

SUPPLEMENTAL MATERIALS

Long Term Response to Circulating Angiogenic Cells, Unstimulated or Atherosclerotic Pre-conditioned, in Critical Limb Ischemic Mice

Lucía Beltrán-Camacho ^{1,2}, Margarita Jiménez-Palomares ^{1,2}, Ismael Sanchez-Gomar ^{1,2}, Antonio Rosal-Vela ^{1,2}, Marta Rojas-Torres ^{1,2}, Sara Eslava-Alcon ^{1,2}, Jose Angel Alonso-Piñero ^{1,2}, Almudena González-Rovira ^{1,2}, M^a Jesús Extremera-García ^{1,2}, Rosario Conejero ³, Esther Doiz ³, Manuel Rodríguez-Piñero ³, Martin R. Larsen ⁴ and M^a Carmen Duran-Ruiz ^{1,2}

^{1.} Biomedicine, Biotechnology, and Public Health Department, Cadiz University, 11002 Cadiz, Spain, lucia.beltrancamacho@alum.uca.es (L.B.-C.); margarita.jimenezpalomares@gm.uca.es (M.J.-P.); ismael.sanchez@uca.es (I.S.-G.); antonio.rosal@uca.es (A.R.-V.); marta.rojas@uca.es (M.R.-T.); sara.eslava@gm.uca.es (S.E.-A.); joseangel.alonsopi@alum.uca.es (J.A.A.-P.); almudena.gonzalez@uca.es (A.G.-R.); maria.jesus.extremera.garcia@gmail.com (M.J.E.-G.).

^{2.} Institute of Research and Innovation in Biomedical Sciences of Cádiz (INiBICA), 11009 Cádiz, Spain

^{3.} Angiology & Vascular Surgery Unit, Hospital Universitario Puerta del Mar, 11009 Cádiz, Spain, rosarioconejero@gmail.com (R.C.); edoiz@comcadiz.com (E.D.); manuel.rodriguez.pinero.sspa@juntadeandalucia.es (M.R.-P.).

^{4.} Department of Biochemistry and Molecular Biology, University of Southern Denmark, 5230 Odense, Denmark, mrl@bmb.sdu.dk (M.R.L.).

* Correspondence: maricarmen.duran@gm.uca.es (M.C.D.-R.)

Supplementary Materials and Methods:

Animals.

Species	Vendor or Source	Background Strain	Sex	Persistent ID / URL
<i>Mus musculus</i>	Charles River Laboratories	Balb-C Nude CAnN.Cg-Foxn1nu/Crl	Female	https://www.criver.com/

Antibodies.

Target antigen	Vendor or Source	Catalog #	Working concentration (µg/ml)	Lot #
CD31-FITC	Biolegend	303103	8	B224876
CD34-APC	Biolegend	343607	2	B223919
CD45-PBlue	Biolegend	368539	4	B264395
CD90-PE	Biolegend	328109	2	B236755
CD73-FITC	Biolegend	344015	16	B224217
CD105-FITC	Biolegend	323203	16	B225651
CD309-PE	Biolegend	359903	8	B245460
CD133-PE	Miltenyi Biotec	130-098-826	1:25 concentration not available	5140404153
CD146-PE	Biolegend	361005	4	B264161
CD14-PB	Biolegend	367121	8	B271628
UEA-1-FITC	Sigma-Aldrich	L9006	3	072M4026V
Dil-ac-LDL	Biomedal	BT-902	0.6	
α-Actin smooth muscle	Sigma	A5228	4	029M4807V
CD31	Abcam	AB32457	2	GR3200348-2
MOMA-2	Sigma-Aldrich	MAB1852	1	3026751
Ly-6G	Biolegend	127601	1	B265458

Alexa Fluor 488 anti-mouse IgG	Thermo Fisher	A10667	4	1962792
Alexa Fluor 555 anti-mouse IgG	Thermo Fisher	A21422	4	1837985
Alexa Fluor 488 anti-rabbit IgG	Thermo Fisher	A11008	4	1832425
Alexa Fluor 555 anti-rat IgG	Thermo Fisher	A21434	4	1907302

Cultured Cells.

Name	Vendor or Source	Sex (F, M, or unknown)
Endothelial progenitor cells (EPCs)	Peripheral blood of healthy donors	Unknown

Atherosclerotic samples.

Donor	Age	Sex (F, M, or unknown)	Smoker	DM2	Dislipidemia	Hypertension
Patient-1	70	M	Yes	Yes	Yes	Yes
Patient-2	64	M	Yes	No	Yes	Yes
Patient-3	Unknown	Unknown	Yes	No	Yes	Yes

Primers.

Description	Sequence	Vendor or Source
Primers forward	5'-GGTGAAACCCCGTCTCTACT-3'	Metabion
Primers reverse	5'-GGTTCAAGCGATTCTCCTGC-3'	Metabion
Hydrolysis FAM label probe	5'-(6-FAM)-CGCCCGGCTAATTTTGTAT-(BHQ-1)-3'	Metabion

Data & Code Availability.

Description	Source / Repository	Persistent ID / URL
MS data with identifier number PXD024132	ProteomeXchange	http://www.proteomexchange.org/

Other.

Description	Source / Repository
Quick-DNA™ Midiprep Plus Kit (D4075)	Zymo Research
Proteinase K (D3001-2-B)	Zymo Research
TaqMan Universal Master Mix II (4440043)	Thermo-Fisher
Mouse Cytokine Antibody Array C3 (AAM-CYT-3)	RayBiotech
TGFβ1 ELISA (CSB-E04726m)	Cusabio

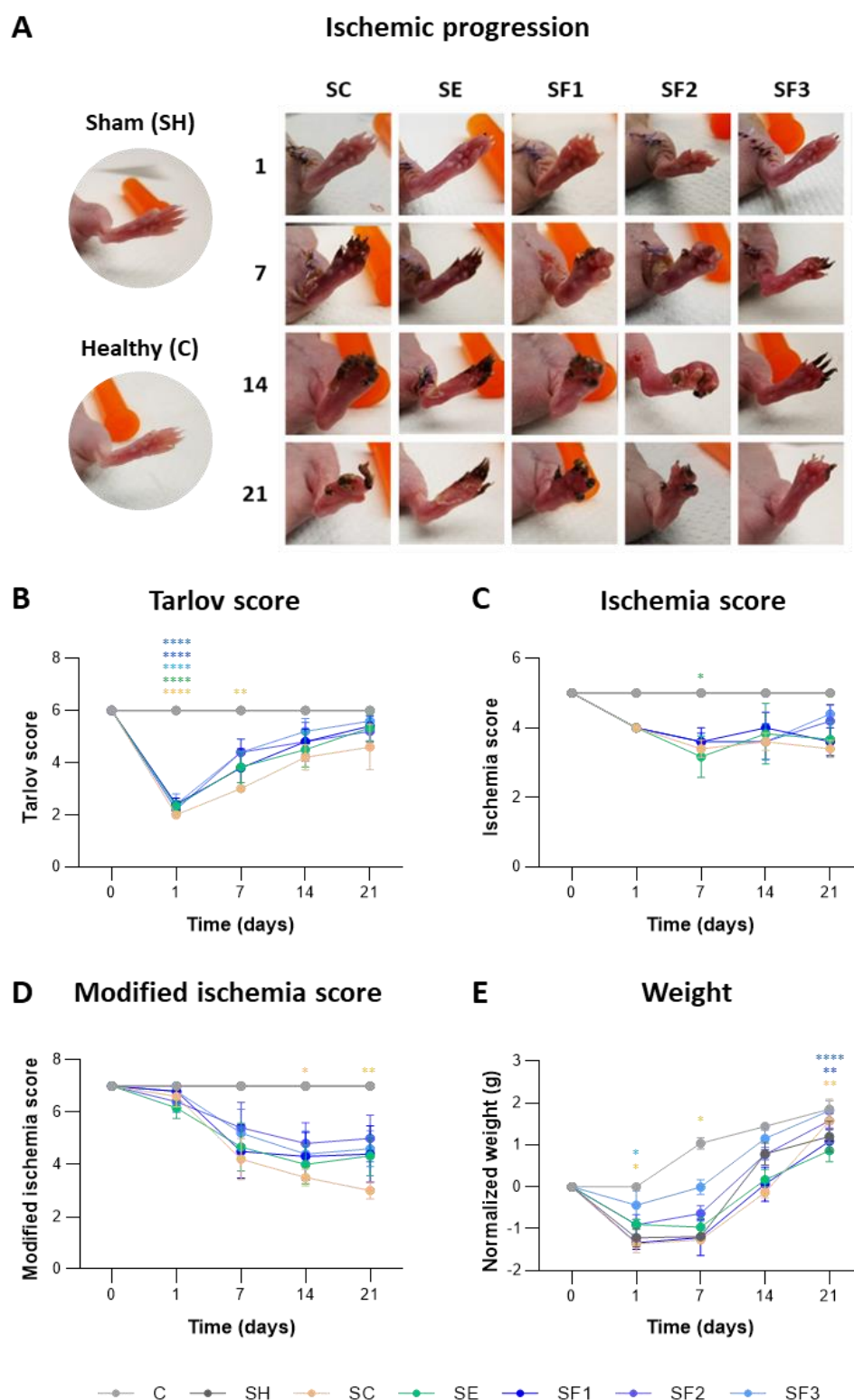


Figure S1. Evaluation of ischemic symptoms within time. (A) Representative images of the evolution of ischemic symptoms in mice. (B) Motility changes (Tarlov score) and Ischemic changes according to (C) Ischemia scores and (D) Modified Ischemia scores, all of them described in supplementary table S2. (E) Weight changes. Groups analyzed: Healthy controls (C, n:2); Sham, surgery controls (SH, n:4); ischemic mice, untreated (SC, n:5); ischemic mice with unstimulated CACs (SE, n:6) or pre-stimulated with atherosclerotic factors (SF: n:15: SF1, n:5; SF2, n:5; SF3, n:5). Data were presented as mean \pm SEM and significant differences were seen by two-way ANOVA and Tukey post-hoc. Statistical differences shown were calculated using the SH group as baseline per day.

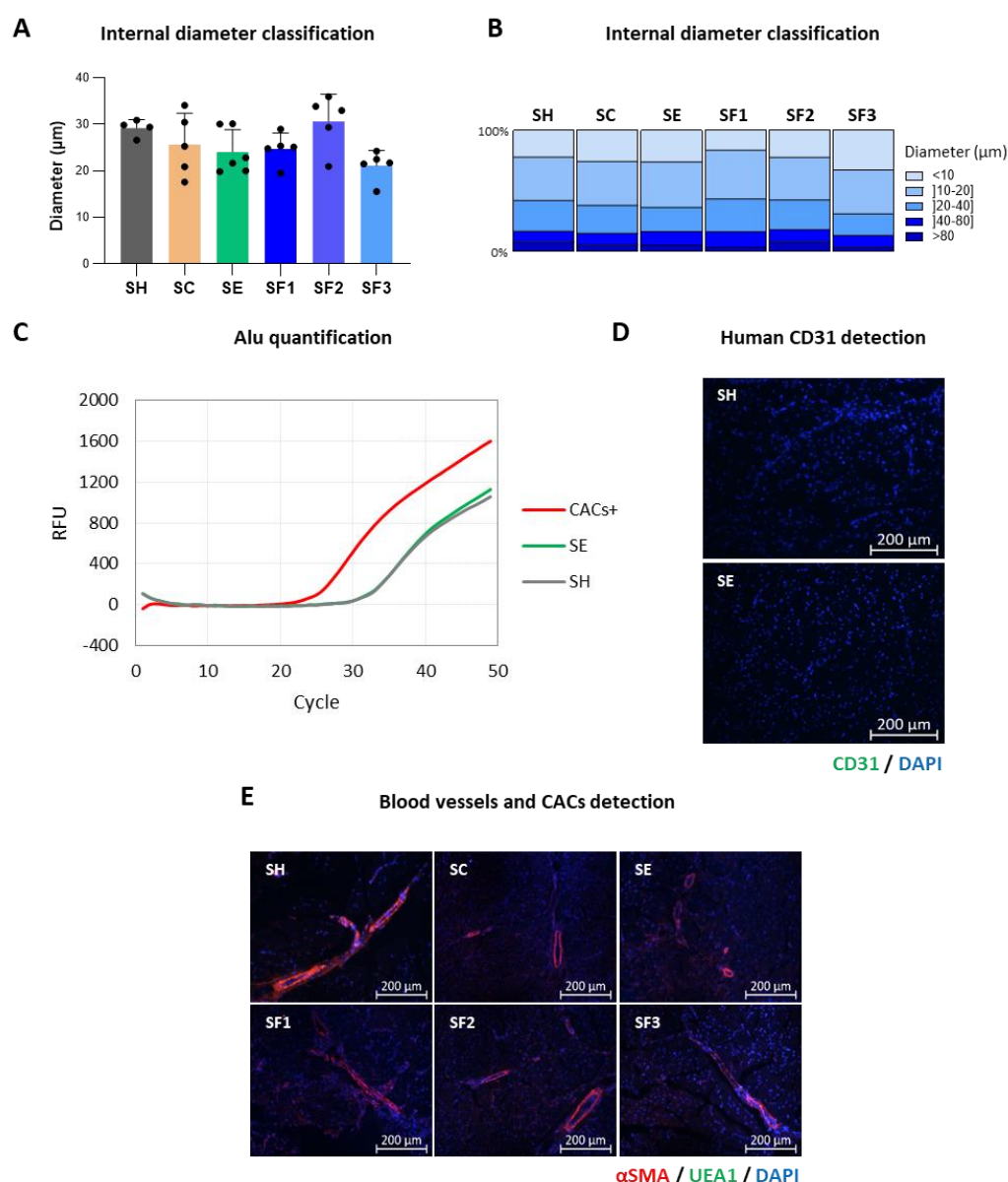


Figure S2. Human CACs detection and vascular density. **A)** Diameter size (μm). **B)** Vessel classification based on abundance (percentage) of different ranges of internal lumen diameter (μm). **C)** Representative results of the amplification of human-specific Alu sequences by qPCR, with the SH group as negative control. A positive result (CACs +, red) obtained from mice sacrificed at early days[1] has also been included. **D)** Representative IHC images using anti-hCD31 (green) and DAPI (blue). **E)** Representative IHC images taken to measure vascular density and diameter size with anti-mouse smooth muscle α -actin (red), and human cells using UEA1 (green) and DAPI (blue). Groups analyzed: SH: Sham, surgery controls (n:4), SC: Ischemic mice, no cell treatment (n:5), ischemic mice treated with unstimulated CACs (SE, n:6) or with pre-stimulated CACs (SF, n:15: SF1, n:5; SF2, n:5; SF3, n:5). Data were presented as mean \pm SD and significant differences were seen by Kruskal-Wallis and Dunn's multiple comparisons test.

Supplementary figure S3

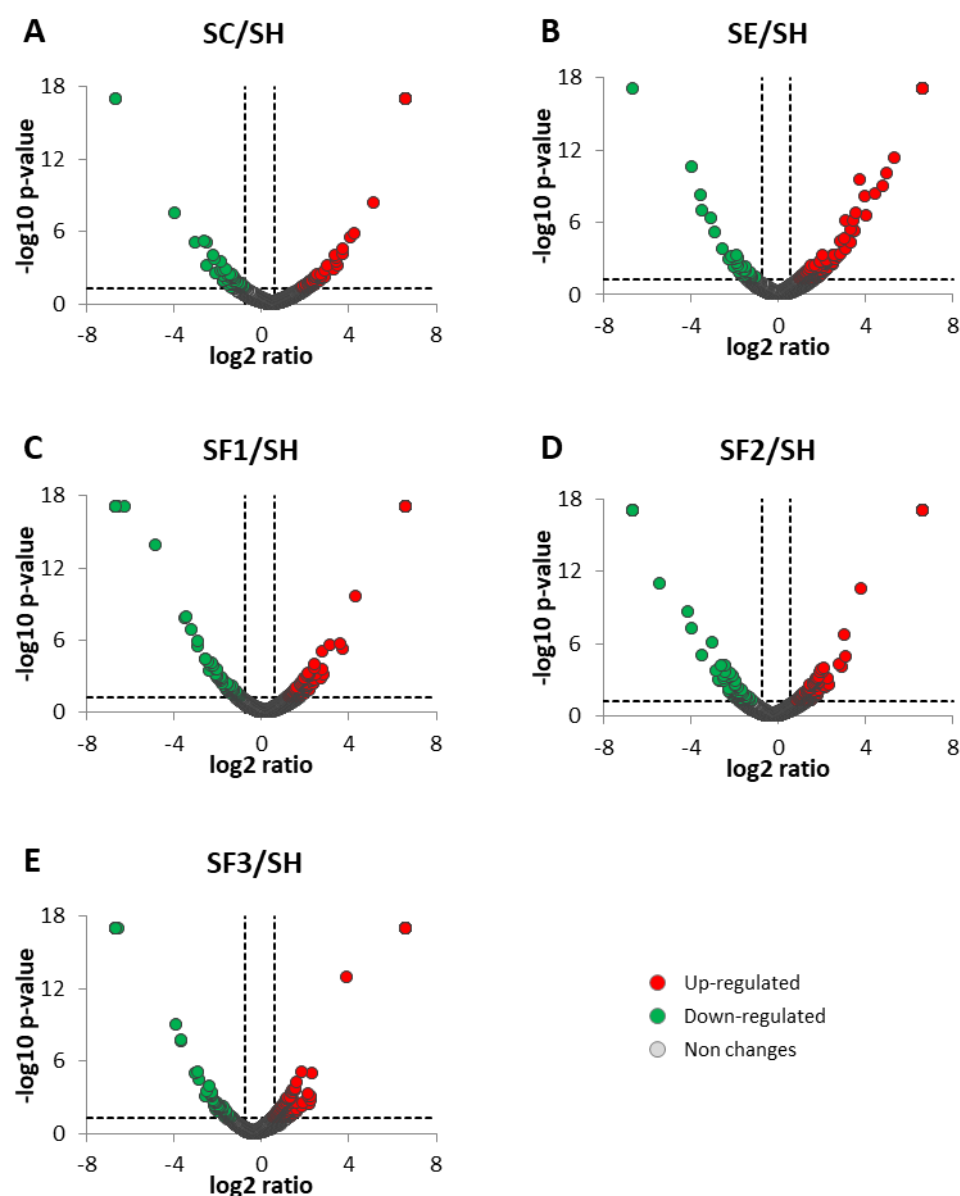


Figure S3. Volcano plots. Volcano plots obtained after label free quantification, comparing protein levels in A) SE, B) SC, C) SF1, D) SF2 and E) SF3 vs SH. Cut-off limits: p-value < 0.05, ratios for up-regulated (> 1.5) and down-regulated (< 0.6) proteins. Groups analyzed: SH: Sham, surgery controls (n:4), SC: Ischemic mice, no cell treatment (n:5), ischemic mice treated with unstimulated CACs (SE, n:6) or with pre-stimulated CACs (SF, n:15: SF1, n:5; SF2, n:5; SF3, n:5).

