Supplementary Table 4: Modulated pathways highlighted by the DAVID annotation tool. Chronically exposed cells vs. unexposed cells

Annotation Cluster 1 Enrichment Score: 3.2045184163200546

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	11	1.3236186932457205E-5	Q923D2, Q9CQU0, P50171, Q8K2B3, Q8CDN6, Q99LC5, P23591, P47791, Q9CZ13, Q64105, P09528	51	676	18082	5.7692887806009985	0.018007438944878107
UP_KEYWORDS	Oxidoreductase	9	1.4388566749678645E-4	Q923D2, P61982, Q9CQU0, P50171, Q8K2B3, P23591, P47791, Q64105, P09528	56	639	22680	5.704225352112676	0.168335993266866
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	9	3.863354499556126E-4	Q923D2, Q9CQU0, P50171, Q8K2B3, Q99LC5, P23591, P47791, Q64105, P09528	53	604	17446	4.904848181931775	0.46841782050119907
UP_KEYWORDS	NADP	4	0.008830386204599647	Q923D2, P23591, P47791, Q64105	56	175	22680	9.257142857142858	9.863773726418612
INTERPRO	IPR016040:NAD(P)-binding domain	4	0.014611110717051392	Q923D2, P50171, P23591, Q64105	54	199	20594	7.66573608784664	16.06719820439031

Annotation Cluster 2 Enrichment Score: 2.2653652261727744

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
UP_KEYWORDS	Transit peptide	7	0.001431504148570666	Q9D2G2, Q9D964, Q8K2B3, Q99LC5, P47791, Q8BMF4, Q9CZ13	56	510	22680	5.558823529411765	1.6632618677438704
UP_KEYWORDS	Tricarboxylic acid cycle	3	0.001671335157719073	Q9D2G2, Q8K2B3, Q8BMF4	56	25	22680	48.6	1.9394333762075555
UP_KEYWORDS	Electron transport	4	0.00224115081127122	Q8K2B3, Q8CDN6, Q99LC5, Q9CZ13	56	107	22680	15.140186915887849	2.5927481146275855
GOTERM_BP_DIRECT	GO:0006099~tricarboxylic acid cycle	3	0.002900680466840862	Q9D2G2, Q8K2B3, Q8BMF4	51	29	18082	36.67748478701826	3.8752672468436944
UP_SEQ_FEATURE	transit peptide:Mitochondrion	7	0.003914036560376206	Q9D2G2, Q9D964, Q8K2B3, Q99LC5, P47791, Q8BMF4, Q9CZ13	56	496	18012	4.539314516129032	4.6807828600375245
KEGG_PATHWAY	mmu00020:Citrate cycle (TCA cycle)	3	0.008659633975128726	Q9D2G2, Q8K2B3, Q8BMF4	35	32	7691	20.600892857142856	9.359113551162535
KEGG_PATHWAY	mmu01130:Biosynthesis of antibiotics	5	0.014056614637970633	Q91ZJ5, Q9D2G2, Q8K2B3, P17751, Q8BMF4	35	214	7691	5.134178905206942	14.780670912737515
KEGG_PATHWAY	mmu01200:Carbon metabolism	4	0.014240436230744568	Q9D2G2, Q8K2B3, P17751, Q8BMF4	35	116	7691	7.577339901477832	14.960010813782997
GOTERM_BP_DIRECT	GO:0008152~metabolic process	5	0.03875764551096013	Q91ZJ5, Q9D2G2, P23591, P17751, Q8BMF4	51	463	18082	3.8288231059162325	41.598069722869454

Annotation Cluster 3 Enrichment Score: 1.9488396529854002

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
UP_KEYWORDS	Transit peptide	7	0.001431504148570666	Q9D2G2, Q9D964, Q8K2B3, Q99LC5, P47791, Q8BMF4, Q9CZ13	56	510	22680	5.558823529411765	1.6632618677438704
UP_SEQ_FEATURE	transit peptide:Mitochondrion	7	0.003914036560376206	Q9D2G2, Q9D964, Q8K2B3, Q99LC5, P47791, Q8BMF4, Q9CZ13	56	496	18012	4.539314516129032	4.6807828600375245
UP_SEQ_FEATURE	nucleotide phosphate-binding region:FAD	3	0.014014411889932106	Q8K2B3, Q99LC5, P47791	56	59	18012	16.354721549636803	15.84608911771912
GOTERM_MF_DIRECT	GO:0050660~flavin adenine dinucleotide binding	3	0.019499371926397203	Q8K2B3, Q99LC5, P47791	53	72	17446	13.715408805031446	21.280008009478724
UP_KEYWORDS	FAD	3	0.03332133081240585	Q8K2B3, Q99LC5, P47791	56	118	22680	10.296610169491524	32.7520940055539
UP_KEYWORDS	Flavoprotein	3	0.03973989857861372	Q8K2B3, Q99LC5, P47791	56	130	22680	9.346153846153847	37.798092739977875

