglycerate dehydrogenase	SERA	56493	D7	D7	D7	
ATP-citrate synthase	ACLY	121471	0,09	0,05	0,12	
Fructosamine-3-kinase-related protein	B2RYN1	34375	0,32	0,08	0,56	D7
Prostaglandin E synthase 3	TEBP	18995	0,23	D7	0,47	D7
Sepiapterin reductase	P18297	28510	0,30	0,19	0,40	D7
Glutamine synthetase	P09606	42982	D7	D7	D7	
Phosphoserine aminotransferase	Q68FU2	40943	D7	D7	D7	
Fatty acid synthase	FAS	275101	0,16	0,07	0,25	
Multifunctional protein ADE2	P51583	47807	0,23	0,07	0,39	
Bifunctional purine biosynthesis protein PURH	PUR9	64681	0,13	0,06	0,19	
Purine nucleoside phosphorylase	PNPH	32566	0,68	0,60	0,75	
UMP-CMP kinase	Q4KM73	22169	D7	D7	D7	
Putative uncharacterized protein Pfas	D4AB17	138461	0,04	D7	0,07	
Gart protein	B5DEG6	45683	D7	D7	D7	
Ctps protein	B1WC02	66640	0,16	0,08	0,24	
Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, cyclohydrolase, formyltetrahydrofolate synthetase	Q5EBC3	101598	0,32	0,13	0,51	D7
Betaine--homocysteine S-methyltransferase 1	O09171	44976	D7	D7	D7	
Protein arginine N-methyltransferase 1	Q63009	40522	0,14	D7	0,28	
Protein arginine N-methyltransferase 5 (Predicted), isoform CRA_a	D4A0E8	72695	D7	D7	D7	
Ribonucleoside-diphosphate reductase	Q5U2Q5	91091	0,25	0,05	0,45	D7
Inosine-5'-monophosphate dehydrogenase	Q6P9U9	56106	0,13	0,14	0,12	
Spermidine synthase	Q99MI5	34545	0,15	D7	0,29	D7
Thimet oligopeptidase	THOP1	79191	0,11	D7	0,23	
Carbonic anhydrase 1	CAH1	28339	1,28	1,43	1,13	1,50
Carbonic anhydrase 2	CAH2	29267	1,24	1,67	0,81	1,00
Catalase	CATA	60062	0,37	0,26	0,49	0,09
Selenium-binding protein 1	Q8VIF7	52532	D7	D7	D7	
Lactoylglutathione lyase	Q6P7Q4	20820	D7	D7	D7	
Obg-like ATPase 1	A0JPD7	44792	0,32	0,32	0,33	D7
Amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (Predicted)	D4AEH9	176729	D7	D7	D7	
Delta-aminolevulinic acid dehydratase	HEM2	36464	0,51	0,47	0,55	
Dihydropteridine reductase	DHPR	25764	D7	D7	D7	
Adenylosuccinate synthetase	D4AEP0	50453	0,14	D7	0,27	
Mannose-1-phosphate guanyltransferase alpha	GMPPA	46504	0,15	D7	0,30	
Pck2 protein (Fragment)	B2RYG2	74080	3,00	3,00	3,00	
Putative uncharacterized protein Hmbs	D3ZJU6	38056	1,09	1,23	0,96	
5'-nucleotidase, cytosolic III	B2GUX5	34073	D7	D7	D7	
GDP-mannose pyrophosphorylase B (Predicted), isoform CRA_a	D4A746	D4A746	D7	D7	D7	
Inosine triphosphatase (Nucleoside triphosphate pyrophosphatase) (Mapped), isoform CRA_a	D3ZW55	22255	D7	D7	D7	
Nicotinamide phosphoribosyltransferase	NAMPT	55689	D7	D7	D7	
Cytosolic acyl coenzyme A thioester hydrolase	BACH	43164	D7	D7	D7	
Tsta3 protein	B0BNN0	31086	0,25	D7	0,50	
LanC-like protein 1	LANC1	45952	0,08	D7	0,17	
Monoglyceride lipase	MGLL	33820	0,25	D7	0,50	
<b>(6) Transmembrane proteins</b>						
4F2 cell-surface antigen heavy chain CD98	4F2	58150	2,39	2,78	2,00	1,85
Aquaporin-1	AQP1	29066	1,51	1,20	1,82	1,72
Cation-dependent mannose-6-phosphate receptor	MPRD	31589	2,17	3,20	1,14	D2
Chloride channel protein 2	CLCN2	100177	8,89	11,50	6,28	D2
H(+)/Cl(-) exchange transporter 3	CLCN3	85419	D2	D2	D2	D2
H(+)/Cl(-) exchange transporter 5	CLCN5	83068	D2	D2	D2	
Putative uncharacterized protein Clcn6	D4A3H5	98352	D2	D2	D2	
H(+)/Cl(-) exchange transporter 7	P51799	88731	D2	D2	D2	
Interferon-inducible protein	INIB	15132	D2	D2	D2	
L-type amino acid transporter 1	LAT1	56551	2,11	2,81	1,40	2,22
Integrin-associated protein, CD47	D4A1U9	33487	2,28	2,22	2,34	5,67
Leukocyte sialoglycoprotein, CD43	LEUK	38402	4,32	3,75	4,88	D2
Monocarboxylate transporter 1	MOT1	53831	1,37	1,48	1,26	2,47
Monocarboxylate transporter 10	MOT10	56368	6,61	9,50	3,71	D2
Metal ion transporter DCT1	NRAM2	62807	16,03	26,50	5,56	D2
Voltage-dependent anion-selective channel protein 3	VDAC3	31178	5,50	8,00	3,01	D2
Voltage-dependent anion-selective channel protein 2	VDAC2	32353	3,63	3,00	4,25	
Voltage-dependent anion-selective channel protein 1	VDAC1	30851	4,08	5,75	2,41	8,03
Two pore calcium channel protein 1	TPC1	94800	25,12	D2	25,12	D2
Intermediate conductance calcium-activated potassium channel protein 4 (KCCN4)	Q9QYW1	48305	D2	D2	D2	
Intermediate conductance K channel isoform 4b (Kcnn4)	A1A5N3	47639	D2	D2	D2	

Putative uncharacterized protein Ttyh3	D3ZP76	52626	25,00	D2	25,00	
Divalent cation transporter 1	O54902	62277	16,01	26,50	5,53	
Solute carrier family 2, facilitated glucose transporter member 3	GTR3	54002	D2		D7	D2
Solute carrier family 2, facilitated glucose transporter member 4	GTR4	54896	D2	D2	D2	
Putative uncharacterized protein Slc2a6	D3ZLC4	55101	D2	D2	D2	
Transporter Slc6a9	D4ABA4	70216	38,54	D2	38,54	
Ecotropic retrovirus receptor	Q8VIA9	68138	2,01	2,36	1,65	
Solute carrier family 12 member 4 (KCC1)	S12A4	121690	D2	D2	D2	D2
Urea transporter Slc14a1	P70633	45214	2,58	2,90	2,26	
Solute carrier family 15 member 4	S15A4	61949	D2	D2	D2	