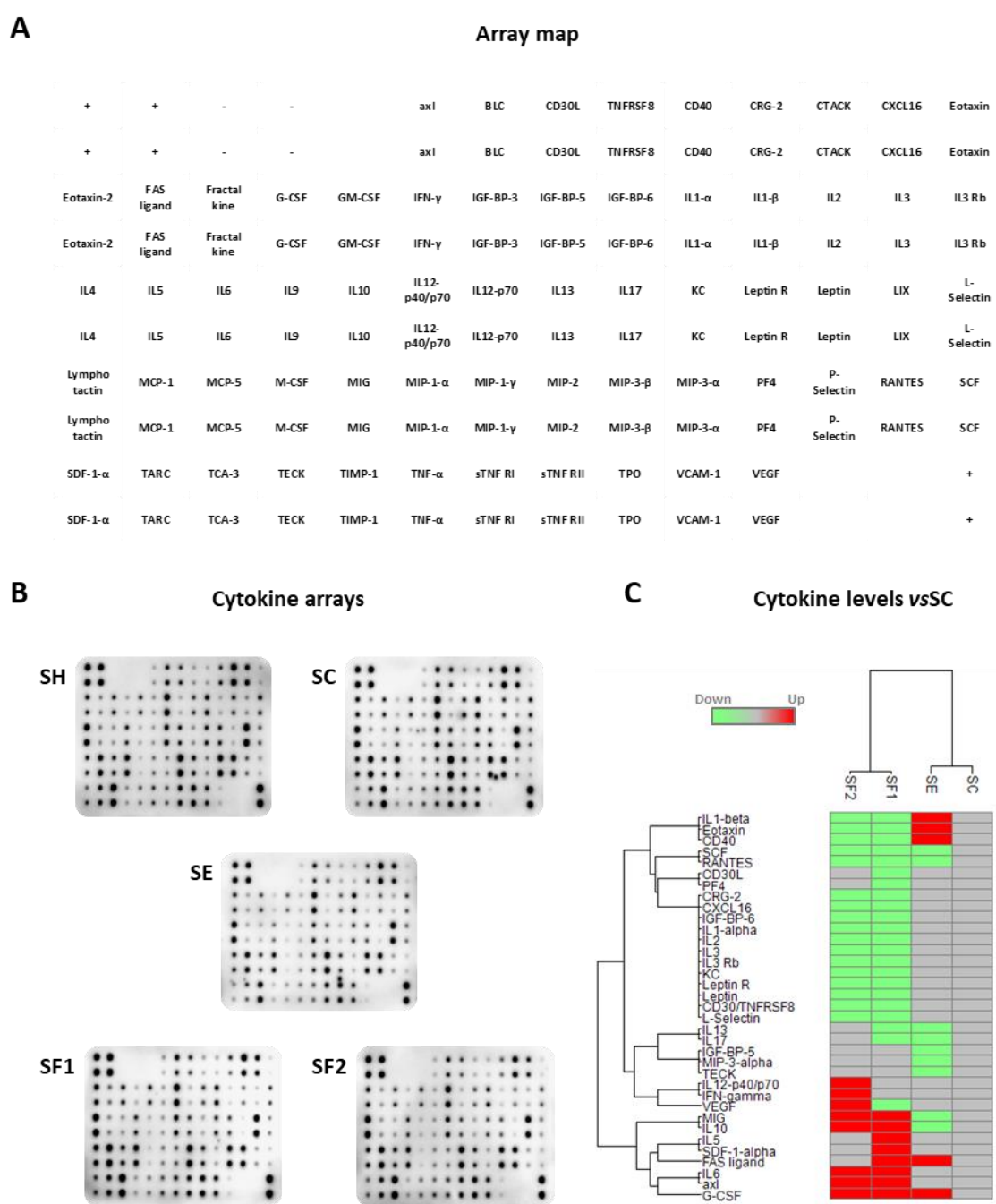


Figure S4 Cytokine expression arrays. (A) Map of Mouse Cytokine Antibody Array C3 (RayBiotech; AAM-CYT-3) (B) Cytokine arrays images acquired with ChemiDoc Touch System (Biorad) (C) Hierarchical cluster with differential levels patterns detected in cytokines arrays SE, SF1 and SF2 *vs* SC group. Groups analyzed: SH: Sham, surgery controls (n:4), SC: Ischemic mice, no cell treatment (n:5), ischemic mice treated with unstimulated CACs (SE, n:6) or with pre-stimulated CACs (SF, n:15: SF1, n:5; SF2, n:5).

Table S1. Functional scoring related to ischemia. The table includes (from left to right): Tarlov score (evaluating motility, leg movement and difficulty walking), ischemia score (ischemic symptoms, advance of the characteristics along the leg) and modified ischemia score (scores adapted to mice studies, evaluating the advance of the characteristics along the leg) [2, 3].

Score	Tarlov	Ischemia	Modified ischemia
0	No movement	Auto-amputation > half lower limb	Auto-amputation of leg

1	Barely perceptible movement, non-weight bearing	Gangrenous tissue > half foot	Leg necrosis
2	Frequent movement, non-weight bearing	Gangrenous tissue < half foot, with lower limb muscle necrosis	Foot necrosis
3	Support weight, partial weight bearing	Gangrenous tissue < half foot, without lower limb muscle necrosis	Discoloration of > two toes
4	Walks with mild deficit	Pale foot or gait abnormalities	Discoloration of one toe
5	Normal but slow walking	Normal	Discoloration of > two nails
6	Full and fast walking		Discoloration of one nail
7			No necrosis

Table S2. Quantitative analysis of proteins differentially expressed (vs SH). The table includes (from left to right): UniProt accession number, protein description, abundance ratio (considering up-regulated ratio > 1.5 and down-regulated ratio < 0.6), p-value (considering P-value < 0.05 as differentially significant), number of amino acids (AAs), number of peptide sequences (PSMs), number of unique peptides and coverage percentage.

Accession	Description	Abundance ratio					P-value					#AAs	#PSMs	#Unique Peptides	Coverage [%]
		SC/S H	SE/S H	SF1/SSF2/SSF3/S H	SC/S H	SE/S H	SF1/SSF2/SSF3/S H	SC/S H	SE/S H	SF1/SSF2/SSF3/S H	SC/S H				
Q9CQI6	Coactosin-like protein	4.853	2.755	2.892	2.642	2.008	0.015	0.014	0.026	0.009	0.007	142	445	9	61
P70333	Heterogeneous nuclear ribonucleoprotein H2	4.631	2.532	2.942	2.384	2.009	0.023	0.031	0.015	0.011	0.004	449	730	7	47
P40124	Adenylyl cyclase-associated protein 1	4.864	2.478	2.779	2.548	1.934	0.013	0.016	0.020	0.013	0.006	474	1637	27	64
Q6R891	Neurabin-2	10.92	6.179	7.281	7.101	4.894	0.000	0.001	0.000	0.000	0.001	817	60	2	2
P40142	Transketolase	4.075	2.319	3.714	3.091	2.327	0.031	0.020	0.002	0.002	0.001	623	3318	41	79
P97352	Protein S100-A13	5.242	3.496	3.599	3.450	2.447	0.016	0.005	0.011	0.000	0.002	98	231	5	46
P14602	Heat shock protein beta-1	4.397	2.898	3.953	3.099	2.689	0.022	0.008	0.001	0.002	0.000	209	776	11	55
Q8VHX6	Filamin-C	4.646	2.771	2.934	2.392	2.041	0.017	0.006	0.014	0.012	0.004	2726	6468	126	66
Q6IRU2	Tropomyosin alpha-4 chain	5.229	3.034	3.377	3.102	1.949	0.013	0.009	0.010	0.002	0.014	248	811	13	55
O89017	Legumain	10.66	4.814	5.151	3.625	2.223	0.000	0.002	0.002	0.000	0.029	435	226	7	21
P13516	Acyl-CoA desaturase 1	7.491	3.195	8.946	3.625	5.043	0.002	0.033	0.000	0.002	0.000	355	183	8	30
P15105	Glutamine synthetase	4.738	2.206	4.507	3.584	2.603	0.015	0.027	0.000	0.000	0.000	373	2095	25	68
Q61553	Fascin	4.656	2.296	2.967	2.764	2.016	0.016	0.027	0.013	0.008	0.004	493	798	21	52
Q9D154	Leukocyte elastase inhibitor A	4.480	2.165	2.457	2.123	1.583	0.020	0.030	0.042	0.023	0.030	379	1610	29	63
P19324	Serpin H1	8.244	2.965	4.758	4.305	3.003	0.000	0.009	0.000	0.000	0.000	417	760	16	53
Q91V92	ATP-citrate synthase	5.596	2.150	5.482	4.115	3.085	0.006	0.032	0.000	0.000	0.000	1091	5085	69	74
P16110	Galectin-3	10.64	4.224	4.736	3.840	2.495	0.000	0.000	0.000	0.000	0.001	264	497	12	38
P07091	Protein S100-A4	5.809	3.024	3.430	3.370	2.840	0.007	0.009	0.012	0.001	0.000	101	179	5	43

P47739	Aldehyde dehydrogenase, dimeric NADP-preferring	6.625	2.439	3.758	8.165	3.019	0.003	0.038	0.005	0.000	0.000	453	473	21	64
		0	0	0	0	0	9	7	9	0	2				
Q9WV32	Actin-related protein 2/3 complex subunit 1B	5.103	2.860	3.227	3.067	2.184	0.012	0.018	0.011	0.002	0.002	372	757	19	60
		0	0	0	0	0	5	1	6	2	2				
Q9ERN0	Secretory carrier-associated membrane protein 2	5.359	3.691	3.857	3.030	2.238	0.014	0.019	0.018	0.018	0.049	329	12	2	4
		0	0	0	0	0	4	6	9	8	9				
P61965	WD repeat-containing protein 5	19.13	15.94	20.23	14.33	15.10	0.000	0.000	0.000	0.000	0.000	334	4	2	10
		70	10	10	20	70	0	0	0	0	0				
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	3.755	2.272	2.558	2.326	1.756	0.044	0.023	0.033	0.014	0.014	353	1562	19	50
		0	0	0	0	0	8	1	6	2	2				
Q9WV54	Acid ceramidase	4.684	2.419	2.672	2.512	2.068	0.021	0.037	0.044	0.010	0.008	394	430	15	46
		0	0	0	0	0	3	1	4	5	2				
P29391	Ferritin light chain 1	5.496	2.689	3.482	2.878	1.822	0.007	0.010	0.004	0.005	0.010	183	773	18	90
		0	0	0	0	0	2	3	5	7	6				
P19096	Fatty acid synthase	6.007	2.390	6.958	3.500	3.634	0.004	0.016	0.000	0.000	0.000	2504	15771	150	78
		0	0	0	0	0	4	8	0	9	0				
P10107	Annexin A1	3.842	2.430	2.522	2.279	1.635	0.040	0.015	0.036	0.016	0.024	346	1800	32	76
		0	0	0	0	0	6	2	4	0	0				
Q9ES30	Complement C1q tumor necrosis factor-related protein 3	35.40	21.65	13.56	7.780	2.703	0.000	0.000	0.000	0.000	0.026	246	26	3	13
		10	70	80	0	0	0	0	0	1	3				
P49312	Heterogeneous nuclear ribonucleoprotein A1	3.845	2.108	2.393	2.168	1.722	0.040	0.042	0.048	0.016	0.016	320	1305	18	55
		0	0	0	0	0	5	3	6	8	4				
Q61233	Plastin-2	4.971	2.737	2.598	2.417	1.550	0.012	0.006	0.030	0.011	0.034	627	1840	42	88
		0	0	0	0	0	1	6	7	4	8				
Q05816	Fatty acid-binding protein 5	5.839	2.935	3.925	3.264	2.282	0.005	0.004	0.001	0.001	0.001	135	1111	11	73
		0	0	0	0	0	2	1	8	5	5				
Q9R1C7	Pre-mRNA-processing factor 40 homolog A	4.366	10.19	3.877	2.865	2.483	0.059	0.000	0.028	0.033	0.049	953	8	3	3
		0	00	0	0	0	8	0	7	5	5				
Q00612	Glucose-6-phosphate 1-dehydrogenase X	2.990	2.040	2.743	2.180	1.772	0.109	0.046	0.022	0.027	0.013	515	1202	33	64
		0	0	0	0	0	7	3	2	3	2				
Q9D9V3	Ethylmalonyl-CoA decarboxylase	4.364	2.142	5.556	2.671	2.626	0.036	0.105	0.000	0.007	0.001	322	273	13	50
		0	0	0	0	0	4	0	2	1	2				
Q62264	Thyroid hormone-inducible hepatic protein	4.828	1.824	4.642	4.015	2.716	0.014	0.177	0.000	0.000	0.000	150	339	4	27
		0	0	0	0	0	0	3	7	1	4				
Q9CZW4	Long-chain-fatty-acid--CoA ligase 3	5.534	3.175	4.217	3.087	3.544	0.021	0.062	0.018	0.021	0.007	720	11	2	6
		0	0	0	0	0	6	5	6	0	1				
P30115	Glutathione S-transferase A3	4.371	1.576	3.609	2.570	1.905	0.030	0.366	0.007	0.009	0.016	221	494	9	66
		0	0	0	0	0	2	7	2	8	8				
Q8BM A6	Signal recognition particle subunit SRP68	6.697	2.472	5.177	5.080	3.820	0.007	0.183	0.004	0.002	0.002	625	78	6	14
		0	0	0	0	0	9	9	3	4	8				
Q91WU0	Carboxylesterase 1F	4.130	1.521	3.994	3.141	2.263	0.029	0.180	0.001	0.002	0.001	561	485	21	55
		0	0	0	0	0	5	1	6	3	6				
Q9CQE1	Protein NipSnap homolog 3B	6.215	2.478	4.648	2.748	2.382	0.008	0.106	0.005	0.012	0.020	247	141	6	22
		0	0	0	0	0	9	3	1	0	0				
Q8VE K3	Heterogeneous nuclear ribonucleoprotein U	3.309	1.976	2.560	2.171	1.601	0.084	0.111	0.033	0.022	0.027	800	565	23	36
		0	0	0	0	0	8	3	4	2	9				
Q8CA Y6	Acetyl-CoA acetyltransferase, cytosolic	3.311	1.673	3.193	2.229	1.864	0.115	0.280	0.015	0.019	0.017	397	518	13	53
		0	0	0	0	0	8	0	3	3	9				
Q3UPL0	Protein transport protein Sec31A	3.307	1.954	2.596	2.058	1.686	0.083	0.123	0.046	0.041	0.027	1230	594	35	39
		0	0	0	0	0	7	1	3	5	6				
P35505	Fumarylacetoacetase	3.024	1.719	2.925	2.096	1.563	0.154	0.221	0.024	0.037	0.047	419	572	14	51
		0	0	0	0	0	8	7	8	8	8				
P35385	Heat shock protein beta-7	4.920	2.380	2.547	2.190	2.182	0.016	0.039	0.055	0.029	0.003	169	538	9	76
		0	0	0	0	0	4	2	4	2	2				
Q62009	Periostin	5.672	3.344	2.226	2.732	2.069	0.006	0.006	0.103	0.006	0.003	838	1131	37	64
		0	0	0	0	0	1	4	8	4	7				
P08226	Apolipoprotein E	4.067	3.278	2.258	2.097	1.610	0.031	0.003	0.071	0.032	0.026	311	975	20	64
		0	0	0	0	0	6	7	6	2	7				

