

Supplementary Information:

“Ionizing Radiation induction of cholesterol biosynthesis in Lung tissue”

Erica Werner, Andrew Alter, Qiudong Deng, Eric B. Dammer, Ya Wang, David S. Yu, Duc M. Duong, Nicholas T. Seyfried and Paul W. Doetsch

Supplementary Table 1: List of proteins regulated by Fe ion exposure.

Gene symbol	Name of the protein	Protein.IDs	f01	f02	f03	n01	n02	n03	log.p	Pvalue	threshold	Differen	fold change(N/	Fold (F/N
ALDH3A1	Aldehyde dehydrogenase 3 fam	tr C9JMC5 C9JMC5_HUMA	7.49601	7.8445	7.978	8.4173	8.714	8.347	-1.773	0.0169	TRUE	-0.72	5.250043	0.19041
HSPB1	Heat shock protein beta 1	sp P04792 HSPB1_HUMAN	9.16436	9.1934	9.147	9.3701	9.721	9.559	-1.694	0.0202	TRUE	-0.38	2.408609	0.41511
BCAM	Basal cell adhesion molecule	tr A0A087WXM8 A0A087V	7.47551	7.4963	7.547	7.6879	8.117	7.82	-1.34	0.0457	TRUE	-0.37	2.337496	0.42781
CA2	Carbonic anhydrase 2	sp P00918 CAH2_HUMAN;	7.66075	7.6376	7.462	7.8712	8.095	7.805	-1.451	0.0354	TRUE	-0.34	2.173935	0.4011
PTK7	Protein Tyrosine Kinase 7	sp Q13308-3 PTK7_HUMA	7.74636	7.9971	7.86	8.0956	8.303	8.128	-1.471	0.0338	TRUE	-0.31	2.031725	0.49211
SPRR1B	Cornifin B	sp P22528 SPRR1B_HUMAN	7.97578	7.8686	7.942	8.1469	8.381	8.157	-1.65	0.0224	TRUE	-0.3	1.993225	0.5011
AKR1C2	Aldo-keto reductase family 1 m	sp P52895 AK1C2_HUMAN	7.82009	7.863	7.891	8.0114	8.241	8.155	-1.778	0.0167	TRUE	-0.28	1.895976	0.52741
PCK2	Phosphoenolpyruvate carboxy	sp Q16822 PCKGM_HUMA	8.33044	8.3008	8.362	8.5664	8.637	8.579	-3.144	0.0007	TRUE	-0.26	1.833137	0.54551
CTSD	Cathepsin D	sp P07339 CATD_HUMAN;	9.12262	9.1886	9.149	9.2976	9.56	9.376	-1.491	0.0323	TRUE	-0.26	1.810984	0.55211
HBB	Hemoglobin beta	CON_P02070;CON_Q35X	7.8013	7.6399	7.777	7.9511	7.936	8.065	-1.713	0.0194	TRUE	-0.24	1.756484	0.56931
HIST1H1C	Histone H1C	sp P16403 H12_HUMAN;sp	9.6761	9.852	9.73	9.9863	9.975	9.967	-1.887	0.013	TRUE	-0.22	1.672775	0.59781
DNAJC2	DnaJ homolog subfamily C mem	sp Q99543-2 DNJC2_HUM	7.53481	7.3096	7.434	7.6012	7.644	7.669	-1.447	0.0358	TRUE	-0.21	1.628764	0.61391
FAHD1	Acylpyruvase	sp Q6P587 FAHD1_HUMA	7.77815	7.9304	7.848	8.0288	8.137	8.013	-1.617	0.0242	TRUE	-0.21	1.612476	0.62011
ECH1	Delta(3,5)-Delta(2,4)-dienoyl-C	sp Q13011 ECH1_HUMAN;	8.04727	8.1538	8.088	8.2642	8.364	8.283	-2.049	0.0089	TRUE	-0.21	1.612273	0.62021
H1FX	Histone 1x	sp Q92522 H1X_HUMAN	8.34009	8.3921	8.368	8.6281	8.484	8.6	-1.921	0.012	TRUE	-0.2	1.59852	0.62551
