

## CONTENT OF SUPPLEMENTARY MATERIAL

\*Material is present in the separate excel file.

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<b>Supplementary Table S7.</b> Results from iTRAQ quantitative protein identification from tree cell lines: HK293, U937 and PBMC. Table is an original result generated in Proteome Discoverer analysis. Channels of iTRAQ label: 114 – HEK293, 115 – U937, 116 and 117 – PBMCs. A and B – cells were lysed in denaturing buffer; C and D – cells were lysed in ‘native’ buffer. Excel file.	*
<b>Supplementary Table S8.</b> Lists of proteins with significantly higher level in each cell line. Sheet “summary” contains calculation of fold differences in the level of all proteins identified in the iTRAQ experiment in tree cell lines. Other sheets in the filecontain lists of protein with significantly higher protein content in each pair of cell lines. A and B – 30 000 cells were	*

lysed in denaturing buffer and analysed with 2D-LC-MSMS; C and D – cells were lysed in ‘native’ buffer; SD – standard deviation, n – number of replicas. Fold difference in protein level is calculated as  $\log_2[\text{iTRAQ ratio}]$ . The protein level was assigned as significantly higher, when absolute value of fold difference in protein level, taking in account standard deviation, was more than 1:  $(\text{ABS}(\log_2[\text{iTRAQ ratio}]) - \text{SD}) > 1$ . Excel file.

**Supplementary Table S9.** List of proteins with significantly higher level in each cell line in comparison with the other in a pairwise comparison.

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**Supplementary Table S10.** Comparison of functional annotation results for quantitative analysis of the three different cell lines: HEK293, U937 and PBMCs. Enrichment of KEGG\_PATHWAY categories.

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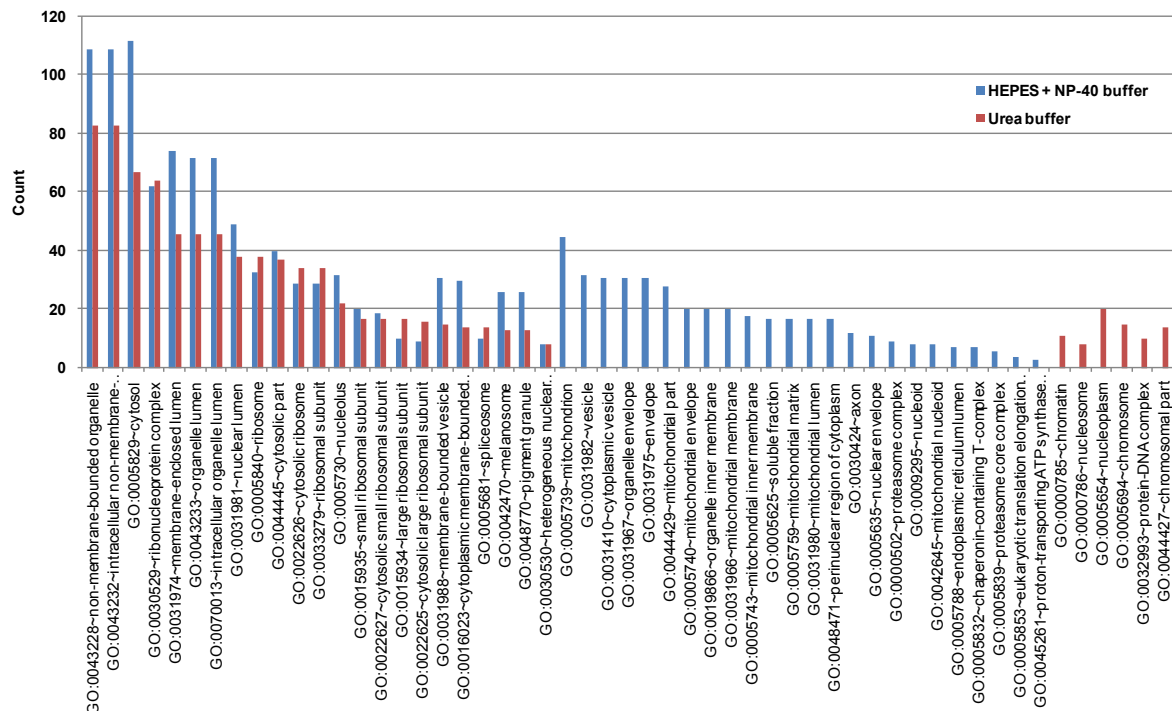
**Supplementary Table S11.** Comparison of functional annotation results for quantitative analysis of 3 different cell lines: HEK293, U937 and PBMCs. Enrichment of GENETIC\_ASSOCIATION\_DB\_DISEASE categories.