Q3UZ3	Leucine-rich repeat flightless-	5.433	4.431	2.673	3.147	2.782	0.012	0.003	0.115	0.011	0.011	729	10	5	9
9	interacting protein 1	0	0	0	0	0	7	2	2	1	5				
P31996	Macrosialin	5.113	8.736	2.235	3.003	4.402	0.020	0.000	0.253	0.017	0.000	326	48	3	14
		0	0	0	0	0	6	0	2	5	5				
Q9Z2X	Heterogeneous nuclear ribonu-	4.539	2.844	2.653	2.579	1.871	0.035	0.022	0.061	0.010	0.022	415	398	9	40
1	cleoprotein F	0	0	0	0	0	3	2	2	4	3				
Q8BX	Golgi integral membrane pro-	5.738	4.182	3.036	4.430	3.091	0.017	0.014	0.106	0.004	0.010	655	103	2	4
A1	tein 4	0	0	0	0	0	4	9	0	2	6				
Q6WV	BTB/POZ domain-containing	4.369	2.578	2.616	2.194	1.690	0.033	0.040	0.069	0.029	0.046	327	350	11	41
G3	protein KCTD12	0	0	0	0	0	3	5	8	9	0				
Q9CQ	Regulator of G-protein signal-	6.590	4.317	2.963	4.396	2.983	0.008	0.012	0.104	0.003	0.015	181	60	3	25
E5	ing 10	0	0	0	0	0	7	2	3	7	1				
Q9WU	Coronin-1C	4.270	2.410	2.392	2.571	2.015	0.034	0.041	0.082	0.011	0.009	474	342	15	35
M4		0	0	0	0	0	5	0	1	1	2				
Q9WU	Cathepsin Z	4.668	3.105	2.441	2.822	1.853	0.018	0.007	0.060	0.003	0.009	306	450	9	47
U7		0	0	0	0	0	7	0	4	4	0				
P97797	Tyrosine-protein phosphatase	4.087	2.427	2.369	2.897	2.515	0.048	0.038	0.112	0.003	0.001	513	33	5	10
	non-receptor type substrate 1	0	0	0	0	0	0	0	6	0	4				
Q569Z	Thyroid hormone receptor-as-	3.917	3.511	2.934	3.718	2.596	0.075	0.018	0.063	0.001	0.011	951	71	9	11
6	sociated protein 3	0	0	0	0	0	6	3	6	6	4				
Q5F2E	Nuclear fragile X mental retar-	4.344	3.461	3.084	8.687	4.810	0.070	0.040	0.094	0.000	0.000	692	41	2	3
7	dation-interacting protein 2	0	0	0	0	0	6	4	6	0	8				
Q9Z0J	NPC intracellular cholesterol	3.595	2.674	2.545	1.994	1.645	0.079	0.027	0.067	0.047	0.048	149	205	8	54
0	transporter 2	0	0	0	0	0	4	5	8	6	6				
Q99PL	Ribosome-binding protein 1	3.830	1.852	2.304	2.290	1.619	0.041	0.072	0.059	0.015	0.025	1605	1686	48	34
5		0	0	0	0	0	2	2	6	5	7				
Q6231	Trans-Golgi network integral	4.874	2.710	3.508	3.480	2.562	0.039	0.138	0.055	0.018	0.035	353	27	2	6
3	membrane protein 1	0	0	0	0	0	9	4	6	6	9				
Q9EQ	Protein SET	4.181	2.166	2.603	2.194	1.760	0.040	0.070	0.051	0.020	0.032	289	396	10	43
U5		0	0	0	0	0	7	1	2	5	3				
Q6444	C-type mannose receptor 2	4.093	1.766	2.243	2.799	1.804	0.036	0.123	0.068	0.005	0.011	1479	463	23	21
9		0	0	0	0	0	1	8	6	0	5				
Q921F	TAR DNA-binding protein 43	2.935	1.967	2.109	2.066	1.588	0.153	0.126	0.134	0.026	0.030	414	615	14	50
2		0	0	0	0	0	8	5	6	5	2				
Q91ZX	Prolow-density lipoprotein re-	3.139	1.852	2.290	2.064	1.630	0.091	0.097	0.061	0.040	0.024	4545	1237	76	20
7	ceptor-related protein 1	0	0	0	0	0	7	0	6	8	5				
Q9CY	Tumor protein D54	2.748	1.795	2.089	2.215	1.608	0.228	0.185	0.152	0.029	0.049	220	429	12	51
Z2		0	0	0	0	0	2	4	6	5	3				
Q9D0J	Parathymosin	3.189	1.759	2.210	2.665	1.604	0.117	0.197	0.107	0.006	0.027	101	161	5	24
8		0	0	0	0	0	1	3	2	6	1				
Q0579	Basement membrane-specific	3.647	1.983	2.369	2.023	1.747	0.050	0.050	0.051	0.031	0.014	3707	3595	94	38
3	heparan sulfate proteoglycan	0	0	0	0	0	6	4	4	0	7				
	core protein														
Q6431	Hematopoietic progenitor cell	3.151	1.962	2.135	2.454	1.738	0.161	0.165	0.205	0.013	0.040	382	226	7	17
4	antigen CD34	0	0	0	0	0	5	1	7	3	1				
Q9QY	Alpha-adducin	3.144	1.849	2.724	2.183	1.942	0.178	0.238	0.079	0.025	0.028	735	217	13	27
C0		0	0	0	0	0	3	8	7	7	9				
Q8BJ7	Nuclear pore complex protein	3.176	1.677	2.372	2.716	1.972	0.169	0.385	0.138	0.007	0.032	819	22	5	7
1	Nup93	0	0	0	0	0	5	1	5	2	8				
B2RXS	Plexin-B2	3.567	2.919	3.167	2.764	2.329	0.105	0.062	0.059	0.030	0.041	1842	19	6	5
4		0	0	0	0	0	7	8	4	9	4				
Q99M	Protein ATP1B4	4.060	2.405	2.013	2.480	2.063	0.061	0.113	0.332	0.047	0.047	356	78	4	13
E6		0	0	0	0	0	8	1	0	1	7				
Q8C65	Septin-10	2.997	1.853	2.519	3.590	2.754	0.249	0.439	0.174	0.015	0.016	452	60	2	6
0		0	0	0	0	0	7	2	3	3	8				
Q9R05	Four and a half LIM domains	2.475	2.276	2.646	2.583	2.233	0.352	0.071	0.065	0.008	0.004	289	305	12	46
9	protein 3	0	0	0	0	0	7	8	4	8	3				

Q6109 3	Cytochrome b-245 heavy chain	3.044	2.397	2.115	3.429	2.255	0.197	0.114	0.280	0.003	0.038	570	45	14	44
		0	0	0	0	0	7	9	2	1	9				
Q8CI9 5	Oxysterol-binding protein-related protein 11	3.197	2.603	3.363	3.055	2.527	0.188	0.152	0.067	0.040	0.033	751	24	5	10
		0	0	0	0	0	4	4	0	3	6				
Q9CQ W9	Interferon-induced transmembrane protein 3	4.677	3.160	3.706	2.152	2.754	0.036	0.032	0.013	0.052	0.003	137	105	2	20
		0	0	0	0	0	8	1	7	1	4				
A6H5X 4	PHD finger protein 11	9.915	31.49	6.780	2.215	4.556	0.001	0.000	0.001	0.099	0.003	337	13	2	12
		0	40	0	0	0	5	0	6	2	9				
P08207	Protein S100-A10	4.083	2.684	3.288	1.620	1.645	0.056	0.025	0.014	0.154	0.043	97	250	5	71
		0	0	0	0	0	5	7	4	2	7				
Q9Z1F 9	SUMO-activating enzyme subunit 2	3.285	2.536	3.053	1.791	1.557	0.087	0.031	0.016	0.083	0.033	638	162	12	29
		0	0	0	0	0	2	2	0	2	7				
Q8R0X 7	Sphingosine-1-phosphate lyase 1	5.231	2.718	3.345	1.894	2.212	0.024	0.066	0.039	0.162	0.044	568	41	3	6
		0	0	0	0	0	6	2	2	5	2				
Q8K4G 1	Latent-transforming growth factor beta-binding protein 4	4.702	2.757	3.490	2.422	2.047	0.039	0.075	0.030	0.061	0.049	1666	73	7	5
		0	0	0	0	0	7	2	6	3	1				
Q9CZ N7	Serine hydroxymethyltransferase, mitochondrial	4.319	2.753	4.057	2.228	3.148	0.053	0.077	0.010	0.088	0.002	504	70	7	23
		0	0	0	0	0	5	7	1	2	9				
P97927	Laminin subunit alpha-4	2.981	1.743	2.505	1.877	1.627	0.110	0.097	0.037	0.062	0.024	1816	631	32	23
		0	0	0	0	0	9	5	8	0	8				
Q8JZU 2	Tricarboxylate transport protein, mitochondrial	3.183	1.697	3.754	1.843	2.127	0.129	0.236	0.005	0.068	0.002	311	345	15	55
		0	0	0	0	0	3	5	0	8	9				
Q9D2R 0	Acetoacetyl-CoA synthetase	2.673	1.548	3.195	1.553	1.827	0.286	0.441	0.017	0.183	0.026	672	247	20	43
		0	0	0	0	0	3	5	2	8	3				
Q6209 3	Serine/arginine-rich splicing factor 2	3.647	2.101	3.981	1.625	2.192	0.082	0.177	0.006	0.207	0.014	221	152	6	22
		0	0	0	0	0	9	6	1	7	4				
P54310	Hormone-sensitive lipase	3.679	1.903	4.422	1.927	2.191	0.068	0.120	0.000	0.058	0.002	759	695	30	63
		0	0	0	0	0	5	8	7	3	2				
P33267	Cytochrome P450 2F2	3.544	1.691	3.030	1.899	1.808	0.082	0.304	0.032	0.069	0.027	491	396	22	53
		0	0	0	0	0	7	7	0	5	0				
O7050 3	Very-long-chain 3-oxoacyl-CoA reductase	4.418	2.674	3.648	2.302	2.479	0.052	0.070	0.020	0.061	0.016	312	95	7	29
		0	0	0	0	0	7	0	5	9	7				
Q6P06 9	Sorcin	3.058	2.200	2.678	1.940	1.693	0.148	0.064	0.043	0.056	0.030	198	379	10	46
		0	0	0	0	0	7	6	8	2	4				
Q99JR 1	Sideroflexin-1	3.351	2.398	3.559	1.502	2.222	0.129	0.174	0.023	0.372	0.041	322	73	7	41
		0	0	0	0	0	1	8	4	6	3				
Q5SW U9	Acetyl-CoA carboxylase 1	3.148	1.802	3.680	1.627	1.846	0.090	0.082	0.003	0.089	0.009	2345	2783	101	66
		0	0	0	0	0	7	9	0	8	6				
Q5EB G6	Heat shock protein beta-6	3.026	1.761	2.788	1.864	1.902	0.113	0.192	0.020	0.062	0.007	162	597	8	71
		0	0	0	0	0	5	2	1	3	5				
Q9ET0 1	Glycogen phosphorylase, liver form	2.764	1.794	2.811	1.631	1.705	0.144	0.084	0.019	0.088	0.017	850	3782	32	61
		0	0	0	0	0	6	8	1	9	7				
P51881	ADP/ATP translocase 2	3.128	1.704	2.721	1.635	1.584	0.092	0.108	0.023	0.087	0.030	298	4970	13	74
		0	0	0	0	0	9	7	3	8	0				
Q8BT M8	Filamin-A	3.681	2.059	2.187	1.711	1.843	0.048	0.041	0.077	0.071	0.009	2647	3788	119	65
		0	0	0	0	0	7	0	8	5	7				
P16675	Lysosomal protective protein	4.023	2.771	2.420	1.821	1.793	0.053	0.017	0.081	0.086	0.026	474	503	10	25
		0	0	0	0	0	0	5	6	4	9				
Q9Z1X 4	Interleukin enhancer-binding factor 3	2.899	2.559	2.554	1.911	1.713	0.172	0.024	0.056	0.071	0.024	898	291	18	28
		0	0	0	0	0	9	9	1	8	1				
P42227	Signal transducer and activator of transcription 3	3.713	3.059	2.610	1.667	2.457	0.094	0.046	0.127	0.268	0.024	770	112	8	19
		0	0	0	0	0	4	3	4	2	7				
O8910 3	Complement component C1q receptor	3.414	2.537	2.585	1.900	1.920	0.118	0.041	0.082	0.072	0.025	644	264	9	19
		0	0	0	0	0	7	5	0	4	1				
Q6Q89 9	Probable ATP-dependent RNA helicase DDX58	4.954	2.425	3.281	2.521	2.494	0.025	0.187	0.063	0.060	0.027	926	114	10	13
		0	0	0	0	0	2	3	4	4	9				
Q6NV F9	Cleavage and polyadenylation specificity factor subunit 6	4.244	2.657	2.800	2.306	2.227	0.045	0.107	0.095	0.070	0.042	551	124	5	14
		0	0	0	0	0	7	1	6	6	0				

P01900	H-2 class I histocompatibility antigen, D-D alpha chain	3.982	1.595	1.857	1.668	1.764	0.047	0.297	0.228	0.109	0.013	365	401	12	55
		0	0	0	0	0	4	4	9	9	2				
P01902	H-2 class I histocompatibility antigen, K-D alpha chain	3.529	2.332	2.681	1.731	1.739	0.089	0.058	0.056	0.111	0.032	368	345	16	48
		0	0	0	0	0	1	3	3	4	8				
P16546	Spectrin alpha chain, non-erythrocytic 1	2.935	1.731	2.020	1.778	1.534	0.117	0.100	0.114	0.059	0.037	2472	4234	141	64
		0	0	0	0	0	3	8	4	6	3				
P61750	ADP-ribosylation factor 4	4.055	1.526	2.465	1.832	1.822	0.059	0.500	0.099	0.081	0.042	180	498	5	83
		0	0	0	0	0	0	9	1	2	8				
Q9JIF0	Protein arginine N-methyltransferase 1	2.665	1.897	2.153	1.737	1.670	0.264	0.151	0.142	0.084	0.036	371	500	14	41
		0	0	0	0	0	2	1	5	3	1				
Q640N1	Adipocyte enhancer-binding protein 1	4.647	7.535	3.394	2.601	1.861	0.041	0.000	0.043	0.039	0.103	1128	63	8	9
		0	0	0	0	0	0	0	2	3	3				
Q80VQ0	Aldehyde dehydrogenase family 3 member B1	4.793	3.198	4.118	2.415	1.596	0.024	0.008	0.004	0.014	0.094	468	104	4	35
		0	0	0	0	0	8	6	4	7	1				
P31324	cAMP-dependent protein kinase type II-beta regulatory subunit	2.891	2.281	2.992	2.238	1.583	0.254	0.157	0.046	0.044	0.145	416	314	7	26
		0	0	0	0	0	0	8	6	3	1				
Q922Q8	Leucine-rich repeat-containing protein 59	4.791	3.532	2.470	2.591	1.881	0.021	0.014	0.133	0.009	0.072	307	183	9	32
		0	0	0	0	0	8	4	4	9	3				
P52840	Sulfotransferase 1A1	5.702	2.988	2.683	2.458	1.578	0.006	0.014	0.060	0.013	0.074	291	8	2	12
		0	0	0	0	0	9	2	3	9	2				
Q91XV3	Brain acid soluble protein 1	5.494	3.073	2.668	2.940	1.698	0.009	0.023	0.080	0.005	0.066	226	230	6	39
		0	0	0	0	0	4	5	5	5	6				
P21995	Embiggin	4.060	4.500	2.774	3.341	1.956	0.070	0.008	0.115	0.010	0.107	330	17	3	9
		0	0	0	0	0	3	8	1	2	3				
Q8BPU7	Engulfment and cell motility protein 1	3.414	6.882	2.692	3.713	2.213	0.147	0.000	0.135	0.007	0.076	727	5	2	3
		0	0	0	0	0	6	7	4	0	2				
Q8BH C4	Dephospho-CoA kinase domain-containing protein	2.353	3.744	2.366	3.187	1.733	0.422	0.025	0.217	0.023	0.167	231	12	3	25
		0	0	0	0	0	3	3	4	5	1				
Q62318	Transcription intermediary factor 1-beta	3.616	2.973	2.057	2.751	1.787	0.114	0.044	0.291	0.024	0.104	834	86	7	16
		0	0	0	0	0	2	0	1	3	7				
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	3.617	2.539	1.906	2.292	1.628	0.098	0.042	0.280	0.024	0.064	114	150	7	79
		0	0	0	0	0	4	7	0	2	1				
P70429	Ena/VASP-like protein	6.311	3.002	2.736	3.752	2.207	0.012	0.080	0.142	0.010	0.071	414	49	6	16
		0	0	0	0	0	8	6	5	2	3				
Q9D8S3	ADP-ribosylation factor GTPase-activating protein 3	3.566	2.472	2.502	2.985	2.124	0.146	0.180	0.203	0.030	0.075	523	17	2	7
		0	0	0	0	0	9	3	9	4	1				
Q8R464	Cell adhesion molecule 4	3.365	1.871	2.284	2.711	1.528	0.169	0.377	0.242	0.034	0.254	388	7	2	6
		0	0	0	0	0	3	0	2	7	7				
P70313	Nitric oxide synthase, endothelial	3.163	1.892	2.718	2.662	1.659	0.162	0.182	0.059	0.007	0.065	1202	9	2	1
		0	0	0	0	0	8	8	3	7	3				
Q9DBE0	Cysteine sulfinic acid decarboxylase	3.143	1.659	2.637	2.710	1.699	0.178	0.380	0.074	0.006	0.050	493	289	15	48
		0	0	0	0	0	1	8	9	1	7				
P33434	72 kDa type IV collagenase	4.231	2.812	2.705	2.860	1.743	0.058	0.115	0.127	0.026	0.148	662	52	7	15
		0	0	0	0	0	7	6	1	6	3				
O08738	Caspase-6	3.588	2.569	2.523	2.938	2.226	0.131	0.155	0.199	0.045	0.069	276	27	5	15
		0	0	0	0	0	5	8	6	3	6				
P02798	Metallothionein-2	3.511	2.251	2.743	3.078	2.232	0.143	0.251	0.121	0.018	0.050	61	56	2	33
		0	0	0	0	0	1	7	8	7	2				
Q9QZD8	Mitochondrial dicarboxylate carrier	3.054	2.607	2.056	2.173	1.551	0.211	0.067	0.213	0.045	0.105	287	162	9	47
		0	0	0	0	0	2	3	7	0	5				
Q6ZPZ3	Zinc finger CCCH domain-containing protein 4	2.547	2.694	2.037	2.547	1.536	0.351	0.125	0.338	0.046	0.284	1304	21	2	3
		0	0	0	0	0	0	8	3	1	5				
Q9Z1Q5	Chloride intracellular channel protein 1	3.514	2.108	2.348	2.014	1.576	0.080	0.084	0.087	0.049	0.050	241	446	16	80
		0	0	0	0	0	3	3	2	5	4				
Q61545	RNA-binding protein EWS	3.336	2.372	2.740	2.206	1.712	0.139	0.073	0.070	0.029	0.082	655	143	4	8
		0	0	0	0	0	6	9	1	6	2				

