

SUPPLEMENTAL INFORMATION**MEMBRANE DISRUPTION, BUT NOT METABOLIC REWIRING, IS THE KEY MECHANISM OF ANTICANCER-ACTION OF FASN-INHIBITORS – A MULTI-OMICS ANALYSIS IN OVARIAN CANCER**

Thomas W. Grunt^{1,2,3,*}, Astrid Slany⁴, Mariya Semkova⁴, Ramón Colomer⁵, María Luz López-Rodríguez⁶, Michael Wuczkowski⁷, Renate Wagner^{1,2}, Christopher Gerner⁴, Gerald Stübiger^{2,7}

¹Cell Signaling & Metabolism Networks Program, Division of Oncology, Department of Medicine I, Medical University of Vienna, Austria; ²Comprehensive Cancer Center, Vienna, Austria; ³Ludwig Boltzmann Institute for Hematology & Oncology, Vienna, Austria; ⁴Department of Analytical Chemistry, University of Vienna, Austria; ⁵Department of Medical Oncology, Hospital Universitario La Princesa and Spanish National Cancer Research Centre (CNIO), Clinical Research Program, Madrid, Spain; ⁶Departamento de Química Orgánica I, Facultad de Ciencias Químicas, Universidad Complutense de Madrid, Spain; ⁷Department of Biomedical Imaging & Image-guided Therapy, Medical University of Vienna, Austria

*Corresponding author: Thomas W. Grunt, Division of Oncology, Department of Medicine I, Medical University of Vienna, Waehringer Guertel 18 – 20, A-1090 Vienna, Austria; P: +43 (0)1 40400-54570, F: +43 (0)1 40400-54650, Email: thomas.grunt@meduniwien.ac.at

SUPPLEMENTAL FIGURE LEGENDS

Supplemental Figure S1. Influence of FASN-inhibition on total amount of lipids per cell in (a) SKOV3 and (b) OVCAR3 cells, and (c) scheme of the action of FASN in *de novo* lipogenesis and the synthesis of the major cellular lipid classes. Relative change of total cellular lipids in (a) SKOV3 and (b) OVCAR3 cells upon G28UCM treatment (20 μ M, 72 hours). A decrease of 60% (SKOV3) to >80% (OVCAR3) in cell number and of about 30% lipid content was observed compared to cells grown in 0.1% DMSO. (c) Palmitate (16:0) as the primary reaction product of FASN is further processed to acyl-CoA via several steps of elongation and desaturation leading to fatty acids with different carbon chain-lengths and number of double bonds. These fatty acids are then esterified to cholesterol or glycerol to generate cholesterol ester (CE), triacylglycerol (TAG), diacylglycerol (DAG) and phospholipids (PL) as the major structural (e.g. membrane), signalling and storage lipid classes.

Supplemental Figure S2. Representative MALDI mass spectra of lipid extracts of untreated and G28UCM treated SKOV3 (a, b) and OVCAR3 (c, d) recorded in positive (a, c) and negative (b, d) ionization mode at 8 hours and 24 hours. Phospholipid class specific internal standards (indicated by asterisks) were added to the samples for semiquantitative analysis of the corresponding lipid species. Abbreviations: LPC, lysophosphatidylcholine; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PS, phosphatidylserine

Supplemental Figure S3. Reproducibility of glycerophospholipid analysis by MALDI-MS. Six individual control cell culture samples were prepared according to the lipid extraction and MS analysis protocols described in Material and Methods. In (a) the data from the independent analysis of the lipid extracts displaying the relative abundances of the sum of individual lipid species relative to class specific internal standards (Ratio vs. Int. Std.) are displayed and in (b) their means $\pm$ SD are shown. Numbers above the error bars indicate the coefficient of variation (CV %). Abbreviations: CL, cardiolipin; LPC, lysophosphatidylcholine; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PS, phosphatidylserine; SM, sphingomyelin.

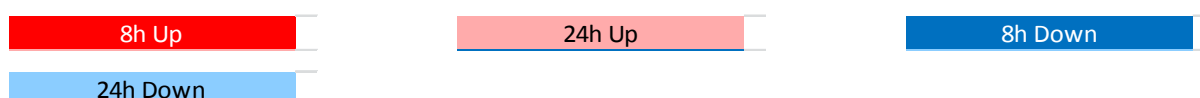
Supplemental Figure S4. Effects of FASN-inhibition on the phosphatidylcholine (PC) composition of SKOV3 and OVCAR3 cells. Changes in the relative composition of PC species containing fatty acid residues with 0-2 total double bonds (DBs) in (a) SKOV3 and (b) OVCAR3 cells treated with 0.1% DMSO and 40 μ M G28UCM for 8 hours and 24 hours. Displayed is the relative composition of PC

species with 0-2 DBs in % of total PC. Values are means $\pm$ SD (n = 3). Letter code of the fatty acid residues: L, linoleate (18:2); O, oleate (18:1); P, palmitate (16:0); S, stearate (18:0).

SUPPLEMENTAL TABLE LEGENDS

Supplemental Table S1: Reproducibility analysis of biological and technical replicates of SKOV3 samples. Glycerophospholipids were quantitatively measured by LC-ESI-MS/MS according to the AbsoluteIDQ p180 kit (see Material and Methods). Samples of three independent cell cultures (biological replica) treated with 0.1% DMSO (control) or 40 μ M G28UCM for 8 hours and 24 hours were measured two times each (technical replica). From that the standard deviation (SD) and coefficient of variation (CV) for the individual lipid species were calculated.

Supplemental Table S2: Shotgun proteomic analysis of SKOV3 (a) and OVCAR3 (b) cells exposed for 8 hours and 24 hours to 40 μ M G28UCM. All proteins identified by MS/MS. Colour Code:

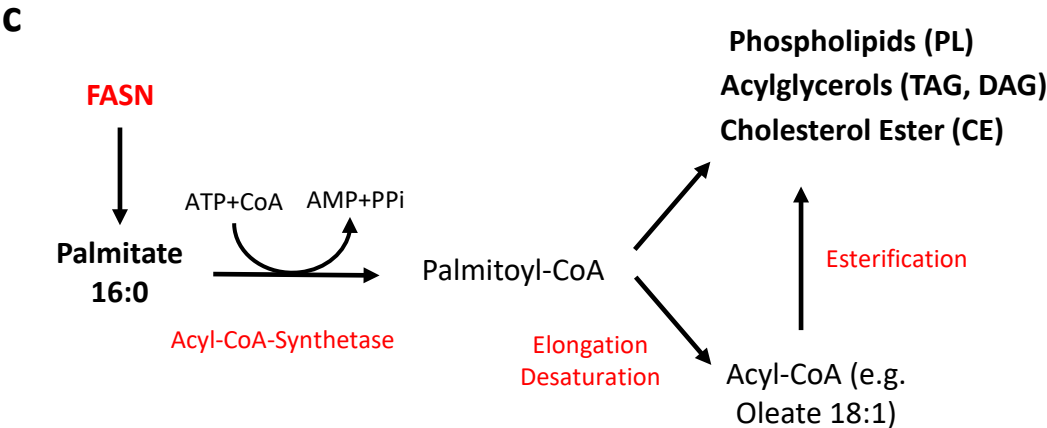
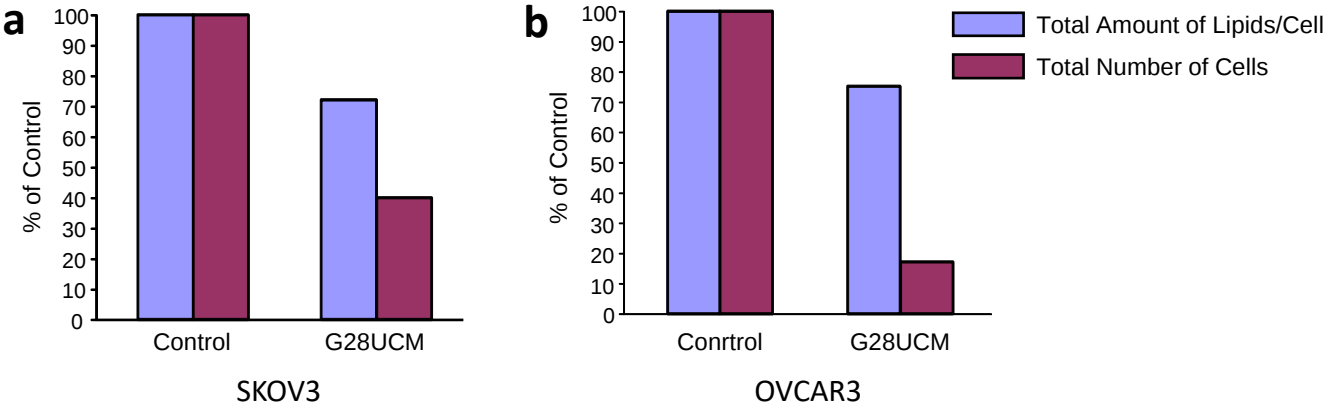


Supplemental Table S3: DAVID-assisted shotgun proteomic analysis of key cell processes in SKOV3 and OVCAR3 cells exposed to 40 μ M G28UCM using BioCarta and KEGG databases.

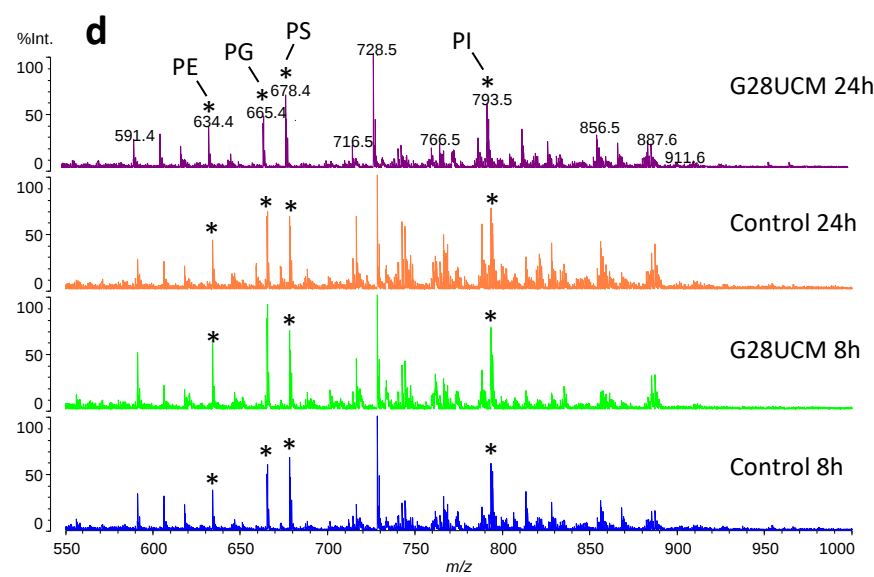
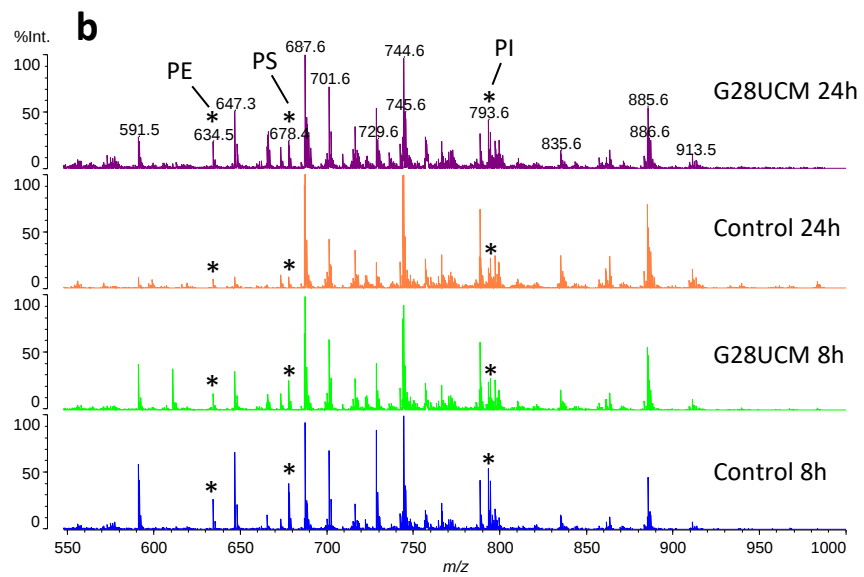
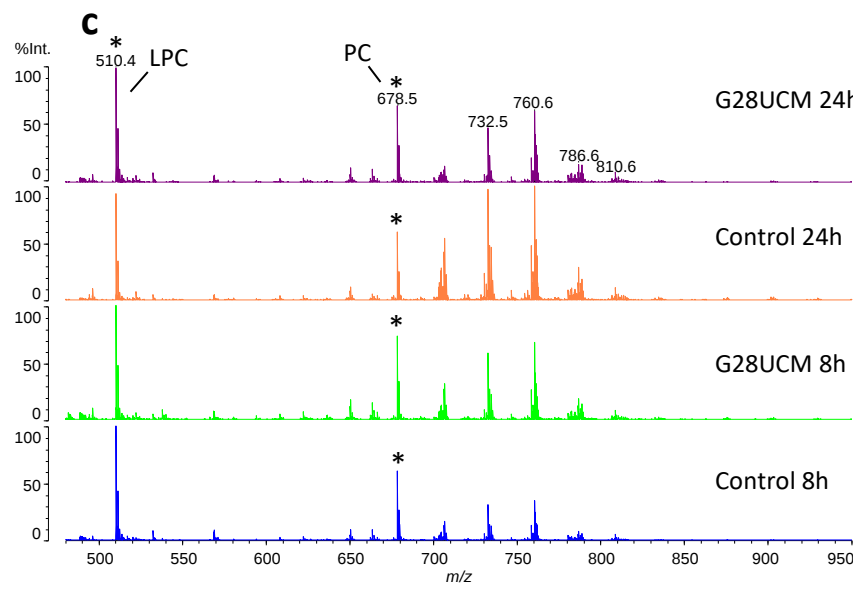
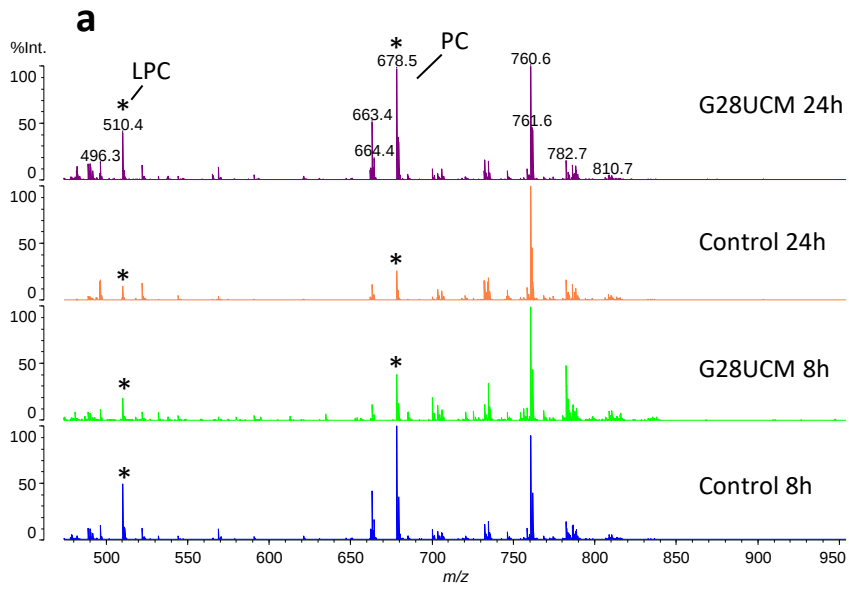
Legend				
Significantly (p < 0.05) downregulated proteins: Blue cell				Blue
Significantly (p < 0.05) upregulated proteins: Red cell				Red
For Individual Proteins				
SKOV3/OVCAR3 Matching Score:				
1,00: uniform regulation at the same time in both cell lines.				
0,00: no uniform regulation in both cell lines at the specific time.				
For Key Cell Processes or Sub-Processes				
Mean SKOV3/OVCAR3 Matching Score:				
Mean of 'Individual Protein SKOV3/OVCAR3 Matching Scores'				

Supplemental Table S4: Summary of all down- (< 50 % of Control) and up-regulated (> 150 % of Control) phosphoproteins as determined by antibody microarray kinomic analysis in SKOV3 (a) and OVCAR3 (b) cells exposed for 24 hours to 40 μ M G28UCM.

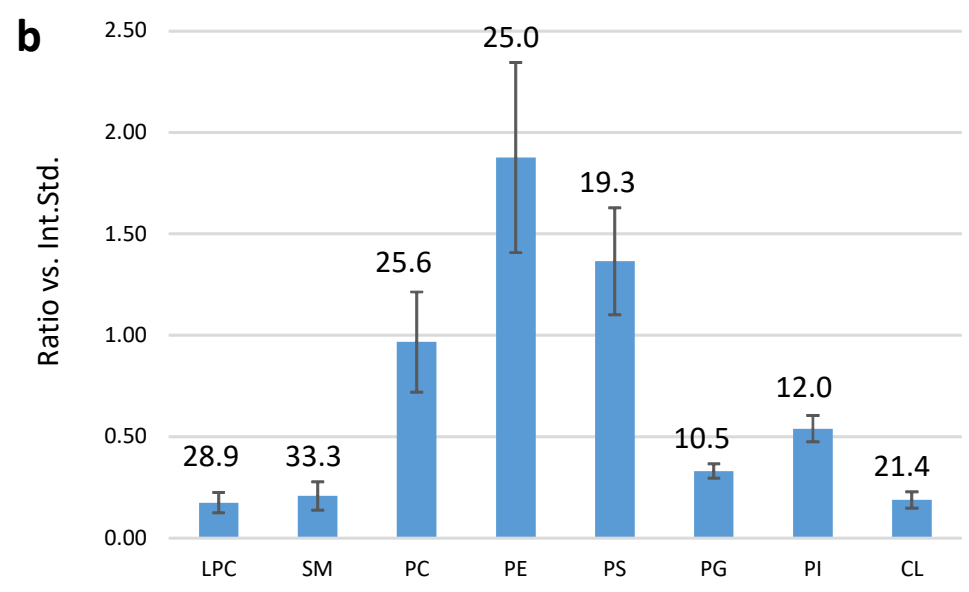
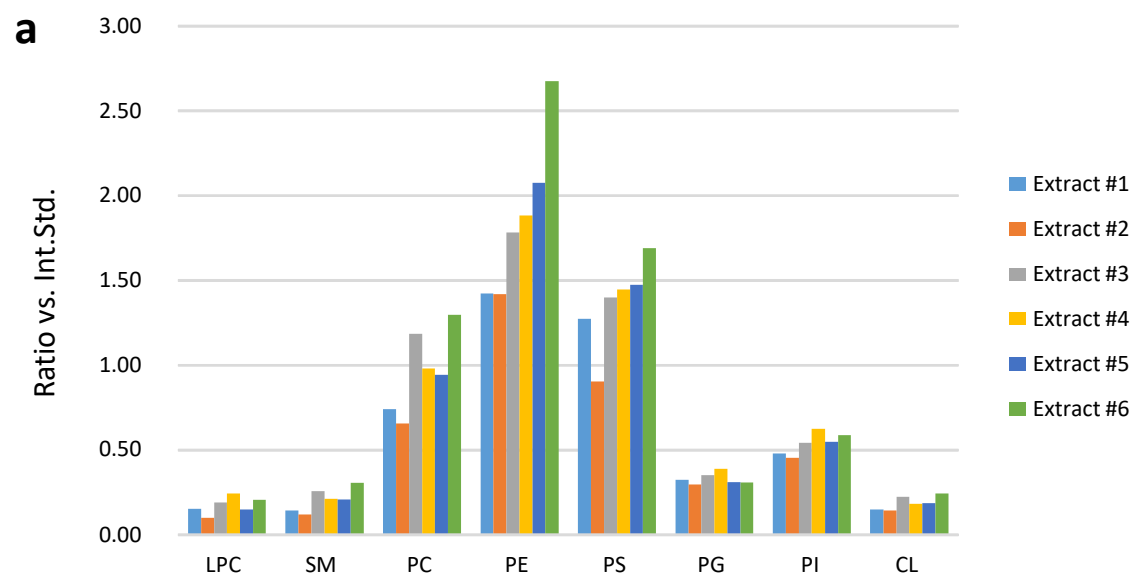
Supplemental Figure S1



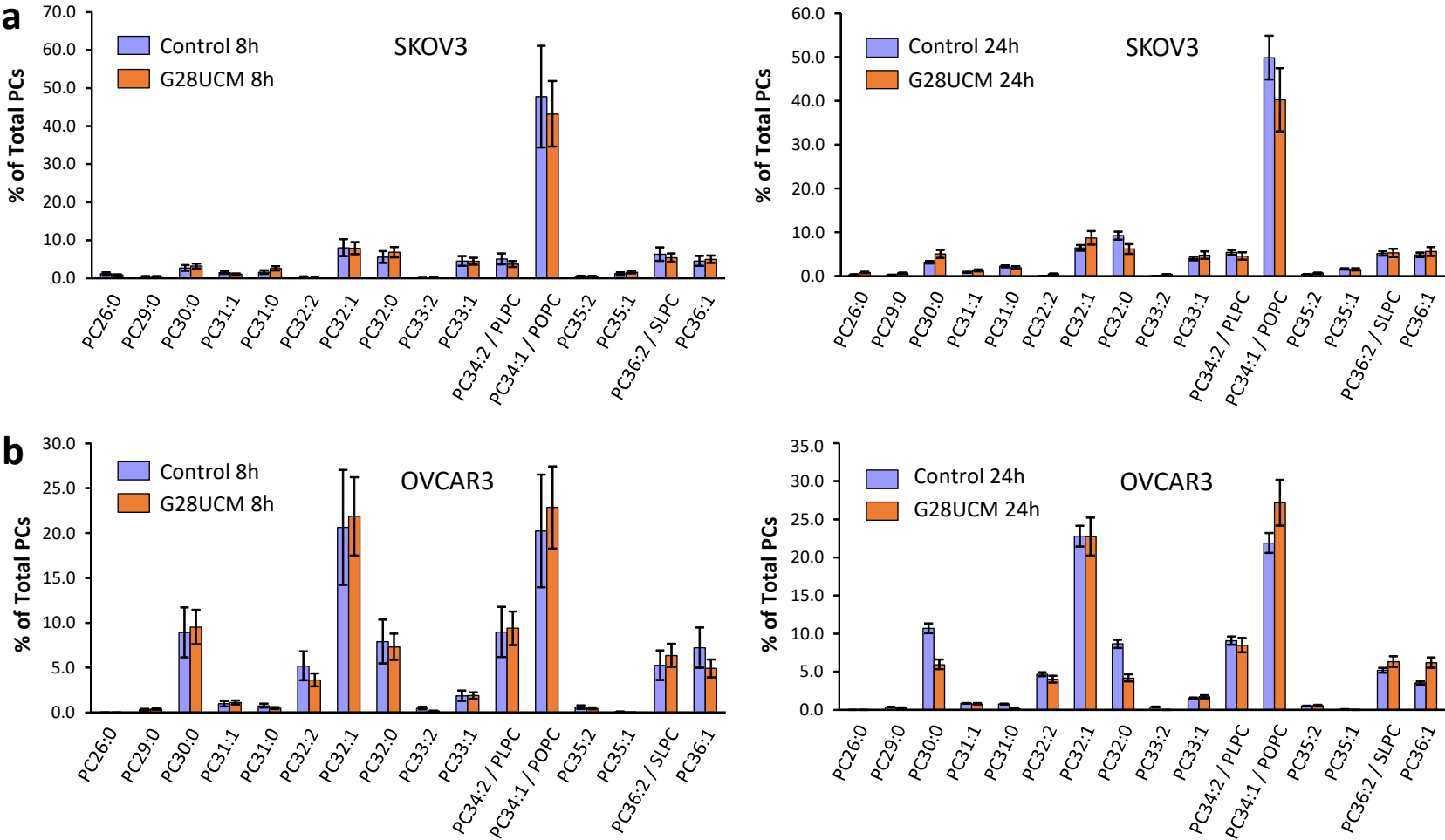
Supplemental Figure S2



Supplemental Figure S3



Supplemental Figure S4



Supplemental Table S1: Reproducibility analysis of biological and technical replicates of SKOV3 samples

8h samples	1 - SKOV con1 8h control	2 - SKOV con2 8h control	3 - SKOV con3 8h control	4 - SKOV FASN1 8h G28UCM	5 - SKOV FASN2 8h G28UCM
lysoPC a C14:0	8,07	9,2	7,75	8,44	11
lysoPC a C16:0	8,33	6,65	9,39	6,52	10,3
lysoPC a C16:1	14,6	19	17,7	15,8	23,6
lysoPC a C17:0	0,622	0,569	0,678	0,503	0,62
lysoPC a C18:0	1,48	0,836	1,71	0,993	1,59
lysoPC a C18:1	50,1	39,3	49,7	43,3	61,6
lysoPC a C18:2	4,7	5,25	5,01	4,45	7,22
lysoPC a C20:3	1,99	1,64	1,97	1,74	2,69
lysoPC a C20:4	4,42	4,87	5,25	3,56	5,07
lysoPC a C24:0	0,852	0,904	1,37	0,689	0,963
lysoPC a C26:0	1,69	1,56	2,83	1,65	2,27
lysoPC a C26:1	0,422	0,373	0,656	0,351	0,418
lysoPC a C28:0	2,22	1,23	2,53	1,31	2,02
lysoPC a C28:1	0,988	0,812	1,37	0,848	1,15
PC aa C24:0	0,269	0,483	0,459	0,309	0,476
PC aa C26:0	1,94	2,36	2,83	2,2	3,24
PC aa C28:1	1,18	1,47	1,69	1,1	1,73
PC aa C30:0	11,9	9,38	13,2	10,9	12,1
PC aa C30:2	0,147	0,164	0,35	0,16	0,359
PC aa C32:0	29,8	16,4	37	23,4	19,4
PC aa C32:1	79,2	45,6	97,5	58,3	88,2
PC aa C32:2	5,71	3,41	7,74	3,82	5,89
PC aa C32:3	0,339	0,296	0,558	0,235	0,362
PC aa C34:1	285	163	343	224	305
PC aa C34:2	47,6	28,9	61,8	34,5	54,6
PC aa C34:3	3,41	2,01	4,39	2,31	3,67
PC aa C34:4	0,452	0,281	0,511	0,274	0,406
PC aa C36:0	2,51	1,57	3,16	2,02	2,69
PC aa C36:1	33,6	16,8	33,9	30,1	28
PC aa C36:2	75,8	46,9	102	65	93,5
PC aa C36:3	14,9	8,83	18,4	11,7	18,5

Supplemental Table S1

PC aa C36:4	9,44	5,08	10,9	5,89	9,37
PC aa C36:5	3,36	1,99	4,02	2,27	3,67
PC aa C36:6	0,524	0,37	0,569	0,371	0,494
PC aa C38:0	3	2,1	4,2	2,51	3,73
PC aa C38:1	1,39	0,71	1,39	1,4	1,12
PC aa C38:3	6,49	3,35	7,97	5,17	6,51
PC aa C38:4	10,5	6,09	12,4	8,18	11,9
PC aa C38:5	13,4	7,93	16,7	10,2	16,5
PC aa C38:6	6,14	3,44	7,17	4,52	7,16
PC aa C40:1	0,417	0,297	0,523	0,392	0,412
PC aa C40:2	0,654	0,437	0,963	0,722	0,689
PC aa C40:3	0,648	0,374	0,922	0,635	0,613
PC aa C40:4	0,982	0,519	1,19	0,865	1,06
PC aa C40:5	3,08	1,7	3,52	2,36	2,97
PC aa C40:6	6,33	3,77	7,53	4,97	7,35
PC aa C42:0	0,138	0,116	0,201	0,118	0,138
PC aa C42:1	0,122	0,082	0,18	0,13	0,127
PC aa C42:2	0,249	0,153	0,339	0,22	0,245
PC aa C42:4	0,233	0,17	0,301	0,178	0,218
PC aa C42:5	0,255	0,147	0,331	0,217	0,285
PC aa C42:6	0,501	0,374	0,624	0,44	0,479
PC ae C30:0	6,36	5,67	7,72	6,02	7,19
PC ae C30:1	2,83	2,57	3,19	2,42	3,22
PC ae C30:2	0,29	0,312	0,348	0,234	0,342
PC ae C32:1	47,5	27,8	61,6	39,2	53
PC ae C32:2	8,32	4,74	10,7	6,25	10,2
PC ae C34:0	4,27	1,8	4,12	3,29	2,85
PC ae C34:1	67,6	36,9	83,3	53,2	69,7
PC ae C34:2	24,7	13,3	28,7	19	27,4
PC ae C34:3	2,5	1,46	2,83	1,8	2,9
PC ae C36:0	2,17	1,41	3,07	1,87	1,78
PC ae C36:1	16,3	8,23	18,8	14,9	14,9
PC ae C36:2	16,2	9,5	20,5	14,1	18,9
PC ae C36:3	10,3	5,59	12,4	8,63	12,2
PC ae C36:4	11,9	7	14,6	8,57	13,5
PC ae C36:5	5,64	3,37	6,41	3,94	6,18
PC ae C38:0	0,98	0,662	1,14	0,867	1,1

Supplemental Table S1

PC ae C38:1	3,07	1,54	3,74	3,15	2,8
PC ae C38:2	4,52	2,46	6	4,56	5,22
PC ae C38:3	3,45	1,77	4,29	2,96	3,74
PC ae C38:4	6,6	3,78	8	5,45	7,32
PC ae C38:5	12,9	7,75	16,2	10,4	15
PC ae C38:6	9,33	5,42	11,2	7,09	10,3
PC ae C40:1	0,995	0,667	1,03	0,771	1,04
PC ae C40:2	0,945	0,419	1,09	0,845	0,918
PC ae C40:3	1,07	0,543	1,41	1,02	1
PC ae C40:4	1,53	0,873	1,91	1,28	1,44
PC ae C40:5	3,65	1,99	4,35	3,13	3,89
PC ae C40:6	4,52	2,52	5,61	3,86	5,5
PC ae C42:0	0,838	0,579	0,889	0,748	0,757
PC ae C42:1	0,486	0,251	0,523	0,34	0,513
PC ae C42:2	0,632	0,419	0,803	0,468	0,687
PC ae C42:3	0,746	0,474	0,827	0,456	0,761
PC ae C42:4	0,261	0,174	0,367	0,257	0,306
PC ae C42:5	0,875	0,544	1,01	0,815	0,893
PC ae C44:3	0,248	0,191	0,272	0,15	0,23
PC ae C44:4	0,234	0,153	0,318	0,207	0,272
PC ae C44:5	0,23	0,144	0,255	0,196	0,242
PC ae C44:6	0,153	0,106	0,186	0,166	0,163

24h samples

	7 - SKOV con1 24h control	8 - SKOV con2 24h control	9 - SKOV con3 24h control	10 - SKOV FASN1 24h G28UCM	11 - SKOV FASN2 24h G28UCM
lysoPC a C14:0	10,3	10,8	10,6	12	9,18
lysoPC a C16:0	12,1	13,6	12,5	10,2	7,92
lysoPC a C16:1	21	23,9	23,2	23,5	21,7
lysoPC a C17:0	0,603	0,609	0,608	0,718	0,547
lysoPC a C18:0	2,16	1,87	1,71	1,38	0,933
lysoPC a C18:1	57,2	59,9	56,8	62	58

Supplemental Table S1

lysoPC a C18:2	5,03	6,03	5,69	6,79	6,39
lysoPC a C20:3	2,32	2,51	2,38	2,09	2,15
lysoPC a C20:4	4,84	5,46	5,16	3,99	3,63
lysoPC a C24:0	1,87	1,61	1,53	0,93	0,948
lysoPC a C26:0	3,57	3,1	3,15	2,07	2,31
lysoPC a C26:1	0,745	0,672	0,742	0,533	0,567
lysoPC a C28:0	3,08	2,6	2,65	2,42	1,9
lysoPC a C28:1	1,63	1,33	1,4	1,26	1,36
PC aa C24:0	0,532	0,64	0,715	0,322	0,46
PC aa C26:0	3,93	3,68	4,03	2,31	3,67
PC aa C28:1	1,97	2	2,11	1,5	2,01
PC aa C30:0	17,1	17,8	17,2	14,5	12,4
PC aa C30:2	0,428	0,361	0,373	0,359	0,466
PC aa C32:0	36,7	39,3	32,9	27,9	16,6
PC aa C32:1	96,2	106	95,8	88,1	68,6
PC aa C32:2	7,81	8,73	7,52	5,47	5,01
PC aa C32:3	0,543	0,556	0,567	0,37	0,326
PC aa C34:1	305	329	318	304	228
PC aa C34:2	57,6	66,3	59,7	49	44,8
PC aa C34:3	4,24	4,83	4,28	2,95	2,79
PC aa C34:4	0,466	0,528	0,511	0,331	0,293
PC aa C36:0	3,01	3,34	3,01	3,06	2,12
PC aa C36:1	29,7	27,3	26	27,5	18,7
PC aa C36:2	91,1	98	91,1	82,4	75,8
PC aa C36:3	16,6	18,6	16,8	14,9	13
PC aa C36:4	9,81	12	10,5	6,97	5,67
PC aa C36:5	3,05	3,47	3,13	2,65	2,16
PC aa C36:6	0,392	0,487	0,51	0,408	0,379
PC aa C38:0	4,44	4,63	4,5	4,26	3,68
PC aa C38:1	1,67	1,6	1,55	1,33	1,07
PC aa C38:3	7,58	8,29	7,58	5,77	5,22
PC aa C38:4	8,8	9,95	8,99	7,6	6,8
PC aa C38:5	11,2	11,7	10,9	9,65	7,93
PC aa C38:6	5,53	6,23	5,67	4,78	3,85
PC aa C40:1	0,578	0,441	0,529	0,473	0,463
PC aa C40:2	1,08	0,973	0,96	0,737	0,726
PC aa C40:3	1,01	0,989	0,881	0,622	0,614

Supplemental Table S1

PC aa C40:4	1,14	1,17	1,09	0,875	0,782
PC aa C40:5	2,57	2,56	2,31	2,14	1,8
PC aa C40:6	4,39	4,46	4,16	4,28	3,86
PC aa C42:0	0,192	0,179	0,197	0,149	0,131
PC aa C42:1	0,188	0,202	0,185	0,11	0,075
PC aa C42:2	0,355	0,336	0,317	0,251	0,237
PC aa C42:4	0,326	0,307	0,318	0,294	0,252
PC aa C42:5	0,283	0,283	0,288	0,209	0,171
PC aa C42:6	0,494	0,582	0,504	0,434	0,391
PC ae C30:0	10,3	9,09	9,52	9,63	7,48
PC ae C30:1	4,34	3,98	4,08	4,13	3,74
PC ae C30:2	0,456	0,473	0,455	0,341	0,464
PC ae C32:1	65,6	67,8	62,1	64,2	49,4
PC ae C32:2	11,8	13,3	12,6	11,2	9,22
PC ae C34:0	4,44	4,29	4,21	3,67	2,59
PC ae C34:1	86	90	82,2	82,8	58,1
PC ae C34:2	31,3	34,7	32,1	29,9	23,5
PC ae C34:3	3,32	3,88	3,51	3,11	2,52
PC ae C36:0	2,14	1,7	1,69	2,27	1,59
PC ae C36:1	21,2	20,1	19,2	18,5	13,1
PC ae C36:2	23,2	24,6	23	21,3	19,2
PC ae C36:3	14,9	15,2	14,8	13,3	11,4
PC ae C36:4	16,7	17,9	17	14,2	12
PC ae C36:5	7,22	7,7	7,46	6,52	5,19
PC ae C38:0	0,868	0,836	0,738	0,834	0,614
PC ae C38:1	4,8	4,16	4,07	3,13	2,65
PC ae C38:2	7,08	6,96	6,51	5,37	4,65
PC ae C38:3	5,54	5,79	5,33	4,17	3,33
PC ae C38:4	9,7	9,95	9,02	8,2	7,06
PC ae C38:5	18,7	19,8	18,7	17,6	14,4
PC ae C38:6	12,8	13,6	12,9	11,7	9,65
PC ae C40:1	0,912	0,786	0,786	0,467	0,484
PC ae C40:2	1,56	1,45	1,36	0,898	0,781
PC ae C40:3	1,72	1,5	1,49	1,25	0,945
PC ae C40:4	2,22	2,26	2,03	1,69	1,4
PC ae C40:5	5,06	5,07	4,66	4,42	3,78
PC ae C40:6	6,82	6,96	6,59	6,34	5,42

Supplemental Table S1

PC ae C42:0	0,684	0,658	0,668	0,674	0,544
PC ae C42:1	0,303	0,276	0,288	0,242	0,182
PC ae C42:2	0,308	0,308	0,249	0,199	0,216
PC ae C42:3	0,397	0,465	0,438	0,254	0,258
PC ae C42:4	0,408	0,373	0,372	0,215	0,193
PC ae C42:5	1,17	1,05	1,02	0,88	0,782
PC ae C44:3	0,136	0,154	0,184	0,091	0,102
PC ae C44:4	0,157	0,174	0,142	0,112	0,112
PC ae C44:5	0,238	0,201	0,253	0,14	0,142
PC ae C44:6	0,254	0,207	0,191	0,169	0,145

Supplemental Table S1

6 - SKOV FASN3 8h G28UCM	1 - SKOV con1 8h repl control	2 - SKOV con2 8h repl control	3 - SKOV con3 8h repl control	4 - SKOV FASN1 8h repl G28UCM	
	12,8	13,3	9,06	6,85	6,92
	11,9	12,7	6,79	10,6	6,32
	27,4	23,2	20,3	16,5	12,5
	0,672	0,728	0,568	0,568	0,444
	2,22	2,69	1,15	1,72	1,18
	67,7	65,9	41,7	52,9	39,3
	9,11	7,31	5,74	4,46	3,95
	3,3	2,76	1,95	2,13	1,66
	6,44	6,03	5,31	5,02	3,22
	1,49	1,24	0,937	1,12	0,798
	3,22	2,67	1,79	2,35	1,84
	0,738	0,648	0,451	0,638	0,387
	2,91	2,43	1,65	2,73	1,38
	1,52	1,1	0,939	1,43	0,826
	0,778	0,651	0,464	0,305	0,356
	4,26	4,42	2,57	2,19	2,21
	1,89	1,84	1,49	1,49	1,14
	12,1	12,3	8,55	13,2	10,4
	0,294	0,197	0,173	0,32	0,203
	16,5	21,8	14,7	32,3	18,1
	65,8	64,9	48,7	102	49,1
	3,86	4,35	3,77	8,48	3,12
	0,283	0,339	0,288	0,521	0,171
	241	249	168	334	201
	41,4	44,4	31,2	64	30,2
	2,73	2,8	2,28	4,54	1,91
	0,356	0,371	0,295	0,481	0,252
	2,08	2,29	1,64	2,88	1,67
	24,3	27,1	15,2	33,4	25,8
	61,8	68,9	46,8	97,3	58,7
	13,2	13,7	9,14	18,5	10,6

Supplemental Table S1

7,91	8,43	5,44	11,3	5,09
3,21	3,07	2,13	3,82	1,89
0,411	0,384	0,304	0,565	0,241
2,4	2,96	2,02	3,72	2,3
1,12	1,37	0,719	1,4	1
4,84	6,22	3,38	7,55	4,71
8,5	10,2	5,77	12	7,2
11,3	12,6	8,52	16	8,71
5,61	5,96	3,9	6,91	3,74
0,381	0,412	0,343	0,437	0,408
0,484	0,653	0,368	0,808	0,618
0,479	0,675	0,391	0,83	0,54
0,75	0,985	0,592	1,14	0,753
2,08	2,91	1,55	3,3	2,22
5,07	5,91	3,71	6,92	4,44
0,114	0,156	0,105	0,152	0,117
0,125	0,146	0,082	0,153	0,12
0,215	0,262	0,157	0,276	0,217
0,175	0,18	0,127	0,236	0,162
0,19	0,251	0,116	0,314	0,212
0,495	0,485	0,326	0,524	0,407
7,22	6,46	5,14	7,6	5,83
3,56	3,35	2,41	3,21	2,43
0,407	0,418	0,27	0,329	0,239
40,2	39,4	29,2	61,4	33,3
7,6	7,31	5,41	11,2	5
2,25	3,41	1,75	3,88	2,57
55,1	56,7	36,5	85,2	49,2
21	21,8	13,5	31,5	16,5
2,26	2,43	1,58	3,22	1,55
1,17	1,7	1,06	2,06	1,71
12,9	14	8,36	19,7	13,5
14,2	14,8	9,33	21,7	12,7
8,85	9,63	5,81	12,7	7,39
10,2	11,2	7,56	14,5	7,58
4,85	5,09	3,72	6,94	3,16
0,806	0,858	0,625	1,06	0,695

Supplemental Table S1

2,16	3,31	1,38	3,65	2,9
3,41	4,75	2,41	6,12	4,1
2,66	3,28	1,87	4,5	2,8
5,23	6,17	3,62	8,22	4,68
10,3	12,1	8,36	16	9,06
7,6	8,6	5,87	11,2	5,93
0,823	1,03	0,604	1,03	0,701
0,722	1,03	0,459	1,16	0,866
0,803	1,03	0,511	1,38	0,892
1,12	1,53	0,786	1,73	1,21
2,73	3,63	1,86	4,25	2,8
3,74	4,59	2,68	5,7	3,51
0,609	0,718	0,557	0,832	0,591
0,439	0,41	0,262	0,514	0,336
0,506	0,618	0,408	0,708	0,413
0,638	0,726	0,475	0,739	0,428
0,253	0,365	0,124	0,354	0,228
0,705	0,915	0,563	0,947	0,754
0,282	0,278	0,169	0,263	0,135
0,256	0,257	0,148	0,253	0,176
0,197	0,241	0,166	0,23	0,191
0,165	0,171	0,071	0,175	0,135

12 - SKOV FASN3 24h G28UCM	7 - SKOV con1 24h repl control	8 - SKOV con2 24h repl control	9 - SKOV con3 24h repl control	10 - SKOV FASN1 24h rep G28UCM	
10,7	11,5	17,2	14	13,4	
8,55	14,7	17,7	15,4	11,1	
18,4	24,1	31	27,2	23,9	
0,479	0,629	0,657	0,62	0,517	
1,16	2,44	2,53	2,46	1,57	
46,5	66,1	72,5	61,5	66,6	

Supplemental Table S1

5,44	5,81	7	6,48	7,18
1,67	2,53	2,78	2,57	2,24
3,07	5,59	6,29	5,56	4,06
1,02	1,53	1,6	1,62	1,02
2,31	3,51	3,5	3,23	2,3
0,437	0,601	0,733	0,66	0,496
2,12	3,31	2,49	2,58	2,24
1,18	1,46	1,37	1,3	1,1
0,315	0,849	0,741	0,773	0,379
2,56	4,5	4,79	4,57	2,83
1,47	1,82	2,31	2,08	1,49
10,1	19,8	19,3	17,4	12,7
0,278	0,434	0,408	0,532	0,245
13,7	44,6	39,9	36,2	15,5
72,4	121	108	96,4	73,7
4,42	10,1	8,41	7,55	4,5
0,307	0,641	0,559	0,58	0,351
238	390	368	316	268
41,4	75,4	66,5	62,2	43,8
2,56	5,82	4,77	4,32	2,73
0,269	0,617	0,516	0,494	0,303
2,29	3,71	3,3	3,1	2,29
15,3	37,8	27,9	26	22
66,2	118	102	92	74,5
12,1	22,7	18,9	17,4	13
5,66	13,3	11,7	11	6,14
2,12	4,15	3,33	3,73	2,22
0,297	0,6	0,479	0,519	0,358
3,14	5,43	4,61	4,58	3,62
0,792	2,09	1,79	1,5	1,17
4,41	10	8,49	7,78	5,4
6,15	11,4	9,77	9,42	6,9
7,4	14,9	12,6	12,7	8,31
3,72	7,36	6,2	6,44	4,31
0,277	0,66	0,498	0,508	0,386
0,573	1,29	1,01	0,868	0,828
0,478	1,21	0,994	0,88	0,612

Supplemental Table S1

0,567	1,43	1,16	1,07	0,721
1,55	3,29	2,72	2,64	1,98
3,25	5,24	4,62	4,73	3,71
0,104	0,224	0,156	0,21	0,133
0,066	0,231	0,194	0,157	0,084
0,215	0,37	0,294	0,324	0,289
0,196	0,415	0,296	0,269	0,256
0,15	0,441	0,309	0,296	0,201
0,307	0,637	0,592	0,587	0,389
6,83	11,2	10,2	9,41	8,08
3,3	4,68	4,11	3,97	3,74
0,357	0,524	0,458	0,488	0,409
50,1	80,3	70,1	62,6	55
9,12	15,2	13,2	11,8	10,1
2,17	5,57	4,39	4,3	3,05
60,4	110	95,9	82,3	68,5
23,5	40,3	35,6	30,9	27,5
2,48	4,47	3,92	3,48	2,75
1,3	2,5	1,67	1,72	1,61
11,4	26,7	22,3	18,9	14,6
16,2	29,7	25,6	22,5	19,1
10,4	18,8	16,6	14,3	11,9
11,3	21,5	18,8	16,5	12,9
5,11	9,15	8,07	7,27	5,59
0,499	1,14	0,912	0,936	0,621
1,85	5,69	4,25	4,02	2,71
3,79	8,76	7,3	6,72	4,81
3,08	7,06	6,01	5,3	3,75
6,19	12,1	10,4	9,52	7,53
13,1	23,4	20,2	18,3	15
8,98	16,3	14,4	12,9	10,6
0,312	1,03	0,899	0,843	0,474
0,593	1,74	1,44	1,39	0,83
0,757	2,03	1,65	1,48	0,964
1,19	2,7	2,34	2	1,47
3,18	6,1	5,19	4,88	4,04
4,92	8,27	7,27	6,48	5,56

Supplemental Table S1

0,547	0,761	0,72	0,677	0,573
0,175	0,37	0,302	0,289	0,189
0,158	0,406	0,31	0,277	0,186
0,171	0,587	0,489	0,459	0,275
0,16	0,491	0,431	0,371	0,206
0,636	1,23	1,07	1,09	0,82
0,08	0,242	0,243	0,169	0,099
0,106	0,209	0,153	0,157	0,113
0,105	0,316	0,242	0,212	0,139
0,099	0,351	0,249	0,247	0,118

Supplemental Table S1

Biological replica:			3 independent cell cultures			
5 - SKOV FASN2 8h repl	6 - SKOV FASN3 8h repl		SKOV cont 8h	SKOV cont repl		
G28UCM	G28UCM		control	8h		SKOV G28UCM 8h
				control	G28UCM	
	9,91	9,48	lysoPC a C14:0	8,34	9,74	10,75
	9,39	8,44	lysoPC a C16:0	8,12	10,03	9,57
	22,9	19,9	lysoPC a C16:1	17,10	20,00	22,27
	0,604	0,573	lysoPC a C17:0	0,62	0,62	0,60
	1,2	1,55	lysoPC a C18:0	1,34	1,85	1,60
	62,2	51,7	lysoPC a C18:1	46,37	53,50	57,53
	7,2	6,14	lysoPC a C18:2	4,99	5,84	6,93
	2,59	2,08	lysoPC a C20:3	1,87	2,28	2,58
	5,23	4,76	lysoPC a C20:4	4,85	5,45	5,02
	1,03	0,989	lysoPC a C24:0	1,04	1,10	1,05
	2,21	2,21	lysoPC a C26:0	2,03	2,27	2,38
	0,58	0,489	lysoPC a C26:1	0,48	0,58	0,50
	1,99	2,66	lysoPC a C28:0	1,99	2,27	2,08
	1,1	1,36	lysoPC a C28:1	1,06	1,16	1,17
	0,507	0,394	PC aa C24:0	0,40	0,47	0,52
	3,56	2,83	PC aa C26:0	2,38	3,06	3,23
	2	1,52	PC aa C28:1	1,45	1,61	1,57
	12,6	11,9	PC aa C30:0	11,49	11,35	11,70
	0,414	0,338	PC aa C30:2	0,22	0,23	0,27
	14,1	19,6	PC aa C32:0	27,73	22,93	19,77
	86,2	87,1	PC aa C32:1	74,10	71,87	70,77
	5,17	5,41	PC aa C32:2	5,62	5,53	4,52
	0,356	0,38	PC aa C32:3	0,40	0,38	0,29
	302	315	PC aa C34:1	263,67	250,33	256,67
	52,1	50,8	PC aa C34:2	46,10	46,53	43,50
	3,33	3,36	PC aa C34:3	3,27	3,21	2,90
	0,431	0,398	PC aa C34:4	0,41	0,38	0,35
	2,35	2,68	PC aa C36:0	2,41	2,27	2,26
	26,4	27,9	PC aa C36:1	28,10	25,23	27,47
	91	82	PC aa C36:2	74,90	71,00	73,43
	17	17,1	PC aa C36:3	14,04	13,78	14,47

Supplemental Table S1

8,91	8,97	PC aa C36:4	8,47	8,39	7,72
3,26	3,61	PC aa C36:5	3,12	3,01	3,05
0,459	0,569	PC aa C36:6	0,49	0,42	0,43
3,42	3,56	PC aa C38:0	3,10	2,90	2,88
1,21	1,05	PC aa C38:1	1,16	1,16	1,21
6,7	6,07	PC aa C38:3	5,94	5,72	5,51
11,1	11,1	PC aa C38:4	9,66	9,32	9,53
14,4	15,6	PC aa C38:5	12,68	12,37	12,67
6,21	6,68	PC aa C38:6	5,58	5,59	5,76
0,404	0,385	PC aa C40:1	0,41	0,40	0,40
0,699	0,598	PC aa C40:2	0,68	0,61	0,63
0,672	0,593	PC aa C40:3	0,65	0,63	0,58
1,07	0,96	PC aa C40:4	0,90	0,91	0,89
3,08	2,9	PC aa C40:5	2,77	2,59	2,47
6,88	7,15	PC aa C40:6	5,88	5,51	5,80
0,132	0,117	PC aa C42:0	0,15	0,14	0,12
0,14	0,126	PC aa C42:1	0,13	0,13	0,13
0,226	0,199	PC aa C42:2	0,25	0,23	0,23
0,24	0,209	PC aa C42:4	0,23	0,18	0,19
0,22	0,233	PC aa C42:5	0,24	0,23	0,23
0,497	0,469	PC aa C42:6	0,50	0,45	0,47
6,8	7,27	PC ae C30:0	6,58	6,40	6,81
3,54	3,49	PC ae C30:1	2,86	2,99	3,07
0,448	0,358	PC ae C30:2	0,32	0,34	0,33
49,6	50,6	PC ae C32:1	45,63	43,33	44,13
9,63	9,6	PC ae C32:2	7,92	7,97	8,02
2,18	2,62	PC ae C34:0	3,40	3,01	2,80
68,6	68	PC ae C34:1	62,60	59,47	59,33
26,5	26,1	PC ae C34:2	22,23	22,27	22,47
2,66	2,87	PC ae C34:3	2,26	2,41	2,32
1,83	2,06	PC ae C36:0	2,22	1,61	1,61
15	14,6	PC ae C36:1	14,44	14,02	14,23
19,5	17,4	PC ae C36:2	15,40	15,28	15,73
12	11,1	PC ae C36:3	9,43	9,38	9,89
13,4	12,8	PC ae C36:4	11,17	11,09	10,76
5,86	6,21	PC ae C36:5	5,14	5,25	4,99
1,02	1,19	PC ae C38:0	0,93	0,85	0,92

Supplemental Table S1

2,72	2,4	PC ae C38:1	2,78	2,78	2,70
5,11	4,32	PC ae C38:2	4,33	4,43	4,40
3,44	3,21	PC ae C38:3	3,17	3,22	3,12
7,15	6,88	PC ae C38:4	6,13	6,00	6,00
14,1	14	PC ae C38:5	12,28	12,15	11,90
9,82	10	PC ae C38:6	8,65	8,56	8,33
0,989	1,05	PC ae C40:1	0,90	0,89	0,88
0,894	0,747	PC ae C40:2	0,82	0,88	0,83
1,17	0,949	PC ae C40:3	1,01	0,97	0,94
1,51	1,42	PC ae C40:4	1,44	1,35	1,28
3,89	3,36	PC ae C40:5	3,33	3,25	3,25
5,02	4,95	PC ae C40:6	4,22	4,32	4,37
0,7	0,755	PC ae C42:0	0,77	0,70	0,70
0,476	0,466	PC ae C42:1	0,42	0,40	0,43
0,67	0,73	PC ae C42:2	0,62	0,58	0,55
0,619	0,646	PC ae C42:3	0,68	0,65	0,62
0,295	0,238	PC ae C42:4	0,27	0,28	0,27
0,794	0,814	PC ae C42:5	0,81	0,81	0,80
0,223	0,264	PC ae C44:3	0,24	0,24	0,22
0,265	0,205	PC ae C44:4	0,24	0,22	0,25
0,163	0,227	PC ae C44:5	0,21	0,21	0,21
0,141	0,125	PC ae C44:6	0,15	0,14	0,16

Biological replica: 3 independent cell cultures

11 - SKOV FASN2 24h rep 12 - SKOV FASN3 24h repl		SKOV cont 24h		SKOV cont repl 24h	SKOV G28UCM 24h
G28UCM	G28UCM	control		control	G28UCM
10,6	7,67	lysoPC a C14:0	10,57	14,23	10,63
8,73	9,4	lysoPC a C16:0	12,73	15,93	8,89
17,3	16,9	lysoPC a C16:1	22,70	27,43	21,20
0,515	0,527	lysoPC a C17:0	0,61	0,64	0,58
1,28	1,33	lysoPC a C18:0	1,91	2,48	1,16
49,1	49,3	lysoPC a C18:1	57,97	66,70	55,50

Supplemental Table S1

4,73	5,24	lysoPC a C18:2	5,58	6,43	6,21
1,58	1,9	lysoPC a C20:3	2,40	2,63	1,97
3,07	3,35	lysoPC a C20:4	5,15	5,81	3,56
0,841	1,56	lysoPC a C24:0	1,67	1,58	0,97
2,15	3,68	lysoPC a C26:0	3,27	3,41	2,23
0,491	0,789	lysoPC a C26:1	0,72	0,66	0,51
2,21	3,46	lysoPC a C28:0	2,78	2,79	2,15
1,14	1,87	lysoPC a C28:1	1,45	1,38	1,27
0,294	0,367	PC aa C24:0	0,63	0,79	0,37
2,03	2,65	PC aa C26:0	3,88	4,62	2,85
1,15	1,61	PC aa C28:1	2,03	2,07	1,66
13,3	13,5	PC aa C30:0	17,37	18,83	12,33
0,236	0,371	PC aa C30:2	0,39	0,46	0,37
26,4	26,1	PC aa C32:0	36,30	40,23	19,40
98,5	111	PC aa C32:1	99,33	108,47	76,37
6,69	7,38	PC aa C32:2	8,02	8,69	4,97
0,436	0,495	PC aa C32:3	0,56	0,59	0,33
315	337	PC aa C34:1	317,33	358,00	256,67
56,8	58,9	PC aa C34:2	61,20	68,03	45,07
3,75	3,85	PC aa C34:3	4,45	4,97	2,77
0,41	0,415	PC aa C34:4	0,50	0,54	0,30
3,16	2,6	PC aa C36:0	3,12	3,37	2,49
23,8	25	PC aa C36:1	27,67	30,57	20,50
90,8	92,9	PC aa C36:2	93,40	104,00	74,80
17,6	17,1	PC aa C36:3	17,33	19,67	13,33
7,85	7,9	PC aa C36:4	10,77	12,00	6,10
2,95	3,17	PC aa C36:5	3,22	3,74	2,31
0,481	0,413	PC aa C36:6	0,46	0,53	0,36
4,42	4,22	PC aa C38:0	4,52	4,87	3,69
1,06	1,11	PC aa C38:1	1,61	1,79	1,06
5,95	6,29	PC aa C38:3	7,82	8,76	5,13
8,54	8,54	PC aa C38:4	9,25	10,20	6,85
10,6	10,9	PC aa C38:5	11,27	13,40	8,33
5,24	5,46	PC aa C38:6	5,81	6,67	4,12
0,401	0,456	PC aa C40:1	0,52	0,56	0,40
0,768	0,768	PC aa C40:2	1,00	1,06	0,68
0,603	0,631	PC aa C40:3	0,96	1,03	0,57

Supplemental Table S1

0,795	0,788	PC aa C40:4	1,13	1,22	0,74
2,25	2,24	PC aa C40:5	2,48	2,88	1,83
4,7	4,73	PC aa C40:6	4,34	4,86	3,80
0,151	0,122	PC aa C42:0	0,19	0,20	0,13
0,09	0,111	PC aa C42:1	0,19	0,19	0,08
0,257	0,263	PC aa C42:2	0,34	0,33	0,23
0,28	0,301	PC aa C42:4	0,32	0,33	0,25
0,215	0,218	PC aa C42:5	0,28	0,35	0,18
0,442	0,446	PC aa C42:6	0,53	0,61	0,38
8,29	9,08	PC ae C30:0	9,64	10,27	7,98
3,33	3,74	PC ae C30:1	4,13	4,25	3,72
0,299	0,363	PC ae C30:2	0,46	0,49	0,39
69,7	74	PC ae C32:1	65,17	71,00	54,57
11,6	12,4	PC ae C32:2	12,57	13,40	9,85
3,88	3,55	PC ae C34:0	4,31	4,75	2,81
86	92,2	PC ae C34:1	86,07	96,07	67,10
30,9	32,7	PC ae C34:2	32,70	35,60	25,63
3,22	3,38	PC ae C34:3	3,57	3,96	2,70
2,68	2,16	PC ae C36:0	1,84	1,96	1,72
17,1	18,2	PC ae C36:1	20,17	22,63	14,33
21,7	22,4	PC ae C36:2	23,60	25,93	18,90
13,5	14,2	PC ae C36:3	14,97	16,57	11,70
15	15,7	PC ae C36:4	17,20	18,93	12,50
6,85	7,05	PC ae C36:5	7,46	8,16	5,61
0,882	0,76	PC ae C38:0	0,81	1,00	0,65
2,88	2,68	PC ae C38:1	4,34	4,65	2,54
5,13	5,33	PC ae C38:2	6,85	7,59	4,60
4,14	4,15	PC ae C38:3	5,55	6,12	3,53
8,6	8,43	PC ae C38:4	9,56	10,67	7,15
18	18,3	PC ae C38:5	19,07	20,63	15,03
12,5	12,3	PC ae C38:6	13,10	14,53	10,11
0,48	0,461	PC ae C40:1	0,83	0,92	0,42
0,719	0,757	PC ae C40:2	1,46	1,52	0,76
1	1	PC ae C40:3	1,57	1,72	0,98
1,56	1,55	PC ae C40:4	2,17	2,35	1,43
4,33	4,27	PC ae C40:5	4,93	5,39	3,79
6,58	6,57	PC ae C40:6	6,79	7,34	5,56

Supplemental Table S1

0,692	0,705	PC ae C42:0	0,67	0,72	0,59
0,249	0,215	PC ae C42:1	0,29	0,32	0,20
0,221	0,24	PC ae C42:2	0,29	0,33	0,19
0,276	0,253	PC ae C42:3	0,43	0,51	0,23
0,185	0,241	PC ae C42:4	0,38	0,43	0,19
0,861	0,762	PC ae C42:5	1,08	1,13	0,77
0,081	0,116	PC ae C44:3	0,16	0,22	0,09
0,121	0,132	PC ae C44:4	0,16	0,17	0,11
0,162	0,152	PC ae C44:5	0,23	0,26	0,13
0,119	0,127	PC ae C44:6	0,22	0,28	0,14

Supplemental Table S1

SKOV FASN repl 8h	SD		SKOV G28UCM 8h	Biological replica CV (%)		Technical replica:	2 measurements c SKOV cont 8h vs. replica control			
	SKOV cont 8h			SKOV cont 8h						
	control	G28UCM		control	G28UCM					
	8,77	0,7618	2,1910	9,1340	20,3878	lysoPC a C14:0	9,04			
	8,05	1,3816	2,7626	17,0083	28,8576	lysoPC a C16:0	9,08			
	18,43	2,2605	5,9138	13,2195	26,5591	lysoPC a C16:1	18,55			
	0,54	0,0545	0,0866	8,7491	14,4666	lysoPC a C17:0	0,62			
	1,31	0,4530	0,6136	33,7591	38,3244	lysoPC a C18:0	1,60			
	51,07	6,1232	12,6982	13,2060	22,0710	lysoPC a C18:1	49,93			
	5,76	0,2757	2,3438	5,5296	33,8375	lysoPC a C18:2	5,41			
	2,11	0,1966	0,7862	10,5297	30,5104	lysoPC a C20:3	2,07			
	4,40	0,4155	1,4406	8,5727	28,6775	lysoPC a C20:4	5,15			
	0,94	0,2852	0,4071	27,3746	38,8706	lysoPC a C24:0	1,07			
	2,09	0,6987	0,7908	34,4772	33,2252	lysoPC a C26:0	2,15			
	0,49	0,1512	0,2068	31,2700	41,1727	lysoPC a C26:1	0,53			
	2,01	0,6790	0,8017	34,0633	38,5426	lysoPC a C28:0	2,13			
	1,10	0,2853	0,3366	26,9969	28,7015	lysoPC a C28:1	1,11			
	0,42	0,1172	0,2377	29,0439	45,6269	PC aa C24:0	0,44			
	2,87	0,4452	1,0300	18,7335	31,8562	PC aa C26:0	2,72			
	1,55	0,2558	0,4177	17,6820	26,5457	PC aa C28:1	1,53			
	11,63	1,9422	0,6928	16,8985	5,9215	PC aa C30:0	11,42			
	0,32	0,1126	0,1015	51,1116	37,4443	PC aa C30:2	0,23			
	17,27	10,4543	3,4646	37,6960	17,5274	PC aa C32:0	25,33			
	74,13	26,3232	15,5565	35,5239	21,9827	PC aa C32:1	72,98			
	4,57	2,1664	1,1837	38,5481	26,1696	PC aa C32:2	5,58			
	0,30	0,1405	0,0641	35,3330	21,8616	PC aa C32:3	0,39			
	272,67	91,8767	42,7122	34,8458	16,6411	PC aa C34:1	257,00			
	44,37	16,5012	10,2132	35,7944	23,4787	PC aa C34:2	46,32			
	2,87	1,1962	0,6964	36,5798	23,9852	PC aa C34:3	3,24			
	0,36	0,1195	0,0666	28,8083	19,2983	PC aa C34:4	0,40			
	2,23	0,7994	0,3707	33,1241	16,3794	PC aa C36:0	2,34			
	26,70	9,7872	2,9366	34,8300	10,6913	PC aa C36:1	26,67			
	77,23	27,5610	17,4517	36,7971	23,7654	PC aa C36:2	72,95			
	14,90	4,8422	3,5726	34,4802	24,6953	PC aa C36:3	13,91			

Supplemental Table S1

7,66	3,0280	1,7475	35,7359	22,6262	PC aa C36:4	8,43
2,92	1,0355	0,7136	33,1533	23,3961	PC aa C36:5	3,07
0,42	0,1044	0,0627	21,3992	14,7508	PC aa C36:6	0,45
3,09	1,0536	0,7382	33,9860	25,6310	PC aa C38:0	3,00
1,09	0,3926	0,1617	33,7477	13,3235	PC aa C38:1	1,16
5,83	2,3592	0,8844	39,7391	16,0613	PC aa C38:3	5,83
9,80	3,2371	2,0616	33,4991	21,6402	PC aa C38:4	9,49
12,90	4,4295	3,3650	34,9423	26,5659	PC aa C38:5	12,53
5,54	1,9263	1,3267	34,5009	23,0190	PC aa C38:6	5,59
0,40	0,1131	0,0157	27,4225	3,9788	PC aa C40:1	0,40
0,64	0,2643	0,1289	38,6082	20,4132	PC aa C40:2	0,65
0,60	0,2740	0,0844	42,2840	14,6674	PC aa C40:3	0,64
0,93	0,3435	0,1567	38,2922	17,5751	PC aa C40:4	0,90
2,73	0,9496	0,4551	34,3228	18,4244	PC aa C40:5	2,68
6,16	1,9206	1,3462	32,6810	23,2229	PC aa C40:6	5,70
0,12	0,0441	0,0129	29,0883	10,4256	PC aa C42:0	0,14
0,13	0,0493	0,0025	38,4959	1,9764	PC aa C42:1	0,13
0,21	0,0930	0,0161	37,6584	7,0909	PC aa C42:2	0,24
0,20	0,0655	0,0240	27,9187	12,6131	PC aa C42:4	0,21
0,22	0,0925	0,0490	37,8428	21,2221	PC aa C42:5	0,24
0,46	0,1250	0,0283	25,0177	6,0022	PC aa C42:6	0,47
6,63	1,0431	0,6843	15,8444	10,0488	PC ae C30:0	6,49
3,15	0,3113	0,5853	10,8734	19,0847	PC ae C30:1	2,93
0,35	0,0293	0,0874	9,2464	26,6692	PC ae C30:2	0,33
44,50	16,9771	7,6950	37,2034	17,4358	PC ae C32:1	44,48
8,08	3,0001	2,0077	37,8796	25,0440	PC ae C32:2	7,95
2,46	1,3848	0,5220	40,7690	18,6668	PC ae C34:0	3,21
61,93	23,6006	9,0279	37,7007	15,2156	PC ae C34:1	61,03
23,03	7,9908	4,3879	35,9408	19,5305	PC ae C34:2	22,25
2,36	0,7150	0,5524	31,5908	23,8125	PC ae C34:3	2,34
1,87	0,8310	0,3808	37,4880	23,7033	PC ae C36:0	1,91
14,37	5,5242	1,1547	38,2473	8,1127	PC ae C36:1	14,23
16,53	5,5435	2,7429	35,9965	17,4335	PC ae C36:2	15,34
10,16	3,4874	2,0007	36,9816	20,2223	PC ae C36:3	9,41
11,26	3,8527	2,5117	34,5018	23,3502	PC ae C36:4	11,13
5,08	1,5805	1,1265	30,7485	22,5760	PC ae C36:5	5,20
0,97	0,2433	0,1552	26,2379	16,7861	PC ae C38:0	0,89

Supplemental Table S1

2,67	1,1277	0,5020	40,5150	18,5707	PC ae C38:1	2,78
4,51	1,7779	0,9160	41,0917	20,8337	PC ae C38:2	4,38
3,15	1,2831	0,5575	40,4770	17,8684	PC ae C38:3	3,19
6,24	2,1494	1,1484	35,0835	19,1406	PC ae C38:4	6,07
12,39	4,2586	2,6851	34,6699	22,5642	PC ae C38:5	12,22
8,58	2,9494	1,7250	34,0970	20,7085	PC ae C38:6	8,60
0,91	0,2002	0,1427	22,3151	16,2511	PC ae C40:1	0,89
0,84	0,3531	0,0991	43,1623	11,9586	PC ae C40:2	0,85
1,00	0,4368	0,1199	43,3524	12,7449	PC ae C40:3	0,99
1,38	0,5246	0,1600	36,4917	12,5000	PC ae C40:4	1,39
3,35	1,2121	0,5892	36,3996	18,1304	PC ae C40:5	3,29
4,49	1,5672	0,9833	37,1662	22,5190	PC ae C40:6	4,27
0,68	0,1662	0,0830	21,6249	11,7746	PC ae C42:0	0,74
0,43	0,1475	0,0868	35,1245	20,1549	PC ae C42:1	0,41
0,60	0,1924	0,1170	31,1298	21,1360	PC ae C42:2	0,60
0,56	0,1849	0,1534	27,0999	24,8164	PC ae C42:3	0,66
0,25	0,0967	0,0295	36,1555	10,8503	PC ae C42:4	0,27
0,79	0,2398	0,0945	29,6136	11,7430	PC ae C42:5	0,81
0,21	0,0416	0,0665	17,5550	30,1328	PC ae C44:3	0,24
0,22	0,0825	0,0339	35,1083	13,8234	PC ae C44:4	0,23
0,19	0,0582	0,0263	27,7710	12,4130	PC ae C44:5	0,21
0,13	0,0402	0,0015	27,1036	0,9276	PC ae C44:6	0,14
			30,7824	20,4662	mean CV (%)	

SD		SKOV G28UCM		Biological replica CV (%)		Technical replica:	2 measurements (SKOV cont 24h vs. replica control)
SKOV G28UCM repl 24h	SKOV cont 24h	24h	24h	SKOV G28UCM	SKOV G28UCM		
G28UCM	control	G28UCM	control	G28UCM	G28UCM		
10,56	0,2517	1,4114	2,3817	13,2820	lysoPC a C14:0	12,40	
9,74	0,7767	1,1774	6,1001	13,2442	lysoPC a C16:0	14,33	
19,37	1,5133	2,5865	6,6664	12,2005	lysoPC a C16:1	25,07	
0,52	0,0032	0,1231	0,5299	21,1829	lysoPC a C17:0	0,62	
1,39	0,2281	0,2235	11,9220	19,3069	lysoPC a C18:0	2,20	
55,00	1,6862	8,0467	2,9089	14,4986	lysoPC a C18:1	62,33	

Supplemental Table S1

5,72	0,5085	0,6934	9,1068	11,1722	lysoPC a C18:2	6,01
1,91	0,0971	0,2615	4,0413	13,2758	lysoPC a C20:3	2,52
3,49	0,3101	0,4636	6,0166	13,0105	lysoPC a C20:4	5,48
1,14	0,1778	0,0476	10,6445	4,9300	lysoPC a C24:0	1,63
2,71	0,2581	0,1386	7,8860	6,2136	lysoPC a C26:0	3,34
0,59	0,0413	0,0674	5,7399	13,1592	lysoPC a C26:1	0,69
2,64	0,2639	0,2610	9,5035	12,1595	lysoPC a C28:0	2,79
1,37	0,1570	0,0902	10,7993	7,1199	lysoPC a C28:1	1,42
0,35	0,0920	0,0818	14,6255	22,3619	PC aa C24:0	0,71
2,50	0,1803	0,7239	4,6463	25,4298	PC aa C26:0	4,25
1,42	0,0737	0,3035	3,6371	18,2819	PC aa C28:1	2,05
13,17	0,3786	2,2008	2,1800	17,8440	PC aa C30:0	18,10
0,28	0,0357	0,0943	9,2235	25,6480	PC aa C30:2	0,42
22,67	3,2187	7,5027	8,8669	38,6735	PC aa C32:0	38,27
94,40	5,7770	10,3375	5,8157	13,5366	PC aa C32:1	103,90
6,19	0,6317	0,5263	7,8771	10,5974	PC aa C32:2	8,35
0,43	0,0120	0,0323	2,1634	9,6658	PC aa C32:3	0,57
306,67	12,0139	41,2957	3,7859	16,0892	PC aa C34:1	337,67
53,17	4,5398	3,8070	7,4180	8,4475	PC aa C34:2	64,62
3,44	0,3297	0,1960	7,4089	7,0859	PC aa C34:3	4,71
0,38	0,0320	0,0313	6,3860	10,5025	PC aa C34:4	0,52
2,68	0,1905	0,5009	6,1066	20,1164	PC aa C36:0	3,25
23,60	1,8771	6,2960	6,7845	30,7123	PC aa C36:1	29,12
86,07	3,9837	8,1462	4,2652	10,8906	PC aa C36:2	98,70
15,90	1,1015	1,4295	6,3549	10,7209	PC aa C36:3	18,50
7,30	1,1197	0,7535	10,3964	12,3518	PC aa C36:4	11,39
2,78	0,2230	0,2951	6,9329	12,7761	PC aa C36:5	3,48
0,42	0,0626	0,0576	13,5106	15,9327	PC aa C36:6	0,50
4,09	0,0971	0,5601	2,1472	15,1657	PC aa C38:0	4,70
1,11	0,0603	0,2691	3,7517	25,2867	PC aa C38:1	1,70
5,88	0,4099	0,6841	5,2442	13,3272	PC aa C38:3	8,29
7,99	0,6165	0,7263	6,6669	10,6028	PC aa C38:4	9,72
9,94	0,4041	1,1763	3,5871	14,1267	PC aa C38:5	12,33
5,00	0,3704	0,5781	6,3753	14,0436	PC aa C38:6	6,24
0,41	0,0694	0,1104	13,4533	27,3010	PC aa C40:1	0,54
0,79	0,0659	0,0917	6,5567	13,5081	PC aa C40:2	1,03
0,62	0,0692	0,0809	7,2101	14,1648	PC aa C40:3	0,99

Supplemental Table S1

0,77	0,0404	0,1580	3,5660	21,3097	PC aa C40:4	1,18
2,16	0,1473	0,2961	5,9399	16,1826	PC aa C40:5	2,68
4,38	0,1570	0,5179	3,6191	13,6412	PC aa C40:6	4,60
0,14	0,0093	0,0226	4,9075	17,6949	PC aa C42:0	0,19
0,10	0,0091	0,0232	4,7341	27,7830	PC aa C42:1	0,19
0,27	0,0190	0,0181	5,6548	7,7443	PC aa C42:2	0,33
0,28	0,0095	0,0492	3,0093	19,8786	PC aa C42:4	0,32
0,21	0,0029	0,0299	1,0141	16,9276	PC aa C42:5	0,32
0,43	0,0482	0,0646	9,1481	17,1184	PC aa C42:6	0,57
8,48	0,6134	1,4654	6,3650	18,3638	PC ae C30:0	9,95
3,60	0,1858	0,4153	4,4959	11,1527	PC ae C30:1	4,19
0,36	0,0101	0,0669	2,1928	17,2656	PC ae C30:2	0,48
66,23	2,8746	8,3500	4,4112	15,3025	PC ae C32:1	68,08
11,37	0,7506	1,1731	5,9726	11,9135	PC ae C32:2	12,98
3,49	0,1168	0,7738	2,7070	27,5381	PC ae C34:0	4,53
82,23	3,9004	13,6451	4,5319	20,3355	PC ae C34:1	91,07
30,37	1,7776	3,6950	5,4362	14,4150	PC ae C34:2	34,15
3,12	0,2848	0,3528	7,9770	13,0487	PC ae C34:3	3,76
2,15	0,2570	0,4979	13,9405	28,9474	PC ae C36:0	1,90
16,63	1,0017	3,7072	4,9669	25,8642	PC ae C36:1	21,40
21,07	0,8718	2,5632	3,6940	13,5619	PC ae C36:2	24,77
13,20	0,2082	1,4731	1,3909	12,5905	PC ae C36:3	15,77
14,53	0,6245	1,5133	3,6308	12,1062	PC ae C36:4	18,07
6,50	0,2400	0,7920	3,2172	14,1257	PC ae C36:5	7,81
0,75	0,0677	0,1702	8,3212	26,2281	PC ae C38:0	0,91
2,76	0,3980	0,6466	9,1643	25,4246	PC ae C38:1	4,50
5,09	0,3005	0,7910	4,3869	17,1839	PC ae C38:2	7,22
4,01	0,2303	0,5710	4,1469	16,1907	PC ae C38:3	5,84
8,19	0,4813	1,0080	5,0361	14,0982	PC ae C38:4	10,12
17,10	0,6351	2,3159	3,3309	15,4050	PC ae C38:5	19,85
11,80	0,4359	1,4171	3,3274	14,0173	PC ae C38:6	13,82
0,47	0,0727	0,0948	8,7858	22,5128	PC ae C40:1	0,88
0,77	0,1002	0,1539	6,8764	20,3175	PC ae C40:2	1,49
0,99	0,1300	0,2488	8,2803	25,2849	PC ae C40:3	1,65
1,53	0,1229	0,2511	5,6628	17,5980	PC ae C40:4	2,26
4,21	0,2339	0,6201	4,7440	16,3473	PC ae C40:5	5,16
6,24	0,1868	0,7203	2,7513	12,9546	PC ae C40:6	7,07

Supplemental Table S1

0,66	0,0131	0,0742	1,9574	12,6127	PC ae C42:0	0,69
0,22	0,0135	0,0368	4,6809	18,4450	PC ae C42:1	0,30
0,22	0,0341	0,0298	11,8140	15,6105	PC ae C42:2	0,31
0,27	0,0342	0,0491	7,9014	21,5734	PC ae C42:3	0,47
0,21	0,0205	0,0277	5,3344	14,6212	PC ae C42:4	0,41
0,81	0,0794	0,1228	7,3493	16,0293	PC ae C42:5	1,11
0,10	0,0242	0,0110	15,3473	12,0879	PC ae C44:3	0,19
0,12	0,0160	0,0035	10,1546	3,1492	PC ae C44:4	0,17
0,15	0,0268	0,0208	11,6031	16,1307	PC ae C44:5	0,24
0,12	0,0327	0,0356	15,0674	25,8389	PC ae C44:6	0,25
			6,3352	16,3825	mean CV (%)	

Supplemental Table S1

If same sample SKOV G28UCM 8h vs. replica G28UCM	SD		SKOV G28UCM 8h G28UCM	Technical replica CV (%)	
	SKOV cont 8h			SKOV cont 8h	SKOVG28UCM 8h
	control			control	G28UCM
	9,76	0,9876	1,3977	10,9267	14,3233
	8,81	1,3482	1,0772	14,8537	12,2242
	20,35	2,0506	2,7106	11,0545	13,3198
	0,57	0,0012	0,0410	0,1894	7,2035
	1,46	0,3616	0,2058	22,6310	14,1373
	54,30	5,0440	4,5726	10,1015	8,4210
	6,35	0,6010	0,8226	11,1064	12,9646
	2,34	0,2923	0,3300	14,0967	14,0818
	4,71	0,4290	0,4384	8,3297	9,3014
	0,99	0,0403	0,0766	3,7651	7,7130
	2,23	0,1721	0,2074	8,0091	9,2874
	0,49	0,0674	0,0120	12,6871	2,4342
	2,05	0,1956	0,0495	9,1775	2,4204
	1,13	0,0705	0,0547	6,3692	4,8221
	0,47	0,0493	0,0721	11,2342	15,3457
	3,05	0,4832	0,2593	17,7752	8,5007
	1,56	0,1131	0,0141	7,4107	0,9046
	11,67	0,1014	0,0471	0,8874	0,4041
	0,29	0,0068	0,0335	3,0357	11,3585
	18,52	3,3941	1,7678	13,3978	9,5469
	72,45	1,5792	2,3806	2,1638	3,2858
	4,55	0,0613	0,0306	1,0989	0,6742
	0,30	0,0106	0,0064	2,7185	2,1368
	264,67	9,4281	11,3137	3,6685	4,2747
	43,93	0,3064	0,6128	0,6616	1,3949
	2,89	0,0448	0,0259	1,3829	0,8987
	0,35	0,0229	0,0106	5,7373	3,0061
	2,25	0,1014	0,0212	4,3282	0,9435
	27,08	2,0270	0,5421	7,6014	2,0017
	75,33	2,7577	2,6870	3,7803	3,5668
	14,68	0,1862	0,3064	1,3385	2,0868

Supplemental Table S1

7,69	0,0589	0,0471	0,6989	0,6130
2,99	0,0825	0,0919	2,6915	3,0795
0,42	0,0495	0,0016	10,9346	0,3890
2,99	0,1414	0,1508	4,7140	5,0508
1,15	0,0002	0,0896	0,0203	7,7884
5,67	0,1556	0,2263	2,6699	3,9931
9,66	0,2404	0,1933	2,5325	2,0001
12,79	0,2145	0,1673	1,7125	1,3089
5,65	0,0047	0,1556	0,0844	2,7517
0,40	0,0106	0,0028	2,6200	0,7125
0,64	0,0530	0,0047	8,1946	0,7424
0,59	0,0113	0,0184	1,7678	3,1231
0,91	0,0061	0,0255	0,6799	2,7984
2,60	0,1273	0,1862	4,7551	7,1571
5,98	0,2569	0,2546	4,5112	4,2592
0,12	0,0099	0,0009	6,8430	0,7686
0,13	0,0007	0,0009	0,5546	0,7366
0,22	0,0108	0,0090	4,5302	4,0651
0,20	0,0379	0,0094	18,2589	4,7858
0,23	0,0123	0,0064	5,2008	2,8138
0,46	0,0387	0,0097	8,1839	2,0805
6,72	0,1296	0,1249	1,9970	1,8585
3,11	0,0896	0,0613	3,0604	1,9705
0,34	0,0158	0,0146	4,8171	4,3235
44,32	1,6263	0,2593	3,6561	0,5850
8,05	0,0377	0,0424	0,4746	0,5273
2,63	0,2711	0,2404	8,4573	9,1529
60,63	2,2156	1,8385	3,6301	3,0321
22,75	0,0236	0,4007	0,1059	1,7613
2,34	0,1037	0,0283	4,4383	1,2087
1,74	0,4313	0,1838	22,5633	10,5862
14,30	0,2993	0,0943	2,1034	0,6593
16,13	0,0872	0,5657	0,5686	3,5063
10,03	0,0354	0,1909	0,3759	1,9038
11,01	0,0566	0,3559	0,5084	3,2331
5,03	0,0778	0,0613	1,4972	1,2175
0,95	0,0563	0,0311	6,3474	3,2877

Supplemental Table S1

2,69	0,0024	0,0212	0,0847	0,7891
4,45	0,0707	0,0801	1,6156	1,7995
3,14	0,0330	0,0212	1,0334	0,6767
6,12	0,0872	0,1673	1,4379	2,7352
12,14	0,0919	0,3441	0,7523	2,8339
8,46	0,0660	0,1791	0,7671	2,1183
0,90	0,0066	0,0250	0,7393	2,7895
0,83	0,0460	0,0052	5,4041	0,6233
0,97	0,0240	0,0443	2,4268	4,5573
1,33	0,0629	0,0707	4,5172	5,3166
3,30	0,0589	0,0707	1,7920	2,1427
4,43	0,0754	0,0896	1,7664	2,0218
0,69	0,0469	0,0160	6,3773	2,3117
0,43	0,0174	0,0033	4,2785	0,7704
0,58	0,0283	0,0358	4,7298	6,1877
0,59	0,0252	0,0382	3,7954	6,4572
0,26	0,0097	0,0130	3,5248	4,9323
0,80	0,0009	0,0120	0,1165	1,5105
0,21	0,0002	0,0094	0,0995	4,4056
0,23	0,0111	0,0210	4,8766	9,1140
0,20	0,0019	0,0127	0,8937	6,2802
0,15	0,0066	0,0219	4,5937	14,6952
			4,9322	4,4209 mean CV (%)

of same sample SKOV G28UCM 24h vs. replica G28UCM	SD		SKOV G28UCM		Technical replica CV (%)	
	SKOV cont 24h		24h		SKOV cont 24h	SKOV G28UCM 24h
	control		G28UCM		control	G28UCM
	10,59	2,5927	0,0495		20,9091	0,4673
	9,32	2,2627	0,6034		15,7866	6,4765
	20,28	3,3470	1,2964		13,3523	6,3913
	0,55	0,0203	0,0436		3,2642	7,9210
	1,28	0,3983	0,1666		18,1475	13,0648
	55,25	6,1754	0,3536		9,9071	0,6399

Supplemental Table S1

5,96	0,5987	0,3465	9,9670	5,8118
1,94	0,1579	0,0448	6,2791	2,3104
3,53	0,4667	0,0495	8,5111	1,4029
1,05	0,0613	0,1233	3,7674	11,7049
2,47	0,0990	0,3394	2,9610	13,7413
0,55	0,0389	0,0563	5,6187	10,2021
2,39	0,0118	0,3465	0,4232	14,4871
1,32	0,0542	0,0731	3,8312	5,5424
0,36	0,1122	0,0134	15,8392	3,7721
2,68	0,5233	0,2428	12,3120	9,0756
1,54	0,0306	0,1721	1,4959	11,1850
12,75	1,0371	0,5893	5,7298	4,6216
0,33	0,0500	0,0592	11,8223	18,1569
21,03	2,7813	2,3099	7,2682	10,9820
85,38	6,4582	12,7515	6,2158	14,9344
5,58	0,4714	0,8650	5,6433	15,5069
0,38	0,0269	0,0658	4,6785	17,2676
281,67	28,7557	35,3553	8,5160	12,5522
49,12	4,8319	5,7276	7,4778	11,6611
3,11	0,3677	0,4785	7,8067	15,4098
0,34	0,0288	0,0554	5,5088	16,4443
2,59	0,1768	0,1367	5,4477	5,2851
22,05	2,0506	2,1920	7,0427	9,9412
80,43	7,4953	7,9667	7,5941	9,9048
14,62	1,6499	1,8149	8,9185	12,4167
6,70	0,8697	0,8462	7,6394	12,6326
2,55	0,3677	0,3323	10,5761	13,0586
0,39	0,0493	0,0396	9,8952	10,1707
3,89	0,2475	0,2781	5,2676	7,1498
1,09	0,1320	0,0349	7,7643	3,2043
5,51	0,6647	0,5280	8,0211	9,5879
7,42	0,6718	0,8085	6,9098	10,8932
9,13	1,5085	1,1384	12,2310	12,4670
4,56	0,6058	0,6270	9,7102	13,7493
0,41	0,0278	0,0071	5,1922	1,7275
0,73	0,0365	0,0773	3,5464	10,5423
0,59	0,0481	0,0311	4,8374	5,2437

Supplemental Table S1

0,75	0,0613	0,0189	5,2082	2,4986
1,99	0,2852	0,2310	10,6352	11,5880
4,09	0,3724	0,4125	8,0959	10,0892
0,13	0,0052	0,0052	2,6868	3,9383
0,09	0,0016	0,0080	0,8556	8,9708
0,25	0,0047	0,0250	1,4170	9,9145
0,26	0,0068	0,0224	2,1239	8,5086
0,19	0,0453	0,0245	14,2910	12,6356
0,40	0,0556	0,0342	9,8279	8,5123
8,23	0,4478	0,3559	4,4993	4,3237
3,66	0,0849	0,0849	2,0235	2,3163
0,37	0,0203	0,0214	4,2615	5,7633
60,40	4,1248	8,2496	6,0584	13,6582
10,61	0,5893	1,0748	4,5386	10,1333
3,15	0,3111	0,4832	6,8631	15,3312
74,67	7,0711	10,7009	7,7647	14,3315
28,00	2,0506	3,3470	6,0047	11,9535
2,91	0,2734	0,2923	7,2652	10,0437
1,94	0,0849	0,3041	4,4581	15,7135
15,48	1,7442	1,6263	8,1505	10,5038
19,98	1,6499	1,5321	6,6618	7,6667
12,45	1,1314	1,0607	7,1757	8,5194
13,52	1,2257	1,4378	6,7841	10,6371
6,05	0,4973	0,6293	6,3665	10,3992
0,70	0,1287	0,0745	14,2203	10,6150
2,65	0,2192	0,1508	4,8730	5,6924
4,85	0,5256	0,3441	7,2783	7,1002
3,77	0,4031	0,3441	6,9035	9,1280
7,67	0,7896	0,7330	7,8063	9,5592
16,07	1,1078	1,4614	5,5809	9,0956
10,96	1,0135	1,1950	7,3355	10,9084
0,45	0,0679	0,0358	7,7491	8,0269
0,76	0,0471	0,0080	3,1638	1,0503
0,99	0,1061	0,0028	6,4478	0,2869
1,48	0,1249	0,0707	5,5316	4,7885
4,00	0,3253	0,2970	6,3037	7,4184
5,90	0,3889	0,4785	5,5047	8,1120

Supplemental Table S1

0,62	0,0349	0,0483	5,0217	7,7621
0,21	0,0222	0,0127	7,2722	6,0996
0,20	0,0302	0,0174	9,7427	8,5780
0,25	0,0554	0,0285	11,7228	11,5077
0,20	0,0330	0,0151	8,0944	7,5425
0,79	0,0354	0,0342	3,1996	4,3253
0,09	0,0424	0,0054	22,5672	5,7165
0,12	0,0108	0,0085	6,5578	7,3149
0,14	0,0184	0,0156	7,5451	11,1117
0,13	0,0460	0,0115	18,3970	8,9185
			7,5163	8,9813 mean CV (%)

Supplemental Table S2a: Shotgun proteomic analysis of SKOV3 cells exposed for 8h and 24h to 40μM G28UCM. All proteins identified by MS/MS.