MUT	Methylmalonyl-CoA mutase	sp P22033 MUTA_HUMAN	7.286	7.1965	7.152	7.4097	7.438	7.366	-1.908	0.0124	TRUE	-0.19	1.560255	0.64091
SDCBP	Syntenin-1	sp Q00560 SDCB1_HUMAN	8.16473	8.1505	8.154	7.9816	7.97	7.991	-4.675	2.11E-05	TRUE	0.175	0.667743	1.49751
TTI1	TELO2-interacting protein 1 hor	sp Q43156 TTI1_HUMAN	7.75163	7.6808	7.637	7.4246	7.569	7.538	-1.503	0.0314	TRUE	0.179	0.661801	1.51101
SCARB1	Scavenger receptor class B mem	sp Q8WTV0-4 SCR1_HUM	7.77851	7.8861	7.795	7.569	7.62	7.728	-1.461	0.0346	TRUE	0.181	0.659439	1.51641
RBMS2	RNA-binding motif, single-stran	sp Q15434 RBMS2_HUMA	7.89264	7.7022	7.791	7.5856	7.602	7.646	-1.473	0.0337	TRUE	0.184	0.654854	1.52701
TTC37	Tetratricopeptide repeat protei	sp Q6PGP7 TTC37_HUMAN	7.91382	7.7741	7.869	7.6294	7.736	7.628	-1.582	0.0262	TRUE	0.188	0.649082	1.54061
LAMC2	Laminin subunit gamma-2	sp Q13753 LAMC2_HUMA	9.23567	9.2228	9.175	9.0962	8.992	8.981	-1.994	0.0101	TRUE	0.188	0.648302	1.54241
WAPL	Wings apart-like protein homol	sp Q7Z5K2 WAPL_HUMAN	7.0271	6.9376	7.043	6.8891	6.733	6.806	-1.591	0.0257	TRUE	0.193	0.640663	1.56081
LPXN	Leupaxin	sp Q60711 LPXN_HUMAN;	8.45487	8.5606	8.528	8.2634	8.33	8.35	-2.101	0.0079	TRUE	0.2	0.630612	1.58571
CSK	Tyrosine-protein kinase CSK	sp P41240 CSK_HUMAN;tr	7.96223	7.9202	7.991	7.71	7.645	7.853	-1.571	0.0268	TRUE	0.221	0.600552	1.66511
SPATS2	Spermatogenesis-associated se	sp Q86XZ4 SPAS2_HUMAN	8.74995	8.7372	8.699	8.4128	8.601	8.499	-1.785	0.0164	TRUE	0.225	0.596101	1.67751
CDKN2AIPNL	CDKN2AIP N-terminal-like prote	sp Q96HQ2 C2AIL_HUMAN	8.22037	8.1923	8.019	7.8805	7.828	8.015	-1.311	0.0488	TRUE	0.236	0.581137	1.72071
CYP51A1	Lanosterol 14-alpha demethyla	sp Q16850 CP51A_HUMAN	8.6308	8.5143	8.586	8.3878	8.39	8.245	-1.8	0.0159	TRUE	0.236	0.580568	1.72241
FSTL1	Follistatin-related protein 1	sp Q12841-2 FSTL1_HUMA	6.7959	6.819	6.776	6.6571	6.524	6.499	-2.023	0.0095	TRUE	0.237	0.579648	1.72511
ATP6V1H	V-type proton ATPase subunit H	sp Q9UI12-2 VATH_HUMA	7.97132	8.132	8.028	7.8374	7.884	7.685	-1.471	0.0338	TRUE	0.242	0.573063	1.74501
HiGD1A	HIG1 domain family member 1A	tr Q9JAW5 C9JAW5_HUMA	8.03587	8.2226	8.062	7.7755	7.859	7.955	-1.452	0.0353	TRUE	0.244	0.570472	1.75291
AAAS	Aladin	tr F8VZ44 F8VZ44_HUMAN	7.88056	7.7601	7.679	7.6426	7.521	7.413	-1.31	0.0489	TRUE	0.248	0.565317	1.76891