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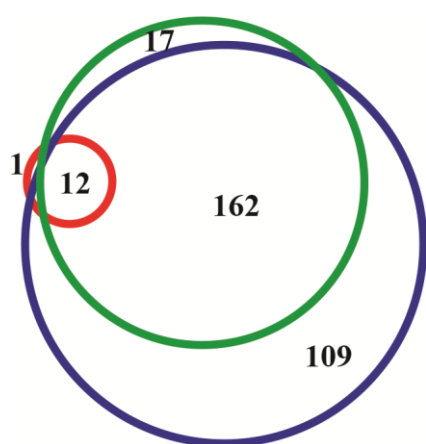
A

Lysis condition	Number of protein IDs
(i) HEPES + NP-40	280
(ii) HEPES without NP-40 + sonication	42
(iii) urea	148
(iv) urea + sonication	100
(v) urea + thiourea + sonication	81

B

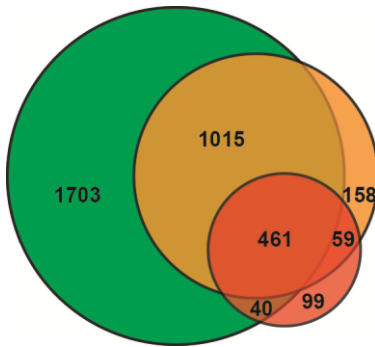


**Supplementary Figure S1.** Evaluation of buffers and lysis conditions for analysis of proteomes from small amount of cell material. (A) Number of proteins identified under different lyses conditions from 1,000 of HEK293cells. In each case an aliquot corresponding to 1,000 cells was taken from a lysate of  $8.7 \times 10^6$  cells. Buffers (i) (50 mM HEPES, 150 mM NaCl, 5 mM EDTA, 0.5% NP-40, pH 8.0) and (iii) (9 M urea, 20 mM HEPES, pH 8.0) were chosen for further evaluation. The details of the lysis conditions are described in section 2.4 of Materials and Methods. (B) Comparison of two buffers, ‘native’ (i) and denaturing (iii), for the efficiency of protein extraction from different cell compartments. GOTERM\_CC\_FAT categories enriched in the Gene Ontology analysis with DAVID Bioinformatics Resources 6.7 are compared; thresholds: Count = 2, EASE = 0.01.



Amount of lysed cells	Number of unique protein identifications
<b>1,000</b>	13
<b>5,000</b>	191
<b>10,000</b>	283
<b>Total number of unique protein identifications</b>	301

**Supplementary Figure S2.** Number of unique protein identifications from different amount of HEK293 cells lysed with urea denaturing buffer. Details of buffer composition are as described in the section 2.7 of Material and Methods: Denaturing lysis and solution tryptic digestion.



**Supplementary Figure S3.** Comparison of three cell types: HEK293 (green); U937 (orange); and human primary PBMCs (red). Number of unique proteins identified in the cell lines. For each cell line, the total number of unique proteins identified is the combination of the data that was generated from both the 5,000 and 10,000 cells lysed with ‘native’ and denaturing buffers and analyzed with 1D- and 2D-LC-MS/MS.