p-Value	x	2 ^x	% of Control	Protein IDs	Protein Names	Gene names
8 h Up						
0,001	3,37	10,36	1036,11	Q9UPV0	Centrosomal protein of 164 kDa	CEP164
0,024	3,23	9,36	935,99	P42338;O00329	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform;Phosphoinositide 3-kinase	PIK3CB;PIK3CD
0,011	3,19	9,11	911,37	P05386	60S acidic ribosomal protein P1	RPLP1
0,001	3,04	8,20	819,72	Q9NV56	MRG-binding protein	MRGBP
0,011	3,02	8,13	813,46	Q5UIP0	Telomere-associated protein RIF1	RIF1
0,000	2,93	7,61	761,42	Q9UER7	Death domain-associated protein 6	DAXX
0,009	2,80	6,95	695,39	O00148	ATP-dependent RNA helicase DDX39A	DDX39A
0,003	2,76	6,77	676,54	Q3ZCM7	Tubulin beta-8 chain	TUBB8
0,000	2,73	6,65	665,06	Q16678	Cytochrome P450 1B1	CYP1B1
0,004	2,73	6,62	661,99	Q9Y2H5	Pleckstrin homology domain-containing family A member 6	PLEKHA6
0,030	2,65	6,27	627,24	Q9Y3B8	Oligoribonuclease, mitochondrial	REXO2
0,030	2,60	6,04	604,32	O43464	Serine protease HTRA2, mitochondrial	HTRA2
0,048	2,59	6,00	600,29	Q9UGU0	Transcription factor 20	TCF20
0,027	2,58	5,98	597,99	Q01780	Exosome component 10	EXOSC10
0,021	2,28	4,86	485,94	Q15021	Condensin complex subunit 1	NCAPD2
0,032	2,26	4,81	480,52	Q8NCA5	Protein FAM98A	FAM98A
0,044	2,25	4,77	477,24	Q12873	Chromodomain-helicase-DNA-binding protein 3	CHD3
0,016	2,23	4,69	469,37	O76027	Annexin A9	ANXA9
0,031	2,21	4,63	463,27	P51808	Dynein light chain Tctex-type 3	DYNLT3
0,002	2,20	4,58	458,02	O00411	DNA-directed RNA polymerase, mitochondrial	POLRMT
0,033	2,16	4,48	448,02	Q9NV88	Integrator complex subunit 9	INTS9
0,004	2,16	4,47	447,08	Q92575	UBX domain-containing protein 4	UBXN4
0,043	2,16	4,47	446,78	Q66PJ3	ADP-ribosylation factor-like protein 6-interacting protein 4	ARL6IP4
0,024	2,15	4,45	445,36	O00442	RNA 3-terminal phosphate cyclase	RTCD1
0,026	2,13	4,38	437,83	Q16629	Serine/arginine-rich splicing factor 7	SRSF7
0,002	2,09	4,26	426,03	Q15528	Mediator of RNA polymerase II transcription subunit 22	MED22
0,037	2,08	4,23	422,59	P15170;Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1

Supplemental Table S2a

0,017	2,05	4,14	414,44	Q9GZR7	ATP-dependent RNA helicase DDX24	DDX24
0,001	2,04	4,12	411,59	Q15428	Splicing factor 3A subunit 2	SF3A2
0,018	2,04	4,11	411,02	Q9UGP8	Translocation protein SEC63 homolog	SEC63
0,012	2,03	4,09	409,43	Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0
0,017	2,02	4,06	406,26	Q05519	Serine/arginine-rich splicing factor 11	SRSF11
0,047	1,98	3,94	394,15	O43264	Centromere/kinetochore protein zw10 homolog	ZW10
0,020	1,96	3,88	388,24	Q9UMN6	Histone-lysine N-methyltransferase MLL4	WBP7
0,034	1,94	3,83	383,32	Q9Y2H1	Serine/threonine-protein kinase 38-like	STK38L
0,018	1,93	3,81	380,71	O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7
0,011	1,92	3,79	378,87	Q9GZS1	DNA-directed RNA polymerase I subunit RPA49	POLR1E
0,022	1,91	3,77	377,08	P62995	Transformer-2 protein homolog beta	TRA2B
0,016	1,89	3,71	371,11	Q8IY17	Neuropathy target esterase	PNPLA6
0,048	1,87	3,66	365,82	P04350;A6NNZ2	Tubulin beta-4A chain	TUBB4A
0,022	1,86	3,62	361,93	Q9NVH0	Exonuclease 3-5 domain-containing protein 2	EXD2
0,037	1,83	3,55	354,67	Q8IYU8	EF-hand domain-containing family member A1	EFHA1
0,023	1,82	3,54	354,25	O00562	Membrane-associated phosphatidylinositol transfer protein 1	PITPNM1
0,022	1,82	3,54	353,71	O95071	E3 ubiquitin-protein ligase UBR5	UBR5
0,031	1,82	3,53	353,39	P27707	Deoxycytidine kinase	DCK
0,014	1,80	3,48	347,74	Q9HC78;Q96K62	Zinc finger and BTB domain-containing protein 20;Zinc finger and BTB domain-containing protein 20	ZBTB20;ZBTB45
0,041	1,80	3,47	347,18	Q9BTD8	RNA-binding protein 42	RBM42
0,048	1,77	3,42	341,81	Q14498;Q86U06	RNA-binding protein 39	RBM39
0,020	1,77	3,40	340,06	P02649	Apolipoprotein E	APOE
0,028	1,76	3,39	339,13	O43716	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	GATC
0,044	1,76	3,38	338,01	Q96SU4	Oxysterol-binding protein-related protein 9	OSBPL9
0,041	1,75	3,35	335,22	Q96FJ2	Dynein light chain 2, cytoplasmic	DYNLL2
0,006	1,75	3,35	335,21	Q96HY6	DDRKG domain-containing protein 1	DDRKG1
0,040	1,73	3,31	331,05	O15042	U2 snRNP-associated SURP motif-containing protein	U2SURP
0,006	1,72	3,30	329,81	P49454	Centromere protein F	CENPF
0,016	1,71	3,26	326,48	Q9P265	Disco-interacting protein 2 homolog B	DIP2B
0,009	1,70	3,26	325,53	Q03701	CCAAT/enhancer-binding protein zeta	CEBPZ
0,026	1,67	3,19	319,28	Q6KC79	Nipped-B-like protein	NIPBL
0,021	1,64	3,12	311,96	P35250	Replication factor C subunit 2	RFC2
0,034	1,63	3,11	310,56	Q5VSL9;Q9ULQ0	Protein FAM40A	FAM40A

Supplemental Table S2a

0,023	1,63	3,09	308,81	Q9Y282	Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3
0,026	1,59	3,02	301,88	Q9H3P2	Negative elongation factor A	WHSC2
0,009	1,59	3,00	300,38	Q86UV5	Ubiquitin carboxyl-terminal hydrolase 48	USP48
0,050	1,59	3,00	300,27	P50851	Lipopolysaccharide-responsive and beige-like anchor protein	LRBA
0,045	1,58	2,99	299,05	Q9Y4F1	FERM, RhoGEF and pleckstrin domain-containing protein 1	FARP1
0,045	1,58	2,99	298,74	Q99729	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
0,044	1,57	2,98	297,65	Q76FK4	Nucleolar protein 8	NOL8
0,026	1,57	2,97	296,75	Q9P1Y5	Calmodulin-regulated spectrin-associated protein 3	CAMSAP3
0,039	1,54	2,91	291,09	Q9NPJ6	Mediator of RNA polymerase II transcription subunit 4	MED4
0,030	1,53	2,90	289,68	P16455	Methylated-DNA--protein-cysteine methyltransferase	MGMT
0,011	1,49	2,81	281,28	Q10713	Mitochondrial-processing peptidase subunit alpha	PMPCA
0,000	1,49	2,81	280,88	Q12872	Splicing factor, suppressor of white-apricot homolog	SFSWAP
0,030	1,48	2,78	278,27	Q8TD47	40S ribosomal protein S4, Y isoform 2	RPS4Y2
0,045	1,47	2,78	277,77	Q96DE0	U8 snoRNA-decapping enzyme	NUDT16
0,042	1,47	2,77	276,95	Q9UKE5	TRAF2 and NCK-interacting protein kinase	TNIK
0,018	1,47	2,77	276,89	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	SH3BGR13
0,023	1,47	2,76	276,36	P54274	Telomeric repeat-binding factor 1	TERF1
0,034	1,46	2,76	275,76	Q9NVC6	Mediator of RNA polymerase II transcription subunit 17	MED17
0,039	1,46	2,75	275,42	Q2TB90	Putative hexokinase HKDC1	HKDC1
0,000	1,46	2,75	275,33	O60563	Cyclin-T1	CCNT1
0,024	1,45	2,73	272,90	Q9UDT6	CAP-Gly domain-containing linker protein 2	CLIP2
0,013	1,44	2,72	272,21	O96019;O94805	Actin-like protein 6A	ACTL6A
0,018	1,43	2,70	269,64	Q7KZ85	Transcription elongation factor SPT6	SUPT6H
0,046	1,43	2,69	268,54	Q08379	Golgin subfamily A member 2	GOLGA2
0,001	1,38	2,59	259,46	Q9P2N5	RNA-binding protein 27	RBM27
0,015	1,37	2,58	258,41	Q92610	Zinc finger protein 592	ZNF592
0,047	1,37	2,58	258,04	Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9
0,014	1,37	2,58	257,92	Q9NRZ9	Lymphoid-specific helicase	HELLS
0,019	1,37	2,58	257,89	Q9NQV6	PR domain zinc finger protein 10	PRDM10
0,000	1,36	2,57	256,82	P52294	Importin subunit alpha-1	KPNA1
0,002	1,35	2,56	255,73	Q96T58	Msx2-interacting protein	SPEN
0,000	1,34	2,53	253,44	O75934	Pre-mRNA-splicing factor SPF27	BCAS2
0,020	1,34	2,53	253,08	Q8WV41	Sorting nexin-33	SNX33

Supplemental Table S2a

0,049	1,33	2,52	252,20	Q96FV9	THO complex subunit 1	THOC1
0,047	1,33	2,51	251,27	Q6ZSJ8	Uncharacterized protein C1orf122	C1orf122
0,027	1,33	2,51	250,68	Q02447	Transcription factor Sp3	SP3
0,020	1,30	2,46	245,77	Q9NQX3	Gephyrin;Molybdopterin adenyltransferase;Molybdopterin molybdenumtransferase	GPHN
0,043	1,28	2,43	242,77	Q7L5D6	Golgi to ER traffic protein 4 homolog	GET4
0,009	1,26	2,40	239,70	Q15050	Ribosome biogenesis regulatory protein homolog	RRS1
0,042	1,26	2,39	238,74	Q70E73	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1
0,041	1,25	2,38	238,03	Q9H267	Vacuolar protein sorting-associated protein 33B	VPS33B
0,013	1,25	2,38	238,01	Q13888;Q6P1K8	General transcription factor IIH subunit 2;General transcription factor IIH subunit 2-variant 1	GTF2H2;GTF2H2C
0,024	1,25	2,38	237,85	Q8N3C7	CAP-Gly domain-containing linker protein 4	CLIP4
0,022	1,25	2,37	237,27	Q96B26	Exosome complex component RRP43	EXOSC8
0,028	1,25	2,37	237,14	P61962	DDB1- and CUL4-associated factor 7	DCAF7
0,002	1,24	2,37	236,90	Q9H008	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP
0,027	1,24	2,36	235,87	Q8WYH8;Q9UNL4	Inhibitor of growth protein 5	ING5
0,002	1,24	2,36	235,56	Q9UKD2	mRNA turnover protein 4 homolog	MRT04
0,023	1,23	2,35	235,37	Q8WXF1	Paraspeckle component 1	PSPC1
0,007	1,23	2,35	234,66	Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase	DECR2
0,015	1,22	2,32	232,24	Q96P48	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	ARAP1
0,030	1,21	2,31	231,35	Q7L2J0	7SK snRNA methylphosphate capping enzyme	MEPCE
0,018	1,21	2,31	230,94	Q6PK04	Coiled-coil domain-containing protein 137	CCDC137
0,044	1,21	2,31	230,80	Q0JRZ9	FCH domain only protein 2	FCHO2
0,001	1,20	2,30	230,06	P09234	U1 small nuclear ribonucleoprotein C	SNRPC
0,000	1,19	2,28	228,23	Q8IUF8	MYC-induced nuclear antigen	MINA
0,025	1,19	2,27	227,41	Q96S94	Cyclin-L2	CCNL2
0,004	1,18	2,27	227,35	Q8N2M8	CLK4-associating serine/arginine rich protein	CLASRP
0,002	1,18	2,26	225,90	Q9Y3B4	Pre-mRNA branch site protein p14	SF3B14
0,038	1,17	2,25	225,23	Q8TF74	WAS/WASL-interacting protein family member 2	WIPF2
0,027	1,15	2,21	221,46	Q8WUA8	Tsukushin	TSKU
0,042	1,15	2,21	221,15	Q96EY4	Translation machinery-associated protein 16	TMA16
0,026	1,13	2,20	219,55	Q9NXV6	CDKN2A-interacting protein	CDKN2AIP
0,011	1,13	2,19	219,34	P62829	60S ribosomal protein L23	RPL23
0,044	1,13	2,18	218,31	Q92769	Histone deacetylase 2	HDAC2
0,021	1,12	2,17	216,61	Q92560	Ubiquitin carboxyl-terminal hydrolase BAP1	BAP1

Supplemental Table S2a

0,029	1,10	2,14	214,35	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1
0,004	1,09	2,13	213,29	P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial	PYCR1
0,031	1,09	2,13	213,22	P17676	CCAAT/enhancer-binding protein beta	CEBPB
0,004	1,09	2,13	212,68	Q76L83	Putative Polycomb group protein ASXL2	ASXL2
0,005	1,07	2,10	210,37	P26599	Polypyrimidine tract-binding protein 1	PTBP1
0,040	1,07	2,10	209,64	Q00013	55 kDa erythrocyte membrane protein	MPP1
0,033	1,06	2,08	208,50	Q9P253	Vacuolar protein sorting-associated protein 18 homolog	VPS18
0,000	1,05	2,07	207,03	Q8IXM2	Chromatin complexes subunit BAP18	BAP18
0,012	1,04	2,05	205,42	P52272	Heterogeneous nuclear ribonucleoprotein M	HNRNPM
0,010	1,03	2,04	204,33	P60953	Cell division control protein 42 homolog	CDC42
0,000	1,01	2,01	201,20	P39060	Collagen alpha-1(XVIII) chain;Endostatin	COL18A1
0,042	0,99	1,98	198,34	O43432	Eukaryotic translation initiation factor 4 gamma 3	EIF4G3
0,044	0,98	1,98	197,82	Q9BVL2	Nucleoporin p58/p45	NUPL1
0,002	0,98	1,98	197,52	Q9NVI7;Q5T2N8	ATPase family AAA domain-containing protein 3A	ATAD3A
0,020	0,98	1,97	196,74	Q9H4I3	TraB domain-containing protein	TRABD
0,015	0,97	1,96	196,08	Q08211	ATP-dependent RNA helicase A	DHX9
0,031	0,97	1,96	195,99	Q14451	Growth factor receptor-bound protein 7	GRB7
0,032	0,96	1,95	195,11	Q9NRW7	Vacuolar protein sorting-associated protein 45	VPS45
0,021	0,96	1,95	194,90	Q99583	Max-binding protein MNT	MNT
0,026	0,95	1,94	193,51	Q14644	Ras GTPase-activating protein 3	RASA3
0,002	0,95	1,93	193,41	Q02880	DNA topoisomerase 2-beta	TOP2B
0,000	0,95	1,93	193,28	Q9UFF9	CCR4-NOT transcription complex subunit 8	CNOT8
0,013	0,94	1,92	192,27	O60232	Sjoegren syndrome/scleroderma autoantigen 1	SSSCA1
0,007	0,93	1,91	191,03	P14902	Indoleamine 2,3-dioxygenase 1	IDO1
0,000	0,93	1,91	190,68	Q9Y5A9	YTH domain family protein 2	YTHDF2
0,033	0,91	1,88	188,41	Q9Y3A2	Probable U3 small nucleolar RNA-associated protein 11	UTP11L
0,035	0,90	1,87	186,56	P51116	Fragile X mental retardation syndrome-related protein 2	FXR2
0,038	0,90	1,86	186,49	P55795	Heterogeneous nuclear ribonucleoprotein H2	HNRNPH2
0,028	0,89	1,85	185,29	O14929	Histone acetyltransferase type B catalytic subunit	HAT1
0,002	0,89	1,85	185,09	Q96EZ8	Microspherule protein 1	MCRS1
0,026	0,89	1,85	184,95	Q9HCJ3	Ribonucleoprotein PTB-binding 2	RAVER2
0,028	0,88	1,84	184,48	Q9NPR2	Semaphorin-4B	SEMA4B
0,035	0,88	1,84	184,45	Q13439	Golgin subfamily A member 4	GOLGA4

Supplemental Table S2a

0,000	0,88	1,83	183,46	Q16186	Proteasomal ubiquitin receptor ADRM1	ADRM1
0,032	0,88	1,83	183,44	Q96FK6	WD repeat-containing protein 89	WDR89
0,018	0,86	1,81	180,88	Q9NP64	Nucleolar protein of 40 kDa	ZCCHC17
0,006	0,85	1,81	180,85	Q8WXA9	Splicing regulatory glutamine/lysine-rich protein 1	SREK1
0,040	0,85	1,81	180,84	Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA
0,004	0,85	1,80	180,19	Q9UHD9	Ubiquilin-2	UBQLN2
0,044	0,84	1,79	179,46	Q9Y3C4	TP53RK-binding protein	TPRKB
0,049	0,83	1,78	178,09	Q9ULU4	Protein kinase C-binding protein 1	ZMYND8
0,010	0,82	1,77	177,11	P33991;Q9UJA3	DNA replication licensing factor MCM4	MCM4
0,003	0,82	1,76	176,47	P51553	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G
0,048	0,81	1,75	175,41	Q13043	Serine/threonine-protein kinase 4;Serine/threonine-protein kinase 4 37kDa subunit	STK4
0,045	0,81	1,75	175,30	Q9NUD5	Zinc finger CCHC domain-containing protein 3	ZCCHC3
0,015	0,80	1,74	173,71	Q8IXK0	Polyhomeotic-like protein 2	PHC2
0,045	0,79	1,73	173,31	O75175	CCR4-NOT transcription complex subunit 3	CNOT3
0,042	0,78	1,72	171,86	Q9UPN4	5-azacytidine-induced protein 1	AZI1
0,021	0,78	1,72	171,62	A9UHW6	MIF4G domain-containing protein	MIF4GD
0,040	0,77	1,71	170,79	Q9BWF3	RNA-binding protein 4	RBM4
0,015	0,77	1,70	170,46	Q13595	Transformer-2 protein homolog alpha	TRA2A
0,009	0,77	1,70	170,27	Q9NVP1	ATP-dependent RNA helicase DDX18	DDX18
0,028	0,76	1,69	169,11	Q6ZNW5	GDP-D-glucose phosphorylase C15orf58	C15orf58
0,043	0,75	1,68	167,79	Q00610;P53675	Clathrin heavy chain 1	CLTC
0,037	0,74	1,67	167,47	Q12906	Interleukin enhancer-binding factor 3	ILF3
0,042	0,74	1,67	166,89	Q5JTW2	Centrosomal protein of 78 kDa	CEP78
0,041	0,74	1,66	166,44	P61964	WD repeat-containing protein 5	WDR5
0,021	0,73	1,66	166,30	Q02750	Dual specificity mitogen-activated protein kinase kinase 1	MAP2K1
0,027	0,73	1,66	165,81	Q53H96	Pyrroline-5-carboxylate reductase 3	PYCRL
0,033	0,72	1,65	165,00	Q9BTC8	Metastasis-associated protein MTA3	MTA3
0,032	0,72	1,64	164,36	O15056	Synaptojanin-2	SYNJ2
0,034	0,71	1,64	163,92	Q969V3	Nicalin	NCLN
0,020	0,71	1,64	163,57	Q13123	Protein Red	IK
0,016	0,70	1,63	162,61	P27540	Aryl hydrocarbon receptor nuclear translocator	ARNT
0,023	0,68	1,60	160,17	Q4LE39	AT-rich interactive domain-containing protein 4B	ARID4B
0,046	0,68	1,60	160,12	Q9BZV1	UBX domain-containing protein 6	UBXN6

Supplemental Table S2a

0,011	0,68	1,60	160,10	P07737;CON__P02584	Profilin-1	PFN1
0,028	0,67	1,59	159,47	Q32P44	Echinoderm microtubule-associated protein-like 3	EML3
0,040	0,67	1,59	159,34	Q15652	Probable JmjC domain-containing histone demethylation protein 2C	JMJD1C
0,040	0,66	1,58	157,62	P83436	Conserved oligomeric Golgi complex subunit 7	COG7
0,007	0,66	1,58	157,54	Q8N3X1	Formin-binding protein 4	
0,005	0,65	1,57	156,80	P52789;P52790	Hexokinase-2	HK2
0,040	0,65	1,56	156,48	Q15418	Ribosomal protein S6 kinase alpha-1	RPS6KA1
0,045	0,63	1,55	155,00	Q8WWQ0	PH-interacting protein	PHIP
0,012	0,62	1,54	153,76	Q08945	FACT complex subunit SSRP1	SSRP1
0,048	0,62	1,53	153,38	Q9HCG8	Pre-mRNA-splicing factor CWC22 homolog	CWC22
0,035	0,61	1,53	152,79	Q9ULV4;Q6QEF8	Coronin-1C	CORO1C
0,000	0,61	1,53	152,55	P53396	ATP-citrate synthase	ACLY
0,032	0,61	1,52	152,23	Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2
0,035	0,60	1,52	151,70	P19338	Nucleolin	NCL
0,037	0,60	1,52	151,70	P51948	CDK-activating kinase assembly factor MAT1	MINAT1
0,008	0,59	1,50	150,16	Q92499	ATP-dependent RNA helicase DDX1	DDX1
0,019	0,58	1,50	150,00	Q9Y388	RNA-binding motif protein, X-linked 2	RBMX2
0,013	0,58	1,49	149,23	Q96DH6	RNA-binding protein Musashi homolog 2	MSI2
0,000	0,56	1,48	147,74	O75083	WD repeat-containing protein 1	WDR1
0,026	0,55	1,46	146,26	P00338;Q6ZMR3;P07864	L-lactate dehydrogenase A chain	LDHA
0,024	0,53	1,44	144,04	Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L
0,028	0,52	1,43	143,14	Q9P0V9	Septin-10	Sep.10
0,030	0,52	1,43	142,99	Q9UHB9	Signal recognition particle 68 kDa protein	SRP68
0,009	0,51	1,43	142,65	P06744	Glucose-6-phosphate isomerase	GPI
0,045	0,51	1,42	142,24	P032;P68133;P62736;P63	Actin, alpha cardiac muscle 1;Actin, alpha skeletal muscle;Actin, aortic smooth muscle	ACTC1;ACTA1;ACTA2
0,007	0,50	1,41	141,06	P000571;Q15523;Q9NQIC	ATP-dependent RNA helicase DDX3X;ATP-dependent RNA helicase DDX3Y	DDX3X;DDX3Y
0,039	0,49	1,40	140,42	Q13330	Metastasis-associated protein MTA1	MTA1
0,009	0,47	1,39	138,68	P52888	Thimet oligopeptidase	THOP1
0,017	0,46	1,37	137,33	P46087	Putative ribosomal RNA methyltransferase NOP2	NOP2
0,023	0,46	1,37	137,23	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA
0,034	0,45	1,37	137,03	Q14974	Importin subunit beta-1	KPNB1
0,045	0,45	1,36	136,24	Q96CW5	Gamma-tubulin complex component 3	TUBGCP3
0,026	0,44	1,36	136,08	Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK

Supplemental Table S2a

0,032	0,41	1,32	132,44	P50454	Serpin H1	SERPINH1
0,027	0,40	1,32	131,88	Q15459	Splicing factor 3A subunit 1	SF3A1
0,024	0,39	1,31	131,38	Q9NW13	RNA-binding protein 28	RBM28
0,037	0,38	1,30	130,15	O14979	Heterogeneous nuclear ribonucleoprotein D-like	HNRPDL
0,043	0,38	1,30	130,02	Q12792	Twinfilin-1	TWF1
0,012	0,31	1,24	124,28	P52788	Spermine synthase	SMS
0,003	0,31	1,24	123,79	Q9Y224	UPF0568 protein C14orf166	C14orf166
0,001	0,30	1,24	123,51	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	PPP1CB
0,020	0,30	1,23	123,31	P35249	Replication factor C subunit 4	RFC4
0,006	0,28	1,22	121,74	Q6NZI2	Polymerase I and transcript release factor	PTRF
0,038	0,26	1,20	119,58	Q9C0J8	pre-mRNA 3 end processing protein WDR33	WDR33
0,013	0,25	1,19	119,08	Q14103	Heterogeneous nuclear ribonucleoprotein D0	HNRNPD
24 h Up						
0,00	5,00	31,99	3199,09	Q3ZCM7	Tubulin beta-8 chain	TUBB8
0,02	3,96	15,51	1551,23	Q9H930	Nuclear body protein SP140-like protein	SP140L
0,02	3,92	15,10	1509,72	Q8TC07	TBC1 domain family member 15	TBC1D15
0,00	3,57	11,89	1189,13	P06748	Nucleophosmin	NPM1
0,00	3,32	10,01	1000,55	Q16678	Cytochrome P450 1B1	CYP1B1
0,02	3,25	9,52	952,43	P13929	Beta-enolase	ENO3
0,01	3,03	8,19	818,82	Q9UBB6	Neurochondrin	NCDN
0,00	2,89	7,42	741,89	Q8NI77	Kinesin-like protein KIF18A	KIF18A
0,00	2,88	7,37	736,58	Q13547	Histone deacetylase 1	HDAC1
0,03	2,86	7,24	723,96	P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70
0,00	2,79	6,94	694,01	Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	HIBCH
0,00	2,78	6,88	687,59	Q15121	Astrocytic phosphoprotein PEA-15	PEA15
0,00	2,76	6,78	678,22	P05386	60S acidic ribosomal protein P1	RPLP1
0,02	2,75	6,72	672,02	Q9NZT1	Calmodulin-like protein 5	CALML5
0,00	2,73	6,62	661,93	33778;Q16778;Q8N257;Q6P996;Q6P474	Histone H2B type 1-J;Histone H2B type 1-O;Histone H2B type 1-B;Histone H2B type 1-A	HIST1H2BJ;HIST1H2B;HIST1H2BA;HIST1H2BE
0,04	2,71	6,56	656,32	Q6P996;Q6P474	Pyridoxal-dependent decarboxylase domain-containing protein 1	PDXDC1
0,00	2,69	6,44	643,66	Q16512	Serine/threonine-protein kinase N1	PKN1
0,00	2,62	6,16	616,43	O14791	Apolipoprotein L1	APOL1
0,00	2,61	6,11	611,44	O76054	SEC14-like protein 2	SEC14L2
0,00	2,60	6,07	606,72	Q08554	Desmocollin-1	DSC1

Supplemental Table S2a

0,01	2,55	5,87	586,99	O14874	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial	BCKDK
0,00	2,53	5,79	578,56	P43490	Nicotinamide phosphoribosyltransferase	NAMPT
0,00	2,50	5,68	567,50	P37108	Signal recognition particle 14 kDa protein	SRP14
0,00	2,49	5,62	561,62	P40306	Proteasome subunit beta type-10	PSMB10
0,02	2,47	5,55	554,86	Q6WKZ4;Q7L804	Rab11 family-interacting protein 1	RAB11FIP1
0,01	2,42	5,36	536,37	P17480	Nucleolar transcription factor 1	UBTF
0,03	2,42	5,36	536,00	P15408	Fos-related antigen 2	FOSL2
0,03	2,39	5,26	525,87	Q8IW19	MAX gene-associated protein	MGA
0,00	2,39	5,23	522,90	Q9Y6X8	Zinc fingers and homeoboxes protein 2	ZHX2
0,00	2,37	5,16	515,58	Q7LFL8	CXXC-type zinc finger protein 5	CXXC5
0,03	2,33	5,04	504,43	P06702	Protein S100-A9	S100A9
0,01	2,33	5,02	501,60	Q9P2R7	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2
0,01	2,32	5,01	500,69	Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3	ADPRHL2
0,02	2,32	5,00	500,40	Q13151	Heterogeneous nuclear ribonucleoprotein A0	HNRNPA0
0,03	2,32	4,98	497,76	Q9HAB8	Phosphopantothenate--cysteine ligase	PPCS
0,01	2,28	4,85	485,01	P47736	Rap1 GTPase-activating protein 1	RAP1GAP
0,04	2,28	4,85	484,93	P28290	Sperm-specific antigen 2	SSFA2
0,05	2,26	4,78	478,04	Q9UHY1	Nuclear receptor-binding protein	NRBP1
0,01	2,21	4,63	463,39	P84103	Serine/arginine-rich splicing factor 3	SRSF3
0,01	2,16	4,48	448,44	Q9Y5V0	Zinc finger protein 706	ZNF706
0,00	2,16	4,46	445,84	P22102	Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine	GART
0,01	2,15	4,45	444,96	P46782	40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed	RPS5
0,03	2,14	4,42	442,26	P48200	Iron-responsive element-binding protein 2	IREB2
0,05	2,12	4,36	435,75	Q4V328	GRIP1-associated protein 1	GRIPAP1
0,03	2,12	4,35	434,67	Q9Y4C8	Probable RNA-binding protein 19	RBM19
0,04	2,08	4,24	423,87	P23246	Splicing factor, proline- and glutamine-rich	SFPQ
0,01	2,08	4,23	423,20	P62993	Growth factor receptor-bound protein 2	GRB2
0,00	2,06	4,17	417,01	Q99715	Collagen alpha-1(XII) chain	COL12A1
0,03	2,05	4,15	415,06	Q9H0A0	N-acetyltransferase 10	NAT10
0,01	2,02	4,06	405,55	Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3	PPIL3
0,01	2,00	4,00	400,45	Q6P4E1	Protein CASC4	CASC4
0,02	1,99	3,98	398,20	P35226;P35227	Polycomb complex protein BMI-1	BMI1
0,00	1,98	3,94	393,99	Q9C0J8	pre-mRNA 3 end processing protein WDR33	WDR33

Supplemental Table S2a

0,00	1,95	3,87	386,85	P12273	Prolactin-inducible protein	PIP
0,03	1,95	3,86	385,63	P29218	Inositol monophosphatase 1	IMPA1
0,01	1,92	3,77	377,35	Q9P013	Protein CWC15 homolog	CWC15
0,03	1,91	3,77	376,92	Q15287	RNA-binding protein with serine-rich domain 1	RNPS1
0,00	1,88	3,67	367,17	P39060	Collagen alpha-1(XVIII) chain;Endostatin	COL18A1
0,03	1,84	3,57	357,02	Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	IARS2
0,01	1,83	3,55	355,15	Q9H008	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP
0,03	1,83	3,55	354,94	Q9NX62	Inositol monophosphatase 3	IMPAD1
0,00	1,80	3,48	347,76	Q9H412	Zinc fingers and homeoboxes protein 3	ZHX3
0,02	1,80	3,47	347,07	Q16629	Serine/arginine-rich splicing factor 7	SRSF7
0,04	1,78	3,44	343,67	P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1
0,03	1,78	3,43	342,54	O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2
0,01	1,75	3,36	335,86	Q9H2U1	Probable ATP-dependent RNA helicase DHX36	DHX36
0,02	1,75	3,36	335,65	Q5ZPR3	CD276 antigen	CD276
0,01	1,74	3,35	334,55	Q14512	Fibroblast growth factor-binding protein 1	FGFBP1
0,03	1,74	3,34	334,45	P16220;P18846	Cyclic AMP-responsive element-binding protein 1	CREB1
0,03	1,73	3,32	332,44	P27540	Aryl hydrocarbon receptor nuclear translocator	ARNT
0,00	1,73	3,32	332,13	Q9UPN9	E3 ubiquitin-protein ligase TRIM33	TRIM33
0,02	1,73	3,32	332,05	Q9Y2R4	Probable ATP-dependent RNA helicase DDX52	DDX52
0,00	1,72	3,29	329,12	Q9UKY1	Zinc fingers and homeoboxes protein 1	ZHX1
0,03	1,71	3,28	327,53	P61225	Ras-related protein Rap-2b	RAP2B
0,02	1,71	3,27	327,40	Q9H7L9	Sin3 histone deacetylase corepressor complex component SDS3	SUDS3
0,03	1,71	3,27	326,68	Q8NFH5	Nucleoporin NUP53	NUP35
0,00	1,71	3,26	326,07	P30042	ES1 protein homolog, mitochondrial	C21orf33
0,01	1,69	3,23	322,75	Q15257	Serine/threonine-protein phosphatase 2A activator	PPP2R4
0,04	1,68	3,21	321,38	P80217	Interferon-induced 35 kDa protein	IFI35
0,01	1,68	3,19	319,38	Q9BY42	UPF0549 protein C20orf43	C20orf43
0,01	1,67	3,18	318,43	Q5JTZ9	Alanine--tRNA ligase, mitochondrial	AARS2
0,01	1,67	3,18	318,24	O00186	Syntaxin-binding protein 3	STXBP3
0,01	1,67	3,18	317,98	O00625	Pirin	PIR
0,00	1,66	3,16	315,87	Q8IVL5	Prolyl 3-hydroxylase 2	LEPREL1
0,01	1,66	3,15	315,01	Q9ULM3	YEATS domain-containing protein 2	YEATS2
0,01	1,66	3,15	314,97	P16333	Cytoplasmic protein NCK1	NCK1

Supplemental Table S2a

0,03	1,65	3,15	314,72	O15145	Actin-related protein 2/3 complex subunit 3	ARPC3
0,00	1,65	3,14	314,50	P02751	Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3	FN1
0,02	1,65	3,14	313,86	O00767	Acyl-CoA desaturase	SCD
0,02	1,63	3,09	308,86	O43291	Kunitz-type protease inhibitor 2	SPINT2
0,03	1,62	3,07	306,85	P51948	CDK-activating kinase assembly factor MAT1	MNAT1
0,01	1,62	3,07	306,68	Q02413	Desmoglein-1	DSG1
0,01	1,60	3,03	303,23	Q9ULG6	Cell cycle progression protein 1	CCPG1
0,02	1,59	3,02	301,99	P57081	tRNA (guanine-N(7)-)-methyltransferase subunit WDR4	WDR4
0,04	1,59	3,02	301,88	Q9NZI7	Upstream-binding protein 1	UBP1
0,02	1,59	3,01	301,06	O75164	Lysine-specific demethylase 4A	KDM4A
0,04	1,59	3,01	300,86	P53634	Dipeptidyl peptidase 1;Dipeptidyl peptidase 1 exclusion domain chain;Dipeptidyl pe	CTSC
0,02	1,59	3,00	300,31	O75683	Surfeit locus protein 6	SURF6
0,00	1,59	3,00	300,17	P68366;Q9NY65	Tubulin alpha-4A chain	TUBA4A
0,01	1,58	2,99	298,63	P00918	Carbonic anhydrase 2	CA2
0,03	1,56	2,95	294,60	Q8WWI1	LIM domain only protein 7	LMO7
0,04	1,54	2,90	289,85	P31949	Protein S100-A11	S100A11
0,01	1,53	2,90	289,63	P52926	High mobility group protein HMGI-C	HMGA2
0,01	1,52	2,87	286,59	Q01081;Q8WU68	Splicing factor U2AF 35 kDa subunit;Splicing factor U2AF 26 kDa subunit	U2AF1;U2AF1L4
0,01	1,52	2,86	286,16	Q9NVZ3;Q8NC96	Adaptin ear-binding coat-associated protein 2	NECAP2
0,04	1,52	2,86	285,97	Q9Y226	Solute carrier family 22 member 13	SLC22A13
0,00	1,51	2,84	284,39	P30838;P43353;P48448	Aldehyde dehydrogenase, dimeric NADP-preferring	ALDH3A1
0,00	1,51	2,84	284,16	Q13795	ADP-ribosylation factor-related protein 1	ARFRP1
0,00	1,50	2,83	282,56	Q12962	Transcription initiation factor TFIID subunit 10	TAF10
0,03	1,49	2,81	280,81	P48506	Glutamate--cysteine ligase catalytic subunit	GCLC
0,00	1,47	2,77	276,89	P43243	Matrin-3	MATR3
0,03	1,47	2,76	276,19	Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2
0,00	1,46	2,76	275,58	Q92766	Ras-responsive element-binding protein 1	RREB1
0,02	1,45	2,72	272,32	P35240	Merlin	NF2
0,02	1,44	2,72	272,06	Q9UKJ3	G patch domain-containing protein 8	GPATCH8
0,00	1,43	2,70	269,92	Q96PU8	Protein quaking	QKI
0,00	1,43	2,69	269,35	Q16254	Transcription factor E2F4	E2F4
0,04	1,42	2,67	266,81	P61163	Alpha-centractin	ACTR1A
0,00	1,42	2,67	266,74	P49903	Selenide, water dikinase 1	SEPHS1

Supplemental Table S2a

0,01	1,41	2,66	266,07	Q5QJE6	Deoxynucleotidyltransferase terminal-interacting protein 2	DNTTIP2
0,04	1,41	2,66	265,75	P19447	TFIIH basal transcription factor complex helicase XPB subunit	ERCC3
0,01	1,41	2,66	265,71	Q9H8M2	Bromodomain-containing protein 9	BRD9
0,00	1,41	2,66	265,60	P09917	Arachidonate 5-lipoxygenase	ALOX5
0,03	1,41	2,66	265,56	Q96F63	Coiled-coil domain-containing protein 97	CCDC97
0,00	1,40	2,65	264,78	Q5W0V3;Q86V87	Protein FAM160B1	FAM160B1
0,04	1,40	2,65	264,70	P24468;P10589	COUP transcription factor 2	NR2F2
0,02	1,40	2,64	263,82	O75607	Nucleoplasmin-3	NPM3
0,03	1,38	2,60	259,56	Q9NX58	Cell growth-regulating nucleolar protein	LYAR
0,04	1,37	2,59	258,57	Q8N3F8	MICAL-like protein 1	MICALL1
0,01	1,36	2,57	257,16	Q9H6R0	Putative ATP-dependent RNA helicase DHX33	DHX33
0,00	1,36	2,57	256,74	Q8IYU8	EF-hand domain-containing family member A1	EFHA1
0,00	1,35	2,56	255,77	P53801	Pituitary tumor-transforming gene 1 protein-interacting protein	PTTG1P
0,02	1,35	2,55	255,14	O00763	Acetyl-CoA carboxylase 2;Biotin carboxylase	ACACB
0,02	1,35	2,55	255,01	Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial	PTRH2
0,00	1,34	2,54	253,92	P54727	UV excision repair protein RAD23 homolog B	RAD23B
0,05	1,34	2,53	253,07	Q13740	CD166 antigen	ALCAM
0,01	1,34	2,52	252,50	Q8WUB8	PHD finger protein 10	PHF10
0,02	1,33	2,52	252,06	P17936	Insulin-like growth factor-binding protein 3	IGFBP3
0,00	1,33	2,51	251,39	Q7L4I2	Arginine/serine-rich coiled-coil protein 2	RSRC2
0,00	1,33	2,51	250,99	Q9BQ61	Uncharacterized protein C19orf43	C19orf43
0,00	1,33	2,51	250,83	Q96LT9	RNA-binding protein 40	RNPC3
0,00	1,33	2,51	250,75	Q6P587	Acylpyruvase FAHD1, mitochondrial	FAHD1
0,02	1,31	2,47	247,49	Q92878	DNA repair protein RAD50	RAD50
0,02	1,31	2,47	247,35	Q5JRA6	Melanoma inhibitory activity protein 3	MIA3
0,04	1,30	2,47	246,96	P35659	Protein DEK	DEK
0,05	1,29	2,45	245,28	Q6PJ69	Tripartite motif-containing protein 65	TRIM65
0,03	1,29	2,44	244,17	P38398	Breast cancer type 1 susceptibility protein	BRCA1
0,03	1,28	2,43	242,99	Q86V81	THO complex subunit 4	ALYREF
0,03	1,27	2,42	241,93	Q8IZ69	tRNA (uracil-5-)-methyltransferase homolog A	TRMT2A
0,02	1,27	2,41	241,26	P50579	Methionine aminopeptidase 2	METAP2
0,03	1,26	2,40	239,62	Q8NEJ9	Neuroguidin	NGDN
0,02	1,25	2,38	238,09	Q96RL1	BRCA1-A complex subunit RAP80	UIMC1

Supplemental Table S2a

0,01	1,24	2,37	236,93	Q3YEC7	Rab-like protein 1	PARF
0,00	1,24	2,36	236,48	P09972	Fructose-bisphosphate aldolase C	ALDOC
0,00	1,24	2,36	236,25	Q2TAK8	PWWP domain-containing protein MUM1	MUM1
0,00	1,24	2,36	235,95	Q9NYH9	U3 small nucleolar RNA-associated protein 6 homolog	UTP6
0,01	1,24	2,36	235,62	Q8IYB3	Serine/arginine repetitive matrix protein 1	SRRM1
0,03	1,22	2,33	233,48	Q9H0A8	COMM domain-containing protein 4	COMMD4
0,00	1,22	2,33	233,46	P07195	L-lactate dehydrogenase B chain	LDHB
0,00	1,21	2,31	231,43	Q8IYH5	ZZ-type zinc finger-containing protein 3	ZZZ3
0,00	1,21	2,31	231,42	Q04828;P52895	Aldo-keto reductase family 1 member C1;Aldo-keto reductase family 1 member C2	AKR1C1;AKR1C2
0,01	1,21	2,31	231,11	Q8N2M8	CLK4-associating serine/arginine rich protein	CLASRP
0,00	1,21	2,31	230,89	Q14686	Nuclear receptor coactivator 6	NCOA6
0,00	1,21	2,31	230,76	O60701	UDP-glucose 6-dehydrogenase	UGDH
0,00	1,20	2,30	230,07	Q96EZ8	Microspherule protein 1	MCRS1
0,01	1,20	2,30	229,78	P11277	Spectrin beta chain, erythrocyte	SPTB
0,04	1,19	2,29	228,69	P16435	NADPH--cytochrome P450 reductase	POR
0,03	1,19	2,28	228,22	Q13428	Treacle protein	TCOF1
0,00	1,18	2,27	226,76	P80188	Neutrophil gelatinase-associated lipocalin	LCN2
0,00	1,18	2,26	226,18	P53355	Death-associated protein kinase 1	DAPK1
0,03	1,17	2,25	225,24	P27361	Mitogen-activated protein kinase 3	MAPK3
0,02	1,17	2,25	224,60	Q8WUA8	Tsukushin	TSKU
0,00	1,16	2,23	223,35	O15031	Plexin-B2	PLXNB2
0,00	1,16	2,23	223,15	Q619Y2	THO complex subunit 7 homolog	THOC7
0,01	1,15	2,21	221,46	Q96BD5	PHD finger protein 21A	PHF21A
0,01	1,14	2,21	220,63	O95503	Chromobox protein homolog 6	CBX6
0,00	1,14	2,20	220,48	O00468	Agrin	AGRN
0,00	1,12	2,18	217,72	Q15427	Splicing factor 3B subunit 4	SF3B4
0,01	1,12	2,18	217,70	Q96S94	Cyclin-L2	CCNL2
0,02	1,11	2,16	216,43	O95232	Luc7-like protein 3	LUC7L3
0,02	1,11	2,16	215,88	Q53GQ0	Estradiol 17-beta-dehydrogenase 12	HSD17B12
0,01	1,11	2,16	215,80	P49720	Proteasome subunit beta type-3	PSMB3
0,00	1,10	2,15	214,58	Q5VZF2;Q93079;Q917;Q5QNW6	Histone H2B type 1-K;Histone H2B type F-S;Histone H2B type 1-D;Histone H2B type 1-E	HIST1H2BK;H2BFS;HIST1H2BE;HIST1H2BD
0,03	1,10	2,14	214,03	Q5VZF2	Muscleblind-like protein 2	MBNL2
0,00	1,10	2,14	213,90	Q96D46	60S ribosomal export protein NMD3	NMD3

Supplemental Table S2a

0,00	1,10	2,14	213,79	Q9NX70	Mediator of RNA polymerase II transcription subunit 29	MED29
0,02	1,09	2,14	213,56	Q9BTD8	RNA-binding protein 42	RBM42
0,03	1,08	2,12	211,61	O14925;Q5SRD1	Mitochondrial import inner membrane translocase subunit Tim23;Putative mitocho	TIMM23;TIMM23B
0,02	1,08	2,12	211,57	P10451;CON__P31096	Osteopontin	SPP1
0,00	1,07	2,11	210,65	Q9NR56	Muscleblind-like protein 1	MBNL1
0,00	1,07	2,10	210,36	Q9H981	Actin-related protein 8	ACTR8
0,00	1,07	2,10	210,00	Q9H0G5	Nuclear speckle splicing regulatory protein 1	NSRP1
0,01	1,06	2,09	208,93	Q06587	E3 ubiquitin-protein ligase RING1	RING1
0,00	1,06	2,08	207,97	Q6P4R8	Nuclear factor related to kappa-B-binding protein	NFRKB
0,00	1,06	2,08	207,97	P06454	Prothymosin alpha;Thymosin alpha-1	PTMA
0,00	1,05	2,08	207,73	P51825	AF4/FMR2 family member 1	AFF1
0,02	1,05	2,06	206,40	Q13889	General transcription factor IIH subunit 3	GTF2H3
0,00	1,04	2,06	206,12	Q15532	Protein SSXT	SS18
0,00	1,04	2,06	205,86	Q9UKI8	Serine/threonine-protein kinase tousled-like 1	TLK1
0,01	1,04	2,05	205,15	Q7Z3B3	KAT8 regulatory NSL complex subunit 1	KANSL1
0,02	1,03	2,04	203,80	Q01469;A8MUU1	Fatty acid-binding protein, epidermal	FABP5
0,00	1,03	2,04	203,70	O95359	Transforming acidic coiled-coil-containing protein 2	TACC2
0,01	1,03	2,04	203,59	Q9NVR2	Integrator complex subunit 10	INTS10
0,01	1,02	2,02	202,24	Q9H0B6	Kinesin light chain 2	KLC2
0,00	1,01	2,02	201,91	P05549;Q92481	Transcription factor AP-2-alpha;Transcription factor AP-2-beta	TFAP2A;TFAP2B
0,00	1,01	2,02	201,64	Q8WUQ7	Uncharacterized protein C19orf29	C19orf29
0,05	1,01	2,02	201,52	Q008S8	Epithelial cell-transforming sequence 2 oncogene-like	ECT2L
0,04	1,01	2,01	201,21	Q9BRD0	BUD13 homolog	BUD13
0,00	1,00	2,01	200,60	Q96JM7	Lethal(3)malignant brain tumor-like protein 3	L3MBTL3
0,00	1,00	2,00	200,44	Q06330	Recombining binding protein suppressor of hairless	RBPJ
0,01	1,00	2,00	200,34	Q01658	Protein Dr1	DR1
0,02	1,00	2,00	199,86	P05067	Amyloid beta A4 protein;N-APP;Soluble APP-alpha;Soluble APP-beta;C99;Beta-amyli	APP
0,05	1,00	2,00	199,53	Q32P28	Prolyl 3-hydroxylase 1	LEPRE1
0,05	1,00	1,99	199,40	Q5T749	Keratinocyte proline-rich protein	KPRP
0,02	1,00	1,99	199,34	Q9P260	LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468
0,00	0,99	1,99	199,11	O60885	Bromodomain-containing protein 4	BRD4
0,04	0,99	1,99	198,97	Q53EL6	Programmed cell death protein 4	PDCD4
0,00	0,99	1,99	198,80	Q9BVJ6;Q5TAP6	U3 small nucleolar RNA-associated protein 14 homolog A	UTP14A

Supplemental Table S2a

0,01	0,99	1,98	198,17	P26583	High mobility group protein B2	HMGB2
0,04	0,98	1,98	197,63	Q76FK4	Nucleolar protein 8	NOL8
0,01	0,98	1,98	197,61	P08651	Nuclear factor 1 C-type	NFIC
0,00	0,98	1,97	196,58	Q9UPQ0	LIM and calponin homology domains-containing protein 1	LIMCH1
0,03	0,97	1,96	196,30	Q86VW0	SEC14 domain and spectrin repeat-containing protein 1	SESTD1
0,00	0,97	1,95	195,35	Q9UPQ3;Q96P47	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	AGAP1
0,02	0,97	1,95	195,21	P35222	Catenin beta-1	CTNNB1
0,04	0,96	1,95	195,17	Q75N03	E3 ubiquitin-protein ligase Hakai	CBLL1
0,02	0,96	1,95	195,08	P80723	Brain acid soluble protein 1	BASP1
0,00	0,96	1,95	194,71	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1
0,00	0,96	1,94	194,18	Q674X7	Kazrin	KAZN
0,00	0,96	1,94	194,11	Q99961;Q99962	Endophilin-A2	SH3GL1
0,00	0,95	1,93	193,46	P46934	E3 ubiquitin-protein ligase NEDD4	NEDD4
0,00	0,95	1,93	193,28	Q03112	MDS1 and EVI1 complex locus protein EVI1	MECOM
0,02	0,95	1,93	192,96	Q8N3C0	Activating signal cointegrator 1 complex subunit 3	ASCC3
0,00	0,95	1,93	192,52	B1AK53	Espin	ESPN
0,00	0,94	1,91	191,37	P13674	Prolyl 4-hydroxylase subunit alpha-1	P4HA1
0,00	0,94	1,91	191,30	Q5TGY3	AT-hook DNA-binding motif-containing protein 1	AHDC1
0,00	0,94	1,91	191,28	Q16352;P41219;P12036	Vimentin	VIM
0,05	0,93	1,91	191,04	P60953	Cell division control protein 42 homolog	CDC42
0,03	0,93	1,91	191,01	O15116	U6 snRNA-associated Sm-like protein LSm1	LSM1
0,00	0,93	1,91	190,53	P35080	Profilin-2	PFN2
0,04	0,92	1,90	189,63	P06744	Glucose-6-phosphate isomerase	GPI
0,05	0,92	1,90	189,61	O00165	HCLS1-associated protein X-1	HAX1
0,00	0,92	1,90	189,52	Q15554	Telomeric repeat-binding factor 2	TERF2
0,02	0,92	1,89	189,47	O75376	Nuclear receptor corepressor 1	NCOR1
0,04	0,92	1,89	189,08	Q53F19	Uncharacterized protein C17orf85	C17orf85
0,04	0,92	1,89	189,07	P35270	Sepiapterin reductase	SPR
0,00	0,91	1,88	188,39	Q9BXP5	Serrate RNA effector molecule homolog	SRRT
0,04	0,91	1,88	188,12	O95067	G2/mitotic-specific cyclin-B2	CCNB2
0,00	0,91	1,88	188,03	Q92541	RNA polymerase-associated protein RTF1 homolog	RTF1
0,00	0,91	1,88	188,01	Q9HCK8	Chromodomain-helicase-DNA-binding protein 8	CHD8
0,02	0,91	1,88	187,82	Q9Y6R0	Numb-like protein	NUMBL

Supplemental Table S2a

0,05	0,91	1,88	187,67	Q6RFH5	WD repeat-containing protein 74	WDR74
0,00	0,91	1,88	187,55	P98160	Basement membrane-specific heparan sulfate proteoglycan core protein;Endorepellin	HSPG2
0,01	0,91	1,88	187,52	Q01167	Forkhead box protein K2	FO XK2
0,01	0,90	1,87	187,16	P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PPP2CA
0,04	0,90	1,87	186,82	O14686	Histone-lysine N-methyltransferase MLL2	MLL2
0,00	0,90	1,87	186,79	P61981	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	YWHAG
0,02	0,90	1,86	186,30	Q8NFW8	N-acetylneuraminase cytidyltransferase	CMAS
0,03	0,89	1,86	185,91	Q86VM9	Zinc finger CCCH domain-containing protein 18	ZC3H18
0,01	0,89	1,86	185,90	Q9UL33	Trafficking protein particle complex subunit 2-like protein	TRAPPC2L
0,00	0,89	1,86	185,89	P62805	Histone H4	HIST1H4A
0,01	0,89	1,86	185,84	O95391	Pre-mRNA-splicing factor SLU7	SLU7
0,01	0,89	1,86	185,55	P29084	Transcription initiation factor IIE subunit beta	GTF2E2
0,00	0,89	1,85	185,43	Q8TF68	Zinc finger protein 384	ZNF384
0,02	0,89	1,85	185,35	Q9NVH1	DnaJ homolog subfamily C member 11	DNAJC11
0,01	0,89	1,85	184,84	Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2
0,01	0,88	1,84	184,28	Q96DH6	RNA-binding protein Musashi homolog 2	MSI2
0,03	0,88	1,84	184,24	P48507	Glutamate--cysteine ligase regulatory subunit	GCLM
0,00	0,87	1,83	183,25	O60828	Polyglutamine-binding protein 1	PQBP1
0,03	0,87	1,83	182,82	P63096	Guanine nucleotide-binding protein G(i) subunit alpha-1	GNAI1
0,05	0,87	1,82	182,25	Q7L7X3	Serine/threonine-protein kinase TAO1	TAOK1
0,01	0,86	1,82	181,76	Q96P16	Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A
0,05	0,86	1,82	181,61	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1
0,01	0,86	1,81	181,37	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21
0,00	0,86	1,81	181,19	Q13501	Sequestosome-1	SQSTM1
0,00	0,86	1,81	181,12	P35052	Glypican-1;Secreted glypican-1	GPC1
0,00	0,86	1,81	181,10	Q16630	Cleavage and polyadenylation specificity factor subunit 6	CPSF6
0,02	0,85	1,81	180,53	P55268	Laminin subunit beta-2	LAMB2
0,04	0,85	1,80	180,49	P35680	Hepatocyte nuclear factor 1-beta	HNF1B
0,00	0,85	1,80	180,32	Q14978	Nucleolar and coiled-body phosphoprotein 1	NOLC1
0,02	0,85	1,80	180,09	Q3KQU3	MAP7 domain-containing protein 1	MAP7D1
0,01	0,85	1,80	179,73	Q9UMN6	Histone-lysine N-methyltransferase MLL4	WBP7
0,01	0,84	1,79	179,47	Q9Y2T2	AP-3 complex subunit mu-1	AP3M1
0,05	0,84	1,79	179,08	P18827	Syndecan-1	SDC1

Supplemental Table S2a

0,00	0,84	1,79	178,74	Q8IY67	Ribonucleoprotein PTB-binding 1	RAVER1
0,00	0,84	1,79	178,57	P37275	Zinc finger E-box-binding homeobox 1	ZEB1
0,01	0,83	1,78	178,04	Q9UFF9	CCR4-NOT transcription complex subunit 8	CNOT8
0,02	0,83	1,78	177,97	Q75QN2	Integrator complex subunit 8	INTS8
0,00	0,83	1,78	177,75	Q96EV2	RNA-binding protein 33	RBM33
0,00	0,83	1,77	177,38	O75937	DnaJ homolog subfamily C member 8	DNAJC8
0,00	0,82	1,77	176,53	P82979	SAP domain-containing ribonucleoprotein	SARNP
0,00	0,82	1,77	176,52	P33240	Cleavage stimulation factor subunit 2	CSTF2
0,00	0,81	1,76	175,81	Q6SPF0	Atherin	SAMD1
0,03	0,81	1,76	175,66	Q99959	Plakophilin-2	PKP2
0,00	0,81	1,76	175,61	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus	ACIN1
0,00	0,81	1,75	175,43	Q5T8P6	RNA-binding protein 26	RBM26
0,00	0,81	1,75	175,32	P35221;Q9UI47	Catenin alpha-1	CTNNA1
0,04	0,81	1,75	175,21	P07311	Acylphosphatase-1	ACYP1
0,00	0,81	1,75	175,09	Q6PJG2	Uncharacterized protein C14orf43	C14orf43
0,02	0,81	1,75	175,07	P54578	Ubiquitin carboxyl-terminal hydrolase 14	USP14
0,01	0,81	1,75	174,83	Q6P6C2	Probable alpha-ketoglutarate-dependent dioxygenase ABH5	ALKBH5
0,01	0,80	1,74	174,43	Q7Z6E9	E3 ubiquitin-protein ligase RBBP6	RBBP6
0,02	0,80	1,74	174,11	P54274	Telomeric repeat-binding factor 1	TERF1
0,00	0,80	1,74	173,96	Q92925;Q6STE5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily 1	SMARCD2
0,00	0,80	1,74	173,92	O94880	PHD finger protein 14	PHF14
0,01	0,79	1,73	173,47	P63165	Small ubiquitin-related modifier 1	SUMO1
0,00	0,79	1,73	173,25	Q6ZSJ8	Uncharacterized protein C1orf122	C1orf122
0,02	0,79	1,73	173,23	Q9NYB0	Telomeric repeat-binding factor 2-interacting protein 1	TERF2IP
0,01	0,79	1,72	172,42	P08237	6-phosphofructokinase, muscle type	PFKM
0,01	0,78	1,72	172,29	O43396	Thioredoxin-like protein 1	TXNL1
0,02	0,78	1,72	172,23	Q99569	Plakophilin-4	PKP4
0,01	0,77	1,71	170,95	O43670	Zinc finger protein 207	ZNF207
0,05	0,77	1,71	170,81	16777;Q9BTM1;Q96KK5	Histone H2A type 1;Histone H2A type 1-D;Histone H2A type 2-A;Histone H2A type 2-B	HIST1H2AG;HIST1H2BD
0,03	0,77	1,71	170,79	Q15208	Serine/threonine-protein kinase 38	STK38
0,02	0,77	1,71	170,66	Q9NQG5	Regulation of nuclear pre-mRNA domain-containing protein 1B	RPRD1B
0,02	0,77	1,70	170,33	O95218	Zinc finger Ran-binding domain-containing protein 2	ZRANB2
0,03	0,77	1,70	170,31	Q96ES7	SAGA-associated factor 29 homolog	CCDC101

Supplemental Table S2a

0,01	0,77	1,70	170,14	P85037	Forkhead box protein K1	FOXK1
0,01	0,76	1,70	169,88	P27695	DNA-(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, n	APEX1
0,00	0,76	1,69	169,48	Q15059	Bromodomain-containing protein 3	BRD3
0,02	0,76	1,69	169,40	Q14011	Cold-inducible RNA-binding protein	CIRBP
0,00	0,76	1,69	169,27	Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	GNL3L
0,03	0,76	1,69	169,16	Q96FK6	WD repeat-containing protein 89	WDR89
0,02	0,76	1,69	168,94	Q9HBM6	Transcription initiation factor TFIID subunit 9B	TAF9B
0,02	0,76	1,69	168,84	Q8TB45	DEP domain-containing mTOR-interacting protein	DEPTOR
0,00	0,75	1,68	168,37	Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein	SNRNP40
0,04	0,75	1,68	168,32	Q6UX04	Peptidyl-prolyl cis-trans isomerase CWC27 homolog	CWC27
0,00	0,75	1,68	168,06	Q01518	Adenylyl cyclase-associated protein 1	CAP1
0,01	0,75	1,68	167,71	Q96CB8	Integrator complex subunit 12	INTS12
0,02	0,74	1,67	167,49	O00291	Huntingtin-interacting protein 1	HIP1
0,00	0,74	1,67	167,41	3;CON__H-INV:HIT0000	Keratin, type I cytoskeletal 18	KRT18
0,00	0,74	1,67	166,66	Q96C57	Uncharacterized protein C12orf43	C12orf43
0,01	0,74	1,67	166,61	Q7Z589	Protein EMSY	EMSY
0,02	0,74	1,67	166,57	O15347	High mobility group protein B3	HMGB3
0,03	0,74	1,66	166,45	Q9HCJ3	Ribonucleoprotein PTB-binding 2	RAVER2
0,01	0,73	1,66	166,20	Q9H8G2	Caspase activity and apoptosis inhibitor 1	CAAP1
0,00	0,73	1,66	166,09	Q9BZL4	Protein phosphatase 1 regulatory subunit 12C	PPP1R12C
0,00	0,73	1,66	165,92	P51608	Methyl-CpG-binding protein 2	MECP2
0,01	0,73	1,66	165,83	P00519	Tyrosine-protein kinase ABL1	ABL1
0,00	0,73	1,66	165,77	Q12888	Tumor suppressor p53-binding protein 1	TP53BP1
0,01	0,73	1,65	165,37	O43719	HIV Tat-specific factor 1	HTATSF1
0,03	0,72	1,65	165,23	P98095	Fibulin-2	FBLN2
0,01	0,72	1,65	165,11	Q8NEF9	Serum response factor-binding protein 1	SRFBP1
0,00	0,72	1,65	165,00	Q9NVC6	Mediator of RNA polymerase II transcription subunit 17	MED17
0,00	0,71	1,64	163,97	P01034	Cystatin-C	CST3
0,00	0,71	1,64	163,69	P39880	Homeobox protein cut-like 1	CUX1
0,03	0,71	1,64	163,56	P21127;Q9UQ88	Cyclin-dependent kinase 11B;Cyclin-dependent kinase 11A	CDK11B;CDK11A
0,00	0,71	1,63	163,49	Q5T5P2	Sickle tail protein homolog	SKT
0,00	0,71	1,63	163,37	P35580	Myosin-10	MYH10
0,01	0,71	1,63	163,05	Q9BRX2	Protein pelota homolog	PELO

Supplemental Table S2a

0,02	0,70	1,63	163,01	Q15637	Splicing factor 1	SF1
0,02	0,70	1,63	162,58	Q7Z6R9	Transcription factor AP-2-delta	TFAP2D
0,00	0,70	1,62	162,49	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1
0,00	0,70	1,62	162,46	Q99497	Protein DJ-1	PARK7
0,01	0,70	1,62	162,37	Q8NFC6;Q96IK1	Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1
0,00	0,70	1,62	162,30	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1
0,03	0,70	1,62	162,27	Q93034	Cullin-5	CUL5
0,01	0,70	1,62	162,25	Q96T60	Bifunctional polynucleotide phosphatase/kinase;Polynucleotide 3-phosphatase;Poly	PNKP
0,02	0,70	1,62	162,17	Q93099	Homogentisate 1,2-dioxygenase	HGD
0,01	0,70	1,62	162,05	Q14151	Scaffold attachment factor B2	SAFB2
0,01	0,70	1,62	161,95	Q9ULL5	Proline-rich protein 12	PRR12
0,01	0,69	1,62	161,65	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B
0,01	0,69	1,61	161,06	Q92785;Q92782	Zinc finger protein ubi-d4	DPF2
0,00	0,69	1,61	160,93	O15231	Zinc finger protein 185	ZNF185
0,00	0,69	1,61	160,78	P39748	Flap endonuclease 1	FEN1
0,00	0,68	1,61	160,72	Q06481	Amyloid-like protein 2	APLP2
0,04	0,68	1,61	160,54	O75962	Triple functional domain protein	TRIO
0,03	0,68	1,60	160,37	Q14687	Genetic suppressor element 1	GSE1
0,02	0,68	1,60	160,27	Q09028	Histone-binding protein RBBP4	RBBP4
0,03	0,67	1,60	159,66	P27797	Calreticulin	CALR
0,00	0,67	1,60	159,56	O75928	E3 SUMO-protein ligase PIAS2	PIAS2
0,02	0,67	1,59	159,37	Q6EEV6;P55854;P61956	Small ubiquitin-related modifier 4;Small ubiquitin-related modifier 3;Small ubiquitin	SUMO4;SUMO3;SUMO5
0,00	0,67	1,59	159,25	P23193;Q15560	Transcription elongation factor A protein 1	TCEA1
0,02	0,67	1,59	159,24	Q13185	Chromobox protein homolog 3	CBX3
0,00	0,67	1,59	159,15	Q9UMS4	Pre-mRNA-processing factor 19	PRPF19
0,04	0,67	1,59	159,12	Q9NP50	Protein FAM60A	FAM60A
0,01	0,67	1,59	158,88	P30504	HLA class I histocompatibility antigen, Cw-4 alpha chain	HLA-C
0,00	0,66	1,58	158,40	Q86WB0	Nuclear-interacting partner of ALK	ZC3HC1
0,02	0,66	1,58	158,22	Q66PJ3	ADP-ribosylation factor-like protein 6-interacting protein 4	ARL6IP4
0,00	0,66	1,58	158,02	Q9NXV6	CDKN2A-interacting protein	CDKN2AIP
0,01	0,66	1,58	157,61	P60174	Triosephosphate isomerase	TPI1
0,01	0,66	1,58	157,50	Q13217	DnaJ homolog subfamily C member 3	DNAJC3
0,02	0,65	1,57	157,41	Q15652	Probable JmjC domain-containing histone demethylation protein 2C	JMJD1C

Supplemental Table S2a

0,05	0,65	1,57	157,40	Q02086	Transcription factor Sp2	SP2
0,00	0,65	1,57	157,37	Q05682	Caldesmon	CALD1
0,00	0,65	1,57	157,12	Q16186	Proteasomal ubiquitin receptor ADRM1	ADRM1
0,04	0,65	1,57	157,08	Q8NAV1	Pre-mRNA-splicing factor 38A	PRPF38A
0,02	0,65	1,57	156,92	Q9UHB6	LIM domain and actin-binding protein 1	LIMA1
0,00	0,65	1,57	156,82	Q9UFW8	CGG triplet repeat-binding protein 1	CGGBP1
0,05	0,65	1,57	156,79	Q4VC44	FLYWCH-type zinc finger-containing protein 1	FLYWCH1
0,00	0,65	1,57	156,76	Q9BTC0	Death-inducer obliterator 1	DIDO1
0,00	0,65	1,57	156,63	P09661	U2 small nuclear ribonucleoprotein A	SNRPA1
0,00	0,65	1,57	156,57	P33176;O60282;Q1284C	Kinesin-1 heavy chain	KIF5B
0,00	0,64	1,56	156,10	Q9UHD8	Septin-9	40057,00
0,00	0,64	1,56	156,08	Q16181	Septin-7	39326,00
0,02	0,64	1,56	155,93	Q01085	Nucleolysin TIAR	TIAL1
0,02	0,64	1,56	155,71	P35251	Replication factor C subunit 1	RFC1
0,02	0,64	1,56	155,52	Q9UKD1	Glucocorticoid modulatory element-binding protein 2	GMEB2
0,05	0,64	1,55	155,39	Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2
0,00	0,63	1,55	155,22	P49915	GMP synthase [glutamine-hydrolyzing]	GMPS
0,00	0,63	1,55	155,01	Q15906	Vacuolar protein sorting-associated protein 72 homolog	VPS72
0,01	0,63	1,55	154,93	P51571	Translocon-associated protein subunit delta	SSR4
0,04	0,63	1,55	154,82	Q9BXB4;Q9BXB5	Oxysterol-binding protein-related protein 11	OSBPL11
0,03	0,63	1,55	154,77	Q08945	FACT complex subunit SSRP1	SSRP1
0,05	0,63	1,55	154,77	P46100	Transcriptional regulator ATRX	ATRX
0,00	0,63	1,55	154,73	P06753	Tropomyosin alpha-3 chain	TPM3
0,00	0,63	1,54	154,47	P25440	Bromodomain-containing protein 2	BRD2
0,02	0,63	1,54	154,31	Q8NDX5	Polyhomeotic-like protein 3	PHC3
0,00	0,63	1,54	154,31	P48059;Q7Z4I7	LIM and senescent cell antigen-like-containing domain protein 1;LIM and senescent	LIMS1;LIMS2
0,01	0,62	1,54	154,07	Q99590	Protein SCAF11	SCAF11
0,03	0,62	1,54	153,53	O95833	Chloride intracellular channel protein 3	CLIC3
0,02	0,62	1,54	153,52	Q9ULR0	Pre-mRNA-splicing factor ISY1 homolog	ISY1
0,00	0,62	1,54	153,50	Q9Y277	Voltage-dependent anion-selective channel protein 3	VDAC3
0,04	0,61	1,53	153,06	Q9H4L4	Sentrin-specific protease 3	SEN3
0,04	0,61	1,53	153,05	Q96SB3	Neurabin-2	PPP1R9B
0,00	0,61	1,53	152,53	Q9UHF7	Zinc finger transcription factor Trps1	TRPS1

Supplemental Table S2a

0,00	0,61	1,52	152,37	O15230	Laminin subunit alpha-5	LAMA5
0,01	0,60	1,52	152,00	P20810	Calpastatin	CAST
0,04	0,60	1,52	151,90	Q6P1N0	Coiled-coil and C2 domain-containing protein 1A	CC2D1A
0,02	0,60	1,51	151,30	Q9UHG0	Doublecortin domain-containing protein 2	DCDC2
0,02	0,60	1,51	151,09	P35637	RNA-binding protein FUS	FUS
0,00	0,59	1,51	150,62	P08572	Collagen alpha-2(IV) chain;Canstatin	COL4A2
0,04	0,59	1,50	150,25	O15047	Histone-lysine N-methyltransferase SETD1A	SETD1A
0,01	0,59	1,50	150,17	P00390	Glutathione reductase, mitochondrial	GSR
0,01	0,58	1,50	149,98	Q9UQR1	Zinc finger protein 148	ZNF148
0,01	0,58	1,49	149,45	P29372	DNA-3-methyladenine glycosylase	MPG
0,00	0,58	1,49	149,36	Q9H307	Pinin	PNN
0,00	0,58	1,49	149,15	Q9NVA2	Septin-11	40787,00
0,00	0,57	1,49	148,97	Q7Z6I8	UPF0461 protein C5orf24	C5orf24
0,01	0,57	1,49	148,79	P37837	Transaldolase	TALDO1
0,00	0,57	1,49	148,68	Q9H0L4	Cleavage stimulation factor subunit 2 tau variant	CSTF2T
0,04	0,57	1,48	148,26	P46087	Putative ribosomal RNA methyltransferase NOP2	NOP2
0,00	0,56	1,48	147,84	Q9Y2S0	DNA-directed RNA polymerases I and III subunit RPAC2	POLR1D
0,02	0,56	1,48	147,82	Q15599	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	SLC9A3R2
0,00	0,56	1,48	147,59	Q6WCQ1	Myosin phosphatase Rho-interacting protein	MPRIP
0,01	0,56	1,47	147,38	P11047	Laminin subunit gamma-1	LAMC1
0,01	0,56	1,47	147,34	Q9UJU6	Drebrin-like protein	DBNL
0,01	0,56	1,47	147,22	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7
0,00	0,56	1,47	147,17	P98175	RNA-binding protein 10	RBM10
0,00	0,56	1,47	147,15	P28799	Granulins;Acrogranin;Paragranulin;Granulin-1;Granulin-2;Granulin-3;Granulin-4;Granulin-5	GRN
0,00	0,56	1,47	147,13	O43290	U4/U6.U5 tri-snRNP-associated protein 1	SART1
0,04	0,55	1,47	146,76	Q9H0E3	Histone deacetylase complex subunit SAP130	SAP130
0,02	0,55	1,46	146,48	Q12959	Disks large homolog 1	DLG1
0,00	0,55	1,46	146,46	Q7Z3K3	Pogo transposable element with ZNF domain	POGZ
0,02	0,55	1,46	146,08	Q99547	M-phase phosphoprotein 6	MPHOSPH6
0,03	0,55	1,46	145,91	Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13
0,00	0,54	1,46	145,65	P45880	Voltage-dependent anion-selective channel protein 2	VDAC2
0,00	0,54	1,46	145,51	P52907	F-actin-capping protein subunit alpha-1	CAPZA1
0,00	0,54	1,45	145,15	Q8N7H5	RNA polymerase II-associated factor 1 homolog	PAF1

Supplemental Table S2a

0,00	0,54	1,45	145,14	P49750	YLP motif-containing protein 1	YLPM1
0,02	0,54	1,45	144,94	P43307	Translocon-associated protein subunit alpha	SSR1
0,00	0,53	1,45	144,85	Q96ST3	Paired amphipathic helix protein Sin3a	SIN3A
0,00	0,53	1,45	144,83	O43684	Mitotic checkpoint protein BUB3	BUB3
0,04	0,53	1,45	144,68	Q9UHD9	Ubiquilin-2	UBQLN2
0,00	0,53	1,44	144,36	Q13363	C-terminal-binding protein 1	CTBP1
0,00	0,53	1,44	144,36	Q9HC52	Chromobox protein homolog 8	CBX8
0,00	0,53	1,44	144,31	IM9;P0DMN0;P50225;P50226		
0,01	0,52	1,44	143,85	Q12830	Nucleosome-remodeling factor subunit BPTF	BPTF
0,01	0,52	1,44	143,84	P18621	60S ribosomal protein L17	RPL17
0,00	0,52	1,44	143,76	Q9Y6X9;Q86VD1	MORC family CW-type zinc finger protein 2	MORC2
0,05	0,52	1,44	143,68	Q8N4P3	Guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase MESH1	HDDC3
0,01	0,52	1,43	142,93	Q9UQE7	Structural maintenance of chromosomes protein 3	SMC3
0,02	0,51	1,43	142,70	Q8WVC0	RNA polymerase-associated protein LEO1	LEO1
0,00	0,51	1,42	142,32	Q9H1B7	Interferon regulatory factor 2-binding protein-like	IRF2BPL
0,01	0,51	1,42	142,14	O43395	U4/U6 small nuclear ribonucleoprotein Prp3	PRPF3
0,00	0,51	1,42	142,14	Q8IX12	Cell division cycle and apoptosis regulator protein 1	CCAR1
0,02	0,51	1,42	142,11	Q08211	ATP-dependent RNA helicase A	DHX9
0,00	0,50	1,42	141,89	P35579	Myosin-9	MYH9
0,05	0,50	1,42	141,84	Q8IXM2	Chromatin complexes subunit BAP18	BAP18
0,02	0,50	1,42	141,71	Q9BZ95	Histone-lysine N-methyltransferase NSD3	WHSC1L1
0,00	0,50	1,42	141,69	Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2
0,01	0,49	1,41	140,79	Q9NVM9	Protein asunder homolog	Asun
0,00	0,49	1,41	140,78	P52701	DNA mismatch repair protein Msh6	MSH6
0,00	0,49	1,41	140,59	P13807	Glycogen [starch] synthase, muscle	GYS1
0,04	0,49	1,41	140,51	O60292	Signal-induced proliferation-associated 1-like protein 3	SIPA1L3
0,00	0,49	1,40	140,31	Q86YP4	Transcriptional repressor p66-alpha	GATAD2A
0,03	0,49	1,40	140,27	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23	DDX23
0,01	0,49	1,40	139,98	P22234	Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthetase	PAICS
0,01	0,48	1,40	139,92	O00712	Nuclear factor 1 B-type	NFIB
0,05	0,48	1,40	139,72	A0AV96;Q9NQ94	RNA-binding protein 47	RBM47
0,03	0,48	1,40	139,64	P33991;Q9UJA3	DNA replication licensing factor MCM4	MCM4
0,01	0,48	1,39	139,48	Q12996	Cleavage stimulation factor subunit 3	CSTF3

Supplemental Table S2a

0,00	0,48	1,39	139,41	P49756	RNA-binding protein 25	RBM25
0,01	0,48	1,39	139,08	Q969V3	Nicalin	NCLN
0,00	0,47	1,39	138,98	O76027	Annexin A9	ANXA9
0,03	0,47	1,39	138,91	Q9UBL3	Set1/Ash2 histone methyltransferase complex subunit ASH2	ASH2L
0,03	0,47	1,39	138,69	P35241	Radixin	RDX
0,00	0,47	1,39	138,56	Q8IVT2	Uncharacterized protein C19orf21	C19orf21
0,00	0,47	1,38	138,42	42;O15405;O94900;Q969V3	TOX high mobility group box family member 4	TOX4
0,02	0,46	1,38	137,87	Q9BRT2	Mitochondrial nucleoid factor 1	MNF1
0,01	0,46	1,38	137,83	Q9NWH9	SAFB-like transcription modulator	SLTM
0,00	0,46	1,38	137,60	Q5JWF2;P63092;P38405	Guanine nucleotide-binding protein G(s) subunit alpha isoforms X1	GNAS
0,00	0,46	1,37	137,34	P18669;Q8N0Y7;P15259	Phosphoglycerate mutase 1	PGAM1
0,01	0,46	1,37	137,32	Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47
0,00	0,46	1,37	137,17	Q9P2E9	Ribosome-binding protein 1	RRBP1
0,01	0,45	1,37	136,58	P52756	RNA-binding protein 5	RBM5
0,00	0,45	1,37	136,52	Q12972	Nuclear inhibitor of protein phosphatase 1;Activator of RNA decay	PPP1R8
0,03	0,45	1,37	136,51	P07237	Protein disulfide-isomerase	P4HB
0,01	0,45	1,36	136,47	316;P01892;P16190;P16191	HLA class I histocompatibility antigen, A-68 alpha chain;HLA class I histocompatibility antigen A-68	HLA-A
0,00	0,45	1,36	136,43	Q14683	Structural maintenance of chromosomes protein 1A	SMC1A
0,03	0,45	1,36	136,28	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2
0,00	0,45	1,36	136,16	O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	OGT
0,01	0,44	1,36	136,09	P14923	Junction plakoglobin	JUP
0,01	0,44	1,36	135,78	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4
0,05	0,44	1,36	135,72	O43823	A-kinase anchor protein 8	AKAP8
0,04	0,44	1,35	135,39	Q9UKM9	RNA-binding protein Raly	RALY
0,01	0,43	1,35	134,57	O75534	Cold shock domain-containing protein E1	CSDE1
0,02	0,43	1,34	134,43	O15014	Zinc finger protein 609	ZNF609
0,00	0,42	1,34	133,87	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1
0,00	0,42	1,34	133,80	Q01082	Spectrin beta chain, brain 1	SPTBN1
0,00	0,41	1,33	132,78	P12429	Annexin A3	ANXA3
0,02	0,41	1,33	132,56	Q13884	Beta-1-syntrophin	SNTB1
0,02	0,41	1,32	132,50	P15144	Aminopeptidase N	ANPEP
0,04	0,41	1,32	132,49	Q8N684	Cleavage and polyadenylation specificity factor subunit 7	CPSF7
0,02	0,41	1,32	132,46	O75940	Survival of motor neuron-related-splicing factor 30	SMNDC1

Supplemental Table S2a

0,01	0,40	1,32	132,38	O60437	Periplakin	PPL
0,00	0,40	1,32	132,36	Q5VUA4	Zinc finger protein 318	ZNF318
0,02	0,40	1,32	132,29	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2
0,00	0,40	1,32	132,01	Q9BZZ5	Apoptosis inhibitor 5	API5
0,04	0,40	1,32	131,66	P63220	40S ribosomal protein S21	RPS21
0,00	0,40	1,32	131,57	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	GNB2
0,00	0,39	1,31	130,94	P33993	DNA replication licensing factor MCM7	MCM7
0,02	0,39	1,31	130,83	Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86
0,00	0,39	1,31	130,78	Q8NB4	Golgi membrane protein 1	GOLM1
0,02	0,39	1,31	130,62	Q9NUU7;Q9UMR2	ATP-dependent RNA helicase DDX19A;ATP-dependent RNA helicase DDX19B	DDX19A;DDX19B
0,00	0,38	1,31	130,54	P09429;B2RPK0	High mobility group protein B1;Putative high mobility group protein B1-like 1	HMGB1;HMGB1P1
0,00	0,38	1,30	130,49	Q14980	Nuclear mitotic apparatus protein 1	NUMA1
0,04	0,38	1,30	130,44	Q5SSJ5	Heterochromatin protein 1-binding protein 3	HP1BP3
0,00	0,38	1,30	130,24	P11021	78 kDa glucose-regulated protein	HSPA5
0,02	0,38	1,30	129,97	P23229	Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain	ITGA6
0,05	0,38	1,30	129,71	Q6NZY4	Zinc finger CCHC domain-containing protein 8	ZCCHC8
0,02	0,37	1,30	129,59	P47755	F-actin-capping protein subunit alpha-2	CAPZA2
0,01	0,37	1,29	129,49	Q86UP2	Kinectin	KTN1
0,00	0,37	1,29	129,49	P12270	Nucleoprotein TPR	TPR
0,00	0,37	1,29	129,27	Q15149	Plectin	PLEC
0,01	0,37	1,29	129,04	Q15019	Septin-2	37500,00
0,02	0,37	1,29	128,94	Q9UJX3	Anaphase-promoting complex subunit 7	ANAPC7
0,03	0,37	1,29	128,84	P25205	DNA replication licensing factor MCM3	MCM3
0,00	0,36	1,29	128,63	P46939	Utrophin	UTRN
0,00	0,36	1,29	128,51	Q9Y230	RuvB-like 2	RUVBL2
0,00	0,36	1,28	128,43	Q9Y2L1	Exosome complex exonuclease RRP44	DIS3
0,03	0,36	1,28	128,39	Q9UHR5	SAP30-binding protein	SAP30BP
0,01	0,36	1,28	128,31	Q13868	Exosome complex component RRP4	EXOSC2
0,03	0,36	1,28	127,98	P40222	Alpha-taxilin	TXLNA
0,03	0,36	1,28	127,97	Q10570	Cleavage and polyadenylation specificity factor subunit 1	CPSF1
0,03	0,36	1,28	127,92	Q9H0S4	Probable ATP-dependent RNA helicase DDX47	DDX47
0,03	0,35	1,28	127,85	Q5TZA2;Q86T23	Rootletin	CROCC
0,03	0,35	1,28	127,76	Q15007	Pre-mRNA-splicing regulator WTAP	WTAP

Supplemental Table S2a

0,05	0,35	1,27	127,25	439;P13746;P30443;P3C	HLA class I histocompatibility antigen, A-3 alpha chain;HLA class I histocompatibility	HLA-A
0,02	0,35	1,27	127,08	P21796	Voltage-dependent anion-selective channel protein 1	VDAC1
0,02	0,34	1,27	126,63	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A
0,02	0,33	1,26	125,97	Q86V48	Leucine zipper protein 1	LUZP1
0,00	0,33	1,26	125,95	Q9NZN4	EH domain-containing protein 2	EHD2
0,03	0,33	1,26	125,85	Q9BWF3	RNA-binding protein 4	RBM4
0,05	0,33	1,26	125,65	P09110	3-ketoacyl-CoA thiolase, peroxisomal	ACAA1
0,01	0,33	1,26	125,60	P43246	DNA mismatch repair protein Msh2	MSH2
0,01	0,33	1,26	125,52	Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1
0,03	0,32	1,25	125,11	P24928	DNA-directed RNA polymerase II subunit RPB1	POLR2A
0,04	0,32	1,25	125,06	Q16204	Coiled-coil domain-containing protein 6	CCDC6
0,00	0,32	1,25	124,90	P15924	Desmoplakin	DSP
0,05	0,31	1,24	124,13	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2
0,01	0,30	1,23	123,44	Q13813	Spectrin alpha chain, brain	SPTAN1
0,02	0,30	1,23	123,27	Q16891	Mitochondrial inner membrane protein	IMMT
0,00	0,30	1,23	122,87	O43491;Q9Y2J2	Band 4.1-like protein 2	EPB41L2
0,00	0,30	1,23	122,71	Q9Y6W5	Wiskott-Aldrich syndrome protein family member 2	WASF2
0,00	0,29	1,22	121,99	O94905	Erlin-2	ERLIN2
0,00	0,29	1,22	121,95	Q07157	Tight junction protein ZO-1	TJP1
0,05	0,28	1,21	121,10	Q9Y490	Talin-1	TLN1
0,04	0,27	1,21	120,52	Q8IX01	SURP and G-patch domain-containing protein 2	SUGP2
0,04	0,26	1,20	120,12	Q86UE4	Protein LYRIC	MTDH
0,02	0,26	1,20	119,80	Q8N163	DBIRD complex subunit KIAA1967	KIAA1967
0,01	0,25	1,19	119,31	O00159	Unconventional myosin-Ic	MYO1C
0,04	0,25	1,19	119,16	P09874	Poly [ADP-ribose] polymerase 1	PARP1
0,04	0,24	1,18	118,17	O00268;Q92750	Transcription initiation factor TFIID subunit 4	TAF4
0,04	0,13	1,10	109,71	Q00341	Vigilin	HDLBP
8 h Down						
0,000	-5,20	0,03	2,72	P82933	28S ribosomal protein S9, mitochondrial	MRPS9
0,009	-3,73	0,08	7,52	P11498	Pyruvate carboxylase, mitochondrial	PC
0,000	-3,54	0,09	8,61	Q8N5N7	39S ribosomal protein L50, mitochondrial	MRPL50
0,003	-3,49	0,09	8,92	O00763	Acetyl-CoA carboxylase 2;Biotin carboxylase	ACACB
0,001	-3,39	0,10	9,57	Q9BUT1	3-hydroxybutyrate dehydrogenase type 2	BDH2

Supplemental Table S2a

0,004	-3,38	0,10	9,60	Q13247	Serine/arginine-rich splicing factor 6	SRSF6
0,024	-3,29	0,10	10,21	Q8NFF5	FAD synthase;Molybdenum cofactor biosynthesis protein-like region;FAD synthase	FLAD1
0,000	-3,28	0,10	10,29	Q9H3P7	Golgi resident protein GCP60	ACBD3
0,002	-3,17	0,11	11,12	Q02952	A-kinase anchor protein 12	AKAP12
0,009	-3,15	0,11	11,23	Q9Y223	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	L GNE
0,005	-3,14	0,11	11,36	P49585;Q9Y5K3	Choline-phosphate cytidyltransferase A;Choline-phosphate cytidyltransferase B	PCYT1A;PCYT1B
0,009	-3,13	0,11	11,44	P49257	Protein ERGIC-53	LMAN1
0,000	-3,11	0,12	11,56	O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B
0,003	-2,98	0,13	12,69	Q9H0U6	39S ribosomal protein L18, mitochondrial	MRPL18
0,004	-2,96	0,13	12,84	O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1
0,002	-2,94	0,13	13,01	Q7Z2W9	39S ribosomal protein L21, mitochondrial	MRPL21
0,041	-2,94	0,13	13,04	Q8IX01	SURP and G-patch domain-containing protein 2	SUGP2
0,010	-2,94	0,13	13,08	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB
0,049	-2,91	0,13	13,28	P61981	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	YWHAG
0,030	-2,85	0,14	13,91	Q03252	Lamin-B2	LMNB2
0,001	-2,80	0,14	14,35	Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7
0,019	-2,80	0,14	14,38	Q4G0N4	NAD kinase domain-containing protein 1	NADKD1
0,002	-2,77	0,15	14,61	Q8TAE8	Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1
0,005	-2,77	0,15	14,68	Q16890	Tumor protein D53	TPD52L1
0,031	-2,77	0,15	14,68	P53041	Serine/threonine-protein phosphatase 5	PPP5C
0,004	-2,75	0,15	14,88	Q9P0M9	39S ribosomal protein L27, mitochondrial	MRPL27
0,004	-2,75	0,15	14,89	O14646	Chromodomain-helicase-DNA-binding protein 1	CHD1
0,042	-2,72	0,15	15,18	Q04206	Transcription factor p65	RELA
0,012	-2,72	0,15	15,19	P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	PDHB
0,002	-2,70	0,15	15,37	P82914	28S ribosomal protein S15, mitochondrial	MRPS15
0,008	-2,68	0,16	15,59	Q9NSE4	Isoleucine--tRNA ligase, mitochondrial	IARS2
0,026	-2,67	0,16	15,69	Q5T653	39S ribosomal protein L2, mitochondrial	MRPL2
0,000	-2,65	0,16	15,93	Q96JH7	Deubiquitinating protein VCIP135	VCIP1
0,006	-2,61	0,16	16,35	Q96FW1	Ubiquitin thioesterase OTUB1	OTUB1
0,000	-2,61	0,16	16,35	P50579	Methionine aminopeptidase 2	METAP2
0,015	-2,61	0,16	16,43	Q8WUX9	Charged multivesicular body protein 7	CHMP7
0,027	-2,58	0,17	16,71	O60493	Sorting nexin-3	SNX3
0,024	-2,56	0,17	17,01	Q8N5M4	Tetratricopeptide repeat protein 9C	TTC9C

Supplemental Table S2a

0,001	-2,55	0,17	17,03	P11532	Dystrophin	DMD
0,039	-2,53	0,17	17,35	P63151;Q00005;Q9Y2T4	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A
0,046	-2,51	0,18	17,53	Q2TBE0	CWF19-like protein 2	CWF19L2
0,001	-2,51	0,18	17,54	P51398	28S ribosomal protein S29, mitochondrial	DAP3
0,010	-2,50	0,18	17,65	Q92783	Signal transducing adapter molecule 1	STAM
0,045	-2,49	0,18	17,76	O14530	Thioredoxin domain-containing protein 9	TXNDC9
0,021	-2,46	0,18	18,12	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK
0,011	-2,46	0,18	18,13	Q9Y3B2	Exosome complex component CSL4	EXOSC1
0,004	-2,45	0,18	18,36	Q99798	Aconitate hydratase, mitochondrial	ACO2
0,002	-2,43	0,19	18,60	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA
0,011	-2,42	0,19	18,66	Q9NR45	Sialic acid synthase	NANS
0,016	-2,40	0,19	18,89	Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1
0,015	-2,40	0,19	18,91	Q15785	Mitochondrial import receptor subunit TOM34	TOMM34
0,007	-2,40	0,19	18,92	A0AVT1	Ubiquitin-like modifier-activating enzyme 6	UBA6
0,014	-2,39	0,19	19,11	Q9Y450	HBS1-like protein	HBS1L
0,006	-2,39	0,19	19,13	P49321	Nuclear autoantigenic sperm protein	NASP
0,001	-2,38	0,19	19,15	Q99598	Translin-associated protein X	TSNAX
0,040	-2,37	0,19	19,33	P49773	Histidine triad nucleotide-binding protein 1	HINT1
0,003	-2,36	0,20	19,52	Q9Y2R0	Coiled-coil domain-containing protein 56	CCDC56
0,043	-2,35	0,20	19,63	Q9HDC9	Adipocyte plasma membrane-associated protein	APMAP
0,031	-2,33	0,20	19,89	P17174	Aspartate aminotransferase, cytoplasmic	GOT1
0,006	-2,33	0,20	19,92	Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA
0,007	-2,32	0,20	19,97	P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase	DLAT
0,000	-2,32	0,20	20,00	Q13795	ADP-ribosylation factor-related protein 1	ARFRP1
0,018	-2,29	0,20	20,43	Q9NZT1	Calmodulin-like protein 5	CALML5
0,020	-2,29	0,20	20,44	Q9UL63	Muskelin	MKLN1
0,004	-2,28	0,21	20,61	Q96A35	39S ribosomal protein L24, mitochondrial	MRPL24
0,007	-2,27	0,21	20,66	O95817	BAG family molecular chaperone regulator 3	BAG3
0,011	-2,27	0,21	20,66	P00387	NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-bound	CYB5R3
0,006	-2,27	0,21	20,78	P22059	Oxysterol-binding protein 1	OSBP
0,004	-2,26	0,21	20,82	Q99707	Methionine synthase	MTR
0,011	-2,26	0,21	20,82	P31151;Q86SG5	Protein S100-A7	S100A7
0,001	-2,26	0,21	20,93	P06737	Glycogen phosphorylase, liver form	PYGL