Annotation Cluster 4 Enrichment Score: 1.8932587888919852

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
GOTERM_CC_DIRECT	GO:0043209~myelin sheath	8	1.0362013419097073E-6	P61982, Q9D2G2, Q9DCX2, Q9DB05, P67778, Q8K2B3, Q8BMF4, Q9CZ13	56	192	19662	14.629464285714285	0.001201682186247055
UP_KEYWORDS	Mitochondrion inner membrane	5	0.0033487765940817455	Q9DCX2, P67778, Q9D964, Q8K2B3, Q9CZ13	56	254	22680	7.97244094488189	3.851305542039518
GOTERM_CC_DIRECT	GO:0005743~mitochondrial inner membrane	5	0.02292722664396589	Q9DCX2, P67778, Q9D964, Q8K2B3, Q9CZ13	56	387	19662	4.536267995570321	23.584439642552535
KEGG_PATHWAY	mmu00190:Oxidative phosphorylation	3	0.12520618705110048	Q9DCX2, Q8K2B3, Q9CZ13	35	139	7691	4.742651593011305	77.93844384629823
KEGG_PATHWAY	mmu05012:Parkinson's disease	3	0.14014627859951423	Q9DCX2, Q8K2B3, Q9CZ13	35	149	7691	4.424352828379674	81.84013992422574
KEGG_PATHWAY	mmu05010:Alzheimer's disease	3	0.1837965571570911	Q9DCX2, Q8K2B3, Q9CZ13	35	177	7691	3.724455205811138	89.91962750847306
KEGG_PATHWAY	mmu05016:Huntington's disease	3	0.21775187110779454	Q9DCX2, Q8K2B3, Q9CZ13	35	198	7691	3.329437229437229	93.76293978653293

Annotation Cluster 5 Enrichment Score: 1.3988787121960118

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
INTERPRO	Cysteine peptidase, asparagine active site	3	6.678640496164755E-4	O70370, P10605, Q9WUU7	54	15	20594	76.27407407407406	0.791866036251454
SMART	SM00645:Pept_C1	3	0.0010471000607657095	O70370, P10605, Q9WUU7	23	23	10425	59.12098298676748	0.826966113978922
INTERPRO	IPR000668:Peptidase C1A, papain C-terminal	3	0.0015881597012858348	O70370, P10605, Q9WUU7	54	23	20594	49.743961352657	1.8736239040144542
UP_SEQ_FEATURE	propeptide:Activation peptide	4	0.001942325364077986	O70370, P10605, Q9WUU7, P18242	56	81	18012	15.883597883597881	2.348573184075642
INTERPRO	IPR013128:Peptidase C1A, papain	3	0.002188876092008921	O70370, P10605, Q9WUU7	54	27	20594	42.374485596707814	2.5738942304716295
UP_KEYWORDS	Thiol protease	4	0.004228005059038943	O70370, P10605, Q7TQI3, Q9WUU7	56	134	22680	12.08955223880597	4.839734855985989
UP_KEYWORDS	Redox-active center	3	0.005820385456546925	Q9CQU0, Q8CDN6, P47791	56	47	22680	25.851063829787233	6.60626656217519
GOTERM_MF_DIRECT	GO:0008234~cysteine-type peptidase activity	4	0.008554573086907396	O70370, P10605, Q7TQI3, Q9WUU7	53	141	17446	9.33815067576609	9.912779905971503
GOTERM_BP_DIRECT	proteolysis involved in cellular protein catabolic process	3	0.01085486886282228	O70370, P10605, Q9WUU7	51	57	18082	18.66047471620227	13.799741483256788
GOTERM_MF_DIRECT	GO:0004197~cysteine-type endopeptidase activity	3	0.013377408385132964	O70370, P10605, Q9WUU7	53	59	17446	16.737448033258715	15.09548697553904
GOTERM_BP_DIRECT	GO:0045454~cell redox homeostasis	3	0.013949750485764327	Q9CQU0, Q8CDN6, P47791	51	65	18082	16.363800904977374	17.397835576665344
UP_KEYWORDS	Zymogen	4	0.014976173146207675	O70370, P10605, Q9WUU7, P18242	56	213	22680	7.605633802816901	16.194525464494514
KEGG_PATHWAY	mmu04142:Lysosome	4	0.016292894646507856	O70370, P10605, Q9WUU7, P18242	35	122	7691	7.204683840749414	16.93919738281008
GOTERM_CC_DIRECT	intracellular membrane-bounded organelle	7	0.018015694170592116	O70370, Q91ZR2, Q9D2G2, P10605, Q9QZ88, Q9WUU7, P46061	56	751	19662	3.272636484687084	19.009148193877845
UP_KEYWORDS	Lysosome	4	0.022561641707407508	O70370, P10605, Q9WUU7, P18242	56	249	22680	6.506024096385542	23.446786328271017
UP_KEYWORDS	Protease	5	0.04226437709246879	O70370, P10605, Q7TQI3, Q9WUU7, P18242	56	542	22680	3.736162361623616	39.685981756031474
GOTERM_CC_DIRECT	GO:0005764~lysosome	4	0.0653736599433696	O70370, P10605, Q9WUU7, P18242	56	331	19662	4.242986620630125	54.34510476800563
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	5	0.0673427689802694	O70370, P10605, Q7TQI3, Q9WUU7, P18242	53	516	17446	3.189629954658476	57.13532945509279
GOTERM_BP_DIRECT	GO:0006508~proteolysis	5	0.0766506754537089	O70370, P10605, Q7TQI3, Q9WUU7, P18242	51	582	18082	3.045953776699683	66.21095634354445
UP_KEYWORDS	Hydrolase	8	0.10160419352863737	O70370, Q61205, P10605, Q7TQI3, Q9WUU7, Q9QXK7, Q9JHW2, P18242	56	1646	22680	1.9684082624544348	71.47761322974821
GOTERM_CC_DIRECT	GO:0005615~extracellular space	8	0.12472746292540123	O70370, Q60854, P10605, Q9WUU7, P17751, P18760, Q91WN1, P18242	56	1504	19662	1.8675911854103342	78.66795579044505
GOTERM_MF_DIRECT	GO:0016787~hydrolase activity	8	0.16875905585098583	O70370, Q61205, P10605, Q7TQI3, Q9WUU7, Q9QXK7, Q9JHW2, P18242	53	1533	17446	1.7177811419217466	89.4167342700843
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	5	0.5113020017603636	Q9ER38, Q6ZQI3, Q9CQU0, Q9WUU7, P31938	56	1323	19662	1.3269355361192094	99.97523803491626
UP_KEYWORDS	Endoplasmic reticulum	3	0.702622231856916	Q9ER38, Q6ZQI3, Q9CQU0	56	997	22680	1.218655967903711	99.99993187042593
UP_KEYWORDS	Disulfide bond	7	0.787288087595317	O70370, P10605, Q9CQU0, Q8CDN6, P47791, Q9WUU7, P18242	56	3124	22680	0.9074903969270166	99.99999865233468
UP_SEQ_FEATURE	disulfide bond	7	0.7969517792476128	O70370, P10605, Q9CQU0, Q8CDN6, P47791, Q9WUU7, P18242	56	2510	18012	0.8970119521912351	99.99999965632486
UP_KEYWORDS	Glycoprotein	7	0.919027236933758	Q9ER38, Q6ZQI3, O70370, P10605, Q9CQU0, Q9WUU7, P18242	56	3815	22680	0.7431192660550459	99.99999999998346
UP_SEQ_FEATURE	signal peptide	7	0.9327318177206512	Q9ER38, Q6ZQI3, O70370, P10605, Q9CQU0, Q9WUU7, P18242	56	3124	18012	0.7207106274007682	99.99999999999953
UP_KEYWORDS	Signal	8	0.9431968129909098	Q9DBP5, Q9ER38, Q6ZQI3, O70370, P10605, Q9CQU0, Q9WUU7, P18242	56	4543	22680	0.713185119964781	99.99999999999974
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	7	0.9733701372063551	Q9ER38, Q6ZQI3, O70370, P10605, Q9CQU0, Q9WUU7, P18242	56	3563	18012	0.631911310693236	100.0