Solute carrier family 22 member 4	Q9R141	62362	D2	D2	D2	
Solute carrier family 40 member 1	S40A1	63286	2,54	3,75	1,33	
Putative uncharacterized protein Slc30a10	D3ZJB7	50970	2,00	2,00	D2	
Na <sup>+</sup> -dependent neutral amino acid transporter, ASCT2 (member 5)	Q9Z1D7	57630	2,67	2,73	2,60	2,55
Sodium-coupled neutral amino acid transporter 5	A2VCW5	52436	D2	D2	D2	
Na <sup>+</sup> /K <sup>+</sup> -transporting ATPase subunit alpha-1	AT1A1	114293	3,05	3,50	2,59	D2
Na <sup>+</sup> /K <sup>+</sup> -transporting ATPase subunit beta-3	AT1B3	32151	2,59	2,75	2,43	
Sodium- and chloride-dependent glycine transporter 1	D4ABA4	71493	38,73	D2	38,73	D2
Sodium-dependent phosphate transporter 1	Q9JJP0	74187	D2	D2	D2	
ATP-binding cassette sub-family G member 2	Q80W57	72961	5,42	6,50	4,34	
Progressive ankylosis protein homolog	D3ZNG7	54304	12,92	10,67	15,18	D2
Plasma membrane calcium-transporting ATPase 4	AT2B4	134094	5,11	6,23	3,98	D2
Copper-transporting ATPase 2	D3ZZB4	157431	2,97	3,35	2,59	
Band 3 anion transport protein (Slc4a1)	Q5U329	103392	0,78	0,93	0,62	0,98
Cd36 protein	Q5BKE5	53559	2,68	2,37	3,00	3,76
Platelet glycoprotein 4 Cd36	CD36	53268	2,62	2,37	2,86	
Putative uncharacterized protein Cd44	D3Z9C5	67923	3,93	D2	3,93	D2
CD48 antigen	CD48	27890	2,20	2,20	D2	D2
CD55	A9CMA5	41019	0,84	0,43	1,25	
CD59 glycoprotein	CD59	14465	1,28	1,50	1,07	1,20
Embigin	EMB	37438	1,66	1,61	1,71	1,44
Basigin (CD147, OX47 antigen)	P26453	42865	2,84	2,54	3,14	D2
Lman2 protein	B0BNG3	40709	D2	D2	D2	D2
Nicastrin	NICA	79035	3,07	3,40	2,75	D2
Rh blood group protein	RHD	46952	0,88	0,72	1,04	0,50
Ammonium transporter Rh type A	RHAG	49258	0,81	0,65	0,96	
Putative uncharacterized protein Ermap	D3Z9R6	53769	2,56	3,38	1,74	
Putative uncharacterized protein Frrs1	D4A8Z3	67063	D2	D2	D2	
Atp11b protein (Fragment)	Q5RJS7	21487	D2	D2	D2	
Putative uncharacterized protein Sppl2a	D3ZNG3	58905	4,25	4,25	D2	
Putative uncharacterized protein Atp6v1a	D4A133	68563	2,59	2,44	2,75	
Putative uncharacterized protein Atp6v1h	D3ZW96	56346	2,67	2,67	2,67	
V-type proton ATPase subunit B	VATB2	56857	2,32	2,78	1,86	D2
V-type proton ATPase subunit C 1	VATC1	44044	5,50	4,60	6,40	D2
ATPase, H <sup>+</sup> transporting, V1 subunit D	Q6P503	28291	4,21	7,00	1,43	
V-type proton ATPase subunit E 1	VATE1	26169	5,36	7,00	3,72	D2
V-type proton ATPase 116 kDa subunit a isoform 1	VPP1	97063	7,03	7,03		20,83
V-H+ATPase subunit a1-III	Q2I6B2	96321	5,52	7,14	3,90	15,20
V-H+ATPase subunit a3	Q2I6B0	93850	D2	D2	D2	D2
Putative uncharacterized protein 682925	D4A3X6	115106	D2	D2	D2	
Transmembrane protein 206	TM206	40333	14,00	14,00	D2	D2
Apolipoprotein B-100	APOB	537740	4,87	1,71	8,02	D2
Disintegrin and metalloproteinase domain-containing protein 10 (Fragment)	ADA10	62401	8,46	11,25	5,67	
Complement regulatory protein Crry	CRRY	63407	8,50	7,00	10,00	
Putative uncharacterized protein Tmem9b	D3ZUR2	22639	D2	D2	D2	
Putative uncharacterized protein Tmem30a	D3ZYA3	41411	D2	D2	D2	D2
Integral membrane protein 2B	ITM2B	30808	D2	D2	D2	
Major prion protein	P13852	27804	D2	D2	D2	
Leucine-rich repeat-containing protein 8C	Q498T9	93372	D2	D2	D2	
Leucine-rich repeat-containing protein 8D	Q5U308	97940	D2	D2	D2	
Putative uncharacterized protein Nptn	NPTN	31501	D2	D2	D2	
Neuropilin-1	NRP1	104271	10,07	D2	10,07	
Podocalyxin	PODXL	52026	2,95	3,60	2,30	D2
Insulin receptor	P15127	156757	D2	D2	D2	
Transmembrane 9 superfamily member 2	TM9S2	76620	7,27	6,00	8,55	D2
Osteopetrosis associated transmembrane protein 1	Q4QQU9	37910	D2	D2	D2	D2
Putative uncharacterized protein Scamp2	D3ZHT9	37330	2,00	D2	2,00	
Putative uncharacterized protein Scamp3	D3ZQ93	34830	13,33	21,00	5,67	D2
Flotillin-1	FLOT1	47755	1,34	1,85	0,83	
Flotillin-2	FLOT2	47408	1,06	1,38	0,74	
Putative uncharacterized protein ENSRNOP0000043743	D3Z841	52597	D2	D2	D2	
Serine incorporator 3	Q5U2V2	52321	D2	D2	D2	
Adiponectin receptor 1	Q6P746	42466	D2	D2	D2	

Sema4b protein (Fragment)	Q4KM50	79479	D2	D2	D2	
Disrupted in renal carcinoma protein 2 homolog	Q66H95	52030	D2	D2	D2	
Putative uncharacterized protein Abcc10	D3ZX04	163822	D2	D2	D2	
Transmembrane protein 127	A2RRU2	25858	D2	D2	D2	
Putative uncharacterized protein Tmem189	D3ZFY8	16458	1,61	1,63	1,60	
Osteopetrosis associated transmembrane protein 1	Q4QQU9	37910	D2	D2	D2	
Coxsackievirus and adenovirus receptor homolog	Q9R066	39949	D2	D2	D2	
Putative uncharacterized protein Enpp4	D3ZVW8	44257	D2	D2	D2	
Leucyl-cystinyl aminopeptidase	P97629	117202	D2	D2	D2	
Transmembrane protein 184A	Q4QQS1	46878	D2	D2	D2	
Transmembrane protein 106B	Q6AYA5	31152	3,00	D2	3,00	
Disintegrin and metalloproteinase domain-containing protein 10 (Fragment) (ADAM 10)	Q10743	60445	8,58	11,25	5,90	
Putative uncharacterized protein Frrs1	D4A8Z3	66308	D2	D2	D2	
STARD3 N-terminal like	Q5U205	26719	D2	D2	D2	
Complement regulatory protein Crry	Q63135	61680	8,71	7,00	10,42	
Putative uncharacterized protein Sspl2a	D3ZNG3	57917	4,25	4,25	D2	
Putative uncharacterized protein Sidt2	D3ZEH5	94454	D2	D2	D2	
Myeloid-associated differentiation marker	Q6VBQ5	35148	3,47	D2	3,47	
Presenilin-2	O88777	50051	D2	D2	D2	
Multidrug resistance-associated protein 4 splice variant	Q6QMG5	144430	D2	D2	D2	
Sn1-specific diacylglycerol lipase beta	P0C1S9	73771	D2	D2	D2	
Putative uncharacterized protein Lrig1	D3ZD84	107876	3,21	D2	3,21	
Choline transporter-like protein 1	CTL1	74582	2,03	2,55	1,51	D2
Transmembrane emp24 protein transport domain containing 9	Q5I0E7	27182	3,33	D2	3,33	
<b>(7) Iron and Globins</b>						
Alpha globin	Q63910	15572	0,44	0,37	0,52	0,14
Epsilon 1 globin (Hemoglobin, epsilon 1)	O88752	16151	0,73	D7	0,73	D7
Hemoglobin subunit alpha-1/2	HBA	15490	0,66	0,70	0,62	0,82
Zero beta-1 globin	Q62669	16069	0,39	0,35	0,42	0,25
Beta Glo	Q6PDU6	16084	0,47	0,47	0,48	0,31
Hemoglobin subunit beta-1	HBB1	16083	0,60	0,59	0,61	0,46
Hemoglobin subunit beta-2	HBB2	16086	0,59	0,58	0,60	0,48
Metalloreductase STEAP3	STEAP3	55095	14,16	21,27	7,04	D2
Putative uncharacterized protein Rfesd	D3ZF58	17557	D7	D7	D7	
Uroporphyrinogen III synthase	Q5XIF2	28439	D7	D7	D7	
Uroporphyrinogen decarboxylase	B0BN55	40842	0,35	0,22	0,47	0,02
Transferrin receptor protein 1 (Fragment) (CD 71)	TFR1	70337	5,73	4,33	7,13	4,62
Biliverdin reductase A	Q6AZ33	33658	0,30	0,11	0,49	D7
Biliverdin reductase B (Flavin reductase (NADPH)) (Predicted), isoform CRA_b)	B5DF65	22194	0,23	0,19	0,27	0,08
Putative uncharacterized protein Mpo	D4A856	80883	2,86	D2	2,86	
Eosinophil peroxidase (Predicted)	D3ZSY4	81281	2,53	2,33	2,73	
Hebp1 protein	B4F7C7	21124	D7	D7	D7	
Ferrochelatase	D3ZBM3	48091	0,78	0,96	0,60	
Ferritin light chain 1	FRIL1	20793	1,20	1,32	1,07	
Ferritin heavy chain	FRIH	21284	1,15	1,55	0,76	
<b>(8) MVB biogenesis</b>						
Alix	PDC6I	97141	1,57	1,75	1,38	D2
BRO1 domain-containing protein BROX	BROX	46676	4,69	6,00	3,39	
<b>ESCRT0</b>						
SNAP-25-interacting protein Hrs-2	HGS	86819	0,32	0,55	0,08	
Epidermal growth factor receptor pathway substrate 15 isoform B	Q5JC29	87189	D7	D7	D7	
Putative uncharacterized protein Stam	D3ZI37	54890	0,22	0,38	0,05	
<b>ESCRTI</b>						
Tumor susceptibility gene 101 protein	TS101	44221	1,00		1,00	
<b>ESCRTII</b>						
<b>ESCRTIII</b>						
Putative uncharacterized protein Chmp4b	D4A9Z8	25094	1,38	1,75	1,00	
IST1 homolog	IST1	40088	2,75	D2	2,75	
Vacuolar protein sorting-associated protein 4A	VPS4A	49161	1,00	D2	1,00	
<b>(9) Signalling proteins</b>						
Major vault protein	Q62667	96081	0,39	0,34	0,44	0,21
<b>14-3-3 proteins</b>						
epsilon	1433E	29326	0,73	0,33	1,13	1,14
eta	1433F	28365	0,86	0,83	0,88	D2
gamma	1433G	28455	0,66	0,44	0,88	
zeta/delta	1433Z	27925	1,20	0,75	1,65	3,33
Rho, GDP dissociation inhibitor (GDI) beta	Q5M860	22927	D2	D2	D2	D2
GTPase-activating protein and VPS9 domain-containing protein 1	D3ZBJ3	162466	D7	D7	D7	

GTP binding protein 1 (Predicted), isoform CRA_a	D2XV59	72489	D7	D7	D7	
Syntenin-1	SDCB1	32631	6,16	6,11	6,20	D2
Transforming protein RhoA	RHOA	22110	1,04	0,76	1,32	D7
Ras homolog gene family, member G, RhoG	Q32PX6	21309	2,08	D2	2,08	
RhoA activator C11orf59 homolog	Q6P791	17824	3,61	4,50	2,72	D2
<b>Guanine nucleotide-binding protein</b>						
G(i), alpha-2 subunit	GNAI2	41043	2,52	3,17	1,88	
G(l)/G(S)/G(T) beta-2	GBB2	38048	1,17	1,40	0,95	
beta-2-like 1	GBLP	35510	1,23	1,07	1,38	
Kinase D-interacting substrate of 220 kDa = ARMS	KDIS	197247	D2	D2	D2	D2
Cell cycle control protein 50A	CC50A	37263	D2	D2		D2
Cell division control protein 42 homolog	CDC42	21587	0,76	0,67	0,86	0,40
<b>(10) Tetraspanins</b>						
Tetraspanin-5	Q68VK5	30337	D2	D2	D2	
D6.1A protein (Tetraspanin 8)	O55158	26212	2,79	4,00	1,58	4,25
Putative uncharacterized protein Tspan14	D4A0Z1	30702	5,21	D2	5,21	
CD9 molecule	B1WBM0	25768	2,44	D2	2,44	D2
CD81 molecule	Q6P9V1	26571	D2		D2	
CD82	Q6IN14	30081	1,80	1,73	1,87	3,00
<b>(11) Transcription and protein synthesis</b>						
<b>Histones</b>						
Histone 1, H1a (Predicted)	D4A3K5	22004	D2	D2	D2	
Putative uncharacterized protein Hist1h1b	D3ZBN0	22649	D2	D2	D2	
Histone H1.2	H12	21974	4,40	5,33	3,48	D2
Histone H2A	D3ZXP3	15115	1,18	D2	1,18	
H2A type 1	H2A1	14068	3,47	6,15	0,78	2,08
Core histone macro-H2A.1	H2AY	39650	D2	D2	D2	
H2A.Z	H2AZ	13545	2,12	D2	2,12	D2
H2B	D3ZNH4	13982	0,55	0,42	0,68	4,00
Histone H3	D3ZJ08	15388	2,35	1,57	3,13	
H3.1	H31	15509	2,35	D7	2,35	2,35
H4	H4	11360	2,54	2,30	2,78	2,40
Putative uncharacterized protein (NAP-1-related protein)	Q6P769	45602	0,20	0,11	0,28	D7
Condensin complex subunit 1	D3ZHP6	155590	0,12	D7	0,25	