Supplemental Table S2a

0,006	-2,25	0,21	20,97	P16144	Integrin beta-4	ITGB4
0,011	-2,25	0,21	20,99	P60891	Ribose-phosphate pyrophosphokinase 1	PRPS1
0,003	-2,25	0,21	21,07	Q96GC5	39S ribosomal protein L48, mitochondrial	MRPL48
0,023	-2,25	0,21	21,09	Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1
0,036	-2,24	0,21	21,12	Q8IXM3	39S ribosomal protein L41, mitochondrial	MRPL41
0,025	-2,24	0,21	21,18	Q9H444	Charged multivesicular body protein 4b	CHMP4B
0,017	-2,24	0,21	21,21	O15355	Protein phosphatase 1G	PPM1G
0,011	-2,23	0,21	21,26	Q9UIS9	Methyl-CpG-binding domain protein 1	MBD1
0,007	-2,21	0,22	21,56	P07954	Fumarate hydratase, mitochondrial	FH
0,003	-2,20	0,22	21,84	Q8N3F8	MICAL-like protein 1	MICALL1
0,030	-2,19	0,22	21,88	P01034	Cystatin-C	CST3
0,015	-2,18	0,22	22,05	Q16851	UTP--glucose-1-phosphate uridylyltransferase	UGP2
0,020	-2,18	0,22	22,14	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA
0,008	-2,17	0,22	22,15	O43252	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1;Sulfate adenylyltran	PAPSS1
0,003	-2,17	0,22	22,20	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1
0,016	-2,17	0,22	22,21	P36915	Guanine nucleotide-binding protein-like 1	GNL1
0,006	-2,16	0,22	22,34	P12268	Inosine-5-monophosphate dehydrogenase 2	IMPDH2
0,029	-2,15	0,22	22,46	Q8N5A5	Zinc finger CCCH-type with G patch domain-containing protein	ZGPAT
0,042	-2,15	0,22	22,48	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS
0,030	-2,13	0,23	22,82	Q9BRA2	Thioredoxin domain-containing protein 17	TXNDC17
0,017	-2,13	0,23	22,84	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF
0,001	-2,12	0,23	22,94	Q8NF50	Dedicator of cytokinesis protein 8	DOCK8
0,031	-2,12	0,23	23,06	P51148;P20339;P61020	Ras-related protein Rab-5C;Ras-related protein Rab-5A;Ras-related protein Rab-5B	RAB5C;RAB5A;RAB
0,038	-2,12	0,23	23,07	Q14257	Reticulocalbin-2	RCN2
0,029	-2,11	0,23	23,16	P22307	Non-specific lipid-transfer protein	SCP2
0,016	-2,10	0,23	23,30	Q12965;O00160	Unconventional myosin-Ie	MYO1E
0,003	-2,10	0,23	23,38	Q96DZ1	Endoplasmic reticulum lectin 1	ERLEC1
0,031	-2,09	0,24	23,52	Q9H2W6	39S ribosomal protein L46, mitochondrial	MRPL46
0,009	-2,09	0,24	23,56	Q9P2T1	GMP reductase 2	GMPR2
0,001	-2,08	0,24	23,63	Q96G25	Mediator of RNA polymerase II transcription subunit 8	MED8
0,015	-2,07	0,24	23,75	Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	NFU1
0,041	-2,07	0,24	23,77	Q5JRX3	Presequence protease, mitochondrial	PITRM1
0,016	-2,06	0,24	23,94	P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1

Supplemental Table S2a

0,007	-2,06	0,24	24,04	O00748	Cocaine esterase	CES2
0,002	-2,05	0,24	24,12	Q96EL3	39S ribosomal protein L53, mitochondrial	MRPL53
0,027	-2,05	0,24	24,12	P49023	Paxillin	PXN
0,049	-2,05	0,24	24,16	Q9P013	Protein CWC15 homolog	CWC15
0,037	-2,05	0,24	24,19	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2
0,001	-2,05	0,24	24,23	O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	PLOD2
0,042	-2,04	0,24	24,28	Q9Y653	G-protein coupled receptor 56	GPR56
0,007	-2,04	0,24	24,29	Q9UNH7;Q86XE0	Sorting nexin-6	SNX6
0,019	-2,04	0,24	24,30	Q96BQ5	Coiled-coil domain-containing protein 127	CCDC127
0,011	-2,04	0,24	24,34	Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP
0,032	-2,03	0,24	24,42	Q8WUM4	Programmed cell death 6-interacting protein	PDCD6IP
0,046	-2,03	0,25	24,50	Q8IVM0	Coiled-coil domain-containing protein 50	CCDC50
0,014	-2,03	0,25	24,51	P62993	Growth factor receptor-bound protein 2	GRB2
0,026	-2,03	0,25	24,51	Q8TEX9	Importin-4	IPO4
0,010	-2,01	0,25	24,86	Q8ND24	RING finger protein 214	RNF214
0,010	-2,01	0,25	24,88	Q99733	Nucleosome assembly protein 1-like 4	NAP1L4
0,032	-2,00	0,25	24,91	O43617	Trafficking protein particle complex subunit 3	TRAPPC3
0,044	-2,00	0,25	24,95	P62899	60S ribosomal protein L31	RPL31
0,044	-2,00	0,25	25,05	Q96C86	m7GpppX diphosphatase	DCPS
0,043	-1,99	0,25	25,09	P60033	CD81 antigen	CD81
0,006	-1,98	0,25	25,32	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial	PCCA
0,001	-1,98	0,25	25,35	Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog	SUGT1
0,024	-1,98	0,25	25,35	Q1W1;P20340;Q9H0N0;Q9Y6K8	Ras-related protein Rab-6B;Ras-related protein Rab-6A	RAB6B;RAB6A
0,000	-1,97	0,26	25,60	Q13214	Semaphorin-3B	SEMA3B
0,009	-1,95	0,26	25,91	P00568;Q9Y6K8	Adenylate kinase isoenzyme 1	AK1
0,041	-1,94	0,26	26,01	Q14019	Coactosin-like protein	COTL1
0,001	-1,94	0,26	26,01	P28838	Cytosol aminopeptidase	LAP3
0,046	-1,92	0,26	26,35	Q8NBN7	Retinol dehydrogenase 13	RDH13
0,018	-1,92	0,26	26,39	Q9ULT8	E3 ubiquitin-protein ligase HECTD1	HECTD1
0,038	-1,92	0,26	26,41	O95336	6-phosphogluconolactonase	PGLS
0,028	-1,91	0,27	26,57	O95834	Echinoderm microtubule-associated protein-like 2	EML2
0,025	-1,91	0,27	26,59	P10074	Zinc finger and BTB domain-containing protein 48	ZBTB48
0,006	-1,91	0,27	26,66	P30085	UMP-CMP kinase	CMPK1

Supplemental Table S2a

0,041	-1,90	0,27	26,74	Q8TDH9	Protein Muted homolog	MUTED
0,005	-1,90	0,27	26,77	O15173	Membrane-associated progesterone receptor component 2	PGRMC2
0,002	-1,90	0,27	26,78	P49419	Alpha-aminoadipic semialdehyde dehydrogenase	ALDH7A1
0,038	-1,89	0,27	26,89	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3
0,029	-1,89	0,27	26,91	Q8WW12	PEST proteolytic signal-containing nuclear protein	PCNP
0,016	-1,89	0,27	26,96	Q9UHD1	Cysteine and histidine-rich domain-containing protein 1	CHORDC1
0,047	-1,88	0,27	27,09	P04632;Q96L46	Calpain small subunit 1	CAPNS1
0,005	-1,88	0,27	27,18	Q5T5X7	BEN domain-containing protein 3	BEND3
0,043	-1,88	0,27	27,25	Q08257	Quinone oxidoreductase	CRYZ
0,031	-1,86	0,27	27,45	Q13596	Sorting nexin-1	SNX1
0,023	-1,86	0,27	27,48	Q96IX5	Up-regulated during skeletal muscle growth protein 5	USMG5
0,035	-1,86	0,27	27,50	P30740	Leukocyte elastase inhibitor	SERPINB1
0,002	-1,86	0,28	27,57	Q9H814	Phosphorylated adapter RNA export protein	PHAX
0,020	-1,86	0,28	27,60	Q6NCE7;Q9GZQ8;Q9H49	Microtubule-associated proteins 1A/1B light chain 3 beta 2;Microtubule-associated	MAP1LC3B2;MAP1
0,038	-1,86	0,28	27,63	P23921	Ribonucleoside-diphosphate reductase large subunit	RRM1
0,003	-1,85	0,28	27,65	P21281;P15313	V-type proton ATPase subunit B, brain isoform	ATP6V1B2
0,012	-1,85	0,28	27,71	P29084	Transcription initiation factor IIE subunit beta	GTF2E2
0,001	-1,85	0,28	27,77	Q13409	Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2
0,004	-1,84	0,28	27,85	P27487	Dipeptidyl peptidase 4;Dipeptidyl peptidase 4 membrane form;Dipeptidyl peptidase	DPP4
0,016	-1,83	0,28	28,09	Q8NFU5	Inositol polyphosphate multikinase	IPMK
0,016	-1,83	0,28	28,14	Q14116	Interleukin-18	IL18
0,014	-1,83	0,28	28,17	P82650	28S ribosomal protein S22, mitochondrial	MRPS22
0,046	-1,82	0,28	28,23	Q5RKV6	Exosome complex component MTR3	EXOSC6
0,027	-1,82	0,28	28,28	Q969S3	Zinc finger protein 622	ZNF622
0,021	-1,82	0,28	28,33	O00116	Alkylidihydroxyacetonephosphate synthase, peroxisomal	AGPS
0,036	-1,81	0,29	28,58	Q96L73	Histone-lysine N-methyltransferase, H3 lysine-36 and H4 lysine-20 specific	NSD1
0,022	-1,80	0,29	28,71	Q7Z422	UPF0485 protein C1orf144	C1orf144
0,037	-1,80	0,29	28,74	Q93062	RNA-binding protein with multiple splicing	RBPM5
0,020	-1,80	0,29	28,76	Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4
0,007	-1,79	0,29	28,90	Q99614	Tetratricopeptide repeat protein 1	TTC1
0,031	-1,78	0,29	29,11	Q08752	Peptidyl-prolyl cis-trans isomerase D	PPID
0,016	-1,78	0,29	29,14	O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2
0,010	-1,78	0,29	29,19	Q9BZE1	39S ribosomal protein L37, mitochondrial	MRPL37

Supplemental Table S2a

0,009	-1,77	0,29	29,24	O75947	ATP synthase subunit d, mitochondrial	ATP5H
0,018	-1,77	0,29	29,28	Q13938	Calcyphosin	CAPS
0,035	-1,77	0,29	29,30	P22681	E3 ubiquitin-protein ligase CBL	CBL
0,014	-1,77	0,29	29,32	O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX
0,002	-1,77	0,29	29,34	Q13084	39S ribosomal protein L28, mitochondrial	MRPL28
0,002	-1,77	0,29	29,36	P82673	28S ribosomal protein S35, mitochondrial	MRPS35
0,010	-1,77	0,29	29,37	Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1
0,014	-1,77	0,29	29,38	Q12962	Transcription initiation factor TFIID subunit 10	TAF10
0,005	-1,77	0,29	29,38	P62699	Protein yippee-like 5	YPEL5
0,029	-1,77	0,29	29,41	P57105	Synaptojanin-2-binding protein	SYNJ2BP
0,003	-1,76	0,29	29,49	Q16762	Thiosulfate sulfurtransferase	TST
0,038	-1,76	0,30	29,57	Q8NBF2	NHL repeat-containing protein 2	NHLRC2
0,029	-1,76	0,30	29,59	Q9Y266	Nuclear migration protein nudC	NUDC
0,000	-1,74	0,30	29,85	Q8NBJ4	Golgi membrane protein 1	GOLM1
0,045	-1,74	0,30	29,85	P14735	Insulin-degrading enzyme	IDE
0,048	-1,74	0,30	29,93	P20839	Inosine-5-monophosphate dehydrogenase 1	IMPDH1
0,049	-1,74	0,30	29,97	P38117	Electron transfer flavoprotein subunit beta	ETFB
0,033	-1,73	0,30	30,08	Q9Y5P6	Mannose-1-phosphate guanylttransferase beta	GMPPB
0,013	-1,73	0,30	30,22	O14907	Tax1-binding protein 3	TAX1BP3
0,044	-1,73	0,30	30,24	Q9UBQ0	Vacuolar protein sorting-associated protein 29	VPS29
0,039	-1,72	0,30	30,25	P53367	Arfaptin-1	ARFIP1
0,000	-1,72	0,30	30,35	Q8N983	39S ribosomal protein L43, mitochondrial	MRPL43
0,046	-1,72	0,30	30,40	Q96DB5	Regulator of microtubule dynamics protein 1	FAM82B
0,011	-1,72	0,30	30,44	Q96GM8	Target of EGR1 protein 1	TOE1
0,000	-1,71	0,31	30,54	P16989	DNA-binding protein A	CSDA
0,030	-1,71	0,31	30,58	Q8IXQ6	Poly [ADP-ribose] polymerase 9	PARP9
0,041	-1,70	0,31	30,68	Q9HD33	39S ribosomal protein L47, mitochondrial	MRPL47
0,001	-1,70	0,31	30,72	Q9NX40	OCIA domain-containing protein 1	OCIAD1
0,038	-1,70	0,31	30,79	O00154	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7
0,026	-1,70	0,31	30,80	P78417	Glutathione S-transferase omega-1	GSTO1
0,013	-1,70	0,31	30,83	Q96S19	UPF0585 protein C16orf13	C16orf13
0,036	-1,69	0,31	30,89	Q15388	Mitochondrial import receptor subunit TOM20 homolog	TOMM20
0,036	-1,69	0,31	30,90	Q9BYT8	Neurolysin, mitochondrial	NLN

Supplemental Table S2a

0,028	-1,69	0,31	30,94	P00966	Argininosuccinate synthase	ASS1
0,003	-1,69	0,31	30,97	P48047	ATP synthase subunit O, mitochondrial	ATP5O
0,007	-1,69	0,31	30,98	P46379	Large proline-rich protein BAG6	BAG6
0,001	-1,69	0,31	31,10	Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L
0,010	-1,68	0,31	31,12	O15067	Phosphoribosylformylglycinamide synthase	PFAS
0,047	-1,68	0,31	31,27	Q92526	T-complex protein 1 subunit zeta-2	CCT6B
0,015	-1,68	0,31	31,29	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1
0,001	-1,67	0,31	31,39	Q96DV4	39S ribosomal protein L38, mitochondrial	MRPL38
0,035	-1,67	0,31	31,40	P58546	Myotrophin	MTPN
0,029	-1,67	0,31	31,43	Q14376	UDP-glucose 4-epimerase	GALE
0,027	-1,67	0,32	31,53	Q8N183	Mimitin, mitochondrial	NDUFAF2
0,003	-1,66	0,32	31,55	P28072	Proteasome subunit beta type-6	PSMB6
0,025	-1,66	0,32	31,61	Q9BXR0	Queuine tRNA-ribosyltransferase	QTRT1
0,042	-1,66	0,32	31,61	Q96HE7;Q86YB8	ERO1-like protein alpha	ERO1L
0,023	-1,66	0,32	31,63	P31431	Syndecan-4	SDC4
0,005	-1,66	0,32	31,66	P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2
0,019	-1,65	0,32	31,77	Q9BT30	Probable alpha-ketoglutarate-dependent dioxygenase ABH7	ALKBH7
0,010	-1,65	0,32	31,82	P06132	Uroporphyrinogen decarboxylase	UROD
0,008	-1,65	0,32	31,83	Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1
0,030	-1,65	0,32	31,90	Q9H8S9	MOB kinase activator 1A	MOB1A
0,022	-1,65	0,32	31,90	Q14697	Neutral alpha-glucosidase AB	GANAB
0,021	-1,65	0,32	31,92	Q16204	Coiled-coil domain-containing protein 6	CCDC6
0,045	-1,65	0,32	31,94	P49356	Protein farnesyltransferase subunit beta	FNTB
0,019	-1,64	0,32	32,00	P27708;P31327	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyl transferase	CAD
0,009	-1,64	0,32	32,13	Q86VX2	COMM domain-containing protein 7	COMMD7
0,018	-1,64	0,32	32,15	Q02818	Nucleobindin-1	NUCB1
0,024	-1,63	0,32	32,25	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1
0,001	-1,63	0,32	32,31	O94979	Protein transport protein Sec31A	SEC31A
0,042	-1,63	0,32	32,40	P55327	Tumor protein D52	TPD52
0,021	-1,62	0,32	32,43	O75348;O95670	V-type proton ATPase subunit G 1;V-type proton ATPase subunit G 2	ATP6V1G1;ATP6V1G2
0,034	-1,62	0,33	32,54	P41250	Glycine--tRNA ligase	GARS
0,013	-1,61	0,33	32,69	P49327	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-acyltransferase	FASN
0,011	-1,61	0,33	32,78	P06730	Eukaryotic translation initiation factor 4E	EIF4E

Supplemental Table S2a

0,016	-1,61	0,33	32,79	Q9H074	Polyadenylate-binding protein-interacting protein 1	PAIP1
0,012	-1,61	0,33	32,82	Q15370	Transcription elongation factor B polypeptide 2	TCEB2
0,027	-1,60	0,33	32,96	Q9UEW8	STE20/SPS1-related proline-alanine-rich protein kinase	STK39
0,016	-1,60	0,33	32,99	Q15293	Reticulocalbin-1	RCN1
0,000	-1,59	0,33	33,25	O75410	Transforming acidic coiled-coil-containing protein 1	TACC1
0,016	-1,59	0,33	33,31	P46199	Translation initiation factor IF-2, mitochondrial	MTIF2
0,040	-1,59	0,33	33,33	O15400	Syntaxin-7	STX7
0,020	-1,58	0,33	33,37	Q5TFE4	5-nucleotidase domain-containing protein 1	NT5DC1
0,009	-1,58	0,33	33,43	Q01518	Adenylyl cyclase-associated protein 1	CAP1
0,006	-1,58	0,33	33,46	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B
0,019	-1,57	0,34	33,58	Q9GZU8	Protein FAM192A	FAM192A
0,039	-1,57	0,34	33,63	Q9BY89	Uncharacterized protein KIAA1671	KIAA1671
0,034	-1,57	0,34	33,66	Q9HCU4	Cadherin EGF LAG seven-pass G-type receptor 2	CELSR2
0,011	-1,57	0,34	33,68	P62834	Ras-related protein Rap-1A	RAP1A
0,001	-1,56	0,34	33,80	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1
0,010	-1,56	0,34	33,84	Q9P2R7	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	SUCLA2
0,005	-1,56	0,34	33,92	Q9BXJ9;Q6N069	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15
0,019	-1,56	0,34	33,97	Q6VY07	Phosphofurin acidic cluster sorting protein 1	PACS1
0,006	-1,56	0,34	34,00	O00264	Membrane-associated progesterone receptor component 1	PGRMC1
0,031	-1,56	0,34	34,02	P25705	ATP synthase subunit alpha, mitochondrial	ATP5A1
0,025	-1,55	0,34	34,08	Q12800	Alpha-globin transcription factor CP2	TFCP2
0,049	-1,55	0,34	34,26	Q2TAY7	WD40 repeat-containing protein SMU1	SMU1
0,000	-1,54	0,34	34,33	P08572	Collagen alpha-2(IV) chain;Canstatin	COL4A2
0,037	-1,54	0,34	34,35	O94906	Pre-mRNA-processing factor 6	PRPF6
0,000	-1,54	0,34	34,45	Q16270	Insulin-like growth factor-binding protein 7	IGFBP7
0,005	-1,54	0,34	34,47	Q9BVQ7	Spermatogenesis-associated protein 5-like protein 1	SPATA5L1
0,015	-1,54	0,34	34,49	Q13510	Acid ceramidase;Acid ceramidase subunit alpha;Acid ceramidase subunit beta	ASAH1
0,021	-1,53	0,35	34,52	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2
0,044	-1,53	0,35	34,59	Q96M27	Protein PRRC1	PRRC1
0,017	-1,53	0,35	34,64	O95453	Poly(A)-specific ribonuclease PARN	PARN
0,001	-1,53	0,35	34,71	Q8NBJ7	Sulfatase-modifying factor 2	SUMF2
0,005	-1,53	0,35	34,72	Q9UNZ2	NSFL1 cofactor p47	NSFL1C
0,004	-1,53	0,35	34,74	P09972	Fructose-bisphosphate aldolase C	ALDOC

Supplemental Table S2a

0,012	-1,52	0,35	34,82	Q14696	LDLR chaperone MESD	MESDC2
0,026	-1,52	0,35	34,90	P04083	Annexin A1	ANXA1
0,012	-1,52	0,35	34,94	P53990	IST1 homolog	IST1
0,034	-1,52	0,35	34,97	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehyd	DLST
0,021	-1,50	0,35	35,33	Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1
0,029	-1,50	0,35	35,44	O60927	Protein phosphatase 1 regulatory subunit 11	PPP1R11
0,041	-1,50	0,35	35,46	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	ETFDH
0,025	-1,49	0,36	35,60	Q92599	Septin-8	Sep.08
0,023	-1,49	0,36	35,63	P18206	Vinculin	VCL
0,009	-1,48	0,36	35,80	Q9Y6Y8	SEC23-interacting protein	SEC23IP
0,008	-1,48	0,36	35,83	Q8IXI1	Mitochondrial Rho GTPase 2	RHOT2
0,045	-1,47	0,36	35,98	O43414	ERI1 exoribonuclease 3	ERI3
0,035	-1,47	0,36	36,06	Q14108	Lysosome membrane protein 2	SCARB2
0,012	-1,47	0,36	36,13	P08758	Annexin A5	ANXA5
0,002	-1,47	0,36	36,14	Q96L92;O60759	Sorting nexin-27	SNX27
0,001	-1,46	0,36	36,28	Q5R115	Cytochrome c oxidase protein 20 homolog	COX20
0,033	-1,45	0,37	36,62	P11413	Glucose-6-phosphate 1-dehydrogenase	G6PD
0,024	-1,45	0,37	36,63	Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	PBXIP1
0,038	-1,44	0,37	36,80	Q9NRS6	Sorting nexin-15	SNX15
0,045	-1,44	0,37	36,84	Q96PZ0	Pseudouridylate synthase 7 homolog	PUS7
0,047	-1,44	0,37	36,95	Q9UJ70	N-acetyl-D-glucosamine kinase	NAGK
0,018	-1,43	0,37	37,08	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1	LRRFIP1
0,033	-1,42	0,37	37,26	Q96EY7	Pentatricopeptide repeat-containing protein 3, mitochondrial	PTCD3
0,017	-1,42	0,37	37,34	Q9BZX2;Q9HA47	Uridine-cytidine kinase 2;Uridine-cytidine kinase 1	UCK2;UCK1
0,006	-1,42	0,37	37,38	P23588	Eukaryotic translation initiation factor 4B	EIF4B
0,035	-1,41	0,38	37,53	Q4G0F5	Vacuolar protein sorting-associated protein 26B	VPS26B
0,045	-1,41	0,38	37,56	Q9NQT4	Exosome complex component RRP46	EXOSC5
0,000	-1,41	0,38	37,59	P05067	Amyloid beta A4 protein;N-APP;Soluble APP-alpha;Soluble APP-beta;C99;Beta-amyloid	APP
0,017	-1,41	0,38	37,61	P10644;P31321	cAMP-dependent protein kinase type I-alpha regulatory subunit	PRKAR1A
0,019	-1,41	0,38	37,76	P29353	SHC-transforming protein 1	SHC1
0,045	-1,40	0,38	37,78	P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1
0,015	-1,40	0,38	37,85	O60749	Sorting nexin-2	SNX2
0,034	-1,40	0,38	37,91	Q16864	V-type proton ATPase subunit F	ATP6V1F

Supplemental Table S2a

0,002	-1,40	0,38	37,98	.Q2;Q5SNT6;Q9Y4E1;Q5	WASH complex subunit FAM21A;WASH complex subunit FAM21B;WASH complex subunit FAM21A;FAM21B;	
0,008	-1,40	0,38	38,02	O60307	Microtubule-associated serine/threonine-protein kinase 3	MAST3
0,011	-1,39	0,38	38,08	Q9Y496;Q9P2E2	Kinesin-like protein KIF3A	KIF3A
0,017	-1,39	0,38	38,15	O95573	Long-chain-fatty-acid--CoA ligase 3	ACSL3
0,021	-1,39	0,38	38,15	P49588	Alanine--tRNA ligase, cytoplasmic	AARS
0,002	-1,39	0,38	38,25	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1
0,050	-1,38	0,38	38,45	Q9NVE7	Pantothenate kinase 4	PANK4
0,015	-1,38	0,38	38,47	P13667	Protein disulfide-isomerase A4	PDIA4
0,001	-1,37	0,39	38,64	P22830	Ferrochelatase, mitochondrial	FECH
0,001	-1,37	0,39	38,79	Q9H6E4	Coiled-coil domain-containing protein 134	CCDC134
0,033	-1,36	0,39	38,84	Q6DKJ4	Nucleoredoxin	NXN
0,013	-1,36	0,39	38,92	Q9NVD7;Q9HBI1	Alpha-parvin	PARVA
0,025	-1,36	0,39	39,08	Q06710	Paired box protein Pax-8	PAX8
0,017	-1,35	0,39	39,10	P40306	Proteasome subunit beta type-10	PSMB10
0,019	-1,35	0,39	39,17	Q9HB07	UPF0160 protein MYG1, mitochondrial	C12orf10
0,042	-1,35	0,39	39,17	Q02127	Dihydroorotate dehydrogenase (quinone), mitochondrial	DHODH
0,046	-1,35	0,39	39,23	Q96AT9;Q2QD12	Ribulose-phosphate 3-epimerase	RPE
0,028	-1,35	0,39	39,32	Q9BVG4	UPF0368 protein Cxorf26	CXorf26
0,046	-1,34	0,39	39,43	P52926	High mobility group protein HMGI-C	HMGA2
0,023	-1,34	0,40	39,51	Q56VL3	OCIA domain-containing protein 2	OCIAD2
0,031	-1,33	0,40	39,64	P0C0S5;Q71UI9;Q8IUE6	Histone H2A.Z;Histone H2A.V	H2AFZ;H2AFV
0,002	-1,33	0,40	39,68	Q96KG9	N-terminal kinase-like protein	SCYL1
0,001	-1,33	0,40	39,72	P62633	Cellular nucleic acid-binding protein	CNBP
0,045	-1,33	0,40	39,75	Q05209	Tyrosine-protein phosphatase non-receptor type 12	PTPN12
0,048	-1,33	0,40	39,78	P14314	Glucosidase 2 subunit beta	PRKCSH
0,034	-1,33	0,40	39,89	Q9BRF8	Calcineurin-like phosphoesterase domain-containing protein 1	CPPED1
0,003	-1,32	0,40	39,97	Q99615	DnaJ homolog subfamily C member 7	DNAJC7
0,001	-1,32	0,40	40,01	O75534	Cold shock domain-containing protein E1	CSDE1
0,008	-1,32	0,40	40,14	P12429	Annexin A3	ANXA3
0,037	-1,31	0,40	40,34	Q8IXQ4	Uncharacterized protein KIAA1704	KIAA1704
0,000	-1,31	0,40	40,43	Q92896	Golgi apparatus protein 1	GLG1
0,000	-1,30	0,41	40,56	O75569	Interferon-inducible double stranded RNA-dependent protein kinase activator A	PRKRA
0,002	-1,30	0,41	40,57	P49407	Beta-arrestin-1	ARRB1

Supplemental Table S2a

0,002	-1,30	0,41	40,57	P85037	Forkhead box protein K1	FOXK1
0,033	-1,30	0,41	40,62	Q9NYL2	Mitogen-activated protein kinase kinase kinase MLT	MLTK
0,000	-1,30	0,41	40,70	P62877	E3 ubiquitin-protein ligase RBX1	RBX1
0,004	-1,30	0,41	40,74	Q9Y617	Phosphoserine aminotransferase	PSAT1
0,000	-1,30	0,41	40,75	P18754	Regulator of chromosome condensation	RCC1
0,000	-1,30	0,41	40,75	Q13740	CD166 antigen	ALCAM
0,029	-1,29	0,41	40,86	Q86WQ0	Nuclear receptor 2C2-associated protein	NR2C2AP
0,049	-1,29	0,41	40,87	Q9BYD3	39S ribosomal protein L4, mitochondrial	MRPL4
0,000	-1,29	0,41	40,94	P52565	Rho GDP-dissociation inhibitor 1	ARHGDI1A
0,029	-1,29	0,41	40,94	Q96RE7	Nucleus accumbens-associated protein 1	NACC1
0,002	-1,28	0,41	41,22	P12081	Histidine--tRNA ligase, cytoplasmic	HARS
0,017	-1,28	0,41	41,23	Q9Y2H0	Disks large-associated protein 4	DLGAP4
0,032	-1,28	0,41	41,29	P21964	Catechol O-methyltransferase	COMT
0,000	-1,27	0,41	41,46	Q8NBJ5	Procollagen galactosyltransferase 1	GLT25D1
0,009	-1,26	0,42	41,72	P20073	Annexin A7	ANXA7
0,016	-1,26	0,42	41,74	Q96EK6	Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1
0,035	-1,26	0,42	41,77	P14635	G2/mitotic-specific cyclin-B1	CCNB1
0,020	-1,26	0,42	41,90	P21283	V-type proton ATPase subunit C 1	ATP6V1C1
0,009	-1,25	0,42	41,91	Q13753	Laminin subunit gamma-2	LAMC2
0,015	-1,25	0,42	41,96	P05455	Lupus La protein	SSB
0,006	-1,25	0,42	42,00	Q9Y291	28S ribosomal protein S33, mitochondrial	MRPS33
0,000	-1,25	0,42	42,05	Q9Y3A5	Ribosome maturation protein SBDS	SBDS
0,003	-1,25	0,42	42,14	P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1
0,019	-1,25	0,42	42,15	O60925	Prefoldin subunit 1	PFDN1
0,004	-1,24	0,42	42,21	P18827	Syndecan-1	SDC1
0,024	-1,24	0,42	42,23	P50502;Q8NFI4;Q8IZP2	Hsc70-interacting protein;Putative protein FAM10A5;Putative protein FAM10A4	ST13;ST13P5;ST13
0,011	-1,24	0,42	42,32	Q9NZR1	Tropomodulin-2	TMOD2
0,019	-1,24	0,42	42,41	Q99436	Proteasome subunit beta type-7	PSMB7
0,039	-1,23	0,43	42,64	O43865	Putative adenosylhomocysteinase 2	AHCYL1
0,031	-1,23	0,43	42,64	Q9HB21	Pleckstrin homology domain-containing family A member 1	PLEKHA1
0,034	-1,23	0,43	42,74	Q13951	Core-binding factor subunit beta	CBFB
0,030	-1,22	0,43	42,83	Q86VW0	SEC14 domain and spectrin repeat-containing protein 1	SESTD1
0,010	-1,22	0,43	42,94	P06396	Gelsolin	GSN

Supplemental Table S2a

0,000	-1,21	0,43	43,09	P11717	Cation-independent mannose-6-phosphate receptor	IGF2R
0,003	-1,21	0,43	43,10	P26639	Threonine--tRNA ligase, cytoplasmic	TARS
0,029	-1,21	0,43	43,10	O75794	Cell division cycle protein 123 homolog	CDC123
0,020	-1,21	0,43	43,14	O75616	GTPase Era, mitochondrial	ERAL1
0,007	-1,21	0,43	43,15	P18859	ATP synthase-coupling factor 6, mitochondrial	ATP5J
0,000	-1,21	0,43	43,18	Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1	UFC1
0,004	-1,20	0,43	43,41	Q9UM11	Fizzy-related protein homolog	FZR1
0,004	-1,20	0,44	43,60	P28482	Mitogen-activated protein kinase 1	MAPK1
0,000	-1,20	0,44	43,64	Q13501	Sequestosome-1	SQSTM1
0,010	-1,19	0,44	43,68	Q99536	Synaptic vesicle membrane protein VAT-1 homolog	VAT1
0,003	-1,19	0,44	43,68	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2
0,027	-1,19	0,44	43,70	Q15758	Neutral amino acid transporter B(0)	SLC1A5
0,006	-1,19	0,44	43,72	Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3
0,018	-1,19	0,44	43,83	Q14137	Ribosome biogenesis protein BOP1	BOP1
0,017	-1,19	0,44	43,86	Q12765	Secernin-1	SCRN1
0,007	-1,18	0,44	44,20	P11234	Ras-related protein Ral-B	RALB
0,003	-1,17	0,44	44,29	P55010	Eukaryotic translation initiation factor 5	EIF5
0,012	-1,17	0,45	44,52	P35080	Profilin-2	PFN2
0,038	-1,17	0,45	44,52	Q01995	Transgelin	TAGLN
0,044	-1,17	0,45	44,54	Q8WWK9	Cytoskeleton-associated protein 2	CKAP2
0,001	-1,17	0,45	44,59	P10155	60 kDa SS-A/Ro ribonucleoprotein	TROVE2
0,000	-1,16	0,45	44,65	O75822	Eukaryotic translation initiation factor 3 subunit J	EIF3J
0,002	-1,16	0,45	44,68	Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	TIMM9
0,001	-1,16	0,45	44,69	O43169	Cytochrome b5 type B	CYB5B
0,002	-1,16	0,45	44,70	P67809	Nuclease-sensitive element-binding protein 1	YBX1
0,030	-1,16	0,45	44,75	O75448	Mediator of RNA polymerase II transcription subunit 24	MED24
0,035	-1,16	0,45	44,88	P32119	Peroxiredoxin-2	PRDX2
0,023	-1,15	0,45	44,99	P07195	L-lactate dehydrogenase B chain	LDHB
0,015	-1,15	0,45	45,00	Q8NFH3	Nucleoporin Nup43	NUP43
0,005	-1,15	0,45	45,07	Q04917	14-3-3 protein eta	YWHAH
0,013	-1,15	0,45	45,17	Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47
0,010	-1,14	0,45	45,35	P27797	Calreticulin	CALR
0,038	-1,14	0,45	45,37	A2A3N6;Q99755	Putative PIP5K1A and PSMD4-like protein;Phosphatidylinositol 4-phosphate 5-kinas	PIPSL;PIP5K1A

Supplemental Table S2a

0,011	-1,14	0,45	45,42	P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B
0,006	-1,14	0,46	45,53	P61758	Prefoldin subunit 3	VBP1
0,006	-1,13	0,46	45,55	Q9BRP8	Partner of Y14 and mago	WIBG
0,040	-1,13	0,46	45,58	Q12972	Nuclear inhibitor of protein phosphatase 1;Activator of RNA decay	PPP1R8
0,001	-1,13	0,46	45,71	O43583	Density-regulated protein	DENR
0,050	-1,13	0,46	45,83	Q96FN4	Copine-2	CPNE2
0,000	-1,12	0,46	45,94	Q9H078	Caseinolytic peptidase B protein homolog	CLPB
0,045	-1,12	0,46	45,99	P27361	Mitogen-activated protein kinase 3	MAPK3
0,008	-1,12	0,46	46,02	Q9UPP1	Histone lysine demethylase PHF8	PHF8
0,007	-1,12	0,46	46,10	P53992	Protein transport protein Sec24C	SEC24C
0,032	-1,12	0,46	46,11	P30101	Protein disulfide-isomerase A3	PDIA3
0,031	-1,12	0,46	46,15	P52209	6-phosphogluconate dehydrogenase, decarboxylating	PGD
0,000	-1,11	0,46	46,20	O75347	Tubulin-specific chaperone A	TBCA
0,038	-1,11	0,46	46,29	Q9UJA5	tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6	TRMT6
0,016	-1,10	0,47	46,52	O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3
0,004	-1,10	0,47	46,54	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2
0,011	-1,10	0,47	46,55	Q9GZT9	Egl nine homolog 1	EGLN1
0,009	-1,10	0,47	46,61	Q9BZ17	Regulator of nonsense transcripts 3B	UPF3B
0,021	-1,10	0,47	46,64	Q9C0E2	Exportin-4	XPO4
0,027	-1,10	0,47	46,76	P61088	Ubiquitin-conjugating enzyme E2 N	UBE2N
0,004	-1,09	0,47	47,13	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2
0,046	-1,09	0,47	47,13	P37837	Transaldolase	TALDO1
0,039	-1,09	0,47	47,14	Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5
0,010	-1,08	0,47	47,28	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2
0,005	-1,08	0,47	47,29	P23526	Adenosylhomocysteinase	AHCY
0,034	-1,08	0,47	47,34	Q9BRT2	Mitochondrial nucleoid factor 1	MNF1
0,021	-1,08	0,47	47,36	P61604	10 kDa heat shock protein, mitochondrial	HSPE1
0,014	-1,08	0,47	47,37	Q96AC1	Fermitin family homolog 2	FERMT2
0,009	-1,08	0,47	47,39	P34932	Heat shock 70 kDa protein 4	HSPA4
0,003	-1,07	0,48	47,53	Q7Z4V5	Hepatoma-derived growth factor-related protein 2	HDGFRP2
0,003	-1,07	0,48	47,54	O95292	Vesicle-associated membrane protein-associated protein B/C	VAPB
0,009	-1,07	0,48	47,68	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1
0,005	-1,07	0,48	47,78	Q9Y3F4	Serine-threonine kinase receptor-associated protein	STRAP

Supplemental Table S2a

0,018	-1,06	0,48	47,94	Q06587	E3 ubiquitin-protein ligase RING1	RING1
0,047	-1,06	0,48	47,96	Q5F1R6	DnaJ homolog subfamily C member 21	DNAJC21
0,019	-1,06	0,48	48,02	P41227;Q9BSU3	N-alpha-acetyltransferase 10	NAA10
0,001	-1,06	0,48	48,04	P07858	Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain	CTSB
0,003	-1,06	0,48	48,13	P50895	Basal cell adhesion molecule	BCAM
0,031	-1,05	0,48	48,18	Q6NZ67;Q6P582	Mitotic-spindle organizing protein 2B;Mitotic-spindle organizing protein 2A	MZT2B;MZT2A
0,032	-1,05	0,48	48,23	Q9P015	39S ribosomal protein L15, mitochondrial	MRPL15
0,000	-1,04	0,48	48,47	Q8TAT6	Nuclear protein localization protein 4 homolog	NPLOC4
0,002	-1,04	0,48	48,48	P60520	Gamma-aminobutyric acid receptor-associated protein-like 2	GABARAPL2
0,016	-1,04	0,49	48,52	Q9BRX2	Protein pelota homolog	PELO
0,000	-1,04	0,49	48,54	Q14677	Clathrin interactor 1	CLINT1
0,000	-1,04	0,49	48,63	O60524	Nuclear export mediator factor NEMF	NEMF
0,046	-1,04	0,49	48,69	Q9UL46	Proteasome activator complex subunit 2	PSME2
0,003	-1,04	0,49	48,73	P30519	Heme oxygenase 2	HMOX2
0,000	-1,03	0,49	48,92	P18669;Q8N0Y7;P15259	Phosphoglycerate mutase 1	PGAM1
0,012	-1,03	0,49	48,95	526;Q15303;P80192;Q5	Receptor tyrosine-protein kinase erbB-2	ERBB2
0,004	-1,03	0,49	49,09	P23193;Q15560	Transcription elongation factor A protein 1	TCEA1
0,002	-1,03	0,49	49,11	P55072	Transitional endoplasmic reticulum ATPase	VCP
0,001	-1,02	0,49	49,15	P61201	COP9 signalosome complex subunit 2	COPS2
0,020	-1,02	0,49	49,16	Q9Y3D9	28S ribosomal protein S23, mitochondrial	MRPS23
0,047	-1,02	0,49	49,18	Q9BYD1	39S ribosomal protein L13, mitochondrial	MRPL13
0,032	-1,02	0,49	49,21	P22314	Ubiquitin-like modifier-activating enzyme 1	UBA1
0,007	-1,02	0,49	49,23	P61221	ATP-binding cassette sub-family E member 1	ABCE1
0,003	-1,02	0,49	49,23	Q92598	Heat shock protein 105 kDa	HSPH1
0,001	-1,02	0,49	49,24	Q9Y5S9	RNA-binding protein 8A	RBM8A
0,041	-1,02	0,49	49,27	Q15907;P62491	Ras-related protein Rab-11B;Ras-related protein Rab-11A	RAB11B;RAB11A
0,013	-1,02	0,49	49,33	Q96AE4	Far upstream element-binding protein 1	FUBP1
0,004	-1,02	0,49	49,42	Q15942	Zyxin	ZYX
0,018	-1,01	0,49	49,49	P27695	DNA-(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, n	APEX1
0,024	-1,01	0,50	49,52	Q13769	THO complex subunit 5 homolog	THOC5
0,035	-1,01	0,50	49,54	P07900;Q14568;Q58FGC	Heat shock protein HSP 90-alpha	HSP90AA1
0,030	-1,01	0,50	49,57	O43676	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3
0,005	-1,01	0,50	49,64	Q8N3E9	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3	PLCD3

Supplemental Table S2a

0,012	-1,01	0,50	49,73	Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1	LRWD1
0,041	-1,01	0,50	49,78	P08238;Q58FF7	Heat shock protein HSP 90-beta;Putative heat shock protein HSP 90-beta-3	HSP90AB1;HSP90A
0,031	-1,00	0,50	49,93	Q96JP5	E3 ubiquitin-protein ligase ZFP91	ZFP91
0,032	-1,00	0,50	49,95	P09493	Tropomyosin alpha-1 chain	TPM1
0,022	-1,00	0,50	49,96	Q06203	Amidophosphoribosyltransferase	PPAT
0,023	-1,00	0,50	49,99	Q9UL15	BAG family molecular chaperone regulator 5	BAG5
0,008	-1,00	0,50	50,04	Q9UI30	tRNA methyltransferase 112 homolog	TRMT112
0,047	-1,00	0,50	50,12	P25490	Transcriptional repressor protein YY1	YY1
0,009	-0,99	0,50	50,19	P46937	Yorkie homolog	YAP1
0,040	-0,99	0,50	50,19	P48163	NADP-dependent malic enzyme	ME1
0,017	-0,99	0,51	50,51	Q9UQ80	Proliferation-associated protein 2G4	PA2G4
0,002	-0,98	0,51	50,55	P18031	Tyrosine-protein phosphatase non-receptor type 1	PTPN1
0,022	-0,98	0,51	50,59	Q9BS26	Endoplasmic reticulum resident protein 44	ERP44
0,013	-0,98	0,51	50,75	Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	PLCB3
0,021	-0,98	0,51	50,82	P11277	Spectrin beta chain, erythrocyte	SPTB
0,013	-0,97	0,51	50,98	P20810	Calpastatin	CAST
0,019	-0,97	0,51	51,00	Q15185	Prostaglandin E synthase 3	PTGES3
0,026	-0,97	0,51	51,05	O95340	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 2;Sulfate adenylyltran	PAPSS2
0,027	-0,97	0,51	51,05	P54577	Tyrosine--tRNA ligase, cytoplasmic	YARS
0,003	-0,97	0,51	51,07	O14818;Q8TAA3	Proteasome subunit alpha type-7	PSMA7
0,023	-0,97	0,51	51,10	P22102	Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine	GART
0,017	-0,97	0,51	51,16	Q99873;Q9NR22	Protein arginine N-methyltransferase 1	PRMT1
0,000	-0,96	0,51	51,26	Q07020	60S ribosomal protein L18	RPL18
0,000	-0,96	0,51	51,31	P48426	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	PIP4K2A
0,006	-0,96	0,51	51,33	Q01105;P0DME0	Protein SET	SET
0,002	-0,96	0,51	51,35	Q12986	Transcriptional repressor NF-X1	NFX1
0,000	-0,96	0,51	51,42	O15230	Laminin subunit alpha-5	LAMA5
0,031	-0,96	0,52	51,53	Q9H019	Protein FAM54B	FAM54B
0,008	-0,95	0,52	51,64	Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1
0,037	-0,95	0,52	51,67	Q8IYA6	Cytoskeleton-associated protein 2-like	CKAP2L
0,039	-0,95	0,52	51,92	P18124	60S ribosomal protein L7	RPL7
0,005	-0,94	0,52	52,04	P16403	Histone H1.2	HIST1H1C
0,004	-0,94	0,52	52,06	O75312	Zinc finger protein ZPR1	ZNF259

Supplemental Table S2a

0,036	-0,94	0,52	52,09	P42566	Epidermal growth factor receptor substrate 15	EPS15
0,009	-0,94	0,52	52,14	Q9ULX3	RNA-binding protein NOB1	NOB1
0,039	-0,94	0,52	52,18	P09525	Annexin A4	ANXA4
0,048	-0,94	0,52	52,20	P00450	Ceruloplasmin	CP
0,024	-0,93	0,52	52,33	Q9UHV9	Prefoldin subunit 2	PFDN2
0,002	-0,93	0,52	52,37	P13611	Versican core protein	VCAN
0,033	-0,93	0,52	52,41	O14653	Golgi SNAP receptor complex member 2	GOSR2
0,021	-0,93	0,52	52,45	P23381	Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS	WARS
0,030	-0,93	0,53	52,59	Q9C035	Tripartite motif-containing protein 5	TRIM5
0,036	-0,93	0,53	52,59	Q15545	Transcription initiation factor TFIID subunit 7	TAF7
0,021	-0,93	0,53	52,63	O43447	Peptidyl-prolyl cis-trans isomerase H	PPIH
0,031	-0,93	0,53	52,63	Q9NZ09	Ubiquitin-associated protein 1	UBAP1
0,002	-0,92	0,53	52,73	Q13185	Chromobox protein homolog 3	CBX3
0,003	-0,92	0,53	52,88	P60866	40S ribosomal protein S20	RPS20
0,029	-0,92	0,53	52,91	Q12931	Heat shock protein 75 kDa, mitochondrial	TRAP1
0,031	-0,91	0,53	53,06	P29762	Cellular retinoic acid-binding protein 1	CRABP1
0,016	-0,91	0,53	53,08	O43148	mRNA cap guanine-N7 methyltransferase	RNMT
0,027	-0,91	0,53	53,33	Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial	PPA2
0,013	-0,91	0,53	53,35	P15586	N-acetylglucosamine-6-sulfatase	GNS
0,007	-0,90	0,54	53,62	P62263	40S ribosomal protein S14	RPS14
0,030	-0,89	0,54	53,97	P20618	Proteasome subunit beta type-1	PSMB1
0,003	-0,89	0,54	54,04	P52943	Cysteine-rich protein 2	CRIP2
0,001	-0,88	0,54	54,16	Q9H0B6	Kinesin light chain 2	KLC2
0,022	-0,88	0,54	54,19	P26885	Peptidyl-prolyl cis-trans isomerase FKBP2	FKBP2
0,012	-0,88	0,54	54,22	P13693;Q56UQ5	Translationally-controlled tumor protein	TPT1
0,003	-0,88	0,54	54,24	P40222	Alpha-taxilin	TXLNA
0,009	-0,88	0,54	54,31	Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein 2	PACSIN2
0,004	-0,88	0,54	54,40	Q9H7E9	UPF0488 protein C8orf33	C8orf33
0,044	-0,88	0,54	54,40	P35222	Catenin beta-1	CTNNB1
0,004	-0,88	0,54	54,40	P23229	Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain	ITGA6
0,029	-0,88	0,54	54,41	Q9H910	Hematological and neurological expressed 1-like protein	HN1L
0,013	-0,88	0,54	54,43	O15212	Prefoldin subunit 6	PFDN6
0,042	-0,88	0,54	54,44	Q13217	DnaJ homolog subfamily C member 3	DNAJC3

Supplemental Table S2a

0,008	-0,88	0,55	54,52	P41567;O60739	Eukaryotic translation initiation factor 1;Eukaryotic translation initiation factor 1b	EIF1;EIF1B
0,003	-0,87	0,55	54,56	P35613	Basigin	BSG
0,033	-0,87	0,55	54,61	Q9BWU0	Kanadaptin	SLC4A1AP
0,048	-0,87	0,55	54,76	O43278	Kunitz-type protease inhibitor 1	SPINT1
0,047	-0,87	0,55	54,78	P28065	Proteasome subunit beta type-9	PSMB9
0,002	-0,87	0,55	54,84	P07741	Adenine phosphoribosyltransferase	APRT
0,000	-0,87	0,55	54,85	Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2
0,046	-0,87	0,55	54,88	P61289	Proteasome activator complex subunit 3	PSME3
0,013	-0,86	0,55	54,95	Q9UBS4	DnaJ homolog subfamily B member 11	DNAJB11
0,008	-0,86	0,55	55,02	P06454	Prothymosin alpha;Thymosin alpha-1	PTMA
0,047	-0,86	0,55	55,09	O75781	Paralemmin-1	PALM
0,043	-0,86	0,55	55,11	Q9Y490	Talin-1	TLN1
0,037	-0,86	0,55	55,16	Q92905	COP9 signalosome complex subunit 5	COPS5
0,048	-0,85	0,55	55,31	Q8TDM6	Disks large homolog 5	DLG5
0,027	-0,85	0,55	55,32	Q71F56	Mediator of RNA polymerase II transcription subunit 13-like	MED13L
0,006	-0,85	0,55	55,34	P07602	Proactivator polypeptide;Saposin-A;Saposin-B-Val;Saposin-B;Saposin-C;Saposin-D	PSAP
0,000	-0,85	0,55	55,42	P52815	39S ribosomal protein L12, mitochondrial	MRPL12
0,008	-0,85	0,55	55,43	P17987	T-complex protein 1 subunit alpha	TCP1
0,045	-0,85	0,56	55,52	P80723	Brain acid soluble protein 1	BASP1
0,036	-0,85	0,56	55,56	Q9BXV9	Uncharacterized protein C14orf142	C14orf142
0,010	-0,85	0,56	55,61	Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	ADI1
0,030	-0,84	0,56	55,74	P15144	Aminopeptidase N	ANPEP
0,013	-0,84	0,56	55,85	P28062	Proteasome subunit beta type-8	PSMB8
0,028	-0,84	0,56	55,95	E9PAV3;Q13765	Nascent polypeptide-associated complex subunit alpha	NACA
0,008	-0,83	0,56	56,14	P82912	28S ribosomal protein S11, mitochondrial	MRPS11
0,002	-0,83	0,56	56,16	P62424	60S ribosomal protein L7a	RPL7A
0,019	-0,83	0,56	56,42	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4
0,011	-0,82	0,56	56,46	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1
0,019	-0,82	0,57	56,50	P00813	Adenosine deaminase	ADA
0,018	-0,82	0,57	56,56	Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP
0,029	-0,82	0,57	56,64	Q14318	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8
0,012	-0,82	0,57	56,65	Q9NRY4	Rho GTPase-activating protein 35	ARHGAP35
0,003	-0,82	0,57	56,67	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10

Supplemental Table S2a

0,011	-0,81	0,57	56,85	P26358	DNA (cytosine-5)-methyltransferase 1	DNMT1
0,009	-0,81	0,57	56,86	P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2
0,004	-0,81	0,57	56,89	Q7Z2T5	TRMT1-like protein	TRMT1L
0,003	-0,81	0,57	56,89	Q9UKY7	Protein CDV3 homolog	CDV3
0,001	-0,81	0,57	56,92	Q92665	28S ribosomal protein S31, mitochondrial	MRPS31
0,018	-0,81	0,57	57,00	P13674	Prolyl 4-hydroxylase subunit alpha-1	P4HA1
0,029	-0,81	0,57	57,12	P40227	T-complex protein 1 subunit zeta	CCT6A
0,027	-0,81	0,57	57,17	P42766	60S ribosomal protein L35	RPL35
0,003	-0,80	0,57	57,33	O43402	Neighbor of COX4	COX4NB
0,038	-0,80	0,57	57,37	P13639	Elongation factor 2	EEF2
0,021	-0,80	0,58	57,63	P10599	Thioredoxin	TXN
0,044	-0,79	0,58	57,64	Q99497	Protein DJ-1	PARK7
0,019	-0,79	0,58	57,67	Q9UK41	Vacuolar protein sorting-associated protein 28 homolog	VPS28
0,001	-0,79	0,58	57,72	P49755	Transmembrane emp24 domain-containing protein 10	TMED10
0,005	-0,79	0,58	57,80	O43709	Uncharacterized methyltransferase WBSCR22	WBSCR22
0,039	-0,79	0,58	57,81	P10768	S-formylglutathione hydrolase	ESD
0,003	-0,79	0,58	57,89	P62750	60S ribosomal protein L23a	RPL23A
0,008	-0,79	0,58	57,94	P63208	S-phase kinase-associated protein 1	SKP1
0,001	-0,78	0,58	58,21	P60842	Eukaryotic initiation factor 4A-I	EIF4A1
0,000	-0,78	0,58	58,23	P30050	60S ribosomal protein L12	RPL12
0,032	-0,78	0,58	58,30	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7
0,040	-0,78	0,58	58,37	P30041	Peroxiredoxin-6	PRDX6
0,045	-0,78	0,58	58,40	P27348	14-3-3 protein theta	YWHAQ
0,025	-0,77	0,58	58,45	Q15075	Early endosome antigen 1	EEA1
0,022	-0,77	0,58	58,47	Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1
0,012	-0,77	0,58	58,49	Q9H4M9	EH domain-containing protein 1	EHD1
0,038	-0,77	0,59	58,61	Q15006	Tetratricopeptide repeat protein 35	TTC35
0,000	-0,77	0,59	58,61	O00468	Agrin	AGRN
0,040	-0,77	0,59	58,65	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35
0,002	-0,77	0,59	58,69	Q9UBK7;Q9UNT1	Rab-like protein 2A;Rab-like protein 2B	RABL2A;RABL2B
0,009	-0,77	0,59	58,72	P25789	Proteasome subunit alpha type-4	PSMA4
0,003	-0,77	0,59	58,84	Q02878	60S ribosomal protein L6	RPL6
0,001	-0,76	0,59	59,01	Q04837	Single-stranded DNA-binding protein, mitochondrial	SSBP1

Supplemental Table S2a

0,006	-0,76	0,59	59,14	P61254;Q9UNX3	60S ribosomal protein L26;60S ribosomal protein L26-like 1	RPL26;RPL26L1
0,015	-0,76	0,59	59,23	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial	ALDH5A1
0,036	-0,76	0,59	59,25	O95630	STAM-binding protein	STAMBP
0,036	-0,75	0,59	59,34	P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1
0,014	-0,75	0,59	59,38	Q96HC4	PDZ and LIM domain protein 5	PDLIM5
0,005	-0,75	0,59	59,46	Q6PKG0;Q659C4	La-related protein 1	LARP1
0,009	-0,75	0,59	59,47	P54819	Adenylate kinase 2, mitochondrial	AK2
0,006	-0,75	0,60	59,53	P00441	Superoxide dismutase [Cu-Zn]	SOD1
0,005	-0,75	0,60	59,54	Q5HYJ3	Protein FAM76B	FAM76B
0,000	-0,75	0,60	59,58	Q14240	Eukaryotic initiation factor 4A-II	EIF4A2
0,036	-0,75	0,60	59,64	P50990	T-complex protein 1 subunit theta	CCT8
0,011	-0,75	0,60	59,65	P51858	Hepatoma-derived growth factor	HDGF
0,014	-0,74	0,60	59,84	Q9GZN8	UPF0687 protein C20orf27	C20orf27
0,004	-0,74	0,60	59,96	O00170	AH receptor-interacting protein	AIP
0,029	-0,74	0,60	59,97	Q13642	Four and a half LIM domains protein 1	FHL1
0,047	-0,74	0,60	60,00	Q9NX24	H/ACA ribonucleoprotein complex subunit 2	NHP2
0,016	-0,74	0,60	60,05	P35606	Coatomer subunit beta	COPB2
0,012	-0,73	0,60	60,11	P07339	Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain	CTSD
0,033	-0,73	0,60	60,14	P62249	40S ribosomal protein S16	RPS16
0,018	-0,73	0,60	60,16	O75390	Citrate synthase, mitochondrial	CS
0,023	-0,73	0,60	60,24	Q8WX93	Palladin	PALLD
0,005	-0,73	0,60	60,36	P46781	40S ribosomal protein S9	RPS9
0,041	-0,73	0,60	60,43	Q92804	TATA-binding protein-associated factor 2N	TAF15
0,007	-0,72	0,61	60,50	P62753	40S ribosomal protein S6	RPS6
0,002	-0,72	0,61	60,55	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1
0,006	-0,72	0,61	60,56	Q06481	Amyloid-like protein 2	APLP2
0,000	-0,72	0,61	60,61	P40429;Q6NVV1	60S ribosomal protein L13a;Putative 60S ribosomal protein L13a-like MGC87657	RPL13A
0,010	-0,72	0,61	60,63	P62851	40S ribosomal protein S25	RPS25
0,043	-0,72	0,61	60,72	O00461	Golgi integral membrane protein 4	GOLIM4
0,004	-0,72	0,61	60,77	Q15436	Protein transport protein Sec23A	SEC23A
0,042	-0,72	0,61	60,90	P61247	40S ribosomal protein S3a	RPS3A
0,035	-0,72	0,61	60,90	P10619	Lysosomal protective protein;Lysosomal protective protein 32 kDa chain;Lysosomal	CTSA
0,015	-0,71	0,61	60,93	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1

Supplemental Table S2a

0,039	-0,71	0,61	60,96	O75935	Dynactin subunit 3	DCTN3
0,038	-0,71	0,61	60,98	Q15056	Eukaryotic translation initiation factor 4H	EIF4H
0,001	-0,71	0,61	61,02	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP
0,014	-0,71	0,61	61,08	P61224;A6NIZ1	Ras-related protein Rap-1b;Ras-related protein Rap-1b-like protein	RAP1B
0,046	-0,71	0,61	61,22	Q16718	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	NDUFA5
0,035	-0,71	0,61	61,26	Q9UGR2	Zinc finger CCCH domain-containing protein 7B	ZC3H7B
0,028	-0,71	0,61	61,34	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1
0,050	-0,70	0,61	61,38	O95571	Protein ETHE1, mitochondrial	ETHE1
0,011	-0,70	0,61	61,49	P08708;P0CW22	40S ribosomal protein S17;40S ribosomal protein S17-like	RPS17;RPS17L
0,009	-0,70	0,62	61,51	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1
0,045	-0,70	0,62	61,54	Q16831	Uridine phosphorylase 1	UPP1
0,015	-0,70	0,62	61,56	P48643	T-complex protein 1 subunit epsilon	CCT5
0,033	-0,70	0,62	61,62	P28066	Proteasome subunit alpha type-5	PSMA5
0,010	-0,69	0,62	61,79	Q9GZZ1	N-alpha-acetyltransferase 50	NAA50
0,015	-0,69	0,62	61,79	P02545	Prelamin-A/C;Lamin-A/C	LMNA
0,003	-0,69	0,62	62,06	P41091;Q2VIR3	Eukaryotic translation initiation factor 2 subunit 3;Putative eukaryotic translation in	EIF2S3;EIF2S3L
0,036	-0,69	0,62	62,07	O60271;Q9UPT6	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9
0,019	-0,69	0,62	62,13	P35269	General transcription factor IIF subunit 1	GTF2F1
0,015	-0,68	0,62	62,32	P54578	Ubiquitin carboxyl-terminal hydrolase 14	USP14
0,014	-0,68	0,62	62,39	Q9H6T3	RNA polymerase II-associated protein 3	RPAP3
0,015	-0,68	0,62	62,45	P62277	40S ribosomal protein S13	RPS13
0,012	-0,68	0,63	62,54	Q9BSD7	Cancer-related nucleoside-triphosphatase	NTPCR
0,005	-0,67	0,63	62,89	P36776	Lon protease homolog, mitochondrial	LONP1
0,045	-0,67	0,63	63,02	Q15599	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	SLC9A3R2
0,031	-0,66	0,63	63,11	P55769	NHP2-like protein 1	NHP2L1
0,010	-0,66	0,63	63,16	Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH
0,001	-0,66	0,63	63,20	Q8ND56	Protein LSM14 homolog A	LSM14A
0,012	-0,66	0,63	63,28	P23396	40S ribosomal protein S3	RPS3
0,027	-0,66	0,63	63,34	O95816	BAG family molecular chaperone regulator 2	BAG2
0,024	-0,66	0,63	63,37	P10636	Microtubule-associated protein tau	MAPT
0,008	-0,66	0,63	63,44	Q3L8U1	Chromodomain-helicase-DNA-binding protein 9	CHD9
0,023	-0,66	0,63	63,47	P53350	Serine/threonine-protein kinase PLK1	PLK1
0,032	-0,65	0,64	63,51	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial	HAGH

Supplemental Table S2a

0,000	-0,65	0,64	63,53	Q9Y520	Protein PRRC2C	PRRC2C
0,005	-0,65	0,64	63,78	Q99832	T-complex protein 1 subunit eta	CCT7
0,045	-0,65	0,64	63,83	O60763	General vesicular transport factor p115	USO1
0,007	-0,65	0,64	63,90	O60841	Eukaryotic translation initiation factor 5B	EIF5B
0,046	-0,64	0,64	63,95	Q9BRJ6	Uncharacterized protein C7orf50	C7orf50
0,019	-0,64	0,64	64,08	P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS
0,042	-0,64	0,64	64,16	Q14558;O60256	Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1
0,028	-0,64	0,64	64,18	P56537	Eukaryotic translation initiation factor 6	EIF6
0,004	-0,64	0,64	64,26	P11279	Lysosome-associated membrane glycoprotein 1	LAMP1
0,002	-0,64	0,64	64,29	Q5T6F2	Ubiquitin-associated protein 2	UBAP2
0,012	-0,64	0,64	64,31	P11047	Laminin subunit gamma-1	LAMC1
0,010	-0,64	0,64	64,32	P46821	Microtubule-associated protein 1B;MAP1 light chain LC1	MAP1B
0,015	-0,64	0,64	64,38	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7
0,009	-0,63	0,64	64,40	P49590	Probable histidine--tRNA ligase, mitochondrial	HARS2
0,044	-0,63	0,65	64,52	P52594	Arf-GAP domain and FG repeat-containing protein 1	AGFG1
0,003	-0,63	0,65	64,67	Q96CT7	Coiled-coil domain-containing protein 124	CCDC124
0,025	-0,63	0,65	64,69	Q9UFW8	CGG triplet repeat-binding protein 1	CGGBP1
0,012	-0,62	0,65	64,85	Q96P16	Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A
0,041	-0,62	0,65	64,85	Q96K21	Zinc finger FYVE domain-containing protein 19	ZFYVE19
0,002	-0,62	0,65	64,93	P05198	Eukaryotic translation initiation factor 2 subunit 1	EIF2S1
0,008	-0,62	0,65	64,98	Q8IV08	Phospholipase D3	PLD3
0,001	-0,62	0,65	65,02	P04075	Fructose-bisphosphate aldolase A	ALDOA
0,043	-0,62	0,65	65,08	O94925	Glutaminase kidney isoform, mitochondrial	GLS
0,009	-0,62	0,65	65,10	Q13287	N-myc-interactor	NMI
0,034	-0,62	0,65	65,16	Q12841	Follistatin-related protein 1	FSTL1
0,005	-0,62	0,65	65,21	Q9NP81	Serine--tRNA ligase, mitochondrial	SARS2
0,004	-0,62	0,65	65,23	P18077	60S ribosomal protein L35a	RPL35A
0,018	-0,61	0,65	65,31	P079;P0CG48;P0CG47;P61	Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Polyubiquitin	RPS27A;UBC;UBB;UBA
0,007	-0,61	0,66	65,70	P131;Q9UBL6;O95741;Q9	Copine-3	CPNE3
0,017	-0,61	0,66	65,73	Q15637	Splicing factor 1	SF1
0,046	-0,60	0,66	65,77	O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10
0,019	-0,60	0,66	65,96	P49915	GMP synthase [glutamine-hydrolyzing]	GMPS
0,006	-0,60	0,66	65,96	Q15008	26S proteasome non-ATPase regulatory subunit 6	PSMD6

Supplemental Table S2a

0,023	-0,60	0,66	65,97	Q9NVA2	Septin-11	Sep.11
0,005	-0,60	0,66	66,01	Q6RFH5	WD repeat-containing protein 74	WDR74
0,019	-0,60	0,66	66,01	P50914	60S ribosomal protein L14	RPL14
0,009	-0,60	0,66	66,16	O94992	Protein HEXIM1	HEXIM1
0,023	-0,59	0,66	66,40	O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3
0,046	-0,59	0,66	66,46	Q9H223	EH domain-containing protein 4	EHD4
0,009	-0,59	0,67	66,57	P55145	Mesencephalic astrocyte-derived neurotrophic factor	MANF
0,017	-0,58	0,67	67,12	P50991	T-complex protein 1 subunit delta	CCT4
0,044	-0,57	0,67	67,16	Q9NVT9	Armadillo repeat-containing protein 1	ARMC1
0,017	-0,57	0,67	67,18	Q8N6T3	ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1
0,022	-0,57	0,67	67,19	Q9NP97;Q8TF09	Dynein light chain roadblock-type 1;Dynein light chain roadblock-type 2	DYNLRB1;DYNLRB2
0,020	-0,57	0,67	67,31	P78371	T-complex protein 1 subunit beta	CCT2
0,013	-0,57	0,67	67,39	O14950;P19105;P24844	Myosin regulatory light chain 12B;Myosin regulatory light chain 12A;Myosin regulatory light chain 12B	MYL12B;MYL12A;MYL12B
0,005	-0,57	0,67	67,41	P63173	60S ribosomal protein L38	RPL38
0,003	-0,57	0,67	67,45	Q9H0F6	Sharpin	SHARPIN
0,020	-0,57	0,67	67,49	Q08378	Golgin subfamily A member 3	GOLGA3
0,000	-0,56	0,68	67,68	P35579	Myosin-9	MYH9
0,026	-0,56	0,68	67,81	P11216	Glycogen phosphorylase, brain form	PYGB
0,023	-0,56	0,68	67,83	P48739	Phosphatidylinositol transfer protein beta isoform	PITPNB
0,031	-0,56	0,68	67,87	P23528	Cofilin-1	CFL1
0,012	-0,56	0,68	67,97	P00390	Glutathione reductase, mitochondrial	GSR
0,033	-0,56	0,68	68,01	Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB
0,005	-0,56	0,68	68,06	P18615	Negative elongation factor E	RDBP
0,019	-0,56	0,68	68,06	P04181	Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form	OAT
0,013	-0,55	0,68	68,08	P62847	40S ribosomal protein S24	RPS24
0,048	-0,55	0,68	68,09	Q16513	Serine/threonine-protein kinase N2	PKN2
0,001	-0,55	0,68	68,26	Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86
0,042	-0,55	0,68	68,40	P62244	40S ribosomal protein S15a	RPS15A
0,014	-0,55	0,68	68,41	P49411	Elongation factor Tu, mitochondrial	TUFM
0,019	-0,55	0,68	68,48	P30622	CAP-Gly domain-containing linker protein 1	CLIP1
0,001	-0,54	0,69	68,60	P13861;P31323	cAMP-dependent protein kinase type II-alpha regulatory subunit	PRKAR2A
0,000	-0,54	0,69	68,71	Q9BY44	Eukaryotic translation initiation factor 2A	EIF2A
0,036	-0,54	0,69	68,71	P38646	Stress-70 protein, mitochondrial	HSPA9

Supplemental Table S2a

0,024	-0,54	0,69	68,77	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB
0,012	-0,54	0,69	68,79	Q96JB5	CDK5 regulatory subunit-associated protein 3	CDK5RAP3
0,045	-0,54	0,69	68,88	P15289	Arylsulfatase A;Arylsulfatase A component B;Arylsulfatase A component C	ARSA
0,025	-0,53	0,69	69,19	Q8N684	Cleavage and polyadenylation specificity factor subunit 7	CPSF7
0,030	-0,53	0,69	69,30	P11142	Heat shock cognate 71 kDa protein	HSPA8
0,009	-0,53	0,69	69,32	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A
0,028	-0,53	0,69	69,33	P36578	60S ribosomal protein L4	RPL4
0,031	-0,53	0,69	69,41	P54652	Heat shock-related 70 kDa protein 2	HSPA2
0,030	-0,53	0,69	69,42	O75976	Carboxypeptidase D	CPD
0,031	-0,53	0,69	69,48	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3
0,017	-0,53	0,69	69,49	P46926	Glucosamine-6-phosphate isomerase 1	GNPDA1
0,042	-0,52	0,70	69,53	Q9BUP3	Oxidoreductase HTATIP2	HTATIP2
0,016	-0,52	0,70	69,60	P48730	Casein kinase I isoform delta	CSNK1D
0,049	-0,52	0,70	69,60	Q6QNY0	Biogenesis of lysosome-related organelles complex 1 subunit 3	BLOC1S3
0,031	-0,52	0,70	69,87	Q96C01	Protein FAM136A	FAM136A
0,008	-0,52	0,70	69,94	P46776	60S ribosomal protein L27a	RPL27A
0,008	-0,51	0,70	70,14	Q7L2E3	Putative ATP-dependent RNA helicase DHX30	DHX30
0,027	-0,51	0,70	70,20	Q9UN81		ORF1
0,038	-0,51	0,70	70,22	Q3KQU3	MAP7 domain-containing protein 1	MAP7D1
0,001	-0,51	0,70	70,25	O95793	Double-stranded RNA-binding protein Staufin homolog 1	STAU1
0,007	-0,51	0,70	70,36	P48634	Protein PRRC2A	PRRC2A
0,031	-0,51	0,70	70,38	P48444	Coatomer subunit delta	ARCN1
0,044	-0,51	0,70	70,40	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2
0,037	-0,51	0,70	70,41	P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC
0,001	-0,51	0,70	70,43	P22392	Nucleoside diphosphate kinase B	NME2
0,010	-0,50	0,71	70,64	Q9NWH9	SAFB-like transcription modulator	SLTM
0,029	-0,50	0,71	70,65	Q9P0R6	GSK3-beta interaction protein	GSKIP
0,033	-0,50	0,71	70,89	Q5TZA2;Q86T23	Rootletin	CROCC
0,005	-0,49	0,71	71,01	P51608	Methyl-CpG-binding protein 2	MECP2
0,016	-0,49	0,71	71,11	P33316	Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT
0,019	-0,48	0,72	71,75	P55084	Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase	HADHB
0,036	-0,47	0,72	72,15	Q8WUQ7	Uncharacterized protein C19orf29	C19orf29
0,033	-0,47	0,72	72,37	P32969	60S ribosomal protein L9	RPL9

Supplemental Table S2a

0,036	-0,47	0,72	72,41	O00233	26S proteasome non-ATPase regulatory subunit 9	PSMD9
0,028	-0,46	0,73	72,51	O00425	Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3
0,014	-0,46	0,73	72,71	Q14258	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25
0,036	-0,46	0,73	72,77	P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70
0,002	-0,46	0,73	72,79	P60660	Myosin light polypeptide 6	MYL6
0,027	-0,46	0,73	72,83	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH
0,038	-0,46	0,73	72,85	Q4J6C6	Prolyl endopeptidase-like	PREPL
0,006	-0,45	0,73	73,19	Q96FV2	Secernin-2	SCRN2
0,006	-0,45	0,73	73,29	Q9NSK0	Kinesin light chain 4	KLC4
0,046	-0,45	0,73	73,36	P31153;Q00266	S-adenosylmethionine synthase isoform type-2	MAT2A
0,013	-0,45	0,73	73,37	Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2
0,027	-0,44	0,74	73,54	Q9BW91	ADP-ribose pyrophosphatase, mitochondrial	NUDT9
0,020	-0,44	0,74	73,74	Q14157	Ubiquitin-associated protein 2-like	UBAP2L
0,030	-0,43	0,74	74,28	P12955	Xaa-Pro dipeptidase	PEPD
0,045	-0,43	0,74	74,44	P28799	Granulins;Acrogranin;Paragranulin;Granulin-1;Granulin-2;Granulin-3;Granulin-4;Granulin-5	GRN
0,024	-0,43	0,74	74,47	Q96G03	Phosphoglucomutase-2	PGM2
0,040	-0,42	0,75	74,66	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	ANP32B
0,017	-0,41	0,75	75,19	Q00341	Vigilin	HDLBP
0,031	-0,41	0,75	75,44	Q53H82	Beta-lactamase-like protein 2	LACTB2
0,034	-0,40	0,76	75,63	Q02543	60S ribosomal protein L18a	RPL18A
0,039	-0,40	0,76	75,91	Q16555;Q14194	Dihydropyrimidinase-related protein 2	DPYSL2
0,005	-0,39	0,76	76,24	Q14151	Scaffold attachment factor B2	SAFB2
0,033	-0,39	0,76	76,37	P62913	60S ribosomal protein L11	RPL11
0,029	-0,39	0,76	76,39	Q15369	Transcription elongation factor B polypeptide 1	TCEB1
0,031	-0,39	0,76	76,43	P35241	Radixin	RDX
0,002	-0,39	0,76	76,45	Q9Y2T3	Guanine deaminase	GDA
0,036	-0,39	0,77	76,55	P27816	Microtubule-associated protein 4	MAP4
0,048	-0,38	0,77	76,81	P20042	Eukaryotic translation initiation factor 2 subunit 2	EIF2S2
0,011	-0,37	0,77	77,22	O43491;Q9Y2J2	Band 4.1-like protein 2	EPB41L2
0,035	-0,37	0,77	77,26	P12814;Q08043	Alpha-actinin-1	ACTN1
0,023	-0,35	0,78	78,41	O15347	High mobility group protein B3	HMGB3
0,008	-0,35	0,78	78,44	P61353	60S ribosomal protein L27	RPL27
0,035	-0,34	0,79	78,81	P13798	Acylamino-acid-releasing enzyme	APEH

Supplemental Table S2a

0,017	-0,34	0,79	78,82	P40939	Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;	HADHA
0,049	-0,34	0,79	79,05	P49770	Translation initiation factor eIF-2B subunit beta	EIF2B2
0,044	-0,34	0,79	79,13	Q8IVF2	Protein AHNAK2	AHNAK2
0,042	-0,33	0,79	79,39	Q9Y310	tRNA-splicing ligase RtcB homolog	C22orf28
0,048	-0,33	0,79	79,47	P49189	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1
0,041	-0,33	0,80	79,55	Q8IW45	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	CARKD
0,042	-0,33	0,80	79,73	Q9NTK5	Obg-like ATPase 1	OLA1
0,025	-0,32	0,80	79,85	Q7Z2W4	Zinc finger CCCH-type antiviral protein 1	ZC3HAV1
0,015	-0,32	0,80	79,89	O95359	Transforming acidic coiled-coil-containing protein 2	TACC2
0,041	-0,32	0,80	80,35	P55081	Microfibrillar-associated protein 1	MFAP1
0,037	-0,30	0,81	81,25	Q9NZB2;Q5T035	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A
0,008	-0,29	0,82	81,68	P51114	Fragile X mental retardation syndrome-related protein 1	FXR1
0,011	-0,28	0,82	82,23	Q14764	Major vault protein	MVP
0,013	-0,27	0,83	82,74	P26196	Probable ATP-dependent RNA helicase DDX6	DDX6
0,049	-0,26	0,83	83,50	Q9Y5P4	Collagen type IV alpha-3-binding protein	COL4A3BP
0,008	-0,26	0,84	83,72	Q86UE4	Protein LYRIC	MTDH
0,010	-0,24	0,85	84,66	P98170	E3 ubiquitin-protein ligase XIAP	XIAP
0,017	-0,24	0,85	84,73	Q9NQR4	Omega-amidase NIT2	NIT2
24 h Down						
0,000	-4,76	0,04	3,70	P61513	60S ribosomal protein L37a	RPL37A
0,000	-4,64	0,04	4,01	P82933	28S ribosomal protein S9, mitochondrial	MRPS9
0,003	-4,12	0,06	5,77	P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial;Cytochrome b-c1 complex	UQCRCF1
0,038	-3,73	0,08	7,52	Q9Y4Y9	U6 snRNA-associated Sm-like protein LSM5	LSM5
0,001	-3,73	0,08	7,53	Q9UNS2	COP9 signalosome complex subunit 3	COPS3
0,003	-3,60	0,08	8,26	Q27J81	Inverted formin-2	INF2
0,000	-3,55	0,09	8,51	P17066;P48741	Heat shock 70 kDa protein 6;Putative heat shock 70 kDa protein 7	HSPA6;HSPA7
0,005	-3,49	0,09	8,90	P14927	Cytochrome b-c1 complex subunit 7	UQCRB
0,013	-3,48	0,09	8,98	O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10
0,002	-3,43	0,09	9,28	Q12849	G-rich sequence factor 1	GRSF1
0,036	-3,39	0,10	9,56	Q15366	Poly(rC)-binding protein 2	PCBP2
0,018	-3,38	0,10	9,64	P47813;O14602	Eukaryotic translation initiation factor 1A, X-chromosomal;Eukaryotic translation ini	EIF1AX;EIF1AY
0,000	-3,37	0,10	9,65	O43181	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	NDUFS4
0,003	-3,31	0,10	10,09	P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2

Supplemental Table S2a

0,000	-3,30	0,10	10,17	P53350	Serine/threonine-protein kinase PLK1	PLK1
0,002	-3,27	0,10	10,35	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K
0,004	-3,27	0,10	10,38	Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUFB9
0,020	-3,24	0,11	10,55	P53618	Coatomer subunit beta	COPB1
0,004	-3,18	0,11	11,02	P57105	Synaptojanin-2-binding protein	SYNJ2BP
0,021	-3,18	0,11	11,07	Q96FJ2	Dynein light chain 2, cytoplasmic	DYNLL2
0,020	-3,11	0,12	11,58	Q9Y262	Eukaryotic translation initiation factor 3 subunit L	EIF3L
0,000	-3,05	0,12	12,11	Q02241	Kinesin-like protein KIF23	KIF23
0,000	-3,02	0,12	12,35	Q9BZE1	39S ribosomal protein L37, mitochondrial	MRPL37
0,000	-3,00	0,13	12,51	Q9H0W8	Protein SMG9	SMG9
0,000	-2,97	0,13	12,74	Q96DC8	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	ECHDC3
0,003	-2,95	0,13	12,91	Q96T51	RUN and FYVE domain-containing protein 1	RUFY1
0,013	-2,94	0,13	13,00	P60228	Eukaryotic translation initiation factor 3 subunit E	EIF3E
0,040	-2,93	0,13	13,16	P15559	NAD(P)H dehydrogenase [quinone] 1	NQO1
0,042	-2,90	0,13	13,44	P09211	Glutathione S-transferase P	GSTP1
0,009	-2,88	0,14	13,58	O95470	Sphingosine-1-phosphate lyase 1	SGPL1
0,015	-2,85	0,14	13,84	O00410;O60518	Importin-5	IPO5
0,001	-2,84	0,14	13,95	Q9P015	39S ribosomal protein L15, mitochondrial	MRPL15
0,032	-2,80	0,14	14,37	P08754	Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3
0,007	-2,75	0,15	14,87	Q9Y2U8	Inner nuclear membrane protein Man1	LEMD3
0,006	-2,75	0,15	14,92	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2
0,011	-2,73	0,15	15,07	Q9H8Y8	Golgi reassembly-stacking protein 2	GORASP2
0,040	-2,72	0,15	15,19	Q9NV56	MRG-binding protein	MRGBP
0,000	-2,72	0,15	15,20	Q9NQ50	39S ribosomal protein L40, mitochondrial	MRPL40
0,011	-2,66	0,16	15,79	Q9UPV0	Centrosomal protein of 164 kDa	CEP164
0,003	-2,66	0,16	15,80	Q8WV24	Pleckstrin homology-like domain family A member 1	PHLDA1
0,009	-2,65	0,16	15,90	Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11
0,015	-2,65	0,16	15,91	Q9BWM7	Sideroflexin-3	SFXN3
0,002	-2,65	0,16	15,93	Q9H118	Activating signal cointegrator 1 complex subunit 2	ASCC2
0,017	-2,65	0,16	15,96	O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS
0,000	-2,64	0,16	16,00	Q9H4L7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily 1	SMARCAD1
0,018	-2,64	0,16	16,01	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1
0,001	-2,64	0,16	16,06	P61923	Coatomer subunit zeta-1	COPZ1

Supplemental Table S2a

0,035	-2,64	0,16	16,08	Q14241	Transcription elongation factor B polypeptide 3	TCEB3
0,014	-2,63	0,16	16,16	O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	NDUFS7
0,045	-2,60	0,17	16,52	P10619	Lysosomal protective protein;Lysosomal protective protein 32 kDa chain;Lysosomal	CTSA
0,014	-2,58	0,17	16,75	Q9H479	Fructosamine-3-kinase	FN3K
0,003	-2,57	0,17	16,81	P62861	40S ribosomal protein S30	FAU
0,033	-2,57	0,17	16,83	O43324	Eukaryotic translation elongation factor 1 epsilon-1	EEF1E1
0,008	-2,57	0,17	16,84	Q9HD33	39S ribosomal protein L47, mitochondrial	MRPL47
0,000	-2,56	0,17	16,96	P62266	40S ribosomal protein S23	RPS23
0,009	-2,55	0,17	17,07	Q9BQG0	Myb-binding protein 1A	MYBBP1A
0,013	-2,54	0,17	17,14	O15379	Histone deacetylase 3	HDAC3
0,000	-2,53	0,17	17,29	Q9Y448	Small kinetochore-associated protein	SKAP
0,007	-2,51	0,18	17,52	P14854	Cytochrome c oxidase subunit 6B1	COX6B1
0,032	-2,51	0,18	17,59	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3
0,002	-2,49	0,18	17,78	Q9P0J0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	NDUFA13
0,001	-2,49	0,18	17,79	P51398	28S ribosomal protein S29, mitochondrial	DAP3
0,020	-2,49	0,18	17,86	Q9UJX2	Cell division cycle protein 23 homolog	CDC23
0,003	-2,49	0,18	17,86	Q8IY17	Neuropathy target esterase	PNPLA6
0,032	-2,48	0,18	17,91	Q9BUF5	Tubulin beta-6 chain	TUBB6
0,032	-2,48	0,18	17,96	Q9UI09	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	NDUFA12
0,013	-2,47	0,18	18,01	P36543	V-type proton ATPase subunit E 1	ATP6V1E1
0,001	-2,45	0,18	18,33	O00743	Serine/threonine-protein phosphatase 6 catalytic subunit	PPP6C
0,024	-2,44	0,18	18,38	Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210
0,007	-2,44	0,18	18,48	Q12769	Nuclear pore complex protein Nup160	NUP160
0,030	-2,43	0,19	18,50	P16455	Methylated-DNA--protein-cysteine methyltransferase	MGMT
0,001	-2,43	0,19	18,52	Q9Y6W3	Calpain-7	CAPN7
0,041	-2,43	0,19	18,57	Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	SLIRP
0,002	-2,43	0,19	18,60	O00148	ATP-dependent RNA helicase DDX39A	DDX39A
0,015	-2,42	0,19	18,66	Q10567	AP-1 complex subunit beta-1	AP1B1
0,034	-2,42	0,19	18,73	O00425	Insulin-like growth factor 2 mRNA-binding protein 3	IGF2BP3
0,023	-2,42	0,19	18,73	Q8NDA2	Hemicentin-2	HMCN2
0,025	-2,37	0,19	19,39	Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9
0,003	-2,35	0,20	19,58	P15407	Fos-related antigen 1	FOSL1
0,039	-2,34	0,20	19,76	P16070	CD44 antigen	CD44

Supplemental Table S2a

0,032	-2,33	0,20	19,89	Q9HCE1	Putative helicase MOV-10	MOV10
0,025	-2,33	0,20	19,89	P56556	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	NDUFA6
0,001	-2,32	0,20	20,03	Q8TB72	Pumilio homolog 2	PUM2
0,003	-2,32	0,20	20,06	P27635;Q96L21	60S ribosomal protein L10;60S ribosomal protein L10-like	RPL10;RPL10L
0,026	-2,32	0,20	20,06	P55209	Nucleosome assembly protein 1-like 1	NAP1L1
0,004	-2,31	0,20	20,21	Q9BUR5	Apolipoprotein O	APOO
0,000	-2,29	0,20	20,38	P14635	G2/mitotic-specific cyclin-B1	CCNB1
0,025	-2,28	0,21	20,58	Q96N67	Dedicator of cytokinesis protein 7	DOCK7
0,036	-2,28	0,21	20,59	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP
0,010	-2,26	0,21	20,91	P60510	Serine/threonine-protein phosphatase 4 catalytic subunit	PPP4C
0,042	-2,22	0,22	21,51	P29992;O95837	Guanine nucleotide-binding protein subunit alpha-11	GNA11
0,015	-2,21	0,22	21,56	Q9BXS5;Q9Y6Q5	AP-1 complex subunit mu-1	AP1M1
0,011	-2,20	0,22	21,77	Q5UIP0	Telomere-associated protein RIF1	RIF1
0,003	-2,19	0,22	21,88	P08240	Signal recognition particle receptor subunit alpha	SRPR
0,043	-2,19	0,22	21,92	Q9Y2Z4	Tyrosine--tRNA ligase, mitochondrial	YARS2
0,017	-2,19	0,22	21,94	O75884	Putative hydrolase RBBP9	RBBP9
0,045	-2,19	0,22	21,95	Q9NU22	Midasin	MDN1
0,001	-2,18	0,22	22,09	O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	NDUFS3
0,034	-2,17	0,22	22,19	O95292	Vesicle-associated membrane protein-associated protein B/C	VAPB
0,036	-2,17	0,22	22,23	Q969H8	UPF0556 protein C19orf10	C19orf10
0,002	-2,17	0,22	22,24	O75616	GTPase Era, mitochondrial	ERAL1
0,014	-2,16	0,22	22,35	Q9NZM5	Glioma tumor suppressor candidate region gene 2 protein	GLTSCR2
0,013	-2,15	0,23	22,53	Q6P2E9	Enhancer of mRNA-decapping protein 4	EDC4
0,014	-2,14	0,23	22,61	P78362	SRSF protein kinase 2;SRSF protein kinase 2 N-terminal;SRSF protein kinase 2 C-term	SRPK2
0,023	-2,14	0,23	22,62	Q13885;Q9BVA1	Tubulin beta-2A chain;Tubulin beta-2B chain	TUBB2A;TUBB2B
0,025	-2,14	0,23	22,67	P02649	Apolipoprotein E	APOE
0,004	-2,14	0,23	22,76	P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST
0,004	-2,13	0,23	22,82	P53007	Tricarboxylate transport protein, mitochondrial	SLC25A1
0,006	-2,12	0,23	22,95	Q9NPA8	Enhancer of yellow 2 transcription factor homolog	ENY2
0,017	-2,11	0,23	23,15	Q93052	Lipoma-preferred partner	LPP
0,025	-2,09	0,23	23,44	Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1	UFC1
0,006	-2,09	0,24	23,52	Q9C0F1	Centrosomal protein of 44 kDa	CEP44
0,044	-2,09	0,24	23,53	O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8

Supplemental Table S2a

0,001	-2,09	0,24	23,54	Q7Z2W9	39S ribosomal protein L21, mitochondrial	MRPL21
0,015	-2,09	0,24	23,57	Q9H9B4	Sideroflexin-1	SFXN1
0,035	-2,07	0,24	23,78	Q9Y6A4	UPF0468 protein C16orf80	C16orf80
0,015	-2,07	0,24	23,82	O14967	Calmegin	CLGN
0,001	-2,07	0,24	23,85	Q14644	Ras GTPase-activating protein 3	RASA3
0,015	-2,07	0,24	23,88	Q9NYK5	39S ribosomal protein L39, mitochondrial	MRPL39
0,023	-2,06	0,24	24,02	O75694	Nuclear pore complex protein Nup155	NUP155
0,000	-2,06	0,24	24,02	Q8IVH8	Mitogen-activated protein kinase kinase kinase kinase 3	MAP4K3
0,007	-2,05	0,24	24,09	Q9Y6K5	2-5-oligoadenylate synthase 3	OAS3
0,037	-2,05	0,24	24,12	P63313	Thymosin beta-10	TMSB10
0,035	-2,05	0,24	24,20	Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7
0,038	-2,04	0,24	24,35	Q8IUR7	Armadillo repeat-containing protein 8	ARMC8
0,006	-2,02	0,25	24,57	Q9NVV4	Poly(A) RNA polymerase, mitochondrial	MTPAP
0,000	-2,02	0,25	24,62	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	SDHB
0,018	-2,02	0,25	24,67	Q92882	Osteoclast-stimulating factor 1	OSTF1
0,045	-2,02	0,25	24,68	Q04917	14-3-3 protein eta	YWHAH
0,014	-2,02	0,25	24,69	O95373	Importin-7	IPO7
0,003	-2,01	0,25	24,77	P46778	60S ribosomal protein L21	RPL21
0,028	-2,01	0,25	24,78	O14617	AP-3 complex subunit delta-1	AP3D1
0,042	-2,01	0,25	24,81	Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial	PGAM5
0,008	-2,01	0,25	24,89	P62857	40S ribosomal protein S28	RPS28
0,001	-2,00	0,25	25,02	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13
0,023	-1,99	0,25	25,14	Q8IXI2	Mitochondrial Rho GTPase 1	RHOT1
0,014	-1,99	0,25	25,15	Q5JPE7;P69849;Q15155	Nodal modulator 2;Nodal modulator 3;Nodal modulator 1	NOMO2;NOMO3;N
0,023	-1,99	0,25	25,18	P12235	ADP/ATP translocase 1	SLC25A4
0,017	-1,98	0,25	25,26	Q9Y6X3	MAU2 chromatid cohesion factor homolog	MAU2
0,016	-1,98	0,25	25,31	Q02833	Ras association domain-containing protein 7	RASSF7
0,007	-1,98	0,25	25,34	Q9H7D7	WD repeat-containing protein 26	WDR26
0,022	-1,98	0,25	25,41	Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L
0,041	-1,97	0,25	25,48	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29
0,002	-1,97	0,26	25,51	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1
0,014	-1,97	0,26	25,58	Q5VTL8	Pre-mRNA-splicing factor 38B	PRPF38B
0,007	-1,97	0,26	25,59	Q9BYD1	39S ribosomal protein L13, mitochondrial	MRPL13