A



B

UniProt AC	UniProt ID	Gene_symbol	Description	Cell type <sup>1</sup>
O00602	<b>FCN1_HUMAN</b>	FCN1	Ficolin-1	<b>Monocytes</b>
Q14005	<b>IL16_HUMAN</b>	IL16	Pro-interleukin-16	<b>T cells</b>
Q14766	<b>LTBP1_HUMAN</b>	LTBP1	Latent-transforming growth factor beta-binding protein 1	<b>T cells</b>
P08514	<b>ITA2B_HUMAN</b>	ITGA2B	Integrin alpha-IIb	<b>platelets</b>
P07359	<b>GP1BA_HUMAN</b>	GP1BA	Platelet glycoprotein Ib alpha chain	<b>platelets</b>
P40197	<b>GPV_HUMAN</b>	GP5	Platelet glycoprotein V	<b>platelets</b>
P12931	<b>SRC_HUMAN</b>	SRC	Proto-oncogene tyrosine-protein kinase Src	<b>platelets</b>
P59665	<b>DEF1_HUMAN</b>	DEFA1B	Neutrophil defensin 1	<b>neutrophils</b>
P69905	<b>HBA_HUMAN</b>	HBA1	Hemoglobin subunit alpha	<b>neutrophils</b>
P68871	<b>HBB_HUMAN</b>	HBB	Hemoglobin subunit beta	<b>neutrophils</b>

**Supplementary Figure S4.** Proteins in PBMCs, those are specific for certain blood cell types. (A) Comparison of total PBMCs proteome identified in our study (List 1) with list of specific blood cell proteins from Haudek et al., 2009 (List 2). (B) Table of proteins in PBMCs from our study that are specific for the cell types. <sup>1</sup>Specificity of protein to the cell type is defined according Haudek et al., 2009.

**Supplementary Table S5.** Comparison of functional annotation results for the three different cell lines: HEK293, U937 and PBMCs. Enrichment of KEGG\_PATHWAY categories performed in DAVID Bioinformatics Resources 6.7; thresholds: Count=2, EASE=0.01. Pathways unique for the cell line are highlighted; color codes as on Figure 5.

KEGG pathway map			Term	Count		
				HEK293	U937	PBMCs
1. Metabolism	1.0 Global and overview maps	1.0	hsa00071:Fatty acid metabolism	22	13	9
	1.1 Carbohydrate metabolism	1.1	hsa00010:Glycolysis / Gluconeogenesis	32	25	20
		1.1	hsa00020:Citrate cycle (TCA cycle)	26	21	
		1.1	hsa00030:Pentose phosphate pathway	15	13	10
		1.1	hsa00052:Galactose metabolism	15	12	
		1.1	hsa00520:Amino sugar and nucleotide sugar metabolism	24		
		1.1	hsa00620:Pyruvate metabolism	25	15	11
		1.1	hsa00630:Glyoxylate and dicarboxylate metabolism	10		
		1.1	hsa00640:Propanoate metabolism	18	12	
	1.2 Energy metabolism	1.2	hsa00190:Oxidative phosphorylation	84	37	17
	1.3 Lipid metaboism	1.3	hsa00062:Fatty acid elongation in mitochondria	7		
	1.4 Nucleotide metabolism	1.4	hsa00230:Purine metabolism	54		
		1.4	hsa00240:Pyrimidine metabolism	42		
	1.5 Amino acid metabolism	1.5	hsa00280:Valine, leucine and isoleucine degradation	30	16	
		1.5	hsa00290:Valine, leucine and isoleucine biosynthesis	9		
		1.5	hsa00310:Lysine degradation	19		
		1.5	hsa00330:Arginine and proline metabolism	23		
	1.6 Metabolism of other amino acids	1.6	hsa00480:Glutathione metabolism	21	17	11
	1.8 Metabolism of cofactors and vitamins	1.8	hsa00670:One carbon pool by folate		8	
2. Genetic information processing	2.1 Transcription	2.1	hsa03040:Spliceosome	89	61	
	2.2 Translation	2.2	hsa00970:Aminoacyl-tRNA biosynthesis	32	20	
		2.2	hsa03010:Ribosome	79	76	30
	2.3 Folding, sorting and degradation	2.3	hsa03018:RNA degradation	31		
		2.3	hsa03050:Proteasome	34	35	11
		2.3	hsa03060:Protein export	8	6	
		2.3	hsa04130:SNARE interactions in vesicular transport	17		
	2.4 Replication and repair	2.4	hsa03030:DNA replication	29	16	
		2.4	hsa03420:Nucleotide excision repair	22		
		2.4	hsa03430:Mismatch repair	16		
4. Cellular processes	4.1 Transport and catabolism	4.1	hsa04142:Lysosome		32	
	4.2 Cell motility	4.2	hsa04810:Regulation of actin cytoskeleton			34
	4.3 Cell growth and death	4.3	hsa04110:Cell cycle	43		
		4.3	hsa04114:Oocyte meiosis	41		
	4.4 Cell communication	4.4	hsa04510:Focal adhesion			26
		4.4	hsa04520:Adherens junction			12
		4.4	hsa04530:Tight junction	47		
5. Organismal systems	5.1 Immune system	5.1	hsa04612:Antigen processing and presentation			17
		5.1	hsa04666:Fc gamma R-mediated phagocytosis		26	
		5.1	hsa04670:Leukocyte transendothelial migration			19
6. Human diseases	6.4 Neurodegenerative diseases	6.4	hsa05010:Alzheimer's disease	82	41	20
		6.4	hsa05012:Parkinson's disease	81	39	21
		6.4	hsa05016:Huntington's disease	99	47	23
	6.6 Cardiovascular diseases	6.6	hsa05416:Viral myocarditis			12
	6.8 Infectious diseases: Bacterial	6.8	hsa05130:Pathogenic Escherichia coli infection	27	21	21