O8879	Junctional adhesion molecule 2	3.395	3.079	2.761	2.865	2.214	0.166	0.074	0.138	0.046	0.066	300	30	2	3
	A	0	0	0	0	0	6	4	2	1	6				
Q6158	Insulin-like growth factor-binding protein 7	5.682	4.697	5.210	2.432	1.982	0.017	0.007	0.004	0.088	0.103	281	46	3	19
		0	0	0	0	0	7	9	5	7	8				
P29416	Beta-hexosaminidase subunit alpha	4.538	2.876	5.529	2.049	1.803	0.037	0.079	0.002	0.125	0.150	528	113	10	27
		0	0	0	0	0	6	9	0	4	5				
Q9WV80	Sorting nexin-1	3.159	2.636	3.270	1.609	1.935	0.194	0.081	0.029	0.269	0.061	522	99	7	16
		0	0	0	0	0	4	2	6	1	0				
Q91VS7	Microsomal glutathione S-transferase 1	3.269	1.918	2.986	1.542	1.612	0.130	0.166	0.035	0.182	0.062	155	141	8	66
		0	0	0	0	0	2	9	1	7	0				
Q8R5A0	N-lysine methyltransferase SMYD2	1.977	1.855	3.275	2.087	1.580	0.669	0.314	0.035	0.101	0.200	433	77	6	14
		0	0	0	0	0	9	1	3	0	9				
Q9CXR1	Dehydrogenase/reductase SDR family member 7	3.134	2.218	3.846	1.663	1.559	0.174	0.173	0.010	0.228	0.127	338	119	10	39
		0	0	0	0	0	4	9	6	3	2				
Q9R0Q9	Mannose-P-dolichol utilization defect 1 protein	3.678	2.221	3.358	1.932	1.675	0.094	0.255	0.044	0.175	0.183	247	38	3	14
		0	0	0	0	0	3	1	9	3	9				
Q9DBL7	Bifunctional coenzyme A synthase	2.667	2.055	2.982	2.031	1.694	0.307	0.189	0.047	0.071	0.111	563	48	6	19
		0	0	0	0	0	1	3	7	5	9				
D3Z6Q9	Bridging integrator 2	11.16	3.941	2.653		1.754	0.000	0.021	0.157		0.221	489	155	2	7
		10	0	0		0	7	3	2		0				
P01921	H-2 class II histocompatibility antigen, A-D beta chain	4.999	3.696	2.230	2.341	1.847	0.023	0.012	0.243	0.059	0.086	265	154	9	41
		0	0	0	0	0	7	5	9	9	4				
Q60766	Immunity-related GTPase family M protein 1	4.544	3.632	3.069	1.889	1.691	0.041	0.016	0.050	0.123	0.131	409	69	10	25
		0	0	0	0	0	5	2	7	4	1				
Q9CXY6	Interleukin enhancer-binding factor 2	3.851	2.992	2.528	1.865	1.671	0.077	0.030	0.107	0.094	0.107	390	146	10	33
		0	0	0	0	0	0	3	1	4	5				
P61290	Proteasome activator complex subunit 3	4.165	2.917	2.316	2.207	1.789	0.050	0.049	0.227	0.086	0.132	254	75	5	23
		0	0	0	0	0	4	9	4	4	9				
P01915	H-2 class II histocompatibility antigen, E-D beta chain	2.411	4.625	2.590	1.664	1.542	0.443	0.009	0.156	0.315	0.248	264	19	6	27
		0	0	0	0	0	0	2	6	6	8				
P47964	60S ribosomal protein L36	3.386	3.961	2.430	1.845	1.672	0.130	0.010	0.169	0.220	0.172	105	24	3	21
		0	0	0	0	0	8	9	8	7	5				
P50543	Protein S100-A11	3.772	1.765	2.946	2.070	1.471	0.061	0.192	0.021	0.036	0.048	98	417	6	72
		0	0	0	0	0	9	4	6	7	6				
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	3.345	2.222	1.996	1.882	1.494	0.071	0.026	0.120	0.045	0.044	379	1463	19	48
		0	0	0	0	0	8	4	9	0	5				
Q9WUM3	Coronin-1B	3.515	1.911	2.042	2.087	1.494	0.058	0.097	0.108	0.041	0.044	484	388	15	41
		0	0	0	0	0	9	6	6	4	4				
Q9WVA4	Transgelin-2	3.401	1.854	2.101	2.110	1.478	0.067	0.071	0.094	0.024	0.047	199	1225	17	81
		0	0	0	0	0	3	8	8	7	7				
P32020	Non-specific lipid-transfer protein	2.582	1.706	2.291	1.865	1.472	0.181	0.163	0.061	0.055	0.049	547	748	13	19
		0	0	0	0	0	2	9	5	0	0				
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	3.487	2.143	2.760	2.049	1.436	0.060	0.032	0.021	0.028	0.057	483	1826	29	73
		0	0	0	0	0	9	6	3	9	2				
Q9WTP6	Adenylate kinase 2, mitochondrial	2.703	1.676	2.596	1.867	1.405	0.155	0.166	0.030	0.046	0.065	239	1432	19	69
		0	0	0	0	0	9	8	8	5	7				
Q9CPW4	Actin-related protein 2/3 complex subunit 5	6.228	3.931	2.901	2.152	1.256	0.004	0.001	0.052	0.043	0.390	151	153	7	60
		0	0	0	0	0	9	9	7	1	6				
P15379	CD44 antigen	5.509	2.717	2.895	3.291	1.089	0.016	0.072	0.076	0.008	0.629	778	77	4	5
		0	0	0	0	0	8	2	5	2	4				
Q6GU68	Immunoglobulin superfamily containing leucine-rich repeat protein	4.687			2.944	1.076	0.035			0.034	0.688	428	55	6	23
		0			0	0	1			5	4				
P30681	High mobility group protein B2	3.271	2.454	2.260	2.160	1.435	0.150	0.089	0.182	0.032	0.201	210	82	5	17
		0	0	0	0	0	8	5	8	9	5				
P28063	Proteasome subunit beta type-8	3.364	1.692	2.600	2.257	1.406	0.127	0.307	0.072	0.023	0.131	276	197	11	46
		0	0	0	0	0	8	7	7	8	9				

P61979	Heterogeneous nuclear ribonucleoprotein K	2.925	1.968	2.138	1.845	1.451	0.118	0.052	0.087	0.049	0.053	463	1705	24	57
Q6Y7W8	GRB10-interacting GYF protein 2	3.887	1.746	2.687	3.115	1.478	0.102	0.383	0.111	0.015	0.238	1291	30	2	2
P11688	Integrin alpha-5	2.607	2.238	1.663	2.533	1.498	0.362	0.213	0.611	0.046	0.273	1053	70	4	4
Q9WV91	Prostaglandin F2 receptor negative regulator	2.429	1.982	1.655	2.294	1.158	0.376	0.139	0.502	0.019	0.338	879	131	11	18
P26645	Myristoylated alanine-rich C-kinase substrate	3.408	1.725	2.035	2.027	1.426	0.066	0.153	0.110	0.038	0.059	309	719	12	64
P70245	3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	2.031	2.554	2.150	4.886	1.465	0.625	0.161	0.323	0.000	0.316	230	17	3	25
P09055	Integrin beta-1	2.564	2.086	1.899	1.904	1.438	0.251	0.078	0.215	0.049	0.056	798	897	26	39
E9Q7G0	Nuclear mitotic apparatus protein 1	2.271	1.642	1.687	2.075	1.498	0.409	0.334	0.408	0.042	0.080	2094	315	30	20
Q9EST5	Acidic leucine-rich nuclear phosphoprotein 32 family member B	3.901	2.975	3.114	1.921	1.425	0.059	0.017	0.021	0.059	0.137	272	229	5	33
O54931	A-kinase anchor protein 2	3.997	1.844	4.489	2.148	1.238	0.084	0.347	0.006	0.081	0.481	893	44	5	9
Q8R422	CD109 antigen	3.194	1.776	7.080	1.966	1.189	0.188	0.480	0.000	0.150	0.568	1442	15	4	4
Q9D0B5	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 3	5.542	3.763	3.494		0.612	0.025	0.024	0.053		0.458	157	31	3	25
P18242	Cathepsin D	4.048	2.412	2.164	1.827	1.254	0.032	0.015	0.082	0.052	0.126	410	1082	12	42
P62962	Profilin-1	3.063	1.990	1.991	1.765	1.401	0.100	0.049	0.122	0.061	0.066	140	1512	11	77
P62889	60S ribosomal protein L30	2.679	5.114	2.294	1.963	1.158	0.297	0.001	0.191	0.117	0.421	115	110	6	54
P18760	Cofilin-1	3.557	2.437	2.351	1.635	1.419	0.056	0.016	0.053	0.128	0.061	166	1516	12	70
Q60972	Histone-binding protein RBBP4	3.161	2.354	1.959	1.612	1.253	0.131	0.048	0.254	0.136	0.232	425	440	9	67
P27773	Protein disulfide-isomerase A3	2.948	2.075	1.869	1.766	1.202	0.115	0.039	0.161	0.061	0.157	505	2006	33	71
Q61543	Golgi apparatus protein 1	2.800	2.144	1.773	1.530	1.121	0.138	0.032	0.201	0.117	0.222	1175	533	22	19
P09541	Myosin light chain 4	6.709	2.827	3.082	2.111	1.272	0.005	0.061	0.059	0.097	0.431	193	232	5	47
Q9D8Y0	EF-hand domain-containing protein D2	4.534	2.128	2.243	1.808	1.432	0.038	0.171	0.214	0.127	0.256	240	167	9	32
P63276	40S ribosomal protein S17	4.714	2.610	3.361	1.470	2.178	0.023	0.030	0.012	0.245	0.006	135	251	6	56
P62702	40S ribosomal protein S4, X isoform	2.801	2.297	3.020	0.827	1.509	0.138	0.047	0.012	0.926	0.041	263	575	23	68
P62245	40S ribosomal protein S15a	3.146	2.598	3.289	0.959	1.652	0.150	0.036	0.012	0.891	0.046	130	261	9	69
P14131	40S ribosomal protein S16	3.606	3.904	3.387	1.049	1.813	0.093	0.001	0.013	0.706	0.022	146	266	6	40
Q9D1R9	60S ribosomal protein L34	3.877	1.840	3.271	0.893	2.141	0.084	0.316	0.037	0.884	0.035	117	200	6	38
P62900	60S ribosomal protein L31	3.089	1.564	3.015	0.802	1.697	0.162	0.393	0.032	0.728	0.046	125	94	3	20
P62270	40S ribosomal protein S18	3.305	1.998	3.142	1.077	1.691	0.082	0.080	0.009	0.519	0.018	152	385	10	45

P01791	Ig heavy chain V region	5.771	10.06	2.153	1.166	2.692	0.018	0.000	0.287	0.723	0.014	123	36	3	49
	HPCM6	0	30	0	0	0	1	0	7	4	9				
Q91VC	Eukaryotic initiation factor 4A-	3.715	1.885	2.173	1.392	2.074	0.105	0.299	0.230	0.443	0.049	411	246	7	26
3	III	0	0	0	0	0	5	2	7	2	4				
P62908	40S ribosomal protein S3	2.890	1.889	2.381	0.913	1.533	0.123	0.065	0.050	0.635	0.037	243	873	21	80
		0	0	0	0	0	9	3	1	8	5				
Q99N9	39S ribosomal protein L27, mi-	2.103	1.706	2.435	0.772	2.740	0.591	0.440	0.172	0.624	0.013	148	21	4	38
2	tochondrial	0	0	0	0	0	4	7	0	9	3				
Q5FW	Rho GTPase-activating protein	3.922	2.177	2.543	1.348	1.801	0.058	0.146	0.102	0.369	0.047	439	229	12	42
K3	1	0	0	0	0	0	8	8	5	0	0				
Q6ZW	60S ribosomal protein L10	2.906	1.568	2.624	0.832	1.629	0.196	0.393	0.068	0.820	0.046	214	254	9	46
V3		0	0	0	0	0	7	0	9	3	8				
P70261	Paladin	2.660	2.054	2.977	1.230	3.045	0.305	0.324	0.092	0.596	0.017	859	6	2	4
		0	0	0	0	0	2	6	2	8	6				
Q9CPR	60S ribosomal protein L17	3.417	1.774	2.470	0.920	1.719	0.098	0.254	0.092	0.967	0.035	184	159	7	42
4		0	0	0	0	0	7	4	9	1	9				
P31725	Protein S100-A9	16.82	8.361	4.926	1.221	1.998	0.000	0.000	0.002	0.651	0.054	113	212	9	74
		90	0	0	0	0	0	0	8	5	4				
Q9JIK9	28S ribosomal protein S34, mi-	2.951	2.465	3.196	1.490	1.665	0.224	0.107	0.042	0.373	0.146	218	10	2	10
	tochondrial	0	0	0	0	0	1	1	0	4	5				
P12970	60S ribosomal protein L7a	3.378	2.119	3.424	0.641	1.544	0.118	0.084	0.011	0.403	0.071	266	251	13	42
		0	0	0	0	0	9	3	2	0	9				
Q6447	Glutathione S-transferase theta-	3.485	2.215	4.089	1.358	1.982	0.122	0.221	0.014	0.532	0.078	240	118	2	19
1	1	0	0	0	0	0	9	7	2	0	8				
P61255	60S ribosomal protein L26	3.788	3.019	2.580	0.723	1.570	0.085	0.031	0.096	0.466	0.105	145	138	7	43
		0	0	0	0	0	2	5	2	4	0				
Q9EPB	Apoptosis-associated speck-	3.486	4.794	2.715	0.810	1.672	0.118	0.001	0.077	0.602	0.127	193	121	10	66
4	like protein containing a	0	0	0	0	0	7	6	1	5	7				
	CARD														
Q9D0T	NHP2-like protein 1	4.215	4.740	2.927	1.429	1.551	0.065	0.002	0.068	0.443	0.218	128	107	5	62
1		0	0	0	0	0	6	1	9	3	5				
Q91W	Protein Dr1	3.068	5.659	2.361	1.363	1.555	0.206	0.002	0.225	0.475	0.278	176	5	2	18
V0		0	0	0	0	0	8	7	0	9	8				
Q6159	Rho GDP-dissociation inhibitor	4.514	3.114	2.734	1.385	1.387	0.028	0.006	0.044	0.293	0.142	200	311	12	66
9	2	0	0	0	0	0	3	7	8	7	4				
P0DO	Interferon-activable protein	7.513	5.672	4.681	0.938	1.138	0.006	0.002	0.013	0.977	0.632	425	32	2	18
V1	205-B	0	0	0	0	0	2	9	2	4	2				
P35979	60S ribosomal protein L12	4.102	2.727	2.856	0.729	1.490	0.042	0.024	0.043	0.521	0.099	165	192	7	59
		0	0	0	0	0	5	9	8	4	9				
Q9CZ	40S ribosomal protein S19	3.298	2.349	2.697	1.211	1.444	0.080	0.041	0.024	0.355	0.055	145	521	9	54
X8		0	0	0	0	0	7	7	6	1	2				
P47911	60S ribosomal protein L6	3.012	2.428	2.672	0.737	1.367	0.146	0.034	0.038	0.659	0.078	296	440	19	47
		0	0	0	0	0	1	3	2	3	7				
P63325	40S ribosomal protein S10	2.907	2.843	3.010	0.884	1.398	0.218	0.022	0.032	0.944	0.139	165	222	7	43
		0	0	0	0	0	7	2	4	7	5				
P97351	40S ribosomal protein S3a	2.714	1.889	2.501	0.899	1.360	0.169	0.145	0.038	0.838	0.079	264	668	18	59
		0	0	0	0	0	2	6	1	3	7				
P25444	40S ribosomal protein S2	2.878	1.511	2.629	0.869	1.104	0.162	0.337	0.032	0.991	0.238	293	535	16	53
		0	0	0	0	0	9	5	7	7	9				
P33622	Apolipoprotein C-III	2.167	1.924	3.184	1.308	1.299	0.550	0.248	0.041	0.467	0.279	99	139	2	27
		0	0	0	0	0	7	2	7	2	5				
P68254	14-3-3 protein theta	2.875	1.751	2.532	1.372	1.367	0.169	0.203	0.049	0.269	0.077	245	1548	11	70
		0	0	0	0	0	4	5	7	4	3				
Q8K2H	Deubiquitinase OTUD6B	2.068	1.642	4.200	1.346	1.261	0.624	0.467	0.012	0.481	0.465	294	24	3	17
2		0	0	0	0	0	4	7	0	3	2				
O5514	60S ribosomal protein L35a	1.908	1.783	2.746	1.171	1.418	0.606	0.199	0.035	0.471	0.062	110	189	6	45
2		0	0	0	0	0	3	3	7	9	1				