Supplemental Table S2a

0,012	-1,97	0,26	25,61	Q9Y3B7	39S ribosomal protein L11, mitochondrial	MRPL11
0,046	-1,95	0,26	25,82	Q15418	Ribosomal protein S6 kinase alpha-1	RPS6KA1
0,015	-1,95	0,26	25,82	P48444	Coatomer subunit delta	ARCN1
0,015	-1,95	0,26	25,84	O14579	Coatomer subunit epsilon	COPE
0,020	-1,95	0,26	25,92	Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	ADI1
0,008	-1,95	0,26	25,92	Q86WA8	Lon protease homolog 2, peroxisomal	LONP2
0,006	-1,94	0,26	26,07	O43169	Cytochrome b5 type B	CYB5B
0,019	-1,94	0,26	26,07	Q9UIV1	CCR4-NOT transcription complex subunit 7	CNOT7
0,005	-1,94	0,26	26,09	Q9BRK5	45 kDa calcium-binding protein	SDF4
0,001	-1,94	0,26	26,10	Q99623	Prohibitin-2	PHB2
0,018	-1,93	0,26	26,17	P82912	28S ribosomal protein S11, mitochondrial	MRPS11
0,006	-1,93	0,26	26,26	Q8NE01	Metal transporter CNNM3	CNNM3
0,017	-1,93	0,26	26,28	Q9UHI6	Probable ATP-dependent RNA helicase DDX20	DDX20
0,001	-1,93	0,26	26,28	P06493	Cyclin-dependent kinase 1	CDK1
0,003	-1,93	0,26	26,29	P04350;A6NNZ2	Tubulin beta-4A chain	TUBB4A
0,027	-1,91	0,27	26,59	Q9Y2D4	Exocyst complex component 6B	EXOC6B
0,012	-1,91	0,27	26,65	P17568	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	NDUFB7
0,018	-1,91	0,27	26,66	Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUFA11
0,001	-1,91	0,27	26,67	Q13753	Laminin subunit gamma-2	LAMC2
0,024	-1,90	0,27	26,81	P07305	Histone H1.0	H1FO
0,036	-1,90	0,27	26,88	O43747	AP-1 complex subunit gamma-1	AP1G1
0,028	-1,89	0,27	26,97	Q9Y5Q9	General transcription factor 3C polypeptide 3	GTF3C3
0,002	-1,89	0,27	26,97	O75223	Gamma-glutamylcyclotransferase	GGCT
0,000	-1,89	0,27	27,01	Q10471	Polypeptide N-acetylgalactosaminyltransferase 2;Polypeptide N-acetylgalactosamin	GALNT2
0,009	-1,89	0,27	27,02	P62888	60S ribosomal protein L30	RPL30
0,019	-1,87	0,27	27,35	Q96GC5	39S ribosomal protein L48, mitochondrial	MRPL48
0,032	-1,86	0,28	27,53	Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2
0,024	-1,85	0,28	27,70	Q66K14	TBC1 domain family member 9B	TBC1D9B
0,000	-1,85	0,28	27,71	Q9Y6A5	Transforming acidic coiled-coil-containing protein 3	TACC3
0,033	-1,84	0,28	27,88	Q9H0U6	39S ribosomal protein L18, mitochondrial	MRPL18
0,008	-1,84	0,28	27,97	Q13405	39S ribosomal protein L49, mitochondrial	MRPL49
0,048	-1,83	0,28	28,04	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	PRPF8
0,024	-1,83	0,28	28,06	Q7Z7A4	PX domain-containing protein kinase-like protein	PXK

Supplemental Table S2a

0,024	-1,83	0,28	28,18	Q9Y6C9	Mitochondrial carrier homolog 2	MTCH2
0,032	-1,81	0,28	28,48	Q9Y3A3	MOB-like protein phocein	MOB4
0,004	-1,80	0,29	28,66	Q9NVU0	DNA-directed RNA polymerase III subunit RPC5	POLR3E
0,000	-1,80	0,29	28,68	P08574	Cytochrome c1, heme protein, mitochondrial	CYC1
0,022	-1,80	0,29	28,76	O95365	Zinc finger and BTB domain-containing protein 7A	ZBTB7A
0,022	-1,79	0,29	28,85	Q69YH5	Cell division cycle-associated protein 2	CDCA2
0,002	-1,79	0,29	28,87	Q9Y606	tRNA pseudouridine synthase A, mitochondrial	PUS1
0,005	-1,79	0,29	28,99	Q3ZCM7	Tubulin beta-8 chain	TUBB8
0,013	-1,78	0,29	29,12	P11182	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase	DBT
0,011	-1,78	0,29	29,22	O43709	Uncharacterized methyltransferase WBSCR22	WBSCR22
0,047	-1,76	0,30	29,51	Q6IAA8	Ragulator complex protein LAMTOR1	LAMTOR1
0,018	-1,76	0,30	29,52	P13716	Delta-aminolevulinic acid dehydratase	ALAD
0,022	-1,76	0,30	29,59	Q9NRY5	Protein FAM114A2	FAM114A2
0,029	-1,76	0,30	29,62	Q9GZQ3	COMM domain-containing protein 5	COMMD5
0,037	-1,75	0,30	29,67	O75381	Peroxisomal membrane protein PEX14	PEX14
0,025	-1,75	0,30	29,75	P34896	Serine hydroxymethyltransferase, cytosolic	SHMT1
0,034	-1,75	0,30	29,75	O60504	Vinexin	SORBS3
0,003	-1,75	0,30	29,80	Q9NXV2	BTB/POZ domain-containing protein KCTD5	KCTD5
0,001	-1,74	0,30	29,85	O75380	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	NDUFS6
0,006	-1,74	0,30	29,93	Q92692	Poliovirus receptor-related protein 2	PVRL2
0,001	-1,73	0,30	30,05	P62269	40S ribosomal protein S18	RPS18
0,011	-1,73	0,30	30,07	Q9NPI6	mRNA-decapping enzyme 1A	DCP1A
0,046	-1,72	0,30	30,40	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	CAND1
0,001	-1,71	0,30	30,47	P12236	ADP/ATP translocase 3	SLC25A6
0,000	-1,71	0,31	30,57	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2
0,007	-1,69	0,31	30,94	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1
0,007	-1,69	0,31	31,01	P62244	40S ribosomal protein S15a	RPS15A
0,017	-1,69	0,31	31,02	Q7Z460	CLIP-associating protein 1	CLASP1
0,033	-1,69	0,31	31,09	Q8IWJ2	GRIP and coiled-coil domain-containing protein 2	GCC2
0,048	-1,68	0,31	31,16	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase	PECR
0,012	-1,68	0,31	31,23	P36404	ADP-ribosylation factor-like protein 2	ARL2
0,030	-1,68	0,31	31,26	Q9BYD3	39S ribosomal protein L4, mitochondrial	MRPL4
0,046	-1,67	0,31	31,42	Q13426	DNA repair protein XRCC4	XRCC4

Supplemental Table S2a

0,004	-1,67	0,32	31,51	Q9BX10	GTP-binding protein 2	GTPBP2
0,039	-1,66	0,32	31,65	Q9BZE9	Tether containing UBX domain for GLUT4	ASPSR1
0,003	-1,66	0,32	31,68	Q99447	Ethanolamine-phosphate cytidyltransferase	PCYT2
0,007	-1,65	0,32	31,90	P26641	Elongation factor 1-gamma	EEF1G
0,003	-1,65	0,32	31,94	Q14165	Malectin	MLEC
0,021	-1,63	0,32	32,24	Q9BQE3	Tubulin alpha-1C chain	TUBA1C
0,038	-1,63	0,32	32,30	Q9BRJ2	39S ribosomal protein L45, mitochondrial	MRPL45
0,004	-1,63	0,32	32,34	P32969	60S ribosomal protein L9	RPL9
0,001	-1,63	0,32	32,41	O60763	General vesicular transport factor p115	USO1
0,006	-1,62	0,32	32,47	Q92542	Nicastrin	NCSTN
0,026	-1,61	0,33	32,76	Q9NVH0	Exonuclease 3-5 domain-containing protein 2	EXD2
0,000	-1,60	0,33	32,96	Q9UF33;P54753;Q15375	Ephrin type-A receptor 2	EPHA2
0,046	-1,59	0,33	33,17	Q14451	Growth factor receptor-bound protein 7	GRB7
0,013	-1,59	0,33	33,33	O14965	Aurora kinase A	AURKA
0,004	-1,59	0,33	33,33	O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	NDUFS5
0,025	-1,58	0,33	33,40	Q00577	Transcriptional activator protein Pur-alpha	PURA
0,029	-1,58	0,33	33,45	O75976	Carboxypeptidase D	CPD
0,027	-1,58	0,33	33,47	Q9NR50	Translation initiation factor eIF-2B subunit gamma	EIF2B3
0,005	-1,58	0,34	33,53	Q8N9B5	Junction-mediating and -regulatory protein	JMY
0,037	-1,58	0,34	33,54	Q96Q15;Q6P435	Serine/threonine-protein kinase SMG1	SMG1
0,031	-1,57	0,34	33,60	Q4KMP7	TBC1 domain family member 10B	TBC1D10B
0,042	-1,57	0,34	33,69	Q6P9B9	Integrator complex subunit 5	INTS5
0,024	-1,56	0,34	33,84	P42345	Serine/threonine-protein kinase mTOR	MTOR
0,001	-1,56	0,34	33,85	P62906	60S ribosomal protein L10a	RPL10A
0,012	-1,56	0,34	33,88	Q9NRS6	Sorting nexin-15	SNX15
0,009	-1,56	0,34	33,91	P05388;Q8NHW5	60S acidic ribosomal protein P0;60S acidic ribosomal protein P0-like	RPLP0;RPLP0P6
0,036	-1,56	0,34	33,96	P15170;Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	GSPT1
0,009	-1,55	0,34	34,07	Q9BQC6	Ribosomal protein 63, mitochondrial	MRP63
0,022	-1,55	0,34	34,16	Q9Y291	28S ribosomal protein S33, mitochondrial	MRPS33
0,007	-1,54	0,34	34,34	O15067	Phosphoribosylformylglycinamide synthase	PFAS
0,004	-1,54	0,34	34,47	P41252	Isoleucine--tRNA ligase, cytoplasmic	IARS
0,020	-1,53	0,35	34,52	O60294	Leucine carboxyl methyltransferase 2	LCMT2
0,042	-1,53	0,35	34,63	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA

Supplemental Table S2a

0,001	-1,53	0,35	34,74	P35232	Prohibitin	PHB
0,041	-1,53	0,35	34,74	Q96IX5	Up-regulated during skeletal muscle growth protein 5	USMG5
0,014	-1,52	0,35	34,77	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10
0,011	-1,52	0,35	34,88	Q14008	Cytoskeleton-associated protein 5	CKAP5
0,015	-1,52	0,35	34,92	Q13445	Transmembrane emp24 domain-containing protein 1	TMED1
0,006	-1,52	0,35	34,92	P11940;Q9H361;Q96DU5	Polyadenylate-binding protein 1;Polyadenylate-binding protein 3	PABPC1;PABPC3
0,039	-1,51	0,35	35,00	Q8N183	Mimitin, mitochondrial	NDUFAF2
0,040	-1,51	0,35	35,04	O95782	AP-2 complex subunit alpha-1	AP2A1
0,001	-1,51	0,35	35,05	Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	EIF3M
0,011	-1,51	0,35	35,13	Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1
0,008	-1,50	0,35	35,24	P61313	60S ribosomal protein L15	RPL15
0,039	-1,49	0,35	35,49	P68036	Ubiquitin-conjugating enzyme E2 L3	UBE2L3
0,008	-1,49	0,36	35,60	Q96JB2	Conserved oligomeric Golgi complex subunit 3	COG3
0,017	-1,49	0,36	35,66	P27824	Calnexin	CANX
0,007	-1,49	0,36	35,69	Q5VSL9;Q9ULQ0	Protein FAM40A	FAM40A
0,014	-1,49	0,36	35,71	Q92783	Signal transducing adapter molecule 1	STAM
0,002	-1,48	0,36	35,80	P52815	39S ribosomal protein L12, mitochondrial	MRPL12
0,008	-1,48	0,36	35,84	Q14789	Golgin subfamily B member 1	GOLGB1
0,002	-1,46	0,36	36,27	Q8WVB6	Chromosome transmission fidelity protein 18 homolog	CHTF18
0,002	-1,46	0,36	36,29	P63173	60S ribosomal protein L38	RPL38
0,026	-1,46	0,36	36,36	P61962	DDB1- and CUL4-associated factor 7	DCAF7
0,026	-1,46	0,36	36,39	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HADH
0,029	-1,46	0,36	36,47	P49327	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] 5	FASN
0,026	-1,45	0,37	36,53	P46199	Translation initiation factor IF-2, mitochondrial	MTIF2
0,000	-1,45	0,37	36,64	O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	NDUFA2
0,001	-1,44	0,37	36,77	Q06203	Amidophosphoribosyltransferase	PPAT
0,004	-1,44	0,37	36,78	P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B
0,000	-1,44	0,37	36,81	Q99988	Growth/differentiation factor 15	GDF15
0,011	-1,44	0,37	36,82	P61421	V-type proton ATPase subunit d 1	ATP6V0D1
0,001	-1,43	0,37	37,08	Q8NBJ7	Sulfatase-modifying factor 2	SUMF2
0,010	-1,43	0,37	37,15	O00151	PDZ and LIM domain protein 1	PDLIM1
0,030	-1,43	0,37	37,21	O00748	Cocaine esterase	CES2
0,019	-1,43	0,37	37,23	Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1

Supplemental Table S2a

0,002	-1,42	0,37	37,46	P62701;P22090	40S ribosomal protein S4, X isoform	RPS4X
0,012	-1,41	0,38	37,57	P25098;P35626	Beta-adrenergic receptor kinase 1;Beta-adrenergic receptor kinase 2	ADRBK1;ADRBK2
0,026	-1,41	0,38	37,60	P46013	Antigen KI-67	MKI67
0,028	-1,41	0,38	37,62	Q8NHV4	Protein NEDD1	NEDD1
0,023	-1,40	0,38	37,84	Q14807	Kinesin-like protein KIF22	KIF22
0,001	-1,40	0,38	37,88	Q96HP0	Dedicator of cytokinesis protein 6	DOCK6
0,017	-1,40	0,38	37,94	Q9NRX2	39S ribosomal protein L17, mitochondrial	MRPL17
0,003	-1,40	0,38	38,01	Q9ULX9	Transcription factor MafF	MAFF
0,037	-1,40	0,38	38,02	Q14558;O60256	Phosphoribosyl pyrophosphate synthase-associated protein 1	PRPSAP1
0,002	-1,39	0,38	38,21	Q7Z6K5	UPF0552 protein C15orf38	C15orf38
0,044	-1,38	0,38	38,29	P36405	ADP-ribosylation factor-like protein 3	ARL3
0,004	-1,38	0,38	38,33	P53621	Coatomer subunit alpha;Xenin;Proxenin	COPA
0,032	-1,38	0,38	38,34	Q15477	Helicase SKI2W	SKIV2L
0,000	-1,38	0,38	38,37	Q9Y3U8	60S ribosomal protein L36	RPL36
0,043	-1,38	0,38	38,41	P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA
0,005	-1,38	0,38	38,46	P54136	Arginine--tRNA ligase, cytoplasmic	RARS
0,025	-1,38	0,39	38,51	P62166	Neuronal calcium sensor 1	NCS1
0,021	-1,37	0,39	38,65	Q9P0L0	Vesicle-associated membrane protein-associated protein A	VAPA
0,043	-1,37	0,39	38,67	Q6ZNW5	GDP-D-glucose phosphorylase C15orf58	C15orf58
0,015	-1,37	0,39	38,69	Q15056	Eukaryotic translation initiation factor 4H	EIF4H
0,017	-1,37	0,39	38,77	Q13084	39S ribosomal protein L28, mitochondrial	MRPL28
0,041	-1,37	0,39	38,81	Q9UJ41	Rab5 GDP/GTP exchange factor	RABGEF1
0,002	-1,36	0,39	38,83	Q9ULF5	Zinc transporter ZIP10	SLC39A10
0,012	-1,35	0,39	39,10	P55884	Eukaryotic translation initiation factor 3 subunit B	EIF3B
0,003	-1,35	0,39	39,12	P18077	60S ribosomal protein L35a	RPL35A
0,036	-1,35	0,39	39,23	Q3MHD2	Protein LSM12 homolog	LSM12
0,025	-1,35	0,39	39,28	Q9UHV7	Mediator of RNA polymerase II transcription subunit 13	MED13
0,030	-1,35	0,39	39,29	Q8WTW3	Conserved oligomeric Golgi complex subunit 1	COG1
0,001	-1,35	0,39	39,30	Q8WX92	Negative elongation factor B	COBRA1
0,014	-1,35	0,39	39,33	Q8WVX9	Fatty acyl-CoA reductase 1	FAR1
0,014	-1,34	0,39	39,42	Q96EE3	Nucleoporin SEH1	SEH1L
0,004	-1,34	0,40	39,59	O60502	Bifunctional protein NCOAT;Protein O-GlcNAcase;Histone acetyltransferase	MGEA5
0,006	-1,33	0,40	39,64	O14618	Copper chaperone for superoxide dismutase	CCS

Supplemental Table S2a

0,039	-1,33	0,40	39,81	Q9Y3E2	BolA-like protein 1	BOLA1
0,016	-1,33	0,40	39,85	P07947	Tyrosine-protein kinase Yes	YES1
0,023	-1,33	0,40	39,88	P00387	NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-bo	CYB5R3
0,045	-1,33	0,40	39,91	Q6ZMI0	Protein phosphatase 1 regulatory subunit 21	PPP1R21
0,030	-1,32	0,40	39,92	O14802	DNA-directed RNA polymerase III subunit RPC1	POLR3A
0,002	-1,32	0,40	39,92	P25398	40S ribosomal protein S12	RPS12
0,034	-1,32	0,40	39,97	Q9UPN4	5-azacytidine-induced protein 1	AZI1
0,045	-1,32	0,40	40,09	Q8IZL8	Proline-, glutamic acid- and leucine-rich protein 1	PELP1
0,038	-1,32	0,40	40,16	P49459	Ubiquitin-conjugating enzyme E2 A	UBE2A
0,000	-1,32	0,40	40,17	Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH
0,047	-1,32	0,40	40,18	Q712K3	Ubiquitin-conjugating enzyme E2 R2	UBE2R2
0,002	-1,31	0,40	40,24	Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1	SLC25A24
0,024	-1,31	0,40	40,43	Q9BYN8	28S ribosomal protein S26, mitochondrial	MRPS26
0,030	-1,31	0,40	40,46	P18074	TFIIH basal transcription factor complex helicase XPD subunit	ERCC2
0,021	-1,31	0,40	40,47	Q86TB9	Protein PAT1 homolog 1	PATL1
0,006	-1,30	0,40	40,49	Q01780	Exosome component 10	EXOSC10
0,011	-1,30	0,41	40,51	Q9BVG4	UPF0368 protein Cxorf26	CXorf26
0,004	-1,30	0,41	40,62	P78344	Eukaryotic translation initiation factor 4 gamma 2	EIF4G2
0,001	-1,29	0,41	40,83	Q99729	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
0,000	-1,29	0,41	40,99	P22695	Cytochrome b-c1 complex subunit 2, mitochondrial	UQCRC2
0,018	-1,29	0,41	41,02	Q9Y4B6	Protein VPRBP	VPRBP
0,035	-1,28	0,41	41,08	Q6P158	Putative ATP-dependent RNA helicase DHX57	DHX57
0,034	-1,28	0,41	41,14	Q9BVL2	Nucleoporin p58/p45	NUPL1
0,002	-1,28	0,41	41,23	Q14847	LIM and SH3 domain protein 1	LASP1
0,030	-1,27	0,41	41,43	Q6UWZ7	BRCA1-A complex subunit Abraxas	FAM175A
0,045	-1,27	0,41	41,48	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	FKBP1A
0,001	-1,27	0,42	41,53	P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8
0,049	-1,27	0,42	41,55	Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1
0,041	-1,27	0,42	41,58	P36873	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	PPP1CC
0,015	-1,25	0,42	42,01	Q99653	Calcium-binding protein p22	CHP
0,022	-1,25	0,42	42,15	O94973	AP-2 complex subunit alpha-2	AP2A2
0,000	-1,24	0,42	42,26	P40429;Q6NVV1	60S ribosomal protein L13a;Putative 60S ribosomal protein L13a-like MGC87657	RPL13A
0,033	-1,24	0,42	42,30	Q2TB90	Putative hexokinase HKDC1	HKDC1

Supplemental Table S2a

0,035	-1,24	0,42	42,40	O95453	Poly(A)-specific ribonuclease PARN	PARN
0,029	-1,23	0,43	42,53	Q9H267	Vacuolar protein sorting-associated protein 33B	VPS33B
0,019	-1,23	0,43	42,57	Q8NFH3	Nucleoporin Nup43	NUP43
0,035	-1,23	0,43	42,64	O15372	Eukaryotic translation initiation factor 3 subunit H	EIF3H
0,014	-1,22	0,43	42,88	Q9NRG0	Chromatin accessibility complex protein 1	CHRA1
0,030	-1,22	0,43	42,91	Q8NE86	Calcium uniporter protein, mitochondrial	MCU
0,035	-1,22	0,43	43,04	O60825;Q16875;P16118	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2;6-phosphofructo-2-kinase	PFKFB2
0,022	-1,21	0,43	43,12	Q9BT30	Probable alpha-ketoglutarate-dependent dioxygenase ABH7	ALKBH7
0,043	-1,21	0,43	43,17	O43824	Putative GTP-binding protein 6	GTPBP6
0,013	-1,21	0,43	43,24	Q9HD26	Golgi-associated PDZ and coiled-coil motif-containing protein	GOPC
0,026	-1,21	0,43	43,25	Q7Z4Q2	HEAT repeat-containing protein 3	HEATR3
0,030	-1,21	0,43	43,27	Q96HQ2	CDKN2AIP N-terminal-like protein	CDKN2AIPNL
0,001	-1,21	0,43	43,29	P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	COX4I1
0,001	-1,20	0,43	43,46	Q8NBJ5	Procollagen galactosyltransferase 1	GLT25D1
0,018	-1,19	0,44	43,77	Q16539	Mitogen-activated protein kinase 14	MAPK14
0,006	-1,19	0,44	43,81	P28288	ATP-binding cassette sub-family D member 3	ABCD3
0,022	-1,19	0,44	43,85	Q9Y678	Coatamer subunit gamma-1	COPG1
0,002	-1,19	0,44	43,93	Q92974	Rho guanine nucleotide exchange factor 2	ARHGEF2
0,035	-1,18	0,44	43,98	Q92797	Symplekin	SYMPK
0,009	-1,18	0,44	44,25	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1
0,038	-1,18	0,44	44,25	Q8IVM0	Coiled-coil domain-containing protein 50	CCDC50
0,001	-1,17	0,44	44,41	Q8TDN6	Ribosome biogenesis protein BRX1 homolog	BRX1
0,021	-1,16	0,45	44,61	Q00610;P53675	Clathrin heavy chain 1	CLTC
0,015	-1,16	0,45	44,67	O75175	CCR4-NOT transcription complex subunit 3	CNOT3
0,014	-1,16	0,45	44,69	Q56VL3	OCIA domain-containing protein 2	OCIAD2
0,014	-1,15	0,45	44,91	Q7L9L4	MOB kinase activator 1B	MOB1B
0,032	-1,15	0,45	44,92	Q9Y3D0	Mitotic spindle-associated MMXD complex subunit MIP18	FAM96B
0,000	-1,15	0,45	44,99	P11717	Cation-independent mannose-6-phosphate receptor	IGF2R
0,025	-1,15	0,45	45,04	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B
0,042	-1,15	0,45	45,16	Q9UGN5	Poly [ADP-ribose] polymerase 2	PARP2
0,016	-1,15	0,45	45,16	Q8N766	Uncharacterized protein KIAA0090	KIAA0090
0,048	-1,15	0,45	45,18	P45877	Peptidyl-prolyl cis-trans isomerase C	PPIC
0,021	-1,14	0,45	45,24	Q99728	BRCA1-associated RING domain protein 1	BARD1

Supplemental Table S2a

0,000	-1,14	0,45	45,26	Q5JTW2	Centrosomal protein of 78 kDa	CEP78
0,018	-1,14	0,45	45,27	Q9Y6E0	Serine/threonine-protein kinase 24;Serine/threonine-protein kinase 24 36 kDa subu	STK24
0,001	-1,14	0,45	45,31	Q9UMX5	Neudesin	NENF
0,018	-1,14	0,45	45,31	O00178	GTP-binding protein 1	GTPBP1
0,000	-1,14	0,46	45,52	Q9H0H5	Rac GTPase-activating protein 1	RACGAP1
0,002	-1,13	0,46	45,60	P20618	Proteasome subunit beta type-1	PSMB1
0,005	-1,13	0,46	45,65	Q96J01	THO complex subunit 3	THOC3
0,000	-1,13	0,46	45,65	Q12882	Dihydropyrimidine dehydrogenase [NADP(+)]	DPYD
0,031	-1,13	0,46	45,72	Q9H8V3	Protein ECT2	ECT2
0,049	-1,13	0,46	45,78	Q8NBN7	Retinol dehydrogenase 13	RDH13
0,001	-1,13	0,46	45,84	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	UQCRC1
0,027	-1,12	0,46	45,95	Q12789	General transcription factor 3C polypeptide 1	GTF3C1
0,025	-1,11	0,46	46,38	P63000;P15153;P60763	Ras-related C3 botulinum toxin substrate 1;Ras-related C3 botulinum toxin substrat	RAC1;RAC2;RAC3
0,001	-1,11	0,46	46,40	Q96II8	Leucine-rich repeat and calponin homology domain-containing protein 3	LRCH3
0,005	-1,10	0,47	46,60	P12814;Q08043	Alpha-actinin-1	ACTN1
0,047	-1,10	0,47	46,65	P28065	Proteasome subunit beta type-9	PSMB9
0,006	-1,10	0,47	46,70	P26640	Valine--tRNA ligase	VARS
0,039	-1,10	0,47	46,71	Q99584	Protein S100-A13	S100A13
0,026	-1,10	0,47	46,80	O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F
0,001	-1,09	0,47	46,89	Q08378	Golgin subfamily A member 3	GOLGA3
0,001	-1,09	0,47	46,93	B5ME19;Q99613	Eukaryotic translation initiation factor 3 subunit C	EIF3CL;EIF3C
0,005	-1,08	0,47	47,18	O00487	26S proteasome non-ATPase regulatory subunit 14	PSMD14
0,012	-1,08	0,47	47,26	Q9BTT6	Leucine-rich repeat-containing protein 1	LRRC1
0,007	-1,08	0,47	47,34	P35613	Basigin	BSG
0,036	-1,08	0,47	47,37	P09651;Q32P51	Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleopro	HNRNPA1;HNRNPA
0,001	-1,08	0,47	47,38	P07437	Tubulin beta chain	TUBB
0,019	-1,08	0,47	47,43	P68104;Q5VTE0	Elongation factor 1-alpha 1;Putative elongation factor 1-alpha-like 3	EEF1A1;EEF1A1P5
0,000	-1,07	0,48	47,51	Q6PIU2	Neutral cholesterol ester hydrolase 1	NCEH1
0,042	-1,06	0,48	47,85	Q8WWH5	Probable tRNA pseudouridine synthase 1	TRUB1
0,017	-1,06	0,48	47,92	Q9BSH4	Translational activator of cytochrome c oxidase 1	TACO1
0,018	-1,06	0,48	47,97	Q9UBP6	tRNA (guanine-N(7)-)-methyltransferase	METTLL1
0,008	-1,06	0,48	47,98	Q9Y333	U6 snRNA-associated Sm-like protein LSm2	LSM2
0,014	-1,06	0,48	48,10	P00441	Superoxide dismutase [Cu-Zn]	SOD1

Supplemental Table S2a

0,028	-1,06	0,48	48,13	P55010	Eukaryotic translation initiation factor 5	EIF5
0,014	-1,05	0,48	48,14	O96008	Mitochondrial import receptor subunit TOM40 homolog	TOMM40
0,038	-1,05	0,48	48,20	P78346	Ribonuclease P protein subunit p30	RPP30
0,048	-1,05	0,48	48,35	Q9BRR8	G patch domain-containing protein 1	GPATCH1
0,029	-1,05	0,48	48,39	Q96IZ7	Serine/Arginine-related protein 53	RSRC1
0,007	-1,05	0,48	48,41	Q9BRJ7	Protein syndesmos	NUDT16L1
0,002	-1,04	0,49	48,51	P83731	60S ribosomal protein L24	RPL24
0,009	-1,04	0,49	48,65	O14907	Tax1-binding protein 3	TAX1BP3
0,035	-1,04	0,49	48,76	Q8WVM8	Sec1 family domain-containing protein 1	SCFD1
0,014	-1,03	0,49	48,83	Q10469	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase	MGAT2
0,009	-1,03	0,49	48,92	Q96CS3	FAS-associated factor 2	FAF2
0,044	-1,03	0,49	48,94	O15020	Spectrin beta chain, brain 2	SPTBN2
0,011	-1,02	0,49	49,22	Q8WXX5	DnaJ homolog subfamily C member 9	DNAJC9
0,040	-1,02	0,49	49,30	Q9UJW0	Dynactin subunit 4	DCTN4
0,020	-1,02	0,49	49,34	Q8WYQ5	Microprocessor complex subunit DGCR8	DGCR8
0,001	-1,02	0,49	49,35	O76003	Glutaredoxin-3	GLRX3
0,015	-1,02	0,49	49,38	Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	TIMM9
0,023	-1,02	0,49	49,42	Q09161	Nuclear cap-binding protein subunit 1	NCBP1
0,010	-1,02	0,49	49,45	Q9ULC3	Ras-related protein Rab-23	RAB23
0,001	-1,02	0,49	49,46	O95881	Thioredoxin domain-containing protein 12	TXNDC12
0,015	-1,01	0,50	49,52	Q7L5Y9	Macrophage erythroblast attacher	MAEA
0,012	-1,01	0,50	49,63	Q96CN7	Isochorismatase domain-containing protein 1	ISOC1
0,021	-1,01	0,50	49,80	Q01968	Inositol polyphosphate 5-phosphatase OCRL-1	OCRL
0,009	-1,00	0,50	49,93	P57740	Nuclear pore complex protein Nup107	NUP107
0,001	-1,00	0,50	49,96	P49755	Transmembrane emp24 domain-containing protein 10	TMED10
0,020	-1,00	0,50	50,05	P26373	60S ribosomal protein L13	RPL13
0,009	-1,00	0,50	50,09	Q13496	Myotubularin	MTM1
0,005	-1,00	0,50	50,11	Q15813	Tubulin-specific chaperone E	TBCE
0,022	-1,00	0,50	50,15	Q92900	Regulator of nonsense transcripts 1	UPF1
0,041	-0,99	0,50	50,21	Q96G01	Protein bicaudal D homolog 1	BICD1
0,017	-0,99	0,50	50,24	P50452	Serpin B8	SERPINB8
0,005	-0,99	0,50	50,45	Q5TA45	Integrator complex subunit 11	CPSF3L
0,002	-0,99	0,50	50,47	Q9Y4W6;Q01484	AFG3-like protein 2	AFG3L2

Supplemental Table S2a

0,024	-0,99	0,50	50,49	Q6ZNB6	NF-X1-type zinc finger protein NFXL1	NFXL1
0,007	-0,99	0,51	50,51	Q9UNN5	FAS-associated factor 1	FAF1
0,015	-0,98	0,51	50,58	Q6IA69	Glutamine-dependent NAD(+) synthetase	NADSYN1
0,032	-0,98	0,51	50,66	Q96SB4;Q9UPE1	SRSF protein kinase 1	SRPK1
0,032	-0,98	0,51	50,68	Q71SY5	Mediator of RNA polymerase II transcription subunit 25	MED25
0,002	-0,98	0,51	50,71	Q9BRT3	Migration and invasion enhancer 1	MIEN1
0,014	-0,98	0,51	50,76	O95248	Myotubularin-related protein 5	SBF1
0,013	-0,98	0,51	50,77	P52948	Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;N	NUP98
0,011	-0,98	0,51	50,79	Q9NRF9	DNA polymerase epsilon subunit 3	POLE3
0,005	-0,98	0,51	50,84	P08865	40S ribosomal protein SA	RPSA
0,002	-0,97	0,51	50,88	P49790	Nuclear pore complex protein Nup153	NUP153
0,023	-0,97	0,51	50,89	Q7L2J0	7SK snRNA methylphosphate capping enzyme	MEPCE
0,000	-0,97	0,51	51,06	P62241	40S ribosomal protein S8	RPS8
0,035	-0,97	0,51	51,18	Q6IN84	rRNA methyltransferase 1, mitochondrial	MRM1
0,000	-0,97	0,51	51,19	Q02543	60S ribosomal protein L18a	RPL18A
0,023	-0,96	0,51	51,30	Q15003	Condensin complex subunit 2	NCAPH
0,029	-0,96	0,51	51,37	Q5C9Z4	Nucleolar MIF4G domain-containing protein 1	NOM1
0,001	-0,96	0,51	51,39	Q9H9T3	Elongator complex protein 3	ELP3
0,000	-0,96	0,51	51,40	P22830	Ferrochelatase, mitochondrial	FECH
0,000	-0,96	0,51	51,41	P62280	40S ribosomal protein S11	RPS11
0,037	-0,96	0,51	51,42	P30419;O60551	Glycylpeptide N-tetradecanoyltransferase 1	NMT1
0,000	-0,95	0,52	51,59	Q92793	CREB-binding protein	CREBBP
0,002	-0,95	0,52	51,70	Q13310;P0CB38	Polyadenylate-binding protein 4	PABPC4
0,001	-0,95	0,52	51,80	P61457	Pterin-4-alpha-carbinolamine dehydratase	PCBD1
0,017	-0,94	0,52	52,07	O43813	LanC-like protein 1	LANCL1
0,046	-0,94	0,52	52,10	Q9UDT6	CAP-Gly domain-containing linker protein 2	CLIP2
0,000	-0,94	0,52	52,22	Q8N1F7	Nuclear pore complex protein Nup93	NUP93
0,042	-0,94	0,52	52,22	P11388	DNA topoisomerase 2-alpha	TOP2A
0,021	-0,94	0,52	52,28	Q15154	Pericentriolar material 1 protein	PCM1
0,006	-0,93	0,52	52,34	Q92615	La-related protein 4B	LARP4B
0,029	-0,93	0,52	52,38	Q13268	Dehydrogenase/reductase SDR family member 2	DHRS2
0,020	-0,93	0,52	52,41	P63261	Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed	ACTG1
0,000	-0,93	0,52	52,43	Q9NZB2;Q5T035	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A

Supplemental Table S2a

0,010	-0,93	0,53	52,54	Q7Z4H3	HD domain-containing protein 2	HDDC2
0,011	-0,93	0,53	52,58	Q9BXR0	Queuine tRNA-ribosyltransferase	QTRT1
0,017	-0,93	0,53	52,62	P05141	ADP/ATP translocase 2	SLC25A5
0,015	-0,92	0,53	52,73	O14787	Transportin-2	TNPO2
0,019	-0,92	0,53	52,76	Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L
0,028	-0,92	0,53	52,78	Q9NRF8	CTP synthase 2	CTPS2
0,000	-0,92	0,53	52,84	O43353	Receptor-interacting serine/threonine-protein kinase 2	RIPK2
0,021	-0,92	0,53	52,87	Q9NV96;Q3MIR4	Cell cycle control protein 50A;Cell cycle control protein 50B	TMEM30A;TMEM3
0,026	-0,92	0,53	52,95	Q13188	Serine/threonine-protein kinase 3;Serine/threonine-protein kinase 3 36kDa subunit	STK3
0,026	-0,92	0,53	52,98	Q14152	Eukaryotic translation initiation factor 3 subunit A	EIF3A
0,002	-0,91	0,53	53,10	P46821	Microtubule-associated protein 1B;MAP1 light chain LC1	MAP1B
0,027	-0,91	0,53	53,13	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4
0,037	-0,91	0,53	53,36	Q53H12	Acylglycerol kinase, mitochondrial	AGK
0,024	-0,90	0,53	53,47	P51452	Dual specificity protein phosphatase 3	DUSP3
0,002	-0,90	0,54	53,63	Q7Z4W1	L-xylulose reductase	DCXR
0,001	-0,90	0,54	53,77	P62829	60S ribosomal protein L23	RPL23
0,000	-0,89	0,54	53,80	Q92896	Golgi apparatus protein 1	GLG1
0,000	-0,89	0,54	53,83	P17812	CTP synthase 1	CTPS
0,003	-0,89	0,54	53,90	Q99661	Kinesin-like protein KIF2C	KIF2C
0,002	-0,89	0,54	53,93	Q13751	Laminin subunit beta-3	LAMB3
0,002	-0,89	0,54	54,14	Q9Y4P3	Transducin beta-like protein 2	TBL2
0,041	-0,88	0,54	54,17	P56962	Syntaxin-17	STX17
0,018	-0,88	0,54	54,33	Q15645	Pachytene checkpoint protein 2 homolog	TRIP13
0,003	-0,88	0,54	54,48	P17980	26S protease regulatory subunit 6A	PSMC3
0,001	-0,88	0,55	54,50	P49736	DNA replication licensing factor MCM2	MCM2
0,005	-0,88	0,55	54,50	Q13895	Bystin	BYSL
0,039	-0,87	0,55	54,55	P17858	6-phosphofructokinase, liver type	PFKL
0,000	-0,87	0,55	54,64	Q8IYA6	Cytoskeleton-associated protein 2-like	CKAP2L
0,030	-0,87	0,55	54,70	O95479	GDH/6PGL endoplasmic bifunctional protein;Glucose 1-dehydrogenase;6-phosphogl	H6PD
0,012	-0,87	0,55	54,73	Q14669	Probable E3 ubiquitin-protein ligase TRIP12	TRIP12
0,011	-0,87	0,55	54,74	P31946	14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed	YWHAB
0,008	-0,87	0,55	54,88	Q99439	Calponin-2	CNN2
0,014	-0,86	0,55	54,97	P43155	Carnitine O-acetyltransferase	CRAT

Supplemental Table S2a

0,041	-0,86	0,55	54,98	Q16740	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	CLPP
0,030	-0,86	0,55	54,99	Q5TDH0	Protein DDI1 homolog 2	DDI2
0,023	-0,86	0,55	55,02	Q9H9A6	Leucine-rich repeat-containing protein 40	LRRC40
0,000	-0,86	0,55	55,07	P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC
0,050	-0,86	0,55	55,11	Q9NWU2	Protein C20orf11	C20orf11
0,047	-0,86	0,55	55,13	Q9NZC9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily 1	SMARCAL1
0,029	-0,86	0,55	55,14	Q6IBS0	Twinfilin-2	TWF2
0,020	-0,86	0,55	55,14	Q9H3P7	Golgi resident protein GCP60	ACBD3
0,006	-0,86	0,55	55,24	P23919	Thymidylate kinase	DTYMK
0,042	-0,86	0,55	55,26	Q7Z392	Trafficking protein particle complex subunit 11	TRAPPC11
0,017	-0,85	0,55	55,35	Q9UMY4	Sorting nexin-12	SNX12
0,035	-0,85	0,56	55,54	P56385	ATP synthase subunit e, mitochondrial	ATP5I
0,002	-0,85	0,56	55,56	P24534	Elongation factor 1-beta	EEF1B2
0,000	-0,85	0,56	55,65	O95834	Echinoderm microtubule-associated protein-like 2	EML2
0,020	-0,84	0,56	55,74	Q8WWM7	Ataxin-2-like protein	ATXN2L
0,001	-0,84	0,56	55,76	P08243	Asparagine synthetase [glutamine-hydrolyzing]	ASNS
0,002	-0,84	0,56	55,94	P54886	Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate transferase	ALDH18A1
0,016	-0,84	0,56	55,99	Q9GZN8	UPF0687 protein C20orf27	C20orf27
0,007	-0,84	0,56	56,00	Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1	ANKHD1
0,002	-0,84	0,56	56,01	O43716	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	GATC
0,009	-0,83	0,56	56,09	P23396	40S ribosomal protein S3	RPS3
0,033	-0,83	0,56	56,13	O75717	WD repeat and HMG-box DNA-binding protein 1	WDHD1
0,005	-0,83	0,56	56,15	Q7Z2W4	Zinc finger CCCH-type antiviral protein 1	ZC3HAV1
0,016	-0,83	0,56	56,21	P84098	60S ribosomal protein L19	RPL19
0,006	-0,83	0,56	56,25	Q05397;Q14289	Focal adhesion kinase 1	PTK2
0,037	-0,83	0,56	56,28	Q9P1U0	DNA-directed RNA polymerase I subunit RPA12	ZNRD1
0,032	-0,83	0,56	56,30	Q13308	Inactive tyrosine-protein kinase 7	PTK7
0,015	-0,83	0,56	56,33	O43707	Alpha-actinin-4	ACTN4
0,024	-0,83	0,56	56,35	O75879	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	PET112
0,000	-0,83	0,56	56,42	P30519	Heme oxygenase 2	HMOX2
0,014	-0,83	0,56	56,42	P28676	Grancalcin	GCA
0,019	-0,82	0,57	56,61	O94906	Pre-mRNA-processing factor 6	PRPF6
0,034	-0,82	0,57	56,62	Q96S44	TP53-regulating kinase	TP53RK

Supplemental Table S2a

0,022	-0,82	0,57	56,65	P04150	Glucocorticoid receptor	NR3C1
0,021	-0,82	0,57	56,69	A6NFE2	Uncharacterized protein C12orf70	C12orf70
0,021	-0,82	0,57	56,72	P23258;Q9NRH3	Tubulin gamma-1 chain;Tubulin gamma-2 chain	TUBG1;TUBG2
0,016	-0,82	0,57	56,75	O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7
0,003	-0,82	0,57	56,77	Q9NR28	Diablo homolog, mitochondrial	DIABLO
0,039	-0,82	0,57	56,78	O60678	Protein arginine N-methyltransferase 3	PRMT3
0,040	-0,82	0,57	56,80	Q14318	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8
0,044	-0,82	0,57	56,81	P48163	NADP-dependent malic enzyme	ME1
0,048	-0,81	0,57	56,85	Q9NWU5	39S ribosomal protein L22, mitochondrial	MRPL22
0,008	-0,81	0,57	56,85	O00499	Myc box-dependent-interacting protein 1	BIN1
0,001	-0,81	0,57	56,98	O95571	Protein ETHE1, mitochondrial	ETHE1
0,021	-0,81	0,57	57,08	Q9NVS2	28S ribosomal protein S18a, mitochondrial	MRPS18A
0,007	-0,81	0,57	57,23	O95817	BAG family molecular chaperone regulator 3	BAG3
0,025	-0,80	0,57	57,28	P43487	Ran-specific GTPase-activating protein	RANBP1
0,022	-0,80	0,58	57,61	Q96MW1	Coiled-coil domain-containing protein 43	CCDC43
0,017	-0,80	0,58	57,63	P67936	Tropomyosin alpha-4 chain	TPM4
0,014	-0,79	0,58	57,72	P04792	Heat shock protein beta-1	HSPB1
0,003	-0,79	0,58	57,86	P12004	Proliferating cell nuclear antigen	PCNA
0,026	-0,79	0,58	57,90	O14737	Programmed cell death protein 5	PDCD5
0,025	-0,79	0,58	57,91	Q96FW1	Ubiquitin thioesterase OTUB1	OTUB1
0,018	-0,79	0,58	57,95	Q6IN85	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1
0,046	-0,79	0,58	58,00	P09038	Fibroblast growth factor 2	FGF2
0,009	-0,79	0,58	58,02	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	GNB2L1
0,006	-0,79	0,58	58,03	P61011	Signal recognition particle 54 kDa protein	SRP54
0,038	-0,78	0,58	58,05	P08238;Q58FF7	Heat shock protein HSP 90-beta;Putative heat shock protein HSP 90-beta-3	HSP90AB1;HSP90A
0,031	-0,78	0,58	58,14	Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I
0,031	-0,78	0,58	58,31	Q9HAV4	Exportin-5	XPO5
0,050	-0,78	0,58	58,36	O15371	Eukaryotic translation initiation factor 3 subunit D	EIF3D
0,016	-0,78	0,58	58,40	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	ETFDH
0,014	-0,78	0,58	58,43	P19623	Spermidine synthase	SRM
0,001	-0,77	0,58	58,49	O60664	Perilipin-3	PLIN3
0,036	-0,77	0,59	58,52	P50502;Q8NFI4;Q8IZP2	Hsc70-interacting protein;Putative protein FAM10A5;Putative protein FAM10A4	ST13;ST13P5;ST13
0,049	-0,77	0,59	58,60	Q6KC79	Nipped-B-like protein	NIPBL

Supplemental Table S2a

0,003	-0,77	0,59	58,79	Q9H5N1	Rab GTPase-binding effector protein 2	RABEP2
0,001	-0,76	0,59	58,92	P60842	Eukaryotic initiation factor 4A-I	EIF4A1
0,019	-0,76	0,59	59,07	Q9NTX5	Ethylmalonyl-CoA decarboxylase	ECHDC1
0,016	-0,76	0,59	59,12	Q02127	Dihydroorotate dehydrogenase (quinone), mitochondrial	DHODH
0,007	-0,76	0,59	59,19	P00374;Q86XF0	Dihydrofolate reductase	DHFR
0,018	-0,75	0,59	59,29	Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1
0,003	-0,75	0,59	59,34	O43175	D-3-phosphoglycerate dehydrogenase	PHGDH
0,013	-0,75	0,59	59,35	Q14331;Q9BZ01	Protein FRG1;Protein FRG1B	FRG1;FRG1B
0,019	-0,75	0,59	59,44	O94874	E3 UFM1-protein ligase 1	UFL1
0,000	-0,75	0,60	59,60	Q99798	Aconitate hydratase, mitochondrial	ACO2
0,002	-0,75	0,60	59,61	Q96EY1	DnaJ homolog subfamily A member 3, mitochondrial	DNAJA3
0,025	-0,75	0,60	59,63	P61081	NEDD8-conjugating enzyme Ubc12	UBE2M
0,013	-0,74	0,60	59,78	Q8WW59	SPRY domain-containing protein 4	SPRYD4
0,000	-0,74	0,60	59,87	Q07065	Cytoskeleton-associated protein 4	CKAP4
0,039	-0,74	0,60	59,99	O43237	Cytoplasmic dynein 1 light intermediate chain 2	DYNC1LI2
0,009	-0,74	0,60	59,99	Q8N9N7	Leucine-rich repeat-containing protein 57	LRRC57
0,003	-0,74	0,60	60,02	Q14258	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25
0,001	-0,74	0,60	60,05	Q9NYU2;Q9NYU1	UDP-glucose:glycoprotein glucosyltransferase 1	UGGT1
0,024	-0,73	0,60	60,12	Q86X55	Histone-arginine methyltransferase CARM1	CARM1
0,003	-0,73	0,60	60,13	O95347	Structural maintenance of chromosomes protein 2	SMC2
0,000	-0,73	0,60	60,21	Q6L8Q7	2,5-phosphodiesterase 12	PDE12
0,044	-0,73	0,60	60,25	Q9BY43	Charged multivesicular body protein 4a	CHMP4A
0,048	-0,73	0,60	60,25	Q9NPA0	UPF0480 protein C15orf24	C15orf24
0,013	-0,73	0,60	60,28	O60925	Prefoldin subunit 1	PFDN1
0,003	-0,73	0,60	60,29	Q8TAE6	Protein phosphatase 1 regulatory subunit 14C	PPP1R14C
0,003	-0,73	0,60	60,33	P51553	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial	IDH3G
0,047	-0,73	0,60	60,38	Q5VW32	BRO1 domain-containing protein BROX	BROX
0,006	-0,73	0,60	60,48	P11142	Heat shock cognate 71 kDa protein	HSPA8
0,001	-0,72	0,61	60,53	Q96S99	Pleckstrin homology domain-containing family F member 1	PLEKHF1
0,026	-0,72	0,61	60,69	P63104	14-3-3 protein zeta/delta	YWHAZ
0,050	-0,72	0,61	60,74	Q8TE77	Protein phosphatase Slingshot homolog 3	SSH3
0,036	-0,72	0,61	60,84	Q96AG4	Leucine-rich repeat-containing protein 59	LRRC59
0,019	-0,71	0,61	60,92	P07741	Adenine phosphoribosyltransferase	APRT

Supplemental Table S2a

0,005	-0,71	0,61	60,95	P46926	Glucosamine-6-phosphate isomerase 1	GNPDA1
0,004	-0,71	0,61	61,02	Q71RC2	La-related protein 4	LARP4
0,005	-0,71	0,61	61,06	Q8IYI6	Exocyst complex component 8	EXOC8
0,034	-0,71	0,61	61,12	P46783;Q9NQ39	40S ribosomal protein S10	RPS10
0,024	-0,71	0,61	61,17	P30044	Peroxisome oxidoreductase 5, mitochondrial	PRDX5
0,011	-0,71	0,61	61,22	Q2NL82	Pre-rRNA-processing protein TSR1 homolog	TSR1
0,035	-0,70	0,61	61,43	Q96A33	Coiled-coil domain-containing protein 47	CCDC47
0,003	-0,70	0,61	61,47	Q04637	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1
0,003	-0,70	0,62	61,69	O43815	Striatin	STRN
0,026	-0,69	0,62	61,78	Q16881	Thioredoxin reductase 1, cytoplasmic	TXNRD1
0,003	-0,69	0,62	61,79	Q9NR45	Sialic acid synthase	NANS
0,023	-0,69	0,62	61,82	P62277	40S ribosomal protein S13	RPS13
0,001	-0,69	0,62	61,85	Q9BTW9	Tubulin-specific chaperone D	TBCD
0,005	-0,69	0,62	61,85	Q9NQT8	Kinesin-like protein KIF13B	KIF13B
0,031	-0,69	0,62	61,86	O95071	E3 ubiquitin-protein ligase UBR5	UBR5
0,019	-0,69	0,62	61,93	P19838	Nuclear factor NF-kappa-B p105 subunit;Nuclear factor NF-kappa-B p50 subunit	NFKB1
0,008	-0,69	0,62	61,94	Q8TBX8	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	PIP4K2C
0,045	-0,69	0,62	62,00	Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B	PDS5B
0,048	-0,69	0,62	62,06	P26196	Probable ATP-dependent RNA helicase DDX6	DDX6
0,026	-0,69	0,62	62,15	P55735	Protein SEC13 homolog	SEC13
0,029	-0,68	0,62	62,25	P50416	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A
0,045	-0,68	0,62	62,31	Q9NZN8	CCR4-NOT transcription complex subunit 2	CNOT2
0,040	-0,68	0,62	62,32	Q9Y2R0	Coiled-coil domain-containing protein 56	CCDC56
0,006	-0,68	0,62	62,35	Q9BUH6	Uncharacterized protein C9orf142	C9orf142
0,000	-0,68	0,62	62,40	Q8NBS9	Thioredoxin domain-containing protein 5	TXNDC5
0,003	-0,68	0,62	62,49	O60524	Nuclear export mediator factor NEMF	NEMF
0,000	-0,68	0,63	62,51	P19174	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	PLCG1
0,001	-0,68	0,63	62,51	Q8IWB7	WD repeat and FYVE domain-containing protein 1	WDFY1
0,012	-0,68	0,63	62,55	Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB
0,001	-0,67	0,63	62,72	P46060	Ran GTPase-activating protein 1	RANGAP1
0,034	-0,67	0,63	62,78	Q96A35	39S ribosomal protein L24, mitochondrial	MRPL24
0,005	-0,67	0,63	62,87	P62263	40S ribosomal protein S14	RPS14
0,028	-0,67	0,63	62,87	Q13951	Core-binding factor subunit beta	CBFB

Supplemental Table S2a

0,001	-0,67	0,63	62,89	P46109	Crk-like protein	CRKL
0,023	-0,67	0,63	62,90	P25815	Protein S100-P	S100P
0,038	-0,67	0,63	63,01	Q8TEQ6	Gem-associated protein 5	GEMIN5
0,042	-0,66	0,63	63,09	Q9NTZ6	RNA-binding protein 12	RBM12
0,021	-0,66	0,63	63,21	Q9UUK9	ADP-sugar pyrophosphatase	NUDT5
0,007	-0,66	0,63	63,34	P52565	Rho GDP-dissociation inhibitor 1	ARHGDIA
0,013	-0,66	0,63	63,39	Q9Y496;Q9P2E2	Kinesin-like protein KIF3A	KIF3A
0,034	-0,66	0,63	63,45	A0FGR8	Extended synaptotagmin-2	ESYT2
0,038	-0,65	0,64	63,51	Q9P0M9	39S ribosomal protein L27, mitochondrial	MRPL27
0,009	-0,65	0,64	63,52	Q9NR19	Acetyl-coenzyme A synthetase, cytoplasmic	ACSS2
0,012	-0,65	0,64	63,64	Q04323	UBX domain-containing protein 1	UBXN1
0,000	-0,65	0,64	63,67	P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2
0,002	-0,65	0,64	63,77	Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1
0,002	-0,65	0,64	63,79	P12081	Histidine--tRNA ligase, cytoplasmic	HARS
0,041	-0,65	0,64	63,86	P60520	Gamma-aminobutyric acid receptor-associated protein-like 2	GABARAPL2
0,013	-0,65	0,64	63,88	P53004	Biliverdin reductase A	BLVRA
0,000	-0,64	0,64	63,95	P30050	60S ribosomal protein L12	RPL12
0,022	-0,64	0,64	63,96	Q6PI48	Aspartate--tRNA ligase, mitochondrial	DARS2
0,003	-0,64	0,64	64,13	Q13162	Peroxisredoxin-4	PRDX4
0,028	-0,64	0,64	64,28	Q9UIJ7	GTP:AMP phosphotransferase, mitochondrial	AK3
0,016	-0,63	0,64	64,42	Q16774	Guanylate kinase	GUK1
0,007	-0,63	0,64	64,44	Q8N6T3	ADP-ribosylation factor GTPase-activating protein 1	ARFGAP1
0,025	-0,63	0,64	64,46	Q96LD4	Tripartite motif-containing protein 47	TRIM47
0,020	-0,63	0,65	64,57	Q13564	NEDD8-activating enzyme E1 regulatory subunit	NAE1
0,018	-0,63	0,65	64,59	O43681	ATPase ASNA1	ASNA1
0,001	-0,63	0,65	64,64	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS
0,030	-0,63	0,65	64,70	Q8N0X7	Spartin	SPG20
0,044	-0,63	0,65	64,75	Q14116	Interleukin-18	IL18
0,004	-0,63	0,65	64,77	P30040	Endoplasmic reticulum resident protein 29	ERP29
0,013	-0,63	0,65	64,83	P12268	Inosine-5-monophosphate dehydrogenase 2	IMPDH2
0,007	-0,62	0,65	64,89	O60610	Protein diaphanous homolog 1	DIAPH1
0,005	-0,62	0,65	64,90	Q96FZ7	Charged multivesicular body protein 6	CHMP6
0,029	-0,62	0,65	64,92	Q9GZS1	DNA-directed RNA polymerase I subunit RPA49	POLR1E

Supplemental Table S2a

0,023	-0,62	0,65	65,20	Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10
0,000	-0,62	0,65	65,21	P52292	Importin subunit alpha-2	KPNA2
0,005	-0,62	0,65	65,25	Q8NHU6	Tudor domain-containing protein 7	TDRD7
0,018	-0,62	0,65	65,25	P55072	Transitional endoplasmic reticulum ATPase	VCP
0,004	-0,61	0,65	65,38	P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	GPD2
0,034	-0,61	0,66	65,51	Q9UHD2	Serine/threonine-protein kinase TBK1	TBK1
0,029	-0,61	0,66	65,53	P49591	Serine--tRNA ligase, cytoplasmic	SARS
0,009	-0,61	0,66	65,68	P01130	Low-density lipoprotein receptor	LDLR
0,025	-0,61	0,66	65,69	P28072	Proteasome subunit beta type-6	PSMB6
0,015	-0,61	0,66	65,71	Q7Z3T8	Zinc finger FYVE domain-containing protein 16	ZFYVE16
0,030	-0,60	0,66	65,78	Q7L5N1	COP9 signalosome complex subunit 6	COPS6
0,004	-0,60	0,66	65,81	O43252	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1;Sulfate adenylyltran	PAPSS1
0,033	-0,60	0,66	65,83	Q9GZP4	PITH domain-containing protein 1	PITHD1
0,018	-0,60	0,66	65,86	Q96G46	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	DUS3L
0,013	-0,60	0,66	65,87	O75390	Citrate synthase, mitochondrial	CS
0,025	-0,60	0,66	65,95	O95163	Elongator complex protein 1	IKBKAP
0,012	-0,60	0,66	65,96	Q9UHY7	Enolase-phosphatase E1	ENOPH1
0,006	-0,60	0,66	66,01	P61221	ATP-binding cassette sub-family E member 1	ABCE1
0,002	-0,60	0,66	66,04	O14950;P19105;P24844	Myosin regulatory light chain 12B;Myosin regulatory light chain 12A;Myosin regulat	MYL12B;MYL12A;M
0,002	-0,60	0,66	66,05	Q8IYB7	DIS3-like exonuclease 2	DIS3L2
0,027	-0,60	0,66	66,17	Q8WUX9	Charged multivesicular body protein 7	CHMP7
0,001	-0,59	0,66	66,21	Q9BUL8	Programmed cell death protein 10	PDCD10
0,040	-0,59	0,66	66,23	O95707	Ribonuclease P protein subunit p29	POP4
0,002	-0,59	0,66	66,24	Q86X76	Nitrilase homolog 1	NIT1
0,004	-0,59	0,66	66,25	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7
0,045	-0,59	0,66	66,26	O60443	Non-syndromic hearing impairment protein 5	DFNA5
0,000	-0,59	0,66	66,38	P29692	Elongation factor 1-delta	EEF1D
0,024	-0,59	0,66	66,42	Q9BYX2	TBC1 domain family member 2A	TBC1D2
0,036	-0,59	0,66	66,43	P15880	40S ribosomal protein S2	RPS2
0,012	-0,59	0,66	66,48	Q9UQ80	Proliferation-associated protein 2G4	PA2G4
0,046	-0,59	0,66	66,49	Q92973	Transportin-1	TNPO1
0,000	-0,59	0,67	66,53	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial	HAGH
0,001	-0,59	0,67	66,60	Q6P179	Endoplasmic reticulum aminopeptidase 2	ERAP2

Supplemental Table S2a

0,003	-0,59	0,67	66,63	O00629	Importin subunit alpha-4	KPNA4
0,015	-0,58	0,67	66,76	Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	MACF1
0,016	-0,58	0,67	66,76	Q9NQP4	Prefoldin subunit 4	PFDN4
0,000	-0,58	0,67	66,78	Q14195	Dihydropyrimidinase-related protein 3	DPYSL3
0,002	-0,58	0,67	66,79	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1
0,033	-0,58	0,67	66,80	P78318	Immunoglobulin-binding protein 1	IGBP1
0,002	-0,58	0,67	66,85	P11086	Phenylethanolamine N-methyltransferase	PNMT
0,013	-0,58	0,67	66,94	P50991	T-complex protein 1 subunit delta	CCT4
0,024	-0,58	0,67	66,95	P52943	Cysteine-rich protein 2	CRIP2
0,000	-0,58	0,67	66,97	Q9ULW0	Targeting protein for Xklp2	TPX2
0,020	-0,58	0,67	67,00	P78417	Glutathione S-transferase omega-1	GSTO1
0,015	-0,58	0,67	67,00	P62847	40S ribosomal protein S24	RPS24
0,000	-0,58	0,67	67,05	O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	IDH3B
0,000	-0,58	0,67	67,06	P17174	Aspartate aminotransferase, cytoplasmic	GOT1
0,024	-0,58	0,67	67,09	Q9H6E4	Coiled-coil domain-containing protein 134	CCDC134
0,045	-0,58	0,67	67,13	P59998	Actin-related protein 2/3 complex subunit 4	ARPC4
0,015	-0,57	0,67	67,17	Q9NSK0	Kinesin light chain 4	KLC4
0,002	-0,57	0,67	67,21	P82650	28S ribosomal protein S22, mitochondrial	MRPS22
0,006	-0,57	0,67	67,21	P06756	Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain	ITGAV
0,009	-0,57	0,67	67,28	P18206	Vinculin	VCL
0,000	-0,57	0,67	67,29	P49368	T-complex protein 1 subunit gamma	CCT3
0,000	-0,57	0,67	67,32	P54819	Adenylate kinase 2, mitochondrial	AK2
0,006	-0,57	0,67	67,35	Q12802	A-kinase anchor protein 13	AKAP13
0,032	-0,57	0,67	67,37	Q96A49	Synapse-associated protein 1	SYAP1
0,004	-0,57	0,67	67,39	P00492	Hypoxanthine-guanine phosphoribosyltransferase	HPRT1
0,004	-0,57	0,67	67,40	Q9NX02	NACHT, LRR and PYD domains-containing protein 2	NLRP2
0,006	-0,57	0,67	67,49	P49796	Regulator of G-protein signaling 3	RGS3
0,001	-0,57	0,68	67,56	Q9NP97;Q8TF09	Dynein light chain roadblock-type 1;Dynein light chain roadblock-type 2	DYNLRB1;DYNLRB2
0,019	-0,56	0,68	67,64	O15382	Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2
0,002	-0,56	0,68	67,66	Q9Y266	Nuclear migration protein nudC	NUDC
0,002	-0,56	0,68	67,66	P46781	40S ribosomal protein S9	RPS9
0,039	-0,56	0,68	67,72	Q96PQ0	VPS10 domain-containing receptor SorCS2	SORCS2
0,014	-0,56	0,68	67,73	Q9UBW8	COP9 signalosome complex subunit 7a	COPS7A

Supplemental Table S2a

0,006	-0,56	0,68	67,81	Q9NP81	Serine--tRNA ligase, mitochondrial	SARS2
0,022	-0,56	0,68	67,88	P39019	40S ribosomal protein S19	RPS19
0,009	-0,56	0,68	67,91	Q8TEX9	Importin-4	IPO4
0,014	-0,56	0,68	67,91	P10599	Thioredoxin	TXN
0,034	-0,56	0,68	67,94	O96033	Molybdopterin synthase sulfur carrier subunit	MOCS2
0,001	-0,56	0,68	67,98	Q15417	Calponin-3	CNN3
0,039	-0,56	0,68	68,01	P40261	Nicotinamide N-methyltransferase	NNMT
0,015	-0,56	0,68	68,04	P49454	Centromere protein F	CENPF
0,035	-0,55	0,68	68,26	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH
0,010	-0,55	0,68	68,29	P49753;Q86TX2	Acyl-coenzyme A thioesterase 2, mitochondrial;Acyl-coenzyme A thioesterase 1	ACOT2;ACOT1
0,016	-0,55	0,68	68,44	Q02218;Q9ULD0	2-oxoglutarate dehydrogenase, mitochondrial	OGDH
0,011	-0,55	0,68	68,44	Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S
0,015	-0,55	0,68	68,45	Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1LI1
0,014	-0,55	0,68	68,45	P42126	Enoyl-CoA delta isomerase 1, mitochondrial	ECI1
0,003	-0,55	0,69	68,51	Q9BZQ8	Protein Niban	FAM129A
0,005	-0,54	0,69	68,57	P16949;Q93045	Stathmin	STMN1
0,029	-0,54	0,69	68,60	O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	INPPL1
0,001	-0,54	0,69	68,65	Q9NR46	Endophilin-B2	SH3GLB2
0,010	-0,54	0,69	68,65	P42166	Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO
0,002	-0,54	0,69	68,66	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial	PCCA
0,028	-0,54	0,69	68,85	Q13642	Four and a half LIM domains protein 1	FHL1
0,032	-0,54	0,69	68,86	P61247	40S ribosomal protein S3a	RPS3A
0,023	-0,54	0,69	68,92	O60271;Q9UPT6	C-Jun-amino-terminal kinase-interacting protein 4	SPAG9
0,002	-0,54	0,69	68,94	Q16851	UTP--glucose-1-phosphate uridylyltransferase	UGP2
0,012	-0,54	0,69	69,01	Q12768	WASH complex subunit strumpellin	KIAA0196
0,028	-0,53	0,69	69,09	Q13425;Q13424	Beta-2-syntrophin	SNTB2
0,002	-0,53	0,69	69,09	Q16555;Q14194	Dihydropyrimidinase-related protein 2	DPYSL2
0,000	-0,53	0,69	69,15	P78371	T-complex protein 1 subunit beta	CCT2
0,014	-0,53	0,69	69,26	Q9BT78	COP9 signalosome complex subunit 4	COPS4
0,029	-0,53	0,69	69,28	Q07020	60S ribosomal protein L18	RPL18
0,003	-0,53	0,69	69,31	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2
0,003	-0,53	0,69	69,32	P62158	Calmodulin	CALM1
0,001	-0,53	0,69	69,40	P63241;Q6IS14	Eukaryotic translation initiation factor 5A-1;Eukaryotic translation initiation factor 5 EIF5A;EIF5AL1	

Supplemental Table S2a

0,032	-0,52	0,70	69,58	Q9Y446	Plakophilin-3	PKP3
0,004	-0,52	0,70	69,63	Q53FA7	Quinone oxidoreductase PIG3	TP53I3
0,012	-0,52	0,70	69,69	P14902	Indoleamine 2,3-dioxygenase 1	IDO1
0,004	-0,52	0,70	69,71	P05387	60S acidic ribosomal protein P2	RPLP2
0,049	-0,52	0,70	69,75	P46937	Yorkie homolog	YAP1
0,000	-0,52	0,70	69,79	Q99832	T-complex protein 1 subunit eta	CCT7
0,029	-0,52	0,70	69,85	O00154	Cytosolic acyl coenzyme A thioester hydrolase	ACOT7
0,001	-0,52	0,70	69,89	P14314	Glucosidase 2 subunit beta	PRKCSH
0,007	-0,52	0,70	69,92	Q96L92;O60759	Sorting nexin-27	SNX27
0,022	-0,52	0,70	69,98	P78330	Phosphoserine phosphatase	PSPH
0,008	-0,51	0,70	70,13	P40925	Malate dehydrogenase, cytoplasmic	MDH1
0,001	-0,51	0,70	70,14	Q15075	Early endosome antigen 1	EEA1
0,042	-0,51	0,70	70,22	Q06323	Proteasome activator complex subunit 1	PSME1
0,013	-0,51	0,70	70,23	P30085	UMP-CMP kinase	CMPK1
0,005	-0,51	0,70	70,27	O95573	Long-chain-fatty-acid--CoA ligase 3	ACSL3
0,017	-0,51	0,70	70,29	Q9HDC9	Adipocyte plasma membrane-associated protein	APMAP
0,000	-0,51	0,70	70,31	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;Endothelial	AIMP1
0,006	-0,51	0,70	70,33	Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	NFU1
0,028	-0,51	0,70	70,34	Q9BS26	Endoplasmic reticulum resident protein 44	ERP44
0,042	-0,51	0,70	70,35	P49902	Cytosolic purine 5-nucleotidase	NT5C2
0,004	-0,51	0,70	70,37	O95757	Heat shock 70 kDa protein 4L	HSPA4L
0,027	-0,51	0,70	70,41	Q96HN2	Putative adenosylhomocysteinase 3	AHCYL2
0,039	-0,51	0,70	70,46	P25685	DnaJ homolog subfamily B member 1	DNAJB1
0,001	-0,50	0,70	70,47	P11586	C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase	MTHFD1
0,000	-0,50	0,70	70,48	Q96AE4	Far upstream element-binding protein 1	FUBP1
0,007	-0,50	0,71	70,50	Q7Z2Z2	Elongation factor Tu GTP-binding domain-containing protein 1	EFTUD1
0,006	-0,50	0,71	70,51	P23528	Cofilin-1	CFL1
0,020	-0,50	0,71	70,60	P16885	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2	PLCG2
0,006	-0,50	0,71	70,62	P22392	Nucleoside diphosphate kinase B	NME2
0,037	-0,50	0,71	70,71	O43583	Density-regulated protein	DENR
0,007	-0,50	0,71	70,72	Q9NTK5	Obg-like ATPase 1	OLA1
0,024	-0,50	0,71	70,75	Q05086	Ubiquitin-protein ligase E3A	UBE3A
0,015	-0,50	0,71	70,76	O14980	Exportin-1	XPO1

Supplemental Table S2a

0,002	-0,50	0,71	70,78	Q15054	DNA polymerase delta subunit 3	POLD3
0,001	-0,50	0,71	70,80	Q9UL15	BAG family molecular chaperone regulator 5	BAG5
0,042	-0,50	0,71	70,81	Q00653	Nuclear factor NF-kappa-B p100 subunit;Nuclear factor NF-kappa-B p52 subunit	NFKB2
0,003	-0,50	0,71	70,82	P33992	DNA replication licensing factor MCM5	MCM5
0,042	-0,50	0,71	70,86	Q96Q11	CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1
0,011	-0,50	0,71	70,89	P23588	Eukaryotic translation initiation factor 4B	EIF4B
0,007	-0,50	0,71	70,90	P28482	Mitogen-activated protein kinase 1	MAPK1
0,022	-0,49	0,71	70,97	Q9UD71	Protein phosphatase 1 regulatory subunit 1B	PPP1R1B
0,000	-0,49	0,71	70,98	Q7Z417	Nuclear fragile X mental retardation-interacting protein 2	NUFIP2
0,020	-0,49	0,71	71,03	Q9UIA9	Exportin-7	XPO7
0,001	-0,49	0,71	71,10	Q5JRX3	Presequence protease, mitochondrial	PITRM1
0,002	-0,49	0,71	71,12	Q86VS8	Protein Hook homolog 3	HOOK3
0,003	-0,49	0,71	71,16	Q13596	Sorting nexin-1	SNX1
0,019	-0,49	0,71	71,21	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35
0,028	-0,49	0,71	71,21	P33316	Deoxyuridine 5-triphosphate nucleotidohydrolase, mitochondrial	DUT
0,009	-0,49	0,71	71,22	P50990	T-complex protein 1 subunit theta	CCT8
0,003	-0,49	0,71	71,24	P51003;Q9BWT3;Q9NRJ1	Poly(A) polymerase alpha	PAPOLA
0,030	-0,49	0,71	71,26	Q9NRY4	Rho GTPase-activating protein 35	ARHGAP35
0,047	-0,49	0,71	71,28	Q53H82	Beta-lactamase-like protein 2	LACTB2
0,036	-0,49	0,71	71,33	Q15435	Protein phosphatase 1 regulatory subunit 7	PPP1R7
0,028	-0,49	0,71	71,34	Q96CW1	AP-2 complex subunit mu	AP2M1
0,006	-0,49	0,71	71,34	Q9UHV9	Prefoldin subunit 2	PFDN2
0,005	-0,49	0,71	71,35	P22314	Ubiquitin-like modifier-activating enzyme 1	UBA1
0,001	-0,49	0,71	71,39	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);AT	DAK
0,001	-0,49	0,71	71,43	A0MZ66	Shootin-1	KIAA1598
0,034	-0,49	0,71	71,43	P15311	Ezrin	EZR
0,040	-0,49	0,71	71,44	Q9UBU9	Nuclear RNA export factor 1	NXF1
0,035	-0,48	0,71	71,49	P00568;Q9Y6K8	Adenylate kinase isoenzyme 1	AK1
0,002	-0,48	0,72	71,52	Q9UNZ2	NSFL1 cofactor p47	NSFL1C
0,019	-0,48	0,72	71,58	Q9BQA1	Methylosome protein 50	WDR77
0,007	-0,48	0,72	71,59	P25705	ATP synthase subunit alpha, mitochondrial	ATP5A1
0,004	-0,48	0,72	71,68	Q14697	Neutral alpha-glucosidase AB	GANAB
0,011	-0,48	0,72	71,75	P07858	Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain	CTSB

Supplemental Table S2a

0,009	-0,48	0,72	71,77	Q04760	Lactoylglutathione lyase	GLO1
0,004	-0,48	0,72	71,86	Q99747	Gamma-soluble NSF attachment protein	NAPG
0,010	-0,48	0,72	71,88	Q9BXJ9;Q6N069	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15
0,008	-0,48	0,72	71,88	Q9BV86	Alpha N-terminal protein methyltransferase 1A	METTTL11A
0,039	-0,47	0,72	71,96	Q15021	Condensin complex subunit 1	NCAPD2
0,008	-0,47	0,72	72,03	P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A
0,005	-0,47	0,72	72,11	P07900;Q14568;Q58FGC	Heat shock protein HSP 90-alpha	HSP90AA1
0,042	-0,47	0,72	72,16	Q9NUQ8	ATP-binding cassette sub-family F member 3	ABCF3
0,049	-0,47	0,72	72,26	P40818	Ubiquitin carboxyl-terminal hydrolase 8	USP8
0,019	-0,47	0,72	72,27	P28838	Cytosol aminopeptidase	LAP3
0,036	-0,47	0,72	72,28	P62937;F5H284;Q9Y536	Peptidyl-prolyl cis-trans isomerase A	PPIA
0,044	-0,47	0,72	72,29	P08758	Annexin A5	ANXA5
0,005	-0,47	0,72	72,36	O60318	80 kDa MCM3-associated protein	MCM3AP
0,030	-0,47	0,72	72,36	O75153	Protein KIAA0664	KIAA0664
0,034	-0,47	0,72	72,38	O95295	SNARE-associated protein Snapin	SNAPIN
0,005	-0,46	0,72	72,49	P55263	Adenosine kinase	ADK
0,001	-0,46	0,73	72,52	Q99460	26S proteasome non-ATPase regulatory subunit 1	PSMD1
0,005	-0,46	0,73	72,62	Q15042	Rab3 GTPase-activating protein catalytic subunit	RAB3GAP1
0,002	-0,46	0,73	72,64	P50995	Annexin A11	ANXA11
0,024	-0,46	0,73	72,69	Q99733	Nucleosome assembly protein 1-like 4	NAP1L4
0,006	-0,46	0,73	72,69	Q96JJ7	Protein disulfide-isomerase TMX3	TMX3
0,003	-0,46	0,73	72,70	P40123	Adenylyl cyclase-associated protein 2	CAP2
0,013	-0,46	0,73	72,71	Q15084	Protein disulfide-isomerase A6	PDIA6
0,002	-0,46	0,73	72,75	Q13085	Acetyl-CoA carboxylase 1;Biotin carboxylase	ACACA
0,007	-0,46	0,73	72,79	P23526	Adenosylhomocysteinase	AHCY
0,034	-0,46	0,73	72,87	Q9BRA2	Thioredoxin domain-containing protein 17	TXNDC17
0,003	-0,46	0,73	72,88	Q99614	Tetratricopeptide repeat protein 1	TTC1
0,008	-0,45	0,73	72,96	Q6DKJ4	Nucleoredoxin	NXN
0,022	-0,45	0,73	73,01	P48426	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	PIP4K2A
0,027	-0,45	0,73	73,02	Q99426	Tubulin-folding cofactor B	TBCB
0,038	-0,45	0,73	73,12	P38117	Electron transfer flavoprotein subunit beta	ETFB
0,022	-0,45	0,73	73,14	O95831	Apoptosis-inducing factor 1, mitochondrial	AIFM1
0,021	-0,45	0,73	73,16	Q9Y371	Endophilin-B1	SH3GLB1

Supplemental Table S2a

0,000	-0,45	0,73	73,21	Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	PNPT1
0,001	-0,45	0,73	73,32	Q92616	Translational activator GCN1	GCN1L1
0,007	-0,45	0,73	73,33	Q9H6T3	RNA polymerase II-associated protein 3	RPAP3
0,005	-0,44	0,73	73,47	P30041	Peroxiredoxin-6	PRDX6
0,013	-0,44	0,74	73,53	Q9Y3A5	Ribosome maturation protein SBDS	SBDS
0,000	-0,44	0,74	73,54	Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1	PPP6R1
0,020	-0,44	0,74	73,56	Q9HAV7	GrpE protein homolog 1, mitochondrial	GRPEL1
0,027	-0,44	0,74	73,64	Q9HB71	Calcyclin-binding protein	CACYBP
0,000	-0,44	0,74	73,65	Q06124	Tyrosine-protein phosphatase non-receptor type 11	PTPN11
0,005	-0,44	0,74	73,69	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1
0,003	-0,44	0,74	73,81	P43034	Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1
0,045	-0,44	0,74	73,86	Q9UPT5	Exocyst complex component 7	EXOC7
0,016	-0,44	0,74	73,89	Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	MTHFD1L
0,045	-0,43	0,74	73,97	O00273	DNA fragmentation factor subunit alpha	DDFA
0,005	-0,43	0,74	73,98	O00764	Pyridoxal kinase	PDXK
0,043	-0,43	0,74	73,99	O94826	Mitochondrial import receptor subunit TOM70	TOMM70A
0,000	-0,43	0,74	73,99	P62826	GTP-binding nuclear protein Ran	RAN
0,007	-0,43	0,74	74,01	Q9UK59	Lariat debranching enzyme	DBR1
0,043	-0,43	0,74	74,03	Q9UBQ0	Vacuolar protein sorting-associated protein 29	VPS29
0,048	-0,43	0,74	74,17	P30626	Sorcin	SRI
0,015	-0,43	0,74	74,18	P41250	Glycine--tRNA ligase	GARS
0,033	-0,43	0,74	74,18	P50453	Serpin B9	SERPINB9
0,008	-0,43	0,74	74,19	P49321	Nuclear autoantigenic sperm protein	NASP
0,016	-0,43	0,74	74,22	Q9UKY7	Protein CDV3 homolog	CDV3
0,028	-0,43	0,74	74,24	Q16401	26S proteasome non-ATPase regulatory subunit 5	PSMD5
0,036	-0,43	0,74	74,27	O95816	BAG family molecular chaperone regulator 2	BAG2
0,012	-0,43	0,74	74,30	O43399	Tumor protein D54	TPD52L2
0,000	-0,43	0,74	74,32	Q8WUM4	Programmed cell death 6-interacting protein	PDCD6IP
0,026	-0,43	0,74	74,33	O00541	Pescadillo homolog	PES1
0,005	-0,43	0,74	74,35	O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	LETM1
0,039	-0,43	0,74	74,36	P55036	26S proteasome non-ATPase regulatory subunit 4	PSMD4
0,011	-0,43	0,74	74,36	Q9H936;Q9H1K4	Mitochondrial glutamate carrier 1	SLC25A22
0,037	-0,43	0,74	74,38	P32321	Deoxycytidylate deaminase	DCTD

Supplemental Table S2a

0,004	-0,43	0,74	74,39	Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1
0,003	-0,42	0,74	74,50	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX
0,002	-0,42	0,75	74,55	P31153;Q00266	S-adenosylmethionine synthase isoform type-2	MAT2A
0,020	-0,42	0,75	74,60	P84090	Enhancer of rudimentary homolog	ERH
0,015	-0,42	0,75	74,62	P30740	Leukocyte elastase inhibitor	SERPINB1
0,039	-0,42	0,75	74,63	P21291	Cysteine and glycine-rich protein 1	CSRP1
0,033	-0,42	0,75	74,68	Q9Y223	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase;L	GNE
0,023	-0,42	0,75	74,69	P23921	Ribonucleoside-diphosphate reductase large subunit	RRM1
0,017	-0,42	0,75	74,71	P38646	Stress-70 protein, mitochondrial	HSPA9
0,005	-0,42	0,75	74,91	Q8TD19	Serine/threonine-protein kinase Nek9	NEK9
0,049	-0,42	0,75	74,95	Q8NFK8	Torsin-1A-interacting protein 2	TOR1AIP2
0,000	-0,42	0,75	74,99	Q8IVF2	Protein AHNK2	AHNK2
0,002	-0,41	0,75	75,01	Q9UM54	Unconventional myosin-VI	MYO6
0,026	-0,41	0,75	75,06	P18031	Tyrosine-protein phosphatase non-receptor type 1	PTPN1
0,008	-0,41	0,75	75,07	O95487	Protein transport protein Sec24B	SEC24B
0,005	-0,41	0,75	75,08	Q13616	Cullin-1	CUL1
0,031	-0,41	0,75	75,12	Q9H9P8	L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2HGDH
0,050	-0,41	0,75	75,14	P11233	Ras-related protein Ral-A	RALA
0,020	-0,41	0,75	75,14	Q96EL3	39S ribosomal protein L53, mitochondrial	MRPL53
0,016	-0,41	0,75	75,18	Q96JB5	CDK5 regulatory subunit-associated protein 3	CDK5RAP3
0,007	-0,41	0,75	75,27	Q13464	Rho-associated protein kinase 1	ROCK1
0,001	-0,41	0,75	75,29	Q13177	Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-2p34	PAK2
0,042	-0,41	0,75	75,29	P46459	Vesicle-fusing ATPase	NSF
0,021	-0,41	0,75	75,32	Q9P2J5	Leucine--tRNA ligase, cytoplasmic	LARS
0,050	-0,41	0,75	75,32	O75828	Carbonyl reductase [NADPH] 3	CBR3
0,002	-0,41	0,75	75,34	P13489	Ribonuclease inhibitor	RNH1
0,000	-0,41	0,75	75,36	P20073	Annexin A7	ANXA7
0,006	-0,41	0,75	75,41	O00429	Dynamin-1-like protein	DNM1L
0,030	-0,41	0,76	75,51	Q13057	Bifunctional coenzyme A synthase;Phosphopantetheine adenylyltransferase;Depho	COASY
0,024	-0,41	0,76	75,52	P61224;A6NIZ1	Ras-related protein Rap-1b;Ras-related protein Rap-1b-like protein	RAP1B
0,032	-0,40	0,76	75,73	Q15942	Zyxin	ZYX
0,035	-0,40	0,76	75,83	P10768	S-formylglutathione hydrolase	ESD
0,004	-0,40	0,76	75,88	Q08257	Quinone oxidoreductase	CRYZ

Supplemental Table S2a

0,001	-0,40	0,76	75,96	Q13045	Protein flightless-1 homolog	FLII
0,006	-0,39	0,76	76,09	P60866	40S ribosomal protein S20	RPS20
0,007	-0,39	0,76	76,17	P40763	Signal transducer and activator of transcription 3	STAT3
0,017	-0,39	0,76	76,21	O15212	Prefoldin subunit 6	PFDN6
0,006	-0,39	0,76	76,23	Q12931	Heat shock protein 75 kDa, mitochondrial	TRAP1
0,021	-0,39	0,76	76,28	P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1
0,003	-0,39	0,76	76,28	P30622	CAP-Gly domain-containing linker protein 1	CLIP1
0,024	-0,39	0,76	76,39	P14550	Alcohol dehydrogenase [NADP(+)]	AKR1A1
0,001	-0,39	0,76	76,40	O43847	Nardilysin	NRD1
0,009	-0,39	0,76	76,41	P13010	X-ray repair cross-complementing protein 5	XRCC5
0,012	-0,39	0,76	76,44	Q92598	Heat shock protein 105 kDa	HSPH1
0,042	-0,39	0,76	76,45	O75569	Interferon-inducible double stranded RNA-dependent protein kinase activator A	PRKRA
0,002	-0,39	0,76	76,48	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS
0,005	-0,39	0,76	76,49	P58546	Myotrophin	MTPN
0,001	-0,39	0,77	76,50	Q9UBC2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1
0,002	-0,39	0,77	76,50	O75822	Eukaryotic translation initiation factor 3 subunit J	EIF3J
0,031	-0,39	0,77	76,51	P24666	Low molecular weight phosphotyrosine protein phosphatase	ACP1
0,010	-0,38	0,77	76,67	Q9NZL9	Methionine adenosyltransferase 2 subunit beta	MAT2B
0,020	-0,38	0,77	76,67	P05556	Integrin beta-1	ITGB1
0,018	-0,38	0,77	76,69	P67809	Nuclease-sensitive element-binding protein 1	YBX1
0,038	-0,38	0,77	76,73	O75439	Mitochondrial-processing peptidase subunit beta	PMPCB
0,001	-0,37	0,77	77,21	P31939	Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarboxamide	ATIC
0,034	-0,37	0,77	77,24	P50570;Q9UQ16;Q05191	Dynamin-2	DNM2
0,004	-0,37	0,77	77,34	Q4G0N4	NAD kinase domain-containing protein 1	NADKD1
0,002	-0,37	0,77	77,34	P07355;A6NMY6	Annexin A2;Putative annexin A2-like protein	ANXA2;ANXA2P2
0,018	-0,37	0,77	77,37	P34897	Serine hydroxymethyltransferase, mitochondrial	SHMT2
0,007	-0,37	0,77	77,45	Q7L523;Q5VZM2	Ras-related GTP-binding protein A;Ras-related GTP-binding protein B	RRAGA;RRAGB
0,004	-0,37	0,77	77,46	P60660	Myosin light polypeptide 6	MYL6
0,038	-0,37	0,78	77,54	P12956	X-ray repair cross-complementing protein 6	XRCC6
0,047	-0,37	0,78	77,54	P54652	Heat shock-related 70 kDa protein 2	HSPA2
0,030	-0,37	0,78	77,64	Q9Y4E8	Ubiquitin carboxyl-terminal hydrolase 15	USP15
0,002	-0,36	0,78	77,77	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK
0,000	-0,36	0,78	77,79	P56537	Eukaryotic translation initiation factor 6	EIF6

Supplemental Table S2a

0,019	-0,36	0,78	77,81	P50454	Serpin H1	SERPINH1
0,026	-0,36	0,78	77,93	P13639	Elongation factor 2	EEF2
0,030	-0,36	0,78	77,96	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15
0,016	-0,36	0,78	78,00	Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK
0,028	-0,36	0,78	78,00	Q6FI81	Anamorsin	CIAPIN1
0,001	-0,36	0,78	78,01	P04632;Q96L46	Calpain small subunit 1	CAPNS1
0,032	-0,35	0,78	78,24	O94979	Protein transport protein Sec31A	SEC31A
0,032	-0,35	0,78	78,47	Q9UKK3	Poly [ADP-ribose] polymerase 4	PARP4
0,024	-0,35	0,78	78,47	P34932	Heat shock 70 kDa protein 4	HSPA4
0,025	-0,35	0,79	78,50	Q12965;O00160	Unconventional myosin-Ie	MYO1E
0,012	-0,35	0,79	78,55	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1
0,038	-0,35	0,79	78,66	P08107	Heat shock 70 kDa protein 1A/1B	HSPA1A
0,023	-0,34	0,79	78,77	P07737;CON__P02584	Profilin-1	PFN1
0,005	-0,34	0,79	78,80	I31;Q9UBL6;O95741;Q9	Copine-3	CPNE3
0,041	-0,34	0,79	78,85	P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehyd	DLST
0,007	-0,34	0,79	78,86	Q9NY33	Dipeptidyl peptidase 3	DPP3
0,017	-0,34	0,79	78,89	P29401	Transketolase	TKT
0,004	-0,34	0,79	78,95	Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog	SUGT1
0,015	-0,34	0,79	79,17	P23381	Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS	WARS
0,005	-0,34	0,79	79,17	O60749	Sorting nexin-2	SNX2
0,042	-0,34	0,79	79,25	P55327	Tumor protein D52	TPD52
0,021	-0,34	0,79	79,25	O94903	Proline synthase co-transcribed bacterial homolog protein	PROSC
0,039	-0,33	0,79	79,29	O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11
0,010	-0,33	0,79	79,30	Q9Y617	Phosphoserine aminotransferase	PSAT1
0,000	-0,33	0,79	79,32	P54577	Tyrosine--tRNA ligase, cytoplasmic	YARS
0,035	-0,33	0,79	79,39	O75351	Vacuolar protein sorting-associated protein 4B	VPS4B
0,019	-0,33	0,79	79,41	Q9NPQ8	Synembryn-A	RIC8A
0,002	-0,33	0,79	79,42	P13611	Versican core protein	VCAN
0,016	-0,33	0,79	79,44	Q6PL18	ATPase family AAA domain-containing protein 2	ATAD2
0,013	-0,33	0,80	79,51	O15270	Serine palmitoyltransferase 2	SPTLC2
0,038	-0,33	0,80	79,56	P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	SUCLG1
0,006	-0,33	0,80	79,57	Q13586	Stromal interaction molecule 1	STIM1
0,003	-0,33	0,80	79,60	Q06787	Fragile X mental retardation protein 1	FMR1

