SUPPLEMENTARY INFORMATION

Myeloperoxidase-derived 2-chlorohexadecanal is generated in mouse heart during endotoxemia and induces modification of distinct cardiomyocyte protein subsets in vitro

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Table S1: Biological process gene ontology (GO) enrichment analysis.

#term ID	term description	observed gene count	background gene count	false discovery rate	matching proteins in network (labels)
GO:0006457	protein folding	10	153	5.21e-09	Cct3,Cct5,Cct8,Fkbp4,Hsp90aa1,Hspa1l,Hspb1,Pdia3,Pdia6,Tcp1
GO:0007339	binding of sperm to zona pellucida	6	36	4.02e-07	Aldoa,Cct3,Cct5,Cct8,Hspa1l,Tcp1
GO:0061077	chaperone-mediated protein folding	6	60	2.67e-06	Cct3,Cct5,Cct8,Fkbp4,Hspb1,Tcp1
GO:0017144	drug metabolic process	11	494	4.06e-06	Aldh2,Aldoa,Eno1,Gapdh,Hsp90aa1,Idh3a,Ldha,Ndufs2,Pgam1,Phgdh,Uqcrc1
GO:2000573	positive regulation of DNA biosynthetic process	6	69	4.16e-06	Cct3,Cct5,Cct8,Ddx39b,Hsp90aa1,Tcp1
GO:0009987	cellular process	47	12459	4.22e-06	Alad,Alb,Aldh2,Aldoa,Cct3,Cct5,Cct8,Dctn2,Ddx39,Ddx39b,Des,Eef1g,Eef2,Eif3f,Eif4a2,Eno1,Fdps,Fkbp4,Gapdh,Hnrnpl,Hsp90aa1,Hspa1l,Hspb1,Idh3a,Ldha,Lmna,Lyz1,Ndufs2,Pcna,Pdia3,Pdia6,Pgam1,Phgdh,Prph,Psmd13,Rpsa,Ruvbl2,Tcp1,Tuba3b,Tubal3,Tubb3,Tubb6,Uap1l1,Uqcrc1,Uqcrc2,Vim,Ywhab
GO:1904851	positive regulation of establishment of protein localization to telomere	4	10	4.22e-06	Cct3,Cct5,Cct8,Tcp1
GO:0046031	ADP metabolic process	5	44	1.07e-05	Aldoa,Eno1,Gapdh,Ldha,Pgam1
GO:0046034	ATP metabolic process	7	162	1.15e-05	Aldoa,Eno1,Gapdh,Ldha,Ndufs2,Pgam1,Uqcrc1
GO:0046496	nicotinamide nucleotide metabolic process	6	101	1.55e-05	Aldoa,Eno1,Gapdh,Idh3a,Ldha,Pgam1
GO:0006090	pyruvate metabolic process	5	62	2.34e-05	Aldoa,Eno1,Gapdh,Ldha,Pgam1
GO:0006091	generation of precursor metabolites and energy	8	295	2.34e-05	Aldoa,Eno1,Gapdh,Idh3a,Ldha,Ndufs2,Pgam1,Uqcrc1
GO:0009167	purine ribonucleoside monophosphate metabolic process	7	196	2.34e-05	Aldoa,Eno1,Gapdh,Ldha,Ndufs2,Pgam1,Uqcrc1
GO:0051054	positive regulation of DNA metabolic process	7	223	3.96e-05	Cct3,Cct5,Cct8,Ddx39b,Hsp90aa1,Pcna,Tcp1
GO:0032212	positive regulation of telomere maintenance via telomerase	4	31	4.95e-05	Cct3,Cct5,Cct8,Tcp1
GO:0032204	regulation of telomere maintenance	5	78	5.10e-05	Cct3,Cct5,Cct8,Lmna,Tcp1
GO:0016052	carbohydrate catabolic process	5	80	5.59e-05	Aldoa,Eno1,Gapdh,Ldha,Pgam1
GO:0006458	'de novo' protein folding	4	35	6.80e-05	Cct3,Cct5,Cct8,Tcp1
GO:0050821	protein stabilization	6	157	6.85e-05	Cct3,Cct5,Cct8,Gapdh,Hsp90aa1,Tcp1
GO:0006096	glycolytic process	4	37	7.79e-05	Aldoa,Eno1,Gapdh,Pgam1
GO:0006757	ATP generation from ADP	4	37	7.79e-05	Aldoa,Eno1,Gapdh,Pgam1
GO:0009166	nucleotide catabolic process	5	90	8.27e-05	Aldoa,Eno1,Gapdh,Ldha,Pgam1
GO:0051052	regulation of DNA metabolic process	8	383	8.94e-05	Cct3,Cct5,Cct8,Ddx39b,Hsp90aa1,Lmna,Pcna,Tcp1
GO:0042866	pyruvate biosynthetic process	4	41	0.00010	Aldoa,Eno1,Gapdh,Pgam1
GO:1901998	toxin transport	4	42	0.00011	Cct3,Cct5,Cct8,Tcp1
GO:0051186	cofactor metabolic process	8	403	0.00012	Alad,Aldoa,Eef1g,Eno1,Gapdh,Idh3a,Ldha,Pgam1
GO:0055086	nucleobase-containing small molecule metabolic process	9	566	0.00016	Aldoa,Eno1,Gapdh,Idh3a,Ldha,Ndufs2,Pgam1,Uap1l1,Uqcrc1
GO:0019359	nicotinamide nucleotide biosynthetic process	4	54	0.00025	Aldoa,Eno1,Gapdh,Pgam1
GO:0009117	nucleotide metabolic process	8	488	0.00039	Aldoa,Eno1,Gapdh,Idh3a,Ldha,Ndufs2,Pgam1,Uqcrc1
GO:0016043	cellular component organization	24	4560	0.00051	Alad,Aldoa,Cct3,Cct8,Dctn2,Ddx39b,Des,Fkbp4,Gapdh,Hsp90aa1,Lmna,Pcna,Phgdh,Prph,Psmd13,Rpsa,Ruvbl2,Tuba3b,Tubal3,Tubb3,Tubb6,Uqcrc