THOC3	THO complex subunit 3	sp Q96J01 THOC3_HUMAN	8.1398	8.0464	8.121	7.8539	7.98	7.723	-1.462	0.0345	TRUE	0.25	0.562218	1.77861
FADD	FAS-associated death domain p	sp Q13158 FADD_HUMAN	8.41752	8.2342	8.383	8.0198	8.061	8.192	-1.532	0.0294	TRUE	0.254	0.557322	1.7941
UCK2	Uridine-cytidine kinase 2	sp Q9BZX2 UCK2_HUMAN;	7.94037	7.9337	7.854	7.798	7.57	7.555	-1.492	0.0322	TRUE	0.268	0.539327	1.85411
CDK4	Cyclin-dependent kinase 4	sp P11802 CDK4_HUMAN;	9.8375	9.8062	9.83	9.5575	9.455	9.534	-3.17	0.0007	TRUE	0.309	0.490678	2.0311
MSMO1	Methylsterol monooxygenase 1	sp Q15800-2 MSMO1_HU	7.90859	8.0245	7.968	7.6981	7.628	7.638	-2.84	0.0014	TRUE	0.312	0.487105	2.05291
SQLE	Squalene monooxygenase	tr E7EVQ6 E7EVQ6_HUMA	8.02901	7.8967	7.89	7.6894	7.723	7.457	-1.527	0.0297	TRUE	0.315	0.483857	2.06671
FN1	Fibronectin	sp P02751-6 FINC_HUMAN	7.99319	7.964	7.953	7.6453	7.642	7.663	-4.722	1.90E-05	TRUE	0.32	0.478235	2.09101
DUT	Deoxyuridine 5'-triphosphate n	sp P33316-2 DUT_HUMAN	8.434	8.4649	8.371	8.2349	7.892	8.167	-1.397	0.0401	TRUE	0.325	0.473068	2.11381
RFTN1	Raft-linking protein, isoform CR	tr G3XAJ6 G3XAJ6_HUMAN	7.79599	7.8211	7.772	7.4566	7.321	7.593	-1.883	0.0131	TRUE	0.34	0.457588	2.18531
IPO11	Importin-11	sp Q9UI16 IPO11_HUMAN	8.2006	8.2281	8.143	7.8818	7.802	7.808	-3.247	0.0006	TRUE	0.36	0.436384	2.29151
FADS2	Fatty acid desaturase 2	sp Q95864 FADS2_HUMAN	8.61977	8.5036	8.553	8.2661	8.096	8.231	-2.371	0.0043	TRUE	0.361	0.435635	2.29511
TRIP12	E3 ubiquitin-protein ligase TRIP	sp Q14669-4 TRIPC_HUMA	7.76426	7.9081	7.634	7.4494	7.231	7.449	-1.662	0.0218	TRUE	0.392	0.405216	2.46781
THBS1	Thrombospondin-1	sp P07996 TSP1_HUMAN;	9.15713	9.0691	9.105	8.8049	8.602	8.689	-2.52	0.003	TRUE	0.412	0.387663	2.57951
HMGCS1	Hydroxymethylglutaryl-CoA syn	sp Q01581 HMGCS1_HUMA	9.4041	9.3766	9.384	9.0986	8.804	9.021	-2.022	0.0095	TRUE	0.413	0.386047	2.59031
FADS1	Fatty acid desaturase 1	sp Q60427 FADS1_HUMAN	7.83135	7.5282	7.768	7.108	7.193	7.46	-1.5	0.0316	TRUE	0.456	0.350233	2.85521
IL1A	Interleukin-1 alpha	sp P01583 IL1A_HUMAN	8.08982	7.9666	7.976	7.6892	7.517	7.452	-2.318	0.0048	TRUE	0.458	0.348204	2.87181
F3	Tissue factor	sp P13726 TF_HUMAN;sp	8.33194	8.3969	8.203	8.0594	7.521	7.819	-1.433	0.0369	TRUE	0.511	0.308524	3.24121
ENAH	Protein enabled homolog	sp Q8N857 ENAH_HUMAN	7.30695	7.5495	7.766	6.8331	6.435	7	-1.67	0.0214	TRUE	0.785	0.164152	6.0911

Western Blots without cropping:

