

Anexos

Anexo I. Proteínas diferencialmente expresadas

ID	Proteína diferencialmente expresada	P-value	FC	T-Student
G1SER8	profilin 1(PFN1)	0,033	1,234	0,033
G1SF32	translocase of outer mitochondrial membrane 70(TOMM70)	0,028	0,860	0,028
G1SG68	karyopherin subunit alpha 4(KPNA4)	0,036	2,830	0,036
G1SGS7	UFM1 specific ligase 1(UFL1)	0,023	-0,667	0,023
G1SHT2	sterol carrier protein 2(SCP2)	0,034	-0,621	0,034
G1SIN4	ELKS/RAB6-interacting/CAST family member 1(ERC1)	0,039	0,476	0,039
G1SN96	paraoxonase 1(PON1)	0,043	1,617	0,043
G1SNC7	dermatopontin(DPT)	0,016	-0,640	0,016
G1SP02	pyruvate dehydrogenase phosphatase regulatory subunit(PDPR)	0,0197	-0,204	0,0197
G1SPD1	myotrophin(MTPN)	0,028	2,368	0,028
G1SQ46	Rho GDP dissociation inhibitor beta(ARHGDI B)	0,043	1,152	0,043
G1SQW0	mitochondrial carrier 2(MTCH2)	0,000	-0,776	0,000
G1SR29	ATPase H+ transporting V1 subunit A(ATP6V1A)	0,043	1,535	0,043
G1SSL9	17-beta-hydroxysteroid dehydrogenase 13(LOC100348252)	0,027	1,607	0,027
G1SU17	NAD(P) dependent steroid dehydrogenase-like(NSDHL)	0,023	-0,378	0,023
G1SVP7	glutathione S-transferase omega 1(GSTO1)	0,005	-0,187	0,005
G1SVZ8	chromosome unknown open reading frame, human C9orf64(LOC100352045)	0,045	-0,507	0,045
G1SXZ9	biphenyl hydrolase like(BPHL)	0,007	1,779	0,007
G1SYC9	RAB8B, member RAS oncogene family(RAB8B)	0,014	-0,568	0,014
G1SZ00	cysteine and glycine rich protein 1(CSRP1)	0,020	-0,605	0,020
G1T0H7	trafficking protein particle complex 3(TRAPPC3)	0,014	-0,711	0,014
G1T2I4	glutamyl-prolyl-tRNA synthetase(EPRS)	0,024	6,176	0,024
G1T6X2	cytochrome P450 2C15-like(LOC100347004)	0,026	-0,478	0,026
G1T726	hydroxyacyl-CoA dehydrogenase(HADH)	0,014	0,781	0,014
G1T8G9	pyruvate kinase, liver and RBC(PKLR)	0,001	3,772	0,001
G1T9I4	sorcini(SRI)	0,041	0,484	0,041
G1T9T6	ethanolamine-phosphate phospho-lyase(ETNPPL)	0,034	-0,562	0,034
G1TAH7	transketolase(TKT)	0,020	13,925	0,020
G1TBR1	NAD(P)H quinone dehydrogenase 2(NQO2)	0,002	-0,376	0,002
G1TBU9	acetyl-CoA acyltransferase 2(ACAA2)	0,037	0,424	0,037
G1TCG5	solute carrier family 27 member 2(SLC27A2)	0,027	3,868	0,027
G1TCT8	major facilitator superfamily domain containing 9(MFSD9)	0,047	-0,447	0,047
G1TES6	hydroxysteroid 17-beta dehydrogenase 10(HSD17B10)	0,005	0,323	0,005
G1TIR9	UDP-glucuronosyltransferase 2B31(LOC100341802)	0,049	1,744	0,049
G1TR70	cytochrome P450 2C4(CYP2C4)	0,000	3,777	0,000
G1TRH9	tropomodulin 3(TMOD3)	0,016	1,337	0,016
G1TTZ8	formimidoyltransferase cyclodeaminase(FTCD)	0,010	0,680	0,010