**Supplementary Table 6.** Comparison of functional annotation results for 3 different cell lines: HEK293, U937 and PBMCs. Enrichment of GENETIC\_ASSOCIATION\_DB\_DISEASE categories performed in DAVID Bioinformatics Resources 6.7; thresholds: Count=2, EASE=0.05. Categories unique for the cell line are highlighted; color codes as on Figure 5.

Term	Counts		
	HEK293	U937	PBMCs
ALS/amyotrophic lateral sclerosis	9		
Alzheimer's Disease			21
Anemia			4
aplastic anemia, acquired	6		
Asthma			22
atherosclerosis, coronary			15
atherosclerosis, coronary myocardial infarct			4
atherosclerosis, coronary; tuberculosis	4	4	3
atherosclerosis, generalized			5
Bernard-Soulier Syndrome			3
bladder cancer	23		
brain hemorrhage			6
carbamazepine hypersensitivity			4
catalase activity		3	3
cerebral infarct			4
cerebrovascular disease; sickle cell anemia			7
cirrhosis, alcoholic			5
coronary artery stent thrombosis			3
coronary disease			4
coronary heart disease			8
Fibrinogen			3
fibrinogen heart disease, ischemic tissue plasminogen activator level			3
fibrinogen II-6 myocardial infarct			3
fibrinogen myocardial infarct			4
fibrinogen protein C resistance ratio prothrombin thrombosis, deep vein			4
head and neck cancer	14		
hyperhomocysteinemia	4		
Hypothyroidism		4	4
intimal medial thickness			3
Leukemia	19		
liver disease, alcoholic			4
Longevity			9
lung function			5
lymphoma, Non-Hodgkin's	8		
lymphoproliferative disorders; blood transfusion complications			3
maternal microchimerism			3
methotrexate toxicity	7		
myocardial infarct			17
myocardial infarct; atherosclerosis, coronary			8
myocardial infarct; heart disease, ischemic			3
myocardial infarct; thromboembolism, venous; thrombosis, deep vein			3
myocardial infarction			12



myocardial infarction; stroke			3
myocardial infarction; stroke, ischemic			3
neural tube defects	12		
obesity; retinal vascular occlusion			3
Pancreatitis			6
pancreatitis, chronic			5
Parkinson's disease			13
Preeclampsia			13
pregnancy loss, recurrent			8
Psoriasis			9
Radiotoxicity			3
retinal vascular occlusion			4
Sarcoidosis			7
Sepsis			6
Spermatogenesis	4		
spondyloarthropathies		4	4
Stroke			14
stroke, ischemic			14
stroke, lacunar			3
Thrombocytopenia			7
thromboembolism, venous			8
Thrombosis			5
thrombosis, deep vein			5
Tuberculosis			9
Vitiligo		4	4

**Supplementary Table S9.** List of proteins with significantly higher level in each cell line in comparison with the other in a pairwise comparison. Summary of denaturing and 'native' buffer lysis conditions.