Supplemental Table S2a

0,042	-0,33	0,80	79,69	P43897	Elongation factor Ts, mitochondrial	TSFM
0,016	-0,33	0,80	79,71	P49137;P51817;O43930	MAP kinase-activated protein kinase 3;MAP kinase-activated protein kinase 2	MAPKAPK3;MAPKAPK2
0,037	-0,33	0,80	79,72	P12277	Creatine kinase B-type	CKB
0,024	-0,33	0,80	79,78	Q9H4A4	Aminopeptidase B	RNPEP
0,016	-0,32	0,80	79,88	Q96JH7	Deubiquitinating protein VCIP135	VCIP1
0,004	-0,32	0,80	79,91	P53992	Protein transport protein Sec24C	SEC24C
0,000	-0,32	0,80	79,91	P17987	T-complex protein 1 subunit alpha	TCP1
0,020	-0,32	0,80	79,99	P13797;P13796	Plastin-3	PLS3
0,004	-0,32	0,80	80,00	O75116	Rho-associated protein kinase 2	ROCK2
0,029	-0,32	0,80	80,03	O14818;Q8TAA3	Proteasome subunit alpha type-7	PSMA7
0,028	-0,32	0,80	80,08	P22059	Oxysterol-binding protein 1	OSBP
0,036	-0,32	0,80	80,16	Q63ZY3;Q14678	KN motif and ankyrin repeat domain-containing protein 2	KANK2
0,045	-0,32	0,80	80,16	P45984;P53779;P45983	Mitogen-activated protein kinase 9	MAPK9
0,033	-0,32	0,80	80,31	Q16513	Serine/threonine-protein kinase N2	PKN2
0,023	-0,31	0,80	80,41	Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2
0,009	-0,31	0,80	80,42	P04083	Annexin A1	ANXA1
0,000	-0,31	0,80	80,44	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA
0,014	-0,31	0,81	80,53	P10809	60 kDa heat shock protein, mitochondrial	HSPD1
0,016	-0,31	0,81	80,61	P52888	Thimet oligopeptidase	THOP1
0,002	-0,31	0,81	80,61	P04040	Catalase	CAT
0,025	-0,31	0,81	80,64	Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5
0,048	-0,31	0,81	80,68	Q9BSJ8	Extended synaptotagmin-1	ESYT1
0,050	-0,31	0,81	80,80	P07902	Galactose-1-phosphate uridylyltransferase	GALT
0,033	-0,31	0,81	80,83	O15027	Protein transport protein Sec16A	SEC16A
0,027	-0,31	0,81	80,89	P27708;P31327	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyl transferase	CAD
0,043	-0,31	0,81	80,94	P17655	Calpain-2 catalytic subunit	CAPN2
0,030	-0,30	0,81	80,98	Q9Y376	Calcium-binding protein 39	CAB39
0,016	-0,30	0,81	81,14	P40227	T-complex protein 1 subunit zeta	CCT6A
0,035	-0,30	0,81	81,20	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D
0,006	-0,30	0,81	81,22	O43852	Calumenin	CALU
0,022	-0,30	0,81	81,29	P35250	Replication factor C subunit 2	RFC2
0,008	-0,30	0,81	81,30	P26038	Moesin	MSN
0,048	-0,30	0,81	81,34	P42566	Epidermal growth factor receptor substrate 15	EPS15

Supplemental Table S2a

0,005	-0,30	0,81	81,36	P52758	Ribonuclease UK114	HRSP12
0,009	-0,30	0,81	81,44	Q15181	Inorganic pyrophosphatase	PPA1
0,003	-0,30	0,81	81,46	Q96C90	Protein phosphatase 1 regulatory subunit 14B	PPP1R14B
0,023	-0,30	0,81	81,50	P29144	Tripeptidyl-peptidase 2	TPP2
0,016	-0,29	0,82	81,53	P49257	Protein ERGIC-53	LMAN1
0,000	-0,29	0,82	81,57	P11498	Pyruvate carboxylase, mitochondrial	PC
0,036	-0,29	0,82	81,57	O00592	Podocalyxin	PODXL
0,015	-0,29	0,82	81,61	Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4
0,015	-0,29	0,82	81,77	P55145	Mesencephalic astrocyte-derived neurotrophic factor	MANF
0,040	-0,29	0,82	81,83	Q13131	5-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1
0,030	-0,29	0,82	81,84	Q9BYT8	Neurolysin, mitochondrial	NLN
0,001	-0,29	0,82	81,88	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1
0,028	-0,28	0,82	82,21	P11216	Glycogen phosphorylase, brain form	PYGB
0,014	-0,28	0,82	82,29	P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADVL
0,004	-0,28	0,82	82,36	Q9HC35	Echinoderm microtubule-associated protein-like 4	EML4
0,001	-0,28	0,82	82,37	Q9UL46	Proteasome activator complex subunit 2	PSME2
0,018	-0,28	0,82	82,39	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1
0,002	-0,28	0,82	82,46	Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2
0,039	-0,28	0,82	82,47	Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial	PPA2
0,016	-0,27	0,83	82,68	P48556	26S proteasome non-ATPase regulatory subunit 8	PSMD8
0,005	-0,27	0,83	82,70	Q07960	Rho GTPase-activating protein 1	ARHGAP1
0,011	-0,27	0,83	82,76	O75886	Signal transducing adapter molecule 2	STAM2
0,041	-0,27	0,83	82,78	P08134;P62745	Rho-related GTP-binding protein RhoC	RHOC
0,045	-0,27	0,83	82,94	P60981	Destrin	DSTN
0,012	-0,27	0,83	82,99	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2
0,035	-0,27	0,83	83,03	O60841	Eukaryotic translation initiation factor 5B	EIF5B
0,025	-0,27	0,83	83,12	Q9UHG3	Prenylcysteine oxidase 1	PCYOX1
0,003	-0,26	0,83	83,41	A0AVT1	Ubiquitin-like modifier-activating enzyme 6	UBA6
0,010	-0,26	0,83	83,44	Q13938	Calcyphosin	CAPS
0,045	-0,26	0,83	83,45	P48643	T-complex protein 1 subunit epsilon	CCT5
0,041	-0,26	0,84	83,75	P56134	ATP synthase subunit f, mitochondrial	ATP5J2
0,046	-0,25	0,84	83,99	P23284	Peptidyl-prolyl cis-trans isomerase B	PIIB
0,006	-0,24	0,84	84,39	O60716	Catenin delta-1	CTNND1

Supplemental Table S2a

0,021	-0,24	0,84	84,41	P379;P0CG48;P0CG47;P61	Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Polyubiquitin	RPS27A;UBC;UBB;U
0,003	-0,24	0,85	84,82	P41091;Q2VIR3	Eukaryotic translation initiation factor 2 subunit 3;Putative eukaryotic translation in	EIF2S3;EIF2S3L
0,006	-0,24	0,85	84,86	P36776	Lon protease homolog, mitochondrial	LONP1
0,001	-0,24	0,85	84,88	P21333	Filamin-A	FLNA
0,032	-0,24	0,85	84,95	Q12792	Twinfilin-1	TWF1
0,049	-0,23	0,85	85,12	P53990	IST1 homolog	IST1
0,035	-0,23	0,85	85,41	Q8TAT6	Nuclear protein localization protein 4 homolog	NPLOC4
0,014	-0,23	0,85	85,41	P49411	Elongation factor Tu, mitochondrial	TUFM
0,002	-0,23	0,85	85,42	P33121;Q9ULC5	Long-chain-fatty-acid--CoA ligase 1	ACSL1
0,041	-0,23	0,86	85,56	P41240	Tyrosine-protein kinase CSK	CSK
0,039	-0,22	0,86	85,56	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	PSMD13
0,001	-0,22	0,86	86,02	O75179	Ankyrin repeat domain-containing protein 17	ANKRD17
0,036	-0,20	0,87	86,83	P16930	Fumarylacetoacetase	FAH
0,038	-0,20	0,87	87,13	P09382	Galectin-1	LGALS1
0,019	-0,19	0,87	87,38	Q14444	Caprin-1	CAPRIN1
0,018	-0,19	0,87	87,41	Q9Y5K6	CD2-associated protein	CD2AP
0,045	-0,19	0,88	87,55	Q96C19;Q9BUP0	EF-hand domain-containing protein D2	EFHD2
0,018	-0,18	0,88	88,37	Q99615	DnaJ homolog subfamily C member 7	DNAJC7
0,020	-0,17	0,89	88,65	P55786;A6NEC2	Puromycin-sensitive aminopeptidase	NPEPPS
0,050	-0,16	0,89	89,23	P51808	Dynein light chain Tctex-type 3	DYNLT3

Color Code

8h Up
24h Up
8h Down
24h Down

Supplemental Table S2b: Shotgun proteomic analysis of OVCAR3 cells exposed for 8h and 24h to 40μM G28UCM. All proteins identified by MS/MS.

p-Value	x	2^x	% of Control	Protein IDs	Protein Names	Gene names
8 h Up						
0,017	5,75	53,86	5386,33	P33527	Multidrug resistance-associated protein 1	ABCC1
0,000	4,73	26,50	2650,38	Q9HBL0	Tensin-1	TNS1
0,005	4,48	22,36	2236,48	O00479	High mobility group nucleosome-binding domain-containing protein 4	HMGN4
0,014	4,13	17,51	1750,87	Q96S55	ATPase WRNIP1	WRNIP1
0,014	4,11	17,26	1725,54	Q9UDY4	DnaJ homolog subfamily B member 4	DNAJB4
0,000	3,99	15,89	1588,95	Q9UMS0	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	NFU1
0,020	3,86	14,55	1455,00	Q6PL18	ATPase family AAA domain-containing protein 2	ATAD2
0,006	3,78	13,71	1371,02	O00584	Ribonuclease T2	RNASSET2
0,017	3,77	13,65	1365,35	Q5VWQ8	Disabled homolog 2-interacting protein	DAB2IP
0,000	3,76	13,52	1351,57	P11166	Solute carrier family 2, facilitated glucose transporter member 1	SLC2A1
0,032	3,62	12,33	1233,50	O75448	Mediator of RNA polymerase II transcription subunit 24	MED24
0,034	3,57	11,88	1187,62	Q96DH6	RNA-binding protein Musashi homolog 2	MSI2
0,001	3,57	11,84	1183,64	Q9GZT9	Egl nine homolog 1	EGLN1
0,002	3,54	11,63	1163,18	Q16665	Hypoxia-inducible factor 1-alpha	HIF1A
0,019	3,52	11,51	1150,86	Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1	DTD1
0,005	3,49	11,27	1126,52	Q9BZV1	UBX domain-containing protein 6	UBXN6
0,005	3,48	11,16	1115,79	Q13423	NAD(P) transhydrogenase, mitochondrial	NNT
0,001	3,48	11,16	1115,79	P17693	HLA class I histocompatibility antigen, alpha chain G	HLA-G
0,027	3,42	10,67	1067,47	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP
0,026	3,35	10,21	1021,05	P05976;P08590	Myosin light chain 1/3, skeletal muscle isoform;Myosin light chain 3	MYL1;MYL3
0,012	3,33	10,06	1005,61	Q6ZSR9	Uncharacterized protein FLJ45252	
0,035	3,30	9,88	987,62	O95208	Epsin-2	EPN2
0,000	3,30	9,84	984,44	Q8NCH0	Carbohydrate sulfotransferase 14	CHST14
0,004	3,27	9,65	964,65	Q3YBR2	Transforming growth factor beta regulator 1	TBRG1
0,020	3,23	9,41	941,18	Q15434	RNA-binding motif, single-stranded-interacting protein 2	RBMS2
0,006	3,21	9,23	922,97	Q14493	Histone RNA hairpin-binding protein	SLBP
0,012	3,14	8,82	881,52	P45985	Dual specificity mitogen-activated protein kinase kinase 4	MAP2K4

Supplemental Table S2b

0,003	3,12	8,69	868,70	Q96CU9	FAD-dependent oxidoreductase domain-containing protein 1	FOXRED1
0,002	3,10	8,59	858,80	Q99996	A-kinase anchor protein 9	AKAP9
0,000	3,06	8,34	834,36	Q9UPQ3	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	AGAP1
0,027	3,04	8,25	824,52	O14907	Tax1-binding protein 3	TAX1BP3
0,000	3,03	8,17	816,82	O76041	Nebulette	NEBL
0,005	2,99	7,96	795,52	Q9UKM9	RNA-binding protein Raly	RALY
0,024	2,89	7,41	741,34	P53803	DNA-directed RNA polymerases I, II, and III subunit RPABC4	POLR2K
0,030	2,84	7,15	715,20	Q5VZF2	Muscleblind-like protein 2	MBNL2
0,005	2,82	7,06	706,16	Q8IWB7	WD repeat and FYVE domain-containing protein 1	WDFY1
0,001	2,81	7,01	701,28	Q9H936	Mitochondrial glutamate carrier 1	SLC25A22
0,029	2,79	6,90	689,75	Q9C0D4	Zinc finger protein 518B	ZNF518B
0,012	2,73	6,63	662,74	O14656	Torsin-1A	TOR1A
0,019	2,66	6,32	632,03	Q9BRQ6	MICOS complex subunit MIC25	CHCHD6
0,001	2,65	6,28	627,67	P06703	Protein S100-A6	S100A6
0,040	2,63	6,19	619,03	Q4G0P3	Hydrocephalus-inducing protein homolog	HYDIN
0,014	2,57	5,94	594,06	P06400	Retinoblastoma-associated protein	RB1
0,005	2,57	5,94	593,64	P17050	Alpha-N-acetylgalactosaminidase	NAGA
0,037	2,55	5,86	586,07	Q9BXW7	Cat eye syndrome critical region protein 5	CECR5
0,003	2,55	5,86	585,63	Q9UEU0	Vesicle transport through interaction with t-SNAREs homolog 1B	VTI1B
0,008	2,51	5,68	567,74	Q9P0U4	CXXC-type zinc finger protein 1	CXXC1
0,044	2,50	5,67	566,75	Q15652	Probable JmjC domain-containing histone demethylation protein 2C	JMJD1C
0,039	2,49	5,62	562,28	P49356	Protein farnesyltransferase subunit beta	FNTB
0,006	2,48	5,60	559,76	Q9BRT6	Protein LLP homolog	LLPH
0,004	2,48	5,58	557,90	Q9BRZ2	E3 ubiquitin-protein ligase TRIM56	TRIM56
0,002	2,47	5,56	555,79	P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70
0,016	2,47	5,52	552,24	Q86WX3	Active regulator of SIRT1	RPS19BP1
0,000	2,45	5,46	546,42	O95498	Vascular non-inflammatory molecule 2	VNN2
0,049	2,43	5,37	537,07	Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1
0,041	2,42	5,35	535,17	Q9P2K3	REST corepressor 3	RCOR3
0,016	2,41	5,33	532,70	P42345	Serine/threonine-protein kinase mTOR	MTOR
0,011	2,41	5,31	531,47	Q9Y421	Protein FAM32A	FAM32A
0,039	2,41	5,30	530,11	O00411	DNA-directed RNA polymerase, mitochondrial	POLRMT
0,038	2,40	5,28	527,80	Q53HC9	Protein TSSC1	TSSC1

Supplemental Table S2b

0,026	2,38	5,21	520,54	Q99439	Calponin-2	CNN2
0,016	2,37	5,17	516,94	Q13796	Protein Shroom2	SHROOM2
0,038	2,37	5,17	516,94	Q4J6C6	Prolyl endopeptidase-like	PREPL
0,046	2,36	5,13	513,08	P09758	Tumor-associated calcium signal transducer 2	TACSTD2
0,050	2,30	4,94	493,99	Q9H3P2	Negative elongation factor A	NELFA
0,047	2,30	4,92	492,46	Q9UDT6	CAP-Gly domain-containing linker protein 2	CLIP2
0,029	2,30	4,92	491,64	Q9NY61	Protein AATF	AATF
0,003	2,29	4,89	489,06	Q5W111	SPRY domain-containing protein 7	SPRYD7
0,001	2,27	4,83	483,47	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1
0,010	2,27	4,82	482,32	O75164	Lysine-specific demethylase 4A	KDM4A
0,019	2,26	4,79	478,99	P49593	Protein phosphatase 1F	PPM1F
0,030	2,24	4,72	471,74	Q9BYD1	39S ribosomal protein L13, mitochondrial	MRPL13
0,016	2,24	4,71	471,22	P04114	Apolipoprotein B-100;Apolipoprotein B-48	APOB
0,024	2,22	4,67	466,68	Q71F56	Mediator of RNA polymerase II transcription subunit 13-like	MED13L
0,016	2,18	4,54	454,21	Q9UJX4	Anaphase-promoting complex subunit 5	ANAPC5
0,009	2,18	4,53	453,15	Q4V328	GRIP1-associated protein 1	GRIPAP1
0,028	2,17	4,50	450,02	Q8N392	Rho GTPase-activating protein 18	ARHGAP18
0,017	2,15	4,44	443,83	P27540	Aryl hydrocarbon receptor nuclear translocator	ARNT
0,038	2,13	4,39	439,23	Q5RKV6	Exosome complex component MTR3	EXOSC6
0,009	2,12	4,34	433,58	Q96B26	Exosome complex component RRP43	EXOSC8
0,016	2,11	4,32	431,69	P42695	Condensin-2 complex subunit D3	NCAPD3
0,012	2,09	4,26	425,75	Q8WWQ0	PH-interacting protein	PHIP
0,008	2,09	4,24	424,47	Q9Y4P3	Transducin beta-like protein 2	TBL2
0,033	2,08	4,24	423,82	Q96S94	Cyclin-L2	CCNL2
0,013	2,08	4,22	422,21	Q96PK6	RNA-binding protein 14	RBM14
0,032	2,06	4,17	416,63	P17676	CCAAT/enhancer-binding protein beta	CEBPB
0,002	2,02	4,07	406,53	Q9UHR4	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	BAIAP2L1
0,005	2,00	4,00	400,29	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	PRPF8
0,005	1,98	3,96	395,80	P60602	Reactive oxygen species modulator 1	ROMO1
0,001	1,98	3,96	395,57	Q9BUQ8	Probable ATP-dependent RNA helicase DDX23	DDX23
0,032	1,98	3,95	395,13	Q9BQG0	Myb-binding protein 1A	MYBBP1A
0,025	1,98	3,94	394,49	Q13889	General transcription factor IIH subunit 3	GTF2H3
0,024	1,96	3,89	389,06	Q6MZP7	Protein lin-54 homolog	LIN54

Supplemental Table S2b

0,010	1,95	3,87	387,11	Q9Y2D4	Exocyst complex component 6B	EXOC6B
0,009	1,95	3,86	386,21	Q16537	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	PPP2R5E
0,002	1,93	3,81	381,44	P48637	Glutathione synthetase	GSS
0,019	1,92	3,78	378,42	Q86YS3	Rab11 family-interacting protein 4	RAB11FIP4
0,010	1,89	3,71	370,57	P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha	PIK3R1
0,007	1,87	3,66	365,53	O00423	Echinoderm microtubule-associated protein-like 1	EML1
0,013	1,84	3,58	358,01	O00418	Eukaryotic elongation factor 2 kinase	EEF2K
0,025	1,83	3,54	354,43	Q9Y6R0	Numb-like protein	NUMBL
0,005	1,82	3,54	353,66	Q9H0S4	Probable ATP-dependent RNA helicase DDX47	DDX47
0,031	1,81	3,51	350,88	Q86W42	THO complex subunit 6 homolog	THOC6
0,028	1,81	3,51	350,64	Q92600	Cell differentiation protein RCD1 homolog	RQCD1
0,024	1,81	3,49	349,43	O95479	GDH/6PGL endoplasmic bifunctional protein;Glucose 1-dehydrogenase;6-phosphogl	H6PD
0,021	1,80	3,48	348,22	Q14119	Vascular endothelial zinc finger 1	VEZF1
0,013	1,80	3,48	348,06	O76021	Ribosomal L1 domain-containing protein 1	RSL1D1
0,007	1,79	3,45	345,02	P98175	RNA-binding protein 10	RBM10
0,001	1,78	3,44	343,97	Q13557	Calcium/calmodulin-dependent protein kinase type II subunit delta	CAMK2D
0,008	1,78	3,43	343,50	Q96L91	E1A-binding protein p400	EP400
0,042	1,78	3,43	343,23	P14902	Indoleamine 2,3-dioxygenase 1	IDO1
0,006	1,77	3,41	341,37	Q9NRS6	Sorting nexin-15	SNX15
0,003	1,77	3,41	340,55	Q8IXT5	RNA-binding protein 12B	RBM12B
0,005	1,74	3,34	333,99	Q9NR30	Nucleolar RNA helicase 2	DDX21
0,003	1,73	3,32	331,59	Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	PDPR
0,040	1,73	3,31	331,28	P82912	28S ribosomal protein S11, mitochondrial	MRPS11
0,032	1,73	3,31	330,77	Q8IY17	Neuropathy target esterase	PNPLA6
0,001	1,72	3,29	328,91	O95197	Reticulon-3	RTN3
0,002	1,71	3,28	328,27	Q01415	N-acetylgalactosamine kinase	GALK2
0,009	1,70	3,25	324,90	Q14203	Dynactin subunit 1	DCTN1
0,020	1,70	3,24	323,90	Q6ZW49	PAX-interacting protein 1	PAXIP1
0,007	1,69	3,23	323,27	Q9NXV2	BTB/POZ domain-containing protein KCTD5	KCTD5
0,028	1,69	3,23	322,81	Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9
0,018	1,69	3,23	322,66	Q92597	Protein NDRG1	NDRG1
0,016	1,68	3,21	321,46	Q96SY0	von Willebrand factor A domain-containing protein 9	VWA9
0,005	1,68	3,21	321,03	Q13596	Sorting nexin-1	SNX1

Supplemental Table S2b

0,040	1,68	3,20	320,26	Q9NY27	Serine/threonine-protein phosphatase 4 regulatory subunit 2	PPP4R2
0,000	1,65	3,14	313,69	Q7RTV0	PHD finger-like domain-containing protein 5A	PHF5A
0,035	1,65	3,13	313,02	P09234	U1 small nuclear ribonucleoprotein C	SNRPC
0,001	1,64	3,11	311,40	P49756	RNA-binding protein 25	RBM25
0,021	1,64	3,11	311,13	Q9NPE3	H/ACA ribonucleoprotein complex subunit 3	NOP10
0,011	1,63	3,11	310,58	Q92820	Gamma-glutamyl hydrolase	GGH
0,045	1,63	3,09	309,14	Q14683	Structural maintenance of chromosomes protein 1A	SMC1A
0,018	1,62	3,07	307,38	Q9BVQ7	Spermatogenesis-associated protein 5-like protein 1	SPATA5L1
0,012	1,59	3,00	300,39	Q9Y570	Protein phosphatase methylesterase 1	PPME1
0,022	1,58	3,00	299,96	Q8IX12	Cell division cycle and apoptosis regulator protein 1	CCAR1
0,028	1,58	2,99	299,29	Q9NZJ6	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	COQ3
0,041	1,56	2,94	293,88	Q5ZPR3	CD276 antigen	CD276
0,028	1,55	2,93	292,82	Q9Y5Z9	UbiA prenyltransferase domain-containing protein 1	UBIAD1
0,002	1,54	2,91	291,03	Q96LD4	Tripartite motif-containing protein 47	TRIM47
0,000	1,52	2,87	287,17	Q9NVR2	Integrator complex subunit 10	INTS10
0,030	1,51	2,85	284,68	Q96FV9	THO complex subunit 1	THOC1
0,041	1,50	2,83	282,84	Q7Z460	CLIP-associating protein 1	CLASP1
0,034	1,50	2,82	282,16	Q9H2W6	39S ribosomal protein L46, mitochondrial	MRPL46
0,015	1,49	2,81	280,89	Q8N442	Translation factor GUF1, mitochondrial	GUF1
0,040	1,48	2,79	279,21	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA
0,039	1,48	2,79	278,95	P21926	CD9 antigen	CD9
0,021	1,48	2,78	278,42	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	ACADSB
0,041	1,47	2,77	277,02	Q15382	Branched-chain-amino-acid aminotransferase, mitochondrial	BCAT2
0,027	1,46	2,75	275,31	Q9BRA0	N-alpha-acetyltransferase 38, NatC auxiliary subunit	NAA38
0,039	1,46	2,75	275,11	P22307	Non-specific lipid-transfer protein	SCP2
0,009	1,46	2,75	275,11	P30622	CAP-Gly domain-containing linker protein 1	CLIP1
0,004	1,46	2,75	274,62	Q9H2J4	Phosducin-like protein 3	PDCL3
0,005	1,46	2,74	274,50	Q8TE58	A disintegrin and metalloproteinase with thrombospondin motifs 15	ADAMTS15
0,043	1,45	2,74	274,01	Q96PV6	Leukocyte receptor cluster member 8	LENG8
0,003	1,45	2,73	273,46	Q96KR1	Zinc finger RNA-binding protein	ZFR
0,012	1,45	2,73	273,21	Q9UGI8	Testin	TES
0,011	1,44	2,72	271,86	Q15014	Mortality factor 4-like protein 2	MORF4L2
0,013	1,44	2,71	270,61	P53582	Methionine aminopeptidase 1	METAP1

Supplemental Table S2b

0,002	1,43	2,70	269,99	Q9BY77	Polymerase delta-interacting protein 3	POLDIP3
0,027	1,43	2,69	269,45	P54619	5-AMP-activated protein kinase subunit gamma-1	PRKAG1
0,033	1,43	2,69	269,45	Q9NYK5	39S ribosomal protein L39, mitochondrial	MRPL39
0,017	1,42	2,68	267,59	Q9C0D5	Protein TANC1	TANC1
0,001	1,42	2,67	267,01	Q9UNX4	WD repeat-containing protein 3	WDR3
0,024	1,40	2,64	263,82	P14866	Heterogeneous nuclear ribonucleoprotein L	HNRNPL
0,024	1,40	2,63	263,24	Q8N983	39S ribosomal protein L43, mitochondrial	MRPL43
0,025	1,38	2,60	260,20	P48553	Trafficking protein particle complex subunit 10	TRAPPC10
0,015	1,38	2,60	260,15	P55265	Double-stranded RNA-specific adenosine deaminase	ADAR
0,043	1,37	2,58	258,47	O95171	Sciellin	SCEL
0,001	1,37	2,58	257,99	Q99459	Cell division cycle 5-like protein	CDC5L
0,044	1,35	2,55	255,11	Q14BN4	Sarcolemmal membrane-associated protein	SLMAP
0,043	1,35	2,55	255,05	Q8TEM1	Nuclear pore membrane glycoprotein 210	NUP210
0,004	1,35	2,55	254,96	Q8WXF1	Paraspeckle component 1	PSPC1
0,008	1,35	2,55	254,91	O00401	Neural Wiskott-Aldrich syndrome protein	WASL
0,024	1,34	2,53	253,15	P29279	Connective tissue growth factor	CTGF
0,006	1,33	2,51	250,76	Q13627;Q9Y463	Dual specificity tyrosine-phosphorylation-regulated kinase 1A;Dual specificity tyrosi	DYRK1A;DYRK1B
0,021	1,32	2,50	250,40	P12270	Nucleoprotein TPR	TPR
0,002	1,32	2,50	250,37	Q9H0B6	Kinesin light chain 2	KLC2
0,007	1,32	2,50	249,67	Q4VC44	FLYWCH-type zinc finger-containing protein 1	FLYWCH1
0,003	1,30	2,46	246,23	P17275	Transcription factor jun-B	JUNB
0,049	1,30	2,46	246,23	Q9Y244	Proteasome maturation protein	POMP
0,003	1,30	2,46	245,50	P51149	Ras-related protein Rab-7a	RAB7A
0,026	1,29	2,45	244,84	Q15233	Non-POU domain-containing octamer-binding protein	NONO
0,002	1,29	2,45	244,53	Q03468	DNA excision repair protein ERCC-6	ERCC6
0,024	1,28	2,42	242,21	Q96T76	MMS19 nucleotide excision repair protein homolog	MMS19
0,017	1,27	2,42	241,75	Q9BX40	Protein LSM14 homolog B	LSM14B
0,043	1,27	2,41	240,74	Q9Y3C4	EKC/KEOPS complex subunit TPRKB	TPRKB
0,037	1,26	2,40	240,08	Q00169	Phosphatidylinositol transfer protein alpha isoform	PITPNA
0,011	1,25	2,38	238,43	Q9UIC8	Leucine carboxyl methyltransferase 1	LCMT1
0,020	1,24	2,36	236,43	P20700	Lamin-B1	LMNB1
0,035	1,24	2,36	236,20	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring	ALDH3A1
0,044	1,23	2,35	234,57	O60610	Protein diaphanous homolog 1	DIAPH1

Supplemental Table S2b

0,020	1,23	2,34	234,40	Q9NQW6	Actin-binding protein anillin	ANLN
0,031	1,23	2,34	234,03	P49354	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	FNTA
0,045	1,22	2,33	233,04	P15170;Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;Eukaryotic pepti	GSPT1;GSPT2
0,048	1,22	2,33	232,55	Q15397	Pumilio domain-containing protein KIAA0020	KIAA0020
0,000	1,22	2,32	232,35	P14406	Cytochrome c oxidase subunit 7A2, mitochondrial	COX7A2
0,030	1,21	2,32	231,78	P46100	Transcriptional regulator ATRX	ATRX
0,040	1,21	2,31	231,31	A6NKD9	Coiled-coil domain-containing protein 85C	CCDC85C
0,047	1,20	2,30	229,68	P11137	Microtubule-associated protein 2	MAP2
0,047	1,20	2,29	229,47	P51610	Host cell factor 1;HCF N-terminal chain 1;HCF N-terminal chain 2;HCF N-terminal cha	HCFC1
0,034	1,19	2,29	228,93	P52732	Kinesin-like protein KIF11	KIF11
0,015	1,19	2,28	228,15	Q15785	Mitochondrial import receptor subunit TOM34	TOMM34
0,003	1,19	2,28	227,85	P01130	Low-density lipoprotein receptor	LDLR
0,024	1,18	2,27	226,58	P48735	Isocitrate dehydrogenase [NADP], mitochondrial	IDH2
0,023	1,18	2,27	226,58	P09429	High mobility group protein B1	HMGB1
0,006	1,16	2,23	223,43	O75663	TIP41-like protein	TIPRL
0,005	1,15	2,22	222,09	Q8N556	Actin filament-associated protein 1	AFAP1
0,015	1,15	2,22	221,91	Q7Z2Z2	Elongation factor Tu GTP-binding domain-containing protein 1	EFTUD1
0,048	1,15	2,22	221,52	Q15459	Splicing factor 3A subunit 1	SF3A1
0,009	1,15	2,21	221,36	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	SNRNP200
0,035	1,14	2,21	220,76	O00567	Nucleolar protein 56	NOP56
0,012	1,14	2,21	220,63	Q01105;P0DMEO	Protein SET;Protein SETSIP	SET;SETSIP
0,035	1,14	2,20	220,43	Q96EY4	Translation machinery-associated protein 16	TMA16
0,003	1,14	2,20	219,87	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfami	SMARCE1
0,003	1,13	2,19	219,29	P49916	DNA ligase 3	LIG3
0,037	1,13	2,19	219,28	P32321	Deoxycytidylate deaminase	DCTD
0,044	1,13	2,19	219,19	Q92466	DNA damage-binding protein 2	DDB2
0,027	1,13	2,19	219,09	Q8WUX9	Charged multivesicular body protein 7	CHMP7
0,031	1,12	2,17	217,35	P26583	High mobility group protein B2	HMGB2
0,023	1,11	2,16	216,32	Q03701	CCAAT/enhancer-binding protein zeta	CEBPZ
0,004	1,11	2,16	215,85	Q04206	Transcription factor p65	RELA
0,032	1,10	2,14	214,16	O94864	STAGA complex 65 subunit gamma	SUPT7L
0,001	1,10	2,14	214,04	P04637	Cellular tumor antigen p53	TP53
0,033	1,09	2,12	212,30	O75150	E3 ubiquitin-protein ligase BRE1B	RNF40

Supplemental Table S2b

0,009	1,08	2,11	211,02	Q15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	INPPL1
0,001	1,08	2,11	210,70	O60341	Lysine-specific histone demethylase 1A	KDM1A
0,020	1,07	2,10	209,94	O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	NDUFA7
0,004	1,07	2,09	209,49	Q92609	TBC1 domain family member 5	TBC1D5
0,028	1,05	2,07	207,23	Q13506	NGFI-A-binding protein 1	NAB1
0,035	1,05	2,07	207,05	Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUFA11
0,023	1,04	2,06	206,07	Q9Y2X3	Nucleolar protein 58	NOP58
0,028	1,04	2,06	205,68	O75674	TOM1-like protein 1	TOM1L1
0,011	1,03	2,05	204,79	Q86X55	Histone-arginine methyltransferase CARM1	CARM1
0,025	1,03	2,05	204,58	Q9BPX3	Condensin complex subunit 3	NCAPG
0,011	1,03	2,04	203,79	O76071	Probable cytosolic iron-sulfur protein assembly protein CIAO1	CIAO1
0,007	1,02	2,03	203,49	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK
0,031	1,02	2,03	202,79	Q92615	La-related protein 4B	LARP4B
0,010	1,02	2,03	202,79	Q9NW82	WD repeat-containing protein 70	WDR70
0,037	1,01	2,02	202,02	Q6GMV3	Putative peptidyl-tRNA hydrolase PTRHD1	PTRHD1
0,001	0,99	1,99	198,88	P35658	Nuclear pore complex protein Nup214	NUP214
0,025	0,99	1,99	198,69	Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23	PTPN23
0,045	0,99	1,99	198,62	P26006	Integrin alpha-3;Integrin alpha-3 heavy chain;Integrin alpha-3 light chain	ITGA3
0,024	0,98	1,97	197,25	Q9Y3Y2	Chromatin target of PRMT1 protein	CHTOP
0,038	0,98	1,97	197,12	P31949	Protein S100-A11;Protein S100-A11, N-terminally processed	S100A11
0,035	0,98	1,97	196,70	Q9BW27	Nuclear pore complex protein Nup85	NUP85
0,007	0,97	1,96	196,46	Q9NUB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	ACSS1
0,008	0,97	1,96	196,21	P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC
0,012	0,97	1,96	195,87	Q96BZ8	Leukocyte receptor cluster member 1	LENG1
0,001	0,97	1,96	195,74	Q9Y5X1	Sorting nexin-9	SNX9
0,030	0,97	1,96	195,73	Q9UKN8	General transcription factor 3C polypeptide 4	GTF3C4
0,008	0,97	1,95	195,26	Q16890	Tumor protein D53	TPD52L1
0,032	0,96	1,95	195,10	Q9H098	Protein FAM107B	FAM107B
0,024	0,96	1,94	194,47	Q9NVH0	Exonuclease 3-5 domain-containing protein 2	EXD2
0,038	0,95	1,93	193,19	P61009	Signal peptidase complex subunit 3	SPCS3
0,007	0,95	1,93	192,97	Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C	ILKAP
0,029	0,95	1,93	192,84	Q9HAV7	GrpE protein homolog 1, mitochondrial	GRPEL1
0,009	0,93	1,91	190,64	Q6PJT7	Zinc finger CCCH domain-containing protein 14	ZC3H14

Supplemental Table S2b

0,007	0,92	1,89	189,21	Q9BY42	Protein RTF2 homolog	RTFDC1
0,022	0,92	1,89	188,94	O75494	Serine/arginine-rich splicing factor 10	SRSF10
0,014	0,92	1,89	188,56	O95602	DNA-directed RNA polymerase I subunit RPA1	POLR1A
0,003	0,90	1,87	186,61	P25205	DNA replication licensing factor MCM3	MCM3
0,043	0,90	1,87	186,61	P32929	Cystathionine gamma-lyase	CTH
0,021	0,90	1,86	186,46	Q9NR12	PDZ and LIM domain protein 7	PDLIM7
0,045	0,89	1,86	185,74	Q96L92	Sorting nexin-27	SNX27
0,023	0,89	1,85	185,21	O15231	Zinc finger protein 185	ZNF185
0,023	0,89	1,85	184,82	O43291	Kunitz-type protease inhibitor 2	SPINT2
0,008	0,88	1,84	184,36	Q96MW1	Coiled-coil domain-containing protein 43	CCDC43
0,039	0,88	1,84	183,99	Q12874	Splicing factor 3A subunit 3	SF3A3
0,007	0,88	1,84	183,86	Q9Y224	UPF0568 protein C14orf166	C14orf166
0,023	0,87	1,83	183,38	Q92575	UBX domain-containing protein 4	UBXN4
0,043	0,86	1,82	181,69	Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9
0,026	0,86	1,81	181,42	Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46
0,000	0,86	1,81	181,29	P52789	Hexokinase-2	HK2
0,024	0,85	1,80	179,91	Q5VZE5	N-alpha-acetyltransferase 35, NatC auxiliary subunit	NAA35
0,032	0,84	1,79	179,50	Q13509	Tubulin beta-3 chain	TUBB3
0,039	0,84	1,79	179,17	Q96RU3	Formin-binding protein 1	FNBP1
0,014	0,84	1,79	179,01	P40938	Replication factor C subunit 3	RFC3
0,001	0,84	1,78	178,47	Q9H553	Alpha-1,3/1,6-mannosyltransferase ALG2	ALG2
0,050	0,83	1,78	177,80	Q9UQ35	Serine/arginine repetitive matrix protein 2	SRRM2
0,025	0,82	1,77	177,12	P52272	Heterogeneous nuclear ribonucleoprotein M	HNRNPM
0,014	0,82	1,76	176,13	Q8IWW6	Rho GTPase-activating protein 12	ARHGAP12
0,023	0,81	1,76	175,62	Q9H7Z7	Prostaglandin E synthase 2;Prostaglandin E synthase 2 truncated form	PTGES2
0,021	0,81	1,75	175,35	Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A
0,020	0,81	1,75	175,32	Q9BTE7	DCN1-like protein 5	DCUN1D5
0,592	0,81	1,75	175,07	O00767	Acyl-CoA desaturase	SCD
0,020	0,81	1,75	175,03	P38159	RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosor	RBMX
0,011	0,81	1,75	174,88	O95470	Sphingosine-1-phosphate lyase 1	SGPL1
0,002	0,80	1,75	174,67	Q8NI27	THO complex subunit 2	THOC2
0,018	0,80	1,74	174,11	Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1
0,002	0,80	1,74	173,85	Q06203	Amidophosphoribosyltransferase	PPAT

Supplemental Table S2b

0,022	0,79	1,73	173,10	P30740	Leukocyte elastase inhibitor	SERPINB1
0,028	0,78	1,72	172,29	O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3
0,018	0,78	1,72	171,81	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL
0,010	0,78	1,72	171,71	Q13561	Dynactin subunit 2	DCTN2
0,035	0,78	1,71	171,49	O15020	Spectrin beta chain, non-erythrocytic 2	SPTBN2
0,016	0,78	1,71	171,31	Q96A49	Synapse-associated protein 1	SYAP1
0,025	0,78	1,71	171,20	P63010	AP-2 complex subunit beta	AP2B1
0,022	0,77	1,71	170,55	P05783	Keratin, type I cytoskeletal 18	KRT18
0,002	0,77	1,70	170,12	Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4
0,038	0,77	1,70	170,00	Q9H967	WD repeat-containing protein 76	WDR76
0,043	0,76	1,69	169,24	P55196	Afadin	MLLT4
0,026	0,76	1,69	169,18	Q12996	Cleavage stimulation factor subunit 3	CSTF3
0,043	0,74	1,67	167,02	Q9NS86	LanC-like protein 2	LANCL2
0,006	0,74	1,67	167,02	P33991	DNA replication licensing factor MCM4	MCM4
0,024	0,74	1,67	167,02	Q04323	UBX domain-containing protein 1	UBXN1
0,049	0,73	1,66	166,25	Q9UIJ7	GTP:AMP phosphotransferase AK3, mitochondrial	AK3
0,010	0,73	1,66	166,08	Q99536	Synaptic vesicle membrane protein VAT-1 homolog	VAT1
0,013	0,73	1,66	165,97	Q05682	Caldesmon	CALD1
0,007	0,73	1,65	165,34	Q9Y3A5	Ribosome maturation protein SBDS	SBDS
0,018	0,72	1,65	164,68	Q147X3	N-alpha-acetyltransferase 30	NAA30
0,022	0,72	1,64	164,40	P36915	Guanine nucleotide-binding protein-like 1	GNL1
0,005	0,71	1,64	163,72	Q15042	Rab3 GTPase-activating protein catalytic subunit	RAB3GAP1
0,032	0,70	1,63	162,51	P35270	Sepiapterin reductase	SPR
0,010	0,70	1,62	162,27	P43243	Matrin-3	MATR3
0,029	0,70	1,62	162,07	Q9UBQ0	Vacuolar protein sorting-associated protein 29	VPS29
0,011	0,69	1,62	161,78	P49757	Protein numb homolog	NUMB
0,022	0,68	1,60	160,39	P29218	Inositol monophosphatase 1	IMPA1
0,038	0,68	1,60	160,21	P51812	Ribosomal protein S6 kinase alpha-3	RPS6KA3
0,010	0,68	1,60	159,93	O00442	RNA 3-terminal phosphate cyclase	RTCA
0,007	0,67	1,59	158,91	O00330	Pyruvate dehydrogenase protein X component, mitochondrial	PDHX
0,048	0,67	1,59	158,57	Q9BRT3	Migration and invasion enhancer 1	MIEN1
0,012	0,66	1,58	158,47	Q14980	Nuclear mitotic apparatus protein 1	NUMA1
0,014	0,66	1,58	158,13	P00441	Superoxide dismutase [Cu-Zn]	SOD1

Supplemental Table S2b

0,001	0,66	1,58	158,01	Q14566	DNA replication licensing factor MCM6	MCM6
0,000	0,66	1,58	157,77	P29317	Ephrin type-A receptor 2	EPHA2
0,005	0,66	1,58	157,61	O15031	Plexin-B2	PLXNB2
0,009	0,66	1,58	157,59	P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1
0,045	0,65	1,57	156,92	Q9BS26	Endoplasmic reticulum resident protein 44	ERP44
0,003	0,65	1,57	156,69	Q01813	ATP-dependent 6-phosphofructokinase, platelet type	PFKP
0,029	0,64	1,56	155,83	Q9H1B7	Interferon regulatory factor 2-binding protein-like	IRF2BPL
0,048	0,64	1,56	155,83	Q99627	COP9 signalosome complex subunit 8	COPS8
0,004	0,63	1,55	154,95	Q9BRX2	Protein pelota homolog	PELO
0,003	0,63	1,55	154,72	P50452	Serpin B8	SERPINB8
0,037	0,63	1,54	154,29	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4	LSM4
0,033	0,62	1,54	153,69	Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK
0,005	0,62	1,53	153,48	P82979	SAP domain-containing ribonucleoprotein	SARNP
0,045	0,61	1,53	153,12	O95817	BAG family molecular chaperone regulator 3	BAG3
0,025	0,61	1,53	152,68	Q9Y6Q5	AP-1 complex subunit mu-2	AP1M2
0,029	0,61	1,53	152,60	Q96AT9	Ribulose-phosphate 3-epimerase	RPE
0,003	0,61	1,52	152,16	Q13136	Liprin-alpha-1	PPFIA1
0,007	0,59	1,51	150,52	P49736	DNA replication licensing factor MCM2	MCM2
0,036	0,59	1,50	150,41	Q6FI81	Anamorsin	CIAPIN1
0,039	0,58	1,50	149,72	Q9NW64	Pre-mRNA-splicing factor RBM22	RBM22
0,027	0,58	1,49	149,48	Q8WZA0	Protein LZIC	LZIC
0,021	0,58	1,49	149,48	Q9BT78	COP9 signalosome complex subunit 4	COPS4
0,047	0,58	1,49	149,37	Q9NQR4	Omega-amidase NIT2	NIT2
0,035	0,58	1,49	149,24	P24821	Tenascin	TNC
0,038	0,57	1,49	148,79	P22033	Methylmalonyl-CoA mutase, mitochondrial	MUT
0,047	0,57	1,49	148,59	Q9P000	COMM domain-containing protein 9	COMMD9
0,046	0,56	1,48	147,80	P41229	Lysine-specific demethylase 5C	KDM5C
0,039	0,56	1,47	147,43	Q7Z3J2	UPF0505 protein C16orf62	C16orf62
0,042	0,56	1,47	147,35	O95163	Elongator complex protein 1	IKBKAP
0,004	0,56	1,47	147,00	Q7Z2E3	Aprataxin	APTX
0,010	0,55	1,47	146,71	Q9ULV0	Unconventional myosin-Vb	MYO5B
0,022	0,55	1,46	146,49	Q9Y6C9	Mitochondrial carrier homolog 2	MTCH2
0,023	0,55	1,46	146,41	Q8IY18	Structural maintenance of chromosomes protein 5	SMC5

Supplemental Table S2b

0,018	0,55	1,46	146,13	Q08211	ATP-dependent RNA helicase A	DHX9
0,020	0,54	1,46	145,74	P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	GPD2
0,008	0,54	1,46	145,54	P18065	Insulin-like growth factor-binding protein 2	IGFBP2
0,034	0,54	1,45	145,46	O15126	Secretory carrier-associated membrane protein 1	SCAMP1
0,021	0,54	1,45	145,40	Q14847	LIM and SH3 domain protein 1	LASP1
0,009	0,54	1,45	145,40	P33993	DNA replication licensing factor MCM7	MCM7
0,000	0,54	1,45	145,08	P52306	Rap1 GTPase-GDP dissociation stimulator 1	RAP1GDS1
0,011	0,53	1,44	144,07	Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1
0,030	0,53	1,44	144,02	Q9H8S9	MOB kinase activator 1A	MOB1A
0,020	0,52	1,44	143,63	P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2
0,004	0,52	1,43	143,40	P28066	Proteasome subunit alpha type-5	PSMA5
0,023	0,51	1,43	142,68	Q99426	Tubulin-folding cofactor B	TBCB
0,023	0,51	1,43	142,61	P02545	Prelamin-A/C;Lamin-A/C	LMNA
0,019	0,51	1,42	142,41	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	HSD17B10
0,000	0,51	1,42	142,41	P40818	Ubiquitin carboxyl-terminal hydrolase 8	USP8
0,031	0,51	1,42	142,41	P17535	Transcription factor jun-D	JUND
0,006	0,49	1,41	140,66	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial	UQCRRH
0,043	0,48	1,40	139,91	P39060	Collagen alpha-1(XVIII) chain;Endostatin	COL18A1
0,048	0,48	1,40	139,54	Q16658	Fascin	FSCN1
0,014	0,48	1,39	139,43	P17844	Probable ATP-dependent RNA helicase DDX5	DDX5
0,007	0,48	1,39	139,39	P20674	Cytochrome c oxidase subunit 5A, mitochondrial	COX5A
0,030	0,48	1,39	139,29	Q9P0J1	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	PDP1
0,020	0,48	1,39	139,13	Q5TA45	Integrator complex subunit 11	CPSF3L
0,025	0,47	1,39	138,93	P20585	DNA mismatch repair protein Msh3	MSH3
0,037	0,47	1,39	138,77	Q13363	C-terminal-binding protein 1	CTBP1
0,019	0,46	1,37	137,38	P33240	Cleavage stimulation factor subunit 2	CSTF2
0,038	0,45	1,37	136,60	Q02833	Ras association domain-containing protein 7	RASSF7
0,047	0,45	1,36	136,30	O43795	Unconventional myosin-Ib	MYO1B
0,021	0,44	1,36	136,06	P49711	Transcriptional repressor CTCF	CTCF
0,020	0,44	1,36	135,95	Q6NXS1;P41236	Protein phosphatase inhibitor 2-like protein 3;Protein phosphatase inhibitor 2	PPP1R2P3;PPP1R2
0,045	0,44	1,36	135,66	O75531	Barrier-to-autointegration factor;Barrier-to-autointegration factor, N-terminally pro	BANF1
0,037	0,44	1,36	135,63	Q9UKL0	REST corepressor 1	RCOR1
0,003	0,43	1,35	134,84	Q9H7E9	UPF0488 protein C8orf33	C8orf33

Supplemental Table S2b

0,000	0,43	1,35	134,72	Q15554	Telomeric repeat-binding factor 2	TERF2
0,002	0,43	1,34	134,35	P38919	Eukaryotic initiation factor 4A-III;Eukaryotic initiation factor 4A-III, N-terminally pro	EIF4A3
0,011	0,42	1,34	133,79	P34897	Serine hydroxymethyltransferase, mitochondrial	SHMT2
0,041	0,42	1,34	133,79	Q9UNZ2	NSFL1 cofactor p47	NSFL1C
0,027	0,42	1,34	133,54	Q9BUR5	Apolipoprotein O	APOO
0,046	0,41	1,33	133,18	Q9NUQ7	Ufm1-specific protease 2	UFSP2
0,014	0,41	1,33	133,10	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7
0,041	0,41	1,33	132,77	P06733	Alpha-enolase	ENO1
0,046	0,41	1,33	132,60	Q15424	Scaffold attachment factor B1	SAFB
0,014	0,40	1,32	132,35	O43447	Peptidyl-prolyl cis-trans isomerase H	PPIH
0,008	0,40	1,32	131,91	Q8TDP1	Ribonuclease H2 subunit C	RNASEH2C
0,027	0,40	1,32	131,79	Q9Y2W2	WW domain-binding protein 11	WBP11
0,029	0,39	1,31	131,12	O43719	HIV Tat-specific factor 1	HTATSF1
0,009	0,39	1,31	130,76	P52758	Ribonuclease UK114	HRSP12
0,045	0,38	1,30	130,41	Q9UBI6	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	GNG12
0,033	0,38	1,30	130,30	Q15061	WD repeat-containing protein 43	WDR43
0,037	0,38	1,30	130,12	Q9NRX1	RNA-binding protein PNO1	PNO1
0,047	0,38	1,30	129,86	Q92696	Geranylgeranyl transferase type-2 subunit alpha	RABGGTA
0,010	0,37	1,29	129,36	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2
0,017	0,37	1,29	129,32	Q9UI12	V-type proton ATPase subunit H	ATP6V1H
0,035	0,37	1,29	129,28	P19474	E3 ubiquitin-protein ligase TRIM21	TRIM21
0,007	0,37	1,29	129,24	P55072	Transitional endoplasmic reticulum ATPase	VCP
0,005	0,37	1,29	129,12	Q86W92	Liprin-beta-1	PPFIBP1
0,015	0,37	1,29	129,06	Q86X76	Nitrilase homolog 1	NIT1
0,044	0,36	1,29	128,77	Q8WX93	Palladin	PALLD
0,049	0,36	1,28	128,16	P07902	Galactose-1-phosphate uridylyltransferase	GALT
0,031	0,36	1,28	128,13	Q7Z2W4	Zinc finger CCCH-type antiviral protein 1	ZC3HAV1
0,048	0,36	1,28	127,91	Q15149	Plectin	PLEC
0,016	0,35	1,28	127,81	P08865	40S ribosomal protein SA	RPSA
0,038	0,35	1,27	127,30	P29144	Tripeptidyl-peptidase 2	TPP2
0,029	0,34	1,27	127,01	Q9H3U1	Protein unc-45 homolog A	UNC45A
0,001	0,34	1,27	126,76	P08195	4F2 cell-surface antigen heavy chain	SLC3A2
0,047	0,34	1,26	126,33	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13

Supplemental Table S2b

0,008	0,34	1,26	126,26	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	PIN4
0,022	0,34	1,26	126,24	Q15427	Splicing factor 3B subunit 4	SF3B4
0,017	0,33	1,26	125,59	P46379	Large proline-rich protein BAG6	BAG6
0,042	0,33	1,25	125,46	P04181	Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form	OAT
0,030	0,32	1,25	125,05	Q9Y617	Phosphoserine aminotransferase	PSAT1
0,009	0,32	1,25	124,66	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2
0,029	0,32	1,24	124,46	Q9NP92	28S ribosomal protein S30, mitochondrial	MRPS30
0,001	0,31	1,24	124,40	P20810	Calpastatin	CAST
0,000	0,31	1,24	124,31	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	CAND1
0,024	0,31	1,24	124,16	P62269	40S ribosomal protein S18	RPS18
0,031	0,31	1,24	124,07	Q9C0C2	182 kDa tankyrase-1-binding protein	TNKS1BP1
0,038	0,31	1,24	124,00	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	ANP32A
0,005	0,31	1,24	123,97	P35998	26S protease regulatory subunit 7	PSMC2
0,031	0,31	1,24	123,94	Q13838	Spliceosome RNA helicase DDX39B	DDX39B
0,030	0,30	1,23	123,25	Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1
0,006	0,30	1,23	122,80	P23396	40S ribosomal protein S3	RPS3
0,045	0,29	1,23	122,53	P60174	Triosephosphate isomerase	TPI1
0,015	0,29	1,22	122,45	Q9NX63	MICOS complex subunit MIC19	CHCHD3
0,026	0,29	1,22	122,26	P24752	Acetyl-CoA acetyltransferase, mitochondrial	ACAT1
0,018	0,29	1,22	122,26	Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3	IMP3
0,012	0,29	1,22	122,26	Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5
0,045	0,29	1,22	122,19	P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	GNB1
0,001	0,28	1,22	121,79	Q7Z4L5	Tetratricopeptide repeat protein 21B	TTC21B
0,010	0,28	1,22	121,79	P32119	Peroxiredoxin-2	PRDX2
0,039	0,28	1,22	121,66	P40926	Malate dehydrogenase, mitochondrial	MDH2
0,017	0,28	1,21	121,11	Q9NP81	Serine--tRNA ligase, mitochondrial	SARS2
0,010	0,27	1,21	120,86	P54577	Tyrosine--tRNA ligase, cytoplasmic;Tyrosine--tRNA ligase, cytoplasmic, N-terminally	YARS
0,022	0,27	1,21	120,62	P16278	Beta-galactosidase	GLB1
0,038	0,27	1,21	120,58	Q8N163	Cell cycle and apoptosis regulator protein 2	CCAR2
0,048	0,27	1,21	120,58	P34932	Heat shock 70 kDa protein 4	HSPA4
0,050	0,27	1,21	120,58	P62195	26S protease regulatory subunit 8	PSMC5
0,041	0,27	1,20	120,45	Q9H3P7	Golgi resident protein GCP60	ACBD3
0,014	0,26	1,20	120,04	P00505	Aspartate aminotransferase, mitochondrial	GOT2

Supplemental Table S2b

0,011	0,26	1,20	119,89	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35
0,027	0,26	1,20	119,84	P12081	Histidine--tRNA ligase, cytoplasmic	HARS
0,024	0,26	1,20	119,75	Q9P258	Protein RCC2	RCC2
0,006	0,26	1,20	119,57	O95373	Importin-7	IPO7
0,048	0,25	1,19	118,93	P69849;Q5JPE7;Q15155	Nodal modulator 3;Nodal modulator 2;Nodal modulator 1	MO3;NOMO2;NOM
0,042	0,25	1,19	118,92	O95391	Pre-mRNA-splicing factor SLU7	SLU7
0,021	0,25	1,19	118,92	P18085	ADP-ribosylation factor 4	ARF4
0,006	0,25	1,19	118,55	Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2
0,007	0,24	1,18	118,13	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2
0,017	0,24	1,18	117,96	Q92973	Transportin-1	TNPO1
0,012	0,23	1,17	117,28	Q15717	ELAV-like protein 1	ELAVL1
0,050	0,22	1,16	116,47	O14818	Proteasome subunit alpha type-7	PSMA7
0,039	0,22	1,16	116,43	P63167	Dynein light chain 1, cytoplasmic	DYNLL1
0,007	0,22	1,16	116,34	P62241	40S ribosomal protein S8	RPS8
0,045	0,21	1,15	115,42	P16949	Stathmin	STMN1
0,024	0,21	1,15	115,36	Q14258	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25
0,041	0,20	1,15	114,87	Q8WUF8	Protein FAM172A	FAM172A
0,013	0,19	1,14	114,19	Q6P1N0	Coiled-coil and C2 domain-containing protein 1A	CC2D1A
0,001	0,19	1,14	114,09	P05455	Lupus La protein	SSB
0,030	0,17	1,12	112,37	Q13131	5-AMP-activated protein kinase catalytic subunit alpha-1	PRKAA1
0,033	0,16	1,12	111,73	Q15020	Squamous cell carcinoma antigen recognized by T-cells 3	SART3
0,031	0,15	1,11	110,67	O76094	Signal recognition particle subunit SRP72	SRP72
24h Up						
0,011	6,44	86,82	8682,27	Q8N3F8	MICAL-like protein 1	MICALL1
0,043	5,94	61,39	6139,29	Q8IYS1	Peptidase M20 domain-containing protein 2	PM20D2
0,013	4,60	24,26	2426,07	P61769	Beta-2-microglobulin;Beta-2-microglobulin form pl 5.3	B2M
0,001	4,35	20,39	2039,30	Q92466	DNA damage-binding protein 2	DDB2
0,006	4,06	16,68	1667,95	O43237	Cytoplasmic dynein 1 light intermediate chain 2	DYNC1L12
0,007	3,99	15,89	1588,95	Q9BYC8	39S ribosomal protein L32, mitochondrial	MRPL32
0,006	3,89	14,80	1480,03	P05090	Apolipoprotein D	APOD
0,009	3,78	13,74	1373,70	Q9HC36	RNA methyltransferase-like protein 1	RNMTL1
0,041	3,70	13,00	1299,60	O60678	Protein arginine N-methyltransferase 3	PRMT3

Supplemental Table S2b

0,030	3,61	12,21	1221,01	Q9Y484	WD repeat domain phosphoinositide-interacting protein 4	WDR45
0,002	3,49	11,24	1123,56	Q9BU02	Thiamine-triphosphatase	THTPA
0,000	3,37	10,34	1033,88	Q8IXM3	39S ribosomal protein L41, mitochondrial	MRPL41
0,004	3,36	10,27	1026,74	Q8N983	39S ribosomal protein L43, mitochondrial	MRPL43
0,003	3,31	9,92	991,77	Q99569	Plakophilin-4	PKP4
0,037	3,23	9,38	938,27	Q9H019	Mitochondrial fission regulator 1-like	MTFR1L
0,000	3,15	8,88	887,66	Q8TAE8	Growth arrest and DNA damage-inducible proteins-interacting protein 1	GADD45GIP1
0,020	3,11	8,66	866,08	Q9Y483	Metal-response element-binding transcription factor 2	MTF2
0,033	3,01	8,07	807,05	P40261	Nicotinamide N-methyltransferase	NNMT
0,008	2,98	7,91	791,17	Q86UE8	Serine/threonine-protein kinase tousled-like 2	TLK2
0,011	2,94	7,67	767,41	O60762	Dolichol-phosphate mannosyltransferase subunit 1	DPM1
0,021	2,89	7,41	741,27	P11086	Phenylethanolamine N-methyltransferase	PNMT
0,046	2,85	7,23	722,72	P16403	Histone H1.2	HIST1H1C
0,033	2,82	7,06	706,13	Q96EK6	Glucosamine 6-phosphate N-acetyltransferase	GNPNAT1
0,037	2,79	6,92	691,63	P49406	39S ribosomal protein L19, mitochondrial	MRPL19
0,000	2,76	6,78	677,83	Q9Y2S6	Translation machinery-associated protein 7	TMA7
0,021	2,76	6,77	677,40	Q9H0U6	39S ribosomal protein L18, mitochondrial	MRPL18
0,023	2,72	6,57	656,59	Q01831	DNA repair protein complementing XP-C cells	XPC
0,000	2,71	6,54	654,32	Q96GC5	39S ribosomal protein L48, mitochondrial	MRPL48
0,043	2,68	6,43	642,63	O60888	Protein CutA	CUTA
0,044	2,66	6,31	630,63	Q9H3L0	Methylmalonic aciduria and homocystinuria type D protein, mitochondrial	MMADHC
0,000	2,62	6,15	614,75	Q0JRZ9	FCH domain only protein 2	FCHO2
0,021	2,61	6,11	610,50	Q9ULX9	Transcription factor MafF	MAFF
0,000	2,60	6,05	604,54	Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1
0,021	2,54	5,82	581,59	Q9UNE7	E3 ubiquitin-protein ligase CHIP	STUB1
0,028	2,53	5,78	577,57	Q9P032	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	NDUFAF4
0,003	2,52	5,74	573,58	Q9P015	39S ribosomal protein L15, mitochondrial	MRPL15
0,027	2,49	5,62	561,78	Q9NQ50	39S ribosomal protein L40, mitochondrial	MRPL40
0,001	2,47	5,52	552,15	Q3ZCW2	Galectin-related protein	LGALS1
0,038	2,46	5,52	551,97	Q15363	Transmembrane emp24 domain-containing protein 2	TMED2
0,000	2,44	5,43	542,64	P49321	Nuclear autoantigenic sperm protein	NASP
0,016	2,39	5,24	524,16	Q92552	28S ribosomal protein S27, mitochondrial	MRPS27
0,010	2,38	5,21	520,50	P06400	Retinoblastoma-associated protein	RB1

Supplemental Table S2b

0,027	2,38	5,20	520,09	Q9H2F5	Enhancer of polycomb homolog 1	EPC1
0,011	2,36	5,13	513,37	Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5	FKBP5
0,031	2,36	5,13	513,37	Q9H5N1	Rab GTPase-binding effector protein 2	RABEP2
0,011	2,33	5,03	502,81	Q2TAL8	Glutamine-rich protein 1	QRICH1
0,003	2,31	4,96	495,88	Q13409	Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2
0,020	2,29	4,89	489,06	Q5T653	39S ribosomal protein L2, mitochondrial	MRPL2
0,003	2,28	4,86	485,68	Q9H974	Queuine tRNA-ribosyltransferase subunit QTRTD1	QTRTD1
0,028	2,28	4,86	485,68	Q9H3N1	Thioredoxin-related transmembrane protein 1	TMX1
0,000	2,28	4,86	485,68	Q9GZP4	PITH domain-containing protein 1	PITHD1
0,000	2,26	4,79	478,99	Q14061	Cytochrome c oxidase copper chaperone	COX17
0,024	2,25	4,77	476,55	Q8WUD4	Coiled-coil domain-containing protein 12	CCDC12
0,000	2,21	4,63	462,68	Q9BZE9	Tether containing UBX domain for GLUT4	ASPSR1
0,037	2,18	4,53	453,19	Q13825	Methylglutaconyl-CoA hydratase, mitochondrial	AUH
0,043	2,18	4,52	452,16	Q676U5	Autophagy-related protein 16-1	ATG16L1
0,002	2,14	4,41	440,67	Q96Q89	Kinesin-like protein KIF20B	KIF20B
0,010	2,13	4,38	437,72	Q96EL3	39S ribosomal protein L53, mitochondrial	MRPL53
0,019	2,12	4,35	434,69	Q3YBR2	Transforming growth factor beta regulator 1	TBRG1
0,003	2,12	4,35	434,69	P46199	Translation initiation factor IF-2, mitochondrial	MTIF2
0,048	2,11	4,32	431,69	Q96FV2	Secernin-2	SCRN2
0,018	2,06	4,17	416,99	Q96PP8	Guanylate-binding protein 5	GBP5
0,040	2,04	4,11	411,25	P08670	Vimentin	VIM
0,006	2,03	4,08	408,40	Q96G01	Protein bicaudal D homolog 1	BICD1
0,014	2,02	4,06	406,13	Q96N67	Dedicator of cytokinesis protein 7	DOCK7
0,026	2,02	4,06	405,58	O60504	Vinexin	SORBS3
0,000	2,01	4,03	402,78	P30622	CAP-Gly domain-containing linker protein 1	CLIP1
0,046	1,99	3,97	397,24	Q9BQA1	Methylosome protein 50	WDR77
0,034	1,96	3,89	389,06	P80303	Nucleobindin-2;Nesfatin-1	NUCB2
0,048	1,95	3,86	385,60	Q9H2Y7	Zinc finger protein 106	ZNF106
0,013	1,93	3,81	381,06	Q96MW1	Coiled-coil domain-containing protein 43	CCDC43
0,013	1,92	3,78	377,53	Q9P246	Stromal interaction molecule 2	STIM2
0,015	1,90	3,73	373,21	Q9H2W6	39S ribosomal protein L46, mitochondrial	MRPL46
0,030	1,89	3,71	370,64	P52735	Guanine nucleotide exchange factor VAV2	VAV2
0,005	1,87	3,66	366,46	Q9NR30	Nucleolar RNA helicase 2	DDX21

Supplemental Table S2b

0,012	1,87	3,66	365,53	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB
0,037	1,86	3,63	362,84	Q8N668	COMM domain-containing protein 1	COMMD1
0,040	1,85	3,60	359,57	P32780	General transcription factor IIH subunit 1	GTF2H1
0,006	1,83	3,55	355,20	P84098	60S ribosomal protein L19	RPL19
0,002	1,82	3,53	353,08	O75164	Lysine-specific demethylase 4A	KDM4A
0,005	1,81	3,51	350,64	Q7L2J0	7SK snRNA methylphosphate capping enzyme	MEPCE
0,036	1,81	3,51	350,64	Q8NDH3	Probable aminopeptidase NPEPL1	NPEPL1
0,007	1,80	3,48	348,22	Q9BYD1	39S ribosomal protein L13, mitochondrial	MRPL13
0,001	1,80	3,48	348,22	O75935	Dynactin subunit 3	DCTN3
0,020	1,79	3,47	346,82	P62072	Mitochondrial import inner membrane translocase subunit Tim10	TIMM10
0,034	1,79	3,47	346,66	Q9BRQ6	MICOS complex subunit MIC25	CHCHD6
0,001	1,78	3,43	343,43	Q13084	39S ribosomal protein L28, mitochondrial	MRPL28
0,001	1,74	3,34	334,04	Q5JTZ9	Alanine--tRNA ligase, mitochondrial	AARS2
0,037	1,72	3,30	329,72	P38935	DNA-binding protein SMUBP-2	IGHMBP2
0,011	1,71	3,27	326,90	P98179	Putative RNA-binding protein 3	RBM3
0,005	1,70	3,25	324,90	Q9NRV9	Heme-binding protein 1	HEBP1
0,012	1,67	3,19	319,10	Q96SY0	von Willebrand factor A domain-containing protein 9	VWA9
0,008	1,67	3,18	318,21	Q9NWU5	39S ribosomal protein L22, mitochondrial	MRPL22
0,031	1,66	3,16	316,49	Q9BVK6	Transmembrane emp24 domain-containing protein 9	TMED9
0,005	1,66	3,15	315,22	Q9H967	WD repeat-containing protein 76	WDR76
0,038	1,62	3,08	308,33	O60244	Mediator of RNA polymerase II transcription subunit 14	MED14
0,040	1,62	3,08	308,25	Q13541	Eukaryotic translation initiation factor 4E-binding protein 1	EIF4EBP1
0,006	1,62	3,07	307,38	Q9NYK5	39S ribosomal protein L39, mitochondrial	MRPL39
0,001	1,61	3,05	305,25	Q9ULA0	Aspartyl aminopeptidase	DNPEP
0,015	1,60	3,03	303,47	Q8WYP5	Protein ELYS	AHCTF1
0,001	1,60	3,03	303,14	Q93034	Cullin-5	CUL5
0,044	1,59	3,01	300,69	Q9P260	LisH domain and HEAT repeat-containing protein KIAA1468	KIAA1468
0,024	1,57	2,96	296,18	Q92766	Ras-responsive element-binding protein 1	RREB1
0,035	1,56	2,95	294,85	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	DDAH2
0,000	1,55	2,93	292,82	P34932	Heat shock 70 kDa protein 4	HSPA4
0,026	1,53	2,89	288,79	O00559	Receptor-binding cancer antigen expressed on SiSo cells	EBAG9
0,028	1,53	2,89	288,79	Q8IVH4	Methylmalonic aciduria type A protein, mitochondrial	MMAA
0,009	1,52	2,87	286,50	P20700	Lamin-B1	LMNB1

Supplemental Table S2b

0,001	1,50	2,83	282,84	Q14203	Dynactin subunit 1	DCTN1
0,000	1,49	2,81	280,89	Q13561	Dynactin subunit 2	DCTN2
0,001	1,48	2,79	278,95	P38646	Stress-70 protein, mitochondrial	HSPA9
0,046	1,47	2,77	277,02	Q96A35	39S ribosomal protein L24, mitochondrial	MRPL24
0,017	1,47	2,77	277,02	Q16352	Alpha-internexin	INA
0,006	1,46	2,75	275,11	Q9GZL7	Ribosome biogenesis protein WDR12	WDR12
0,035	1,44	2,71	271,32	O75832	26S proteasome non-ATPase regulatory subunit 10	PSMD10
0,043	1,44	2,71	271,24	P61960	Ubiquitin-fold modifier 1	UFM1
0,010	1,43	2,69	269,45	P12268	Inosine-5-monophosphate dehydrogenase 2	IMPDH2
0,000	1,42	2,68	267,59	Q12765	Secernin-1	SCRN1
0,028	1,42	2,68	267,59	Q8NBZ0	INO80 complex subunit E	INO80E
0,012	1,40	2,65	264,55	O00515	Ladinin-1	LAD1
0,019	1,40	2,64	264,36	P61916	Epididymal secretory protein E1	NPC2
0,001	1,40	2,64	263,90	Q9BYD2	39S ribosomal protein L9, mitochondrial	MRPL9
0,002	1,37	2,58	258,47	Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1	DYNC1L1
0,004	1,37	2,58	258,07	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus	ACIN1
0,003	1,35	2,55	255,24	Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial	ACOT9
0,001	1,35	2,55	254,91	P10768	S-formylglutathione hydrolase	ESD
0,010	1,34	2,53	253,15	Q9Y2S7	Polymerase delta-interacting protein 2	POLDIP2
0,000	1,33	2,51	251,40	P08727	Keratin, type I cytoskeletal 19	KRT19
0,001	1,32	2,50	249,67	O14744	Protein arginine N-methyltransferase 5;Protein arginine N-methyltransferase 5, N-ter	PRMT5
0,042	1,32	2,50	249,67	P25789	Proteasome subunit alpha type-4	PSMA4
0,021	1,32	2,50	249,67	P49585;Q9Y5K3	Choline-phosphate cytidylyltransferase A;Choline-phosphate cytidylyltransferase B	PCYT1A;PCYT1B
0,001	1,31	2,48	247,94	O95171	Sciellin	SCEL
0,011	1,30	2,47	246,70	Q8NDT2	Putative RNA-binding protein 15B	RBM15B
0,036	1,30	2,46	246,23	Q9UL15	BAG family molecular chaperone regulator 5	BAG5
0,030	1,29	2,45	244,53	Q96EY8	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	MMAB
0,015	1,28	2,43	242,84	Q9UJW0	Dynactin subunit 4	DCTN4
0,008	1,28	2,43	242,84	P11586	C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogen	MTHFD1
0,009	1,27	2,41	241,16	P51784	Ubiquitin carboxyl-terminal hydrolase 11	USP11
0,002	1,26	2,40	240,07	Q9H3H3	UPF0696 protein C11orf68	C11orf68
0,000	1,25	2,38	237,84	Q09666	Neuroblast differentiation-associated protein AHNAK	AHNAK
0,010	1,25	2,38	237,84	Q14137	Ribosome biogenesis protein BOP1	BOP1

Supplemental Table S2b

0,004	1,24	2,36	236,20	Q96JH7	Deubiquitinating protein VCIP135	VCPIP1
0,001	1,24	2,36	236,20	O75323	Protein NipSnap homolog 2	GBAS
0,033	1,23	2,35	235,20	Q99729	Heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
0,001	1,23	2,35	234,57	Q06323	Proteasome activator complex subunit 1	PSME1
0,001	1,23	2,34	234,25	Q969Q0;P83881	60S ribosomal protein L36a-like;60S ribosomal protein L36a	RPL36AL;RPL36A
0,000	1,22	2,33	232,95	P33991	DNA replication licensing factor MCM4	MCM4
0,001	1,21	2,31	231,34	P02794	Ferritin heavy chain;Ferritin heavy chain, N-terminally processed	FTH1
0,000	1,20	2,30	229,91	P52789	Hexokinase-2	HK2
0,007	1,19	2,28	228,28	O76021	Ribosomal L1 domain-containing protein 1	RSL1D1
0,001	1,18	2,27	226,58	Q9NVN8	Guanine nucleotide-binding protein-like 3-like protein	GNL3L
0,035	1,18	2,27	226,58	Q9H3P7	Golgi resident protein GCP60	ACBD3
0,038	1,18	2,27	226,58	O00743	Serine/threonine-protein phosphatase 6 catalytic subunit;Serine/threonine-protein	PPP6C
0,008	1,17	2,25	225,01	Q9BYD6	39S ribosomal protein L1, mitochondrial	MRPL1
0,001	1,16	2,23	223,46	Q04726	Transducin-like enhancer protein 3	TLE3
0,000	1,16	2,23	223,46	Q15020	Squamous cell carcinoma antigen recognized by T-cells 3	SART3
0,007	1,16	2,23	223,46	Q13938	Calcyphosin	CAPS
0,028	1,14	2,21	221,03	P48163	NADP-dependent malic enzyme	ME1
0,000	1,14	2,20	220,38	Q14566	DNA replication licensing factor MCM6	MCM6
0,006	1,14	2,20	220,38	Q8TE68	Epidermal growth factor receptor kinase substrate 8-like protein 1	EPS8L1
0,018	1,13	2,20	219,58	P06703	Protein S100-A6	S100A6
0,006	1,13	2,19	218,86	P61201	COP9 signalosome complex subunit 2	COPS2
0,000	1,13	2,19	218,86	O60437	Periplakin	PPL
0,007	1,12	2,17	217,37	Q96C57	Uncharacterized protein C12orf43	C12orf43
0,021	1,12	2,17	217,35	Q9ULJ3	Zinc finger and BTB domain-containing protein 21	ZBTB21
0,041	1,12	2,17	217,35	Q9Y5V0	Zinc finger protein 706	ZNF706
0,046	1,12	2,17	217,35	Q16555	Dihydropyrimidinase-related protein 2	DPYSL2
0,015	1,12	2,17	217,35	P05455	Lupus La protein	SSB
0,001	1,11	2,16	215,85	P82914	28S ribosomal protein S15, mitochondrial	MRPS15
0,000	1,11	2,16	215,85	Q15149	Plectin	PLEC
0,024	1,11	2,16	215,85	Q99627	COP9 signalosome complex subunit 8	COPS8
0,024	1,11	2,16	215,85	Q92890	Ubiquitin fusion degradation protein 1 homolog	UFD1L
0,034	1,11	2,15	215,46	Q7Z6B7	SLIT-ROBO Rho GTPase-activating protein 1	SRGAP1
0,003	1,10	2,14	214,35	Q9Y5U2	Protein TSSC4	TSSC4

Supplemental Table S2b

0,017	1,09	2,13	212,87	P47985	Cytochrome b-c1 complex subunit Rieske, mitochondrial;Cytochrome b-c1 complex	UQCRCF1
0,035	1,09	2,13	212,87	P56747	Claudin-6	CLDN6
0,050	1,09	2,13	212,87	Q15785	Mitochondrial import receptor subunit TOM34	TOMM34
0,002	1,09	2,13	212,87	P52815	39S ribosomal protein L12, mitochondrial	MRPL12
0,000	1,09	2,13	212,87	P55072	Transitional endoplasmic reticulum ATPase	VCP
0,026	1,09	2,13	212,87	O75525	KH domain-containing, RNA-binding, signal transduction-associated protein 3	KHDRBS3
0,000	1,09	2,13	212,87	O14530	Thioredoxin domain-containing protein 9	TXNDC9
0,000	1,09	2,13	212,87	Q9Y3C1	Nucleolar protein 16	NOP16
0,047	1,09	2,13	212,87	Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	NDUFB9
0,000	1,08	2,11	211,40	P25205	DNA replication licensing factor MCM3	MCM3
0,003	1,07	2,10	209,94	Q96D46	60S ribosomal export protein NMD3	NMD3
0,000	1,07	2,10	209,94	Q92817	Envoplakin	EVPL
0,000	1,06	2,08	208,49	Q9HCS7	Pre-mRNA-splicing factor SYF1	XAB2
0,020	1,06	2,08	208,49	Q7LBC6	Lysine-specific demethylase 3B	KDM3B
0,012	1,06	2,08	207,94	P46821	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B
0,011	1,05	2,07	207,05	Q8TD16	Protein bicaudal D homolog 2	BICD2
0,013	1,04	2,06	205,62	Q9NRX2	39S ribosomal protein L17, mitochondrial	MRPL17
0,007	1,04	2,06	205,62	Q9P253	Vacuolar protein sorting-associated protein 18 homolog	VPS18
0,002	1,04	2,06	205,62	Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog	SUGT1
0,030	1,04	2,06	205,62	Q16851	UTP--glucose-1-phosphate uridylyltransferase	UGP2
0,008	1,04	2,06	205,62	Q8TAT6	Nuclear protein localization protein 4 homolog	NPLOC4
0,000	1,04	2,06	205,62	Q92598	Heat shock protein 105 kDa	HSPH1
0,000	1,03	2,04	204,20	Q02539	Histone H1.1	HIST1H1A
0,017	1,03	2,04	204,20	Q16401	26S proteasome non-ATPase regulatory subunit 5	PSMD5
0,002	1,03	2,04	204,20	P43034	Platelet-activating factor acetylhydrolase IB subunit alpha	PAFAH1B1
0,004	1,02	2,03	202,79	P09001	39S ribosomal protein L3, mitochondrial	MRPL3
0,022	1,01	2,01	201,39	P10155	60 kDa SS-A/Ro ribonucleoprotein	TROVE2
0,016	1,01	2,01	201,39	Q00577	Transcriptional activator protein Pur-alpha	PURA
0,034	1,01	2,01	201,39	Q9NQV6	PR domain zinc finger protein 10	PRDM10
0,019	1,00	2,00	200,33	Q9H5X1	MIP18 family protein FAM96A	FAM96A
0,010	1,00	2,00	199,69	O43716	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	GATC
0,001	0,99	1,99	198,62	Q99700	Ataxin-2	ATXN2
0,002	0,99	1,99	198,62	Q7L5N1	COP9 signalosome complex subunit 6	COPS6

Supplemental Table S2b

0,009	0,98	1,98	197,52	Q9H269	Vacuolar protein sorting-associated protein 16 homolog	VPS16
0,001	0,98	1,97	197,48	P32929	Cystathionine gamma-lyase	CTH
0,003	0,98	1,97	197,25	P49411	Elongation factor Tu, mitochondrial	TUFM
0,000	0,98	1,97	197,25	P33992	DNA replication licensing factor MCM5	MCM5
0,000	0,98	1,97	197,25	P07900	Heat shock protein HSP 90-alpha	HSP90AA1
0,003	0,97	1,96	195,88	P05783	Keratin, type I cytoskeletal 18	KRT18
0,002	0,97	1,96	195,88	Q9UL40	Zinc finger protein 346	ZNF346
0,010	0,97	1,95	195,32	Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	TOMM22
0,005	0,96	1,95	194,95	Q16629	Serine/arginine-rich splicing factor 7	SRSF7
0,044	0,96	1,95	194,53	Q96RP9	Elongation factor G, mitochondrial	GFM1
0,049	0,96	1,95	194,53	Q92989	Polyribonucleotide 5-hydroxyl-kinase Clp1	CLP1
0,017	0,95	1,93	193,19	Q5VZK9	Leucine-rich repeat-containing protein 16A	LRRC16A
0,040	0,95	1,93	193,19	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4;Peptidyl-prolyl cis-trans isomerase FKBP4,	FKBP4
0,031	0,95	1,93	193,19	Q8NCH0	Carbohydrate sulfotransferase 14	CHST14
0,007	0,94	1,92	191,85	Q16881	Thioredoxin reductase 1, cytoplasmic	TXNRD1
0,008	0,94	1,92	191,85	Q14204	Cytoplasmic dynein 1 heavy chain 1	DYNC1H1
0,022	0,94	1,92	191,85	Q9Y3B7	39S ribosomal protein L11, mitochondrial	MRPL11
0,006	0,93	1,91	190,53	P41250	Glycine--tRNA ligase	GARS
0,014	0,93	1,91	190,53	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	SLC9A3R1
0,012	0,93	1,91	190,53	P50750	Cyclin-dependent kinase 9	CDK9
0,047	0,93	1,91	190,53	Q9NW08	DNA-directed RNA polymerase III subunit RPC2	POLR3B
0,044	0,93	1,91	190,53	Q969S3	Zinc finger protein 622	ZNF622
0,026	0,92	1,90	189,67	P33764	Protein S100-A3	S100A3
0,013	0,92	1,89	189,21	Q8TBX8	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	PIP4K2C
0,001	0,91	1,88	187,90	Q9BT78	COP9 signalosome complex subunit 4	COPS4
0,018	0,91	1,88	187,90	P51608	Methyl-CpG-binding protein 2	MECP2
0,034	0,91	1,88	187,90	P25787	Proteasome subunit alpha type-2	PSMA2
0,007	0,91	1,88	187,90	Q9HCY8	Protein S100-A14	S100A14
0,004	0,90	1,87	186,61	Q14197	Peptidyl-tRNA hydrolase ICT1, mitochondrial	ICT1
0,046	0,90	1,87	186,58	Q5SW79	Centrosomal protein of 170 kDa	CEP170
0,001	0,89	1,86	185,57	Q9Y2X3	Nucleolar protein 58	NOP58
0,000	0,87	1,83	182,93	P39060	Collagen alpha-1(XVIII) chain;Endostatin	COL18A1
0,035	0,87	1,83	182,86	Q9UNH6	Sorting nexin-7	SNX7

Supplemental Table S2b

0,030	0,87	1,83	182,77	Q9H9B4	Sideroflexin-1	SFXN1
0,001	0,87	1,83	182,77	P17066;P48741	Heat shock 70 kDa protein 6;Putative heat shock 70 kDa protein 7	HSPA6;HSPA7
0,029	0,86	1,82	181,50	P08754	Guanine nucleotide-binding protein G(k) subunit alpha	GNAI3
0,039	0,85	1,80	180,25	Q86TI2	Dipeptidyl peptidase 9	DPP9
0,000	0,85	1,80	180,25	P33993	DNA replication licensing factor MCM7	MCM7
0,004	0,84	1,79	179,01	Q93009	Ubiquitin carboxyl-terminal hydrolase 7	USP7
0,043	0,83	1,78	177,91	Q9H307	Pinin	PNN
0,001	0,83	1,78	177,77	P13639	Elongation factor 2	EEF2
0,029	0,83	1,78	177,77	P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A
0,000	0,83	1,78	177,77	P31948	Stress-induced-phosphoprotein 1	STIP1
0,002	0,83	1,78	177,77	P25786	Proteasome subunit alpha type-1	PSMA1
0,004	0,83	1,78	177,77	Q9UBW8	COP9 signalosome complex subunit 7a	COPS7A
0,001	0,82	1,77	176,54	P15927	Replication protein A 32 kDa subunit	RPA2
0,000	0,82	1,77	176,54	P49736	DNA replication licensing factor MCM2	MCM2
0,003	0,82	1,77	176,54	P28066	Proteasome subunit alpha type-5	PSMA5
0,002	0,82	1,77	176,54	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCC2
0,037	0,81	1,76	175,93	Q8IYB8	ATP-dependent RNA helicase SUPV3L1, mitochondrial	SUPV3L1
0,022	0,81	1,75	175,42	O94906	Pre-mRNA-processing factor 6	PRPF6
0,025	0,81	1,75	175,18	Q9Y2U5;Q99759	Mitogen-activated protein kinase kinase kinase 2;Mitogen-activated protein kinase	MAP3K2;MAP3K3
0,024	0,81	1,75	175,00	Q07955	Serine/arginine-rich splicing factor 1	SRSF1
0,003	0,80	1,74	174,11	O94992	Protein HEXIM1	HEXIM1
0,018	0,80	1,74	173,95	P09651;Q32P51	Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein	NRNPA1;HNRNPA1
0,006	0,80	1,74	173,83	P49589	Cysteine--tRNA ligase, cytoplasmic	CARS
0,030	0,80	1,74	173,61	P38159	RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome	RBMX
0,005	0,79	1,73	172,91	Q9Y4C8	Probable RNA-binding protein 19	RBM19
0,038	0,78	1,72	171,95	Q5SNT6;Q641Q2;Q9Y4E1	WASH complex subunit FAM21B;WASH complex subunit FAM21A;WASH complex subunit FAM21B;FAM21A;FAM21B	FAM21B;FAM21A;FAM21B
0,029	0,78	1,72	171,89	P04279	Semenogelin-1;Alpha-inhibin-92;Alpha-inhibin-31;Seminal basic protein	SEMG1
0,003	0,78	1,72	171,77	Q13247	Serine/arginine-rich splicing factor 6	SRSF6
0,045	0,78	1,72	171,71	P82673	28S ribosomal protein S35, mitochondrial	MRPS35
0,010	0,78	1,72	171,71	Q9UKD1	Glucocorticoid modulatory element-binding protein 2	GMEB2
0,000	0,78	1,72	171,71	P11142	Heat shock cognate 71 kDa protein	HSPA8
0,009	0,77	1,71	170,53	Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	UCHL5
0,040	0,76	1,69	169,42	Q96A26	Protein FAM162A	FAM162A

Supplemental Table S2b

0,003	0,76	1,69	169,35	P62333	26S protease regulatory subunit 10B	PSMC6
0,000	0,76	1,69	169,35	P50502;Q8NFI4;Q8IZP2	Hsc70-interacting protein;Putative protein FAM10A5;Putative protein FAM10A4	ST13;ST13P5;ST13P4
0,018	0,76	1,69	169,35	Q8N2M8	CLK4-associating serine/arginine rich protein	CLASRP
0,000	0,76	1,69	169,35	P51149	Ras-related protein Rab-7a	RAB7A
0,026	0,76	1,69	169,29	Q96JC1	Vam6/Vps39-like protein	VPS39
0,009	0,75	1,68	168,18	P40227	T-complex protein 1 subunit zeta	CCT6A
0,027	0,75	1,68	168,18	Q9Y676	28S ribosomal protein S18b, mitochondrial	MRPS18B
0,043	0,75	1,68	168,18	Q8WZA0	Protein LZIC	LZIC
0,030	0,75	1,68	168,18	O43681	ATPase ASNA1	ASNA1
0,045	0,75	1,68	168,18	Q9NX24	H/ACA ribonucleoprotein complex subunit 2	NHP2
0,007	0,73	1,66	165,86	Q9UL46	Proteasome activator complex subunit 2	PSME2
0,017	0,73	1,66	165,86	P60510	Serine/threonine-protein phosphatase 4 catalytic subunit	PPP4C
0,011	0,73	1,66	165,86	Q13426	DNA repair protein XRCC4	XRCC4
0,006	0,73	1,66	165,86	O43395	U4/U6 small nuclear ribonucleoprotein Prp3	PRPF3
0,001	0,73	1,66	165,72	P08195	4F2 cell-surface antigen heavy chain	SLC3A2
0,015	0,72	1,65	164,72	P29590	Protein PML	PML
0,017	0,72	1,65	164,72	P12532	Creatine kinase U-type, mitochondrial	CKMT1A
0,046	0,71	1,64	163,85	P48723	Heat shock 70 kDa protein 13	HSPA13
0,000	0,71	1,64	163,58	P20618	Proteasome subunit beta type-1	PSMB1
0,001	0,70	1,62	162,45	P25788	Proteasome subunit alpha type-3	PSMA3
0,002	0,70	1,62	162,45	P49721	Proteasome subunit beta type-2	PSMB2
0,038	0,69	1,61	161,33	Q13619	Cullin-4A	CUL4A
0,004	0,69	1,61	161,33	Q9Y2R9	28S ribosomal protein S7, mitochondrial	MRPS7
0,037	0,68	1,60	160,21	Q00059	Transcription factor A, mitochondrial	TFAM
0,025	0,68	1,60	160,21	P62316	Small nuclear ribonucleoprotein Sm D2	SNRPD2
0,022	0,68	1,60	160,21	Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1QBP
0,001	0,68	1,60	160,21	Q9NW13	RNA-binding protein 28	RBM28
0,000	0,68	1,60	160,21	P28070	Proteasome subunit beta type-4	PSMB4
0,026	0,68	1,60	160,21	P15408	Fos-related antigen 2	FOSL2
0,002	0,67	1,59	159,11	O14818	Proteasome subunit alpha type-7	PSMA7
0,040	0,67	1,59	159,11	O43719	HIV Tat-specific factor 1	HTATSF1
0,011	0,66	1,58	158,07	Q14116	Interleukin-18	IL18
0,000	0,66	1,58	158,01	P27694	Replication protein A 70 kDa DNA-binding subunit;Replication protein A 70 kDa DNA-binding subunit	RPA1

Supplemental Table S2b

0,028	0,66	1,58	158,01	Q9NRA8	Eukaryotic translation initiation factor 4E transporter	EIF4ENIF1
0,002	0,66	1,58	158,01	Q99436	Proteasome subunit beta type-7	PSMB7
0,000	0,66	1,58	158,01	P08107	Heat shock 70 kDa protein 1A/1B	HSPA1A
0,041	0,66	1,58	158,01	Q9Y399	28S ribosomal protein S2, mitochondrial	MRPS2
0,037	0,65	1,57	157,38	P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	HNRNPC
0,289	0,65	1,57	157,24	O00767	Acyl-CoA desaturase	SCD
0,012	0,63	1,55	154,76	O95456	Proteasome assembly chaperone 1	PSMG1
0,002	0,63	1,55	154,76	O15355	Protein phosphatase 1G	PPM1G
0,034	0,63	1,55	154,76	P62877	E3 ubiquitin-protein ligase RBX1;E3 ubiquitin-protein ligase RBX1, N-terminally proc	RBX1
0,016	0,63	1,55	154,76	Q02040	A-kinase anchor protein 17A	AKAP17A
0,037	0,62	1,54	153,69	Q8NF91	Nesprin-1	SYNE1
0,002	0,62	1,54	153,69	P62191	26S protease regulatory subunit 4	PSMC1
0,014	0,61	1,53	152,63	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial	UQCRH
0,010	0,60	1,52	151,57	P28072	Proteasome subunit beta type-6	PSMB6
0,001	0,60	1,52	151,57	P17980	26S protease regulatory subunit 6A	PSMC3
0,003	0,60	1,52	151,57	P17987	T-complex protein 1 subunit alpha	TCP1
0,027	0,60	1,51	151,36	Q9BZJ0	Crooked neck-like protein 1	CRNKL1
0,034	0,59	1,51	150,88	Q05BQ5	MBT domain-containing protein 1	MBTD1
0,014	0,59	1,51	150,83	O95834	Echinoderm microtubule-associated protein-like 2	EML2
0,002	0,59	1,51	150,52	O75381	Peroxisomal membrane protein PEX14	PEX14
0,000	0,59	1,51	150,52	P35998	26S protease regulatory subunit 7	PSMC2
0,043	0,58	1,49	149,48	P25685	DnaJ homolog subfamily B member 1	DNAJB1
0,033	0,58	1,49	149,48	P42704	Leucine-rich PPR motif-containing protein, mitochondrial	LRPPRC
0,005	0,56	1,48	147,61	P29317	Ephrin type-A receptor 2	EPHA2
0,010	0,56	1,47	147,43	O00232	26S proteasome non-ATPase regulatory subunit 12	PSMD12
0,006	0,56	1,47	147,43	P55036	26S proteasome non-ATPase regulatory subunit 4	PSMD4
0,015	0,56	1,47	147,04	P67936	Tropomyosin alpha-4 chain	TPM4
0,041	0,55	1,46	146,41	O00170	AH receptor-interacting protein	AIP
0,016	0,55	1,46	146,41	P28074	Proteasome subunit beta type-5	PSMB5
0,000	0,54	1,45	145,40	P13995	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochond	MTHFD2
0,016	0,54	1,45	145,40	Q04837	Single-stranded DNA-binding protein, mitochondrial	SSBP1
0,013	0,54	1,45	145,40	P68400;Q8NEV1	Casein kinase II subunit alpha;Casein kinase II subunit alpha 3	CSNK2A1;CSNK2A3
0,003	0,53	1,44	144,39	P49368	T-complex protein 1 subunit gamma	CCT3

Supplemental Table S2b

0,035	0,53	1,44	144,39	Q8N556	Actin filament-associated protein 1	AFAP1
0,012	0,53	1,44	144,39	Q9H6R0	Putative ATP-dependent RNA helicase DHX33	DHX33
0,012	0,53	1,44	144,39	Q9UL63	Muskelin	MKLN1
0,010	0,53	1,44	144,39	Q9UBP9	PTB domain-containing engulfment adapter protein 1	GULP1
0,019	0,52	1,43	143,40	P08621	U1 small nuclear ribonucleoprotein 70 kDa	SNRNP70
0,003	0,52	1,43	143,40	P31942	Heterogeneous nuclear ribonucleoprotein H3	HNRNPH3
0,029	0,51	1,42	142,41	Q9Y6X4	Soluble lamin-associated protein of 75 kDa	FAM169A
0,003	0,51	1,42	142,41	Q9UJZ1	Stomatin-like protein 2, mitochondrial	STOML2
0,036	0,50	1,41	141,42	O95232	Luc7-like protein 3	LUC7L3
0,000	0,50	1,41	141,42	Q13263	Transcription intermediary factor 1-beta	TRIM28
0,016	0,50	1,41	141,42	Q15424	Scaffold attachment factor B1	SAFB
0,003	0,50	1,41	141,42	Q99733	Nucleosome assembly protein 1-like 4	NAP1L4
0,000	0,50	1,41	141,42	Q8N163	Cell cycle and apoptosis regulator protein 2	CCAR2
0,004	0,50	1,41	141,42	P53396	ATP-citrate synthase	ACLY
0,018	0,50	1,41	141,42	P52907	F-actin-capping protein subunit alpha-1	CAPZA1
0,001	0,49	1,40	140,44	P56537	Eukaryotic translation initiation factor 6	EIF6
0,022	0,49	1,40	140,44	Q13217	DnaJ homolog subfamily C member 3	DNAJC3
0,002	0,49	1,40	140,44	P78332	RNA-binding protein 6	RBM6
0,019	0,49	1,40	140,44	Q96S82	Ubiquitin-like protein 7	UBL7
0,017	0,49	1,40	140,44	P50552	Vasodilator-stimulated phosphoprotein	VASP
0,018	0,49	1,40	140,44	P28062	Proteasome subunit beta type-8	PSMB8
0,021	0,48	1,40	139,93	Q96L91	E1A-binding protein p400	EP400
0,004	0,48	1,39	139,47	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1
0,005	0,47	1,39	138,51	P07355;A6NMY6	Annexin A2;Putative annexin A2-like protein	ANXA2;ANXA2P2
0,034	0,47	1,39	138,51	Q96JY6	PDZ and LIM domain protein 2	PDLIM2
0,031	0,47	1,39	138,51	Q9Y221	60S ribosome subunit biogenesis protein NIP7 homolog	NIP7
0,000	0,47	1,39	138,51	Q15008	26S proteasome non-ATPase regulatory subunit 6	PSMD6
0,007	0,47	1,39	138,51	Q9UHB6	LIM domain and actin-binding protein 1	LIMA1
0,042	0,47	1,39	138,51	Q6PI48	Aspartate--tRNA ligase, mitochondrial	DARS2
0,001	0,47	1,39	138,51	P51665	26S proteasome non-ATPase regulatory subunit 7	PSMD7
0,027	0,47	1,39	138,51	Q96GQ7	Probable ATP-dependent RNA helicase DDX27	DDX27
0,028	0,47	1,38	138,31	Q66K74	Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain	MAP1S
0,004	0,46	1,38	137,55	Q15717	ELAV-like protein 1	ELAVL1

Supplemental Table S2b

0,045	0,46	1,38	137,55	Q9UKK9	ADP-sugar pyrophosphatase	NUDT5
0,048	0,45	1,37	136,62	Q13769	THO complex subunit 5 homolog	THOC5
0,015	0,45	1,37	136,60	P08579	U2 small nuclear ribonucleoprotein B	SNRPB2
0,041	0,45	1,37	136,60	Q8IUD2	ELKS/Rab6-interacting/CAST family member 1	ERC1
0,010	0,45	1,37	136,60	Q9BWU0	Kanadaptin	SLC4A1AP
0,035	0,44	1,36	135,91	P02545	Prelamin-A/C;Lamin-A/C	LMNA
0,000	0,44	1,36	135,66	P62195	26S protease regulatory subunit 8	PSMC5
0,020	0,44	1,36	135,66	P00367	Glutamate dehydrogenase 1, mitochondrial	GLUD1
0,029	0,44	1,36	135,66	Q16527	Cysteine and glycine-rich protein 2	CSRP2
0,013	0,44	1,36	135,66	P48643	T-complex protein 1 subunit epsilon	CCT5
0,006	0,44	1,36	135,66	Q99460	26S proteasome non-ATPase regulatory subunit 1	PSMD1
0,001	0,44	1,36	135,66	Q4G0J3	La-related protein 7	LARP7
0,019	0,43	1,35	134,79	P05387	60S acidic ribosomal protein P2	RPLP2
0,010	0,43	1,35	134,72	O43818	U3 small nucleolar RNA-interacting protein 2	RRP9
0,034	0,43	1,35	134,72	P08238	Heat shock protein HSP 90-beta	HSP90AB1
0,025	0,43	1,35	134,72	Q13098	COP9 signalosome complex subunit 1	GPS1
0,013	0,41	1,33	133,07	Q15366	Poly(rC)-binding protein 2	PCBP2
0,011	0,41	1,33	132,87	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	SGTA
0,002	0,40	1,32	132,04	Q13242	Serine/arginine-rich splicing factor 9	SRSF9
0,041	0,39	1,31	131,04	Q9UNP9	Peptidyl-prolyl cis-trans isomerase E	PPIE
0,010	0,39	1,31	131,04	P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3
0,001	0,39	1,31	131,04	O43823	A-kinase anchor protein 8	AKAP8
0,000	0,39	1,31	131,04	P48556	26S proteasome non-ATPase regulatory subunit 8	PSMD8
0,019	0,39	1,31	131,04	P52298	Nuclear cap-binding protein subunit 2	NCBP2
0,007	0,38	1,30	130,13	O60716	Catenin delta-1	CTNND1
0,001	0,38	1,30	130,13	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	HNRNPA2B1
0,015	0,38	1,30	130,13	Q96IR2;A2RRD8	Zinc finger protein 845;Zinc finger protein 320	ZNF845;ZNF320
0,007	0,37	1,29	129,24	P50990	T-complex protein 1 subunit theta	CCT8
0,023	0,37	1,29	129,20	Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein	NIFK
0,038	0,36	1,29	128,74	Q9UBS4	DnaJ homolog subfamily B member 11	DNAJB11
0,023	0,36	1,28	128,42	Q01813	ATP-dependent 6-phosphofructokinase, platelet type	PFKP
0,004	0,36	1,28	128,34	Q9H0L4	Cleavage stimulation factor subunit 2 tau variant	CSTF2T
0,006	0,36	1,28	128,34	Q9NRL3	Striatin-4	STRN4

Supplemental Table S2b

0,006	0,36	1,28	128,34	O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11
0,023	0,35	1,27	127,46	Q13951	Core-binding factor subunit beta	CBFB
0,020	0,35	1,27	127,46	Q9UHX1	Poly(U)-binding-splicing factor PUF60	PUF60
0,001	0,35	1,27	127,46	P15924	Desmoplakin	DSP
0,046	0,34	1,27	126,58	Q13952	Nuclear transcription factor Y subunit gamma	NFYC
0,005	0,34	1,27	126,58	Q99832	T-complex protein 1 subunit eta	CCT7
0,027	0,34	1,27	126,58	P49750	YLP motif-containing protein 1	YLPM1
0,023	0,33	1,26	125,70	Q14690	Protein RRP5 homolog	PDCD11
0,007	0,33	1,26	125,70	P43686	26S protease regulatory subunit 6B	PSMC4
0,022	0,33	1,26	125,70	Q9NZL9	Methionine adenosyltransferase 2 subunit beta	MAT2B
0,006	0,33	1,26	125,70	Q01130	Serine/arginine-rich splicing factor 2	SRSF2
0,026	0,32	1,25	124,83	P35579	Myosin-9	MYH9
0,030	0,32	1,25	124,83	P20810	Calpastatin	CAST
0,034	0,32	1,25	124,83	O75880	Protein SCO1 homolog, mitochondrial	SCO1
0,015	0,31	1,24	123,97	P67870	Casein kinase II subunit beta	CSNK2B
0,026	0,31	1,24	123,97	Q8IX12	Cell division cycle and apoptosis regulator protein 1	CCAR1
0,002	0,31	1,24	123,66	O43707	Alpha-actinin-4	ACTN4
0,032	0,30	1,23	123,33	P19338	Nucleolin	NCL
0,040	0,30	1,23	123,32	P00558	Phosphoglycerate kinase 1	PGK1
0,028	0,30	1,23	123,11	P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase	NOP2
0,030	0,29	1,22	122,26	Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2
0,048	0,29	1,22	122,26	O15160	DNA-directed RNA polymerases I and III subunit RPAC1	POLR1C
0,008	0,28	1,21	121,42	Q8IZ69	tRNA (uracil-5-)-methyltransferase homolog A	TRMT2A
0,033	0,28	1,21	121,42	Q9UQE7	Structural maintenance of chromosomes protein 3	SMC3
0,033	0,28	1,21	121,06	P15311	Ezrin	EZR
0,007	0,27	1,21	120,63	P11021	78 kDa glucose-regulated protein	HSPA5
0,013	0,27	1,21	120,58	P09874	Poly [ADP-ribose] polymerase 1	PARP1
0,016	0,27	1,20	120,27	Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1
0,001	0,26	1,20	119,75	Q12906	Interleukin enhancer-binding factor 3	ILF3
0,033	0,25	1,19	118,92	O43242	26S proteasome non-ATPase regulatory subunit 3	PSMD3
0,030	0,25	1,19	118,90	P23528	Cofilin-1	CFL1
0,027	0,24	1,18	118,46	P23284	Peptidyl-prolyl cis-trans isomerase B	PPIB
0,043	0,24	1,18	118,30	Q9Y617	Phosphoserine aminotransferase	PSAT1

Supplemental Table S2b

0,006	0,24	1,18	117,74	Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47
0,029	0,24	1,18	117,73	O76094	Signal recognition particle subunit SRP72	SRP72
0,012	0,23	1,17	117,03	P04083	Annexin A1	ANXA1
0,042	0,23	1,17	117,00	Q9BRP8	Partner of Y14 and mago	WIBG
0,038	0,22	1,17	116,75	Q14103	Heterogeneous nuclear ribonucleoprotein D0	HNRNP
0,042	0,22	1,17	116,67	P06753	Tropomyosin alpha-3 chain	TPM3
0,002	0,22	1,16	116,47	P35580	Myosin-10	MYH10
0,002	0,22	1,16	116,47	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	EFTUD2
0,030	0,21	1,16	115,83	P62241	40S ribosomal protein S8	RPS8
0,005	0,21	1,16	115,67	P55769	NHP2-like protein 1;NHP2-like protein 1, N-terminally processed	NHP2L1
0,013	0,19	1,14	113,77	O60307	Microtubule-associated serine/threonine-protein kinase 3	MAST3
0,033	0,18	1,13	113,29	Q6VN20	Ran-binding protein 10	RANBP10
0,040	0,17	1,12	112,31	P36578	60S ribosomal protein L4	RPL4
0,039	0,16	1,12	111,94	P62750	60S ribosomal protein L23a	RPL23A
0,012	0,12	1,09	108,87	P61088	Ubiquitin-conjugating enzyme E2 N	UBE2N
8 h Down						
0,026	-0,16	0,90	89,59	P48739	Phosphatidylinositol transfer protein beta isoform	PITPNB
0,030	-0,17	0,89	88,91	P35221	Catenin alpha-1	CTNNA1
0,033	-0,18	0,88	88,27	P46060	Ran GTPase-activating protein 1	RANGAP1
0,018	-0,18	0,88	88,17	P11142	Heat shock cognate 71 kDa protein	HSPA8
0,010	-0,19	0,88	87,66	P11021	78 kDa glucose-regulated protein	HSPA5
0,012	-0,20	0,87	87,21	P08238	Heat shock protein HSP 90-beta	HSP90AB1
0,028	-0,20	0,87	87,06	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	DHX15
0,024	-0,20	0,87	86,85	P49411	Elongation factor Tu, mitochondrial	TUFM
0,023	-0,21	0,86	86,46	P46940	Ras GTPase-activating-like protein IQGAP1	IQGAP1
0,039	-0,21	0,86	86,23	P15311	Ezrin	EZR
0,001	-0,22	0,86	85,86	P11234	Ras-related protein Ral-B	RALB
0,024	-0,22	0,86	85,70	P08574	Cytochrome c1, heme protein, mitochondrial	CYC1
0,021	-0,24	0,85	84,67	Q9NRG0	Chromatin accessibility complex protein 1	CHRAC1
0,018	-0,27	0,83	83,18	P61353	60S ribosomal protein L27	RPL27
0,013	-0,27	0,83	83,02	P35580	Myosin-10	MYH10
0,049	-0,27	0,83	82,90	P78371	T-complex protein 1 subunit beta	CCT2
0,045	-0,27	0,83	82,82	P28482	Mitogen-activated protein kinase 1	MAPK1

Supplemental Table S2b

0,033	-0,28	0,82	82,42	P63220	40S ribosomal protein S21	RPS21
0,048	-0,29	0,82	82,01	P18669	Phosphoglycerate mutase 1	PGAM1
0,045	-0,29	0,82	81,79	Q16630	Cleavage and polyadenylation specificity factor subunit 6	CPSF6
0,031	-0,29	0,82	81,79	P40429;Q6NVV1	60S ribosomal protein L13a;Putative 60S ribosomal protein L13a protein RPL13AP3	RPL13A;RPL13AP3
0,033	-0,29	0,82	81,79	P48444	Coatomer subunit delta	ARCN1
0,014	-0,29	0,82	81,77	Q8IXI1	Mitochondrial Rho GTPase 2	RHOT2
0,019	-0,29	0,82	81,60	Q15019	Septin-2	37500,000
0,007	-0,29	0,82	81,54	P35222	Catenin beta-1	CTNNB1
0,016	-0,30	0,81	81,37	O00231	26S proteasome non-ATPase regulatory subunit 11	PSMD11
0,026	-0,30	0,81	81,23	P42677	40S ribosomal protein S27	RPS27
0,033	-0,30	0,81	81,18	O96019	Actin-like protein 6A	ACTL6A
0,013	-0,31	0,81	80,66	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21
0,043	-0,31	0,81	80,66	Q9H307	Pinin	PNN
0,050	-0,31	0,81	80,66	P54578	Ubiquitin carboxyl-terminal hydrolase 14	USP14
0,013	-0,31	0,81	80,55	P25786	Proteasome subunit alpha type-1	PSMA1
0,041	-0,32	0,80	80,35	P62993	Growth factor receptor-bound protein 2	GRB2
0,022	-0,33	0,79	79,37	P62333	26S protease regulatory subunit 10B	PSMC6
0,011	-0,33	0,79	79,34	O76031	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	CLPX
0,038	-0,34	0,79	79,00	Q86XP3	ATP-dependent RNA helicase DDX42	DDX42
0,000	-0,35	0,78	78,46	P49327	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] 5	FASN
0,025	-0,37	0,77	77,38	Q52LJ0	Protein FAM98B	FAM98B
0,041	-0,37	0,77	77,25	Q9Y371	Endophilin-B1	SH3GLB1
0,028	-0,38	0,77	76,91	P82094	TATA element modulatory factor	TMF1
0,041	-0,38	0,77	76,84	O00303	Eukaryotic translation initiation factor 3 subunit F	EIF3F
0,008	-0,39	0,76	76,31	Q96SI9	Spermatid perinuclear RNA-binding protein	STRBP
0,033	-0,39	0,76	76,31	O94906	Pre-mRNA-processing factor 6	PRPF6
0,019	-0,39	0,76	76,31	Q9Y3C1	Nucleolar protein 16	NOP16
0,006	-0,39	0,76	76,22	P16422	Epithelial cell adhesion molecule	EPCAM
0,002	-0,40	0,76	75,79	P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B
0,042	-0,41	0,75	75,26	Q7L576	Cytoplasmic FMR1-interacting protein 1	CYFIP1
0,050	-0,42	0,75	74,74	Q9NP79	Vacuolar protein sorting-associated protein VTA1 homolog	VTA1
0,000	-0,43	0,74	74,24	P57764	Gasdermin-D	GSDMD
0,012	-0,43	0,74	74,23	A6NHQ2	rRNA/tRNA 2-O-methyltransferase fibrillarin-like protein 1	FBLL1

Supplemental Table S2b

0,020	-0,44	0,74	73,96	P11802	Cyclin-dependent kinase 4	CDK4
0,022	-0,44	0,74	73,84	Q8N7H5	RNA polymerase II-associated factor 1 homolog	PAF1
0,050	-0,44	0,74	73,76	P53007	Tricarboxylate transport protein, mitochondrial	SLC25A1
0,002	-0,44	0,74	73,67	Q13867	Bleomycin hydrolase	BLMH
0,047	-0,45	0,73	73,20	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1
0,045	-0,46	0,73	72,80	Q01844	RNA-binding protein EWS	EWSR1
0,014	-0,47	0,72	72,20	O15550;O14607	Lysine-specific demethylase 6A;Histone demethylase UTY	KDM6A;UTY
0,000	-0,47	0,72	72,12	Q14165	Malectin	MLEC
0,028	-0,48	0,72	71,92	Q9BY43	Charged multivesicular body protein 4a	CHMP4A
0,004	-0,49	0,71	71,05	O95861	3(2),5-bisphosphate nucleotidase 1	BPNT1
0,005	-0,50	0,71	70,86	Q13098	COP9 signalosome complex subunit 1	GPS1
0,013	-0,50	0,71	70,71	P26358	DNA (cytosine-5)-methyltransferase 1	DNMT1
0,028	-0,50	0,71	70,71	P49792	E3 SUMO-protein ligase RanBP2	RANBP2
0,036	-0,50	0,71	70,71	P63165	Small ubiquitin-related modifier 1	SUMO1
0,045	-0,52	0,70	69,74	O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1
0,007	-0,53	0,69	69,36	Q12888	Tumor suppressor p53-binding protein 1	TP53BP1
0,019	-0,53	0,69	69,26	O75822	Eukaryotic translation initiation factor 3 subunit J	EIF3J
0,019	-0,53	0,69	69,26	P43246	DNA mismatch repair protein Msh2	MSH2
0,041	-0,54	0,69	68,72	Q86Y56	HEAT repeat-containing protein 2	HEATR2
0,015	-0,55	0,68	68,19	O43847	Nardilysin	NRD1
0,030	-0,56	0,68	67,83	Q9P2T1	GMP reductase 2	GMPR2
0,029	-0,56	0,68	67,83	Q9Y388	RNA-binding motif protein, X-linked 2	RBMX2
0,023	-0,57	0,67	67,36	Q9H981	Actin-related protein 8	ACTR8
0,041	-0,57	0,67	67,36	Q9H6T3	RNA polymerase II-associated protein 3	RPAP3
0,004	-0,57	0,67	67,32	P63241;Q6IS14	Eukaryotic translation initiation factor 5A-1;Eukaryotic translation initiation factor 5	EIF5A;EIF5AL1
0,043	-0,57	0,67	67,25	P31153	S-adenosylmethionine synthase isoform type-2	MAT2A
0,039	-0,57	0,67	67,19	Q96BP3	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	PPWD1
0,026	-0,57	0,67	67,19	O94992	Protein HEXIM1	HEXIM1
0,036	-0,58	0,67	66,90	O14653	Golgi SNAP receptor complex member 2	GOSR2
0,022	-0,59	0,67	66,63	Q6P1N9	Putative deoxyribonuclease TATDN1	TATDN1
0,047	-0,59	0,67	66,61	P13591	Neural cell adhesion molecule 1	NCAM1
0,028	-0,59	0,67	66,53	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2
0,045	-0,59	0,66	66,43	Q92830	Histone acetyltransferase KAT2A	KAT2A

Supplemental Table S2b

0,009	-0,59	0,66	66,31	P24386	Rab proteins geranylgeranyltransferase component A 1	CHM
0,025	-0,61	0,66	65,70	Q9UFN0	Protein NipSnap homolog 3A	NIPSNAP3A
0,041	-0,61	0,66	65,52	Q9UNQ2	Probable dimethyladenosine transferase	DIMT1
0,039	-0,62	0,65	65,26	P09496	Clathrin light chain A	CLTA
0,012	-0,62	0,65	65,07	Q7Z589	Protein EMSY	EMSY
0,042	-0,63	0,65	64,62	Q14764	Major vault protein	MVP
0,000	-0,63	0,65	64,53	P07686	Beta-hexosaminidase subunit beta;Beta-hexosaminidase subunit beta chain B;Beta-	HEXB
0,027	-0,63	0,64	64,42	Q13501	Sequestosome-1	SQSTM1
0,028	-0,64	0,64	64,17	O75347	Tubulin-specific chaperone A	TBCA
0,013	-0,65	0,64	63,85	Q9Y5K8	V-type proton ATPase subunit D	ATP6V1D
0,018	-0,65	0,64	63,73	O60307	Microtubule-associated serine/threonine-protein kinase 3	MAST3
0,003	-0,67	0,63	62,85	Q9HCG8	Pre-mRNA-splicing factor CWC22 homolog	CWC22
0,043	-0,67	0,63	62,85	Q99567	Nuclear pore complex protein Nup88	NUP88
0,042	-0,67	0,63	62,85	Q13442	28 kDa heat- and acid-stable phosphoprotein	PDAP1
0,002	-0,67	0,63	62,74	Q96P16	Regulation of nuclear pre-mRNA domain-containing protein 1A	RPRD1A
0,028	-0,68	0,63	62,58	Q9H7P9	Pleckstrin homology domain-containing family G member 2	PLEKHG2
0,007	-0,68	0,62	62,42	Q49AG3	Zinc finger BED domain-containing protein 5	ZBED5
0,022	-0,68	0,62	62,42	O94880	PHD finger protein 14	PHF14
0,005	-0,68	0,62	62,42	O95490	Latrophilin-2	LPHN2
0,000	-0,68	0,62	62,39	P49585;Q9Y5K3	Choline-phosphate cytidylyltransferase A;Choline-phosphate cytidylyltransferase B	PCYT1A;PCYT1B
0,011	-0,69	0,62	61,99	P46013	Antigen KI-67	MKI67
0,006	-0,69	0,62	61,99	P12004	Proliferating cell nuclear antigen	PCNA
0,030	-0,69	0,62	61,82	O14893	Gem-associated protein 2	GEMIN2
0,012	-0,70	0,62	61,64	Q9BSV6	tRNA-splicing endonuclease subunit Sen34	TSEN34
0,031	-0,70	0,62	61,56	Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase	NSUN2
0,007	-0,71	0,61	61,13	Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18
0,002	-0,71	0,61	61,13	P50502;Q8NFI4;Q8IZP2	Hsc70-interacting protein;Putative protein FAM10A5;Putative protein FAM10A4	IT13;ST13P5;ST13P
0,011	-0,71	0,61	61,05	P08047	Transcription factor Sp1	SP1
0,009	-0,72	0,61	60,90	Q9NQX6	Zinc finger protein 331	ZNF331
0,017	-0,73	0,60	60,36	O96008	Mitochondrial import receptor subunit TOM40 homolog	TOMM40
0,050	-0,73	0,60	60,35	Q01995	Transgelin	TAGLN
0,003	-0,73	0,60	60,33	Q96Q11	CCA tRNA nucleotidyltransferase 1, mitochondrial	TRNT1
0,049	-0,73	0,60	60,29	P53992	Protein transport protein Sec24C	SEC24C

Supplemental Table S2b

0,033	-0,73	0,60	60,29	P08048;P17010	Zinc finger Y-chromosomal protein;Zinc finger X-chromosomal protein	ZFY;ZFX
0,026	-0,73	0,60	60,16	P10155	60 kDa SS-A/Ro ribonucleoprotein	TROVE2
0,042	-0,74	0,60	60,04	Q96HW7	Integrator complex subunit 4	INTS4
0,030	-0,74	0,60	59,87	Q9H078	Caseinolytic peptidase B protein homolog	CLPB
0,023	-0,74	0,60	59,87	Q01804	OTU domain-containing protein 4	OTUD4
0,044	-0,74	0,60	59,87	Q92614	Unconventional myosin-XVIIIa	MYO18A
0,010	-0,74	0,60	59,81	O00217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	NDUFS8
0,015	-0,74	0,60	59,72	Q16539	Mitogen-activated protein kinase 14	MAPK14
0,018	-0,75	0,59	59,44	P23458	Tyrosine-protein kinase JAK1	JAK1
0,041	-0,76	0,59	59,05	Q6ISB3	Grainyhead-like protein 2 homolog	GRHL2
0,050	-0,76	0,59	59,05	Q96EZ8	Microspherule protein 1	MCRS1
0,003	-0,78	0,58	58,40	Q13617	Cullin-2	CUL2
0,028	-0,78	0,58	58,27	Q9UG63	ATP-binding cassette sub-family F member 2	ABCF2
0,027	-0,78	0,58	58,24	Q9BZJ0	Crooked neck-like protein 1	CRNKL1
0,011	-0,79	0,58	57,86	Q9Y2S0	DNA-directed RNA polymerases I and III subunit RPAC2	POLR1D
0,009	-0,79	0,58	57,83	Q14192	Four and a half LIM domains protein 2	FHL2
0,020	-0,79	0,58	57,83	Q9UHV7	Mediator of RNA polymerase II transcription subunit 13	MED13
0,021	-0,79	0,58	57,78	Q15382	GTP-binding protein Rheb	RHEB
0,027	-0,80	0,57	57,35	Q13144	Translation initiation factor eIF-2B subunit epsilon	EIF2B5
0,025	-0,81	0,57	57,20	Q96PE2	Rho guanine nucleotide exchange factor 17	ARHGEF17
0,036	-0,81	0,57	57,16	P43307	Translocon-associated protein subunit alpha	SSR1
0,037	-0,81	0,57	57,04	Q9Y2A7	Nck-associated protein 1	NCKAP1
0,031	-0,81	0,57	57,04	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial	HAGH
0,007	-0,82	0,57	56,64	P41227	N-alpha-acetyltransferase 10	NAA10
0,028	-0,82	0,57	56,61	O95166;Q9H0R8	Gamma-aminobutyric acid receptor-associated protein;Gamma-aminobutyric acid receptor-associated protein 1	GABARAP;GABARAPL1
0,009	-0,82	0,57	56,56	Q53GQ0	Estradiol 17-beta-dehydrogenase 12	HSD17B12
0,040	-0,83	0,56	56,41	Q92817	Envoplakin	EVPL
0,036	-0,83	0,56	56,25	A1L020	RNA-binding protein MEX3A	MEX3A
0,024	-0,83	0,56	56,25	P53621	Coatomer subunit alpha;Xenin;Proxenin	COPA
0,001	-0,84	0,56	55,86	P51858	Hepatoma-derived growth factor	HDGF
0,017	-0,85	0,55	55,50	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR
0,007	-0,85	0,55	55,48	P52948	Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;Nup96	NUP98
0,037	-0,85	0,55	55,46	Q6P1L8	39S ribosomal protein L14, mitochondrial	MRPL14

Supplemental Table S2b

0,034	-0,85	0,55	55,32	Q14241	Transcription elongation factor B polypeptide 3	TCEB3
0,008	-0,86	0,55	55,19	Q14134	Tripartite motif-containing protein 29	TRIM29
0,042	-0,86	0,55	55,10	P21283	V-type proton ATPase subunit C 1	ATP6V1C1
0,018	-0,86	0,55	55,09	Q8NEL9	Phospholipase DDHD1	DDHD1
0,022	-0,88	0,54	54,34	Q96CW1	AP-2 complex subunit mu	AP2M1
0,001	-0,88	0,54	54,34	Q8IYB3	Serine/arginine repetitive matrix protein 1	SRRM1
0,035	-0,88	0,54	54,34	Q8NEM2	SHC SH2 domain-binding protein 1	SHCBP1
0,022	-0,89	0,54	53,96	Q6UXN9	WD repeat-containing protein 82	WDR82
0,025	-0,89	0,54	53,96	Q9H0W8	Protein SMG9	SMG9
0,019	-0,89	0,54	53,96	P12236	ADP/ATP translocase 3;ADP/ATP translocase 3, N-terminally processed	SLC25A6
0,039	-0,89	0,54	53,96	P55010	Eukaryotic translation initiation factor 5	EIF5
0,038	-0,89	0,54	53,96	Q8IV08	Phospholipase D3	PLD3
0,032	-0,89	0,54	53,79	Q9P015	39S ribosomal protein L15, mitochondrial	MRPL15
0,013	-0,90	0,54	53,71	Q9Y4B6	Protein VPRBP	VPRBP
0,037	-0,90	0,54	53,57	Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3
0,050	-0,91	0,53	53,22	P50416	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A
0,009	-0,91	0,53	53,04	Q969T7	7-methylguanosine phosphate-specific 5-nucleotidase	NT5C3B
0,018	-0,92	0,53	53,03	Q8TDH9	Biogenesis of lysosome-related organelles complex 1 subunit 5	BLOC1S5
0,001	-0,92	0,53	52,99	Q5VTR2	E3 ubiquitin-protein ligase BRE1A	RNF20
0,037	-0,92	0,53	52,80	Q9H993	UPF0364 protein C6orf211	C6orf211
0,010	-0,94	0,52	52,29	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	GFPT1
0,010	-0,94	0,52	52,12	Q9H6W3	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	NO66
0,029	-0,94	0,52	52,12	P69905	Hemoglobin subunit alpha	HBA1
0,021	-0,94	0,52	51,99	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADS
0,034	-0,95	0,52	51,76	Q96KQ7	Histone-lysine N-methyltransferase EHMT2	EHMT2
0,023	-0,96	0,51	51,48	Q9H0E9	Bromodomain-containing protein 8	BRD8
0,042	-0,96	0,51	51,41	Q7Z7C8	Transcription initiation factor TFIID subunit 8	TAF8
0,006	-0,96	0,51	51,41	Q92576	PHD finger protein 3	PHF3
0,033	-0,96	0,51	51,41	Q9H4L4	Sentrin-specific protease 3	SEN3
0,035	-0,97	0,51	51,05	Q9NPI6	mRNA-decapping enzyme 1A	DCP1A
0,035	-0,97	0,51	51,05	P38606	V-type proton ATPase catalytic subunit A	ATP6V1A
0,029	-0,98	0,51	50,70	P19224	UDP-glucuronosyltransferase 1-6	UGT1A6
0,045	-0,99	0,50	50,35	Q14967	Calmequin	CLGN

Supplemental Table S2b

0,009	-0,99	0,50	50,35	Q92563	Testican-2	SPOCK2
0,011	-0,99	0,50	50,35	P06756	Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain	ITGAV
0,027	-0,99	0,50	50,28	Q92667	A-kinase anchor protein 1, mitochondrial	AKAP1
0,023	-1,00	0,50	50,08	Q8NDH3	Probable aminopeptidase NPEPL1	NPEPL1
0,016	-1,01	0,50	49,67	Q9NVS9	Pyridoxine-5-phosphate oxidase	PNPO
0,010	-1,01	0,50	49,65	Q9UBW7	Zinc finger MYM-type protein 2	ZMYM2
0,042	-1,01	0,50	49,65	Q8WXE1	ATR-interacting protein	ATRIP
0,026	-1,01	0,50	49,65	Q9NTZ6	RNA-binding protein 12	RBM12
0,031	-1,02	0,49	49,31	Q14669	E3 ubiquitin-protein ligase TRIP12	TRIP12
0,002	-1,02	0,49	49,31	Q9Y580	RNA-binding protein 7	RBM7
0,048	-1,03	0,49	48,97	Q8IUC4	Rhopilin-2	RHPN2
0,046	-1,03	0,49	48,97	Q15811	Intersectin-1	ITSN1
0,026	-1,04	0,49	48,67	Q96GA3	Protein LTV1 homolog	LTV1
0,025	-1,04	0,49	48,63	Q6P1J9	Parafibromin	CDC73
0,041	-1,04	0,49	48,63	Q15004	PCNA-associated factor	KIAA0101
0,044	-1,04	0,49	48,63	P35241	Radixin	RDX
0,029	-1,05	0,48	48,38	Q92544	Transmembrane 9 superfamily member 4	TM9SF4
0,030	-1,05	0,48	48,33	O95394	Phosphoacetylglucosamine mutase	PGM3
0,035	-1,05	0,48	48,30	Q9H8V3	Protein ECT2	ECT2
0,008	-1,05	0,48	48,30	Q8WUM0	Nuclear pore complex protein Nup133	NUP133
0,043	-1,06	0,48	47,96	P11086	Phenylethanolamine N-methyltransferase	PNMT
0,000	-1,07	0,48	47,80	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4
0,039	-1,07	0,48	47,63	O95453	Poly(A)-specific ribonuclease PARN	PARN
0,021	-1,09	0,47	46,98	O75367	Core histone macro-H2A.1	H2AFY
0,022	-1,09	0,47	46,98	Q9NZN4	EH domain-containing protein 2	EHD2
0,000	-1,09	0,47	46,89	Q96C86	m7GpppX diphosphatase	DCPS
0,049	-1,10	0,47	46,66	Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	NUCKS1
0,034	-1,10	0,47	46,66	O43768	Alpha-endosulfine	ENSA
0,045	-1,10	0,47	46,55	Q69YN4	Protein virilizer homolog	KIAA1429
0,042	-1,11	0,46	46,47	P27448	MAP/microtubule affinity-regulating kinase 3	MARK3
0,034	-1,12	0,46	46,10	Q8WVX9	Fatty acyl-CoA reductase 1	FAR1
0,021	-1,12	0,46	46,08	Q8N1G2	Cap-specific mRNA (nucleoside-2-O-)-methyltransferase 1	CMTR1
0,014	-1,12	0,46	46,01	O60318	Germinal-center associated nuclear protein	MCM3AP

Supplemental Table S2b

0,012	-1,13	0,46	45,55	Q9UKK6	NTF2-related export protein 1	NXT1
0,007	-1,14	0,45	45,38	Q13162	Peroxioredoxin-4	PRDX4
0,005	-1,14	0,45	45,38	9BWW4;P81877;Q9BWC	Single-stranded DNA-binding protein 3;Single-stranded DNA-binding protein 2;Single-stranded DNA-binding protein 1	SSBP3;SSBP2;SSBP4
0,006	-1,16	0,45	44,75	P30504	HLA class I histocompatibility antigen, Cw-4 alpha chain	HLA-C
0,007	-1,16	0,45	44,75	Q5VZL5	Zinc finger MYM-type protein 4	ZMYM4
0,046	-1,16	0,45	44,60	P46736	Lys-63-specific deubiquitinase BRCC36	BRCC3
0,013	-1,17	0,44	44,32	Q9Y6H1;Q5T1J5	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial;Putative mitochondrial protein	CHCHD2;CHCHD2P9
0,017	-1,18	0,44	44,26	O15042	U2 snRNP-associated SURP motif-containing protein	U2SURP
0,031	-1,18	0,44	44,14	Q9HCM1	Uncharacterized protein KIAA1551	KIAA1551
0,002	-1,19	0,44	43,83	Q53H12	Acylglycerol kinase, mitochondrial	AGK
0,049	-1,19	0,44	43,83	Q8N5C6	S1 RNA-binding domain-containing protein 1	SRBD1
0,012	-1,19	0,44	43,73	Q9NTX5	Ethylmalonyl-CoA decarboxylase	ECHDC1
0,004	-1,20	0,44	43,66	Q7L3B6	Hsp90 co-chaperone Cdc37-like 1	CDC37L1
0,022	-1,20	0,44	43,60	P31350	Ribonucleoside-diphosphate reductase subunit M2	RRM2
0,006	-1,20	0,44	43,53	Q13503	Mediator of RNA polymerase II transcription subunit 21	MED21
0,043	-1,21	0,43	43,23	Q9BRD0	BUD13 homolog	BUD13
0,050	-1,22	0,43	42,98	Q6PK04	Coiled-coil domain-containing protein 137	CCDC137
0,036	-1,22	0,43	42,93	Q8TF74	WAS/WASL-interacting protein family member 2	WIPF2
0,001	-1,22	0,43	42,93	Q15545	Transcription initiation factor TFIID subunit 7	TAF7
0,049	-1,22	0,43	42,90	Q9Y5L0	Transportin-3	TNPO3
0,038	-1,22	0,43	42,90	P55210	Caspase-7;Caspase-7 subunit p20;Caspase-7 subunit p11	CASP7
0,007	-1,23	0,43	42,63	O95071	E3 ubiquitin-protein ligase UBR5	UBR5
0,006	-1,25	0,42	42,04	P29375	Lysine-specific demethylase 5A	KDM5A
0,036	-1,25	0,42	42,04	O15460	Prolyl 4-hydroxylase subunit alpha-2	P4HA2
0,049	-1,26	0,42	41,75	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	ACAT2
0,050	-1,27	0,41	41,47	Q9BZQ8	Protein Niban	FAM129A
0,050	-1,27	0,41	41,47	P23921	Ribonucleoside-diphosphate reductase large subunit	RRM1
0,002	-1,27	0,41	41,47	Q9BQ39	ATP-dependent RNA helicase DDX50	DDX50
0,009	-1,28	0,41	41,21	O94855	Protein transport protein Sec24D	SEC24D
0,048	-1,28	0,41	41,18	P51572	B-cell receptor-associated protein 31	BCAP31
0,038	-1,29	0,41	40,90	P84090	Enhancer of rudimentary homolog	ERH
0,029	-1,29	0,41	40,77	Q9H267	Vacuolar protein sorting-associated protein 33B	VPS33B
0,007	-1,30	0,41	40,73	O15347	High mobility group protein B3	HMGB3

Supplemental Table S2b

0,034	-1,30	0,41	40,61	Q92796	Disks large homolog 3	DLG3
0,009	-1,30	0,41	40,61	P50402	Emerin	EMD
0,014	-1,30	0,41	40,61	Q8TEX9	Importin-4	IPO4
0,046	-1,30	0,41	40,61	Q9Y2R5	28S ribosomal protein S17, mitochondrial	MRPS17
0,047	-1,31	0,40	40,33	Q12797	Aspartyl/asparaginyl beta-hydroxylase	ASPH
0,043	-1,33	0,40	39,78	Q9NXX6	Non-structural maintenance of chromosomes element 4 homolog A	NSMCE4A
0,049	-1,33	0,40	39,78	Q9BWM7	Sideroflexin-3	SFXN3
0,007	-1,34	0,40	39,50	Q9Y4F1	FERM, RhoGEF and pleckstrin domain-containing protein 1	FARP1
0,032	-1,34	0,40	39,50	Q5VWG9	Transcription initiation factor TFIID subunit 3	TAF3
0,048	-1,35	0,39	39,24	Q96E29	Transcription termination factor 3, mitochondrial	MTERF3
0,037	-1,35	0,39	39,12	Q9BZ23	Pantothenate kinase 2, mitochondrial	PANK2
0,028	-1,36	0,39	38,96	Q8IWA0	WD repeat-containing protein 75	WDR75
0,039	-1,36	0,39	38,96	Q9HCS7	Pre-mRNA-splicing factor SYF1	XAB2
0,004	-1,36	0,39	38,96	P40692	DNA mismatch repair protein Mlh1	MLH1
0,003	-1,37	0,39	38,75	Q9NZ45	CDGSH iron-sulfur domain-containing protein 1	CISD1
0,000	-1,37	0,39	38,75	Q9H488	GDP-fucose protein O-fucosyltransferase 1	POFUT1
0,009	-1,37	0,39	38,72	Q9NX08	COMM domain-containing protein 8	COMMD8
0,024	-1,37	0,39	38,69	O14980	Exportin-1	XPO1
0,015	-1,38	0,38	38,42	Q69YH5	Cell division cycle-associated protein 2	CDCA2
0,049	-1,38	0,38	38,42	439;P13746;P30455;P3C	HLA class I histocompatibility antigen, A-3 alpha chain;HLA class I histocompatibility	HLA-A
0,034	-1,38	0,38	38,41	Q9Y314	Nitric oxide synthase-interacting protein	NOSIP
0,004	-1,39	0,38	38,24	Q9HD26	Golgi-associated PDZ and coiled-coil motif-containing protein	GOPC
0,001	-1,39	0,38	38,16	Q16706	Alpha-mannosidase 2	MAN2A1
0,021	-1,39	0,38	38,16	P52209	6-phosphogluconate dehydrogenase, decarboxylating	PGD
0,030	-1,40	0,38	38,02	P12830	Cadherin-1;E-Cad/CTF1;E-Cad/CTF2;E-Cad/CTF3	CDH1
0,010	-1,40	0,38	37,89	Q12849	G-rich sequence factor 1	GRSF1
0,004	-1,40	0,38	37,82	Q8IY67	Ribonucleoprotein PTB-binding 1	RAVER1
0,017	-1,41	0,38	37,63	Q96T58	Msx2-interacting protein	SPEN
0,045	-1,41	0,38	37,63	O75436	Vacuolar protein sorting-associated protein 26A	VPS26A
0,038	-1,42	0,37	37,49	Q6UN15	Pre-mRNA 3-end-processing factor FIP1	FIP1L1
0,001	-1,43	0,37	37,11	P54886	Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl pho	ALDH18A1
0,016	-1,44	0,37	36,86	Q92616	Translational activator GCN1	GCN1L1
0,026	-1,45	0,37	36,60	O60306	Intron-binding protein aquarius	AQR

Supplemental Table S2b

0,047	-1,45	0,37	36,58	O15047	Histone-lysine N-methyltransferase SETD1A	SETD1A
0,025	-1,46	0,36	36,35	Q9BQ69	O-acetyl-ADP-ribose deacetylase MACROD1	MACROD1
0,049	-1,46	0,36	36,35	O00170	AH receptor-interacting protein	AIP
0,047	-1,46	0,36	36,35	Q96MX6	WD repeat-containing protein 92	WDR92
0,006	-1,46	0,36	36,34	Q13505	Metaxin-1	MTX1
0,002	-1,48	0,36	35,85	Q68CP9	AT-rich interactive domain-containing protein 2	ARID2
0,030	-1,49	0,36	35,61	Q8TCZ2	CD99 antigen-like protein 2	CD99L2
0,028	-1,49	0,36	35,60	P62166	Neuronal calcium sensor 1	NCS1
0,040	-1,49	0,36	35,60	P09001	39S ribosomal protein L3, mitochondrial	MRPL3
0,035	-1,49	0,36	35,60	P19387	DNA-directed RNA polymerase II subunit RPB3	POLR2C
0,006	-1,50	0,35	35,36	Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13
0,029	-1,51	0,35	35,11	P22234	Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide s	PAICS
0,023	-1,51	0,35	35,11	Q15528	Mediator of RNA polymerase II transcription subunit 22	MED22
0,009	-1,51	0,35	35,11	O15027	Protein transport protein Sec16A	SEC16A
0,049	-1,52	0,35	34,87	Q6VMQ6	Activating transcription factor 7-interacting protein 1	ATF7IP
0,010	-1,52	0,35	34,87	Q12769	Nuclear pore complex protein Nup160	NUP160
0,030	-1,52	0,35	34,87	P48634	Protein PRRC2A	PRRC2A
0,033	-1,53	0,35	34,51	Q9H9Y6	DNA-directed RNA polymerase I subunit RPA2	POLR1B
0,005	-1,54	0,34	34,39	Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1
0,003	-1,55	0,34	34,23	O94762	ATP-dependent DNA helicase Q5	RECQL5
0,048	-1,55	0,34	34,19	Q9H6I2	Transcription factor SOX-17	SOX17
0,015	-1,55	0,34	34,15	Q8NEJ9	Neuroguidin	NGDN
0,039	-1,55	0,34	34,15	P38432	Coilin	COIL
0,003	-1,57	0,34	33,68	Q9NYV4	Cyclin-dependent kinase 12	CDK12
0,001	-1,58	0,33	33,47	P40261	Nicotinamide N-methyltransferase	NNMT
0,007	-1,60	0,33	32,99	Q9UM13	Anaphase-promoting complex subunit 10	ANAPC10
0,038	-1,61	0,33	32,84	Q9P1Y5	Calmodulin-regulated spectrin-associated protein 3	CAMSAP3
0,039	-1,62	0,33	32,56	Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	PPP2R5D
0,025	-1,62	0,33	32,53	O75534	Cold shock domain-containing protein E1	CSDE1
0,013	-1,63	0,32	32,31	Q9HCN4	GPN-loop GTPase 1	GPN1
0,012	-1,64	0,32	32,09	Q8N2Z9	Centromere protein S	APITD1
0,046	-1,64	0,32	32,09	P36776	Lon protease homolog, mitochondrial	LONP1
0,027	-1,64	0,32	32,09	P49591	Serine--tRNA ligase, cytoplasmic	SARS

Supplemental Table S2b

0,033	-1,65	0,32	31,91	P0CG12	Chromosome transmission fidelity protein 8 homolog isoform 2	CHTF8
0,048	-1,65	0,32	31,86	Q9P2R6	Arginine-glutamic acid dipeptide repeats protein	RERE
0,042	-1,66	0,32	31,64	Q2NL82	Pre-rRNA-processing protein TSR1 homolog	TSR1
0,025	-1,66	0,32	31,64	Q9UGP8	Translocation protein SEC63 homolog	SEC63
0,017	-1,66	0,32	31,64	P33897	ATP-binding cassette sub-family D member 1	ABCD1
0,041	-1,67	0,32	31,53	O43414	ERI1 exoribonuclease 3	ERI3
0,008	-1,67	0,31	31,43	Q9Y2T2	AP-3 complex subunit mu-1	AP3M1
0,022	-1,67	0,31	31,43	P16152	Carbonyl reductase [NADPH] 1	CBR1
0,031	-1,68	0,31	31,21	Q96Q05	Trafficking protein particle complex subunit 9	TRAPPC9
0,012	-1,68	0,31	31,21	Q13084	39S ribosomal protein L28, mitochondrial	MRPL28
0,022	-1,69	0,31	30,99	Q8N5N7	39S ribosomal protein L50, mitochondrial	MRPL50
0,047	-1,72	0,30	30,35	P37837	Transaldolase	TALDO1
0,008	-1,73	0,30	30,22	P31749	RAC-alpha serine/threonine-protein kinase	AKT1
0,033	-1,73	0,30	30,15	P14927	Cytochrome b-c1 complex subunit 7	UQCRB
0,027	-1,74	0,30	29,94	P35573	Glycogen debranching enzyme;4-alpha-glucanotransferase;Amylo-alpha-1,6-glucosi	AGL
0,014	-1,74	0,30	29,87	Q16864	V-type proton ATPase subunit F	ATP6V1F
0,040	-1,76	0,30	29,52	P48730	Casein kinase I isoform delta	CSNK1D
0,012	-1,76	0,30	29,52	P62491;Q15907	Ras-related protein Rab-11A;Ras-related protein Rab-11B	RAB11A;RAB11B
0,017	-1,77	0,29	29,42	Q9NZD8	Maspardin	SPG21
0,015	-1,77	0,29	29,38	Q9UJX6	Anaphase-promoting complex subunit 2	ANAPC2
0,032	-1,77	0,29	29,37	P62070	Ras-related protein R-Ras2	RRAS2
0,017	-1,79	0,29	28,92	P30626	Sorcin	SRI
0,004	-1,80	0,29	28,72	Q9H9A5	CCR4-NOT transcription complex subunit 10	CNOT10
0,018	-1,81	0,29	28,52	Q8WUB8	PHD finger protein 10	PHF10
0,004	-1,81	0,29	28,52	A8MW92	PHD finger protein 20-like protein 1	PHF20L1
0,006	-1,81	0,29	28,52	O60293	Zinc finger C3H1 domain-containing protein	ZFC3H1
0,018	-1,81	0,28	28,45	Q14331;Q9BZ01	Protein FRG1;Protein FRG1B	FRG1;FRG1B
0,001	-1,82	0,28	28,32	Q969Z3;Q5VT66	Mitochondrial amidoxime reducing component 2;Mitochondrial amidoxime-reducin	MARC2;MARC1
0,028	-1,83	0,28	28,11	Q13535	Serine/threonine-protein kinase ATR	ATR
0,016	-1,84	0,28	27,86	O75928	E3 SUMO-protein ligase PIAS2	PIAS2
0,021	-1,85	0,28	27,74	Q9Y399	28S ribosomal protein S2, mitochondrial	MRPS2
0,024	-1,89	0,27	27,01	Q5R314	Tetratricopeptide repeat protein 38	TTC38
0,046	-1,91	0,27	26,61	Q08722	Leukocyte surface antigen CD47	CD47

Supplemental Table S2b

0,005	-1,91	0,27	26,56	Q9UGM6	Tryptophan--tRNA ligase, mitochondrial	WARS2
0,007	-1,94	0,26	26,06	O95155	Ubiquitin conjugation factor E4 B	UBE4B
0,028	-1,94	0,26	26,06	Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11
0,038	-1,94	0,26	26,06	Q8NI36	WD repeat-containing protein 36	WDR36
0,021	-1,94	0,26	26,06	Q86XZ4	Spermatogenesis-associated serine-rich protein 2	SPATS2
0,007	-1,95	0,26	25,94	O95989	Diphosphoinositol polyphosphate phosphohydrolase 1	NUDT3
0,006	-1,96	0,26	25,70	Q9NY93	Probable ATP-dependent RNA helicase DDX56	DDX56
0,041	-1,97	0,26	25,53	P55060	Exportin-2	CSE1L
0,039	-1,99	0,25	25,17	P31939	Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarbo	ATIC
0,016	-1,99	0,25	25,16	P38935	DNA-binding protein SMUBP-2	IGHMBP2
0,039	-2,04	0,24	24,32	O95235	Kinesin-like protein KIF20A	KIF20A
0,004	-2,06	0,24	23,97	P98088	Mucin-5AC	MUC5AC
0,000	-2,08	0,24	23,71	Q8NF37	Lysophosphatidylcholine acyltransferase 1	LPCAT1
0,005	-2,08	0,24	23,65	P55011	Solute carrier family 12 member 2	SLC12A2
0,031	-2,09	0,24	23,57	Q9NZJ9	Diphosphoinositol polyphosphate phosphohydrolase 2	NUDT4
0,039	-2,10	0,23	23,30	Q06481	Amyloid-like protein 2	APLP2
0,038	-2,12	0,23	23,00	O75616	GTPase Era, mitochondrial	ERAL1
0,030	-2,13	0,23	22,88	P42898	Methylenetetrahydrofolate reductase	MTHFR
0,001	-2,13	0,23	22,80	Q16352	Alpha-internexin	INA
0,043	-2,13	0,23	22,78	P01891	HLA class I histocompatibility antigen, A-68 alpha chain	HLA-A
0,027	-2,14	0,23	22,69	P16402	Histone H1.3	HIST1H1D
0,011	-2,15	0,23	22,51	Q6P179	Endoplasmic reticulum aminopeptidase 2	ERAP2
0,002	-2,17	0,22	22,22	Q9H5H4	Zinc finger protein 768	ZNF768
0,021	-2,19	0,22	21,92	P49406	39S ribosomal protein L19, mitochondrial	MRPL19
0,038	-2,20	0,22	21,76	Q9Y2X0	Mediator of RNA polymerase II transcription subunit 16	MED16
0,000	-2,20	0,22	21,76	Q9Y6W5	Wiskott-Aldrich syndrome protein family member 2	WASF2
0,028	-2,20	0,22	21,76	Q9NRY4	Rho GTPase-activating protein 35	ARHGAP35
0,016	-2,22	0,21	21,48	Q96B36	Proline-rich AKT1 substrate 1	AKT1S1
0,044	-2,22	0,21	21,40	Q6NXR4	TELO2-interacting protein 2	TTI2
0,015	-2,23	0,21	21,34	P11171	Protein 4.1	EPB41
0,016	-2,23	0,21	21,32	Q12824	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfami	SMARCB1
0,021	-2,24	0,21	21,17	Q9NYJ1	Cytochrome c oxidase assembly factor 4 homolog, mitochondrial	COA4
0,017	-2,25	0,21	21,02	P13807	Glycogen [starch] synthase, muscle	GYS1

Supplemental Table S2b

0,047	-2,28	0,21	20,66	Q8TB45	DEP domain-containing mTOR-interacting protein	DEPTOR
0,038	-2,28	0,21	20,59	Q9BYG5	Partitioning defective 6 homolog beta	PARD6B
0,016	-2,28	0,21	20,59	Q5SVZ6	Zinc finger MYM-type protein 1	ZMYM1
0,032	-2,28	0,21	20,59	Q92665	28S ribosomal protein S31, mitochondrial	MRPS31
0,002	-2,28	0,21	20,59	Q15054	DNA polymerase delta subunit 3	POLD3
0,029	-2,33	0,20	19,89	Q9UHG0	Doublecortin domain-containing protein 2	DCDC2
0,029	-2,34	0,20	19,80	Q9H2Y7	Zinc finger protein 106	ZNF106
0,034	-2,35	0,20	19,61	Q8ND04	Protein SMG8	SMG8
0,018	-2,35	0,20	19,61	Q13630	GDP-L-fucose synthase	TSTA3
0,023	-2,36	0,19	19,48	Q04760	Lactoylglutathione lyase	GLO1
0,038	-2,36	0,19	19,47	O75962	Triple functional domain protein	TRIO
0,001	-2,37	0,19	19,34	Q9Y2Q3	Glutathione S-transferase kappa 1	GSTK1
0,003	-2,41	0,19	18,82	Q9UIV1	CCR4-NOT transcription complex subunit 7	CNOT7
0,021	-2,44	0,18	18,43	Q96JM3	Chromosome alignment-maintaining phosphoprotein 1	CHAMP1
0,023	-2,44	0,18	18,43	P01034	Cystatin-C	CST3
0,015	-2,45	0,18	18,30	Q14527	Helicase-like transcription factor	HLTF
0,043	-2,47	0,18	18,05	P25208	Nuclear transcription factor Y subunit beta	NFYB
0,003	-2,47	0,18	18,03	Q96EA4	Protein Spindly	SPDL1
0,005	-2,49	0,18	17,80	P07339	Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain	CTSD
0,001	-2,50	0,18	17,73	Q9Y3A4	Ribosomal RNA-processing protein 7 homolog A	RRP7A
0,008	-2,50	0,18	17,68	P10746	Uroporphyrinogen-III synthase	UROS
0,048	-2,50	0,18	17,68	O95298;E9PQ53	NADH dehydrogenase [ubiquinone] 1 subunit C2;NADH dehydrogenase [ubiquinone] 1 subunit C2	NDUFC2;NDUFC2-KCTD13
0,011	-2,51	0,18	17,56	O94973	AP-2 complex subunit alpha-2	AP2A2
0,045	-2,51	0,18	17,56	Q05D32	CTD small phosphatase-like protein 2	CTDSPL2
0,005	-2,52	0,17	17,43	Q14257	Reticulocalbin-2	RCN2
0,027	-2,52	0,17	17,39	P16401	Histone H1.5	HIST1H1B
0,024	-2,53	0,17	17,36	O75362	Zinc finger protein 217	ZNF217
0,014	-2,53	0,17	17,26	Q8N5A5	Zinc finger CCCH-type with G patch domain-containing protein	ZGPAT
0,035	-2,55	0,17	17,08	P30042	ES1 protein homolog, mitochondrial	C21orf33
0,001	-2,56	0,17	16,95	P98179	Putative RNA-binding protein 3	RBM3
0,019	-2,57	0,17	16,84	Q96KP1	Exocyst complex component 2	EXOC2
0,002	-2,66	0,16	15,82	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1
0,041	-2,73	0,15	15,11	Q08AD1	Calmodulin-regulated spectrin-associated protein 2	CAMSAP2

Supplemental Table S2b

0,002	-2,73	0,15	15,07	Q4FZB7	Histone-lysine N-methyltransferase SUV420H1	SUV420H1
0,010	-2,75	0,15	14,83	P78346	Ribonuclease P protein subunit p30	RPP30
0,002	-2,77	0,15	14,62	O94916	Nuclear factor of activated T-cells 5	NFAT5
0,000	-2,84	0,14	13,97	O43716	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	GATC
0,032	-2,85	0,14	13,87	Q9Y4E5	Zinc finger protein 451	ZNF451
0,034	-2,96	0,13	12,85	Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5	FKBP5
0,010	-2,96	0,13	12,85	Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCC1
0,002	-2,98	0,13	12,70	Q15361	Transcription termination factor 1	TTF1
0,020	-3,02	0,12	12,33	Q06587	E3 ubiquitin-protein ligase RING1	RING1
0,000	-3,05	0,12	12,04	Q8TD47	40S ribosomal protein S4, Y isoform 2	RPS4Y2
0,036	-3,06	0,12	11,99	P29034	Protein S100-A2	S100A2
0,001	-3,07	0,12	11,91	Q96CV9	Optineurin	OPTN
0,002	-3,11	0,12	11,62	Q96MU7	YTH domain-containing protein 1	YTHDC1
0,003	-3,11	0,12	11,56	A1X283	SH3 and PX domain-containing protein 2B	SH3PXD2B
0,043	-3,22	0,11	10,77	Q9BVK2	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	ALG8
0,009	-3,24	0,11	10,58	Q9NVV4	Poly(A) RNA polymerase, mitochondrial	MTPAP
0,026	-3,25	0,11	10,51	Q8N5L8	Ribonuclease P protein subunit p25-like protein	RPP25L
0,000	-3,27	0,10	10,37	Q99798	Aconitate hydratase, mitochondrial	ACO2
0,007	-3,29	0,10	10,24	Q17RN3	Protein FAM98C	FAM98C
0,008	-3,33	0,10	9,95	Q969Y2	tRNA modification GTPase GTPBP3, mitochondrial	GTPBP3
0,011	-3,35	0,10	9,82	Q92766	Ras-responsive element-binding protein 1	RREB1
0,032	-3,36	0,10	9,77	P07711	Cathepsin L1;Cathepsin L1 heavy chain;Cathepsin L1 light chain	CTSL
0,010	-3,36	0,10	9,74	Q49MG5	Microtubule-associated protein 9	MAP9
0,028	-3,38	0,10	9,61	O75843	AP-1 complex subunit gamma-like 2	AP1G2
0,048	-3,48	0,09	8,96	Q9HCN8	Stromal cell-derived factor 2-like protein 1	SDF2L1
0,036	-3,56	0,08	8,48	P58107	Epiplakin	EPPK1
0,034	-3,66	0,08	7,90	Q96TC7	Regulator of microtubule dynamics protein 3	RMDN3
0,000	-3,68	0,08	7,81	Q8NDT2	Putative RNA-binding protein 15B	RBM15B
0,001	-3,72	0,08	7,59	O00193	Small acidic protein	SMAP
0,017	-3,86	0,07	6,89	Q96S44	TP53-regulating kinase	TP53RK
0,050	-3,87	0,07	6,84	P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H
0,001	-3,91	0,07	6,65	Q8TDD1	ATP-dependent RNA helicase DDX54	DDX54
0,010	-3,94	0,07	6,52	Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	ARPC5L

Supplemental Table S2b

0,027	-4,21	0,05	5,40	Q70E73	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1
0,014	-4,28	0,05	5,15	P63272	Transcription elongation factor SPT4	SUPT4H1
0,035	-4,45	0,05	4,58	Q5K651	Sterile alpha motif domain-containing protein 9	SAMD9
0,000	-4,50	0,04	4,42	Q92626	Peroxidasin homolog	PXDN
0,003	-4,95	0,03	3,24	P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	PPIF
24h Down						
0,047	-0,12	0,92	92,02	Q9Y230	RuvB-like 2	RUVBL2
0,024	-0,12	0,92	92,02	Q9BY44	Eukaryotic translation initiation factor 2A;Eukaryotic translation initiation factor 2A	EIF2A
0,005	-0,12	0,92	91,79	P06746	DNA polymerase beta	POLB
0,046	-0,16	0,90	89,50	Q9NXV6	CDKN2A-interacting protein	CDKN2AIP
0,022	-0,16	0,90	89,50	Q9Y265	RuvB-like 1	RUVBL1
0,019	-0,16	0,90	89,50	P50402	Emerin	EMD
0,017	-0,16	0,90	89,50	O95400	CD2 antigen cytoplasmic tail-binding protein 2	CD2BP2
0,044	-0,17	0,89	88,93	P61586	Transforming protein RhoA	RHOA
0,029	-0,17	0,89	88,88	Q12788	Transducin beta-like protein 3	TBL3
0,018	-0,19	0,88	87,74	P11940	Polyadenylate-binding protein 1	PABPC1
0,024	-0,19	0,88	87,66	O43809	Cleavage and polyadenylation specificity factor subunit 5	NUDT21
0,022	-0,19	0,87	87,44	Q9H2G2	STE20-like serine/threonine-protein kinase	SLK
0,001	-0,20	0,87	87,25	P45880	Voltage-dependent anion-selective channel protein 2	VDAC2
0,047	-0,20	0,87	87,15	Q86UP2	Kinectin	KTN1
0,019	-0,20	0,87	87,06	Q15046	Lysine--tRNA ligase	KARS
0,041	-0,20	0,87	87,06	Q7L014	Probable ATP-dependent RNA helicase DDX46	DDX46
0,019	-0,20	0,87	87,06	O14776	Transcription elongation regulator 1	TCERG1
0,010	-0,20	0,87	86,86	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	PSMD13
0,026	-0,21	0,86	86,45	Q92841	Probable ATP-dependent RNA helicase DDX17	DDX17
0,015	-0,22	0,86	85,86	P13010	X-ray repair cross-complementing protein 5	XRCC5
0,010	-0,22	0,86	85,86	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	PPP1CA
0,033	-0,22	0,86	85,86	Q16630	Cleavage and polyadenylation specificity factor subunit 6	CPSF6
0,015	-0,23	0,85	85,26	Q9UHD8	Septin-9	40057,000
0,024	-0,23	0,85	85,26	Q15287	RNA-binding protein with serine-rich domain 1	RNPS1
0,027	-0,24	0,85	84,85	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	RPN1
0,001	-0,24	0,85	84,71	Q9NVT9	Armadillo repeat-containing protein 1	ARMC1
0,009	-0,24	0,85	84,67	Q9UQB8	Brain-specific angiogenesis inhibitor 1-associated protein 2	BAIAP2

Supplemental Table S2b

0,001	-0,24	0,85	84,67	Q5T280	Uncharacterized protein C9orf114	C9orf114
0,029	-0,25	0,84	83,91	Q15365	Poly(rC)-binding protein 1	PCBP1
0,014	-0,26	0,84	83,70	P26640	Valine--tRNA ligase	VARS
0,033	-0,26	0,84	83,51	Q13573	SNW domain-containing protein 1	SNW1
0,025	-0,27	0,83	83,17	P22102	Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine	GART
0,024	-0,28	0,83	82,63	Q9BZK7	F-box-like/WD repeat-containing protein TBL1XR1	TBL1XR1
0,043	-0,28	0,83	82,52	P28482	Mitogen-activated protein kinase 1	MAPK1
0,033	-0,28	0,82	82,48	Q86XP3	ATP-dependent RNA helicase DDX42	DDX42
0,024	-0,28	0,82	82,45	P12931	Proto-oncogene tyrosine-protein kinase Src	SRC
0,009	-0,28	0,82	82,36	Q92820	Gamma-glutamyl hydrolase	GGH
0,042	-0,29	0,82	82,04	P48444	Coatomer subunit delta	ARCN1
0,011	-0,29	0,82	82,02	Q9P2E9	Ribosome-binding protein 1	RRBP1
0,007	-0,29	0,82	81,79	P41223	Protein BUD31 homolog	BUD31
0,002	-0,30	0,81	81,23	Q96QK1	Vacuolar protein sorting-associated protein 35	VPS35
0,036	-0,30	0,81	81,23	P61978	Heterogeneous nuclear ribonucleoprotein K	HNRNPK
0,006	-0,30	0,81	81,04	P54136	Arginine--tRNA ligase, cytoplasmic	RARS
0,039	-0,31	0,81	80,66	Q8TEQ6	Gem-associated protein 5	GEMIN5
0,004	-0,31	0,81	80,66	P35637	RNA-binding protein FUS	FUS
0,012	-0,31	0,81	80,63	Q9Y5S2	Serine/threonine-protein kinase MRCK beta	CDC42BPB
0,015	-0,31	0,81	80,60	Q00610	Clathrin heavy chain 1	CLTC
0,049	-0,31	0,80	80,45	Q9UMX0	Ubiquilin-1	UBQLN1
0,030	-0,32	0,80	80,37	P26196	Probable ATP-dependent RNA helicase DDX6	DDX6
0,014	-0,32	0,80	80,11	P78347	General transcription factor II-I	GTF2I
0,024	-0,32	0,80	80,11	P49792	E3 SUMO-protein ligase RanBP2	RANBP2
0,038	-0,32	0,80	80,11	Q13503	Mediator of RNA polymerase II transcription subunit 21	MED21
0,015	-0,33	0,80	79,72	P49327	Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] 4	FASN
0,014	-0,33	0,80	79,55	P63279	SUMO-conjugating enzyme UBC9	UBE2I
0,049	-0,33	0,80	79,55	P09497	Clathrin light chain B	CLTB
0,031	-0,33	0,80	79,55	Q9Y2W2	WW domain-binding protein 11	WBP11
0,039	-0,33	0,80	79,51	Q5T6F2	Ubiquitin-associated protein 2	UBAP2
0,011	-0,33	0,79	79,39	Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A
0,046	-0,34	0,79	79,28	P61970	Nuclear transport factor 2	NUTF2
0,025	-0,34	0,79	78,99	O00203	AP-3 complex subunit beta-1	AP3B1

Supplemental Table S2b

0,044	-0,35	0,79	78,60	P42166	Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin	TMPO
0,016	-0,35	0,79	78,60	Q9UI10	Translation initiation factor eIF-2B subunit delta	EIF2B4
0,004	-0,35	0,79	78,51	Q99613;B5ME19	Eukaryotic translation initiation factor 3 subunit C;Eukaryotic translation initiation f	EIF3C;EIF3CL
0,011	-0,35	0,78	78,46	O00571;O15523	ATP-dependent RNA helicase DDX3X;ATP-dependent RNA helicase DDX3Y	DDX3X;DDX3Y
0,002	-0,35	0,78	78,34	Q9UMS4	Pre-mRNA-processing factor 19	PRPF19
0,029	-0,35	0,78	78,27	Q8WX93	Palladin	PALLD
0,004	-0,35	0,78	78,27	P46060	Ran GTPase-activating protein 1	RANGAP1
0,042	-0,35	0,78	78,19	P00918	Carbonic anhydrase 2	CA2
0,000	-0,35	0,78	78,19	P38432	Coilin	COIL
0,039	-0,36	0,78	77,92	P52926	High mobility group protein HMGI-C	HMGA2
0,039	-0,36	0,78	77,92	Q13685	Angio-associated migratory cell protein	AAMP
0,010	-0,36	0,78	77,92	O00148	ATP-dependent RNA helicase DDX39A	DDX39A
0,038	-0,36	0,78	77,92	O75083	WD repeat-containing protein 1	WDR1
0,023	-0,36	0,78	77,90	O43684	Mitotic checkpoint protein BUB3	BUB3
0,019	-0,36	0,78	77,85	Q9P031	Thyroid transcription factor 1-associated protein 26	CCDC59
0,021	-0,36	0,78	77,84	Q99873	Protein arginine N-methyltransferase 1	PRMT1
0,046	-0,37	0,78	77,54	Q8TD47	40S ribosomal protein S4, Y isoform 2	RPS4Y2
0,013	-0,37	0,77	77,38	P61247	40S ribosomal protein S3a	RPS3A
0,031	-0,37	0,77	77,35	P52597	Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprote	HNRNPF
0,015	-0,37	0,77	77,22	Q00341	Vigilin	HDLBP
0,046	-0,37	0,77	77,16	P35222	Catenin beta-1	CTNNB1
0,020	-0,38	0,77	77,08	Q14152	Eukaryotic translation initiation factor 3 subunit A	EIF3A
0,014	-0,38	0,77	76,87	P48047	ATP synthase subunit O, mitochondrial	ATP5O
0,017	-0,38	0,77	76,84	Q9BY77	Polymerase delta-interacting protein 3	POLDIP3
0,048	-0,38	0,77	76,84	Q7Z3B4	Nucleoporin p54	NUP54
0,023	-0,38	0,77	76,84	Q4LE39	AT-rich interactive domain-containing protein 4B	ARID4B
0,034	-0,38	0,77	76,68	Q9Y5A9	YTH domain-containing family protein 2	YTHDF2
0,009	-0,38	0,77	76,64	O15031	Plexin-B2	PLXNB2
0,026	-0,39	0,77	76,55	Q9H4A4	Aminopeptidase B	RNPEP
0,021	-0,39	0,76	76,48	P56192	Methionine--tRNA ligase, cytoplasmic	MARS
0,016	-0,39	0,76	76,31	Q9HCN4	GPN-loop GTPase 1	GPN1
0,023	-0,39	0,76	76,31	Q8N9M1	Uncharacterized protein C19orf47	C19orf47
0,030	-0,39	0,76	76,31	Q14839	Chromodomain-helicase-DNA-binding protein 4	CHD4

Supplemental Table S2b

0,049	-0,40	0,76	75,99	P04181	Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form	OAT
0,031	-0,40	0,76	75,82	P61163	Alpha-centractin	ACTR1A
0,028	-0,40	0,76	75,82	P19388	DNA-directed RNA polymerases I, II, and III subunit RPABC1	POLR2E
0,041	-0,40	0,76	75,79	Q13347	Eukaryotic translation initiation factor 3 subunit I	EIF3I
0,013	-0,40	0,76	75,79	Q9P0U4	CXXC-type zinc finger protein 1	CXXC1
0,000	-0,40	0,76	75,79	Q9ULL5	Proline-rich protein 12	PRR12
0,030	-0,40	0,76	75,76	Q92506	Estradiol 17-beta-dehydrogenase 8	HSD17B8
0,015	-0,40	0,76	75,55	P60842	Eukaryotic initiation factor 4A-I	EIF4A1
0,027	-0,40	0,76	75,55	Q96S99	Pleckstrin homology domain-containing family F member 1	PLEKHF1
0,000	-0,41	0,75	75,43	Q96GX2	Putative ataxin-7-like protein 3B	ATXN7L3B
0,030	-0,41	0,75	75,34	Q92541	RNA polymerase-associated protein RTF1 homolog	RTF1
0,008	-0,41	0,75	75,29	Q9H6S0	Probable ATP-dependent RNA helicase YTHDC2	YTHDC2
0,009	-0,41	0,75	75,26	P35611	Alpha-adducin	ADD1
0,003	-0,41	0,75	75,17	P07602	Prosaposin;Saposin-A;Saposin-B-Val;Saposin-B;Saposin-C;Saposin-D	PSAP
0,049	-0,41	0,75	75,11	P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	GNAI2
0,001	-0,41	0,75	75,04	Q9UDY2	Tight junction protein ZO-2	TJP2
0,011	-0,42	0,75	74,74	Q9BZH6	WD repeat-containing protein 11	WDR11
0,035	-0,42	0,75	74,72	Q99615	DnaJ homolog subfamily C member 7	DNAJC7
0,017	-0,42	0,75	74,67	P46379	Large proline-rich protein BAG6	BAG6
0,045	-0,42	0,75	74,61	Q9P265	Disco-interacting protein 2 homolog B	DIP2B
0,033	-0,43	0,74	74,44	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	SLC25A13
0,031	-0,43	0,74	74,34	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	EPS8L2
0,015	-0,43	0,74	74,23	Q15084	Protein disulfide-isomerase A6	PDIA6
0,016	-0,43	0,74	74,23	P35249	Replication factor C subunit 4	RFC4
0,038	-0,43	0,74	74,23	P30050	60S ribosomal protein L12	RPL12
0,011	-0,44	0,74	73,71	P62913	60S ribosomal protein L11	RPL11
0,002	-0,44	0,74	73,71	P63173	60S ribosomal protein L38	RPL38
0,044	-0,44	0,74	73,71	Q02543	60S ribosomal protein L18a	RPL18A
0,014	-0,44	0,74	73,59	P60900	Proteasome subunit alpha type-6	PSMA6
0,040	-0,45	0,73	73,36	O95470	Sphingosine-1-phosphate lyase 1	SGPL1
0,034	-0,45	0,73	73,29	Q6VY07	Phosphofurin acidic cluster sorting protein 1	PACS1
0,049	-0,45	0,73	73,28	O60869	Endothelial differentiation-related factor 1	EDF1
0,010	-0,45	0,73	73,20	P42285	Superkiller viralicidic activity 2-like 2	SKIV2L2

Supplemental Table S2b

0,033	-0,45	0,73	73,20	Q13523	Serine/threonine-protein kinase PRP4 homolog	PRPF4B
0,011	-0,45	0,73	73,17	Q15031	Probable leucine--tRNA ligase, mitochondrial	LARS2
0,028	-0,45	0,73	73,08	P61011	Signal recognition particle 54 kDa protein	SRP54
0,008	-0,45	0,73	73,00	P52948	Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;N	NUP98
0,030	-0,46	0,73	72,94	Q9NSK7	Protein C19orf12	C19orf12
0,049	-0,46	0,73	72,87	P17931	Galectin-3	LGALS3
0,003	-0,46	0,73	72,70	Q8WWQ0	PH-interacting protein	PHIP
0,013	-0,46	0,73	72,70	Q92522	Histone H1x	H1FX
0,031	-0,46	0,73	72,70	Q9ULW0	Targeting protein for Xklp2	TPX2
0,033	-0,46	0,73	72,59	O95793	Double-stranded RNA-binding protein Staufin homolog 1	STAU1
0,050	-0,46	0,73	72,54	Q9Y4W2	Ribosomal biogenesis protein LAS1L	LAS1L
0,004	-0,46	0,72	72,49	O43852	Calumenin	CALU
0,032	-0,47	0,72	72,25	Q9BQE3	Tubulin alpha-1C chain	TUBA1C
0,010	-0,47	0,72	72,22	Q92973	Transportin-1	TNPO1
0,001	-0,47	0,72	72,20	Q7Z6R9	Transcription factor AP-2-delta	TFAP2D
0,014	-0,47	0,72	72,20	Q00839	Heterogeneous nuclear ribonucleoprotein U	HNRNPU
0,006	-0,47	0,72	72,20	P62158	Calmodulin	CALM1
0,026	-0,47	0,72	72,20	P55084	Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase	HADHB
0,029	-0,47	0,72	71,99	P56545	C-terminal-binding protein 2	CTBP2
0,014	-0,47	0,72	71,96	Q01844	RNA-binding protein EWS	EWSR1
0,010	-0,48	0,72	71,74	Q8N1F7	Nuclear pore complex protein Nup93	NUP93
0,019	-0,48	0,72	71,70	P41567;O60739	Eukaryotic translation initiation factor 1;Eukaryotic translation initiation factor 1b	EIF1;EIF1B
0,029	-0,48	0,72	71,70	P57772	Selenocysteine-specific elongation factor	EEFSEC
0,004	-0,48	0,72	71,70	P62888	60S ribosomal protein L30	RPL30
0,049	-0,48	0,71	71,47	O75663	TIP41-like protein	TIPRL
0,009	-0,49	0,71	71,31	Q9H6T3	RNA polymerase II-associated protein 3	RPAP3
0,036	-0,49	0,71	71,20	Q9NUD5	Zinc finger CCHC domain-containing protein 3	ZCCHC3
0,006	-0,49	0,71	71,20	P32969	60S ribosomal protein L9	RPL9
0,037	-0,49	0,71	71,20	Q10570	Cleavage and polyadenylation specificity factor subunit 1	CPSF1
0,016	-0,49	0,71	71,20	Q86V48	Leucine zipper protein 1	LUZP1
0,021	-0,50	0,71	70,82	Q92905	COP9 signalosome complex subunit 5	COPS5
0,030	-0,50	0,71	70,71	Q6EEV6;P61956;P55854	Small ubiquitin-related modifier 4;Small ubiquitin-related modifier 2;Small ubiquitin-related modifier 1	SMO4;SUMO2;SUMO1
0,028	-0,50	0,71	70,71	P39023	60S ribosomal protein L3	RPL3

Supplemental Table S2b

0,030	-0,50	0,71	70,71	Q5JVS0	Intracellular hyaluronan-binding protein 4	HABP4
0,025	-0,50	0,70	70,47	Q6EEV4	DNA-directed RNA polymerase II subunit GRINL1A, isoforms 4/5	POLR2M
0,006	-0,51	0,70	70,42	Q9Y3D8	Adenylate kinase isoenzyme 6	AK6
0,018	-0,51	0,70	70,33	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	CAND1
0,001	-0,51	0,70	70,28	Q9UHD1	Cysteine and histidine-rich domain-containing protein 1	CHORDC1
0,016	-0,51	0,70	70,26	A0FGR8	Extended synaptotagmin-2	ESYT2
0,001	-0,51	0,70	70,22	Q2TAK8	PWWP domain-containing protein MUM1	MUM1
0,005	-0,51	0,70	70,22	Q9UPT8	Zinc finger CCCH domain-containing protein 4	ZC3H4
0,015	-0,51	0,70	70,22	P11233	Ras-related protein Ral-A	RALA
0,009	-0,51	0,70	70,22	P47897	Glutamine--tRNA ligase	QARS
0,027	-0,51	0,70	70,20	P07737	Profilin-1	PFN1
0,022	-0,52	0,70	69,85	O95373	Importin-7	IPO7
0,038	-0,52	0,70	69,78	O15371	Eukaryotic translation initiation factor 3 subunit D	EIF3D
0,005	-0,52	0,70	69,74	Q9UHV9	Prefoldin subunit 2	PFDN2
0,009	-0,52	0,70	69,74	Q8WVK2	U4/U6.U5 small nuclear ribonucleoprotein 27 kDa protein	SNRNP27
0,027	-0,52	0,70	69,74	Q96BK5	PIN2/TERF1-interacting telomerase inhibitor 1	PINX1
0,045	-0,53	0,69	69,47	Q9BPX6	Calcium uptake protein 1, mitochondrial	MICU1
0,007	-0,53	0,69	69,33	Q99798	Aconitate hydratase, mitochondrial	ACO2
0,003	-0,53	0,69	69,26	Q8WUZ0	B-cell CLL/lymphoma 7 protein family member C	BCL7C
0,017	-0,53	0,69	69,26	Q9UN86	Ras GTPase-activating protein-binding protein 2	G3BP2
0,036	-0,53	0,69	69,26	P24534	Elongation factor 1-beta	EEF1B2
0,021	-0,53	0,69	69,20	Q76FK4	Nucleolar protein 8	NOL8
0,009	-0,53	0,69	69,11	Q12888	Tumor suppressor p53-binding protein 1	TP53BP1
0,032	-0,53	0,69	69,05	Q9UHD9	Ubiquilin-2	UBQLN2
0,023	-0,53	0,69	69,04	P54819	Adenylate kinase 2, mitochondrial;Adenylate kinase 2, mitochondrial, N-terminally	AK2
0,040	-0,54	0,69	68,87	O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal	AGPS
0,000	-0,54	0,69	68,84	P35221	Catenin alpha-1	CTNNA1
0,003	-0,54	0,69	68,78	Q13308	Inactive tyrosine-protein kinase 7	PTK7
0,040	-0,54	0,69	68,78	P07437	Tubulin beta chain	TUBB
0,014	-0,54	0,69	68,78	Q15637	Splicing factor 1	SF1
0,005	-0,54	0,69	68,78	A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	SMCHD1
0,002	-0,54	0,69	68,78	Q9UQ80	Proliferation-associated protein 2G4	PA2G4
0,039	-0,54	0,69	68,78	P25490	Transcriptional repressor protein YY1	YY1

Supplemental Table S2b

0,028	-0,54	0,69	68,78	P28370	Probable global transcription activator SNF2L1	SMARCA1
0,046	-0,54	0,69	68,72	P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	DDOST
0,026	-0,54	0,69	68,59	Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	SSU72
0,030	-0,55	0,68	68,43	O75616	GTPase Era, mitochondrial	ERAL1
0,036	-0,55	0,68	68,42	Q96TA1	Niban-like protein 1	FAM129B
0,021	-0,55	0,68	68,41	P21266	Glutathione S-transferase Mu 3	GSTM3
0,022	-0,55	0,68	68,30	Q8TAQ2	SWI/SNF complex subunit SMARCC2	SMARCC2
0,046	-0,55	0,68	68,30	Q00403	Transcription initiation factor IIB	GTF2B
0,001	-0,55	0,68	68,30	Q5TA45	Integrator complex subunit 11	CPSF3L
0,014	-0,55	0,68	68,30	Q7Z3B3	KAT8 regulatory NSL complex subunit 1	KANSL1
0,003	-0,55	0,68	68,26	P68371	Tubulin beta-4B chain	TUBB4B
0,045	-0,55	0,68	68,23	P00491	Purine nucleoside phosphorylase	PNP
0,004	-0,56	0,68	67,88	Q5T1M5	FK506-binding protein 15	FKBP15
0,041	-0,56	0,68	67,83	Q9BVC4	Target of rapamycin complex subunit LST8	MLST8
0,012	-0,56	0,68	67,83	Q14157	Ubiquitin-associated protein 2-like	UBAP2L
0,014	-0,56	0,68	67,83	O15164	Transcription intermediary factor 1-alpha	TRIM24
0,003	-0,56	0,68	67,83	Q9BXB4	Oxysterol-binding protein-related protein 11	OSBPL11
0,017	-0,56	0,68	67,83	Q14694	Ubiquitin carboxyl-terminal hydrolase 10	USP10
0,007	-0,56	0,68	67,83	Q15906	Vacuolar protein sorting-associated protein 72 homolog	VPS72
0,012	-0,56	0,68	67,80	Q9H3G5	Probable serine carboxypeptidase CPVL	CPVL
0,033	-0,56	0,68	67,61	P08047	Transcription factor Sp1	SP1
0,004	-0,56	0,68	67,60	Q9Y277	Voltage-dependent anion-selective channel protein 3	VDAC3
0,011	-0,57	0,67	67,49	P40855	Peroxisomal biogenesis factor 19	PEX19
0,014	-0,57	0,67	67,46	Q9HB07	UPF0160 protein MYG1, mitochondrial	C12orf10
0,005	-0,57	0,67	67,36	Q96S94	Cyclin-L2	CCNL2
0,045	-0,57	0,67	67,36	Q06124	Tyrosine-protein phosphatase non-receptor type 11	PTPN11
0,023	-0,57	0,67	67,36	O15372	Eukaryotic translation initiation factor 3 subunit H	EIF3H
0,022	-0,57	0,67	67,25	P15144	Aminopeptidase N	ANPEP
0,019	-0,58	0,67	67,12	Q01085	Nucleolysin TIAR	TIAL1
0,011	-0,58	0,67	67,00	Q7Z434	Mitochondrial antiviral-signaling protein	MAVS
0,010	-0,58	0,67	66,93	Q14696	LDLR chaperone MESD	MESDC2
0,012	-0,58	0,67	66,92	Q15628	Tumor necrosis factor receptor type 1-associated DEATH domain protein	TRADD
0,020	-0,58	0,67	66,90	P63244	Guanine nucleotide-binding protein subunit beta-2-like 1;Guanine nucleotide-bindin	GNB2L1

Supplemental Table S2b

0,007	-0,58	0,67	66,90	Q6IQ23	Pleckstrin homology domain-containing family A member 7	PLEKHA7
0,013	-0,58	0,67	66,90	Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A	FAHD2A
0,015	-0,58	0,67	66,90	P62424	60S ribosomal protein L7a	RPL7A
0,005	-0,58	0,67	66,90	Q9GZS1	DNA-directed RNA polymerase I subunit RPA49	POLR1E
0,043	-0,59	0,67	66,54	Q14671	Pumilio homolog 1	PUM1
0,042	-0,59	0,66	66,43	P22033	Methylmalonyl-CoA mutase, mitochondrial	MUT
0,032	-0,59	0,66	66,43	O60220	Mitochondrial import inner membrane translocase subunit Tim8 A	TIMM8A
0,021	-0,59	0,66	66,43	P08134	Rho-related GTP-binding protein RhoC	RHOC
0,002	-0,59	0,66	66,43	Q12792	Twinfilin-1	TWF1
0,048	-0,59	0,66	66,43	Q9Y6X9	MORC family CW-type zinc finger protein 2	MORC2
0,002	-0,59	0,66	66,43	P20290	Transcription factor BTF3	BTF3
0,011	-0,59	0,66	66,43	P61254	60S ribosomal protein L26	RPL26
0,034	-0,59	0,66	66,27	Q9NQR4	Omega-amidase NIT2	NIT2
0,050	-0,59	0,66	66,21	P61224;A6NIZ1	Ras-related protein Rap-1b;Ras-related protein Rap-1b-like protein	RAP1B
0,047	-0,60	0,66	66,14	Q9Y508	E3 ubiquitin-protein ligase RNF114	RNF114
0,009	-0,60	0,66	65,98	Q8WUM0	Nuclear pore complex protein Nup133	NUP133
0,017	-0,60	0,66	65,98	O15042	U2 snRNP-associated SURP motif-containing protein	U2SURP
0,014	-0,60	0,66	65,98	Q6P3W7	SCY1-like protein 2	SCYL2
0,026	-0,60	0,66	65,98	P98175	RNA-binding protein 10	RBM10
0,030	-0,60	0,66	65,98	Q7L4I2	Arginine/serine-rich coiled-coil protein 2	RSRC2
0,026	-0,60	0,66	65,85	Q9BWF3	RNA-binding protein 4	RBM4
0,047	-0,61	0,66	65,63	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial	HMGCL
0,004	-0,61	0,66	65,52	P50995	Annexin A11	ANXA11
0,014	-0,61	0,66	65,52	Q4VCS5	Angiomotin	AMOT
0,032	-0,61	0,66	65,52	Q7Z4W1	L-xylulose reductase	DCXR
0,011	-0,61	0,66	65,52	P07195	L-lactate dehydrogenase B chain	LDHB
0,047	-0,61	0,66	65,52	Q15436	Protein transport protein Sec23A	SEC23A
0,036	-0,61	0,65	65,39	P10599	Thioredoxin	TXN
0,049	-0,61	0,65	65,32	P11047	Laminin subunit gamma-1	LAMC1
0,021	-0,62	0,65	65,18	Q9NVS9	Pyridoxine-5-phosphate oxidase	PNPO
0,029	-0,62	0,65	65,18	Q92878	DNA repair protein RAD50	RAD50
0,012	-0,62	0,65	65,07	P18077	60S ribosomal protein L35a	RPL35A
0,000	-0,62	0,65	65,07	P17844	Probable ATP-dependent RNA helicase DDX5	DDX5