Thyroid receptor-interacting protein 13	Q5XHZ9	48434	0,07	D7	0,15	
DNA damage-binding protein 1	Q9ESW0	126862	D7	D7	D7	
Nucleosome assembly protein 1-like 4	NP1L4	44118	D7	D7	D7	
Putative uncharacterized protein Hdac6	D3ZVD8	21876	D7	D7	D7	
Putative uncharacterized protein Dhx9	D3Z9Q9	151358	0,58	0,23	0,93	
BRCA1-A complex subunit BRE	BRE	43987	0,50	D7	0,50	
Da2-35	Q7TP02	31827	D7	D7	D7	
<b>Ribosomal proteins</b>						
Small nuclear ribonucleoprotein D1	B2RZB7	13282	D2	D2	D2	
Putative uncharacterized protein RGD1561333	D4A6W6	28367	3,21	2,50	3,93	D2
Rpl14 protein (RCG25732, isoform CRA_b)	B5DEM5	23879	2,96	3,50	2,42	D2
Rpl7 protein (RCG30479, isoform CRA_b)	B0K031	30351	4,24	3,25	5,23	D2
Rps16 protein (Fragment)	B0K038	18074	4,55	5,50	3,61	D2
Putative uncharacterized protein Rps11	D3ZE37	18917	2,03	1,33	2,72	
40S ribosomal protein S4, X isoform	RS4X	29807	1,58	1,11	2,05	
Ribosomal protein S5, isoform CRA_b	B0BN81	23063	1,67	1,11	2,22	
40S ribosomal protein S6	RS6	28834	2,60	2,17	3,02	D2
Ribosomal protein S8	B2RYR8	24475	3,29	1,44	5,14	
40S ribosomal protein S9	RS9	22634	3,93	D2	3,93	D2
40S ribosomal protein S10	RS10	18904	1,60	2,00	1,20	1,00
40S ribosomal protein S11	RS11	18590	1,97	1,33	2,60	3,00
40S ribosomal protein S12	RS12	14858	3,13	D2	3,13	
40S ribosomal protein S13	RS13	17212	0,75	D2	0,75	5,00
40S ribosomal protein S15a	P62246	14840	D2	D2	D2	
40S ribosomal protein S2	RS2	31497	2,42	1,95	2,89	D2
40S ribosomal protein S23	RS23	15969	5,23	D2	5,23	D2
40S ribosomal protein S24	D4A6H5	15197	D2	D2	D2	
40S ribosomal protein S25	RS25	13791	1,00	D2	1,00	
40S ribosomal protein S26	RS26	13292	1,85	1,33	2,38	1,00
40S ribosomal protein S3	RS3	26828	1,86	D2	1,86	D2
40S ribosomal protein S3a	RS3A	30154	2,53	3,00	2,05	
40S ribosomal protein SA	RSSA	32917	2,02	1,83	2,21	3,00
60S acidic ribosomal protein P0	RLA0	34365	0,66	0,61	0,70	0,50
60S acidic ribosomal protein P1	RLA1	11605	0,50	0,75	0,25	D7
60S ribosomal protein L10	Q6PDV7	24604	2,00	2,00	D2	
60S ribosomal protein L10a	RL10A	24986	1,39	1,00	1,77	
60S ribosomal protein L11	RL11	20468	1,85	2,33	1,38	
RCG45615, isoform CRA_a	B2RYU2	18005	0,64	0,40	0,88	

60S ribosomal protein L13	RL13	24351	2,47	2,00	2,93	D2
Ribosomal protein L13A	Q5RK10	23545	9,55	D2	9,55	
60S ribosomal protein L15	RL15	24245	6,11	6,50	5,72	D2
Putative uncharacterized protein RGD1562402	D3ZF07	16587	6,25	D2	6,25	
60S ribosomal protein L17	RL17	21611	3,78	2,00	5,56	2,00
60S ribosomal protein L18	RL18	21702	6,01	2,43	9,60	D2
60S ribosomal protein L18a	RL18A	21004	2,43	1,60	3,25	
60S ribosomal protein L19	RL19	23565	9,07	D2	9,07	D2
60S ribosomal protein L23 (RL23P)	D3ZTH8	14970	D2	D2	D2	D2
60S ribosomal protein L24	RL24	17779	D2	D2	D2	
60S ribosomal protein L26	RL26	17277	8,96	D2	8,96	
60S ribosomal protein L27	RL27	15788	3,84	D2	3,84	D2
60S ribosomal protein L3	RL3	46392	4,76	2,94	6,57	
60S ribosomal protein L30	RL30	12947	2,44	D2	2,44	D2
60S ribosomal protein L32	RL32	15860	D2	D2	D2	
60S ribosomal protein L37a	P61515	10275	D2	D2	D2	
60S ribosomal protein L5	RL5	34665	5,26	5,14	5,37	
Ribosomal protein L4	Q6P3V9	47556	11,50	12,50	10,50	
60S ribosomal protein L6 (Fragment)	D4ADN2	33510	3,60	4,83	2,38	D2
Putative uncharacterized protein ENSRNOP0000046090	D3ZM33	17787	2,44	D2	2,44	D2
Putative uncharacterized protein ENSRNOP0000044275	D3ZX87	14263	2,78	D2	2,78	
Heterogeneous nuclear ribonucleoprotein K	P61980	50976	0,22	D7	0,45	
Polyadenylate-binding protein 1	PABP1	70883	D7	D7	D7	
ATP-binding cassette sub-family F member 1	ABCF1	95649	D7	D7	D7	
Probable tRNA(His) guanylyltransferase	THG1	35170	D7	D7	D7	
<b>tRNAaminoacyl synthetases</b>						
Aspartyl-tRNA synthetase	SYDC	57546	0,23	0,18	0,29	D7
Arginyl-tRNA synthetase	SYRC	76503	0,19	0,13	0,24	
Leucyl-tRNA synthetase	Q5PPJ6	135504	0,20	0,17	0,23	D7
Lysyl-tRNA synthetase	D4ABR8	72091	0,08	D7	0,17	
Phenylalanyl-tRNA synthetase alpha chain	SYFA	57798	0,95	0,60	1,30	1,00
Phenylalanyl-tRNA synthetase, beta subunit	Q68FT7	66294	0,30	D7	0,60	
Seryl-tRNA synthetase, cytoplasmic	SYSC	59064	0,27	D7	0,55	D7
Tryptophanyl-tRNA synthetase, cytoplasmic	SYWC	54622	0,15	D7	0,29	D7
Valyl-tRNA synthetase	SYVC	141535	0,19	0,06	0,32	D7
Glycyl-tRNA synthetase	SYG	72669	0,21	D7	0,42	D7
glutamyl and prolyl-tRNA synthetase	Q6TXE9	168558	0,13	0,05	0,20	D7
aspartyl- asparaginy-tRNA synthetase	Q6TUD1	57975	0,13	D7	0,26	D7
Histidyl-tRNA synthetase	Q4QQV4	57780	D7	D7	D7	
lars protein (Fragment) isoleucine-tRNA synthetase activity	Q5BJR3	31490	0,12	D7	0,23	
Glutamyl-tRNA synthetase	Q66H61	88557	0,19	D7	0,39	
Alanyl-tRNA synthetase, cytoplasmic	SYAC	69001	0,18	0,07	0,29	D7
Threonyl-tRNA synthetase, cytoplasmic	D3ZHY1	81437	0,12	D7	0,25	
Tyrosyl-tRNA synthetase, cytoplasmic	SYYC	59420	D7	D7	D7	