114/115 HEK293/U937	115/114 U937/HEK293	114/(116+117) HEK293/PBMCs	115/(116+117) U937/PBMCs	(116+117)/114 PBMCs/HEK293	(116+117)/115 PBMCs/U937
Q01469	Q7Z2W4-3	P68366	Q9BVP2-2	P02533	P01040
P18887	P33241	P49588	P27144	P35908	P13647
P17980	Q9UJU6-1	P06744-1	Q9UQ35-1	P13645	P13645
P25705	P10253	P23141-1	P09622	P35527	P29508-2
P13010	Q96G03	P00441	P13797	P01040	P01857
Q99714-1	Q9NQC3-2	P54136-2	P02545-3	Q86YZ3	P12544-2
Q92499	P21333-2	P21333-2	P00918	P13647	P02775
Q8IX12-2	P78527-2	Q96G03	P14314-2	Q15517	Q9H4B7
Q14684-2	O95319-5	O95319-5	P16403	P62328	P07996
O00571-2	P49588	P04406	Q01082-3	Q15404-2	P02671-2
P61604	P26038	P04179-1	P62316	Q06323	P05109
P63220	Q13423	Q13510-1	P33241	P02679-2	Q9Y3Z3-2
Q9UII2-1	P04439	P61224	P04406	P30740	P05106-1
P49411	O00299	P07305-2	Q9Y265-2	P01857	P68871
Q14137	P04083	Q8WUM4	P31942-2	Q14141-2	P02768-1
P38646	P08133	P52597	P11387	P04083	P15121
P60900	P14317	Q92900-2	Q13813-3	P52566	
Q9H8H0	P04792	P26038	P78371-2	P31146	
O75347	P21291	P31943	Q15050	P07996	
P46778	O75368	P62266	Q9Y3T9	Q14019	
P62158	P68366	P07339	Q05048	Q9Y3Z3-2	
Q9Y224	P05107	Q02543	P52597	P05109	
P39023	P23141-1	P60174-1	P43034-1	P08575-2	
O00148	Q9BV40	P16070-15	P00390-5	P02671-2	
O75947-2	P31146	Q9NSD9	Q9UMX5	P02768-1	
Q9P2R7-2	Q9UBR2	P62191	P08311	P12544-2	
Q9Y2W1	P61626	P60763	P62805	Q86UX7-2	
Q13561-1	P52566	P78371-2	Q15233	P61626	
P22392-1	P16401	P09622	O75947-2	P13796	
Q15233	P31930	P07686	Q02543	P08514-3	
Q07020	P49736	P53634-1	P52292	P68366	
P06576	P02671-2	Q9UMX5	Q14684-2	P19971	
Q15029-2	P33993-1	Q15149-7	P54136-2	Q14005-3	
P25789-1	Q9UL46	P00390-5	P61626	P11215	
Q9Y265-2	P47756-2	P61160	O43660-2	P06396-2	
P09622	P60709	P29401	Q15293	Q9H299	
P38919	P50995	P09661	P49821-2	P06702	
Q9UHX1-4	P28838-2	Q9UII7-1	P50990	P50453	
Q92945	P18669	O00115	P35232	P41218	
P50990	P38919	P13798	P46776	O60234	
P40227	P41250	P27144	P00505	P02775	
P15311	P61981	P42704	Q8N6T3-1	P20292	
Q15393-1	P30086	Q14157-4	P62910	P08246	
Q15424	P23528	P04040	P25789-1	P05106-1	
P35613-2	Q96QK1	P62917	Q9Y3F4		
P52292	Q53EL6	Q7L014	P25786-1		
Q7RTV0	P49748-2	Q16891-3	P07305-2		
O43660-2	Q13451	Q9Y265-2	P09661		
P08559-3	Q16563-2	P35659-1	P10606		
Q99832-3	P17858-1	P06753-3	P82979		
Q9UJZ1	P27695	P27797	P60174-1		
P49321-1	P07910-2	O75947-2	P0C0S5		
Q05048	P61160	P47914	O75400-2		
Q13347	P00558	P43034-1	Q8IZP2		
P22626-1	Q15404-2	P39687	P62424		
P28072	P04406	P62910	Q15149-7		
P62258-1	Q96C19	P35579-1	P07910-2		
P19338	P06744-1	Q9UQ35-1	P67936-1		
Q15050	P36871-1	P56181-2	P35659-1		
Q01130	Q16851-2	O95777	P28072		
Q9Y3F4	AOFG8-2	P04066	Q96BR5		
P17987	P07384	Q9BQ39	P30405		
Q9Y3T9	P08514-3	P36542-2	P46777		
P27635	P13645	Q13257	P61254		