P62242	40S ribosomal protein S8	2.966	1.959	2.800	0.848	1.471	0.153	0.115	0.034	0.881	0.076	208	381	13	59
Q3V1T4	Prolyl 3-hydroxylase 1	7.024	4.119	2.324	0.753	1.204	0.007	0.015	0.253	0.670	0.532	739	60	5	9
P61514	60S ribosomal protein L37a	5.843	3.187	2.587	0.688	1.466	0.013	0.027	0.119	0.549	0.271	92	66	6	47
P97742	Carnitine O-palmitoyltransferase 1, liver isoform	2.026	3.541	1.915	0.724	1.067	0.654	0.036	0.446	0.631	0.716	773	82	5	13
Q9CR57	60S ribosomal protein L14	3.351	2.875	2.491	0.667	1.449	0.120	0.020	0.087	0.366	0.118	217	170	7	32
Q8CCFU0	small nuclear ribonucleoprotein Prp31	2.323	4.918	2.285	0.831	0.850	0.469	0.006	0.278	0.831	0.918	499	11	3	11
P21958	Antigen peptide transporter 1	1.980	4.304	1.633	1.046	1.340	0.676	0.005	0.651	0.834	0.421	724	17	5	10
Q99MD9	Nuclear autoantigenic sperm protein	3.121	3.911	2.608	1.497	1.217	0.205	0.025	0.175	0.402	0.526	773	10	2	5
P53026	60S ribosomal protein L10a	4.118	2.019	2.076	0.815	1.281	0.044	0.104	0.151	0.888	0.130	217	210	8	38
P56528	ADP-ribosyl cyclase/cyclic ADP-ribose hydrolase 1	13.19	6.010	2.289	0.641	0.574	0.000	0.000	0.260	0.459	0.400	304	11	2	8
P27005	Protein S100-A8	3.414	40.17	12.34	0.468	4.419	0.154	0.000	0.000	0.209	0.001	89	201	7	82
Q6ZWV7	60S ribosomal protein L35	3.488	1.752	3.145	0.535	1.670	0.112	0.267	0.025	0.160	0.045	123	120	4	28
Q9CZM2	60S ribosomal protein L15	3.094	3.065	2.754	0.569	1.812	0.165	0.019	0.054	0.179	0.032	204	244	11	43
P47963	60S ribosomal protein L13	3.365	2.516	3.644	0.564	1.550	0.115	0.039	0.010	0.184	0.078	211	146	7	35
Q8R3F5	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	3.354	2.014	2.733	0.091	0.173	0.156	0.367	0.147	0.000	0.000	381	63	2	6
Q9R0P6	Signal peptidase complex catalytic subunit SEC11A	1.599	2.437		0.406	0.257	0.968	0.155		0.094	0.015	179	10	3	26
Q6WKZ8	E3 ubiquitin-protein ligase UBR2	4.926	2.887		0.498	0.343	0.033	0.095		0.205	0.068	1755	9	2	1
P24668	Cation-dependent mannose-6-phosphate receptor	2.593	2.283	0.806	3.629	2.281	0.307	0.082	0.323	0.000	0.005	278	53	3	11
P01831	Thy-1 membrane glycoprotein	3.786	1.849	1.328	2.100	1.607	0.076	0.195	0.814	0.040	0.062	162	148	4	31
Q9DBR3	Armadillo repeat-containing protein 8	3.625	0.956		1.894		0.033	0.587		0.188		673	3	2	4
Q99LX8	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4	2.781	3.438	0.940	1.638	2.130	0.298	0.044	0.571	0.286	0.083	37	28	2	100
P21614	Vitamin D-binding protein	2.829	2.522	1.463	1.787	1.252	0.133	0.011	0.405	0.065	0.127	476	896	24	61
P47856	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	2.450	7.432	1.331	1.837	0.619	0.375	0.000	0.970	0.202	0.420	697	30	10	20
Q91VH2	Sorting nexin-9	1.963	3.020	1.348	1.803	0.010	0.672	0.076	0.863	0.253	0.000	595	3	3	7
P97369	Neutrophil cytosol factor 4	3.000	0.837		0.532		0.032	0.446		0.296		339	5	3	14
Q9JI91	Alpha-actinin-2	2.515	1.613	1.332	1.209	1.484	0.196	0.139	0.538	0.285	0.046	894	4531	47	79
Q8VDW0	ATP-dependent RNA helicase DDX39A	1.584	3.679	0.689	1.274	0.805	0.969	0.011	0.257	0.558	0.832	427	592	3	37

O7043 9	Syntaxin-7	2.013	2.776	1.382	1.220	0.954	0.408	0.021	0.706	0.609	0.857	261	74	7	30
		0	0	0	0	0	6	1	3	6	2				
P06800	Receptor-type tyrosine-protein phosphatase C	1.823	6.365	1.316	0.891	0.694	0.814	0.000	0.946	0.783	0.577	1293	125	24	28
		0	0	0	0	0	2	6	8	5	7				
Q3UN D0	Src kinase-associated phospho-protein 2	1.819	3.300	1.143	1.058	0.597	0.771	0.049	0.872	0.832	0.419	358	20	6	19
		0	0	0	0	0	4	4	0	9	9				
Q571E 4	N-acetylgalactosamine-6-sulfatase	4.059	3.473	1.257	0.494		0.093	0.040	0.978	0.235		520	25	4	10
		0	0	0	0		7	8	1	3					
E9QAT 4	Protein transport protein Sec16A	4.022	2.051	1.361	0.010	1.241	0.083	0.329	0.881	0.000	0.522	2357	23	2	1
		0	0	0	0	0	3	2	3	0	3				
Q6NV8 3	U2 snRNP-associated SURP motif-containing protein	1.746	4.335	1.194	0.555	0.757	0.784	0.012	0.910	0.283	0.727	1029	6	2	2
		0	0	0	0	0	0	7	0	2	2				
O3589 2	Nuclear autoantigen Sp-100	1.860	2.650	1.214	0.394	0.010	0.785	0.070	0.921	0.095	0.000	482	4	2	3
		0	0	0	0	0	2	2	7	3	0				
Q6229 3	T-cell-specific guanine nucleotide triphosphate-binding protein 1	13.50	3.069	0.840	0.595	0.470	0.000	0.072	0.396	0.403	0.204	415	29	9	36
		40	0	0	0	0	1	4	1	0	3				
P56542	Deoxyribonuclease-2-alpha	1.950	4.945	0.460	0.776	1.051	0.698	0.001	0.072	0.719	0.753	353	8	2	4
		0	0	0	0	0	3	7	6	7	5				
Q3UR D3	Sarcolemmal membrane-associated protein	4.272	1.462	3.719	2.733	2.177	0.044	0.512	0.008	0.006	0.007	845	32	6	10
		0	0	0	0	0	1	9	5	2	5				
Q8CG N5	Perilipin-1	3.419	1.380	4.225	2.765	2.274	0.065	0.448	0.001	0.002	0.001	517	1444	30	71
		0	0	0	0	0	9	7	0	9	6				
Q8R0Y 6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	3.402	1.470	3.459	2.482	1.921	0.067	0.351	0.004	0.013	0.006	902	1412	44	68
		0	0	0	0	0	2	1	7	5	9				
P04117	Fatty acid-binding protein, adipocyte	2.949	1.453	2.598	2.208	1.760	0.115	0.217	0.030	0.019	0.013	132	7545	8	65
		0	0	0	0	0	3	1	6	2	9				
Q6NZ B0	DnaJ homolog subfamily C member 8	2.870	1.393	2.318	1.898	1.606	0.181	0.473	0.081	0.044	0.027	253	119	7	23
		0	0	0	0	0	1	1	7	2	1				
Q9WV L0	Maleylacetoacetate isomerase	2.852	1.252	2.932	1.898	1.620	0.129	0.590	0.014	0.064	0.025	216	956	14	82
		0	0	0	0	0	8	2	6	6	5				
Q0542 1	Cytochrome P450 2E1	2.829	1.393	3.139	1.629	1.953	0.289	0.704	0.029	0.239	0.033	493	100	15	44
		0	0	0	0	0	2	6	7	5	5				
P52196	Thiosulfate sulfurtransferase	2.349	1.248	2.210	1.931	1.539	0.268	0.594	0.073	0.057	0.036	297	640	11	44
		0	0	0	0	0	1	2	9	3	5				
P50462	Cysteine and glycine-rich protein 3	2.326	0.790	1.706	1.669	1.787	0.336	0.442	0.339	0.117	0.011	194	395	9	62
		0	0	0	0	0	2	4	7	6	7				
O5502 8	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial		1.017	1.552	2.530	2.957		0.631	0.733	0.068	0.018	412	28	4	17
			0	0	0	0		1	8	9	4				
Q8R05 9	UDP-glucose 4-epimerase	2.381	1.420	2.102	2.702	1.597	0.418	0.680	0.270	0.019	0.162	347	79	6	27
		0	0	0	0	0	1	3	0	6	2				
P50285	Dimethylaniline monooxygenase [N-oxide-forming] 1	2.565	1.381	2.764	1.656	1.580	0.280	0.599	0.039	0.119	0.062	532	413	18	41
		0	0	0	0	0	0	0	9	3	0				
Q9Z1T 2	Thrombospondin-4	2.810	1.409	2.124	1.739	1.490	0.136	0.253	0.090	0.066	0.045	963	1230	23	37
		0	0	0	0	0	6	0	0	2	2				
Q66K0 8	Cartilage intermediate layer protein 1	4.024	1.282	1.716	2.427	1.161	0.050	0.614	0.381	0.014	0.267	1184	300	15	15
		0	0	0	0	0	5	4	6	7	8				
Q91V7 6	Ester hydrolase C11orf54 homolog	2.834	1.381	2.111	1.976	1.389	0.132	0.353	0.092	0.029	0.070	315	417	14	70
		0	0	0	0	0	7	5	8	5	3				
P99024	Tubulin beta-5 chain	3.292	1.366	2.530	1.299	1.666	0.076	0.275	0.035	0.222	0.020	444	1511	4	73
		0	0	0	0	0	5	3	7	4	9				
O5472 4	Caveolae-associated protein 1	2.789	1.440	2.671	1.342	1.503	0.140	0.233	0.026	0.241	0.042	392	1107	15	42
		0	0	0	0	0	3	5	0	4	7				
Q0592 0	Pyruvate carboxylase, mitochondrial	2.319	1.211	2.544	1.156	1.528	0.265	0.567	0.034	0.431	0.038	1178	1055	46	54
		0	0	0	0	0	2	6	6	9	4				
Q6391 8	Caveolae-associated protein 2	2.218	1.223	2.465	1.424	1.561	0.308	0.630	0.041	0.202	0.033	418	542	11	33
		0	0	0	0	0	8	2	3	0	2				

P17225	Polypyrimidine tract-binding protein 1	3.634	1.399	2.200	1.474	1.564	0.068	0.458	0.113	0.204	0.032	527	365	9	39
O3567	Monoglyceride lipase	2.224	1.168	2.538	1.165	1.354	0.369	0.697	0.035	0.411	0.081	303	708	15	67
Q6071	Long-chain fatty acid transport protein 1	1.858	1.329	2.600	1.153	1.339	0.677	0.560	0.049	0.510	0.115	646	319	21	45
Q9CQ	Endoplasmic reticulum-Golgi intermediate compartment protein 3	2.025	1.474	5.720	1.123	1.032	0.656	0.621	0.000	0.763	0.718	383	5	2	4
P68369	Tubulin alpha-1A chain	2.813	1.425	2.383	1.102	1.416	0.136	0.320	0.049	0.482	0.062	451	1279	6	69
P62862	40S ribosomal protein S30	2.368	0.805	1.154	2.721	2.139	0.449	0.336	0.842	0.042	0.064	59	9	2	19
Q9D0L	mRNA cap guanine-N7 methyltransferase	1.915	1.130	0.658	3.056	0.791	0.709	0.957	0.142	0.014	0.771	465	19	3	10
P02535	Keratin, type I cytoskeletal 10	5.114	1.151	0.779	1.676	0.745	0.024	0.955	0.295	0.197	0.675	570	29	3	8
P70444	BH3-interacting domain death agonist	2.244	0.896	1.042	1.145	0.323	0.505	0.577	0.664	0.770	0.019	195	5	3	19
P41241	Tyrosine-protein kinase CSK	1.835	1.335	1.298	0.404	0.258	0.792	0.827	0.996	0.135	0.010	450	12	7	24
O5478	Epididymis-specific alpha-mannosidase	1.758	0.779	1.396	0.398	0.010	0.859	0.357	0.864	0.106	0.000	1018	4	2	3
Q9Z2V	Phosphoenolpyruvate carbox-kinase, cytosolic [GTP]		1.493	0.888	0.520	0.341		0.709	0.456	0.209	0.041	622	12	3	8
Q8BQ3	Phostensin	2.875	1.195	0.357	0.509	0.624	0.253	0.931	0.016	0.254	0.496	594	9	2	4
P16460	Argininosuccinate synthase		0.067	0.013	0.010	0.011		0.000	0.000	0.000	0.000	412	18	7	18
Q6168	Chromobox protein homolog 5	0.854		1.565	3.064	1.186	0.239		0.673	0.018	0.563	191	19	3	27
P97494	Glutamate--cysteine ligase catalytic subunit	1.330	3.514	2.539	2.012	1.469	0.722	0.014	0.145	0.119	0.271	637	24	4	8
O8887	Apoptotic protease-activating factor 1	1.465	11.70	1.681	0.010	0.967	0.931	0.000	0.605	0.000	0.921	1249	4	2	2
Q0132	DNA topoisomerase 2-alpha	1.271	3.658	1.762	0.010	0.010	0.771	0.032	0.507	0.000	0.000	1528	4	2	1
O3564	Annexin A8	0.648			0.549	0.237	0.104			0.293	0.007	327	3	3	10
O7014	Neutrophil cytosol factor 2	1.169	10.96	0.826	1.251		0.656	0.000	0.413	0.572		525	21	5	13
P35175	Stefin-1	1.177	27.65	1.285	1.497	1.364	0.633	0.000	0.990	0.396	0.377	97	31	3	40
Q8K42	Resistin-like gamma	1.215	13.86	1.191	0.810	1.357	0.710	0.000	0.959	0.798	0.403	117	10	2	23
Q99KV	DnaJ homolog subfamily B member 11	1.249	2.660	1.081	0.691	0.010	0.749	0.114	0.772	0.540	0.000	358	3	2	11
Q3THE	Myosin regulatory light chain 12B	1.163	4.756	1.114	0.682	0.528	0.613	0.002	0.754	0.561	0.293	172	7	2	12
P48025	Tyrosine-protein kinase SYK	0.768	2.305	0.663	0.435	0.271	0.219	0.187	0.200	0.150	0.010	629	13	5	12
O0904	Napsin-A	0.641	5.755	1.141	0.489	0.453	0.129	0.000	0.892	0.209	0.185	419	18	5	28
Q6154	Adhesion G protein-coupled receptor E1	1.215	12.24	0.010	1.754	0.010	0.663	0.000	0.000	0.258	0.000	931	4	2	4
P10810	Monocyte differentiation antigen CD14	1.340	8.574	0.532	0.742	0.756	0.794	0.000	0.105	0.651	0.726	366	37	9	38