Putative uncharacterized protein Mars (Methionyl-tRNA synthetase)	D3Z941	102772	0,12	D7	0,23	
Aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	AIMP2	35705	0,20	0,14	0,26	D7
<b>Elongation factors (EF)</b>						
EF 1-alpha 1	EF1A1	50424	0,81	0,90	0,72	0,27
EF 1-gamma	EF1G	50371	0,25	0,15	0,36	0,04
EF 1 beta 2 (RCG22471, isoform CRA_b)	B5DEN5	24831	0,19	0,20	0,17	D7
EF 1-delta	Q68FR9	72653	0,12	D7	0,23	D7
Eukaryotic translation elongation factor 1 epsilon 1	B2RYN3	19887	0,20	D7	0,40	
EF 2	EF2	96192	0,55	0,47	0,64	0,26
<b>Release factors (RF)</b>						
Eukaryotic peptide chain release factor subunit 1	Q5U2Q7	49031	D7	D7	D7	
<b>Initiation factors (IF)</b>						
Eukaryotic IF 4A-II	IF4A2	46601	D7	D7	D7	0,20
Eukaryotic translation IF 2 subunit 1	IF2A	36371	0,34	0,17	0,50	D7
Eukaryotic translation initiation factor 2A, isoform CRA_b	D3ZUV3	64379	D7	D7	D7	
Eukaryotic translation initiation factor 2-alpha kinase 1	Q63185	69599	D7	D7	D7	
Translation initiation factor eIF-2B subunit epsilon	E12BE	80898	D7	D7	D7	
Eukaryotic translation initiation factor 2 subunit 3	IF2G	51617	0,19	0,04	0,34	
Eukaryotic translation IF 3						
subunit A	Q1JU68	163496	0,09	D7	0,18	D7
subunit B	D3ZUK5	91253	0,10	D7	0,21	D7
subunit C	EIF3C		0,08	D7	0,15	
subunit D	EIF3D	64575	0,08	D7	0,16	
subunit E	EIF3E		0,27	0,14	0,41	D7
subunit F	D4AC36	37997	0,20	0,17	0,24	
subunit G	EIF3G	35914	0,06	D7	0,13	
subunit H	EIF3H	40051	0,10	0,09	0,10	D7
subunit I	EIF3I	36837	0,47	0,41	0,53	
subunit K	D3Z9H3	25115	D7	D7	D7	
Eukaryotic translation IF 5A-1	IF5A1	17049	D7	D7	D7	

Eukaryotic translation initiation factor 5	IF5	48954	0,07	D7	0,15	
Eukaryotic translation initiation factor 4A1	Q6P3V8	46352	0,68	0,52	0,83	
Putative uncharacterized protein Eif4g1	D3ZU13	176394	D7	D7	D7	
Eukaryotic translation initiation factor 4E	IF4E	25266	0,21	D7	0,42	
Eukaryotic translation initiation factor 6	Q3KRD8	27067	D7	D7	D7	
Eukaryotic translation initiation factor 3, subunit 6 interacting protein	Q498D2	45281	0,22	D7	0,44	D7
<b>Ubiquitine and proteasome</b>						
Ubiquitin (Ub)	UBIQ	8560	1,24	1,41	1,07	1,44
Ub thioesterase OTU1	OTU1	37949	0,11	0,13	0,08	D7
Ubiquitin thioesterase OTUB1	OTUB1	31478	D7	D7	D7	
Ubiquitin-like modifier-activating enzyme 1	UBA1	118910	0,34	0,05	0,62	0,02
Ubiquitin-like modifier-activating enzyme 5	UBA5	44895	D7	D7	D7	
Ub-associated domain-containing protein 1	UBAC1	45746	D7	D7	D7	D7
Ub-conjugating enzyme E2 N	UBE2N	17170	1,13	D2	1,13	D2
Ubiquitin carrier protein	D3ZI82	19571	D7	D7	D7	
Ubiquitin carrier protein	D3ZNQ6	21172	D7	D7	D7	
E3 ubiquitin-protein ligase UBR4	D3ZZA2	580498	0,06	D7	0,12	D7
E3 ubiquitin-protein ligase RNF123	D3ZXK7	149077	0,05	D7	0,09	
WW domain containing E3 ubiquitin protein ligase 2	B4F767	99286	8,68	D2	8,68	
Cullin-associated NEDD8-dissociated protein 1	CAND1	137985	0,07	0,04	0,11	D7
Transitional endoplasmic reticulum ATPase	TERA	89977	0,28	0,16	0,40	D7
Ubiquitin carboxyl-terminal hydrolase	Q9R085	110440	D7	D7	D7	
Ubiquitin carboxyl-terminal hydrolase	D3ZC84	289440	0,08	D7	0,15	
Ubiquitin carboxyl-terminal hydrolase	D3ZVQ0	95779	D7	D7	D7	
Ubiquitin carboxyl-terminal hydrolase 7	UBP7	129432	D7	D7	D7	
Ubiquitin carboxyl-terminal hydrolase isozyme L3	UCHL3	26278	D7	D7	D7	
Nedd4l	D7NIW0	51989	D2	D2	D2	
Putative uncharacterized protein Stub1	D4A4T0	35320	D2	D2	D2	
Cullin-5	CUL5	91403	D7	D7	D7	
OTU domain, ubiquitin aldehyde binding 2 (Predicted), isoform CRA_a	D3ZAR8	27258	D7	D7	D7	
Lys-63-specific deubiquitinase BRCC36	BRCC3	33451	D7	D7	D7	
<b>26S proteasome</b>						
26S protease regulatory subunit 4	PRS4	49325	0,08	D7	0,15	D7
26S protease regulatory subunit 6A	PRS6A	49415	0,25	0,12	0,37	D7
26S protease regulatory subunit 6B	PRS6B	47493	0,23	0,07	0,38	D7
26S protease regulatory subunit 7	PRS7	48943	0,23	0,06	0,39	
26S protease regulatory subunit 8	PRS8	45768	0,20	0,02	0,38	D7
Psmc6 protein (Fragment)	Q32PW9	43288	0,21	0,15	0,27	
Proteasome subunit alpha type	Q6P9V6	26411	D7	D7	D7	
Proteasome subunit alpha type-2	PSA2	26024	D7	D7	D7	
Proteasome subunit alpha type-6	PSA6	27399	0,09	D7	0,17	
Proteasome subunit alpha type-7	PSA7	28326	0,13	D7	0,26	
Proteasome subunit beta type-1	PSB1	26690		D7	D2	
Proteasome subunit beta type-2	PSB2	22912	D7	D7	D7	
Proteasome subunit beta type-5	PSB5	28738	D7	D7	D7	
<b>20S proteasome</b>						
26S proteasome non-ATPase regulatory subunit 1	PSMD1	106707	0,09	0,04	0,14	D7
26S proteasome non-ATPase regulatory subunit 2	PSMD2	100922	0,18	D7	0,37	D7
Putative uncharacterized protein Psm�4	D4A9C9	39335	D7	D7	D7	
26S proteasome non-ATPase regulatory subunit 8	Q3B8P5	32337	0,15	D7	0,31	
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 11	B5DEP6	48280	0,23	0,11	0,35	D7