P12270	P31153	Q9Y5J9	Q7L014		
P11310-1	P50395-1	P07910-2	P31943		
P07910-2	P61158	P12268	Q02878		
P10606	Q13510-1	Q9H9B4	P62191		
Q99848	O60568	Q14684-2	Q9H8H0		
P25786-1	Q14141-2	Q16629-3	O75390		
Q13435	P27797	Q12849-5	P28070		
P22307-2	P11279	P50990	P14866-1		
P09661	Q7Z4W1	Q05048	P11021		
P52272-2	P13489	Q15050	P06576		
Q96C01	Q96KP4-2	O95433	Q9UIJZ1		
P62910	Q15126	Q9Y3T9	P18124		
P32969	P50897-2	P62277	P36578		
P78371-2	P09525	P09874	P62266		
Q15019-1	P07339	P52292	Q03252		
Q8N4H5	P00491	P05388	P12270		
P35637-2	Q14847-1	P26639	P10515		
P61254	P15586	Q9BUQ8	P35637-2		
Q16531	Q13576-1	P62937	Q15393-1		
Q00839-2	P02538	O75718	P06744-1		
Q9UMS4	P26447	P62861	P12268		
Q08945	Q8NBJ7-5	O75306	P07339		
P14314-2	P52209	Q9NWS0-1	Q15424		
P10809	Q06323	Q15393-1	P26373		
P38117-1	P07237	P11021	P52272-2		
P16403	Q14019	P28070	Q8WUM4		
Q92841-1	O60664-3	P51659	Q16531		
Q14974	P35908	Q9UKM9-2	P18887		
Q9H3K6-2	P04040	Q9UBQ0-1	Q92900-2		
P45880-2	P09382	P55072	Q12931		
P04179-1	P28062-2	P40429	Q9NSD9		
Q9H9B4	Q86UX7-2	Q15029-2	P04792		
P48643	Q7L591-1	P20962	Q13257		
P00505	P11413-1	Q99848	Q9H307-1		
P61978-3	Q96B97-1	P25789-1	P17980		
P10515	P08575-2	Q9Y3A5	O75494-5		
P84103	P13796	O75367-2	P61247		
O14979-3	P24158	Q6UXN9	P38646		
P14866-1	P30740	O43660-2	P40429		
P40926	Q9ULZ3-3	O75390	Q99714-1		
P11177-2		P30405	Q9UKM9-2		
P26373		Q8WWM7-6	Q9Y2W1		
O43684-2		Q03252	Q8N4H5		
Q96BR5		P23396	P62979		
Q14978-1		P54577	Q6UXN9		
Q13185		P11387	Q15029-2		
Q9UQ35-1		Q9NQZ2	P20618		
O75400-2		P68431	Q13435		
P23246-1		P14314-2	Q8IX12-2		
P35232		Q9H8H0	Q00839-2		
P06748-3		P20618	Q9NWS0-1		
P62424		P18887	P42704		
P49207		P60709	O95433		
P22102-2		P55884-1	Q92945		
O00115		P19105	O75718		
P49821-2		O15511-1	P36542-2		
P62917		Q12906-5	P62258-1		
Q8N6T3-1		Q9Y4L1	Q14157-4		
P14678-2		Q15424	Q92879-2		
Q16629-3		Q9NR30-2	O14979-3		
Q12849-5		P14618-1	P49321-1		
Q9NQZ2		Q99497	Q09028-3		
P62805		P17980	P29401		
P11387		P31930	Q9BUQ8		
Q13813-3		P62316	P43686-2		
Q02878		P46777	Q9UII2-1		
O94788-2		Q96CT7	P51659		
Q12931		P15586	P23246-1		
P62316		Q01082-3	Q13561-1		
P0C0S5		P25788-2	P17987		
Q01082-3		Q9Y266	P40926		
P09651-2		P40227	P34897-3		
P13797		P23246-1	P61224		

P14854		P07237	O95777		
Q9Y5J9		P54819-5	P22102-2		
Q9H307-1		Q9UJZ1	Q92499		
Q9BVP2-2		Q14697-1	P04066		
P46776		P42765	P05388		
Q9NZI8		P25786-1	P48444		
P02545-3		P00505	P10809		
P47914		P10606	P55884-1		
Q13642-1		P49821-2	Q9Y224		
P31942-2		P48444	Q9Y3A5		
P00918		P38646	P25788-2		
P20962		O43818	P15311		
P32119-1		P62424	P60900		
P07355-1		P28072	Q14137		
P36578		Q9Y3F4	P20700		
Q15293		P40939	P16070-15		
P08670		Q9NVI7-3	P25705		
P07197		Q01081-4	Q9UHX1-4		
P06899		O94788-2	P06753-3		
P07196		P62979	P61978-3		
Q16630-3		P61254	P14854		
P60983		Q8IZP2	Q8WWM7-6		
Q12769-2		P13797	P22626-1		
P61081		Q09028-3	P46778		
P47985		P46778	P49411		
P62750		Q99714-1	Q13347		
Q15075		Q9BVP2-2	Q9UIJ7-1		
P61956-2		O94826	Q01081-4		
P08865		P49321-1	Q92841-1		
P31948		P43686-2	Q92922		
P50991		P27635	Q07020		
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		Q8WTV0-3	Q6FI81-3		
			Q9Y240		
			P20839-2		
			Q15056-2		
			Q9Y5M8		
			Q02880-2		
			Q9Y333		
			O43765		
			Q9NR28-2		
			Q9BQG0-1		
			Q96KR1		
			P69849		
			Q92878-3		
			P31483-2		
			Q7Z4K8-3		
			Q9BTE6-1		
			Q02809		
			Q7L576-3		
			P55060-3		
			P42285		
			Q9BRP4-3		
			Q8NBJ7-5		
			Q5TBB1		
			Q06330-3		
			Q9H9Y6-2		
			Q8WU90		
			Q9UNX4		
			P42766		
			Q9BXJ9-4		
			O14647-2		
			Q6KC79-2		
			O60493-2		
			Q9P2J5		
			Q99848		
			Q00341		
			Q9HB07		
			Q15382		
			O43847-1		
			Q9NVP1		
			Q6NUQ4-2		
			P43246		
			Q86UK7-2		
			Q9NTJ3-2		
			Q8N983-4		
			P28370-2		
			P48595		
			Q9BVG4		
			O00154-2		
			Q9HC07		
			Q14690		
			Q16822-1		
			Q12849-5		
			O00418		
			O43324		
			O00422		
			Q92544		
			Q06265-3		
			Q8NBL1		
			Q15738		
			Q14676-4		
			Q01650		
			Q9UBB4-2		
			P18583-6		
			O15427		
			Q15021		
			Q9NU22		
			Q6P2E9-1		
			P23921		
			P30533		

			P49915		
			Q9UBX3-1		
			Q9UM22-2		
			P48507		
			Q8TCT9-5		
			Q9Y617-2		
			P02792		
			Q16576-1		
			P04818		
			Q8WTV0-3		
			P78329		
			P50897-2		

**Supplementary Table S10.** Comparison of functional annotation results for the proteins that are of higher levels in the cell lines in quantitative pairwise analysis of HEK293, U937 and PBMCs. Enrichment of KEGG\_PATHWAY categories performed in DAVID Bioinformatics Resources 6.7; thresholds: Count=2, EASE=0.01 (\*EASE≤0.02, \*\*EASE≤0.1).

KEGG pathway map			Term	Count					
				114/ 115	115/ 114	114/ (116- 117)	115/ (116- 117)	(116- 117)/ 114*	(116- 117)/ 115**
1. Metabolism	1.0 Global and overview maps 1.1 Carbohydrate metabolism	1.0	hsa00071:Fatty acid metabolism			15	17		
		1.1	hsa00010:Glycolysis / Gluconeogenesis		7	20	23		
		1.1	hsa00020:Citrate cycle (TCA cycle)	9		18	20		
		1.1	hsa00030:Pentose phosphate pathway		6		11		
		1.1	hsa00052:Galactose metabolism		5				
		1.1	hsa00500:Starch and sucrose metabolism		5				
		1.1	hsa00520:Amino sugar and nucleotide sugar metabolism			13	15		
		1.1	hsa00620:Pyruvate metabolism	6		16	16		
		1.1	hsa00630:Glyoxylate and dicarboxylate metabolism				7		
		1.1	hsa00640:Propanoate metabolism			12	12		
	1.2 Energy metabolism	1.2	hsa00190:Oxidative phosphorylation	15		36	32		
	1.3 Lipid metabolism	1.3	hsa00062:Fatty acid elongation in mitochondria			6	6		
	1.5 Amino acid metabolism	1.5	hsa00250:Alanine, aspartate and glutamate metabolism			10			
		1.5	hsa00270:Cysteine and methionine metabolism			11	12		
		1.5	hsa00280:Valine, leucine and isoleucine degradation			16	16		
		1.5	hsa00290:Valine, leucine and isoleucine biosynthesis			6	6		
	1.8 Metabolism of cofactors and vitamins	1.8	hsa00670:One carbon pool by folate			7	7		
2. Genetic information processing	2.1 Transcription	2.1	hsa03040:Spliceosome	39		66	67		
	2.2 Translation	2.2	hsa00970:Aminoacyl tRNA biosynthesis			19	20		
		2.2	hsa03010:Ribosome	25		67	65		
	2.3 Folding, sorting and degradation	2.3	hsa03018:RNA degradation			15	17		
		2.3	hsa03050:Proteasome			24	25		
3. Environmental information processing	3.3 Signaling molecules and interaction	3.3	hsa04512:ECM receptor interaction					3	2
4. Cellular processes	4.1 Transport and catabolism	4.1	hsa04142:Lysosome		7	24			
	4.2 Cell motility	4.2	hsa04810:Regulation of actin cytoskeleton					4	
5. Organismal systems	5.1 Immune system	5.1	hsa04640:Hematopoietic cell lineage					3	
6. Human diseases	6.4 Neurodegenerative diseases	6.4	hsa05010:Alzheimer's disease	16		39	35		
		6.4	hsa05012:Parkinson's disease	19		42	37		
		6.4	hsa05016:Huntington's disease	22		53	45		
	6.8 Infectious diseases: Bacterial	6.8	hsa05130:Pathogenic Escherichia coli infection			17	21		

**Supplementary Table S11.** Comparison of functional annotation results for the quantitative analysis of proteomes from 3 different cell lines: HEK293, U937 and PBMCs. Enrichment of GENETIC\_ASSOCIATION\_DB\_DISEASE categories performed in DAVID Bioinformatics Resources 6.7; thresholds: Count=2, EASE=0.05.

Term	Count					
	114/115	115/114	114/ (116-117)	115/ (116-117)	(116-117)/ 114	(116-117)/ 115
Aalpha and gamma fibrinogen plasma levels					2	
atherosclerosis, coronary atherosclerosis, generalized					2	
atherosclerosis, coronary; tuberculosis			3	4		
benign breast disease breast cancer	2					
cerebrovascular disease; sickle cell anemia					3	
coronary artery stent thrombosis					2	
diabetes, type 1		6				
endometrial cancer; cervical cancer; radiosensitivity, clinical	2					
fibrinogen					2	
fibrinogen heart disease, ischemic tissue plasminogen activator level					2	
fibrinogen II-6 myocardial infarct					2	
fibrinogen myocardial infarct					2	
lymphoproliferative disorders; blood transfusion complications					2	
metabolism disorders						2
metabolism disorders; myocardial infarction; stroke, ischemic					2	
myocardial infarct					6	
myocardial infarct; atherosclerosis, coronary					3	
myocardial infarct; lymphoproliferative disorders; restenosis					2	
myocardial infarct; thromboembolism, venous; thrombosis, deep vein					2	
myocardial infarction					4	
myocardial infarction; stroke					2	
Parkinson's disease	6					
skin lesions, arsenic-induced				3		
stroke					3	
stroke, ischemic					4	