					2,Vim,Ywhab
GO:0006754	ATP biosynthetic process	4	70	0.00054	Aldoa,Eno1,Gapdh,Pgam1
GO:0046394	carboxylic acid biosynthetic process	6	256	0.00061	Aldoa,Eno1,Gapdh,Ldha,Pgam1,Phgdh
GO:0055114	oxidation-reduction process	10	898	0.00069	Aldh2,Gapdh,Idh3a,Ldha,Ndufs2,Pdia3,Pdia6,Phgdh,Uqcrc1,Uqcrc2
GO:0051701	interaction with host	4	78	0.00073	Alb,Ddx39b,Gapdh,Tcp1
GO:0007010	cytoskeleton organization	10	916	0.00080	Dctn2,Des,Gapdh,Lmna,Prph,Tuba3b,Tubal3,Tubb3,Tubb6,Vim
GO:0072330	monocarboxylic acid biosynthetic process	5	164	0.00080	Aldoa,Eno1,Gapdh,Ldha,Pgam1
GO:1901566	organonitrogen compound biosynthetic process	11	1122	0.00080	Alad,Aldoa,Eef1g,Eef2,Eif3f,Eif4a2,Eno1,Gapdh,Pgam1,Phgdh,Rpsa
GO:2001252	positive regulation of chromosome organization	5	166	0.00080	Cct3,Cct5,Cct8,Ruvbl2,Tcp1
GO:0051704	multi-organism process	14	1840	0.00091	Alad,Alb,Aldoa,Cct3,Cct5,Cct8,Ddx39b,Eif3f,Fkbp4,Gapdh,Hspa1l,Hspb1,Lyz1,Tcp1
GO:1904951	positive regulation of establishment of protein localization	7	424	0.00094	Cct3,Cct5,Cct8,Gapdh,Hsp90aa1,Hspa1l,Tcp1
GO:0051188	cofactor biosynthetic process	5	175	0.00097	Alad,Aldoa,Eno1,Gapdh,Pgam1

Table S2: KEGG pathway analysis.

#term ID	term description	observed gene count	background gene count	false discovery rate	matching proteins in network (labels)
mmu00010	Glycolysis / Gluconeogenesis	6	65	1.25e-06	Aldh2,Aldoa,Eno1,Gapdh,Ldha,Pgam1
mmu01230	Biosynthesis of amino acids	6	75	1.40e-06	Aldoa,Eno1,Gapdh,Idh3a,Pgam1,Phgdh
mmu01200	Carbon metabolism	6	118	1.19e-05	Aldoa,Eno1,Gapdh,Idh3a,Pgam1,Phgdh
mmu01100	Metabolic pathways	14	1296	2.21e-05	Alad,Aldh2,Aldoa,Eno1,Fdps,Gapdh,Idh3a,Ldha,Ndufs2,Pgam1,Phgdh,Uap1l1,Uqcrc1,Uqcrc2