Supplemental Table S2b

0,048	-0,62	0,65	65,07	Q9BYG5	Partitioning defective 6 homolog beta	PARD6B
0,045	-0,62	0,65	65,07	P62987;P0CG47;P0C	Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Ubiquitin	UBA52;UBB;U
0,004	-0,62	0,65	65,07	P62753	40S ribosomal protein S6	RPS6
0,014	-0,62	0,65	65,07	Q5T200	Zinc finger CCCH domain-containing protein 13	ZC3H13
0,008	-0,62	0,65	65,00	P05141	ADP/ATP translocase 2;ADP/ATP translocase 2, N-terminally processed	SLC25A5
0,049	-0,62	0,65	64,91	Q9UBF2	Coatomer subunit gamma-2	COPG2
0,035	-0,63	0,65	64,72	O96019	Actin-like protein 6A	ACTL6A
0,014	-0,63	0,65	64,64	Q99805	Transmembrane 9 superfamily member 2	TM9SF2
0,027	-0,63	0,65	64,62	P57740	Nuclear pore complex protein Nup107	NUP107
0,004	-0,63	0,65	64,53	Q16763	Ubiquitin-conjugating enzyme E2 S	UBE2S
0,038	-0,63	0,64	64,44	Q53H96	Pyrroline-5-carboxylate reductase 3	PYCR1
0,050	-0,63	0,64	64,40	Q7Z2W9	39S ribosomal protein L21, mitochondrial	MRPL21
0,007	-0,64	0,64	64,22	Q96RU2	Ubiquitin carboxyl-terminal hydrolase 28	USP28
0,031	-0,64	0,64	64,17	P26373	60S ribosomal protein L13	RPL13
0,000	-0,64	0,64	64,17	P68104;Q5VTE0	Elongation factor 1-alpha 1;Putative elongation factor 1-alpha-like 3	EEF1A1;EEF1A1P5
0,007	-0,64	0,64	64,17	P08865	40S ribosomal protein SA	RPSA
0,018	-0,64	0,64	64,17	P62906	60S ribosomal protein L10a	RPL10A
0,027	-0,64	0,64	63,99	O75179	Ankyrin repeat domain-containing protein 17	ANKRD17
0,035	-0,64	0,64	63,95	Q96S59	Ran-binding protein 9	RANBP9
0,004	-0,65	0,64	63,82	Q56VL3	OCIA domain-containing protein 2	OCIAD2
0,050	-0,65	0,64	63,79	P20585	DNA mismatch repair protein Msh3	MSH3
0,007	-0,65	0,64	63,78	O00391	Sulfhydryl oxidase 1	QSOX1
0,042	-0,65	0,64	63,75	P14923	Junction plakoglobin	JUP
0,025	-0,65	0,64	63,73	Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial	HINT2
0,001	-0,65	0,64	63,73	Q9NWH9	SAFB-like transcription modulator	SLTM
0,007	-0,65	0,64	63,73	Q8NI77	Kinesin-like protein KIF18A	KIF18A
0,006	-0,65	0,64	63,73	P62851	40S ribosomal protein S25	RPS25
0,023	-0,66	0,63	63,46	P32970	CD70 antigen	CD70
0,015	-0,66	0,63	63,29	P62847	40S ribosomal protein S24	RPS24
0,012	-0,66	0,63	63,29	P69849;Q5JPE7;Q15155	Nodal modulator 3;Nodal modulator 2;Nodal modulator 1	MO3;NOMO2;NON
0,008	-0,66	0,63	63,29	Q9BZZ5	Apoptosis inhibitor 5	API5
0,004	-0,66	0,63	63,29	Q96C36	Pyrroline-5-carboxylate reductase 2	PYCR2
0,019	-0,66	0,63	63,29	O75436	Vacuolar protein sorting-associated protein 26A	VPS26A

Supplemental Table S2b

0,041	-0,66	0,63	63,29	P06396	Gelsolin	GSN
0,037	-0,66	0,63	63,29	Q04637	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1
0,015	-0,66	0,63	63,29	Q13765;E9PAV3	Nascent polypeptide-associated complex subunit alpha;Nascent polypeptide-associated complex subunit alpha	NACA
0,022	-0,66	0,63	63,29	Q02880	DNA topoisomerase 2-beta	TOP2B
0,000	-0,66	0,63	63,24	P35606	Coatamer subunit beta	COPB2
0,025	-0,66	0,63	63,21	Q16204	Coiled-coil domain-containing protein 6	CCDC6
0,017	-0,67	0,63	63,03	Q14160	Protein scribble homolog	SCRIB
0,007	-0,67	0,63	63,02	Q9H8W4	Pleckstrin homology domain-containing family F member 2	PLEKHF2
0,021	-0,67	0,63	63,02	Q9UUK3	Poly [ADP-ribose] polymerase 4	PARP4
0,014	-0,67	0,63	62,96	P10398	Serine/threonine-protein kinase A-Raf	ARAF
0,007	-0,67	0,63	62,94	Q9NYV4	Cyclin-dependent kinase 12	CDK12
0,028	-0,67	0,63	62,93	P51571	Translocon-associated protein subunit delta	SSR4
0,006	-0,67	0,63	62,91	Q9Y6X8	Zinc fingers and homeoboxes protein 2	ZHX2
0,024	-0,67	0,63	62,85	O75151	Lysine-specific demethylase PHF2	PHF2
0,026	-0,67	0,63	62,85	P27708	CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyl transferase	CAD
0,007	-0,67	0,63	62,78	Q13200	26S proteasome non-ATPase regulatory subunit 2	PSMD2
0,036	-0,67	0,63	62,76	P15170;Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;Eukaryotic peptide chain release factor GTP-binding subunit	GSPT1;GSPT2
0,009	-0,67	0,63	62,76	Q15643	Thyroid receptor-interacting protein 11	TRIP11
0,026	-0,68	0,62	62,42	P51858	Hepatoma-derived growth factor	HDGF
0,024	-0,68	0,62	62,42	Q96FW1	Ubiquitin thioesterase OTUB1	OTUB1
0,013	-0,68	0,62	62,42	P78527	DNA-dependent protein kinase catalytic subunit	PRKDC
0,014	-0,68	0,62	62,42	P07942	Laminin subunit beta-1	LAMB1
0,023	-0,68	0,62	62,42	P40429;Q6NVV1	60S ribosomal protein L13a;Putative 60S ribosomal protein L13a protein RPL13AP3	RPL13A;RPL13AP3
0,005	-0,68	0,62	62,42	P46783;Q9NQ39	40S ribosomal protein S10;Putative 40S ribosomal protein S10-like	RPS10;RPS10P5
0,003	-0,68	0,62	62,42	P42677	40S ribosomal protein S27	RPS27
0,034	-0,68	0,62	62,42	O95785	Protein Wiz	WIZ
0,021	-0,68	0,62	62,36	Q15654	Thyroid receptor-interacting protein 6	TRIP6
0,017	-0,69	0,62	62,14	Q13616	Cullin-1	CUL1
0,001	-0,69	0,62	62,10	A0AV96	RNA-binding protein 47	RBM47
0,020	-0,69	0,62	61,99	Q9BXS5	AP-1 complex subunit mu-1	AP1M1
0,026	-0,69	0,62	61,99	O75718	Cartilage-associated protein	CRTAP
0,005	-0,69	0,62	61,99	O94776	Metastasis-associated protein MTA2	MTA2
0,032	-0,69	0,62	61,99	Q8NDX5	Polyhomeotic-like protein 3	PHC3

Supplemental Table S2b

0,049	-0,69	0,62	61,99	P53350	Serine/threonine-protein kinase PLK1	PLK1
0,012	-0,70	0,62	61,70	Q86WR0	Coiled-coil domain-containing protein 25	CCDC25
0,005	-0,70	0,62	61,56	P52594	Arf-GAP domain and FG repeat-containing protein 1	AGFG1
0,009	-0,70	0,62	61,56	Q9BZ95	Histone-lysine N-methyltransferase NSD3	WHSC1L1
0,019	-0,70	0,62	61,56	Q14004	Cyclin-dependent kinase 13	CDK13
0,008	-0,70	0,62	61,56	O00178	GTP-binding protein 1	GTPBP1
0,036	-0,70	0,62	61,56	P62699	Protein yippee-like 5	YPEL5
0,018	-0,70	0,62	61,55	P55011	Solute carrier family 12 member 2	SLC12A2
0,021	-0,70	0,61	61,37	P54105	Methylosome subunit pICln	CLNS1A
0,015	-0,71	0,61	61,26	P17706	Tyrosine-protein phosphatase non-receptor type 2	PTPN2
0,017	-0,71	0,61	61,15	Q8N6H7	ADP-ribosylation factor GTPase-activating protein 2	ARFGAP2
0,028	-0,71	0,61	61,13	Q99584	Protein S100-A13	S100A13
0,029	-0,71	0,61	61,13	Q9BYE7	Polycomb group RING finger protein 6	PCGF6
0,023	-0,71	0,61	61,11	O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	NDUFS5
0,043	-0,71	0,61	61,10	P46778	60S ribosomal protein L21	RPL21
0,018	-0,71	0,61	61,01	Q99570	Phosphoinositide 3-kinase regulatory subunit 4	PIK3R4
0,049	-0,71	0,61	60,96	Q00765	Receptor expression-enhancing protein 5	REEP5
0,049	-0,72	0,61	60,89	P53985	Monocarboxylate transporter 1	SLC16A1
0,021	-0,72	0,61	60,74	Q16762	Thiosulfate sulfurtransferase	TST
0,017	-0,72	0,61	60,72	Q9NPQ8	Synembryn-A	RIC8A
0,030	-0,72	0,61	60,71	Q5TGY3	AT-hook DNA-binding motif-containing protein 1	AHDC1
0,002	-0,72	0,61	60,71	Q92900	Regulator of nonsense transcripts 1	UPF1
0,004	-0,72	0,61	60,71	Q9P0K7	Ankyrin	RAI14
0,034	-0,72	0,61	60,71	Q8NFF5	FAD synthase;Molybdenum cofactor biosynthesis protein-like region;FAD synthase i	FLAD1
0,000	-0,72	0,61	60,71	P23258;Q9NRH3	Tubulin gamma-1 chain;Tubulin gamma-2 chain	TUBG1;TUBG2
0,029	-0,72	0,61	60,71	Q8NFC6	Biorientation of chromosomes in cell division protein 1-like 1	BOD1L1
0,008	-0,72	0,61	60,59	Q96CW1	AP-2 complex subunit mu	AP2M1
0,004	-0,72	0,61	60,54	P43246	DNA mismatch repair protein Msh2	MSH2
0,010	-0,73	0,60	60,46	P00374	Dihydrofolate reductase	DHFR
0,018	-0,73	0,60	60,43	P53007	Tricarboxylate transport protein, mitochondrial	SLC25A1
0,041	-0,73	0,60	60,43	Q9NRN7	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	AASDHPPT
0,018	-0,73	0,60	60,34	Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50	TIMM50
0,044	-0,73	0,60	60,33	Q7Z6K5	Arpin	ARPIN

Supplemental Table S2b

0,002	-0,73	0,60	60,29	P27816	Microtubule-associated protein 4	MAP4
0,004	-0,73	0,60	60,29	Q9NRR4	Ribonuclease 3	DROSHA
0,012	-0,73	0,60	60,29	Q96DA6	Mitochondrial import inner membrane translocase subunit TIM14	DNAJC19
0,044	-0,73	0,60	60,29	Q8NCN4	E3 ubiquitin-protein ligase RNF169	RNF169
0,036	-0,73	0,60	60,29	Q96SI9	Spermatid perinuclear RNA-binding protein	STRBP
0,004	-0,73	0,60	60,29	P40424	Pre-B-cell leukemia transcription factor 1	PBX1
0,004	-0,73	0,60	60,27	Q9H0U4;Q92928;P62820	Ras-related protein Rab-1B;Putative Ras-related protein Rab-1C;Ras-related protein AB1B;RAB1C;RAB1D	
0,013	-0,74	0,60	60,06	P49770	Translation initiation factor eIF-2B subunit beta	EIF2B2
0,003	-0,74	0,60	60,04	P60228	Eukaryotic translation initiation factor 3 subunit E	EIF3E
0,010	-0,74	0,60	59,87	Q14807	Kinesin-like protein KIF22	KIF22
0,022	-0,74	0,60	59,87	P18124	60S ribosomal protein L7	RPL7
0,013	-0,74	0,60	59,87	Q8N5C6	S1 RNA-binding domain-containing protein 1	SRBD1
0,017	-0,74	0,60	59,87	P61353	60S ribosomal protein L27	RPL27
0,046	-0,74	0,60	59,87	Q14676	Mediator of DNA damage checkpoint protein 1	MDC1
0,009	-0,74	0,60	59,87	POCW22;P08708	40S ribosomal protein S17-like;40S ribosomal protein S17	RPS17L;RPS17
0,003	-0,75	0,60	59,54	Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like	HNRNPLL
0,049	-0,75	0,60	59,51	Q99471	Prefoldin subunit 5	PFDN5
0,048	-0,75	0,59	59,46	O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate	HGS
0,033	-0,75	0,59	59,46	Q9BQ04	RNA-binding protein 4B	RBM4B
0,001	-0,75	0,59	59,46	P25398	40S ribosomal protein S12	RPS12
0,002	-0,75	0,59	59,46	P23396	40S ribosomal protein S3	RPS3
0,006	-0,75	0,59	59,46	P46776	60S ribosomal protein L27a	RPL27A
0,014	-0,75	0,59	59,46	Q92896	Golgi apparatus protein 1	GLG1
0,020	-0,75	0,59	59,43	P27448	MAP/microtubule affinity-regulating kinase 3	MARK3
0,034	-0,75	0,59	59,43	P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUFA8
0,005	-0,75	0,59	59,40	P11717	Cation-independent mannose-6-phosphate receptor	IGF2R
0,017	-0,75	0,59	59,31	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K	EIF3K
0,001	-0,76	0,59	59,19	Q9Y5J9	Mitochondrial import inner membrane translocase subunit Tim8 B	TIMM8B
0,000	-0,76	0,59	59,18	Q16531	DNA damage-binding protein 1	DDB1
0,034	-0,76	0,59	59,14	Q9BTC8	Metastasis-associated protein MTA3	MTA3
0,009	-0,76	0,59	59,13	Q96N66	Lysophospholipid acyltransferase 7	MBOAT7
0,029	-0,76	0,59	59,11	Q96RU3	Formin-binding protein 1	FNBP1
0,047	-0,76	0,59	59,05	Q9UJV9	Probable ATP-dependent RNA helicase DDX41	DDX41

Supplemental Table S2b

0,001	-0,76	0,59	59,05	P62249	40S ribosomal protein S16	RPS16
0,035	-0,76	0,59	58,96	Q9HB40	Retinoid-inducible serine carboxypeptidase	SCPEP1
0,006	-0,76	0,59	58,94	P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	PDHA1
0,049	-0,77	0,59	58,75	Q8WXE0	Caskin-2	CASKIN2
0,010	-0,77	0,59	58,64	Q92922	SWI/SNF complex subunit SMARCC1	SMARCC1
0,002	-0,77	0,59	58,64	Q9UKJ3	G patch domain-containing protein 8	GPATCH8
0,001	-0,77	0,59	58,64	P46013	Antigen KI-67	MKI67
0,002	-0,77	0,59	58,64	Q14444	Caprin-1	CAPRIN1
0,009	-0,77	0,59	58,64	Q14258	E3 ubiquitin/ISG15 ligase TRIM25	TRIM25
0,034	-0,77	0,59	58,64	Q14134	Tripartite motif-containing protein 29	TRIM29
0,007	-0,77	0,59	58,64	P62487	DNA-directed RNA polymerase II subunit RPB7	POLR2G
0,012	-0,77	0,59	58,64	Q96EV2	RNA-binding protein 33	RBM33
0,022	-0,77	0,58	58,50	Q9C0C9	E2/E3 hybrid ubiquitin-protein ligase UBE2O	UBE2O
0,012	-0,78	0,58	58,38	Q9UIJ7	GTP:AMP phosphotransferase AK3, mitochondrial	AK3
0,041	-0,78	0,58	58,36	Q8IWB7	WD repeat and FYVE domain-containing protein 1	WDFY1
0,007	-0,78	0,58	58,24	P62701	40S ribosomal protein S4, X isoform	RPS4X
0,027	-0,78	0,58	58,24	Q9H6I2	Transcription factor SOX-17	SOX17
0,036	-0,78	0,58	58,15	Q9HCE1	Putative helicase MOV-10	MOV10
0,035	-0,78	0,58	58,07	Q9NZ01	Very-long-chain enoyl-CoA reductase	TECR
0,036	-0,79	0,58	57,90	P61313	60S ribosomal protein L15	RPL15
0,033	-0,79	0,58	57,83	P26641	Elongation factor 1-gamma	EEF1G
0,005	-0,79	0,58	57,83	Q9Y5Q8	General transcription factor 3C polypeptide 5	GTF3C5
0,049	-0,79	0,58	57,83	Q9H0E9	Bromodomain-containing protein 8	BRD8
0,010	-0,79	0,58	57,83	P50570	Dynamin-2	DNM2
0,016	-0,79	0,58	57,83	Q9NVC6	Mediator of RNA polymerase II transcription subunit 17	MED17
0,050	-0,79	0,58	57,83	Q8WXI9	Transcriptional repressor p66-beta	GATAD2B
0,002	-0,79	0,58	57,79	P07686	Beta-hexosaminidase subunit beta;Beta-hexosaminidase subunit beta chain B;Beta-	HEXB
0,008	-0,79	0,58	57,72	Q9NPL8	Complex I assembly factor TIMMDC1, mitochondrial	TIMMDC1
0,000	-0,80	0,58	57,57	Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2	BZW2
0,005	-0,80	0,58	57,54	P32456	Interferon-induced guanylate-binding protein 2	GBP2
0,016	-0,80	0,57	57,43	Q6I9Y2	THO complex subunit 7 homolog	THOC7
0,016	-0,80	0,57	57,43	P57088	Transmembrane protein 33	TMEM33
0,020	-0,80	0,57	57,43	P63313	Thymosin beta-10	TMSB10

Supplemental Table S2b

0,008	-0,80	0,57	57,35	Q9Y3T9	Nucleolar complex protein 2 homolog	NOC2L
0,006	-0,80	0,57	57,28	Q9UK41	Vacuolar protein sorting-associated protein 28 homolog	VPS28
0,042	-0,81	0,57	57,07	Q6P1N0	Coiled-coil and C2 domain-containing protein 1A	CC2D1A
0,004	-0,81	0,57	57,04	Q9H0E3	Histone deacetylase complex subunit SAP130	SAP130
0,011	-0,81	0,57	57,04	Q9GZZ1	N-alpha-acetyltransferase 50	NAA50
0,003	-0,81	0,57	57,04	Q9BSC4	Nucleolar protein 10	NOL10
0,020	-0,81	0,57	57,02	O95602	DNA-directed RNA polymerase I subunit RPA1	POLR1A
0,048	-0,81	0,57	56,94	Q9BVL2	Nucleoporin p58/p45	NUPL1
0,001	-0,81	0,57	56,92	Q9HCU4	Cadherin EGF LAG seven-pass G-type receptor 2	CELSR2
0,019	-0,82	0,57	56,64	Q9BV38	WD repeat-containing protein 18	WDR18
0,001	-0,82	0,57	56,64	Q07157	Tight junction protein ZO-1	TJP1
0,013	-0,82	0,57	56,64	Q9NP50	Protein FAM60A	FAM60A
0,000	-0,82	0,57	56,64	Q8TAF3	WD repeat-containing protein 48	WDR48
0,002	-0,82	0,57	56,64	O15294	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subun	OGT
0,001	-0,82	0,57	56,64	Q7KZF4	Staphylococcal nuclease domain-containing protein 1	SND1
0,014	-0,82	0,57	56,64	P62244	40S ribosomal protein S15a	RPS15A
0,010	-0,82	0,57	56,64	Q15428	Splicing factor 3A subunit 2	SF3A2
0,018	-0,82	0,57	56,64	Q8ND04	Protein SMG8	SMG8
0,000	-0,82	0,57	56,64	O94832	Unconventional myosin-IId	MYO1D
0,021	-0,82	0,57	56,64	P20073	Annexin A7	ANXA7
0,035	-0,82	0,57	56,63	Q9UPT5	Exocyst complex component 7	EXOC7
0,043	-0,82	0,57	56,60	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	HIBADH
0,014	-0,82	0,57	56,55	Q5VYK3	Proteasome-associated protein ECM29 homolog	ECM29
0,000	-0,82	0,56	56,46	P0C1Z6	TCF3 fusion partner	TFPT
0,035	-0,83	0,56	56,41	Q7KZ85	Transcription elongation factor SPT6	SUPT6H
0,029	-0,83	0,56	56,34	O14639	Actin-binding LIM protein 1	ABLIM1
0,027	-0,83	0,56	56,33	P82933	28S ribosomal protein S9, mitochondrial	MRPS9
0,041	-0,83	0,56	56,30	Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	IKBIP
0,033	-0,83	0,56	56,29	P20719	Homeobox protein Hox-A5	HOXA5
0,008	-0,83	0,56	56,25	O75351	Vacuolar protein sorting-associated protein 4B	VPS4B
0,045	-0,83	0,56	56,25	Q8WUA2	Peptidyl-prolyl cis-trans isomerase-like 4	PPIL4
0,007	-0,83	0,56	56,25	Q8IYI6	Exocyst complex component 8	EXOC8
0,021	-0,83	0,56	56,22	P84090	Enhancer of rudimentary homolog	ERH

Supplemental Table S2b

0,004	-0,83	0,56	56,12	Q9UKX7	Nuclear pore complex protein Nup50	NUP50
0,030	-0,83	0,56	56,12	Q969Z3;Q5VT66	Mitochondrial amidoxime reducing component 2;Mitochondrial amidoxime-reducin	MARC2;MARC1
0,002	-0,84	0,56	55,86	P46108	Adapter molecule crk	CRK
0,042	-0,84	0,56	55,86	P78406	mRNA export factor	RAE1
0,034	-0,84	0,56	55,86	O75400	Pre-mRNA-processing factor 40 homolog A	PRPF40A
0,012	-0,84	0,56	55,83	O00159	Unconventional myosin-Ic	MYO1C
0,013	-0,84	0,56	55,80	Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9
0,034	-0,85	0,56	55,58	P35269	General transcription factor IIF subunit 1	GTF2F1
0,006	-0,85	0,56	55,51	P17655	Calpain-2 catalytic subunit	CAPN2
0,026	-0,85	0,55	55,48	Q71F56	Mediator of RNA polymerase II transcription subunit 13-like	MED13L
0,034	-0,85	0,55	55,48	Q9ULL0	Uncharacterized protein KIAA1210	KIAA1210
0,030	-0,85	0,55	55,36	Q63ZY3	KN motif and ankyrin repeat domain-containing protein 2	KANK2
0,002	-0,85	0,55	55,32	P55268	Laminin subunit beta-2	LAMB2
0,031	-0,86	0,55	55,28	Q8ND56	Protein LSM14 homolog A	LSM14A
0,008	-0,86	0,55	55,22	P07384	Calpain-1 catalytic subunit	CAPN1
0,041	-0,86	0,55	55,17	P54725	UV excision repair protein RAD23 homolog A	RAD23A
0,013	-0,86	0,55	55,14	Q5T4S7	E3 ubiquitin-protein ligase UBR4	UBR4
0,006	-0,86	0,55	55,10	P39019	40S ribosomal protein S19	RPS19
0,010	-0,86	0,55	55,10	Q5JTV8	Torsin-1A-interacting protein 1	TOR1AIP1
0,000	-0,86	0,55	55,10	Q92614	Unconventional myosin-XVIIIa	MYO18A
0,010	-0,86	0,55	55,10	Q86W42	THO complex subunit 6 homolog	THOC6
0,019	-0,86	0,55	55,00	P31689	DnaJ homolog subfamily A member 1	DNAJA1
0,030	-0,87	0,55	54,79	Q16890	Tumor protein D53	TPD52L1
0,041	-0,87	0,55	54,71	Q9Y4K4	Mitogen-activated protein kinase kinase kinase kinase 5	MAP4K5
0,002	-0,87	0,55	54,71	Q96FV9	THO complex subunit 1	THOC1
0,016	-0,87	0,55	54,71	Q9BSJ2	Gamma-tubulin complex component 2	TUBGCP2
0,001	-0,87	0,55	54,71	A8MW92	PHD finger protein 20-like protein 1	PHF20L1
0,004	-0,87	0,55	54,69	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	IDI1
0,002	-0,87	0,55	54,62	Q05048	Cleavage stimulation factor subunit 1	CSTF1
0,016	-0,88	0,54	54,49	Q5JTJ3	Cytochrome c oxidase assembly factor 6 homolog	COA6
0,028	-0,88	0,54	54,41	Q9Y3B4	Splicing factor 3B subunit 6	SF3B6
0,003	-0,88	0,54	54,34	P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	PPP2R1B
0,004	-0,88	0,54	54,34	P46781	40S ribosomal protein S9	RPS9

Supplemental Table S2b

0,002	-0,88	0,54	54,34	Q9H0H5	Rac GTPase-activating protein 1	RACGAP1
0,008	-0,88	0,54	54,34	Q9P206	Uncharacterized protein KIAA1522	KIAA1522
0,009	-0,88	0,54	54,34	Q96KQ7	Histone-lysine N-methyltransferase EHMT2	EHMT2
0,020	-0,88	0,54	54,34	Q92879	CUGBP Elav-like family member 1	CELF1
0,038	-0,88	0,54	54,25	Q96EP5	DAZ-associated protein 1	DAZAP1
0,007	-0,88	0,54	54,22	P21964	Catechol O-methyltransferase	COMT
0,037	-0,88	0,54	54,19	Q96J02	E3 ubiquitin-protein ligase Itchy homolog	ITCH
0,043	-0,89	0,54	54,14	Q96EB1	Elongator complex protein 4	ELP4
0,023	-0,89	0,54	54,05	Q9Y5Z9	UbiA prenyltransferase domain-containing protein 1	UBIAD1
0,015	-0,89	0,54	54,03	Q9UK76	Hematological and neurological expressed 1 protein;Hematological and neurologica	HN1
0,038	-0,89	0,54	53,96	Q92793	CREB-binding protein	CREBBP
0,050	-0,89	0,54	53,96	P46100	Transcriptional regulator ATRX	ATRX
0,021	-0,89	0,54	53,90	Q9HB71	Calcyclin-binding protein	CACYBP
0,007	-0,89	0,54	53,84	P82675	28S ribosomal protein S5, mitochondrial	MRPS5
0,019	-0,90	0,54	53,59	Q9NRG0	Chromatin accessibility complex protein 1	CHRA1
0,004	-0,90	0,54	53,59	P11388	DNA topoisomerase 2-alpha	TOP2A
0,002	-0,90	0,54	53,59	P12004	Proliferating cell nuclear antigen	PCNA
0,032	-0,90	0,54	53,59	P30085	UMP-CMP kinase	CMPK1
0,023	-0,90	0,54	53,57	Q96ER3	Protein SAAL1	SAAL1
0,042	-0,90	0,54	53,57	P32004	Neural cell adhesion molecule L1	L1CAM
0,003	-0,90	0,54	53,50	O94964	Protein SOGA1;N-terminal form;C-terminal 80 kDa form	SOGA1
0,027	-0,91	0,53	53,37	P46063	ATP-dependent DNA helicase Q1	RECQL
0,003	-0,91	0,53	53,37	Q5T440	Putative transferase CAF17, mitochondrial	IBA57
0,015	-0,91	0,53	53,32	Q9HD15	Steroid receptor RNA activator 1	SRA1
0,011	-0,91	0,53	53,22	P15880	40S ribosomal protein S2	RPS2
0,002	-0,91	0,53	53,22	P17096	High mobility group protein HMG-I/HMG-Y	HMG1
0,036	-0,91	0,53	53,22	P62834	Ras-related protein Rap-1A	RAP1A
0,003	-0,91	0,53	53,16	Q13438	Protein OS-9	OS9
0,031	-0,92	0,53	53,00	P50416	Carnitine O-palmitoyltransferase 1, liver isoform	CPT1A
0,000	-0,92	0,53	52,97	O15230	Laminin subunit alpha-5	LAMA5
0,003	-0,92	0,53	52,90	O75534	Cold shock domain-containing protein E1	CSDE1
0,000	-0,92	0,53	52,85	P62633	Cellular nucleic acid-binding protein	CNBP
0,050	-0,92	0,53	52,77	Q15003	Condensin complex subunit 2	NCAPH

Supplemental Table S2b

0,007	-0,93	0,53	52,52	Q9BSJ8	Extended synaptotagmin-1	ESYT1
0,036	-0,93	0,52	52,49	P55081	Microfibrillar-associated protein 1	MFAP1
0,007	-0,93	0,52	52,49	P09012	U1 small nuclear ribonucleoprotein A	SNRPA
0,007	-0,93	0,52	52,49	Q9NV88	Integrator complex subunit 9	INTS9
0,035	-0,93	0,52	52,38	P31153	S-adenosylmethionine synthase isoform type-2	MAT2A
0,004	-0,94	0,52	52,24	Q9Y2U8	Inner nuclear membrane protein Man1	LEMD3
0,005	-0,94	0,52	52,18	Q9NRR5	Ubiquilin-4	UBQLN4
0,022	-0,94	0,52	52,16	O95163	Elongator complex protein 1	IKBKAP
0,034	-0,94	0,52	52,12	Q6PGP7	Tetratricopeptide repeat protein 37	TTC37
0,018	-0,94	0,52	52,12	Q9BW27	Nuclear pore complex protein Nup85	NUP85
0,047	-0,94	0,52	52,12	O43660	Pleiotropic regulator 1	PLRG1
0,012	-0,94	0,52	52,12	Q9BQ61	Uncharacterized protein C19orf43	C19orf43
0,015	-0,94	0,52	52,12	P14324	Farnesyl pyrophosphate synthase	FDPS
0,009	-0,94	0,52	52,03	Q969U7	Proteasome assembly chaperone 2	PSMG2
0,015	-0,94	0,52	51,94	Q9H936	Mitochondrial glutamate carrier 1	SLC25A22
0,039	-0,95	0,52	51,92	P61962	DDB1- and CUL4-associated factor 7	DCAF7
0,010	-0,95	0,52	51,86	Q6IN85	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	SMEK1
0,019	-0,95	0,52	51,77	P61619;Q9H9S3	Protein transport protein Sec61 subunit alpha isoform 1;Protein transport protein Sec61A1;SEC61A2	SEC61A1;SEC61A2
0,007	-0,95	0,52	51,76	Q96J01	THO complex subunit 3	THOC3
0,003	-0,95	0,52	51,76	Q9UGU0	Transcription factor 20	TCF20
0,005	-0,96	0,52	51,53	Q9Y282	Endoplasmic reticulum-Golgi intermediate compartment protein 3	ERGIC3
0,002	-0,96	0,52	51,50	Q6NXG1	Epithelial splicing regulatory protein 1	ESRP1
0,031	-0,96	0,51	51,50	Q8WVC0	RNA polymerase-associated protein LEO1	LEO1
0,011	-0,96	0,51	51,41	Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit	RAB3GAP2
0,005	-0,96	0,51	51,41	Q9UBL3	Set1/Ash2 histone methyltransferase complex subunit ASH2	ASH2L
0,022	-0,96	0,51	51,41	Q8NHQ9	ATP-dependent RNA helicase DDX55	DDX55
0,001	-0,96	0,51	51,41	Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1	DTD1
0,003	-0,96	0,51	51,41	Q9C0F1	Centrosomal protein of 44 kDa	CEP44
0,001	-0,96	0,51	51,41	P62495	Eukaryotic peptide chain release factor subunit 1	ETF1
0,002	-0,96	0,51	51,41	Q9NVM9	Protein asunder homolog	ASUN
0,000	-0,96	0,51	51,41	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	SERBP1
0,038	-0,96	0,51	51,40	P42224	Signal transducer and activator of transcription 1-alpha/beta	STAT1
0,036	-0,96	0,51	51,37	Q96K76	Ubiquitin carboxyl-terminal hydrolase 47	USP47

Supplemental Table S2b

0,007	-0,97	0,51	51,17	P28288	ATP-binding cassette sub-family D member 3	ABCD3
0,003	-0,97	0,51	51,13	Q9BZX2	Uridine-cytidine kinase 2	UCK2
0,027	-0,97	0,51	51,11	Q9UNS2	COP9 signalosome complex subunit 3	COPS3
0,011	-0,97	0,51	51,05	Q96JM2	Zinc finger protein 462	ZNF462
0,030	-0,97	0,51	51,05	P21399	Cytoplasmic aconitate hydratase	ACO1
0,001	-0,97	0,51	51,05	P40926	Malate dehydrogenase, mitochondrial	MDH2
0,042	-0,97	0,51	51,05	Q00325	Phosphate carrier protein, mitochondrial	SLC25A3
0,005	-0,97	0,51	51,05	P62280	40S ribosomal protein S11	RPS11
0,020	-0,97	0,51	51,03	O43813	LanC-like protein 1	LANCL1
0,005	-0,97	0,51	51,01	P48730	Casein kinase I isoform delta	CSNK1D
0,040	-0,97	0,51	50,97	Q8IWS0	PHD finger protein 6	PHF6
0,026	-0,98	0,51	50,83	P05556	Integrin beta-1	ITGB1
0,019	-0,98	0,51	50,82	Q14008	Cytoskeleton-associated protein 5	CKAP5
0,043	-0,98	0,51	50,70	Q8TDD1	ATP-dependent RNA helicase DDX54	DDX54
0,024	-0,98	0,51	50,70	P63092;Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	GNAS
0,007	-0,98	0,51	50,56	O15162	Phospholipid scramblase 1	PLSCR1
0,013	-0,98	0,51	50,54	Q13206	Probable ATP-dependent RNA helicase DDX10	DDX10
0,020	-0,99	0,51	50,52	Q27J81	Inverted formin-2	INF2
0,006	-0,99	0,51	50,51	Q14318	Peptidyl-prolyl cis-trans isomerase FKBP8	FKBP8
0,001	-0,99	0,50	50,35	Q9BQ39	ATP-dependent RNA helicase DDX50	DDX50
0,048	-0,99	0,50	50,35	Q00535	Cyclin-dependent-like kinase 5	CDK5
0,001	-0,99	0,50	50,35	Q13257	Mitotic spindle assembly checkpoint protein MAD2A	MAD2L1
0,004	-0,99	0,50	50,35	Q13330	Metastasis-associated protein MTA1	MTA1
0,001	-0,99	0,50	50,33	O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	INPPL1
0,010	-0,99	0,50	50,25	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1	HUWE1
0,007	-0,99	0,50	50,20	P33121	Long-chain-fatty-acid--CoA ligase 1	ACSL1
0,026	-1,00	0,50	50,00	Q96GM8	Target of EGR1 protein 1	TOE1
0,002	-1,00	0,50	50,00	Q9H444	Charged multivesicular body protein 4b	CHMP4B
0,000	-1,00	0,50	50,00	P26599	Polypyrimidine tract-binding protein 1	PTBP1
0,004	-1,00	0,50	50,00	Q9H910	Hematological and neurological expressed 1-like protein	HN1L
0,023	-1,01	0,50	49,80	Q9NUY8	TBC1 domain family member 23	TBC1D23
0,043	-1,01	0,50	49,73	Q9UBI6	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	GNG12
0,014	-1,01	0,50	49,71	Q9Y6Q5	AP-1 complex subunit mu-2	AP1M2

Supplemental Table S2b

0,009	-1,01	0,50	49,66	Q9HBL0	Tensin-1	TNS1
0,010	-1,01	0,50	49,65	Q99986	Serine/threonine-protein kinase VRK1	VRK1
0,028	-1,01	0,50	49,65	O43639	Cytoplasmic protein NCK2	NCK2
0,003	-1,01	0,50	49,65	O96028	Histone-lysine N-methyltransferase NSD2	WHSC1
0,041	-1,01	0,50	49,65	Q14191	Werner syndrome ATP-dependent helicase	WRN
0,002	-1,01	0,50	49,65	Q8TEX9	Importin-4	IPO4
0,003	-1,01	0,50	49,63	Q14108	Lysosome membrane protein 2	SCARB2
0,007	-1,01	0,50	49,62	Q9Y520	Protein PRRC2C	PRRC2C
0,025	-1,02	0,49	49,44	Q9H6W3	Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66	NO66
0,008	-1,02	0,49	49,43	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	RPN2
0,003	-1,02	0,49	49,31	Q8NFW8	N-acylneuraminate cytidyltransferase	CMAS
0,002	-1,02	0,49	49,31	Q8NDF8	Non-canonical poly(A) RNA polymerase PAPD5	PAPD5
0,006	-1,02	0,49	49,31	Q13283	Ras GTPase-activating protein-binding protein 1	G3BP1
0,003	-1,02	0,49	49,31	Q96AG4	Leucine-rich repeat-containing protein 59	LRRC59
0,026	-1,02	0,49	49,31	O15514	DNA-directed RNA polymerase II subunit RPB4	POLR2D
0,030	-1,02	0,49	49,31	O00471	Exocyst complex component 5	EXOC5
0,011	-1,02	0,49	49,31	Q96M96	FYVE, RhoGEF and PH domain-containing protein 4	FGD4
0,014	-1,02	0,49	49,31	Q9H8S9	MOB kinase activator 1A	MOB1A
0,003	-1,02	0,49	49,31	Q13506	NGFI-A-binding protein 1	NAB1
0,002	-1,02	0,49	49,28	Q99828	Calcium and integrin-binding protein 1	CIB1
0,035	-1,02	0,49	49,26	Q96HY6	DDR GK domain-containing protein 1	DDR GK1
0,018	-1,02	0,49	49,22	9BWW4;P81877;Q9BWC	Single-stranded DNA-binding protein 3;Single-stranded DNA-binding protein 2;Single-stranded DNA-binding protein 1	SSBP3;SSBP2;SSBP4
0,010	-1,02	0,49	49,16	Q9NXW2	DnaJ homolog subfamily B member 12	DNAJB12
0,016	-1,03	0,49	49,07	Q9H5V8	CUB domain-containing protein 1	CDCP1
0,015	-1,03	0,49	49,05	Q92563	Testican-2	SPOCK2
0,020	-1,03	0,49	48,98	Q9H3U1	Protein unc-45 homolog A	UNC45A
0,039	-1,03	0,49	48,97	O75909	Cyclin-K	CCNK
0,019	-1,03	0,49	48,97	P12235	ADP/ATP translocase 1	SLC25A4
0,025	-1,03	0,49	48,97	Q7Z4L5	Tetratricopeptide repeat protein 21B	TTC21B
0,001	-1,03	0,49	48,97	Q7Z5J4	Retinoic acid-induced protein 1	RAI1
0,010	-1,03	0,49	48,97	Q7Z2T5	TRMT1-like protein	TRMT1L
0,008	-1,03	0,49	48,93	Q9UFC0	Leucine-rich repeat and WD repeat-containing protein 1	LRWD1
0,030	-1,04	0,49	48,65	Q7L2E3	Putative ATP-dependent RNA helicase DHX30	DHX30

Supplemental Table S2b

0,018	-1,04	0,49	48,65	Q460N5	Poly [ADP-ribose] polymerase 14	PARP14
0,012	-1,04	0,49	48,63	Q9UJX3	Anaphase-promoting complex subunit 7	ANAPC7
0,009	-1,04	0,49	48,63	Q5JVF3	PCI domain-containing protein 2	PCID2
0,001	-1,04	0,49	48,63	P23588	Eukaryotic translation initiation factor 4B	EIF4B
0,045	-1,04	0,49	48,57	Q15477	Helicase SKI2W	SKI2L
0,010	-1,04	0,49	48,52	Q9UIQ6	Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum fc	LNPEP
0,000	-1,05	0,48	48,39	O60232	Sjogren syndrome/scleroderma autoantigen 1	SSSCA1
0,036	-1,05	0,48	48,30	Q14697	Neutral alpha-glucosidase AB	GANAB
0,011	-1,05	0,48	48,30	Q9HCK8	Chromodomain-helicase-DNA-binding protein 8	CHD8
0,013	-1,05	0,48	48,21	P63165	Small ubiquitin-related modifier 1	SUMO1
0,010	-1,05	0,48	48,20	P26358	DNA (cytosine-5)-methyltransferase 1	DNMT1
0,007	-1,06	0,48	48,11	Q8NBJ7	Sulfatase-modifying factor 2	SUMF2
0,013	-1,06	0,48	48,07	P06756	Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain	ITGAV
0,014	-1,06	0,48	48,04	P40222	Alpha-taxilin	TXLNA
0,047	-1,06	0,48	47,87	Q6XQN6	Nicotinate phosphoribosyltransferase	NAPRT
0,047	-1,07	0,48	47,75	P46976	Glycogenin-1	GYG1
0,016	-1,07	0,48	47,71	O75781	Paralemmin-1	PALM
0,006	-1,07	0,48	47,64	O43847	Nardilysin	NRD1
0,013	-1,07	0,48	47,63	Q75QN2	Integrator complex subunit 8	INTS8
0,022	-1,07	0,48	47,63	O43929	Origin recognition complex subunit 4	ORC4
0,018	-1,07	0,48	47,63	O95239	Chromosome-associated kinesin KIF4A	KIF4A
0,018	-1,07	0,48	47,63	Q9Y2T2	AP-3 complex subunit mu-1	AP3M1
0,001	-1,07	0,48	47,63	Q14966	Zinc finger protein 638	ZNF638
0,010	-1,07	0,48	47,63	O15013	Rho guanine nucleotide exchange factor 10	ARHGEF10
0,025	-1,07	0,48	47,62	O15258	Protein RER1	RER1
0,007	-1,07	0,48	47,52	O60610	Protein diaphanous homolog 1	DIAPH1
0,007	-1,07	0,48	47,52	O75175	CCR4-NOT transcription complex subunit 3	CNOT3
0,038	-1,07	0,48	47,50	O43676	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	NDUFB3
0,000	-1,08	0,47	47,36	Q8IZH2	5-3 exoribonuclease 1	XRN1
0,026	-1,08	0,47	47,31	Q13153	Serine/threonine-protein kinase PAK 1	PAK1
0,001	-1,08	0,47	47,30	P33176	Kinesin-1 heavy chain	KIF5B
0,005	-1,08	0,47	47,30	P62277	40S ribosomal protein S13	RPS13
0,037	-1,08	0,47	47,30	Q9H270	Vacuolar protein sorting-associated protein 11 homolog	VPS11

Supplemental Table S2b

0,010	-1,09	0,47	47,10	Q9UKU6	Thyrotropin-releasing hormone-degrading ectoenzyme	TRHDE
0,008	-1,09	0,47	47,06	Q02818	Nucleobindin-1	NUCB1
0,022	-1,09	0,47	47,03	Q96T23	Remodeling and spacing factor 1	RSF1
0,039	-1,09	0,47	46,98	Q99719	Septin-5	38596,000
0,002	-1,09	0,47	46,98	Q96DE0	U8 snoRNA-decapping enzyme	NUDT16
0,001	-1,09	0,47	46,98	Q96BZ8	Leukocyte receptor cluster member 1	LENG1
0,011	-1,10	0,47	46,77	Q9H0D6	5-3 exoribonuclease 2	XRN2
0,008	-1,10	0,47	46,66	Q86Y56	HEAT repeat-containing protein 2	HEATR2
0,008	-1,10	0,47	46,65	O00429	Dynamin-1-like protein	DNM1L
0,032	-1,10	0,47	46,65	P13693	Translationally-controlled tumor protein	TPT1
0,000	-1,10	0,47	46,65	Q6UXN9	WD repeat-containing protein 82	WDR82
0,012	-1,10	0,47	46,60	P04818	Thymidylate synthase	TYMS
0,015	-1,11	0,46	46,40	P62714	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	PPP2CB
0,023	-1,11	0,46	46,37	Q9UKF6	Cleavage and polyadenylation specificity factor subunit 3	CPSF3
0,041	-1,11	0,46	46,37	P11274	Breakpoint cluster region protein	BCR
0,005	-1,11	0,46	46,33	Q07020	60S ribosomal protein L18	RPL18
0,015	-1,11	0,46	46,33	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	UCHL1
0,007	-1,11	0,46	46,33	P41227	N-alpha-acetyltransferase 10	NAA10
0,004	-1,11	0,46	46,33	Q8NEM2	SHC SH2 domain-binding protein 1	SHCBP1
0,009	-1,12	0,46	46,01	Q16698	2,4-dienoyl-CoA reductase, mitochondrial	DECR1
0,029	-1,12	0,46	46,01	Q6ZYL4	General transcription factor IIH subunit 5	GTF2H5
0,007	-1,12	0,46	46,01	Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2	CPSF2
0,022	-1,12	0,46	46,01	P62266	40S ribosomal protein S23	RPS23
0,008	-1,12	0,46	46,01	Q9UHF7	Zinc finger transcription factor Trps1	TRPS1
0,025	-1,12	0,46	46,01	P18074	TFIIH basal transcription factor complex helicase XPD subunit	ERCC2
0,000	-1,12	0,46	46,01	Q9BWU1;P49336	Cyclin-dependent kinase 19;Cyclin-dependent kinase 8	CDK19;CDK8
0,002	-1,12	0,46	46,01	Q9GZR2	RNA exonuclease 4	REXO4
0,017	-1,12	0,46	45,99	Q9NYJ1	Cytochrome c oxidase assembly factor 4 homolog, mitochondrial	COA4
0,006	-1,13	0,46	45,73	O60563	Cyclin-T1	CCNT1
0,049	-1,13	0,46	45,71	Q7L266	Isoaspartyl peptidase/L-asparaginase;Isoaspartyl peptidase/L-asparaginase alpha ch	ASRGL1
0,031	-1,13	0,46	45,69	Q8IWZ3	Ankyrin repeat and KH domain-containing protein 1	ANKHD1
0,023	-1,14	0,45	45,38	Q8NB78	Lysine-specific histone demethylase 1B	KDM1B
0,027	-1,14	0,45	45,38	Q69YN2	CWF19-like protein 1	CWF19L1

Supplemental Table S2b

0,001	-1,14	0,45	45,38	Q9UHV7	Mediator of RNA polymerase II transcription subunit 13	MED13
0,003	-1,15	0,45	45,16	Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	USP9X
0,036	-1,15	0,45	45,06	P49257	Protein ERGIC-53	LMAN1
0,012	-1,15	0,45	45,06	O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUFB10
0,021	-1,15	0,45	45,06	Q96G46	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like	DUS3L
0,003	-1,15	0,45	45,00	Q7Z5L9	Interferon regulatory factor 2-binding protein 2	IRF2BP2
0,014	-1,15	0,45	44,93	Q8N3C0	Activating signal cointegrator 1 complex subunit 3	ASCC3
0,005	-1,15	0,45	44,93	O96013	Serine/threonine-protein kinase PAK 4	PAK4
0,010	-1,16	0,45	44,80	Q00534	Cyclin-dependent kinase 6	CDK6
0,016	-1,16	0,45	44,75	Q9H8H2	Probable ATP-dependent RNA helicase DDX31	DDX31
0,003	-1,16	0,45	44,75	Q8IZP0	Abl interactor 1	ABI1
0,045	-1,16	0,45	44,75	O43776	Asparagine--tRNA ligase, cytoplasmic	NARS
0,001	-1,17	0,44	44,44	Q13127	RE1-silencing transcription factor	REST
0,045	-1,17	0,44	44,38	O14976	Cyclin-G-associated kinase	GAK
0,002	-1,18	0,44	44,23	P55060	Exportin-2	CSE1L
0,046	-1,18	0,44	44,14	Q9UJX2	Cell division cycle protein 23 homolog	CDC23
0,050	-1,18	0,44	44,14	Q9NVH2	Integrator complex subunit 7	INTS7
0,004	-1,18	0,44	44,00	Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	NDUFA9
0,011	-1,19	0,44	43,95	Q96HW7	Integrator complex subunit 4	INTS4
0,043	-1,19	0,44	43,85	P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	OXCT1
0,000	-1,19	0,44	43,83	Q9BRJ7	Protein syndesmos	NUDT16L1
0,031	-1,19	0,44	43,83	O76003	Glutaredoxin-3	GLRX3
0,018	-1,19	0,44	43,83	Q9H0P0	Cytosolic 5-nucleotidase 3A	NT5C3A
0,010	-1,19	0,44	43,83	P30876	DNA-directed RNA polymerase II subunit RPB2	POLR2B
0,038	-1,19	0,44	43,80	O95782	AP-2 complex subunit alpha-1	AP2A1
0,002	-1,20	0,44	43,53	Q96RN5	Mediator of RNA polymerase II transcription subunit 15	MED15
0,012	-1,20	0,44	43,53	Q674X7	Kazrin	KAZN
0,018	-1,20	0,43	43,45	O43592	Exportin-T	XPOT
0,005	-1,20	0,43	43,44	Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31	PRPF31
0,049	-1,20	0,43	43,43	Q12824	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfami	SMARCB1
0,026	-1,20	0,43	43,41	Q9P273	Teneurin-3	TENM3
0,025	-1,21	0,43	43,23	Q7Z4G1	COMM domain-containing protein 6	COMMD6
0,002	-1,21	0,43	43,23	Q15398	Disks large-associated protein 5	DLGAP5

Supplemental Table S2b

0,021	-1,21	0,43	43,23	P51531	Probable global transcription activator SNF2L2	SMARCA2
0,023	-1,21	0,43	43,09	Q13501	Sequestosome-1	SQSTM1
0,014	-1,21	0,43	43,08	Q7L576	Cytoplasmic FMR1-interacting protein 1	CYFIP1
0,007	-1,22	0,43	42,93	P30260	Cell division cycle protein 27 homolog	CDC27
0,006	-1,22	0,43	42,93	O60890	Oligophrenin-1	OPHN1
0,005	-1,22	0,43	42,83	Q86X29	Lipolysis-stimulated lipoprotein receptor	LSR
0,003	-1,23	0,43	42,63	Q96QC0	Serine/threonine-protein phosphatase 1 regulatory subunit 10	PPP1R10
0,014	-1,23	0,43	42,63	Q8N201	Integrator complex subunit 1	INTS1
0,008	-1,24	0,42	42,42	O95155	Ubiquitin conjugation factor E4 B	UBE4B
0,049	-1,24	0,42	42,34	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopenti	TMPO
0,048	-1,24	0,42	42,34	Q9UKS7	Zinc finger protein Helios	IKZF2
0,035	-1,24	0,42	42,34	O00443	Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha	PIK3C2A
0,008	-1,24	0,42	42,34	Q53F19	Uncharacterized protein C17orf85	C17orf85
0,013	-1,24	0,42	42,34	Q9Y262	Eukaryotic translation initiation factor 3 subunit L	EIF3L
0,018	-1,24	0,42	42,23	Q8IY81	pre-rRNA processing protein FTSJ3	FTSJ3
0,018	-1,25	0,42	42,14	Q8IV08	Phospholipase D3	PLD3
0,026	-1,25	0,42	42,07	Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	GBF1
0,013	-1,25	0,42	42,04	O95861	3(2),5-bisphosphate nucleotidase 1	BPNT1
0,017	-1,25	0,42	42,04	Q96IZ7	Serine/Arginine-related protein 53	RSRC1
0,000	-1,25	0,42	42,04	Q14320	Protein FAM50A	FAM50A
0,010	-1,26	0,42	41,77	P62330	ADP-ribosylation factor 6	ARF6
0,043	-1,26	0,42	41,75	Q7Z7C8	Transcription initiation factor TFIID subunit 8	TAF8
0,003	-1,26	0,42	41,75	O60216	Double-strand-break repair protein rad21 homolog	RAD21
0,026	-1,26	0,42	41,72	P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit;cAMP-dependent p	PRKAR1A
0,006	-1,27	0,41	41,47	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	FKBP3
0,043	-1,27	0,41	41,47	Q9BVG4	Protein PBDC1	PBDC1
0,002	-1,27	0,41	41,47	Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3	PLCB3
0,006	-1,27	0,41	41,47	Q96II8	Leucine-rich repeat and calponin homology domain-containing protein 3	LRCH3
0,000	-1,27	0,41	41,46	Q96ER9	Coiled-coil domain-containing protein 51	CCDC51
0,006	-1,27	0,41	41,42	P00533	Epidermal growth factor receptor	EGFR
0,016	-1,28	0,41	41,23	P04637	Cellular tumor antigen p53	TP53
0,049	-1,28	0,41	41,18	Q9UHR4	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	BAIAP2L1
0,026	-1,28	0,41	41,18	Q99816	Tumor susceptibility gene 101 protein	TSG101

Supplemental Table S2b

0,005	-1,28	0,41	41,18	Q86YP4	Transcriptional repressor p66-alpha	GATAD2A
0,026	-1,28	0,41	41,18	P06493	Cyclin-dependent kinase 1	CDK1
0,046	-1,28	0,41	41,17	P23634	Plasma membrane calcium-transporting ATPase 4	ATP2B4
0,000	-1,28	0,41	41,09	O00468	Agrin;Agrin N-terminal 110 kDa subunit;Agrin C-terminal 110 kDa subunit;Agrin C-te	AGRN
0,008	-1,28	0,41	41,07	Q9BSV6	tRNA-splicing endonuclease subunit Sen34	TSEN34
0,015	-1,29	0,41	40,90	P12236	ADP/ATP translocase 3;ADP/ATP translocase 3, N-terminally processed	SLC25A6
0,001	-1,29	0,41	40,90	Q6PJT7	Zinc finger CCCH domain-containing protein 14	ZC3H14
0,032	-1,29	0,41	40,90	Q9UPN6	Protein SCAF8	SCAF8
0,009	-1,29	0,41	40,90	A1L020	RNA-binding protein MEX3A	MEX3A
0,012	-1,29	0,41	40,90	Q9Y5B6	PAX3- and PAX7-binding protein 1	PAXBP1
0,012	-1,29	0,41	40,90	Q8IX18	Probable ATP-dependent RNA helicase DHX40	DHX40
0,007	-1,29	0,41	40,90	Q9H8V3	Protein ECT2	ECT2
0,011	-1,29	0,41	40,81	Q8NFH4	Nucleoporin Nup37	NUP37
0,001	-1,30	0,41	40,61	P62861	40S ribosomal protein S30	FAU
0,006	-1,30	0,41	40,61	Q9NZQ3	NCK-interacting protein with SH3 domain	NCKIPSD
0,034	-1,30	0,41	40,55	O95436	Sodium-dependent phosphate transport protein 2B	SLC34A2
0,005	-1,31	0,40	40,42	Q99567	Nuclear pore complex protein Nup88	NUP88
0,013	-1,31	0,40	40,33	Q9Y421	Protein FAM32A	FAM32A
0,000	-1,31	0,40	40,33	P50238	Cysteine-rich protein 1	CRIP1
0,004	-1,31	0,40	40,33	Q6IN84	rRNA methyltransferase 1, mitochondrial	MRM1
0,001	-1,31	0,40	40,33	P30533	Alpha-2-macroglobulin receptor-associated protein	LRPAP1
0,003	-1,31	0,40	40,29	Q9BW91	ADP-ribose pyrophosphatase, mitochondrial	NUDT9
0,019	-1,32	0,40	40,05	Q8WXA9	Splicing regulatory glutamine/lysine-rich protein 1	SREK1
0,001	-1,32	0,40	40,05	Q99728	BRCA1-associated RING domain protein 1	BARD1
0,034	-1,32	0,40	40,05	Q9ULU4	Protein kinase C-binding protein 1	ZMYND8
0,009	-1,32	0,40	40,05	Q13144	Translation initiation factor eIF-2B subunit epsilon	EIF2B5
0,026	-1,32	0,40	40,05	P49459	Ubiquitin-conjugating enzyme E2 A	UBE2A
0,002	-1,32	0,40	39,94	Q147X3	N-alpha-acetyltransferase 30	NAA30
0,031	-1,33	0,40	39,80	Q9NYY8	FAST kinase domain-containing protein 2	FASTKD2
0,020	-1,33	0,40	39,78	Q5SY16	Polynucleotide 5-hydroxyl-kinase NOL9	NOL9
0,021	-1,33	0,40	39,78	Q9HDC9	Adipocyte plasma membrane-associated protein	APMAP
0,015	-1,33	0,40	39,71	Q9Y6C9	Mitochondrial carrier homolog 2	MTCH2
0,000	-1,33	0,40	39,66	Q9H7P9	Pleckstrin homology domain-containing family G member 2	PLEKHG2

Supplemental Table S2b

0,004	-1,34	0,40	39,60	Q8IWA0	WD repeat-containing protein 75	WDR75
0,016	-1,34	0,40	39,50	Q6IA86	Elongator complex protein 2	ELP2
0,006	-1,34	0,40	39,50	Q13356	Peptidyl-prolyl cis-trans isomerase-like 2	PPIL2
0,008	-1,34	0,39	39,47	Q13423	NAD(P) transhydrogenase, mitochondrial	NNT
0,000	-1,34	0,39	39,37	O95140	Mitofusin-2	MFN2
0,002	-1,35	0,39	39,29	P18065	Insulin-like growth factor-binding protein 2	IGFBP2
0,003	-1,35	0,39	39,23	Q99496	E3 ubiquitin-protein ligase RING2	RNF2
0,028	-1,35	0,39	39,23	Q56N19	N-acetyltransferase ESCO2	ESCO2
0,002	-1,35	0,39	39,23	Q9P270	SLAIN motif-containing protein 2	SLAIN2
0,000	-1,36	0,39	39,02	Q13191	E3 ubiquitin-protein ligase CBL-B	CBLB
0,032	-1,36	0,39	38,96	Q86Y91	Kinesin-like protein KIF18B	KIF18B
0,012	-1,36	0,39	38,96	Q15648	Mediator of RNA polymerase II transcription subunit 1	MED1
0,034	-1,36	0,39	38,96	P54132	Bloom syndrome protein	BLM
0,007	-1,36	0,39	38,83	O15347	High mobility group protein B3	HMGB3
0,019	-1,37	0,39	38,69	Q8NFI3	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1	TSTD1
0,004	-1,37	0,39	38,69	P12081	Histidine--tRNA ligase, cytoplasmic	HARS
0,015	-1,37	0,39	38,65	Q9H1B7	Interferon regulatory factor 2-binding protein-like	IRF2BPL
0,039	-1,38	0,39	38,52	Q6WCQ1	Myosin phosphatase Rho-interacting protein	MPRIP
0,001	-1,38	0,38	38,42	Q5UIP0	Telomere-associated protein RIF1	RIF1
0,048	-1,38	0,38	38,31	P11117	Lysosomal acid phosphatase	ACP2
0,037	-1,39	0,38	38,23	Q9ULT8	E3 ubiquitin-protein ligase HECTD1	HECTD1
0,006	-1,39	0,38	38,20	O75717	WD repeat and HMG-box DNA-binding protein 1	WDHD1
0,015	-1,39	0,38	38,16	Q14508	WAP four-disulfide core domain protein 2	WFDC2
0,001	-1,39	0,38	38,16	Q86U86	Protein polybromo-1	PBRM1
0,012	-1,39	0,38	38,16	P62854;Q5JNZ5	40S ribosomal protein S26;Putative 40S ribosomal protein S26-like 1	RPS26;RPS26P11
0,023	-1,39	0,38	38,14	P05067	Amyloid beta A4 protein;N-APP;Soluble APP-alpha;Soluble APP-beta;C99;Beta-amyl	APP
0,005	-1,39	0,38	38,14	Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1
0,037	-1,39	0,38	38,14	O75382	Tripartite motif-containing protein 3	TRIM3
0,001	-1,40	0,38	37,99	P02649	Apolipoprotein E	APOE
0,005	-1,40	0,38	37,89	Q9UBW7	Zinc finger MYM-type protein 2	ZMYM2
0,002	-1,40	0,38	37,89	O00567	Nucleolar protein 56	NOP56
0,001	-1,40	0,38	37,89	Q96BP3	Peptidylprolyl isomerase domain and WD repeat-containing protein 1	PPWD1
0,041	-1,40	0,38	37,89	Q5VSL9	Striatin-interacting protein 1	STRIP1

Supplemental Table S2b

0,018	-1,40	0,38	37,83	Q14527	Helicase-like transcription factor	HLTF
0,003	-1,41	0,38	37,68	P23458	Tyrosine-protein kinase JAK1	JAK1
0,011	-1,41	0,38	37,68	O14893	Gem-associated protein 2	GEMIN2
0,026	-1,41	0,38	37,67	Q9BQ52	Zinc phosphodiesterase ELAC protein 2	ELAC2
0,011	-1,41	0,38	37,63	Q9H501	ESF1 homolog	ESF1
0,003	-1,41	0,38	37,63	Q96SB4	SRSF protein kinase 1	SRPK1
0,021	-1,41	0,38	37,63	Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	PBXIP1
0,004	-1,41	0,38	37,63	P63098	Calcineurin subunit B type 1	PPP3R1
0,013	-1,41	0,38	37,63	O15047	Histone-lysine N-methyltransferase SETD1A	SETD1A
0,002	-1,41	0,38	37,58	Q8WXI7	Mucin-16	MUC16
0,002	-1,41	0,38	37,56	Q9Y6H1;Q5T1J5	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial;Putative	CHCHD2;CHCHD2P5
0,002	-1,42	0,37	37,37	Q8NCW5	NAD(P)H-hydrate epimerase	APOA1BP
0,001	-1,42	0,37	37,37	Q68D10	Protein SPT2 homolog	SPTY2D1
0,019	-1,42	0,37	37,31	Q9BY42	Protein RTF2 homolog	RTFDC1
0,002	-1,42	0,37	37,31	Q9NP92	28S ribosomal protein S30, mitochondrial	MRPS30
0,008	-1,43	0,37	37,13	P40763	Signal transducer and activator of transcription 3	STAT3
0,008	-1,43	0,37	37,11	Q5VUA4	Zinc finger protein 318	ZNF318
0,022	-1,43	0,37	37,11	Q9NPI1	Bromodomain-containing protein 7	BRD7
0,043	-1,44	0,37	36,86	Q99543	DnaJ homolog subfamily C member 2;DnaJ homolog subfamily C member 2, N-termi	DNAJC2
0,005	-1,44	0,37	36,86	P46939	Utrophin	UTRN
0,000	-1,44	0,37	36,85	Q99538	Legumain	LGMN
0,040	-1,44	0,37	36,79	Q9Y6I4	Ubiquitin carboxyl-terminal hydrolase 3	USP3
0,008	-1,45	0,37	36,60	P36776	Lon protease homolog, mitochondrial	LONP1
0,022	-1,45	0,37	36,60	P51648	Fatty aldehyde dehydrogenase	ALDH3A2
0,002	-1,45	0,37	36,60	Q03252	Lamin-B2	LMNB2
0,000	-1,45	0,37	36,60	P48729	Casein kinase I isoform alpha	CSNK1A1
0,005	-1,45	0,37	36,60	Q03112	MDS1 and EVI1 complex locus protein EVI1	MECOM
0,033	-1,45	0,37	36,60	Q9UER7	Death domain-associated protein 6	DAXX
0,016	-1,45	0,37	36,59	Q96P70	Importin-9	IPO9
0,007	-1,46	0,36	36,35	Q5VZL5	Zinc finger MYM-type protein 4	ZMYM4
0,024	-1,46	0,36	36,35	P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2
0,014	-1,46	0,36	36,31	Q96EE3	Nucleoporin SEH1	SEH1L
0,024	-1,46	0,36	36,23	P11802	Cyclin-dependent kinase 4	CDK4

Supplemental Table S2b

0,030	-1,47	0,36	36,16	Q96BN8	Ubiquitin thioesterase otulin	OTULIN
0,044	-1,47	0,36	36,10	O95503	Chromobox protein homolog 6	CBX6
0,027	-1,47	0,36	36,10	Q13405	39S ribosomal protein L49, mitochondrial	MRPL49
0,007	-1,47	0,36	36,09	P49821	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	NDUFV1
0,024	-1,47	0,36	36,02	Q15819	Ubiquitin-conjugating enzyme E2 variant 2	UBE2V2
0,045	-1,47	0,36	35,99	P05023	Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1
0,001	-1,48	0,36	35,92	O43278	Kunitz-type protease inhibitor 1	SPINT1
0,037	-1,48	0,36	35,85	Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3	ADPRHL2
0,031	-1,48	0,36	35,85	Q15269	Periodic tryptophan protein 2 homolog	PWP2
0,003	-1,48	0,36	35,83	Q9H792	Pseudopodium-enriched atypical kinase 1	PEAK1
0,002	-1,48	0,36	35,75	P63151;Q66LE6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	PPP2R2A;PPP2R2D
0,002	-1,49	0,36	35,64	Q9H3S7	Tyrosine-protein phosphatase non-receptor type 23	PTPN23
0,024	-1,49	0,36	35,63	Q9BTW9	Tubulin-specific chaperone D	TBCD
0,002	-1,49	0,36	35,60	O14578	Citron Rho-interacting kinase	CIT
0,023	-1,49	0,36	35,60	Q14669	E3 ubiquitin-protein ligase TRIP12	TRIP12
0,002	-1,49	0,36	35,60	Q99661	Kinesin-like protein KIF2C	KIF2C
0,032	-1,49	0,36	35,60	Q96CN7	Isochorismatase domain-containing protein 1	ISOC1
0,033	-1,50	0,35	35,45	P63000;P60763;P15153	Ras-related C3 botulinum toxin substrate 1; Ras-related C3 botulinum toxin substrate 1	RAC1;RAC3;RAC2
0,001	-1,50	0,35	35,36	P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	STT3A
0,033	-1,50	0,35	35,36	Q9UBR2	Cathepsin Z	CTSZ
0,001	-1,50	0,35	35,36	Q9Y6W5	Wiskott-Aldrich syndrome protein family member 2	WASF2
0,015	-1,50	0,35	35,28	Q9HCJ3	Ribonucleoprotein PTB-binding 2	RAVER2
0,014	-1,50	0,35	35,25	P53680	AP-2 complex subunit sigma	AP2S1
0,001	-1,51	0,35	35,11	Q9C0J8	pre-mRNA 3 end processing protein WDR33	WDR33
0,007	-1,51	0,35	35,06	P57076	UPF0769 protein C21orf59	C21orf59
0,017	-1,52	0,35	34,99	P18615	Negative elongation factor E	NELFE
0,006	-1,52	0,35	34,75	Q96EI5	Transcription elongation factor A protein-like 4	TCEAL4
0,028	-1,53	0,35	34,73	Q6NZY4	Zinc finger CCHC domain-containing protein 8	ZCCHC8
0,022	-1,53	0,35	34,63	O60763	General vesicular transport factor p115	USO1
0,047	-1,53	0,35	34,63	Q8N3U4	Cohesin subunit SA-2	STAG2
0,002	-1,54	0,34	34,47	Q9NPD8	Ubiquitin-conjugating enzyme E2 T	UBE2T
0,002	-1,54	0,34	34,39	O15027	Protein transport protein Sec16A	SEC16A
0,025	-1,54	0,34	34,39	Q70E73	Ras-associated and pleckstrin homology domains-containing protein 1	RAPH1

Supplemental Table S2b

0,001	-1,54	0,34	34,32	Q5VT25	Serine/threonine-protein kinase MRCK alpha	CDC42BPA
0,031	-1,55	0,34	34,27	P23229	Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain;Processed	ITGA6
0,008	-1,55	0,34	34,15	P06744	Glucose-6-phosphate isomerase	GPI
0,019	-1,55	0,34	34,14	Q16678	Cytochrome P450 1B1	CYP1B1
0,021	-1,55	0,34	34,11	O15213	WD repeat-containing protein 46	WDR46
0,025	-1,56	0,34	33,83	O14617	AP-3 complex subunit delta-1	AP3D1
0,018	-1,58	0,33	33,45	Q9NQZ2	Something about silencing protein 10	UTP3
0,010	-1,58	0,33	33,45	P55786	Puromycin-sensitive aminopeptidase	NPEPPS
0,003	-1,58	0,33	33,45	Q96B54	Zinc finger protein 428	ZNF428
0,002	-1,58	0,33	33,38	Q6P1L8	39S ribosomal protein L14, mitochondrial	MRPL14
0,012	-1,58	0,33	33,37	O95166;Q9H0R8	Gamma-aminobutyric acid receptor-associated protein;Gamma-aminobutyric acid rABARAP;GABARAP	
0,014	-1,59	0,33	33,32	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	NDUFS1
0,010	-1,59	0,33	33,22	Q13724	Mannosyl-oligosaccharide glucosidase	MOGS
0,005	-1,59	0,33	33,22	P21741	Midkine	MDK
0,028	-1,59	0,33	33,22	Q7Z5K2	Wings apart-like protein homolog	WAPAL
0,013	-1,59	0,33	33,22	P49757	Protein numb homolog	NUMB
0,002	-1,59	0,33	33,19	Q14739	Lamin-B receptor	LBR
0,039	-1,60	0,33	32,99	Q92947	Glutaryl-CoA dehydrogenase, mitochondrial	GCDH
0,004	-1,60	0,33	32,99	Q9UNX4	WD repeat-containing protein 3	WDR3
0,040	-1,60	0,33	32,99	Q6NV74	Uncharacterized protein KIAA1211-like	KIAA1211L
0,015	-1,60	0,33	32,96	Q06203	Amidophosphoribosyltransferase	PPAT
0,043	-1,60	0,33	32,95	P18084	Integrin beta-5	ITGB5
0,001	-1,60	0,33	32,91	Q9NTJ3	Structural maintenance of chromosomes protein 4	SMC4
0,019	-1,61	0,33	32,76	Q12955	Ankyrin-3	ANK3
0,013	-1,61	0,33	32,76	P36404	ADP-ribosylation factor-like protein 2	ARL2
0,004	-1,61	0,33	32,76	P40937	Replication factor C subunit 5	RFC5
0,016	-1,61	0,33	32,76	Q92618	Zinc finger protein 516	ZNF516
0,001	-1,62	0,33	32,53	Q6PL18	ATPase family AAA domain-containing protein 2	ATAD2
0,002	-1,62	0,33	32,53	Q69YH5	Cell division cycle-associated protein 2	CDCA2
0,014	-1,63	0,32	32,41	O43760	Synaptogyrin-2	SYNGR2
0,000	-1,63	0,32	32,40	O43252	Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1;Sulfate adenylyltran	PAPSS1
0,002	-1,63	0,32	32,24	P50851	Lipopolysaccharide-responsive and beige-like anchor protein	LRBA
0,025	-1,64	0,32	32,09	O75182	Paired amphipathic helix protein Sin3b	SIN3B

Supplemental Table S2b

0,021	-1,64	0,32	32,09	Q8WXH0	Nesprin-2	SYNE2
0,005	-1,64	0,32	32,09	Q8N1G0	Zinc finger protein 687	ZNF687
0,003	-1,65	0,32	31,86	Q8N726	Cyclin-dependent kinase inhibitor 2A, isoform 4	CDKN2A
0,046	-1,65	0,32	31,86	Q14BN4	Sarcolemmal membrane-associated protein	SLMAP
0,005	-1,65	0,32	31,86	Q9Y5J1	U3 small nucleolar RNA-associated protein 18 homolog	UTP18
0,032	-1,65	0,32	31,78	Q86WA8	Lon protease homolog 2, peroxisomal	LONP2
0,028	-1,66	0,32	31,68	O14786	Neuropilin-1	NRP1
0,000	-1,66	0,32	31,60	P31350	Ribonucleoside-diphosphate reductase subunit M2	RRM2
0,032	-1,67	0,31	31,43	Q13535	Serine/threonine-protein kinase ATR	ATR
0,008	-1,68	0,31	31,22	Q9Y6D9	Mitotic spindle assembly checkpoint protein MAD1	MAD1L1
0,000	-1,68	0,31	31,21	Q9NYF8	Bcl-2-associated transcription factor 1	BCLAF1
0,003	-1,68	0,31	31,21	Q06710	Paired box protein Pax-8	PAX8
0,007	-1,69	0,31	31,03	A5YKK6	CCR4-NOT transcription complex subunit 1	CNOT1
0,035	-1,69	0,31	30,99	Q13017	Rho GTPase-activating protein 5	ARHGAP5
0,002	-1,69	0,31	30,99	P49848	Transcription initiation factor TFIID subunit 6	TAF6
0,041	-1,70	0,31	30,86	P84103	Serine/arginine-rich splicing factor 3	SRSF3
0,002	-1,70	0,31	30,78	P30419	Glycylpeptide N-tetradecanoyltransferase 1	NMT1
0,002	-1,71	0,30	30,48	O95347	Structural maintenance of chromosomes protein 2	SMC2
0,015	-1,72	0,30	30,37	O75438	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	NDUFB1
0,040	-1,72	0,30	30,36	Q9Y5L0	Transportin-3	TNPO3
0,007	-1,72	0,30	30,35	Q49AG3	Zinc finger BED domain-containing protein 5	ZBED5
0,034	-1,72	0,30	30,35	Q93074	Mediator of RNA polymerase II transcription subunit 12	MED12
0,021	-1,72	0,30	30,33	P61024	Cyclin-dependent kinases regulatory subunit 1	CKS1B
0,002	-1,72	0,30	30,29	Q9BZE1	39S ribosomal protein L37, mitochondrial	MRPL37
0,045	-1,73	0,30	30,25	P60953	Cell division control protein 42 homolog	CDC42
0,013	-1,73	0,30	30,24	Q9Y2D4	Exocyst complex component 6B	EXOC6B
0,004	-1,73	0,30	30,22	Q9NR31	GTP-binding protein SAR1a	SAR1A
0,002	-1,73	0,30	30,15	Q14692	Ribosome biogenesis protein BMS1 homolog	BMS1
0,008	-1,73	0,30	30,15	Q96GM5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfam	SMARCD1
0,010	-1,73	0,30	30,08	Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	ADI1
0,030	-1,73	0,30	30,06	O14907	Tax1-binding protein 3	TAX1BP3
0,001	-1,74	0,30	30,01	Q9NX47	E3 ubiquitin-protein ligase MARCH5	MARCH5
0,006	-1,74	0,30	29,94	O60934	Nibrin	NBN

Supplemental Table S2b

0,025	-1,74	0,30	29,94	Q96K17	Transcription factor BTF3 homolog 4	BTF3L4
0,009	-1,74	0,30	29,94	O75147	Obscurin-like protein 1	OBSL1
0,037	-1,75	0,30	29,73	Q07866	Kinesin light chain 1	KLC1
0,013	-1,76	0,30	29,60	Q8IWR0	Zinc finger CCCH domain-containing protein 7A	ZC3H7A
0,009	-1,76	0,30	29,60	Q96EX3	WD repeat-containing protein 34	WDR34
0,046	-1,76	0,30	29,52	Q6P9B9	Integrator complex subunit 5	INTS5
0,041	-1,77	0,29	29,33	Q9H0U9	Testis-specific Y-encoded-like protein 1	TSPYL1
0,032	-1,77	0,29	29,32	Q6P597	Kinesin light chain 3	KLC3
0,044	-1,77	0,29	29,32	Q9NU22	Midasin	MDN1
0,001	-1,77	0,29	29,32	P57721	Poly(rC)-binding protein 3	PCBP3
0,022	-1,78	0,29	29,12	Q71RC2	La-related protein 4	LARP4
0,007	-1,78	0,29	29,12	P14635	G2/mitotic-specific cyclin-B1	CCNB1
0,026	-1,79	0,29	28,95	Q15291	Retinoblastoma-binding protein 5	RBBP5
0,000	-1,79	0,29	28,86	Q9Y448	Small kinetochore-associated protein	KNSTRN
0,007	-1,80	0,29	28,72	Q9Y4A5	Transformation/transcription domain-associated protein	TRRAP
0,006	-1,80	0,29	28,72	P18887	DNA repair protein XRCC1	XRCC1
0,018	-1,80	0,29	28,72	O60293	Zinc finger C3H1 domain-containing protein	ZFC3H1
0,009	-1,80	0,29	28,72	Q15750	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	TAB1
0,046	-1,81	0,29	28,52	O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	PLOD3
0,013	-1,83	0,28	28,17	Q5VT52	Regulation of nuclear pre-mRNA domain-containing protein 2	RPRD2
0,047	-1,84	0,28	28,02	Q8N9B5	Junction-mediating and -regulatory protein	JMY
0,041	-1,84	0,28	27,97	O75410	Transforming acidic coiled-coil-containing protein 1	TACC1
0,006	-1,84	0,28	27,89	P23921	Ribonucleoside-diphosphate reductase large subunit	RRM1
0,041	-1,85	0,28	27,74	Q92547	DNA topoisomerase 2-binding protein 1	TOPBP1
0,015	-1,86	0,28	27,59	Q8N0X7	Spartin	SPG20
0,010	-1,86	0,28	27,55	Q5PRF9	Protein Smaug homolog 2	SAMD4B
0,039	-1,86	0,28	27,55	A3KN83	Protein strawberry notch homolog 1	SBNO1
0,001	-1,86	0,28	27,55	Q5VYS8	Terminal uridylyltransferase 7	ZCCHC6
0,021	-1,87	0,27	27,40	P55285	Cadherin-6	CDH6
0,032	-1,87	0,27	27,27	O15260	Surfeit locus protein 4	SURF4
0,002	-1,88	0,27	27,23	Q9H9T3	Elongator complex protein 3	ELP3
0,041	-1,88	0,27	27,17	Q9H977	WD repeat-containing protein 54	WDR54
0,004	-1,88	0,27	27,17	Q9P2M7	Cingulin	CGN

Supplemental Table S2b

0,004	-1,88	0,27	27,17	Q9HBE1	POZ-, AT hook-, and zinc finger-containing protein 1	PATZ1
0,000	-1,88	0,27	27,14	Q9BVK2	Probable dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glucosyltransferase	ALG8
0,028	-1,89	0,27	27,04	Q9Y5Y6	Suppressor of tumorigenicity 14 protein	ST14
0,030	-1,89	0,27	26,99	Q5R3I4	Tetratricopeptide repeat protein 38	TTC38
0,002	-1,89	0,27	26,98	B1AK53	Espin	ESPN
0,005	-1,89	0,27	26,98	Q96PE2	Rho guanine nucleotide exchange factor 17	ARHGEF17
0,001	-1,90	0,27	26,87	Q8N7H5	RNA polymerase II-associated factor 1 homolog	PAF1
0,012	-1,90	0,27	26,79	P78563	Double-stranded RNA-specific editase 1	ADARB1
0,027	-1,91	0,27	26,61	Q6ZSR9	Uncharacterized protein FLJ45252	
0,026	-1,91	0,27	26,61	Q14202	Zinc finger MYM-type protein 3	ZMYM3
0,001	-1,92	0,26	26,45	O95298;E9PQ53	NADH dehydrogenase [ubiquinone] 1 subunit C2;NADH dehydrogenase [ubiquinone]	UFC2;NDUFC2-KCTD
0,009	-1,92	0,26	26,44	P57678	Gem-associated protein 4	GEMIN4
0,024	-1,92	0,26	26,43	Q15811	Intersectin-1	ITSN1
0,003	-1,92	0,26	26,43	Q68E01	Integrator complex subunit 3	INTS3
0,006	-1,93	0,26	26,26	P24928	DNA-directed RNA polymerase II subunit RPB1	POLR2A
0,040	-1,93	0,26	26,24	P19404	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	NDUFV2
0,002	-1,94	0,26	26,06	P18583	Protein SON	SON
0,031	-1,95	0,26	25,96	Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase	PBK
0,011	-1,95	0,26	25,88	Q13867	Bleomycin hydrolase	BLMH
0,019	-1,96	0,26	25,70	Q6ZNB6	NF-X1-type zinc finger protein NFXL1	NFXL1
0,002	-1,97	0,26	25,53	P82663	28S ribosomal protein S25, mitochondrial	MRPS25
0,001	-1,97	0,26	25,53	Q9BRA0	N-alpha-acetyltransferase 38, NatC auxiliary subunit	NAA38
0,016	-1,97	0,26	25,53	P13473	Lysosome-associated membrane glycoprotein 2	LAMP2
0,020	-1,98	0,25	25,40	P04626	Receptor tyrosine-protein kinase erbB-2	ERBB2
0,004	-1,98	0,25	25,28	P35240	Merlin	NF2
0,003	-1,99	0,25	25,23	P35573	Glycogen debranching enzyme;4-alpha-glucanotransferase;Amylo-alpha-1,6-glucosidase	AGL
0,014	-1,99	0,25	25,17	O14646	Chromodomain-helicase-DNA-binding protein 1	CHD1
0,007	-1,99	0,25	25,10	Q6UWZ7	BRCA1-A complex subunit Abraxas	FAM175A
0,045	-2,00	0,25	25,00	Q3L8U1	Chromodomain-helicase-DNA-binding protein 9	CHD9
0,007	-2,00	0,25	25,00	P29372	DNA-3-methyladenine glycosylase	MPG
0,006	-2,00	0,25	25,00	Q9HCB6	Spondin-1	SPON1
0,030	-2,01	0,25	24,90	Q9GZN8	UPF0687 protein C20orf27	C20orf27
0,005	-2,01	0,25	24,83	O00268	Transcription initiation factor TFIID subunit 4	TAF4

Supplemental Table S2b

0,000	-2,01	0,25	24,83	Q9NSD9	Phenylalanine--tRNA ligase beta subunit	FARSB
0,035	-2,02	0,25	24,74	O15397	Importin-8	IPO8
0,000	-2,02	0,25	24,66	Q99715	Collagen alpha-1(XII) chain	COL12A1
0,000	-2,02	0,25	24,66	P51946	Cyclin-H	CCNH
0,023	-2,02	0,25	24,66	P53992	Protein transport protein Sec24C	SEC24C
0,040	-2,02	0,25	24,57	Q9UPN9	E3 ubiquitin-protein ligase TRIM33	TRIM33
0,019	-2,04	0,24	24,32	Q4FZB7	Histone-lysine N-methyltransferase SUV420H1	SUV420H1
0,013	-2,05	0,24	24,22	Q8IXQ6	Poly [ADP-ribose] polymerase 9	PARP9
0,036	-2,05	0,24	24,14	Q9NUQ6	SPATS2-like protein	SPATS2L
0,003	-2,06	0,24	23,91	O00762	Ubiquitin-conjugating enzyme E2 C	UBE2C
0,017	-2,07	0,24	23,80	Q13509	Tubulin beta-3 chain	TUBB3
0,021	-2,08	0,24	23,73	P13591	Neural cell adhesion molecule 1	NCAM1
0,000	-2,08	0,24	23,72	O95573	Long-chain-fatty-acid--CoA ligase 3	ACSL3
0,002	-2,08	0,24	23,65	P35251	Replication factor C subunit 1	RFC1
0,013	-2,08	0,24	23,65	Q9NUQ3	Gamma-taxilin	TXLNG
0,006	-2,08	0,24	23,65	Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit	NAA15
0,018	-2,08	0,24	23,65	O43768	Alpha-endosulfine	ENSA
0,020	-2,09	0,23	23,49	Q9NRL2	Bromodomain adjacent to zinc finger domain protein 1A	BAZ1A
0,013	-2,09	0,23	23,43	Q9UJX6	Anaphase-promoting complex subunit 2	ANAPC2
0,030	-2,10	0,23	23,33	Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit	UBA3
0,025	-2,10	0,23	23,33	Q8NBT2	Kinetochore protein Spc24	SPC24
0,006	-2,12	0,23	23,00	Q9UL03	Integrator complex subunit 6	INTS6
0,025	-2,12	0,23	22,95	P54198	Protein HIRA	HIRA
0,015	-2,13	0,23	22,85	P98095	Fibulin-2	FBLN2
0,020	-2,13	0,23	22,85	Q9UBC2	Epidermal growth factor receptor substrate 15-like 1	EPS15L1
0,004	-2,13	0,23	22,85	P30040	Endoplasmic reticulum resident protein 29	ERP29
0,004	-2,13	0,23	22,85	Q9UBX3	Mitochondrial dicarboxylate carrier	SLC25A10
0,031	-2,15	0,23	22,55	Q9UQR0	Sex comb on midleg-like protein 2	SCML2
0,005	-2,15	0,23	22,53	Q9C0J9	Class E basic helix-loop-helix protein 41	BHLHE41
0,001	-2,15	0,22	22,47	Q12800	Alpha-globin transcription factor CP2	TFCP2
0,007	-2,16	0,22	22,38	Q12830	Nucleosome-remodeling factor subunit BPTF	BPTF
0,000	-2,17	0,22	22,26	O43291	Kunitz-type protease inhibitor 2	SPINT2
0,004	-2,18	0,22	22,07	Q8NI27	THO complex subunit 2	THOC2

Supplemental Table S2b

0,000	-2,19	0,22	21,92	Q8NEM7	Transcription factor SPT20 homolog	SUPT20H
0,023	-2,20	0,22	21,72	Q58FF6	Putative heat shock protein HSP 90-beta 4	HSP90AB4P
0,031	-2,22	0,21	21,46	Q9UHY1	Nuclear receptor-binding protein	NRBP1
0,046	-2,22	0,21	21,40	Q5QJE6	Deoxynucleotidyltransferase terminal-interacting protein 2	DNTTIP2
0,000	-2,23	0,21	21,32	Q9Y3D3	28S ribosomal protein S16, mitochondrial	MRPS16
0,013	-2,23	0,21	21,32	Q9Y3A2	Probable U3 small nucleolar RNA-associated protein 11	UTP11L
0,038	-2,24	0,21	21,22	P29375	Lysine-specific demethylase 5A	KDM5A
0,005	-2,24	0,21	21,17	P33897	ATP-binding cassette sub-family D member 1	ABCD1
0,008	-2,24	0,21	21,17	Q99622	Protein C10	C12orf57
0,006	-2,24	0,21	21,14	O95167	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	NDUFA3
0,029	-2,24	0,21	21,11	P80188	Neutrophil gelatinase-associated lipocalin	LCN2
0,021	-2,25	0,21	21,00	Q2M389	WASH complex subunit 7	KIAA1033
0,020	-2,25	0,21	20,96	P16144	Integrin beta-4	ITGB4
0,045	-2,26	0,21	20,90	Q8TCT9	Minor histocompatibility antigen H13	HM13
0,008	-2,26	0,21	20,88	Q9NV70	Exocyst complex component 1	EXOC1
0,011	-2,27	0,21	20,75	O14980	Exportin-1	XPO1
0,008	-2,27	0,21	20,73	Q92797	Symplekin	SYMPK
0,017	-2,28	0,21	20,59	Q8N6M0	OTU domain-containing protein 6B	OTUD6B
0,000	-2,28	0,21	20,59	P36954	DNA-directed RNA polymerase II subunit RPB9	POLR2I
0,023	-2,29	0,20	20,45	P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3	POLR2H
0,022	-2,30	0,20	20,33	Q96Q15	Serine/threonine-protein kinase SMG1	SMG1
0,021	-2,30	0,20	20,32	Q562R1	Beta-actin-like protein 2	ACTBL2
0,020	-2,31	0,20	20,17	O75362	Zinc finger protein 217	ZNF217
0,025	-2,31	0,20	20,17	Q8NI36	WD repeat-containing protein 36	WDR36
0,011	-2,33	0,20	19,89	Q9Y4C2	Protein FAM115A	FAM115A
0,017	-2,33	0,20	19,88	Q9UBD5	Origin recognition complex subunit 3	ORC3
0,005	-2,35	0,20	19,61	Q66PJ3	ADP-ribosylation factor-like protein 6-interacting protein 4	ARL6IP4
0,006	-2,35	0,20	19,58	P22087	rRNA 2-O-methyltransferase fibrillarin	FBL
0,000	-2,36	0,19	19,48	Q92576	PHD finger protein 3	PHF3
0,000	-2,36	0,19	19,48	Q9Y285	Phenylalanine--tRNA ligase alpha subunit	FARSA
0,006	-2,37	0,19	19,36	P22681	E3 ubiquitin-protein ligase CBL	CBL
0,039	-2,38	0,19	19,21	A1X283	SH3 and PX domain-containing protein 2B	SH3PXD2B
0,035	-2,38	0,19	19,17	Q8TB45	DEP domain-containing mTOR-interacting protein	DEPTOR

Supplemental Table S2b

0,049	-2,39	0,19	19,08	Q8N680	Zinc finger and BTB domain-containing protein 2	ZBTB2
0,023	-2,40	0,19	18,95	Q9NVF7	F-box only protein 28	FBXO28
0,028	-2,43	0,19	18,58	Q6RFH5	WD repeat-containing protein 74	WDR74
0,027	-2,43	0,19	18,52	P01876;P01877	Ig alpha-1 chain C region;Ig alpha-2 chain C region	IGHA1;IGHA2
0,013	-2,44	0,18	18,43	Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1
0,003	-2,44	0,18	18,38	Q8WVX9	Fatty acyl-CoA reductase 1	FAR1
0,001	-2,45	0,18	18,27	P30504	HLA class I histocompatibility antigen, Cw-4 alpha chain	HLA-C
0,016	-2,46	0,18	18,23	O95159	Zinc finger protein-like 1	ZFPL1
0,023	-2,46	0,18	18,17	Q92917	G patch domain and KOW motifs-containing protein	GPKOW
0,000	-2,48	0,18	17,97	Q9UHG0	Doublecortin domain-containing protein 2	DCDC2
0,028	-2,48	0,18	17,97	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	ATP2A2
0,028	-2,48	0,18	17,92	Q6DKI1	60S ribosomal protein L7-like 1	RPL7L1
0,001	-2,49	0,18	17,80	Q15047	Histone-lysine N-methyltransferase SETDB1	SETDB1
0,044	-2,51	0,18	17,56	Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein	SLC25A11
0,046	-2,51	0,18	17,56	P04150	Glucocorticoid receptor	NR3C1
0,000	-2,52	0,17	17,43	Q9UIV1	CCR4-NOT transcription complex subunit 7	CNOT7
0,001	-2,52	0,17	17,43	Q15542	Transcription initiation factor TFIID subunit 5	TAF5
0,000	-2,52	0,17	17,41	O14672	Disintegrin and metalloproteinase domain-containing protein 10	ADAM10
0,001	-2,53	0,17	17,31	P35250	Replication factor C subunit 2	RFC2
0,000	-2,56	0,17	16,93	Q9Y580	RNA-binding protein 7	RBM7
0,002	-2,57	0,17	16,90	Q15021	Condensin complex subunit 1	NCAPD2
0,007	-2,57	0,17	16,79	Q9H944	Mediator of RNA polymerase II transcription subunit 20	MED20
0,007	-2,58	0,17	16,77	P10909	Clusterin;Clusterin beta chain;Clusterin alpha chain	CLU
0,005	-2,58	0,17	16,72	Q9UI12	V-type proton ATPase subunit H	ATP6V1H
0,001	-2,59	0,17	16,61	O75153	Clustered mitochondria protein homolog	CLUH
0,010	-2,59	0,17	16,61	Q14644	Ras GTPase-activating protein 3	RASA3
0,002	-2,60	0,16	16,50	Q86YS3	Rab11 family-interacting protein 4	RAB11FIP4
0,002	-2,60	0,16	16,49	Q6KC79	Nipped-B-like protein	NIPBL
0,000	-2,60	0,16	16,45	Q14687	Genetic suppressor element 1	GSE1
0,044	-2,63	0,16	16,15	Q9H204	Mediator of RNA polymerase II transcription subunit 28	MED28
0,027	-2,63	0,16	16,15	Q9UPP1	Histone lysine demethylase PHF8	PHF8
0,014	-2,63	0,16	16,15	Q92616	Translational activator GCN1	GCN1L1
0,003	-2,64	0,16	16,06	Q8TCG1	Protein CIP2A	KIAA1524

Supplemental Table S2b

0,015	-2,64	0,16	16,05	P62273	40S ribosomal protein S29	RPS29
0,041	-2,64	0,16	16,00	O15551	Claudin-3	CLDN3
0,026	-2,65	0,16	15,93	Q9BQ70	Transcription factor 25	TCF25
0,001	-2,66	0,16	15,82	Q9BTY7;P0CB43	Protein HGH1 homolog	HGH1
0,020	-2,66	0,16	15,78	P01034	Cystatin-C	CST3
0,000	-2,70	0,15	15,39	Q9HCM1	Uncharacterized protein KIAA1551	KIAA1551
0,035	-2,72	0,15	15,19	P06865	Beta-hexosaminidase subunit alpha	HEXA
0,048	-2,72	0,15	15,18	Q92794	Histone acetyltransferase KAT6A	KAT6A
0,000	-2,73	0,15	15,07	Q68CP9	AT-rich interactive domain-containing protein 2	ARID2
0,002	-2,73	0,15	15,07	Q9NV06	DDB1- and CUL4-associated factor 13	DCAF13
0,001	-2,73	0,15	15,07	P14373	Zinc finger protein RFP	TRIM27
0,016	-2,74	0,15	14,97	Q9NQW7	Xaa-Pro aminopeptidase 1	XPNPEP1
0,000	-2,75	0,15	14,89	Q53EL6	Programmed cell death protein 4	PDCD4
0,046	-2,77	0,15	14,69	Q8ND76	Cyclin-Y	CCNY
0,015	-2,79	0,14	14,46	Q8IYA6	Cytoskeleton-associated protein 2-like	CKAP2L
0,003	-2,80	0,14	14,32	P0CG12	Chromosome transmission fidelity protein 8 homolog isoform 2	CHTF8
0,002	-2,81	0,14	14,24	Q9Y320	Thioredoxin-related transmembrane protein 2	TMX2
0,024	-2,81	0,14	14,21	Q9P0P0	E3 ubiquitin-protein ligase RNF181	RNF181
0,035	-2,82	0,14	14,16	P0CAP2	DNA-directed RNA polymerase II subunit GRINL1A	POLR2M
0,035	-2,82	0,14	14,16	Q9NYH9	U3 small nucleolar RNA-associated protein 6 homolog	UTP6
0,000	-2,84	0,14	13,97	Q92610	Zinc finger protein 592	ZNF592
0,002	-2,86	0,14	13,77	Q52LW3	Rho GTPase-activating protein 29	ARHGAP29
0,035	-2,87	0,14	13,68	Q69YN4	Protein virilizer homolog	KIAA1429
0,047	-2,88	0,14	13,58	P28340	DNA polymerase delta catalytic subunit	POLD1
0,021	-2,88	0,14	13,58	Q14686	Nuclear receptor coactivator 6	NCOA6
0,042	-2,89	0,14	13,52	Q9Y653	G-protein coupled receptor 56;GPR56 N-terminal fragment;GPR56 C-terminal fragm	GPR56
0,029	-2,89	0,13	13,49	P04114	Apolipoprotein B-100;Apolipoprotein B-48	APOB
0,013	-2,91	0,13	13,30	Q96GN5	Cell division cycle-associated 7-like protein	CDCA7L
0,011	-2,92	0,13	13,21	P50613	Cyclin-dependent kinase 7	CDK7
0,003	-2,92	0,13	13,17	P29083	General transcription factor IIE subunit 1	GTF2E1
0,026	-2,95	0,13	12,94	P40938	Replication factor C subunit 3	RFC3
0,005	-2,96	0,13	12,85	P98160	Basement membrane-specific heparan sulfate proteoglycan core protein;Endorepell	HSPG2
0,021	-2,96	0,13	12,85	Q9H2U1	ATP-dependent RNA helicase DHX36	DHX36

Supplemental Table S2b

0,024	-2,96	0,13	12,85	P09211	Glutathione S-transferase P	GSTP1
0,002	-2,98	0,13	12,67	P49454	Centromere protein F	CENPF
0,013	-3,00	0,13	12,52	Q7Z392	Trafficking protein particle complex subunit 11	TRAPPC11
0,000	-3,00	0,13	12,50	P54886	Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase	ALDH18A1
0,024	-3,01	0,12	12,41	Q13554;Q13555;Q9UQM	Calcium/calmodulin-dependent protein kinase type II subunit beta;Calcium/calmodulin-dependent protein kinase type II subunit gamma	CaMK2B;CAMK2G;CAMK2D
0,001	-3,01	0,12	12,41	Q9BZI7	Regulator of nonsense transcripts 3B	UPF3B
0,012	-3,03	0,12	12,26	Q03426	Mevalonate kinase	MVK
0,000	-3,03	0,12	12,24	Q9BXY0	Protein MAK16 homolog	MAK16
0,009	-3,06	0,12	12,02	Q9C037	Tripartite motif-containing protein 4	TRIM4
0,013	-3,07	0,12	11,91	O14503	Class E basic helix-loop-helix protein 40	BHLHE40
0,005	-3,09	0,12	11,74	Q16513	Serine/threonine-protein kinase N2	PKN2
0,016	-3,12	0,12	11,50	P49902	Cytosolic purine 5-nucleotidase	NT5C2
0,002	-3,12	0,12	11,50	Q9NQW6	Actin-binding protein anillin	ANLN
0,048	-3,12	0,11	11,50	O94819	Kelch repeat and BTB domain-containing protein 11	KBTBD11
0,003	-3,13	0,11	11,42	Q15545	Transcription initiation factor TFIID subunit 7	TAF7
0,006	-3,14	0,11	11,34	Q6VMQ6	Activating transcription factor 7-interacting protein 1	ATF7IP
0,034	-3,15	0,11	11,24	Q9Y4P1	Cysteine protease ATG4B	ATG4B
0,036	-3,16	0,11	11,19	Q4U2R6	39S ribosomal protein L51, mitochondrial	MRPL51
0,016	-3,20	0,11	10,88	Q8N5L8	Ribonuclease P protein subunit p25-like protein	RPP25L
0,002	-3,20	0,11	10,88	Q96BD5	PHD finger protein 21A	PHF21A
0,004	-3,22	0,11	10,70	O75882	Attractin	ATRN
0,024	-3,23	0,11	10,68	Q9H0A8	COMM domain-containing protein 4	COMMD4
0,031	-3,23	0,11	10,66	Q99470	Stromal cell-derived factor 2	SDF2
0,000	-3,28	0,10	10,29	P16333	Cytoplasmic protein NCK1	NCK1
0,030	-3,28	0,10	10,29	Q96QE3	ATPase family AAA domain-containing protein 5	ATAD5
0,031	-3,30	0,10	10,15	Q15054	DNA polymerase delta subunit 3	POLD3
0,010	-3,31	0,10	10,08	Q9HD26	Golgi-associated PDZ and coiled-coil motif-containing protein	GOPC
0,024	-3,41	0,09	9,41	P17535	Transcription factor jun-D	JUND
0,013	-3,46	0,09	9,09	Q9UNQ2	Probable dimethyladenosine transferase	DIMT1
0,001	-3,47	0,09	9,02	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA
0,016	-3,56	0,08	8,48	Q9Y2P8	RNA 3-terminal phosphate cyclase-like protein	RCL1
0,041	-3,62	0,08	8,12	Q15434	RNA-binding motif, single-stranded-interacting protein 2	RBMS2
0,006	-3,65	0,08	7,97	Q49MG5	Microtubule-associated protein 9	MAP9

Supplemental Table S2b

0,000	-3,72	0,08	7,59	Q9NXX6	Non-structural maintenance of chromosomes element 4 homolog A	NSMCE4A
0,002	-3,73	0,08	7,55	Q96AX1	Vacuolar protein sorting-associated protein 33A	VPS33A
0,010	-3,73	0,08	7,54	Q9BXR0	Queuine tRNA-ribosyltransferase	QTRT1
0,020	-3,73	0,08	7,54	Q9Y2Z4	Tyrosine--tRNA ligase, mitochondrial	YARS2
0,001	-3,74	0,07	7,47	O15075	Serine/threonine-protein kinase DCLK1	DCLK1
0,000	-3,85	0,07	6,93	Q9BXS6	Nucleolar and spindle-associated protein 1	NUSAP1
0,015	-4,02	0,06	6,17	Q9Y2Q5	Ragulator complex protein LAMTOR2	LAMTOR2
0,000	-4,03	0,06	6,12	Q9Y2W1	Thyroid hormone receptor-associated protein 3	THRAP3
0,002	-4,07	0,06	5,95	P78549	Endonuclease III-like protein 1	NTHL1
0,023	-4,15	0,06	5,62	Q0VGL1	Ragulator complex protein LAMTOR4;Ragulator complex protein LAMTOR4, N-termi	LAMTOR4
0,000	-4,30	0,05	5,07	O14773	Tripeptidyl-peptidase 1	TPP1
0,018	-4,48	0,04	4,48	O14965	Aurora kinase A	AURKA
0,000	-4,72	0,04	3,79	O95235	Kinesin-like protein KIF20A	KIF20A
0,001	-5,21	0,03	2,70	Q9NRZ9	Lymphoid-specific helicase	HELLS
0,000	-5,55	0,02	2,13	Q5XUX1	F-box/WD repeat-containing protein 9	FBXW9
0,000	-6,23	0,01	1,33	Q9P2K8	Eukaryotic translation initiation factor 2-alpha kinase 4	EIF2AK4
0,000	-6,25	0,01	1,31	P62875	DNA-directed RNA polymerases I, II, and III subunit RPABC5	POLR2L

Color Code

8h Up
24h Up
8h Down
24h Down

Supplemental Table S3

Supplemental Table S3: DAVID-assisted shotgun proteomic analysis of key cell processes in SKOV3 and OVCAR3 cells exposed to 40μM G28UCM using BioCarta and KEGG databases.