Annotation Cluster 6 Enrichment Score: 1.3345970983825508

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
UP_KEYWORDS	Transport	11	0.01500170980907873	Q91ZR2, Q9DCX2, Q9DB05, Q9QZ88, Q8K2B3, Q8CDN6, Q99LC5, O35345, Q9CZ13, Q9QYB1, Q64152	56	1901	22680	2.343503419253025	16.21995998252378
GOTERM_BP_DIRECT	GO:0006810~transport	11	0.025540454930451876	Q91ZR2, Q9DCX2, Q9DB05, Q9QZ88, Q8K2B3, Q8CDN6, Q99LC5, O35345, Q9CZ13, Q9QYB1, Q64152	51	1822	18082	2.1405264630550356	29.67297028822823
UP_KEYWORDS	Protein transport	5	0.05109368847623009	Q91ZR2, Q9DB05, Q9QZ88, O35345, Q64152	56	577	22680	3.509532062391681	45.88422516518106

GOTERM_BP_DIRECT	GO:0015031~protein transport	5	0.08046843953391572	Q91ZR2, Q9DB05, Q9QZ88, O35345, Q64152	51	592	18082	2.9945018547959723	68.0630373933872
GOTERM_BP_DIRECT	GO:0006886~intracellular protein transport	3	0.13478832732804558	Q91ZR2, Q9DB05, Q9QZ88	51	232	18082	4.584685598377282	86.05247457135572

Annotation Cluster 7 Enrichment Score: 1.0776372050152074

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
GOTERM_MF_DIRECT	GO:0051015~actin filament binding	3	0.0589444921723316	P47753, Q99K51, P18760	53	132	17446	7.481132075471698	52.20255893818941
GOTERM_MF_DIRECT	GO:0003779~actin binding	4	0.07958572259563038	P61982, P47753, Q99K51, P18760	53	338	17446	3.8955007256894048	63.493547016800875
UP_KEYWORDS	Actin-binding	3	0.12468378876640601	P47753, Q99K51, P18760	56	252	22680	4.821428571428571	78.96948550839168

Annotation Cluster 8 Enrichment Score: 0.6743894218938593

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
UP_SEQ_FEATURE	metal ion-binding site:Zinc 2	3	0.02314502303195136	Q9QZ88, Q9QYJ0, Q9QXK7	56	77	18012	12.531539888682746	24.892400743162668
UP_SEQ_FEATURE	metal ion-binding site:Zinc 1	3	0.024851495687748585	Q9QZ88, Q9QYJ0, Q9QXK7	56	80	18012	12.061607142857142	26.480620019238632
UP_KEYWORDS	Metal-binding	7	0.8509583520237127	Q91ZJ5, Q99K51, P62748, Q9QZ88, Q9QYJ0, Q9QXK7, P09528	56	3395	22680	0.8350515463917526	99.99999997906686
GOTERM_MF_DIRECT	GO:0046872~metal ion binding	8	0.8958621946495704	Q91ZJ5, Q99K51, P62748, Q9QZ88, Q9QYJ0, Q9QXK7, Q9CZ13, P09528	53	3355	17446	0.7849056603773584	99.99999999988434
UP_KEYWORDS	Zinc	3	0.9684857308057782	Q9QZ88, Q9QYJ0, Q9QXK7	56	2099	22680	0.5788470700333492	100.0

Annotation Cluster 9 Enrichment Score: 0.05610641107297198

Category	Term	Count	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	FDR
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	3	0.8004574716716117	Q9DBP5, Q9ER38, P31938	56	963	18012	1.0020026702269693	99.99999972222713
GOTERM_MF_DIRECT	GO:0005524~ATP binding	4	0.8384216205187112	Q9DBP5, Q9ER38, Q9QYJ0, P31938	53	1507	17446	0.8737088555295415	99.99999997594306
UP_KEYWORDS	ATP-binding	3	0.8509188788683362	Q9DBP5, Q9ER38, P31938	56	1363	22680	0.8914159941305942	99.99999997900186
UP_KEYWORDS	Nucleotide-binding	3	0.9331846344947521	Q9DBP5, Q9ER38, P31938	56	1754	22680	0.6927023945267958	99.99999999999825
GOTERM_MF_DIRECT	GO:0000166~nucleotide binding	3	0.983584042914668	Q9DBP5, Q9ER38, P31938	53	1936	17446	0.5100771869639794	100.0