G1TUB8	ribosomal protein L11(RPL11)	0,040	-0,773	0,040
G1TUC2	CCHC-type zinc finger nucleic acid binding protein(CNBP)	0,042	4,497	0,042
G1TUC5	succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial(LOC100346169)	0,006	4,208	0,006
G1TUX5	protein HP-25 homolog 2(LOC100352752)	0,017	1,009	0,017
G1TWP4	valyl-tRNA synthetase(VARS)	0,001	0,794	0,001
G1TYJ3	dihydropyrimidinase(DPYS)	0,037	0,860	0,037
G1TYM3	cytochrome P450, family 2, subfamily b, polypeptide 4(CYP2B4)	0,004	-0,702	0,004
G1U2K8	cytochrome P450-like(CYP2C)	0,009	-0,525	0,009
G1U4I6	fatty acid amide hydrolase(FAAH)	0,003	2,414	0,003
G1U522	protein kinase cAMP-dependent type II regulatory subunit alpha(PRKAR2A)	0,001	6,382	0,001
P04068	epoxide hydrolase 1(EPHX1)	0,044	-0,613	0,044
P79226	aldolase, fructose-bisphosphate B(ALDOB)	0,008	4,266	0,008
Q95J97	protein kinase cAMP-activated catalytic subunit alpha(PRKACA)	0,024	-0,700	0,024
U3KLZ1	flavin containing monooxygenase 3(FMO3)	0,043	3,680	0,043
U3KM06	UDP-glucuronosyltransferase 2A3(LOC100351592)	0,003	-0,547	0,003
U3KM31	CNDP dipeptidase 2 (metallopeptidase M20 family)(CNDP2)	0,023	-0,855	0,023
U3KPP4	cytochrome P450 2C30(CYP2C30)	0,027	-0,644	0,027

Anexo II. Rutas KEGG

Ruta KEGG	Descripción	Número de proteínas	Proteínas (%)	P-Value
ocu01100:	Metabolic pathways	22	40,7	6,10E-09
ocu05204:	Chemical carcinogenesis	8	14,8	3,20E-07
ocu00830:	Retinol metabolism	6	11,1	3,30E-05
ocu00140:	Steroid hormone biosynthesis	6	11,1	3,90E-05
ocu01130:	Biosynthesis of antibiotics	8	14,8	5,70E-05
ocu00982:	Drug metabolism - cytochrome P450	4	7,4	5,50E-03
ocu00980:	Metabolism of xenobiotics by cytochrome P450	4	7,4	7,60E-03
ocu00590:	Arachidonic acid metabolism	4	7,4	9,30E-03
ocu04750:	Inflammatory mediator regulation of TRP channels	4	7,4	1,00E-02
ocu00591:	Linoleic acid metabolism	3	5,6	1,20E-02
ocu04726:	Serotonergic synapse	4	7,4	1,30E-02
ocu01200:	Carbon metabolism	4	7,4	1,70E-02
ocu00860:	Porphyryn and chlorophyll metabolism	3	5,6	2,20E-02
ocu00280:	Valine, leucine and isoleucine degradation	3	5,6	2,70E-02
ocu00983:	Drug metabolism - other enzymes	3	5,6	3,50E-02
ocu01230:	Biosynthesis of amino acids	3	5,6	4,40E-02

Anexo III. Términos GO

	Términos GO	Descripción	Número de proteínas	Proteínas (%)	P-Value
Biological Process	GO:0008152	metabolic process	4	7,4	5,3E-03
	GO:0019439	aromatic compound catabolic process	2	3,7	1,0E-02
	GO:0060315	negative regulation of ryanodine-sensitive calcium-release channel activity	2	3,7	1,7E-02
	GO:0032781	positive regulation of ATPase activity	2	3,7	2,8E-02
Cellular component	GO:0070062	extracellular exosome	25	46,3	5,4E-09
	GO:0031090	organelle membrane	6	11,1	5,8E-07
	GO:0005789	endoplasmic reticulum membrane	8	14,8	6,4E-06
	GO:0005739	mitochondrion	9	16,7	4,4E-03
Molecular function	GO:0070330	aromatase activity	4	7,4	7,7E-05
	GO:0020037	heme binding	5	9,3	1,5E-03
	GO:0005506	iron ion binding	5	9,3	1,9E-03
	GO:0004497	monooxygenase activity	3	5,6	6,5E-03
	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	3	5,6	8,7E-03
	GO:0003857	3-hydroxyacyl-CoA dehydrogenase activity	2	3,7	2,4E-02
	GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	2	3,7	3,6E-02