Q8BT V2	Cleavage and polyadenylation specificity factor subunit 7	0.922	1.647	0.010	0.519	0.726	0.358	0.619	0.000	0.280	0.693	471	22	2	7
		0	0	0	0	0	9	7	0	6	1				
P28293	Cathepsin G	0.643	2.341	0.348	0.321	0.315	0.126	0.124	0.013	0.054	0.036	261	22	7	30
		0	0	0	0	0	5	3	2	4	8				
O7045 6	14-3-3 protein sigma	0.892	1.084	1.818	0.189	0.067	0.267	0.955	0.332	0.000	0.000	248	524	3	32
		0	0	0	0	0	6	3	2	1	0				
Q6P9Q 6	FK506-binding protein 15	0.707	0.856	1.571	0.305	0.536	0.104	0.488	0.706	0.007	0.254	1216	16	3	3
		0	0	0	0	0	9	3	5	6	0				
Q9CQ N6	Transmembrane protein 14C	0.826	0.861	0.981	0.358	0.851	0.174	0.514	0.558	0.043	0.912	114	95	5	75
		0	0	0	0	0	4	7	5	4	7				
Q9CQ G1	Putative glutathione-specific gamma-glutamylcyclotransferase 2	1.291	0.736	0.879	0.584	0.318	0.724	0.283	0.469	0.367	0.026	178	5	2	11
		0	0	0	0	0	1	3	7	7	0				
Q9WV G6	Histone-arginine methyltransferase CARM1	0.731	0.846	0.660	0.450	0.216	0.143	0.492	0.154	0.119	0.001	608	11	2	4
		0	0	0	0	0	1	7	9	9	9				
P01820	Ig heavy chain V region PJ14	0.716	0.744	0.904	0.366	0.548	0.143	0.337	0.438	0.048	0.273	115	26	2	28
		0	0	0	0	0	8	0	4	2	3				
Q8JZS 9	39S ribosomal protein L48, mitochondrial	0.906	0.701	0.835	0.327	0.389	0.270	0.272	0.353	0.011	0.053	211	17	3	23
		0	0	0	0	0	1	0	3	3	5				
P97825	Jupiter microtubule associated homolog 1	1.374	0.969	0.901	0.283	0.448	0.771	0.683	0.450	0.004	0.115	154	42	3	38
		0	0	0	0	0	9	9	0	2	9				
Q8BFQ 4	WD repeat-containing protein 82	0.789	0.605	0.997	0.392	0.421	0.165	0.161	0.607	0.031	0.084	313	26	3	9
		0	0	0	0	0	8	9	9	9	0				
Q3UIU 2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	1.044	0.645	0.915	0.419	0.597	0.403	0.214	0.487	0.045	0.380	128	136	3	25
		0	0	0	0	0	2	8	3	4	7				
Q921L 3	Calcium load-activated calcium channel	0.707	0.748	0.694	0.261	0.375	0.156	0.332	0.200	0.016	0.064	188	8	2	15
		0	0	0	0	0	0	0	9	5	6				
Q6P9J9	Anoctamin-6	1.262	1.002	0.010	2.080	0.720	0.717	0.635	0.000	0.154	0.658	911	3	2	6
		0	0	0	0	0	1	5	0	6	6				
Q9JK3 8	Glucosamine 6-phosphate N-acetyltransferase	0.839	0.722	0.315	0.869	0.804	0.278	0.289	0.007	0.884	0.827	184	20	3	41
		0	0	0	0	0	9	9	2	9	5				
P50428	Arylsulfatase A	0.967	0.643	0.465	0.731	0.667	0.320	0.201	0.028	0.516	0.503	506	18	4	14
		0	0	0	0	0	9	3	0	0	2				
Q9QX K3	Coatomer subunit gamma-2	0.693	0.711	0.010	0.705	0.010	0.310	0.670	0.000	0.942	0.000	871	46	2	6
		0	0	0	0	0	7	2	0	1	0				
Q3TTY 5	Keratin, type II cytoskeletal 2 epidermal	0.986	0.617	0.333	1.216	0.230	0.410	0.160	0.010	0.653	0.005	707	17	4	6
		0	0	0	0	0	4	8	6	4	0				
P00687	Alpha-amylase 1	1.287	1.187	0.421	0.657	0.392	0.742	0.968	0.036	0.503	0.096	511	3	2	5
		0	0	0	0	0	2	0	5	1	8				
Q8K1X 4	Nck-associated protein 1-like	1.060	1.322	0.011	0.010	0.717	0.450	0.829	0.000	0.000	0.607	1134	13	3	5
		0	0	0	0	0	3	1	0	0	9				
P48999	Arachidonate 5-lipoxygenase	0.647	1.042	0.400	0.337	0.846	0.127	0.720	0.030	0.073	0.907	674	7	4	6
		0	0	0	0	0	1	7	8	9	3				
P18528	Ig heavy chain V region 6.96	0.666	0.740	0.338	0.507	0.819	0.069	0.313	0.004	0.130	0.852	98	38	2	42
		0	0	0	0	0	3	8	7	0	7				
Q91Z8 3	Myosin-7	0.803	0.632	0.478	0.188	0.277	0.181	0.194	0.036	0.000	0.006	1935	516	3	15
		0	0	0	0	0	6	1	6	2	5				
Q6064 8	Ganglioside GM2 activator	0.730	0.789	0.551	0.376	0.267	0.115	0.411	0.065	0.030	0.007	193	11	2	16
		0	0	0	0	0	6	4	8	4	3				
Q9JHK 5	Pleckstrin	1.014	1.197	0.293	0.427	0.331	0.374	0.982	0.001	0.054	0.021	350	29	5	26
		0	0	0	0	0	3	8	4	4	7				
O0869 2	Neutrophilic granule protein	0.853	1.391	0.592	0.410	0.315	0.279	0.475	0.122	0.078	0.016	167	96	11	60
		0	0	0	0	0	7	6	5	6	4				
Q9CY4 5	EEF1A lysine methyltransferase 1	0.849	0.655	0.552	0.495	0.255	0.271	0.224	0.090	0.230	0.006	214	6	2	15
		0	0	0	0	0	1	4	9	9	8				
Q9WV 60	Glycogen synthase kinase-3 beta	0.799	0.607	0.577	0.444	0.361	0.176	0.177	0.085	0.052	0.036	420	135	4	24
		0	0	0	0	0	2	1	2	5	7				

Q9D71 5	Phospholysine phosphohisti- dine inorganic pyrophosphate phosphatase	0.610	0.613	0.592	0.403	0.363	0.087	0.180	0.119	0.078	0.043	270	369	10	62
		0	0	0	0	0	9	8	9	9	0				
Q6071 6	Prolyl 4-hydroxylase subunit alpha-2	0.849	0.890	0.571	0.530	0.350	0.184	0.530	0.097	0.206	0.038	537	9	5	12
		0	0	0	0	0	7	9	5	3	6				
Q69Z2 3	Dynein heavy chain 17, ax- onemal	1.034	0.674	0.594	0.405	0.403	0.402	0.258	0.106	0.030	0.062	4481	107	2	0
		0	0	0	0	0	9	4	3	4	4				
P63300	Selenoprotein W	0.714	0.778	0.508	0.473	0.406	0.113	0.365	0.048	0.084	0.070	88	115	3	50
		0	0	0	0	0	5	8	8	3	2				
P13542	Myosin-8	0.704	0.640	0.471	0.459	0.387	0.130	0.206	0.031	0.104	0.054	1937	1448	3	31
		0	0	0	0	0	1	1	9	0	8				
Q0809 3	Calponin-2	0.917	0.940	0.488	0.492	0.446	0.260	0.701	0.035	0.137	0.109	305	32	4	22
		0	0	0	0	0	7	7	3	1	4				
P70158	Acid sphingomyelinase-like phosphodiesterase 3a	0.904	0.813	0.462	0.539	0.498	0.301	0.492	0.029	0.216	0.222	445	56	5	22
		0	0	0	0	0	2	5	2	8	5				
Q91ZR 1	Ras-related protein Rab-4B	1.298	0.730	0.351	0.568	0.574	0.696	0.334	0.008	0.278	0.319	213	3	2	11
		0	0	0	0	0	1	7	4	1	4				
P01723	Ig lambda-1 chain V region	0.740	0.838	0.488	0.581	0.572	0.142	0.531	0.039	0.298	0.407	117	26	3	42
		0	0	0	0	0	3	4	9	3	3				
P48772	Cytochrome c oxidase subunit 8B, mitochondrial	0.753	0.267	0.718	0.299	0.480	0.224	0.000	0.324	0.011	0.247	70	366	3	56
		0	0	0	0	0	9	6	6	0	9				
O0860 0	Endonuclease G, mitochondrial	0.782	0.550	0.804	0.360	0.527	0.192	0.107	0.364	0.027	0.294	294	261	10	36
		0	0	0	0	0	0	4	5	8	9				
Q8C0L 9	Glycerophosphocholine phos- phodiesterase GPCPD1	0.648	0.464	1.067	0.503	0.421	0.077	0.040	0.715	0.104	0.094	675	12	4	8
		0	0	0	0	0	2	9	7	8	7				
Q9R0G 6	Cartilage oligomeric matrix protein	0.699	0.428	0.633	0.425	0.452	0.169	0.049	0.200	0.114	0.202	755	449	17	35
		0	0	0	0	0	5	2	0	3	4				
P51912	Neutral amino acid transporter B(0)	0.862	0.443	1.065	0.355	0.388	0.262	0.036	0.703	0.068	0.084	553	16	4	16
		0	0	0	0	0	0	3	2	3	1				
Q8BL Y2	Threonine--tRNA ligase 2, cy- toplasmic	0.910	0.413	0.976	0.516	0.580	0.265	0.024	0.573	0.118	0.334	790	101	6	11
		0	0	0	0	0	0	8	6	3	7				
Q9EPU 0	Regulator of nonsense tran- scripts 1	1.004	0.435	0.475	0.795	0.660	0.374	0.035	0.034	0.660	0.533	1124	67	8	10
		0	0	0	0	0	7	2	1	0	8				
P0C0A 3	Charged multivesicular body protein 6	0.789	0.522	0.405	0.759	0.620	0.158	0.068	0.013	0.532	0.411	200	7	3	18
		0	0	0	0	0	8	5	4	1	2				
Q69ZS 7	HBS1-like protein	0.826	0.501	0.036	0.738	0.598	0.204	0.073	0.000	0.528	0.382	682	11	2	4
		0	0	0	0	0	7	2	0	4	5				
P01654	Ig kappa chain V-III region PC 2880/PC 1229	0.710	0.514	0.394	0.226	0.305	0.098	0.052	0.007	0.000	0.007	111	87	4	63
		0	0	0	0	0	6	9	5	6	1				
Q3V0K 9	Plastin-1	0.766	0.417	0.526	0.441	0.251	0.154	0.024	0.056	0.049	0.003	630	159	2	16
		0	0	0	0	0	4	0	4	7	3				
Q8R0 W0	Epiplakin	0.693	0.431	0.421	0.481	0.387	0.098	0.018	0.013	0.118	0.044	6548	215	2	4
		0	0	0	0	0	8	3	8	9	1				
Q8BMJ 3	Eukaryotic translation initiation factor 1A, X-chromosomal	0.756	0.356	0.513	0.590	0.324	0.138	0.005	0.044	0.296	0.013	144	76	5	36
		0	0	0	0	0	0	8	2	0	1				
E9Q55 5	E3 ubiquitin-protein ligase RNF213	0.773	0.588	0.419	0.469	0.175	0.182	0.137	0.015	0.128	0.000	5152	29	3	1
		0	0	0	0	0	4	7	1	8	3				
Q9D0 M5	Dynein light chain 2, cytoplas- mic	0.711	0.555	0.492	0.434	0.325	0.105	0.103	0.037	0.070	0.015	89	605	2	79
		0	0	0	0	0	5	5	1	4	1				
Q9QX Z0	Microtubule-actin cross-linking factor 1	0.613	0.504	0.476	0.368	0.225	0.064	0.090	0.035	0.061	0.002	7354	37	8	2
		0	0	0	0	0	4	7	8	2	5				
Q91V W3	SH3 domain-binding glutamic acid-rich-like protein 3	0.643	0.501	0.250	0.494	0.334	0.075	0.051	0.000	0.146	0.019	93	81	4	68
		0	0	0	0	0	6	6	2	9	7				
P52760	2-iminobutanoate/2-iminopro- panoate deaminase	0.602	0.545	0.566	0.423	0.383	0.043	0.087	0.083	0.061	0.045	135	67	6	54
		0	0	0	0	0	4	3	6	5	1				
Q80VJ 3	2'-deoxynucleoside 5'-phos- phate N-hydrolase 1	0.616	0.545	0.525	0.391	0.362	0.056	0.110	0.055	0.059	0.042	173	47	3	25
		0	0	0	0	0	8	0	8	3	1				

Q5SX3 9	Myosin-4	0.634	0.596	0.550	0.361	0.337	0.240	0.403	0.151	0.135	0.037	1939	2260	24	54
		0	0	0	0	0	4	6	8	9	5				
Q9JM9 9	Proteoglycan 4	0.634	0.388	0.599	0.244	0.512	0.078	0.014	0.099	0.000	0.200	1054	70	7	22
		0	0	0	0	0	4	1	5	5	8				
Q925I1	ATPase family AAA domain- containing protein 3	0.607	0.551	0.520	0.288	0.430	0.108	0.093	0.109	0.020	0.157	591	10	2	4
		0	0	0	0	0	2	2	8	7	8				
P21956	Lactadherin	1.026	0.533	0.536	0.330	0.484	0.385	0.112	0.076	0.049	0.170	463	5	3	6
		0	0	0	0	0	7	9	1	7	9				
Q8R55 0	SH3 domain-containing kinase- binding protein 1	0.745	0.599	0.460	0.455	0.399	0.121	0.139	0.019	0.093	0.051	709	81	6	11
		0	0	0	0	0	7	0	9	0	4				
Q91W G0	Acylcarnitine hydrolase	0.642	0.506	0.349	0.449	0.441	0.249	0.224	0.013	0.304	0.180	561	36	9	26
		0	0	0	0	0	6	5	0	3	5				
Q9CQ8 6	Migration and invasion en- hancer 1	0.869	0.509	0.471	0.506	0.453	0.226	0.067	0.032	0.103	0.135	115	21	4	38
		0	0	0	0	0	8	5	6	7	1				
Q9D2 M8	Ubiquitin-conjugating enzyme E2 variant 2	0.782	0.586	0.515	0.482	0.551	0.154	0.125	0.041	0.120	0.320	145	424	3	61
		0	0	0	0	0	4	2	8	7	6				
Q91W5 9	RNA-binding motif, single- stranded-interacting protein 1	0.702	0.459	0.573	0.430	0.489	0.088	0.047	0.082	0.081	0.179	403	5	3	8
		0	0	0	0	0	3	2	0	6	6				
P30355	Arachidonate 5-lipoxygenase- activating protein	0.489	2.832	1.967	2.231	1.061	0.028	0.098	0.411	0.114	0.739	161	26	5	58
		0	0	0	0	0	5	0	3	1	5				
P83870	PHD finger-like domain-con- taining protein 5A	0.489	1.763	1.713	1.022	0.598	0.030	0.476	0.583	0.878	0.411	110	11	3	23
		0	0	0	0	0	5	7	6	4	3				
P51437	Cathelicidin antimicrobial pep- tide	0.541	16.32	1.837	0.535	0.591	0.046	0.000	0.461	0.246	0.351	172	14	3	25
		0	50	0	0	0	4	0	7	5	3				
Q8VCI 0	Phospholipase B-like 1	0.583	2.191	0.593	0.581	0.387	0.034	0.179	0.088	0.258	0.061	550	79	18	43
		0	0	0	0	0	7	4	4	9	5				
Q921E 2	Ras-related protein Rab-31	0.562	0.637		0.281		0.063	0.202		0.023		194	36	2	24
		0	0		0		5	9		1					
Q3UQ S2	Leucine-rich single-pass mem- brane protein 1	0.167	0.899	0.630	0.681	0.479	0.000	0.579	0.137	0.376	0.155	128	13	2	17
		0	0	0	0	0	0	4	8	3	5				
Q9Z1T 1	AP-3 complex subunit beta-1	0.433	0.949	0.674	0.596	0.642	0.007	0.766	0.187	0.309	0.559	1105	40	6	8
		0	0	0	0	0	6	0	3	7	4				
Q99L2 0	Glutathione S-transferase theta- 3	0.509	0.751	0.708	0.244	0.248	0.021	0.351	0.199	0.009	0.005	241	18	2	24
		0	0	0	0	0	6	6	3	4	2				
Q7TSC 1	Protein PRRC2A	0.439	0.627	0.653	0.179	0.233	0.030	0.150	0.203	0.001	0.011	2158	9	2	2
		0	0	0	0	0	7	3	7	2	1				
Q7TN V0	Protein DEK	0.500	0.715	0.689	0.385	0.360	0.030	0.336	0.235	0.056	0.042	380	39	2	7
		0	0	0	0	0	6	2	1	5	0				
Q5I2A 0	Serine protease inhibitor A3G	0.591	1.431	0.636	0.314	0.433	0.086	0.776	0.181	0.041	0.141	440	363	2	12
		0	0	0	0	0	7	6	6	8	0				
Q8R4E 4	Myozenin-3	0.563	0.713	0.626	0.438	0.460	0.049	0.306	0.136	0.075	0.160	245	163	8	40
		0	0	0	0	0	7	0	9	8	9				
Q80W2 1	Glutathione S-transferase Mu 7	0.486	0.600	0.772	0.461	0.488	0.037	0.177	0.308	0.151	0.176	218	1194	2	51
		0	0	0	0	0	1	1	0	2	6				
Q9QZ Q8	Core histone macro-H2A.1	0.339	0.643	0.954	0.412	0.464	0.003	0.178	0.519	0.070	0.148	372	10	2	5
		0	0	0	0	0	6	5	4	8	8				
Q9R09 9	Transducin beta-like protein 2	0.345	1.094	0.193			0.009	0.765	0.000			442	4	2	4
		0	0	0			4	3	4						
Q8R5F 7	Interferon-induced helicase C domain-containing protein 1	0.476	0.689	0.200	0.140	0.232	0.026	0.282	0.000	0.000	0.003	1025	12	2	2
		0	0	0	0	0	3	0	1	2	3				
Q8BFY 6	Peflin	0.530	0.737	0.492	0.366	0.212	0.030	0.331	0.038	0.019	0.000	275	25	3	12
		0	0	0	0	0	8	2	9	0	9				
P18181	CD48 antigen	0.449	1.138	0.411	0.213	0.240	0.021	0.882	0.031	0.005	0.006	240	5	2	7
		0	0	0	0	0	0	1	6	6	8				
O7020 0	Allograft inflammatory factor 1	0.504	0.646	0.530	0.296	0.201	0.024	0.215	0.061	0.007	0.000	147	8	2	14
		0	0	0	0	0	3	9	9	0	5				
P00375	Dihydrofolate reductase	0.577	0.938	0.494	0.468	0.362	0.040	0.648	0.039	0.084	0.040	187	7	2	14
		0	0	0	0	0	6	1	3	1	0				