		SKOV3/OVCAR3		SKOV3		OVCAR3	
UniProt-ID	Protein Name	Matching Score		Expression		Expression	
		8h	24h	8h	24h	8h	24h
FATTY ACID METABOLISM AND BETA OXIDATION							
P24752	acetyl-CoA acetyltransferase 1(ACAT1)						
Q9BWD1	acetyl-CoA acetyltransferase 2(ACAT2)						
P09110	acetyl-CoA acyltransferase 1(ACAA1)						
Q13085	acetyl-CoA carboxylase alpha(ACACA)		1,00				
P16219	acyl-CoA dehydrogenase, C-2 to C-3 short chain(ACADS)						
P45954	acyl-CoA dehydrogenase, short/branched chain(ACADSB)						
P49748	acyl-CoA dehydrogenase, very long chain(ACADVL)						
P33121	acyl-CoA synthetase long-chain family member 1(ACSL1)		1,00				
O95573	acyl-CoA synthetase long-chain family member 3(ACSL3)		1,00				
P49419	aldehyde dehydrogenase 7 family member A1(ALDH7A1)						
P49189	aldehyde dehydrogenase 9 family member A1(ALDH9A1)						
P50416	carnitine palmitoyltransferase 1A(CPT1A)		1,00				
P42126	enoyl-CoA delta isomerase 1(ECI1)						
P49327	fatty acid synthase(FASN)	1,00	1,00				
P40939	hydroxyacyl-CoA dehydrogenase (trifunctional protein), alpha subunit(HADHA)						
P55084	hydroxyacyl-CoA dehydrogenase (trifunctional protein), beta subunit(HADHB)						
Q16836	hydroxyacyl-CoA dehydrogenase(HADH)						
Q53GQ0	hydroxysteroid 17-beta dehydrogenase 12(HSD17B12), very-long-chain 3-oxoacyl-CoA reductase		1,00				
Q9BY49	peroxisomal trans-2-enoyl-CoA reductase(PECR)						
O00767	stearoyl-CoA desaturase(SCD)	1,00	1,00				
	Mean SKOV3/OVCAR3 Matching Score for fatty acid metabolism and beta oxidation	0,10	0,35				
CENTRAL CARBON METABOLISM							
General carbon metabolism							
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase(HIBCH)						
O95336	6-phosphogluconolactonase(PGLS)						
P24752	acetyl-CoA acetyltransferase 1(ACAT1)						
Q9BWD1	acetyl-CoA acetyltransferase 2(ACAT2)						
Q99798	aconitase 2(ACO2)	1,00	1,00				
P16219	acyl-CoA dehydrogenase, C-2 to C-3 short chain(ACADS)						
Q9NUB1	acyl-CoA synthetase short-chain family member 1(ACSS1)						
Q9NR19	acyl-CoA synthetase short-chain family member 2(ACSS2)						
P04075	aldolase, fructose-bisphosphate A(ALDOA)						
P09972	aldolase, fructose-bisphosphate C(ALDOC)						
P04040	catalase(CAT)						
O75390	citrate synthase(CS)						
P10515	dihydrolipoamide S-acetyltransferase(DLAT)						

Supplemental Table S3

P36957	dihydrolipoamide S-succinyltransferase(DLST)							
P13929	enolase 3(ENO3)							
P10768	esterase D(ESD)							
P07954	fumarate hydratase(FH)							
P11413	glucose-6-phosphate dehydrogenase(G6PD)							
P06744	glucose-6-phosphate isomerase(GPI)							
P17174	glutamic-oxaloacetic transaminase 1(GOT1)							
P00505	glutamic-oxaloacetic transaminase 2(GOT2)							
P52789	hexokinase 2(HK2)	1,00						
Q2TB90	hexokinase domain containing 1(HKDC1)							
O95479	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase(H6PD)							
P40939	hydroxyacyl-CoA dehydrogenase (trifunctional protein), alpha subunit(HADHA)							
P50213	isocitrate dehydrogenase 3 (NAD(+)) alpha(IDH3A)							
O43837	isocitrate dehydrogenase 3 (NAD(+)) beta(IDH3B)							
P51553	isocitrate dehydrogenase 3 (NAD(+)) gamma(IDH3G)							
P40925	malate dehydrogenase 1(MDH1)							
P40926	malate dehydrogenase 2(MDH2)							
P48163	malic enzyme 1(ME1)							
Q02218	oxoglutarate dehydrogenase(OGDH)							
P17858	phosphofructokinase, liver type(PFKL)							
P08237	phosphofructokinase, muscle(PFKM)							
Q01813	phosphofructokinase, platelet(PFKP)							
P52209	phosphogluconate dehydrogenase(PGD)	1,00						
O43175	phosphoglycerate dehydrogenase(PHGDH)							
P18669	phosphoglycerate mutase 1(PGAM1)	1,00						
P60891	phosphoribosyl pyrophosphate synthetase 1(PRPS1)							
Q9Y617	phosphoserine aminotransferase 1(PSAT1)							
P78330	phosphoserine phosphatase(PSPH)							
P05165	propionyl-CoA carboxylase alpha subunit(PCCA)							
P05166	propionyl-CoA carboxylase beta subunit(PCCB)							
P11498	pyruvate carboxylase(PC)							
P11177	pyruvate dehydrogenase (lipoamide) beta(PDHB)							
Q96AT9	ribulose-5-phosphate-3-epimerase(RPE)							
P34896	serine hydroxymethyltransferase 1(SHMT1)							
P34897	serine hydroxymethyltransferase 2(SHMT2)							
P31040	succinate dehydrogenase complex flavoprotein subunit A(SDHA)							
P21912	succinate dehydrogenase complex iron sulfur subunit B(SDHB)							
Q9P2R7	succinate-CoA ligase ADP-forming beta subunit(SUCLA2)							
P53597	succinate-CoA ligase alpha subunit(SUCLG1)							
P37837	transaldolase 1(TALDO1)	1,00						
P29401	transketolase(TKT)							
Q3LXA3	triokinase and FMN cyclase(TKFC)							
P60174	triosephosphate isomerase 1(TPI1)							
	Mean SKOV3/OVCAR3 Matching Score for general carbon metabolism	0,09	0,02					
Glycolysis								

Supplemental Table S3

Q9NR19	acyl-CoA synthetase short-chain family member 2(ACSS2)							
P30838	aldehyde dehydrogenase 3 family member A1(ALDH3A1)							
P49419	aldehyde dehydrogenase 7 family member A1(ALDH7A1)							
P49189	aldehyde dehydrogenase 9 family member A1(ALDH9A1)	1,00						
P14550	aldo-keto reductase family 1 member A1(AKR1A1)							
P04075	aldolase, fructose-bisphosphate A(ALDOA)							
P09972	aldolase, fructose-bisphosphate C(ALDOC)							
P10515	dihydrolipoamide S-acetyltransferase(DLAT)							
P13929	enolase 3(ENO3)							
P06744	glucose-6-phosphate isomerase(GPI)							
P52789	hexokinase 2(HK2)	1,00						
Q2TB90	hexokinase domain containing 1(HKDC1)							
P00338	lactate dehydrogenase A(LDHA)							
P07195	lactate dehydrogenase B(LDHB)							
P17858	phosphofructokinase, liver type(PFKL)							
P08237	phosphofructokinase, muscle(PFKM)							
Q96G03	phosphoglucomutase 2(PGM2)							
P18669	phosphoglycerate mutase 1(PGAM1)	1,00						
P11177	pyruvate dehydrogenase (lipoamide) beta(PDHB)							
P60174	triosephosphate isomerase 1(TPI1)							
	Mean SKOV3/OVCAR3 Matching Score for glycolysis	0,15	0,00					
Pentose phosphate pathway								
O95336	6-phosphogluconolactonase(PGLS)							
P04075	aldolase, fructose-bisphosphate A(ALDOA)							
P09972	aldolase, fructose-bisphosphate C(ALDOC)							
P11413	glucose-6-phosphate dehydrogenase(G6PD)							
P06744	glucose-6-phosphate isomerase(GPI)							
O95479	hexose-6-phosphate dehydrogenase (H6PD)							
P17858	phosphofructokinase, liver type(PFKL)							
P08237	phosphofructokinase, muscle(PFKM)							
Q96G03	phosphoglucomutase 2(PGM2)							
P52209	phosphogluconate dehydrogenase(PGD)	1,00						
P60891	phosphoribosyl pyrophosphate synthetase 1(PRPS1)							
Q96AT9	ribulose-5-phosphate-3-epimerase(RPE)							
P37837	transaldolase 1(TALDO1)	1,00						
P29401	transketolase(TKT)							
	Mean SKOV3/OVCAR3 Matching Score for pentose phosphate pathway	0,14	0,00					
TCA cycle								
Q99798	aconitase 2(ACO2)	1,00	1,00					
P53396	ATP citrate lyase(ACLY)							
O75390	citrate synthase(CS)							
P10515	dihydrolipoamide S-acetyltransferase(DLAT)							
P36957	dihydrolipoamide S-succinyltransferase(DLST)							
P07954	fumarate hydratase(FH)							
P50213	isocitrate dehydrogenase 3 (NAD(+)) alpha(IDH3A)							

Supplemental Table S3

O43837	isocitrate dehydrogenase 3 (NAD(+)) beta(IDH3B)						
P51553	isocitrate dehydrogenase 3 (NAD(+)) gamma(IDH3G)						
P40925	malate dehydrogenase 1(MDH1)						
Q02218	oxoglutarate dehydrogenase(OGDH)						
P11498	pyruvate carboxylase(PC)						
P11177	pyruvate dehydrogenase (lipoamide) beta(PDHB)						
P31040	succinate dehydrogenase complex flavoprotein subunit A(SDHA)						
P21912	succinate dehydrogenase complex iron sulfur subunit B(SDHB)						
Q9P2R7	succinate-CoA ligase ADP-forming beta subunit(SUCLA2)						
P53597	succinate-CoA ligase alpha subunit(SUCLG1)						
	Mean SKOV3/OVCAR3 Matching Score for TCA cycle	0,06	0,06				
	Mean SKOV3/OVCAR3 Matching Score for central carbon metabolism	0,10	0,02				
OXIDATIVE PHOSPHORYLATION AND ELECTRON TRANSPORT							
P25705	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1 (ATP5A1)						
P48047	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit(ATP5O)						
O75947	ATP synthase, H+ transporting, mitochondrial Fo complex subunit D(ATP5H)						
P56385	ATP synthase, H+ transporting, mitochondrial Fo complex subunit E(ATP5I)						
P56134	ATP synthase, H+ transporting, mitochondrial Fo complex subunit F2(ATP5J2)						
P18859	ATP synthase, H+ transporting, mitochondrial Fo complex subunit F6(ATP5J)						
P61421	ATPase H+ transporting V0 subunit d1(ATP6V0D1)						
P38606	ATPase H+ transporting V1 subunit A(ATP6V1A)						
P21281	ATPase H+ transporting V1 subunit B2(ATP6V1B2)	1,00					
P21283	ATPase H+ transporting V1 subunit C1(ATP6V1C1)	1,00					
Q9Y5K8	ATPase H+ transporting V1 subunit D(ATP6V1D)						
P36543	ATPase H+ transporting V1 subunit E1(ATP6V1E1)						
Q16864	ATPase H+ transporting V1 subunit F(ATP6V1F)	1,00					
O75348	ATPase H+ transporting V1 subunit G1(ATP6V1G1)						
Q9UI12	ATPase H+ transporting V1 subunit H(ATP6V1H)						
P13073	cytochrome c oxidase subunit 4I1(COX4I1)						
P20674	cytochrome c oxidase subunit 5A(COX5A)						
P10606	cytochrome c oxidase subunit 5B(COX5B)						
P14854	cytochrome c oxidase subunit 6B1(COX6B1)						
P14406	cytochrome c oxidase subunit 7A2(COX7A2)						
P08574	cytochrome c1(CYC1)						
P43304	glycerol-3-phosphate dehydrogenase 2(GPD2)						
P28331	NADH:ubiquinone oxidoreductase core subunit S1(NDUFS1)		1,00				
O75489	NADH:ubiquinone oxidoreductase core subunit S3(NDUFS3)						
O75251	NADH:ubiquinone oxidoreductase core subunit S7(NDUFS7)						
O00217	NADH:ubiquinone oxidoreductase core subunit S8(NDUFS8)						
P49821	NADH:ubiquinone oxidoreductase core subunit V1(NDUFV1)		1,00				
P19404	NADH:ubiquinone oxidoreductase core subunit V2(NDUFV2)	1,00	1,00				
Q86Y39	NADH:ubiquinone oxidoreductase subunit A11(NDUFA11)						
Q9UI09	NADH:ubiquinone oxidoreductase subunit A12(NDUFA12)						

Supplemental Table S3

Q9P0J0	NADH:ubiquinone oxidoreductase subunit A13(NDUFA13)							
O43678	NADH:ubiquinone oxidoreductase subunit A2(NDUFA2)							
Q16718	NADH:ubiquinone oxidoreductase subunit A5(NDUFA5)							
P56556	NADH:ubiquinone oxidoreductase subunit A6(NDUFA6)							
O95182	NADH:ubiquinone oxidoreductase subunit A7(NDUFA7)							
P51970	NADH:ubiquinone oxidoreductase subunit A8(NDUFA8)		1,00					
O96000	NADH:ubiquinone oxidoreductase subunit B10(NDUFB10)		1,00					
O43676	NADH:ubiquinone oxidoreductase subunit B3(NDUFB3)							
P17568	NADH:ubiquinone oxidoreductase subunit B7(NDUFB7)							
Q9Y6M9	NADH:ubiquinone oxidoreductase subunit B9(NDUFB9)							
O95298	NADH:ubiquinone oxidoreductase subunit C2(NDUFC2)							
O43181	NADH:ubiquinone oxidoreductase subunit S4(NDUFS4)							
O43920	NADH:ubiquinone oxidoreductase subunit S5(NDUFS5)		1,00					
O75380	NADH:ubiquinone oxidoreductase subunit S6(NDUFS6)							
E9PQ53	NDUFC2-KCTD14 readthrough(NDUFC2-KCTD14)							
Q9H008	phospholysine phosphohistidine inorganic pyrophosphate phosphatase(LHPP)							
Q15181	pyrophosphatase (inorganic) 1(PPA1)							
Q9H2U2	pyrophosphatase (inorganic) 2(PPA2)							
P12235	solute carrier family 25 member 4(SLC25A4)		1,00					
P12236	solute carrier family 25 member 6(SLC25A6)		1,00					
P31040	succinate dehydrogenase complex flavoprotein subunit A(SDHA)							
P21912	succinate dehydrogenase complex iron sulfur subunit B(SDHB)							
P14927	ubiquinol-cytochrome c reductase binding protein(UQCRB)							
P31930	ubiquinol-cytochrome c reductase core protein I(UQCRC1)							
P22695	ubiquinol-cytochrome c reductase core protein II(UQCRC2)							
P07919	ubiquinol-cytochrome c reductase hinge protein(UQCRH)							
P47985	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1(UQCRCF1)							
	Mean SKOV3/OVCAR3 Matching Score for oxidative phosphorylation and electron transport	0,07	0,14					
PROTEIN EXPRESSION								
Basal transcription factors								
P18074	ERCC excision repair 2, TFIIH core complex helicase subunit(ERCC2)		1,00					
P19447	ERCC excision repair 3, TFIIH core complex helicase subunit(ERCC3)							
Q00403	general transcription factor IIB(GTF2B)							
P29083	general transcription factor IIE subunit 1(GTF2E1)							
P29084	general transcription factor IIE subunit 2(GTF2E2)							
P35269	general transcription factor IIF subunit 1(GTF2F1)							
P32780	general transcription factor IIH subunit 1(GTF2H1)							
Q13888	general transcription factor IIH subunit 2(GTF2H2)							
Q13889	general transcription factor IIH subunit 3(GTF2H3)							
Q6ZYL4	general transcription factor IIH subunit 5(GTF2H5)							
P78347	general transcription factor Ili(GTF2I)							
P51948	MNAT1, CDK activating kinase assembly factor(MNAT1)							
Q12962	TATA-box binding protein associated factor 10(TAF10)							
Q92804	TATA-box binding protein associated factor 15(TAF15)							

Supplemental Table S3

O00268	TATA-box binding protein associated factor 4(TAF4)							
Q15542	TATA-box binding protein associated factor 5(TAF5)							
P49848	TATA-box binding protein associated factor 6(TAF6)							
Q15545	TATA-box binding protein associated factor 7(TAF7)	1,00						
Q727C8	TATA-box binding protein associated factor 8(TAF8)							
Q9HBM6	TATA-box binding protein associated factor 9b(TAF9B)							
	Mean SKOV3/OVCAR3 Matching Score for basal transcription factors	0,05	0,05					
Aminoacyl-tRNA biosynthesis								
Q5JTZ9	alanyl-tRNA synthetase 2, mitochondrial(AARS2)							
P49588	alanyl-tRNA synthetase(AARS)							
P54136	arginyl-tRNA synthetase(RARS)	1,00						
Q6PI48	aspartyl-tRNA synthetase 2, mitochondrial(DARS2)							
P49589	cysteinyl-tRNA synthetase(CARS)							
O75879	glutamyl-tRNA amidotransferase subunit B(GATB)							
O43716	glutamyl-tRNA amidotransferase subunit C(GATC)							
P41250	glycyl-tRNA synthetase(GARS)							
P49590	histidyl-tRNA synthetase 2, mitochondrial(HARS2)							
P12081	histidyl-tRNA synthetase(HARS)	1,00						
Q9NSE4	isoleucyl-tRNA synthetase 2, mitochondrial(IARS2)							
P41252	isoleucyl-tRNA synthetase(IARS)	1,00						
Q9P2J5	leucyl-tRNA synthetase(LARS)							
Q15046	lysyl-tRNA synthetase(KARS)							
P56192	methionyl-tRNA synthetase(MARS)							
Q9Y285	phenylalanyl-tRNA synthetase alpha subunit(FARSA)							
Q9NSD9	phenylalanyl-tRNA synthetase beta subunit(FARSB)	1,00						
Q9NP81	seryl-tRNA synthetase 2, mitochondrial(SARS2)							
P49591	seryl-tRNA synthetase(SARS)							
P26639	threonyl-tRNA synthetase(TARS)							
P23381	tryptophanyl-tRNA synthetase(WARS)							
Q9Y2Z4	tyrosyl-tRNA synthetase 2(YARS2)	1,00						
P54577	tyrosyl-tRNA synthetase(YARS)							
P26640	valyl-tRNA synthetase(VARS)	1,00						
	Mean SKOV3/OVCAR3 Matching Score for aminoacyl-tRNA biosynthesis	0,00	0,25					
Protein translation								
P13639	eukaryotic translation elongation factor 2(EEF2)							
P41567	eukaryotic translation initiation factor 1(EIF1)							
P47813	eukaryotic translation initiation factor 1A, X-linked(EIF1AX)							
P05198	eukaryotic translation initiation factor 2 subunit alpha(EIF2S1)							
P20042	eukaryotic translation initiation factor 2 subunit beta(EIF2S2)							
P41091	eukaryotic translation initiation factor 2 subunit gamma(EIF2S3)							
Q14152	eukaryotic translation initiation factor 3 subunit A(EIF3A)	1,00						
Q04637	eukaryotic translation initiation factor 4 gamma 1(EIF4G1)	1,00						
P78344	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)							
O43432	eukaryotic translation initiation factor 4 gamma 3(EIF4G3)							
P60842	eukaryotic translation initiation factor 4A1(EIF4A1)	1,00						

Supplemental Table S3

Q14240	eukaryotic translation initiation factor 4A2(EIF4A2)	1,00					
P06730	eukaryotic translation initiation factor 4E(EIF4E)						
P55010	eukaryotic translation initiation factor 5(EIF5)	1,00					
P56537	eukaryotic translation initiation factor 6(EIF6)						
	Mean SKOV3/OVCAR3 Matching Score for protein translation	0,13	0,20				
Ribosome							
Q7Z2Z2	elongation factor like GTPase 1(EFL1)						
P56537	eukaryotic translation initiation factor 6(EIF6)						
O14980	exportin 1(XPO1)		1,00				
P62861	FAU, ubiquitin like and ribosomal protein S30 fusion(FAU)		1,00				
Q9NVN8	G protein nucleolar 3 like(GNL3L)		1,00				
Q9NU22	midasin AAA ATPase 1(MDN1)		1,00				
Q9BYD6	mitochondrial ribosomal protein L1(MRPL1)						
Q9Y3B7	mitochondrial ribosomal protein L11(MRPL11)		1,00				
P52815	mitochondrial ribosomal protein L12(MRPL12)		1,00				
Q9BYD1	mitochondrial ribosomal protein L13(MRPL13)		1,00				
Q9P015	mitochondrial ribosomal protein L15(MRPL15)	1,00					
Q9NRX2	mitochondrial ribosomal protein L17(MRPL17)						
Q9H0U6	mitochondrial ribosomal protein L18(MRPL18)	1,00					
Q5T653	mitochondrial ribosomal protein L2(MRPL2)						
Q7Z2W9	mitochondrial ribosomal protein L21(MRPL21)		1,00				
Q9NWU5	mitochondrial ribosomal protein L22(MRPL22)		1,00				
Q96A35	mitochondrial ribosomal protein L24(MRPL24)						
Q9P0M9	mitochondrial ribosomal protein L27(MRPL27)						
Q13084	mitochondrial ribosomal protein L28(MRPL28)	1,00					
Q9BYD3	mitochondrial ribosomal protein L4(MRPL4)	1,00					
P82912	mitochondrial ribosomal protein S11(MRPS11)						
Q9BYD1	mitochondrial ribosomal protein L13(MRPL13)						
Q6P1L8	mitochondrial ribosomal protein L14(MRPL14)						
P82914	mitochondrial ribosomal protein S15(MRPS15)						
P49406	mitochondrial ribosomal protein L19(MRPL19)						
P09001	mitochondrial ribosomal protein L3(MRPL3)						
Q9BYC8	mitochondrial ribosomal protein L32(MRPL32)						
Q9BYD2	mitochondrial ribosomal protein L9(MRPL9)						
Q9Y2R5	mitochondrial ribosomal protein S17(MRPS17)						
Q9NV52	mitochondrial ribosomal protein S18A(MRPS18A)						
Q9Y399	mitochondrial ribosomal protein S2(MRPS2)						
Q9Y2R9	mitochondrial ribosomal protein S7(MRPS7)						
P82933	mitochondrial ribosomal protein S9(MRPS9)	1,00					
Q9H0A0	N-acetyltransferase 10(NAT10)						
Q9NX24	NHP2 ribonucleoprotein(NHP2)						
Q9ULX3	NIN1/PSMD8 binding protein 1 homolog(NOBI)						
Q96D46	NMD3 ribosome export adaptor(NMD3)		1,00				
Q9UBU9	nuclear RNA export factor 1(NXF1)						
Q95707	POP4 homolog, ribonuclease P/MRP subunit(POP4)						

Supplemental Table S3

P62826	RAN, member RAS oncogene family(RAN)							
P78346	ribonuclease P/MRP subunit p30(RPP30)							
P27635	ribosomal protein L10(RPL10)							
P62906	ribosomal protein L10a(RPL10A)		1,00					
P62913	ribosomal protein L11(RPL11)							
P30050	ribosomal protein L12(RPL12)		1,00					
P26373	ribosomal protein L13(RPL13)		1,00					
P40429	ribosomal protein L13a(RPL13A)	1,00	1,00					
P50914	ribosomal protein L14(RPL14)							
P61313	ribosomal protein L15(RPL15)		1,00					
P18621	ribosomal protein L17(RPL17)							
Q07020	ribosomal protein L18(RPL18)		1,00					
Q02543	ribosomal protein L18a(RPL18A)		1,00					
P84098	ribosomal protein L19(RPL19)							
P46778	ribosomal protein L21(RPL21)		1,00					
P62829	ribosomal protein L23(RPL23)		1,00					
P62750	ribosomal protein L23a(RPL23A)							
P83731	ribosomal protein L24(RPL24)		1,00					
P61254	ribosomal protein L26(RPL26)							
P61353	ribosomal protein L27(RPL27)	1,00						
P46776	ribosomal protein L27a(RPL27A)							
P62888	ribosomal protein L30(RPL30)		1,00					
P62899	ribosomal protein L31(RPL31)							
P42766	ribosomal protein L35(RPL35)							
P18077	ribosomal protein L35a(RPL35A)							
Q9Y3U8	ribosomal protein L36(RPL36)		1,00					
P61513	ribosomal protein L37a(RPL37A)							
P63173	ribosomal protein L38(RPL38)		1,00					
P36578	ribosomal protein L4(RPL4)							
Q02878	ribosomal protein L6(RPL6)							
P18124	ribosomal protein L7(RPL7)	1,00						
P62424	ribosomal protein L7a(RPL7A)							
P32969	ribosomal protein L9(RPL9)		1,00					
P05388	ribosomal protein lateral stalk subunit P0(RPLP0)							
P05386	ribosomal protein lateral stalk subunit P1(RPLP1)							
P05387	ribosomal protein lateral stalk subunit P2(RPLP2)							
P46783	ribosomal protein S10(RPS10)		1,00					
P62280	ribosomal protein S11(RPS11)		1,00					
P25398	ribosomal protein S12(RPS12)		1,00					
P62277	ribosomal protein S13(RPS13)		1,00					
P62263	ribosomal protein S14(RPS14)							
P62244	ribosomal protein S15a(RPS15A)		1,00					
P62249	ribosomal protein S16(RPS16)							
P08708	ribosomal protein S17(RPS17)							
P62269	ribosomal protein S18(RPS18)							

Supplemental Table S3

P39019	ribosomal protein S19(RPS19)		1,00					
P15880	ribosomal protein S2(RPS2)		1,00					
P60866	ribosomal protein S20(RPS20)		1,00					
P63220	ribosomal protein S21(RPS21)		1,00					
P62266	ribosomal protein S23(RPS23)		1,00					
P62847	ribosomal protein S24(RPS24)		1,00					
P62851	ribosomal protein S25(RPS25)							
P42677	ribosomal protein S27(RPS27)							
P62979	ribosomal protein S27a(RPS27A)		1,00					
P62857	ribosomal protein S28(RPS28)		1,00					
P23396	ribosomal protein S3(RPS3)		1,00					
P61247	ribosomal protein S3A(RPS3A)		1,00					
P62701	ribosomal protein S4, X-linked(RPS4X)		1,00					
Q8TD47	ribosomal protein S4, Y-linked 2(RPS4Y2)							
P46782	ribosomal protein S5(RPS5)							
P62753	ribosomal protein S6(RPS6)							
P62241	ribosomal protein S8(RPS8)		1,00					
P46781	ribosomal protein S9(RPS9)		1,00					
P08865	ribosomal protein SA(RPSA)		1,00					
Q9NW13	RNA binding motif protein 28(RBM28)							
Q9Y3B8	RNA exonuclease 2(REXO2)							
Q9Y3A5	SBDS ribosome assembly guanine nucleotide exchange factor(SBDS)							
P55769	SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5)(SNU13)							
Q13428	treacle ribosome biogenesis factor 1(TCOF1)		1,00					
P62987	ubiquitin A-52 residue ribosomal protein fusion product 1(UBA52)							
Q9BVJ6	UTP14A small subunit processome component(UTP14A)							
Q9NYH9	UTP6, small subunit processome component(UTP6)							
	Mean SKOV3/OVCAR3 Matching Score for ribosome	0,07	0,40					
Proteasome								
P62191	proteasome 26S subunit, ATPase 1(PSMC1)							
P35998	proteasome 26S subunit, ATPase 2(PSMC2)							
P17980	proteasome 26S subunit, ATPase 3(PSMC3)							
P62195	proteasome 26S subunit, ATPase 5(PSMC5)							
P62333	proteasome 26S subunit, ATPase 6(PSMC6)							
Q99460	proteasome 26S subunit, non-ATPase 1(PSMD1)							
O00231	proteasome 26S subunit, non-ATPase 11(PSMD11)							
O00232	proteasome 26S subunit, non-ATPase 12(PSMD12)							
Q9UNM6	proteasome 26S subunit, non-ATPase 13(PSMD13)		1,00					
O00487	proteasome 26S subunit, non-ATPase 14(PSMD14)							
Q13200	proteasome 26S subunit, non-ATPase 2(PSMD2)		1,00					
P55036	proteasome 26S subunit, non-ATPase 4(PSMD4)							
Q15008	proteasome 26S subunit, non-ATPase 6(PSMD6)							
P51665	proteasome 26S subunit, non-ATPase 7(PSMD7)							
P48556	proteasome 26S subunit, non-ATPase 8(PSMD8)							
Q06323	proteasome activator subunit 1(PSME1)							

Supplemental Table S3

Q9UL46	proteasome activator subunit 2(PSME2)						
P61289	proteasome activator subunit 3(PSME3)						
Q9Y244	proteasome maturation protein(POMP)						
P25786	proteasome subunit alpha 1(PSMA1)						
P25789	proteasome subunit alpha 4(PSMA4)						
P28066	proteasome subunit alpha 5(PSMA5)						
P60900	proteasome subunit alpha 6(PSMA6)						
O14818	proteasome subunit alpha 7(PSMA7)						
P20618	proteasome subunit beta 1(PSMB1)						
P40306	proteasome subunit beta 10(PSMB10)						
P49720	proteasome subunit beta 3(PSMB3)						
P28072	proteasome subunit beta 6(PSMB6)						
Q99436	proteasome subunit beta 7(PSMB7)						
P28062	proteasome subunit beta 8(PSMB8)						
P28065	proteasome subunit beta 9(PSMB9)						
	Mean SKOV3/OVCAR3 Matching Score for proteasome	0,00	0,06				
	Mean SKOV3/OVCAR3 Matching Score for protein expression	0,05	0,28				
KINASE SIGNALING							
Receptor tyrosine kinase and MAPK signaling							
Q13085	acetyl-CoA carboxylase alpha(ACACA)		1,00				
O00763	acetyl-CoA carboxylase beta(ACACB)						
Q9UQM7	calcium/calmodulin dependent protein kinase II alpha(CAMK2A)						
Q13554	calcium/calmodulin dependent protein kinase II beta(CAMK2B)						
Q13555	calcium/calmodulin dependent protein kinase II gamma(CAMK2G)						
P62158	calmodulin 1(CALM1)		1,00				
Q9N2T1	calmodulin like 5(CALML5)						
P22681	Cbl proto-oncogene(CBL)						
O75131	copine 3(CPNE3)						
P46109	CRK like proto-oncogene, adaptor protein(CRKL)						
P00533	epidermal growth factor receptor(EGFR)						
P04626	erb-b2 receptor tyrosine kinase 2(ERBB2)						
P06730	eukaryotic translation initiation factor 4E(EIF4E)						
Q13541	eukaryotic translation initiation factor 4E binding protein 1(EIF4EBP1)						
Q9UPT5	exocyst complex component 7(EXOC7)		1,00				
P49327	fatty acid synthase(FASN)	1,00	1,00				
P62873	G protein subunit beta 1(GNB1)						
P13807	glycogen synthase 1(GYS1)						
Q5JWF2	GNAS complex locus(GNAS)		1,00				
P62993	growth factor receptor bound protein 2(GRB2)	1,00	1,00				
P52789	hexokinase 2(HK2)	1,00					
Q2TB90	hexokinase domain containing 1(HKDC1)						
O15357	inositol polyphosphate phosphatase like 1(INPPL1)						
P05556	integrin subunit beta 1(ITGB1)		1,00				
P42345	mechanistic target of rapamycin(MTOR)		1,00				

Supplemental Table S3

P28482	mitogen-activated protein kinase 1(MAPK1) = ERK-2	1,00	1,00						
Q16539	mitogen-activated protein kinase 14(MAPK14)								
P27361	mitogen-activated protein kinase 3(MAPK3) = ERK-1								
P45984	mitogen-activated protein kinase 9(MAPK9)								
Q02750	mitogen-activated protein kinase kinase 1(MAP2K1) = MEK-1								
P49023	paxillin(PXN)								
P42338	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta(PIK3CB)								
P27986	phosphoinositide-3-kinase regulatory subunit 1(PIK3R1)								
P19174	phospholipase C gamma 1(PLCG1)								
P06737	phosphorylase, glycogen, liver(PYGL)								
P11216	phosphorylase, glycogen; brain(PYGB)								
Q13131	protein kinase AMP-activated catalytic subunit alpha 1(PRKAA1)								
P10644	protein kinase cAMP-dependent type I regulatory subunit alpha(PRKAR1A)								
P13861	protein kinase cAMP-dependent type II regulatory subunit alpha(PRKAR2A)								
P62136	protein phosphatase 1 catalytic subunit alpha(PPP1CA)								
P62140	protein phosphatase 1 catalytic subunit beta(PPP1CB)								
P36873	protein phosphatase 1 catalytic subunit gamma(PPP1CC)								
P67775	protein phosphatase 2 catalytic subunit alpha(PPP2CA)								
Q05397	protein tyrosine kinase 2(PTK2) = FAK1								
P18031	protein tyrosine phosphatase, non-receptor type 1(PTPN1)								
Q06124	protein tyrosine phosphatase, non-receptor type 11(PTPN11) = SHP-2		1,00						
P62834	RAP1A, member of RAS oncogene family(RAP1A)								
P61224	RAP1B, member of RAS oncogene family(RAP1B)		1,00						
P63244	receptor for activated C kinase 1(RACK1)		1,00						
Q15418	ribosomal protein S6 kinase A1(RPS6KA1)								
P62753	ribosomal protein S6(RPS6)								
Q13501	sequestosome 1(SQSTM1)	1,00							
P29353	SHC adaptor protein 1(SHC1)								
P40763	signal transducer and activator of transcription 3(STAT3)		1,00						
P12931	SRC proto-oncogene, non-receptor tyrosine kinase(SRC)								
O75312	ZPR1 zinc finger(ZPR1)								
	Mean SKOV3/OVCAR3 Matching Score for receptor tyrosine kinase and MAPK signaling	0,09	0,23						
mTOR signaling									
P31749	AKT serine/threonine kinase 1(AKT1)								
Q96B36	AKT1 substrate 1(AKT1S1)								
Q14152	eukaryotic translation initiation factor 3 subunit A(EIF3A)		1,00						
Q04637	eukaryotic translation initiation factor 4 gamma 1(EIF4G1)		1,00						
P78344	eukaryotic translation initiation factor 4 gamma 2(EIF4G2)								
O43432	eukaryotic translation initiation factor 4 gamma 3(EIF4G3)								
P60842	eukaryotic translation initiation factor 4A1(EIF4A1)		1,00						
Q14240	eukaryotic translation initiation factor 4A2(EIF4A2)								
P23588	eukaryotic translation initiation factor 4B(EIF4B)	1,00	1,00						
P06730	eukaryotic translation initiation factor 4E(EIF4E)								
P62942	FK506 binding protein 1A(FKBP1A)								
P42345	mechanistic target of rapamycin(MTOR)		1,00						

Supplemental Table S3

P27986	phosphoinositide-3-kinase regulatory subunit 1(PIK3R1)								
P67775	protein phosphatase 2 catalytic subunit alpha(PPP2CA)								
Q15382	Ras homolog enriched in brain(RHEB)								
P62753	ribosomal protein S6(RPS6)								
P51812	ribosomal protein S6 kinase A3(RPS6KA3)								
	Mean SKOV3/OVCAR3 Matching Score for mTOR signaling	0,06	0,29						
Cell cycle									
P00519	ABL proto-oncogene 1, non-receptor tyrosine kinase(ABL1)								
Q9UM13	anaphase promoting complex subunit 10(ANAPC10)								
Q9UJX6	anaphase promoting complex subunit 2(ANAPC2)								
Q9UJX4	anaphase promoting complex subunit 5(ANAPC5)								
Q9UJX3	anaphase promoting complex subunit 7(ANAPC7)								
Q13535	ATR serine/threonine kinase(ATR)								
O43684	BUB3, mitotic checkpoint protein(BUB3)								
Q9UJX2	cell division cycle 23(CDC23)		1,00						
P30260	cell division cycle 27(CDC27)								
Q92793	CREB binding protein(CREBBP)								
Q13616	cullin 1(CUL1)		1,00						
P14635	cyclin B1(CCNB1)		1,00						
O95067	cyclin B2(CCNB2)								
P51946	cyclin H(CCNH)								
P06493	cyclin dependent kinase 1(CDK1)		1,00						
P11802	cyclin dependent kinase 4(CDK4)								
Q00534	cyclin dependent kinase 6(CDK6)								
P50613	cyclin dependent kinase 7(CDK7)								
Q16254	E2F transcription factor 4(E2F4)								
Q9UM11	fizzy/cell division cycle 20 related 1(FZR1)								
Q13547	histone deacetylase 1(HDAC1)								
Q92769	histone deacetylase 2(HDAC2)								
P49736	minichromosome maintenance complex component 2(MCM2)								
P25205	minichromosome maintenance complex component 3(MCM3)		1,00						
P33991	minichromosome maintenance complex component 4(MCM4)	1,00	1,00						
P33992	minichromosome maintenance complex component 5(MCM5)								
Q14566	minichromosome maintenance complex component 6(MCM6)								
P33993	minichromosome maintenance complex component 7(MCM7)		1,00						
P53350	polo like kinase 1(PLK1)		1,00						
P12004	proliferating cell nuclear antigen(PCNA)		1,00						
P06400	RB transcriptional corepressor 1(RB1)								
P62877	ring-box 1(RBX1)								
P63208	S-phase kinase associated protein 1(SKP1)								
Q14683	structural maintenance of chromosomes 1A(SMC1A)								
Q9UQE7	structural maintenance of chromosomes 3(SMC3)		1,00						
P04637	tumor protein p53(TP53)								
P31946	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein beta(YWHAB)								
Q04917	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta(YWHAH)								

Supplemental Table S3

P61981	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma(YWHAG)							
P27348	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta(YWHAQ)							
P63104	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta(YWHAZ)							
	Mean SKOV3/OVCAR3 Matching Score for cell cycle	0,02	0,24					
	Mean SKOV3/OVCAR3 Matching Score for kinase signaling	0,06	0,25					
MEMBRANE INTEGRITY, MOLECULAR UPTAKE/TRANSPORT								
Intracellular protein transport pathways								
O43707	actinin alpha 4(ACTN4)							
Q9BX55	adaptor related protein complex 1 mu 1 subunit(AP1M1)		1,00					
Q8N6T3	ADP ribosylation factor GTPase activating protein 1(ARFGAP1)							
Q8N6H7	ADP ribosylation factor GTPase activating protein 2(ARFGAP2)							
O43823	A-kinase anchoring protein 8(AKAP8)		1,00					
P48444	archain 1(ARCN1)	1,00	1,00					
Q9UPQ3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 1(AGAP1)							
P49407	arrestin beta 1(ARRB1)							
P49454	centromere protein F(CENPF)		1,00					
Q92526	chaperonin containing TCP1 subunit 6B(CCT6B)							
Q96F27	charged multivesicular body protein 6(CHMP6)							
Q8WUX9	charged multivesicular body protein 7(CHMP7)							
O14579	coatamer protein complex subunit epsilon(COPE)		1,00					
P61923	coatamer protein complex subunit zeta 1(COPZ1)							
Q8WTW3	component of oligomeric golgi complex 1(COG1)							
Q9NUU7	DEAD-box helicase 19A(DDX19A)							
Q9NPA8	ENY2, transcription and export complex 2 subunit(ENY2)							
P42566	epidermal growth factor receptor pathway substrate 15(EPS15)							
Q9H8V3	epithelial cell transforming 2(ECT2)		1,00					
Q9Y2D4	exocyst complex component 6B(EXOC6B)							
Q9UPT5	exocyst complex component 7(EXOC7)		1,00					
Q8IYI6	exocyst complex component 8(EXOC8)		1,00					
Q641Q2	family with sequence similarity 21 member A(FAM21A)							
P60520	GABA type A receptor associated protein like 2(GABARAPL2)							
Q9HD26	golgi associated PDZ and coiled-coil motif containing(GOPC)		1,00					
Q86V58	hook microtubule tethering protein 3(HOOK3)							
Q8TEX9	importin 4(IPO4)	1,00	1,00					
P53990	IST1, ESCRT-III associated factor(IST1)							
Q12768	KIAA0196(KIAA0196)							
Q86UP2	kinectin 1(KTN1)							
Q8NI77	kinesin family member 18A(KIF18A)							
P49257	lectin, mannose binding 1(LMAN1)		1,00					
Q14764	major vault protein(MVP)	1,00						
Q5JRA6	MIA family member 3, ER export factor(MIA3)							
P35579	myosin heavy chain 9(MYH9)		1,00					
Q13496	myotubularin 1(MTM1)							
E9PAV3	nascent polypeptide-associated complex alpha subunit(NACA)							

Supplemental Table S3

Q9NVZ3	NECAP endocytosis associated 2(NECAP2)							
Q96D46	NMD3 ribosome export adaptor(NMD3)		1,00					
P49321	nuclear autoantigenic sperm protein(NASP)							
Q12769	nucleoporin 160(NUP160)		1,00					
Q8TEM1	nucleoporin 210(NUP210)							
Q8NFH3	nucleoporin 43(NUP43)	1,00	1,00					
Q08752	peptidylprolyl isomerase D(PPID)							
O00562	phosphatidylinositol transfer protein membrane associated 1(PITPNM1)							
Q9H814	phosphorylated adaptor for RNA export(PHAX)							
Q8WUM4	programmed cell death 6 interacting protein(PDCD6IP)							
Q6WKZ4	RAB11 family interacting protein 1(RAB11FIP1)							
P62491	RAB11A, member RAS oncogene family(RAB11A)							
Q15907	RAB11B, member RAS oncogene family(RAB11B)							
Q9ULC3	RAB23, member RAS oncogene family(RAB23)							
P51148	RAB5C, member RAS oncogene family(RAB5C)							
Q9NRW1	RAB6B, member RAS oncogene family(RAB6B)							
P51149	RAB7A, member RAS oncogene family(RAB7A)							
Q9H5N1	rabaptin, RAB GTPase binding effector protein 2(RABEP2)							
P62834	RAP1A, member of RAS oncogene family(RAP1A)							
Q9P2E9	ribosome binding protein 1(RRBP1)							
Q96T51	RUN and FYVE domain containing 1(RUFY1)							
Q8WVM8	sec1 family domain containing 1(SCFD1)							
O15027	SEC16 homolog A, endoplasmic reticulum export factor(SEC16A)		1,00					
O94979	SEC31 homolog A, COPII coat complex component(SEC31A)							
Q96EE3	SEH1 like nucleoporin(SEH1L)		1,00					
Q9UMY4	sorting nexin 12(SNX12)							
O60493	sorting nexin 3(SNX3)							
Q99598	translin associated factor X(TSNAX)							
Q9Y5J7	translocase of inner mitochondrial membrane 9(TIMM9)							
Q13445	transmembrane p24 trafficking protein 1(TMED1)							
Q9BVK6	transmembrane p24 trafficking protein 9(TMED9)							
Q9NZ09	ubiquitin associated protein 1(UBAP1)							
O75351	vacuolar protein sorting 4 homolog B(VPS4B)		1,00					
O75436	VPS26, retromer complex component A(VPS26A)							
Q9UBQ0	VPS29, retromer complex component(VPS29)							
Q9H267	VPS33B, late endosome and lysosome associated(VPS33B)							
Q96QK1	VPS35, retromer complex component(VPS35)							
O43264	zw10 kinetochore protein(ZW10)							
	Mean SKOV3/OVCAR3 Matching Score for intracellular protein transport pathways	0,05	0,24					
Solute carrier family proteins								
P12235	ADP/ATP translocase 1 (SLC25A4)		1,00					
P05141	ADP/ATP translocase 2 (SLC25A5)		1,00					
P12236	ADP/ATP translocase 3 (SLC25A6)		1,00					
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 (SLC25A13)		1,00					
Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1 (SLC25A24)							

Supplemental Table S3

Q9BWU0	Kanadaptn (SLC4A1AP)						
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein (SLC25A11)		1,00				
Q9H936	Mitochondrial glutamate carrier 1 (SLC25A22)		1,00				
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 (SLC9A3R1)						
Q15599	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 (SLC9A3R2)						
Q15758	Neutral amino acid transporter B(0) (SLC1A5)						
P55011	Solute carrier family 12 member 2						
P11166	solute carrier family 2 member 1(SLC2A1)						
Q9Y226	Solute carrier family 22 member 13 (SLC22A13)						
P53007	Tricarboxylate transport protein, mitochondrial (SLC25A1)		1,00				
Q9ULF5	Zinc transporter ZIP10 (SLC39A10)						
	Mean SKOV3/OVCAR3 Matching Score for solute carrier family proteins	0,00	0,44				
Transport vesicles/endosomal transport							
Q12904	aminoacyl tRNA synthetase complex interacting multifunctional protein 1(AIMP1)						
P48444	archain 1(ARCN1)	1,00	1,00				
Q6QNY0	biogenesis of lysosomal organelles complex 1 subunit 3(BLOC1S3)						
Q8TDH9	biogenesis of lysosomal organelles complex 1 subunit 5(BLOC1S5)						
Q99653	calcineurin like EF-hand protein 1(CHP1)						
Q9B43	charged multivesicular body protein 4A(CHMP4A)						
Q9H444	charged multivesicular body protein 4B(CHMP4B)						
Q96FZ7	charged multivesicular body protein 6(CHMP6)						
Q8WUX9	charged multivesicular body protein 7(CHMP7)						
P53621	coatomer protein complex subunit alpha(COPA)						
P53618	coatomer protein complex subunit beta 1(COPB1)						
P35606	coatomer protein complex subunit beta 2(COPB2)		1,00				
O14579	coatomer protein complex subunit epsilon(COPE)						
Q9Y678	coatomer protein complex subunit gamma 1(COPG1)						
P61923	coatomer protein complex subunit zeta 1(COPZ1)						
P30040	endoplasmic reticulum protein 29(ERP29)		1,00				
O00461	golgi integral membrane protein 4(GOLIM4)						
O14964	hepatocyte growth factor-regulated tyrosine kinase substrate(HGS)		1,00				
P11717	insulin like growth factor 2 receptor(IGF2R)		1,00				
Q12768	KIAA0196(KIAA0196)						
O60664	perilipin 3(PLIN3)						
P62979	ribosomal protein S27a(RPS27A)		1,00				
Q13501	sequestosome 1(SQSTM1)	1,00					
O75886	signal transducing adaptor molecule 2(STAM2)						
Q92783	signal transducing adaptor molecule(STAM)						
Q8WV41	sorting nexin 33(SNX33)						
Q96L92	sorting nexin family member 27(SNX27)						
P49755	transmembrane p24 trafficking protein 10(TMED10)						
Q9BVK6	transmembrane p24 trafficking protein 9(TMED9)						
O60763	USO1 vesicle transport factor(USO1)						
O75351	vacuolar protein sorting 4 homolog B(VPS4B)		1,00				
Q9UK41	VPS28, ESCRT-I subunit(VPS28)						

Supplemental Table S3

Q7Z3T8	zinc finger FYVE-type containing 16(ZFYVE16)							
	Mean SKOV3/OVCAR3 Matching Score for transport vesicles/endosomal transport	0,06	0,21					
Nuclear pore complex								
P57740	nucleoporin 107(NUP107)		1,00					
P49790	nucleoporin 153(NUP153)							
O75694	nucleoporin 155(NUP155)							
Q12769	nucleoporin 160(NUP160)		1,00					
Q8TEM1	nucleoporin 210(NUP210)							
P35658	nucleoporin 214(NUP214)							
Q8NFH5	nucleoporin 35(NUP35)							
Q8NFH3	nucleoporin 43(NUP43)		1,00					
Q9BVL2	nucleoporin 58(NUP58)		1,00					
Q8N1F7	nucleoporin 93(NUP93)		1,00					
P52948	nucleoporin 98(NUP98)		1,00					
Q96EE3	SEH1 like nucleoporin(SEH1L)		1,00					
P12270	translocated promoter region, nuclear basket protein(TPR)							
	Mean SKOV3/OVCAR3 Matching Score for nuclear pore complex	0,00	0,54					
	Mean SKOV3/OVCAR3 Matching Score for membrane integrity, molecular uptake/transport	0,04	0,28					
STRESS PATHWAYS								
HIF signaling								
P31749	AKT serine/threonine kinase 1(AKT1)							
P27540	aryl hydrocarbon receptor nuclear translocator(ARNT)							
Q92793	CREB binding protein(CREBBP)		1,00					
Q9GZT9	egl-9 family hypoxia inducible factor 1(EGLN1)							
P13929	enolase 3(ENO3)							
P04626	erb-b2 receptor tyrosine kinase 2(ERBB2)							
P06730	eukaryotic translation initiation factor 4E(EIF4E)							
P52789	hexokinase 2(HK2)	1,00						
Q2TB90	hexokinase domain containing 1(HKDC1)							
Q16665	hypoxia inducible factor 1 alpha subunit(HIF1A)							
P42345	mechanistic target of rapamycin(MTOR)		1,00					
P28482	mitogen-activated protein kinase 1(MAPK1) = ERK-2	1,00	1,00					
P27361	mitogen-activated protein kinase 3(MAPK3) = ERK-1							
Q02750	mitogen-activated protein kinase kinase 1(MAP2K1) = MEK-1							
P19838	nuclear factor kappa B subunit 1(NFKB1)							
P42338	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta(PIK3CB)							
P27986	phosphoinositide-3-kinase regulatory subunit 1(PIK3R1)							
P19174	phospholipase C gamma 1(PLCG1)							
P16885	phospholipase C gamma 2(PLCG2)							
P11177	pyruvate dehydrogenase (lipoamide) beta(PDHB)							
Q04206	RELA proto-oncogene, NF-kB subunit(RELA)							
P62753	ribosomal protein S6(RPS6)		1,00					
P62877	ring-box 1(RBX1)							
P40763	signal transducer and activator of transcription 3(STAT3)		1,00					

Supplemental Table S3

Q15369	transcription elongation factor B subunit 1(TCEB1)						
Q15370	transcription elongation factor B subunit 2(TCEB2)						
	Mean SKOV3/OVCAR3 Matching Score for HIF signaling	0,08	0,19				
Processing ER							
O95816	BCL2 associated athanogene 2(BAG2)						
P27824	calnexin(CANX)						
P17655	calpain 2(CAPN2)		1,00				
P27797	calreticulin(CALR)						
Q13616	cullin 1(CUL1)		1,00				
Q07065	cytoskeleton associated protein 4(CKAP4)						
P31689	DnaJ heat shock protein family (Hsp40) member A1(DNAJA1)						
P25685	DnaJ heat shock protein family (Hsp40) member B1(DNAJB1)						
Q9UBS4	DnaJ heat shock protein family (Hsp40) member B11(DNAJB11)						
Q9NXW2	DnaJ heat shock protein family (Hsp40) member B12(DNAJB12)						
Q13217	DnaJ heat shock protein family (Hsp40) member C3(DNAJC3)						
P39656	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit(DDOST)		1,00				
Q96DZ1	endoplasmic reticulum lectin 1(ERLEC1)						
Q96HE7	endoplasmic reticulum oxidoreductase 1 alpha(ERO1A)						
P30040	endoplasmic reticulum protein 29(ERP29)		1,00				
P05198	eukaryotic translation initiation factor 2 subunit alpha(EIF2S1)						
Q14697	glucosidase II alpha subunit(GANAB)						
P07900	heat shock protein 90 alpha family class A member 1(HSP90AA1)						
P08238	heat shock protein 90 alpha family class B member 1(HSP90AB1)	1,00					
P08107	heat shock protein family A (Hsp70) member 1A(HSPA1A)						
P54652	heat shock protein family A (Hsp70) member 2(HSPA2)						
O95757	heat shock protein family A (Hsp70) member 4 like(HSPA4L)						
P11021	heat shock protein family A (Hsp70) member 5(HSPA5)		1,00				
P17066	heat shock protein family A (Hsp70) member 6(HSPA6)						
P11142	heat shock protein family A (Hsp70) member 8(HSPA8)	1,00	1,00				
Q92598	heat shock protein family H (Hsp110) member 1(HSPH1)						
P49257	lectin, mannose binding 1(LMAN1)		1,00				
Q13724	mannosyl-oligosaccharide glucosidase(MOGS)						
P45984	mitogen-activated protein kinase 9(MAPK9)						
Q8TAT6	NPL4 homolog, ubiquitin recognition factor(NPLOC4)		1,00				
Q9UNZ2	NSFL1 cofactor(NSFL1C)						
P07237	prolyl 4-hydroxylase subunit beta(P4HB)						
P30101	protein disulfide isomerase family A member 3(PDIA3)						
P13667	protein disulfide isomerase family A member 4(PDIA4)						
Q15084	protein disulfide isomerase family A member 6(PDIA6)		1,00				
P14314	protein kinase C substrate 80K-H(PRKCSH)						
P54727	RAD23 homolog B, nucleotide excision repair protein(RAD23B)						
P04843	ribophorin I(RPN1)		1,00				
P04844	ribophorin II(RPN2)		1,00				
Q9P2E9	ribosome binding protein 1(RRBP1)						
P62877	ring-box 1(RBX1)						

Supplemental Table S3

P55735	SEC13 homolog, nuclear pore and COPII coat complex component(SEC13)						
Q15436	Sec23 homolog A, coat complex II component(SEC23A)						
O95487	SEC24 homolog B, COPII coat complex component(SEC24B)						
P53992	SEC24 homolog C, COPII coat complex component(SEC24C)	1,00	1,00				
O94979	SEC31 homolog A, COPII coat complex component(SEC31A)						
Q9UGP8	SEC63 homolog, protein translocation regulator(SEC63)	1,00					
P43307	signal sequence receptor subunit 1(SSR1)						
P51571	signal sequence receptor subunit 4(SSR4)		1,00				
P63208	S-phase kinase associated protein 1(SKP1)						
Q8NBS9	thioredoxin domain containing 5(TXNDC5)						
Q9UHD9	ubiquilin 2(UBQLN2)						
Q92890	ubiquitin fusion degradation 1 like (yeast)(UFD1L)						
O95155	ubiquitination factor E4B(UBE4B)						
Q9BZV1	UBX domain protein 6(UBXN6)						
Q9NYU2	UDP-glucose glycoprotein glucosyltransferase 1(UGGT1)						
P55072	valosin containing protein(VCP)						
	Mean SKOV3/OVCAR3 Matching Score for processing ER	0,07	0,23				
	Mean SKOV3/OVCAR3 Matching Score for stress pathways	0,07	0,22				
APOPTOSIS							
O95831	Apoptosis-inducing factor 1, mitochondrial(AIFM1)						
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus(ACIN1)		1,00				
Q9H8G2	Caspase activity and apoptosis inhibitor 1(CAAP1)						
Q8IX12	Cell division cycle and apoptosis regulator protein 1(CCAR1)		1,00				
Q9UER7	Death domain-associated protein 6(DAAX)						
P53355	Death-associated protein kinase 1(DAPK1)		1,00				
Q9BTC0	Death-inducer obliterator 1(DIDO1)						
Q8WUM4	Programmed cell death 6-interacting protein(PDCD6IP)						
Q9BUL8	Programmed cell death protein 10(PDCD10)		1,00				
Q53EL6	Programmed cell death protein 4(PDCD4)						
O14737	Programmed cell death protein 5(PDCD5)		1,00				
	Mean SKOV3/OVCAR3 Matching Score for apoptosis	0,00	0,45				
	Legend						
	Significantly (p < 0.05) downregulated proteins: Blue cell						
	Significantly (p < 0.05) upregulated proteins: Red cell						
	For Individual Proteins						
	SKOV3/OVCAR3 Matching Score:						
	1,00: uniform regulation at the same time in both cell lines.						
	0,00: no uniform regulation in both cell lines at the specific time.						
	For Key Cell Processes or Sub-Processes						
	Mean SKOV3/OVCAR3 Matching Score:						
	Mean of 'Individual Protein SKOV3/OVCAR3 Matching Scores'						

Supplemental Table S4a

Supplemental Table S4a: Summary of all down- (< 50 % of Control) and up-regulated (> 150 % of Control) phosphoproteins as determined by antibody microarray kinomic analysis in SKOV3 cells exposed for 24h to 40μM G28UCM.

Target Name	Full Target Protein Name	P-Site	UniProt #	% of Untreated Control
I. Down-regulated Phosphoproteins (< 50% of Control)				
GFAP	Glial fibrillary acidic protein	S8	P14136	3
Csk	C-terminus of Src tyrosine kinase	Y184	P41240	3
ATF2 (CRE-BP1)	Cyclic AMP-dependent transcription factor ATF-2	S112	P15336	6
CFL1	Cofilin 1	S3	P23528	6
B-Myb (MYBL2)	Myb-related protein B	T487	P10244	7
CK2a1 (CSNK2A1)	Casein protein-serine kinase 2 alpha/ alpha prime	T360+S362	P68400	8
ENFB2	Ephrin-B2	Y316	P52799	8
CDK5	Cyclin-dependent protein-serine kinase 5	S159	Q00535	12
UBF	Nucleolar transcription factor 1	S484	P17480	15
CFL1	Cofilin 1	S3	P23528	16
CrkL	Crk-like protein	Y251	P46109	16
CaMKK1 (CaMKK)	Calcium/calmodulin-dependent protein-serine kinase kinase	S74	Q8N5S9	19
Cbl	E3 ubiquitin-protein ligase CBL	Y700	P22681	25
HDAC4/5/9	Histone deacetylase 4	S246/259/220	P56524	27
Huntingtin	Huntington's disease protein	S419	P42858	28
eEF2K	Eukaryotic elongation factor 2 kinase	S366	O00418	28
CTNNB1	Catenin (cadherin-associated protein) beta 1	Y333	P35222	28
H2AFX	Histone H2A.X	S139	P16104	29
CTNNB1	Catenin (cadherin-associated protein) beta 1	S33+S37	P35222	30
SNCA (a-Synuclein)	Alpha-synuclein	S129	P37840	31
CDK1 (CDC2)	Cyclin-dependent protein-serine kinase 1	T161	P06493	32
DDR1	Epithelial discoidin domain-containing receptor 1	Y796+Y797	Q08345	32
PLCE1	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase epsilon-1	S1096+T1100	Q9P212	33
Jun (c-Jun)	Jun proto-oncogene-encoded AP1 transcription factor	T91+T93	P05412	34
CLK1	Dual specificity protein kinase CLK1	S337	P49759	34
DYRK1A	Dual specificity tyrosine-phosphorylation-regulated kinase 1A	Y321	Q13627	35
MEK1 (MKK1, MAP2K1)	MAPK/ERK protein-serine kinase 1 (MKK1)	S222	Q02750	35
CSF1R (Fms)	Macrophage colony-stimulating factor 1 receptor	Y809	P07333	36
CTNNA1	Catenin alpha-1	S641	P35221	36
Abl (Abl1)	Abelson murine leukemia viral oncogene homologue 1	Y413	P00519	36
EGFR (ErbB1)	Epidermal growth factor receptor-tyrosine kinase	Y1110	P00533	37
MDM2	E3 ubiquitin-protein ligase double minute 2 protein	S166	Q00987	37
Caveolin 1	Caveolin 1	Y14	Q03135	38

Supplemental Table S4a

Gab1	GRB2-associated-binding protein 1	Y627	Q13480	38
ROCK2 (ROKa)	Rho-associated protein kinase 2	Y722	O75116	39
EGFR (ErbB1)	Epidermal growth factor receptor-tyrosine kinase	Y1172	P00533	39
Connexin 43	Gap junction alpha-1 protein	S368	P17302	40
NMDAR2B (GRIN2B)	Glutamate [NMDA] receptor subunit epsilon-2	Y1474	Q13224	40
VIM	Vimentin	S34	P08670	41
ERK1 (MAPK3)	Extracellular regulated protein-serine kinase 1 (p44 MAP kinase)	Y204	P27361	42
DLK (ZPK)	Mitogen-activated protein kinase kinase kinase 12	S269	Q12852	43
CSF1R (Fms)	Macrophage colony-stimulating factor 1 receptor	Y699	P07333	43
COX2	Prostaglandin G/H synthase 2	Y446	P35354	44
HePTP (PTPN7)	Tyrosine-protein phosphatase non-receptor type 7	S44	P35236	47
Cbl	E3 ubiquitin-protein ligase CBL	Y674	P22681	47
CTNNB1	Catenin (cadherin-associated protein) beta 1	S33	P35222	48
ERK1 (MAPK3)	Extracellular regulated protein-serine kinase 1 (p44 MAP kinase)	Y204	P27361	48
SIK (SNF1LK)	Salt-inducible serine/threonine-protein kinase SIK1	T182	P57059	49
CDK5	Cyclin-dependent protein-serine kinase 5	Y15	Q00535	49
HDAC5	Histone deacetylase 5	S498	Q9UQL6	49
Dynamin I	Dynamin-1	S795	Q05193	49
II. Up-regulated Phosphoproteins (> 150% of Control)				
p53 (TP53)	Cellular tumor antigen p53	S392	P04637	152
Fyn	Fyn proto-oncogene-encoded protein-tyrosine kinase	T12	P06241	152
PCYT1A (CTPCT; CCTA)	CTP: phosphocholine cytidyltransferase isoform A	Y359+S362	P49585	152
Src	Src oncogene-encoded protein-tyrosine kinase	Y530	P12931	153
FAK (PTK2)	Focal adhesion protein-tyrosine kinase	Y397	Q05397	153
NFKB1 (NFkB-p105)	Nuclear factor NF-kappa-B p105 subunit	S932	P19838	154
SMC1A	Structural maintenance of chromosomes protein 1A	S957	Q14683	155
SMARCB1	SWI/SNF-rel. matrix-assoc. actin-dep. Regul. of chromatin subf.B memb.1	T134	Q12824	160
SLK	STE20-like serine/threonine-protein kinase; CTCL tumour antigen se20-9	S189	Q9H2G2	160
PKD1 (PRKCM, PKCm, PRKD1)	Protein-serine kinase C mu (Protein kinase D)	S910	Q15139	160
PDGFRb	Platelet-derived growth factor receptor kinase beta	Y716	P09619	162
Syk	Spleen protein-tyrosine kinase	Y352	P43405	162
PKCt (PRKCQ)	Protein-serine kinase C theta	T538	Q04759	164
PKCg (PRKCG)	Protein-serine kinase C gamma	T655	P05129	165
Src	Src oncogene-encoded protein-tyrosine kinase	Y419	P12931	168
PTEN	Protein phosphatase and tensin homolog deleted on chromosome 10	S380+T382+T383	P60484	168
PKCz (PRKCZ)	Protein-serine kinase C zeta	T410	Q05513	170
TrkB (NTRK2)	BNDF/NT3/4/5 receptor- tyrosine kinase	Y702	Q16620	171
Src	Src oncogene-encoded protein-tyrosine kinase	Y419	P12931	172
Cip (WAF1; p21) p21(WAF1/CIP1)	Cyclin-dependent kinase inhibitor 1	T145	P38936	172
Syk	Spleen protein-tyrosine kinase	Y525+Y526	P43405	173
TRIM28 (TIF1B)	Transcription intermediary factor 1-beta	Y517	Q13263	174

Supplemental Table S4a

PKD1 (PRKCM, PKCm, PRKD1)	Protein-serine kinase C mu (Protein kinase D)	S738+S742	Q15139	176
p53 (TP53)	Cellular tumor antigen p53	S6	P04637	180
ILK1 (ILK)	Integrin-linked protein-serine kinase-1	Y351	Q13418	180
THRAP3	Thyroid hormone receptor-associated protein 3	S253	Q9Y2W1	181
SRF	Serum response factor	S224	P11831	183
PKCd (PRKCD)	Protein-serine kinase C delta	S645	Q05655	185
Lck	Lymphocyte-specific protein-tyrosine kinase	Y394	P06239	195
p53 (TP53)	Cellular tumor antigen p53	T155	P04637	200
p70S6K (S6Ka, RPS6KB1)	Ribosomal protein S6 kinase beta-1; Ribosomal protein S6 kinase 1	S434	P23443	206
hnRNP-K	Heterogeneous nuclear ribonucleoprotein K	S302	P61978	208
p53 (TP53)	Cellular tumor antigen p53	T55	P04637	212
PKCa (PRKCA)	Protein-serine kinase C alpha	Y195	P17252	214
Tau	Microtubule-associated protein tau	S713	P10636	222
Caveolin 2	Caveolin 2	S36	P51636	239
PKCd (PRKCD)	Protein-serine kinase C delta	Y334	Q05655	242
MEK1 (MKK1, MAP2K1)	MAPK/ERK protein-serine kinase 1 (MKK1)	S222	Q02750	243
ASK1 (MAP3K5)	Apoptosis signal regulating protein-serine kinase 1	S966	Q99683	243
Adducin a/g (ADD3)	Adducin-alpha/gamma	S726	Q9UEY8	278
Cip (WAF1; p21) p21(WAF1/CIP1)	Cyclin-dependent kinase inhibitor 1	S146	P38936	279
ErbB4 (HER4)	ErbB4 receptor-tyrosine kinase	Y875	Q15303	286
IkbBa	Inhibitor of NF-kappa-B alpha (MAD3)	S32	P25963	293
eIF4E	Eukaryotic translation initiation factor 4 (mRNA cap binding protein)	S209	P06730	310
p53 (TP53)	Cellular tumor antigen p53	S46	P04637	322
PRKAR2A (PKA2RA)	cAMP-dependent protein kinase type II-alpha regulatory subunit	S99	P13861	353
p40-phox	Neutrophil cytosol factor 4	T154	Q15080	418
Smad2	Mothers against decapentaplegic homologue 2	T220	Q15796	529
PKCd (PRKCD)	Protein-serine kinase C delta	S664	Q05655	610
Tau	Microtubule-associated protein tau	T522	P10636	690
RSK1 (RPS6KA1, p90RSK)	Ribosomal S6 protein-serine kinase 1	T348	Q15418	1252

Supplemental Table S4b

Supplemental Table S4b: Summary of all down- (< 50 % of Control) and up-regulated (> 150 % of Control) phosphoproteins as determined by antibody microarray kinomic analysis in OVCAR3 cells exposed for 24h to 40μM G28UCM.

Target Name	Full Target Protein Name	P-Site	UniProt #	% of Untreated Control
I. Down-regulated Phosphoproteins (< 50% of Control)				
eIF4B	Eukaryotic translation initiation factor 4B	S422	P23588	3
JUN	Jun proto-oncogene-encoded AP1 transcription factor (c-Jun)	Y170	P05412	8
Smad1	Mothers against decapentaplegic homologs 1	S465	Q15797	9
MYC	Myc proto-oncogene protein	T58	P01106	10
Tau	Microtubule-associated protein tau	S713	P10636	12
p53	Tumor suppressor protein p53 (antigenNY-CO-13) (TP53)	S392	P04637	15
MEK2	MAPK/ERK protein-serine kinase 2 (MKK2, MAP2K2)	T394	P36507	15
NFkappaB p65	NF-kappa-B p65 nuclear transcription factor (Rel A)	S276	Q04206	16
TRKB	BNDF/NT3/4/5 receptor- tyrosine kinase (NTRK2)	Y706	Q16620	16
CHK2	Checkpoint protein-serine kinase 2 (CHEK2)	T68	O96017	17
LCK	Lymphocyte-specific protein-tyrosine kinase	Y505	P06239	20
FES	Fes/Fps protein-tyrosine kinase	Y713	P07332	22
IRS1	Insulin receptor substrate 1	Y612	P35568	27
JNK1	Jun N-terminus protein-serine kinase (stress-activated protein kinase (SAPK)) 1 (SAPKg, MAPKJ)	Y185	P45983	29
PKCd	Protein-serine kinase C delta (PRKCD)	S645	Q05655	29
p53	Tumor suppressor protein p53 (antigenNY-CO-13) (TP53)	S37	P04637	30
p53	Tumor suppressor protein p53 (antigenNY-CO-13) (TP53)	S6	P04637	30
IGF1R	Insulin-like growth factor 1 receptor protein-tyrosine kinase	Y1280	P08069	32
A6	Twinfilin-1	Y309	Q12792	32
CLK1	Dual specificity protein kinase CLK1	S337	P49759	32
PAK1	p21-activated kinase 1 (alpha) (serine/threonine-protein kinase PAK 1) (PAKa)	S144/S141/S154	Q13153	33
Gab1	GRB2-associated binder 1	Y627	Q13480	34
JUN	Jun proto-oncogene-encoded AP1 transcription factor (c-Jun)	S243	P05412	37
JAK2	Janus protein-tyrosine kinase 2	Y1007+Y1008	O60674	38
p38d MAPK	Mitogen-activated protein-serine kinase p38 delta (MAPK13)	T180+Y182	O15264	38
MEK1	MAPK/ERK protein-serine kinase 1 (MKK1, MAP2K1)	T386	Q02750	38
ERK1 (MAPK3)	Extracellular regulated protein-serine kinase 1 (p44 MAP kinase)	T202	P27361	41
TRKB	BNDF/NT3/4/5 receptor- tyrosine kinase (NTRK2)	Y516	Q16620	42
Tau	Microtubule-associated protein tau	S516	P10636	42
EGFR	Epidermal growth factor receptor-tyrosine kinase (ErbB1)	Y1197	P00533	43

Supplemental Table S4b

SMC1	Structural maintenance of chromosomes protein 1A	S957	Q14683	44
JNK 1/2/3	Jun N-terminus protein-serine kinase (stress-activated protein kinase (SAPK)) 1 (SAPKg, MA	T183+Y185	P45983	44
FYN	Fyn proto-oncogene-encoded protein-tyrosine kinase	Y213+Y214	P06241	44
PDGFRa	Platelet-derived growth factor receptor kinase alpha	Y754	P16234	45
p70 S6K	Ribosomal protein S6 kinase beta-1 (RPS6KB1, p70S6Ka)	S447	P23443	45
PAK2	p21-activated kinase 2 (gamma) (serine/threonine-protein kinase PAK 2) (PAKg)	S141	Q13177	45
ZAP70	Zeta-chain (TCR) associated protein-tyrosine kinase, 70 kDa	Y292	P43403	46
Caveolin 1	Caveolin 1 (CAV1)	Y14	Q03135	47
WASP	Wiskott-Aldrich syndrome protein	Y291	P42768	48
CaMK1d	Calcium/calmodulin-dependent protein-serine kinase 1 delta	T180	Q8IU85	48
ENO1	Alpha-enolase	Y44	P06733	48
AKT1 (PKBa)	RAC-alpha serine/threonine-protein kinase	Y315	P31749	48
ALK	Anaplastic lymphoma kinase	Y1507	Q9UM73	48
InsR (IR)	Insulin receptor beta chain	Y1189	P06213	49
4E-BP1	Eukaryotic translation initiation factor 4E binding protein 1 (PHAS1)		Q13541	49
STAT1	Signal transducer and activator of transcription 1 beta	S727	P42224	49
CSF1R	Macrophage colony-stimulating factor 1 receptor (Fms)	Y809	P07333	49
MSK1	Mitogen & stress-activated protein-serine kinase 1 (RPS6KA5)	S376	O75582	49
II. Up-regulated Phosphoproteins (> 150% of Control)				
BCR	Breakpoint cluster region protein	Y591	P11274	151
p70 S6K	Ribosomal protein S6 kinase beta-1 (RPS6KB1 p70S6Ka)	T412	P23443	153
Fused	Serine/threonine-protein kinase 36 (STK36)	S159	Q9NRP7	156
SYK	Spleen protein-tyrosine kinase	Y525+Y526	P43405	157
PLK4	Polo-like protein kinase 3 (cytokine- inducible kinase (CNK) (SAK, STK18)	T170	O00444	158
B-Raf (RafB)	RafB proto-oncogene-encoded protein-serine kinase	S729	P15056	158
RSK1	Ribosomal S6 protein-serine kinase 1 (RPS6KA1, p90RSK)	Y220+S221	Q15418	159
RSK1/2	Ribosomal S6 protein-serine kinase 1/2 (RPS6KA1/A3, p90RSK)	S363/S369	Q15418	160
ERK4 (MAPK4)	Extracellular regulated protein-serine kinase 4	S186	P31152	160
GSK3a	Glycogen synthase-serine kinase 3 alpha	T19+S21	P49840	161
FER (TYK3)	Fer (fps/fes related) tyrosine kinase	Y402	P16591	163
RSK1	Ribosomal S6 protein-serine kinase 1 (RPS6KA1, p90RSK)	S380	Q15418	163
FAK (PTK2)	Focal adhesion protein-tyrosine kinase	Y576+Y577	Q05397	164
Rb	Retinoblastoma-associated protein 1	T821	P06400	164
FLT3	Receptor-type tyrosine-protein kinase FLT3 (STK1)	Y842	P36888	164
VEGFR2 (KDR)	Vascular endothelial growth factor receptor-tyrosine kinase 2 (Flk1)	Y1059	P35968	166
RSK1	Ribosomal S6 protein-serine kinase 1 (RPS6KA1, p90RSK)	S221	Q15418	167
Tau	Microtubule-associated protein tau	T522	P10636	168
PRKX	Serine/threonine-protein kinase PRKX	T201+T203	P51817	168

Supplemental Table S4b

eIF2a	Eukaryotic translation initiation factor 2 alpha	S52	P05198	169
RPS6	40S ribosomal protein S6	S235	P62753	170
RIPK2	Receptor-interacting serine/threonine-protein kinase 2 (RIPK2, RIP2, RICK)	S176	O43353	170
PLCg1	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1	Y783	P19174	170
STAT5A	Signal transducer and activator of transcription 5A	Y694	P42229	171
SIT	Signaling threshold-regulating transmembrane adapter 1	Y90	Q9Y3P8	174
Adducin a/g	Adducin alpha, gamma (ADD 1/3)	S726	Q9UEY8	174
MKK4	MAPK/ERK protein-serine kinase 4 (MEK4, MAP2K4)	S257	P45985	177
Sgk223	Tyrosine-protein kinase SgK223	Y413	Q86YV5	178
EGFR	Epidermal growth factor receptor-tyrosine kinase (ErbB1)	Y1172	P00533	178
Ezrin	Cytovillin 2	T567	P15311	179
CHK2	Checkpoint protein-serine kinase 2 (CHEK2)	T383	O96017	179
PLCg2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2 (PLC R)	Y753	P16885	184
FKHR	Forkhead box protein O1 (FOXO1A)	S319	Q12778	192
APP	Amyloid beta A4 protein	T743	P05067	196
MOK	MOK protein kinase (RAGE)	Y167	Q9UQ07	196
MYPT1	Myosin phosphatase target 1 (PPP1R12A)	T696	O14974	197
PBK	Lymphokine-activated killer T-cell-originated protein kinase	Y74	Q96KB5	198
PRKACB	cAMP-dependent protein-serine kinase catalytic subunit beta	S339	P22694	202
MOK	MOK protein kinase (RAGE)	T159+Y161	Q9UQ07	202
MSK1	Mitogen & stress-activated protein-serine kinase 1 (RPS6KA5)	S212	O75582	202
PLCg2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2 (PLC R)	Y759	P16885	205
Catenin b	Catenin (cadherin-associated protein) beta 1 (CTNNB1)	Y333	P35222	215
NEK2	NIMA (never-in-mitosis)-related protein-serine kinase 2	S171	P51955	218
NUAK1	NUAK family SNF1-like kinase 1 (ARK5)/Nuak2	T211	O60285	230
p38a MAPK	Mitogen-activated protein-serine kinase p38 alpha (MAPK14)	T180+Y182	Q16539	237
GSK3a	Glycogen synthase-serine kinase 3 alpha	S278+Y279	P49840	248
p70 S6K	Ribosomal protein S6 kinase beta-1 (RPS6KB1, p70S6Ka)	T252	P23443	254
SIK2 (QIK)	Salt-inducible kinase 2	S358	Q9H0K1	257
SYK	Spleen protein-tyrosine kinase	Y323	P43405	261
NBS1	Nijmegen breakage syndrome protein 1 (NBN, Nibrin)	S343	O60934	285
KHS1	Kinase homologous to SPS1/STE20 (MAP kinase kinase kinase protein-serine kinase 5 (MEK	Y31	Q9Y4K4	333
JAK1	Janus protein-tyrosine kinase 1	Y1034	P23458	385
Rb	Retinoblastoma-associated protein 1	S795	P06400	393
SgK269	Tyrosine-protein kinase SgK269 (PEAK1)	Y635	Q9H792	393
RSK1	Ribosomal S6 protein-serine kinase 1 (RPS6KA1, p90RSK)	S363	Q15418	422
STAT1	Signal transducer and activator of transcription 1 beta	Y701	P42224	490
ErbB3 (HER3)	Tyrosine kinase-type cell surface receptor HER3	Y1328	P21860	538

Supplemental Table S4b

KIT	Mast/stem cell growth factor receptor Kit	Y721	P10721	607
MET	Hepatocyte growth factor (HGF) receptor-tyrosine kinase	Y1230+Y1234+Y1235	P08581	675
Vimentin	VIM (Vimentin)	S34	P08670	998
ATF2	Activating transcription factor 2 (CRE-BP1)	S112	P15336	1279
EGFR	Epidermal growth factor receptor-tyrosine kinase (ErbB1)	Y1110	P00533	1472
CK2a1	Casein protein-serine kinase 2 alpha/ alpha prime (CSNK2A1)	T360+S362	P68400	2690