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12	Q5XIC6	53302	0,13	0,03	0,24	
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13 (Predicted)	B0BN93	43075	0,16	D7	0,33	
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 14	Q4V8E2	34577	0,05	0,10	D7	
26S proteasome non-ATPase regulatory subunit 13	PSD13	43075	0,16	D7	0,33	D7
Proteasome (macropain) 26S subunit, non-ATPase, 3	Q5U2S7	60764	0,10	D7	0,19	D7
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 5	B2RYP1	36962	0,32	D7	0,55	
Proteasome (macropain) 26S subunit, non-ATPase, 6	Q6PCT9	45854	0,24	0,12	0,36	0,07
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 7 (Predicted)	D4AEH3	36492	0,21	0,16	0,25	
Proteasome inhibitor PI31 subunit	PSMF1	30007	0,18	D7	0,36	D7
Down syndrome critical region homolog 2 (Human) (Predicted), isoform CRA_b (Psmg1)	D4AAH6	33238	D7	D7	D7	
Putative uncharacterized protein RGD1564425	D3Z8J0	23316	D7	D7	D7	
<b>COP9</b>						
COP9 signalosome complex subunit 2	CSN2	51597	D7	D7	D7	
COP9 signalosome complex subunit 3	CSN3	48398	0,27	0,09	0,45	D7
COP9 signalosome complex subunit 4	CSN4	46546	D7	D7	D7	
COP9 (Constitutive photomorphogenic) homolog, subunit 5	Q4KM69	37579	D7	D7	D7	
Prolyl endopeptidase	PPCE	81659	0,18	D7	0,36	
Tripeptidyl-peptidase 2	TPP2	139688	0,09	0,02	0,15	
Dipeptidyl peptidase 3	DPP3	83386	0,21	D7	0,42	
Insulin-degrading enzyme	IDE	118376	D7	D7	D7	



<b>(10) Trafficking and membrane fusion</b>							
Annexins							
	A1	ANXA1	38829	10,31	18,00	2,63	
	A2	ANXA2	38938	6,02	D2	6,02	D2
	A11	Q5XI77	54468	6,53	5,33	7,73	D2
	Putative uncharacterized protein Anxa6	D4ABR6	75511	D2	D2	D2	D2
ARFs							
	ADP-ribosylation factor 5	ARF5	20631	1,42	1,35	1,49	0,83
	ADP-ribosylation factor-like protein 8B	ARL8B	21753	1,13	1,40	0,86	
AP-1 complex subunit mu-1							
		AP1M1	105377	0,72	0,66	0,77	
AP-2 complex							
	Putative uncharacterized protein Ap2a1	D3ZMB9	106468	0,53	0,61	0,45	
	subunit alpha-2	AP2A2	104891	0,64	0,68	0,60	
	subunit beta-1	AP2B1	105398	0,78	0,80	0,76	
	subunit mu-1	AP2M1	49965	0,64	0,52	0,76	
	subunit sigma-1	AP2S1	17177	0,29	D7	0,57	
Clathrin heavy chain 1							
		CLH	193187	0,60	0,60		0,23
Clta protein							
		Q5PPP1	23608	0,36	0,43	0,29	0,25
Putative uncharacterized protein Cltc							
		D4AD25	193666	0,55	0,58	0,51	
Enthoprotin							
		Q6DGF2	52222	0,32	0,44	0,19	D7
Synptojanin-1							
		SYNJ1	173970	0,08	D7	0,17	
Rab GDP dissociation inhibitor							
	beta	GDIB	51018	0,53	0,50	0,55	0,25
Ras related protein rab							
	1A	RAB1A	22891	1,56	1,45	1,67	3,78
	1B	RAB1B	22320	1,23	1,27	1,20	
	4A	D4ADS8	24232	1,67	D2	1,67	
	4B	P51146	23629	2,11	2,20	2,01	
	5A, member RAS oncogene family	O88565	23827	2,09	2,15	2,04	2,19
	5B	A1L1J8	23887	1,95	2,27	1,63	D2
	5c	B0BNK1	23639	2,08	1,88	2,28	D2
	6A	D3ZGP4	23644	1,56	1,30	1,82	
	7A	RAB7A	23773	2,56	3,40	1,71	D2
	8A	RAB8A	23824	1,37	1,48	1,26	2,40
	8B	RAB8B	23759	1,53	1,77	1,29	D2
	9A	RAB9A	23166	4,54	D2	4,54	D2
	10	Q7TQ88	15561	1,52	1,70	1,34	D2
	11B	RB11B	24588	2,84	3,64	2,05	4,00
	14	B0BMW0	24140	2,66	3,14	2,17	3,65
	18	RAB18	23246	0,50	0,50	0,50	
	21	RAB21	24547	1,57	1,65	1,49	1,20
	35	RAB35	23295	2,21	D2	2,21	
Synaptosomal-associated protein 23							
		SNP23	23505	2,09	D2	2,09	D2
Syntaxins							
	2	STX2	33452	3,24	4,83	1,66	D2
	6	STX6	29096	D2	D2	D2	D2
	7	STX7	29946	4,63	6,91	2,35	4,74
	8	STX8	27122	6,39	6,50	6,28	D2
	13	O70319	30563	4,32	4,80	3,84	3,65
	16	B5DF99	25639	D2	D2	D2	
Syntaxin-binding protein 1							
		STXB1	67925	2,41	3,66	1,17	
Syntaxin-binding protein 2							
		STXB2	67109	3,33	1,40	5,25	
Sorting nexin-3							
		SNX3	18808	5,00	D2	5,00	D2
Snx5 protein							
		B1H267	47049	1,00	1,00	1,00	
Microtubule-associated proteins 1A/1B light chain 3B							
		MLP3B	16441	D2	D2	D2	D2
Gamma-aminobutyric acid receptor-associated protein-like 2							
		GBRL2	13715	3,47	D2	3,47	D2
Alpha-soluble NSF attachment protein							
		SNAA	33627	2,56	2,52	2,60	2,92
EH domain-containing protein 3							
		EHD3	60810	0,80	0,48	1,12	
EH domain-containing protein 4							
		Q8R3Z7	61656	0,44	D7	0,88	
28 kDa cis-Golgi SNARE p28							
		GOSR1	28630	D2	D2	D2	D2
GTPase Ran							
		RAN	24579	0,37	0,16	0,59	D7
RAN GTPase activating protein 1							
		Q66H32	46947	D7	D7	D7	
Importin subunit beta-1							
		IMB1	98373	0,20	0,11	0,28	D7
Putative uncharacterized protein Ipo4							
		D4A2D7	119095	D7	D7	D7	
Putative uncharacterized protein Ipo5							
		D4A781	123706	0,12	0,11	0,12	
Importin 7 (Predicted), isoform CRA_c							
		D4AE96	119488	0,11	0,02	0,19	
Putative uncharacterized protein Ipo9							
		D4A857	116650	D7	D7	D7	
Tnpo1 protein (Fragment)							
		Q5D008	89439	D7	D7	D7	
Putative uncharacterized protein Tnpo2							
		D3ZER6	105557	D7	D7	D7	
Putative uncharacterized protein Tnpo3							