Q8BHJ	F-box-like/WD repeat-contain-	0.594	0.803	0.337	0.360	0.329	0.057	0.422	0.004	0.055	0.027	514	9	3	5
5	ing protein TBL1XR1	0	0	0	0	0	1	1	2	5	0				
A2VD	Leucine-rich repeat-containing	0.010	0.938	0.594	0.529	0.010	0.000	0.536	0.162	0.310	0.000	298	4	2	9
H3	protein 38	0	0	0	0	0	0	8	0	4	0				
Q6428	Interferon-induced protein with	0.574	0.993	0.524	0.323	0.530	0.079	0.711	0.076	0.045	0.246	463	7	5	12
2	tetratricopeptide repeats 1	0	0	0	0	0	7	6	9	3	9				
A2A86	Integrin beta-4	0.065	0.092		0.024		0.000	0.000		0.000		1818	6	3	2
3		0	0		0		0	0		0					
Q80XN	D-beta-hydroxybutyrate dehy-	0.494	0.449	0.626	0.409	0.293	0.024	0.037	0.137	0.032	0.007	343	22	5	15
0	drogenase, mitochondrial	0	0	0	0	0	0	8	7	8	4				
P01636	Ig kappa chain V-V region	0.283	0.532	0.724	0.249	0.292	0.002	0.109	0.219	0.014	0.014	108	10	2	26
	MOPC 149	0	0	0	0	0	0	3	1	0	3				
Q8CHS	Dehydrogenase/reductase SDR	0.488	0.523	0.694	0.368	0.345	0.040	0.136	0.291	0.051	0.043	311	361	16	61
7	family member 7C	0	0	0	0	0	8	5	8	3	5				
P10922	Histone H1.0	0.417	0.290	0.643	0.264	0.441	0.007	0.000	0.155	0.002	0.118	194	181	5	28
		0	0	0	0	0	1	9	7	9	6				
Q8R1Q	Angiopoietin-related protein 7	0.598	0.451	0.793	0.010	0.572	0.105	0.037	0.358	0.000	0.366	337	3	2	5
3		0	0	0	0	0	4	6	1	0	0				
Q9R02	Zinc finger Ran-binding do-	0.432	0.366	0.686	0.573	0.458	0.029	0.010	0.238	0.341	0.205	330	2	2	6
0	main-containing protein 2	0	0	0	0	0	8	7	9	2	2				
Q0901	Neutrophil cytosol factor 1	0.408	0.500	0.611	0.410	0.538	0.005	0.066	0.123	0.055	0.299	390	26	9	19
4		0	0	0	0	0	8	2	0	8	8				
Q8VE	Mitochondrial intermembrane	0.541	0.518	0.458	0.678	0.515	0.040	0.061	0.028	0.472	0.208	139	70	4	42
A4	space import and assembly pro-	0	0	0	0	0	8	9	9	5	6				
	tein 40														
P68134	Actin, alpha skeletal muscle	0.364	0.339	0.245	0.219	0.266	0.030	0.031	0.001	0.010	0.006	377	12040	8	89
		0	0	0	0	0	4	8	0	7	3				
Q5ND3	WD repeat-containing protein	0.434	0.469	0.368	0.378	0.210	0.012	0.041	0.006	0.039	0.000	1934	19	2	1
4	81	0	0	0	0	0	4	0	0	3	4				
P09542	Myosin light chain 3	0.181	0.171	0.173	0.153	0.326	0.000	0.000	0.000	0.000	0.029	204	1136	10	70
		0	0	0	0	0	6	2	0	9	6				
P61458	Pterin-4-alpha-carbinolamine	0.010	0.010	0.010	0.010	0.010	0.000	0.000	0.000	0.000	0.000	104	32	3	32
	dehydratase	0	0	0	0	0	0	0	0	0	0				
Q99K	T-cell immunomodulatory pro-	0.273	0.237	0.212	0.183	0.143	0.000	0.000	0.000	0.000	0.000	610	3	2	8
W9	tein	0	0	0	0	0	4	7	1	4	0				
P01639	Ig kappa chain V-V region	0.424	0.421	0.279	0.167	0.133	0.009	0.030	0.001	0.000	0.000	130	5	2	28
	MOPC 41	0	0	0	0	0	1	6	3	1	0				
P58771	Tropomyosin alpha-1 chain	0.306	0.253	0.184	0.213	0.256	0.013	0.004	0.000	0.009	0.004	284	4093	13	68
		0	0	0	0	0	2	8	1	1	5				
Q6411	Interferon-induced protein with	0.177	0.433	0.108	0.059	0.125	0.000	0.034	0.000	0.000	0.000	472	13	6	17
2	tetratricopeptide repeats 2	0	0	0	0	0	0	9	0	0	0				
P21107	Tropomyosin alpha-3 chain	0.390	0.312	0.298	0.281	0.314	0.041	0.019	0.004	0.043	0.023	285	1688	15	69
		0	0	0	0	0	2	1	3	6	0				
Q0518	Reticulocalbin-1	0.228	0.278	0.215	0.225	0.190	0.000	0.002	0.000	0.000	0.000	325	13	3	10
6		0	0	0	0	0	2	3	1	3	1				
P19123	Troponin C, slow skeletal and	0.303	0.250	0.132	0.182	0.301	0.005	0.001	0.000	0.000	0.016	161	220	8	55
	cardiac muscles	0	0	0	0	0	6	2	0	9	9				
Q6W8	Purkinje cell protein 4-like pro-	0.328	0.323	0.238	0.264	0.288	0.001	0.005	0.000	0.003	0.009	68	24	2	32
Q3	tein 1	0	0	0	0	0	6	4	3	3	2				
Q9WU	Troponin I, slow skeletal mus-	0.122	0.088	0.088	0.066	0.212	0.000	0.000	0.000	0.000	0.000	187	147	7	41
Z5	cle	0	0	0	0	0	0	0	0	0	8				
Q99J47	Dehydrogenase/reductase SDR	0.218	0.138	0.210	0.127	0.079	0.000	0.000	0.000	0.000	0.000	323	8	2	7
	family member 7B	0	0	0	0	0	1	0	1	0	0				
Q8R2E	ERO1-like protein beta	0.406	0.122	0.092	0.391	0.080	0.004	0.000	0.000	0.036	0.000	467	4	2	7
9		0	0	0	0	0	3	0	0	4	0				
Q9JLH	Tropomodulin-4	0.469	0.389	0.358	0.323	0.295	0.035	0.033	0.011	0.036	0.014	345	511	8	44
8		0	0	0	0	0	0	1	3	8	6				

Q8K2Q5	Coiled-coil-helix-coiled-coil-helix domain-containing protein 7	0.482	0.383	0.424	0.264	0.289	0.028	0.027	0.020	0.011	0.013	85	3	2	19
		0	0	0	0	0	7	6	9	2	0				
Q9JL62	Glycolipid transfer protein	0.234	0.211	0.137	0.161	0.210	0.003	0.001	0.000	0.001	0.000	209	35	2	19
		0	0	0	0	0	1	1	0	4	7				
O88346	Troponin T, slow skeletal muscle	0.434	0.377	0.406	0.232	0.203	0.064	0.038	0.032	0.006	0.000	262	453	10	44
		0	0	0	0	0	3	2	7	0	5				
Q9QZ47	Troponin T, fast skeletal muscle	0.474	0.348	0.256	0.265	0.290	0.090	0.037	0.001	0.032	0.012	272	4577	13	36
		0	0	0	0	0	7	1	4	1	5				
P58774	Tropomyosin beta chain	0.416	0.296	0.235	0.246	0.294	0.054	0.013	0.000	0.021	0.014	284	3802	18	66
		0	0	0	0	0	0	8	7	4	1				
Q8BZA9	Fructose-2,6-bisphosphatase TIGAR	0.380	0.495	0.479	0.312	0.332	0.009	0.075	0.049	0.018	0.028	269	322	10	59
		0	0	0	0	0	2	5	5	8	0				
P05977	Myosin light chain 1/3, skeletal muscle isoform	0.396	0.375	0.251	0.258	0.294	0.043	0.055	0.001	0.027	0.014	188	4378	15	74
		0	0	0	0	0	8	9	2	7	2				
P70695	Fructose-1,6-bisphosphatase isozyme 2	0.307	0.431	0.341	0.238	0.282	0.013	0.111	0.011	0.017	0.010	339	974	14	63
		0	0	0	0	0	5	6	2	6	0				
P35487	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial	0.529	0.547	0.390	0.399	0.351	0.021	0.088	0.009	0.049	0.034	391	99	2	12
		0	0	0	0	0	7	4	2	0	3				
Q8CC35	Synaptopodin	0.536	0.517	0.415	0.349	0.356	0.024	0.069	0.013	0.019	0.030	929	151	13	16
		0	0	0	0	0	2	2	4	2	0				
Q9CU62	Structural maintenance of chromosomes protein 1A	0.471	0.542	0.408	0.299	0.230	0.037	0.120	0.029	0.045	0.005	1233	4	3	4
		0	0	0	0	0	4	8	6	7	4				
Q9JIK5	Nucleolar RNA helicase 2	0.489	0.495	0.393	0.318	0.236	0.030	0.078	0.014	0.024	0.003	851	4	2	5
		0	0	0	0	0	2	5	9	6	3				
Q8C494	Proline-rich protein 33	0.426	0.469	0.407	0.297	0.337	0.025	0.096	0.022	0.015	0.037	260	432	16	63
		0	0	0	0	0	0	1	9	8	4				
Q8VC R8	Myosin light chain kinase 2, skeletal/cardiac muscle	0.304	0.416	0.466	0.267	0.298	0.012	0.094	0.069	0.033	0.015	613	967	22	53
		0	0	0	0	0	8	8	6	1	5				
Q99J08	SEC14-like protein 2	0.543	0.555	0.590	0.316	0.316	0.029	0.114	0.098	0.006	0.017	403	21	2	4
		0	0	0	0	0	3	1	0	4	5				
O08911	Mitogen-activated protein kinase 12	0.530	0.514	0.592	0.353	0.349	0.062	0.118	0.154	0.040	0.047	367	441	13	53
		0	0	0	0	0	8	5	2	0	5				
Q8CD91	SPARC-related modular calcium-binding protein 2	0.573	0.543	0.568	0.332	0.315	0.080	0.078	0.138	0.042	0.040	447	7	2	4
		0	0	0	0	0	7	3	9	0	5				
Q8C5H8	NAD kinase 2, mitochondrial	0.406	0.293	0.246	0.382	0.304	0.014	0.006	0.000	0.070	0.017	452	4	2	6
		0	0	0	0	0	6	3	9	3	1				
O55239	Nicotinamide N-methyltransferase	0.482	0.345	0.448	0.511	0.369	0.018	0.010	0.025	0.137	0.035	264	20	2	8
		0	0	0	0	0	7	0	6	0	8				
Q9WU R9	Adenylate kinase 4, mitochondrial	0.300	0.331	0.516	0.421	0.302	0.001	0.010	0.046	0.083	0.015	223	22	3	13
		0	0	0	0	0	8	4	3	6	6				
Q8R1G2	Carboxymethylenebutenolidase homolog	0.304	0.398	0.391	0.332	0.342	0.012	0.076	0.026	0.095	0.041	245	787	13	66
		0	0	0	0	0	9	0	3	4	3				
P13412	Troponin I, fast skeletal muscle	0.409	0.377	0.265	0.297	0.311	0.050	0.057	0.001	0.056	0.021	182	4779	12	49
		0	0	0	0	0	3	2	8	8	3				
Q8CI70	Leucine-rich repeat-containing protein 20	0.474	0.529	0.422	0.323	0.338	0.090	0.266	0.040	0.084	0.038	184	443	10	73
		0	0	0	0	0	4	5	9	0	0				
P97457	Myosin regulatory light chain 2, skeletal muscle isoform	0.416	0.448	0.295	0.317	0.318	0.053	0.134	0.004	0.077	0.024	169	3239	20	91
		0	0	0	0	0	9	2	1	8	8				
Q9WU Z7	SH3 domain-binding glutamic acid-rich protein	0.475	0.410	0.362	0.336	0.338	0.091	0.076	0.016	0.065	0.038	214	511	9	64
		0	0	0	0	0	1	9	3	5	4				
Q9D7X8	Gamma-glutamylcyclotransferase	0.562	0.505	0.543	0.514	0.393	0.040	0.040	0.058	0.165	0.046	188	78	5	34
		0	0	0	0	0	2	1	3	9	6				
Q08091	Calponin-1	0.532	0.525	0.597	0.432	0.390	0.031	0.052	0.093	0.066	0.046	297	26	4	24
		0	0	0	0	0	8	4	3	5	2				
Q9ERT9	Protein phosphatase 1 regulatory subunit 1A	0.476	0.534	0.538	0.421	0.322	0.019	0.075	0.063	0.076	0.019	171	79	4	27
		0	0	0	0	0	0	9	8	8	1				

P50431	Serine hydroxymethyltransferase, cytosolic	0.556	0.523	0.592	0.417	0.347	0.076	0.133	0.153	0.105	0.045	478	136	11	35
		0	0	0	0	0	9	9	4	6	5				
Q3TM	Secernin-3	0.497	0.521	0.481	0.367	0.325	0.107	0.251	0.081	0.144	0.028	418	993	20	53
		0	0	0	0	0	4	4	0	8	9				
Q6466	NAD(P)H dehydrogenase [quinone] 1	0.393	0.413	0.419	0.332	0.388	0.004	0.012	0.016	0.015	0.054	274	139	10	42
		0	0	0	0	0	7	6	8	7	1				
P51667	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	0.303	0.288	0.239	0.233	0.386	0.005	0.004	0.000	0.007	0.088	166	294	9	56
		0	0	0	0	0	6	5	8	9	1				
Q6141	GTPase HRas	0.418	0.435	0.354	0.343	0.365	0.023	0.056	0.008	0.038	0.062	189	213	2	51
		0	0	0	0	0	9	7	9	4	3				
P13597	Intercellular adhesion molecule 1	0.504	0.484	0.409	0.260	0.409	0.022	0.056	0.013	0.001	0.078	537	10	5	11
		0	0	0	0	0	8	6	6	4	2				
P40936	Indolethylamine N-methyltransferase	0.377	0.548	0.399	0.344	0.412	0.003	0.078	0.011	0.019	0.087	264	108	8	33
		0	0	0	0	0	5	4	4	1	2				
A3KG5	Peptidase M20 domain-containing protein 2	0.538	0.505	0.588	0.384	0.402	0.026	0.060	0.094	0.036	0.064	431	191	12	41
		0	0	0	0	0	6	6	5	1	1				
Q9JKL	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	0.516	0.343	0.169	0.435	0.398	0.044	0.011	0.000	0.091	0.073	185	7	2	12
		0	0	0	0	0	6	8	0	1	5				
P16125	L-lactate dehydrogenase B chain	0.366	0.312	0.373	0.291	0.386	0.031	0.019	0.019	0.051	0.087	334	3262	21	74
		0	0	0	0	0	0	3	9	7	7				
Q91ZV	Melanoma inhibitory activity protein 2	0.476	0.432	0.407	0.493	0.428	0.021	0.042	0.013	0.155	0.101	1396	11	3	2
		0	0	0	0	0	7	0	0	9	1				
P56375	Acylphosphatase-2	0.423	0.385	0.337	0.362	0.366	0.057	0.064	0.010	0.138	0.063	106	774	7	62
		0	0	0	0	0	8	5	2	1	9				
P20801	Troponin C, skeletal muscle	0.484	0.370	0.281	0.307	0.362	0.098	0.052	0.002	0.067	0.059	160	6398	12	84
		0	0	0	0	0	1	0	8	2	3				
Q9ESZ	General transcription factor II-I	0.596	0.471	0.559	0.396	0.340	0.098	0.046	0.115	0.114	0.055	998	9	3	3
		0	0	0	0	0	7	9	8	5	3				
P70266	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1	0.524	0.516	0.586	0.468	0.453	0.036	0.071	0.101	0.102	0.151	471	166	12	23
		0	0	0	0	0	6	9	1	9	7				
Q6120	Platelet-activating factor acetylhydrolase IB subunit gamma	0.382	0.536	0.566	0.390	0.380	0.021	0.180	0.172	0.111	0.079	232	77	9	63
		0	0	0	0	0	3	9	2	3	7				

Table S3. Functional classification of proteins differentially expressed due to administration of AP-prestimulated CACs. Proteins changes between SF and SE were classified with IPA. The most probable functions of proteins of interest are shown. Legend: ↑ up-regulated; ↓ down-regulated; ▲ predicted activation increased; ▼ predicted activation decreased.

Cat- e- go- ries.	Functions	p-value	Activa- tion z- score	Molecules	Proteins
Cardiovascular Disease	Artery Occlu- sion	6,89E-07	-2,328 ▼	FABP4↑, PLIN1↑, YAP1↑, ABCA1↓, ALOX5↓, ALOX5AP↓, ARG2↓, CA13↓, CD14↓, CD44↓, CD68↓, CTSS↓, F13A1↓, FN1↓, Hrg↓, ITGAM↓, ITGB2↓, LAMP2↓, LCN2↓, LGALS3↓, MPO↓, PCNA↓, PLA2G15↓, PLIN2↓, PLTP↓, PTGES↓, S100A8↓, S100A9↓, THBS1↓	29
	Atherosclerosis	1,34E-07	-2,328 ▼	FABP4↑, PLIN1↑, YAP1↑, ABCA1↓, ALOX5↓, ALOX5AP↓, ARG2↓, CA13↓, CD14↓, CD44↓, CD68↓, CTSS↓, F13A1↓, FN1↓, ITGAM↓, ITGB2↓, LAMP2↓, LCN2↓, LGALS3↓, MPO↓, PCNA↓, PLA2G15↓, PLIN2↓, PLTP↓, PTGES↓, S100A8↓, S100A9↓, THBS1↓	28
Cell Death and Survival	Cell viability	9,78E-08	-3,278 ▼	ACLY↑, BCKDK↑, CRYAB↑, THRSP↑, YAP1↑, ABCA1↓, ACTN4↓, APAF1↓, ASS1↓, B2M↓, CAMP↓, CASP8↓, CD38↓, CD44↓, CD48↓, CYBA↓, EIF3E↓, EMILIN2↓, FLNA↓, FN1↓, HK3↓, IFIH1↓, IGHM↓, IL1RN↓, IQGAP1↓, ITGAM↓, ITGB2↓, LAMP2↓, LCN2↓, LGALS3↓, LGALS3BP↓, LGALS7/LGALS7B↓, LMNA↓, LTF↓, NCF2↓, PCNA↓, PNKP↓, POSTN↓, PRKCD↓, PRPF8↓, PRTN3↓, PTGR1↓, PTPN1↓, PTPN6↓, PTPRC↓, PYCARD↓, RBM39↓, RPL27↓, S100A8↓, S100A9↓, Saa3↓, SEL1L↓, SLC2A3↓, SMARCC2↓, SND1↓, SRC↓, STAT1↓, STAT2↓, SYK↓, THBS1↓, TRIM28↓, UBE2I↓	62
	Cell cytotoxi- city	3,13E-07	-2,382 ▼	B2M↓, CD38↓, CD44↓, CD48↓, FN1↓, ITGAM↓, ITGB2↓, LGALS3↓, PLTP↓, PRKCD↓, PTPN6↓, PTPRC↓, SRC↓, STAT1↓, STX7↓, SYK↓, TAP2↓	17
Cellular Move- ment	Cell movement	4,63E-14	-4,512 ▼	CRYAB↑, FABP4↑, GLUL↑, YAP1↑, ABCA1↓, ABI1↓, ACTB↓, ACTN1↓, ACTN4↓, AGK↓, AIF1↓, ALOX5↓, ALOX5AP↓, AP2M1↓, APAF1↓, APBB1IP↓, ARG1↓, ARHGDIB↓, BGN↓, BIN2↓, C5AR1↓, CAMP↓, CASP8↓, CD14↓, CD38↓, CD44↓, CD48↓, CFH↓, CFL1↓, CLIC1↓, CSK↓, CTSC↓, CTSG↓, CTSH↓, CTSS↓, CTSZ↓, DDX58↓, EIF3E↓, ELANE↓, ELMO1↓, EMILIN2↓, F13A1↓, FLNA↓, FN1↓, FYB1↓, GBP2↓, GC↓, GIT2↓, GNAI2↓, HCLS1↓, Hrg↓, IFI16↓, IFIT2↓, IGHM↓, IL1RN↓, IQGAP1↓, Irgm1↓, ITGAM↓, ITGB2↓, JCHAIN↓, LCN2↓, LCP1↓, LGALS3↓, LGALS3BP↓, LGMN↓, LIPA↓, LMNA↓, LMNB2↓, LSP1↓, LTF↓, MARCKSL1↓, MBOAT7↓, MPO↓, MYL12A↓, NCF2↓, NCF4↓, NCKAP1L↓, NSF↓, OLFM4↓, Orm1↓, P2RX4↓, PARVG↓, PLTP↓, POSTN↓, PRKCD↓, PRTN3↓, PTGES↓, PTPN1↓, PTPN6↓, PTPRC↓, PYCARD↓, RCC2↓, Retnlg↓, RPL13A↓, S100A8↓, S100A9↓, Saa3↓, SKAP2↓, SLC9A3R1↓, SND1↓, SRC↓, STAT1↓, STAT2↓, SYK↓, THBS1↓, UBE2I↓, WASF2↓	107
Inflammatory Response	Inflammatory response	1,81E-16	-3,232 ▼	CSRP3↑, FABP4↑, YAP1↑, AIF1↓, ALOX5↓, ALOX5AP↓, AOAHL↓, C1QTNF3↓, C5AR1↓, CAMP↓, CASP8↓, CD14↓, CD38↓, CD44↓, CFH↓, CTSG↓, CTSS↓, CYBA↓, ELANE↓, ELMO1↓, Flg↓, FN1↓, GC↓, GIT2↓, GNAI2↓, IGHM↓, IL1RN↓, ITGAM↓, ITGB2↓, LCN2↓, LCP1↓, LGALS3↓, LGALS3BP↓, LGALS9B↓, LGMN↓, LIPA↓, LSP1↓, LTF↓, Mbl1↓, MPO↓, NCKAP1L↓, Orm1↓, PLIN2↓, PRDX5↓, PRKCD↓, PRTN3↓, PTGES↓, PTPN6↓, PYCARD↓, RPL13A↓, S100A8↓, S100A9↓, SRC↓, STAT1↓, SYK↓, THBS1↓, UBE2I↓, ZBP1↓	58
	Cellular im- mune response	2,12E-17	-4,607 ▼	YAP1↑, ABCA1↓, C5AR1↓, CAMP↓, CASP8↓, CD14↓, CD180↓, CD38↓, CD44↓, CD48↓, CD68↓, CFH↓, CSK↓, CTSG↓, CTSS↓, CYBA↓, DDX58↓, ELANE↓, ELMO1↓, FLNA↓, FN1↓, HLA-DQB1↓, IFIH1↓, Ighg2a↓, IGHM↓, ITGAM↓, ITGB2↓, LCN2↓, LGALS3↓, LTF↓, Mbl1↓, MPO↓, PLD4↓	49

				POSTN↓, PRKCD↓, PRTN3↓, PTPN6↓, PTPRC↓, PYCARD↓, RAB31↓, S100A8↓, S100A9↓, SRC↓, STAT1↓, SYK↓, TAP1↓, TAPBP↓, THBS1↓, TOP2A↓	
	Neutrophils immune response	6,52E-06	-2,756 ▼	CAMP↓, CD44↓, CFH↓, FN1↓, ITGAM↓, ITGB2↓, LCN2↓, SYK↓, THBS1↓	9
	Macrophages immune response	1,40E-06	-2,272 ▼	ABCA1↓, CAMP↓, CD14↓, CD38↓, CD44↓, DDX58↓, ELMO1↓, ITGAM↓, ITGB2↓, LGALS3↓, Mbl1↓, PTPRC↓, S100A9↓, THBS1↓	14
Free Radical Scavenging	Synthesis of reactive oxygen species	2,11E-15	-3,391 ▼	CRYAB↑, ABCA1↓, ACTB↓, ALOX5↓, ARG1↓, ARHGDIB↓, C5AR1↓, CAMP↓, CASP8↓, CD14↓, CD44↓, CFH↓, CLIC1↓, CSTB↓, CTSG↓, CYBA↓, ELANE↓, FLNA↓, FN1↓, HK3↓, IQGAP1↓, ITGAM↓, ITGB2↓, ITIH4↓, LGALS3↓, LIPA↓, LTF↓, MPO↓, NCF2↓, NCF4↓, PNKP↓, PRKCD↓, PRTN3↓, PTGES↓, PTPN1↓, PTPN6↓, PYCARD↓, RPL26↓, S100A8↓, SLC9A3R1↓, SRC↓, SYK↓	42

Table 4. Classification of protein changes seen between SF (mice treated with pre-stimulated CACs, SF1, SF2 and SF3) and SE (mice treated with unstimulated CACs) was made with IPA, a software based on biomedical literature and integrated databases. The table shows proteins differentially expressed related to DM; including main categories and related functions, p-value, activation z-score, molecules (protein names) and the number of proteins. Legend: ↑ up-regulated; ↓ down-regulated.

	Functions	p-value	Activation z-score	Molecules	Proteins
SF1/S E	Diabetes mellitus	1,74E-10	1,166	AACS↑, ABCA1↓, ACACA↑, AEBP1↓, AGPAT2↑, ALDH2↑, ALOX5AP↓, APOBR↓, ARG1↓, C1QTNF3↓, CA13↓, CA5B↑, CAPZA1↓, CASP8↓, CAT↑, CAVIN1↑, CD180↓, CD38↓, CD44↓, COL12A1↓, CYBA↓, CYBB↓, CYP2E1↑, ELMO1↓, EPHX2↑, FABP4↑, FAH↑, FN1↓, HCLS1↓, HLA-DQB1↓, IFI44↓, IFIH1↓, IFIT2↓, IL1RN↓, ITGAM↓, ITGB2↓, LGALS9B↓, ME1↑, MGST1↑, MOGS↓, MPEG1↓, MSR1↑, NCF2↓, PLBD1↓, PLD4↓, PLEK↓, PLIN1↑, PTPN1↓, PTPN6↓, PTPRC↓, SCD↑, Slc25a1↑, SMYD1↑, STAT1↓, STAT2↓, TAP1↓, TAP2↓, ZBP1↓	58
	Insulin-dependent diabetes mellitus	3,17E-07		ABCA1↓, ALDH2↑, ALOX5AP↓, APOBR↓, CD180↓, CD38↓, CYBB↓, HCLS1↓, HLA-DQB1↓, IFI44↓, IFIH1↓, IFIT2↓, ITGB2↓, MOGS↓, MPEG1↓, PLBD1↓, PLD4↓, PLEK↓, PTPRC↓, SCD↑, STAT1↓, STAT2↓, TAP1↓, TAP2↓, ZBP1↓	25
	Lipid conversion	6,86E-08	1,425	ABHD5↑, ACACA↑, ACLY↑, ACOX1↑, ALOX5AP↓, CAT↑, CPT1B↑, CYP2E1↑, FABP4↑, FGFR2↑, LIPE↑, PTGES↓, SCD↑, TECR↑	14
	Fatty acid conversion	1,89E-11	1,394	ACACA↑, ACLY↑, ACOX1↑, ALOX5AP↓, CPT1B↑, CYP2E1↑, FABP4↑, FGFR2↑, LIPE↑, PTGES↓, TECR↑	11
	Lipid Oxidation	6,64E-10	0,910	ABCA1↓, ABHD5↑, ACACA↑, ACADS↑, ACOX1↑, Aldh1a7↑, CAT↑, CPT1B↑, CYP2E1↑, ECI1↑, FABP4↑, HADHB↑, LIPE↑, LRPPRC↑, NUCB2↓, PLIN1↑, PNPLA2↑, SCD↑, SLC27A1↑, SLN↓	20
SF2/S E	Fatty acid Oxidation	7,53E-10	0,891	ABCA1↓, ABHD5↑, ACACA↑, ACADS↑, ACOX1↑, CPT1B↑, CYP2E1↑, ECI1↑, FABP4↑, HADHB↑, LIPE↑, LRPPRC↑, NUCB2↓, PLIN1↑, PNPLA2↑, SCD↑, SLC27A1↑, SLN↓	18
	Carbohydrate Metabolism	4,66E-05	1,364	ABHD5↑, AGPAT2↑, ALDH2↑, AOAH↓, CD44↓, COQ3↑, CYP2E1↑, FABP4↑, GALNS↓, GBE1↑, GFPT1↓, GNAI1↑, IL1RN↓, ITGB2↓, LIPE↑, MBOAT7↓, PHOSPHO1↑, PLA2G15↓, PLEK↓, PLIN1↑, POSTN↓, PTPN1↓, PTPRC↓, SCD↑, SFN↑, SLC27A1↑, SLC2A3↓, SLC9A3R1↓, SYK↓	29
	Diabetes mellitus	5,67E-10	-0,687	ABCA1↓, AIF1↓, APOBR↓, ARG1↓, ATXN2↑, B2M↓, C1QTNF3↓, C1S↓, CACNG1↓, CAPZA1↓, CASP8↓, CD180↓, CD38↓, CFH↓, COL12A1↓, COL14A1↓, CP↓, CTSH↓, CTSS↓, CYBA↓, ELMO1↓, FABP4↑, FN1↓, GBP2↓, HCLS1↓, Hrg↓, IFI16↓, IFI44↓, IFIH1↓, IFIT2↓, IGHM↓, IL1RN↓, ITGAM↓, ITGB2↓, ITIH4↓, LCP1↓, LGALS3↓, LMNA↓, ME1↑, MOGS↓, MPEG1↓, NCF2↓, OAS1↓, PDXK↓, PLBD1↓, PLD4↓, PLEK↓, PLIN1↑, PRKCD↓, PRRC2A↓, PTPN1↓, PTPN6↓, PTPRC↓, SERPINC1↓, STAT1↓, STAT2↓, TAP1↓, TAP2↓, TTR↓	59
SF3/S E	Insulin-dependent diabetes mellitus	1,23E-11	-1,090	ABCA1↓, AIF1↓, APOBR↓, ATXN2↑, B2M↓, CACNG1↓, CD180↓, CD38↓, CFH↓, CTSH↓, CTSS↓, GBP2↓, HCLS1↓, IFI16↓, IFI44↓, IFIH1↓, IFIT2↓, IGHM↓, ITGB2↓, ITIH4↓, LCP1↓, MOGS↓, MPEG1↓, OAS1↓, PLBD1↓, PLD4↓, PLEK↓, PRRC2A↓, PTPRC↓, STAT1↓, STAT2↓, TAP1↓, TAP2↓	33
	Diabetes mellitus	1,50E-13	-0,193	ABCA1↓, AEBP1↓, AIF1↓, APOBR↓, APOE↓, ARG1↓, B2M↓, C1QTNF3↓, C1S↓, CA13↓, CACNG1↓, CAPZA1↓, CASP8↓, CD180↓, CD38↓, CD44↓, CFH↓, COL12A1↓, COL14A1↓, CP↓, CTSD↓, CTSH↓, CTSS↓, CYBA↓, ELMO1↓, FN1↓, GBP2↓, GPNMB↓, HLA-DQA1↓, IFI16↓, IFI44↓, IFIT2↓, IGHM↓, IL1RN↓, Irgm1↓, ITGAM↓, ITGB2↓, LCP1↓, LGALS3↓, LGALS9B↓, LMNA↓, MOGS↓, MPEG1↓, NCF2↓, PDXK↓, PEA15↓, PLBD1↓, PLD4↓, PLEK↓, PRRC2A↓, PTPN1↓, PTPN6↓, PTPRC↓, SRC↓, STAT1↓, STAT2↓, TAP1↓, TAP2↓, ZBP1↓	59
	Insulin-dependent diabetes mellitus	3,40E-13	-1,090	ABCA1↓, AIF1↓, APOBR↓, B2M↓, CACNG1↓, CD180↓, CD38↓, CFH↓, CTSH↓, CTSS↓, GBP2↓, GPNMB↓, HLA-DQA1↓, IFI16↓, IFI44↓, IFIT2↓	32

IGHM↓, Irgm1↓, ITGB2↓, LCP1↓, MOGS↓, MPEG1↓, PLBD1↓, PLD4↓,
PLEK↓, PRRC2A↓, PTPRC↓, STAT1↓, STAT2↓, TAP1↓, TAP2↓, ZBP1↓

Supplementary references:

1. Beltran-Camacho, L.; Jimenez-Palomares, M.; Rojas-Torres, M.; Sanchez-Gomar, I.; Rosal-Vela, A.; Eslava-Alcon, S.; Perez-Segura, M. C.; Serrano, A.; Antequera-Gonzalez, B.; Alonso-Pinero, J. A.; Gonzalez-Rovira, A.; Extremera-Garcia, M. J.; Rodriguez-Pinero, M.; Moreno-Luna, R.; Larsen, M. R.; Duran-Ruiz, M. C., Identification of the initial molecular changes in response to circulating angiogenic cells-mediated therapy in critical limb ischemia. *Stem Cell Res Ther* **2020**, *11*, (1), 106.
2. Garcia, S.; Marston, N.; Sandoval, Y.; Pierpont, G.; Adabag, S.; Brenes, J.; Santilli, S.; McFalls, E. O., Prognostic value of 12-lead electrocardiogram and peak troponin I level after vascular surgery. *J Vasc Surg* **2013**, *57*, (1), 166-72.
3. Tarlov, I. M., Spinal cord compression studies. III. Time limits for recovery after gradual compression in dogs. *AMA Arch Neurol Psychiatry* **1954**, *71*, (5), 588-97.