		D4AAM0	104203	D7	D7	D7	
Exportin-1							
		XPO1	124099	0,20	0,09	0,30	
Exportin 7, isoform CRA_a							
		D3ZBB4	17569	0,77	0,71	0,84	
Xpo7 protein (Fragment)							
		Q5U3Y1	7833	0,20	D7	0,39	D7
Vesicle-associated membrane protein 3							
		VAMP3	11587	13,82	24,00	3,64	5,84

Vesicle-associated membrane protein 5	VAMP5	11495	D2	D2	D2	
Vesicle-associated membrane protein 7	VAMP7	24776	7,29	D2	7,29	
Vesicle-associated membrane protein 8	VAMP8	11370	12,14	10,67	13,61	D2
Vesicle transport through interaction with t-SNAREs homolog 1A	QQJ151	26027	2,39	D2	2,39	D2
Vesicle transport through interaction with t-SNAREs homolog 1B	VT11B	26687	12,52	20,50	4,54	D2
Vacuolar protein sorting-associated protein 29	B2RZ78	20626	1,11	D2	1,11	
Vacuolar protein sorting-associated protein 26A	VP26A	38205	D2	D2	D2	
Vacuolar protein sorting-associated protein 45	VPS45	65251	18,05	17,00	19,10	D2
Vps35 protein (Fragment)	B5DFC1	72978	1,87	2,20	1,54	
Vesicle-fusing ATPase	NSF	82652	0,09	D7	0,17	
Vesicle-trafficking protein SEC22b	SC22B	24895	1,69	1,75	1,64	
Secretory carrier-associated membrane protein 1	SCAM1	38373	D2	D2	D2	
Transmembrane emp24 domain-containing protein 10	TMEDA	25013	2,25	4,00	0,50	D2
Dysf	D4A6X1	233191	2,58	3,96	1,20	
General vesicular transport factor p115	P41542	107162	D7	D7	D7	
Ankyrin-1	D3Z9M4	208680	0,12	0,08	0,16	
Autophagy-related protein 9A	ATG9A	95397	12,25	12,25	D2	
General vesicular transport factor p115	USO1	108122	D7	D7	D7	
COPI vesicle coat						
	Copa protein	B5DFK1	139926	1,76	D7	1,76
	subunit beta	COPB	108083	2,42	D7	2,42
	subunit beta'	COPB2	103342	1,08	D7	1,08
	subunit delta	COPD	57619	0,75	D7	0,75
	subunit gamma	COPG	98806	0,92	0,67	1,16
	Coatomer protein complex, subunit zeta 1 (Predicted)	D4A8T3	20242	0,80	1,00	0,60
	Transmembrane emp24 domain-containing protein 2	TMED2	22832	1,33	1,66	1,00
<b>(11) Other cytoplasmic proteins</b>						
Ac1873	Q7TQ70	87344	24,77	D2	24,77	D2
Ac2-269	Q7TPI7	37728	D7	D7	D7	
PKC-theta-interacting protein - Glutaredoxin-3	GLRX3	38111	0,29	0,20	0,37	D7
Peptidyl-prolyl cis-trans isomerase A	PPIA	18091	1,34	1,54	1,14	1,33
Dipeptidyl-peptidase 3	O55096	83386	0,22	D7	0,44	
Protein disulfide-isomerase A3	PDIA3	57044	1,18	1,50	0,85	1,40
Putative uncharacterized protein Wbp2	D4A0J1	37484	2,51	2,90	2,12	D2
Protein MEMO1	MEMO1	34057	0,60	0,38	0,81	D7
Phosphatidylinositol 4-kinase type 2-alpha	P4K2A	54727	D2	D2	D2	
Phosphatidylinositol 4-kinase type 2-beta	P4K2B	55000	D2	D2	D2	D2
Protein phosphatase 1 regulatory subunit 7	PP1R7	41385	D7	D7	D7	D7
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PP2AA	36156	0,34	0,12	0,57	D7
Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6	35821	0,79	D7	0,79	
Serine/threonine Ste20-like kinase 3	B0LT89	47990	D7	D7	D7	
Protein phosphatase 1B	PPM1B	43488	D7	D7	D7	
Xaa-Pro aminopeptidase 1	XPP1	70354	0,15	D7	0,30	
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	P56558	115606	0,27	0,33	0,21	
Calcium-regulated heat stable protein 1	Q9WU49	15906	0,40	0,40	0,39	
Putative uncharacterized protein Tll12	D4A1Q9	74404	0,13	0,05	0,22	
Regucalcin	Q03336	33390	D7	D7	D7	
Huntingtin	HD	347478	D7	D7	D7	
NHL repeat containing 2 (Predicted)	D3ZLM5	79254	D7	D7	D7	
Thioredoxin-like protein 1	Q920J4	32249	0,22	D7	0,45	
Thioredoxin-like protein 2	Q9JLZ1	37849	0,29	0,20	0,37	
Tissue-type transglutaminase	Q9WVJ6	76935	0,07	D7	0,15	
Placenta-specific 8 (Predicted)	B5DF36	13173	2,09	D2	2,09	D2
Obg-like ATPase 1	OLA1	44792	0,32	0,32	0,31	D7
Tyrosine-protein phosphatase non-receptor type 23 (Fragment)	PTN23	163978	D7	D7	D7	
Casein kinase II subunit alpha	CSK21	45158	1,11	0,96	1,26	
Casein kinase II subunit beta	CSK2B	25268	0,94	1,00	0,89	
Calreticulin	CALR	48136	1,15	1,50	0,80	
Phospholipase A-2-activating protein	PLAP	88510	D7	D7	D7	
cAMP-dependent protein kinase type II-alpha regulatory subunit	KAP2	45797	D7	D7	D7	
Map2k3 protein	B1H230	39627	D2	D2	D2	
Protein disulfide-isomerase	PDIA1	57315	4,38	1,75	7,00	
Translationally-controlled tumor protein	TCTP	19563	0,50	0,43	0,58	
Calcium-regulated heat stable protein 1	CHSP1	16124	0,39	0,40	0,38	
Tyrosine-protein kinase Lyn	LYN	59079	D2		D2	
<b>(12) Mitochondrial proteins</b>						
ATP-binding cassette sub-family B member 6, mitochondrial	ABCB6	93305	11,79	18,29	5,29	D2
Dihydrolipoyl dehydrogenase, mitochondrial	DLDH	54574	1,00	D2	1,00	D2
Prohibitin	PHB	29859	0,73	0,89	0,57	2,60
Prohibitin-2	PHB2	33292	1,25	2,00	0,50	3,00

Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3	28563	2,12	2,25	1,98	D2
Serine hydroxymethyltransferase	Q5U3Z7	56243	0,37	0,18	0,55	
Cytochrome b-c1 complex subunit 1, mitochondrial	QCR1	53499	0,74	0,86	0,61	
Cytochrome c oxidase subunit 2	COX2	26096	0,93	1,00	0,86	
Voltage-dependent anion-selective channel protein 2	P81155	31746	3,71	3,00	4,43	
Hydroxyacylglutathione hydrolase, mitochondrial	O35952	34109	0,17	D7	0,35	
UMP-CMP kinase 2, mitochondrial	D3ZC63	50113	0,18	0,04	0,33	
ATP synthase subunit alpha, mitochondrial	ATPA	59830	0,78	0,81	0,75	2,00
ATP synthase subunit beta, mitochondrial	ATPB	56318	0,56	0,48	0,64	0,60
ATP synthase subunit delta, mitochondrial	ATPD	17584	0,50	D7	1,00	
ATP synthase subunit gamma, mitochondrial	ATPG	30228	0,15	D7	0,31	
ATP synthase subunit O, mitochondrial	ATPO	23439	0,58	0,67	0,50	
60 kDa HSP mitochondrial	CH60	61088	1,02	1,51	0,53	2,08
ATP-binding cassette, sub-family E (OABP), member 1	D3ZD23	68226	0,33	0,21	0,46	
ATP-binding cassette, sub-family B (MDR/TAP), member 10	Q5FVL8	77688	1,17	D2	1,17	
Coproporphyrinogen-III oxidase, mitochondrial	HEM6	49817	1,14	1,00	1,27	0,95
ADP/ATP translocase 2	ADT2	33108	1,13	1,30	0,95	
Putative uncharacterized protein Cmpk2	D3ZC63	50880	0,16	D7	0,31	
Citrate synthase, mitochondrial	CISY	52175	0,87	0,63	1,10	
Malate dehydrogenase, mitochondrial	MDHM	36116	0,73	0,85	0,62	
2-oxoglutarate dehydrogenase, mitochondrial	ODO1	117418	0,56	0,71	0,40	
Aconitate hydratase, mitochondrial	ACON	86121	0,46	D7	0,91	
Stress-70 protein, mitochondrial	GRP75	74096	0,44	D7	0,88	
Slc25a3 protein	Q6IRH6	40051	1,00	1,25	0,75	
Aldehyde dehydrogenase, mitochondrial	ALDH2	56966	0,73	0,67	0,80	
Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	35272	0,88	1,00	0,75	
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	Q561S0	NDUAA	D7	D7	D7	
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	ODPB	39299	0,50	0,67	0,33	
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A	40044	0,62	0,57	0,67	
<b>(13) Lysosomal proteins</b>						
Lysosomal acid lipase/cholesterol ester hydrolase	LICH	45186	D2	D2	D2	
Lysosome membrane protein 2	SCRB2	54513	D2	D2	D2	D2
LAMP-2	Q6P6W1	45571	2,36	D2	2,36	D2
LAMP-1	LAMP1	44397	9,93	16,50	3,35	D2
V-H+ATPase subunit a2 (ATPase, H+ transporting, lysosomal V0 subunit A2)	Q2I6B1	99118	D2	D2	D2	
ATPase, H transporting, lysosomal V1 subunit G1	B2GUV5	13816	5,23	D2	5,23	D2
ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1	Q5M7T6	40301	7,85	7,41	8,28	
ATPase, H+ transporting, lysosomal accessory protein 1	Q6IRF8	51185	D2	D2	D2	D2
Cytochrome b ascorbate-dependent protein 3	Q5U2W7	28650	D2	D2	D2	
Lysosomal acid phosphatase	PPAL	48320	9,19	9,00	9,38	
Cathepsin B	P00787	37470	D2	D2	D2	
Cathepsin D	P24268	44681	D2	D2	D2	
H(+)/Cl(-) exchange transporter 7	CLCN7	89187	D2	D2	D2	
Tripeptidyl-peptidase 1	TPP1	61332	D2	D2	D2	
V-type proton ATPase 16 kDa proteolipid subunit	VATL	15798	9,00	9,00	D2	
ATP-binding cassette sub-family B member 9	ABC9	84379	D2	D2	D2	D2
<b>(14) Extracellular proteins</b>						
Fibrinogen beta chain	FIBB	54828	D2	D2	D2	D2
Fibrinogen gamma chain	FIBG	51228	D2	D2	D2	D2
Fibronectin	FINC	275990	3,00	3,62	2,39	D2
Fga protein	A1L114	60505	24,65	D2	24,65	
von Willebrand factor (Fragment)	VWF	48394	4,36	6,00	2,72	D2
Serotransferrin	TRFE	78512	11,14	15,76	6,52	19,70
Complement C3	CO3	187825	0,32	D7	0,64	D7
CRAMP (Fragment)	Q71KM5	19536	D2	D2	D2	D2
Cathepsin Z	Q9R1T3	34194	D2	D2	D2	
Neutrophilic granule protein (Predicted)	D3ZY96	19381	2,24	D2	2,24	
Galectin-3-binding protein	O70513	63742	D2	D2	D2	
Lectin, galactoside-binding, soluble, 9	Q6P7Q6	36341	3,56	4,00	3,13	
Alpha-1-macroglobulin	Q63041	167125	D7	D7	D7	
<b>(15) Unknow functions</b>						
LOC683667 protein	B0BNJ1	21952	7,99	D2	7,99	D2
p55 protein	Q5BK33	51343	0,63	0,54	0,73	0,33
Solute carrier family 43, member 1 (Predicted)	B1WBX5	67972	1,82	2,39	1,25	1,63
Small inducible cytokine subfamily E, member 1	Q4G079	34951	0,10	D7	0,21	D7
Glucocorticoid-attenuated response gene 16 product	Q9JTT1	54006	0,27	0,25	0,30	D7
Alpha-2 antiplasmin	Q80ZA3	46493	0,21	D7	0,42	0,21
Putative uncharacterized protein ENSRNOP0000036443	D3ZFH5	106826	0,20	D7	0,41	D7
Serine peptidase inhibitor, Kunitz type 1	Q4V8Q2	58285	D2	D2	D2	D2

**Table S2**

Summary of the proteins identified by MS/MS spectrometry with an increased abundance at D4

Identified protein	Gene	MW	mean ratio					
			Run 1		Run 2		Qstar	
			D2/D4	D4/D7	D2/D4	D4/D7	D2/D4	D4/D7
Solute carrier family 2, facilitated glucose transporter member 3	GTR3	54002	D4	D4	D4	9.50	0.15	D4
Integrin beta	B2RYB8	87955	D4	D4	0.68	1.81	0.22	D4
CD151 antigen	CD151	29192	D4	D4	0.43	D4	D4	D4
Histone H2A type 1	P02262		1,35	4,53	0,31	2,61		
Endoplasmin	Q66HD0	92998	0.26	3.80	0.36	1.86		
Filamin alpha	C0JPT7		0.43	0.94	0.37	2.96		
Protein disulfide-isomerase A3	PDIA3	57043	0.83	2.00	0.38	2.25	1.40	D4
DnaJ homolog subfamily B member 6	Q6AYU3		0.50	D4	0.40	5.00		
Putative uncharacterized protein Itga2b	D3ZAC0		0.41	6.50	0.45	2.40		
Calnexin	P35565		0.37	D4	0.29	2.33		