

Supplementary Table S1. List of all autoantigens identified by MALDI-TOF-MS/MS corresponding to autoantibodies generated in two mouse strains (A.BY/SnJ and C57BL/6) after infection with Coxsackie virus B3

[illegible]

B_54	KCRS	IPI00120076	Ckmt2	Creatine kinase, sarcomeric mitochondrial	14.0	9.8	7.1	11.0	11.6	15.54	4.07	1.39	3.40	2.67	+	+
B_31	KPYM	IPI00407130	Pkm2	Pyruvate kinase isozyme M2	46.5	60.4	10.8	9.8	5.8	9.78	7.90	0.53	21.73	0.00	+	
B_30	KPYM	IPI00407130	Pkm2	Pyruvate kinase isozyme M2	5.8	14.9	1.7	2.6	0.3						+	
A_143	LDHB	IPI00229510	Ldhb	L-lactate dehydrogenase B chain	6.9	12.2	1.7	4.6	4.9	16.45	3.56	1.91	3.08	0.60	+	
A_132	MANA	IPI00125807	Mpi1	Mannose-6-phosphate isomerase	2.1	6.4	0.9	0.9	1.6	1.11	0.56	1.97	9.29	15.96	+	
A_146	MDHC	IPI00336324	Mdh1	Malate dehydrogenase, cytoplasmic	11.4	11.1	11.1	3.6	3.2	34.84	9.58	13.15	5.62	2.46	+	
B_74	MDHM	IPI00331590	Mdh2	Malate dehydrogenase 2, NAD	28.7	12.1	36.3	12.2	4.7	6.96	0.86	0.82	1.02	0.80	+	
A_137	NDUAA	IPI00116748	Ndufa10	NADH-ubiquinone oxidoreductase 42 kDa subunit, mitochondrial	20.2	31.6	9.6	19.6	9.4						+	
B_97	NDUB6	IPI00341322	Ndufb6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	10.9	0.5	0.0	0.2	0.1						+	
A_44	NDUS1	IPI00308882	Ndufs1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	39.7	71.3	9.7	269.2	12.0	6.02	1.31	0.19	1.32	0.49	+	
A_48	NDUS1	IPI00308882	Ndufs1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	11.4	2.3	1.8	0.4	0.0						+	
A_123	NDUS2	IPI00128023	Ndufs2	NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial	16.2	15.9	4.1	11.9	3.6	5.96	2.37	0.83	2.56	1.61	+	
A_151	NDUS3	IPI00121309	Ndufs3	NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial	7.1	12.5	30.3	4.7	3.5	14.33	2.63	10.34	2.46	1.23	+	
B_45	NDUV1	IPI00130460	Ndufv1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	29.6	19.1	28.7	19.9	12.6	359.16	19.33	437.49	77.00	24.00	+	
A_22	ODO1	IPI00719841	Ogdh	Oxoglutarate dehydrogenase	25.6	13.1	0.8	2.4	6.7						+	
A_112	ODO2	IPI00134809	Dlst	Dihydropyridyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase	68.3	49.4	5.1	1.5	3.7	8.62	1.56	0.00	0.05	0.39	+	
A_113	ODO2	IPI00134809	Dlst	Dihydropyridyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase	26.8	12.4	1.5	1.0	3.2						+	
A_74	ODP2	IPI00153660	Dlat	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	68.4	101.1	4.2	18.6	5.6	15.24	4.57	6.74	7.08	1.00	+	
A_78	ODP2	IPI00153660	Dlat	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	151.5	240.7	11.9	16.1	15.4						+	
B_51	ODPA	IPI00337893	Pdha1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial	30.7	32.7	4.1	8.6	3.0	16.85	6.38	0.85	9.06	3.92	+	
A_125	ODPA	IPI00337893	Pdha1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial	1.8	13.1	1.7	0.7	1.3						+	
A_145	ODPB	IPI00132042	Pdhb	Pyruvate dehydrogenase E1 component beta subunit, mitochondrial	20.8	16.0	4.1	5.1	6.1	18.09	4.01	4.90	4.33	3.59	+	
A_109	ODPX	IPI00222767	Pdhx	Pyruvate dehydrogenase protein X component, mitochondrial	37.1	32.0	13.0	2.5	7.3	57.96	49.01	0.00	3.02	0.00	+	
A_57	PCCA	IPI00330523	Pcca	Propionyl-CoA carboxylase alpha chain, mitochondrial	213.0	80.5	32.8	35.2	59.6						+	
B_88	PGAM2	IPI00230706	Pgam2	Phosphoglycerate mutase 2	6.8	1.6	1.7	2.3	2.0	2.47	1.22	0.21	1.08	1.47	+	
B_60	PGK1	IPI00230002	Pgk1	Phosphoglycerate kinase 1	6.3	5.3	2.0	3.9	7.4	3.94	0.96	7.64	3.57	1.19	+	
B_29	PGM1	IPI00555140	Pgm2	Phosphoglucomutase-1	13.7	14.6	2.2	2.3	1.5	37.73	0.41	0.00	6.04	4.27	+	
A_86	PGM1	IPI00555140	Pgm2	Phosphoglucomutase-1	6.4	19.8	1.1	0.9	0.4						+	
A_84	PGM1	IPI00555140	Pgm2	Phosphoglucomutase-1	18.4	19.6	1.5	2.6	1.4						+	
A_88	PGM5	IPI00269750	Pgm5	Phosphoglucomutase 5	3.0	20.4	1.0	0.4	0.8						+	
A_90	PPP5	IPI00119180	Ppp5c	Serine/threonine-protein phosphatase 5	0.0	1.5	1.4	0.0	46.5						+	+
B_22	Q3TB39	IPI00223092	Hadha	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A h	3.1	3.7	0.7	2.1	1.7	15.15	1.94	3.23	34.82	2.96	+	+
B_84	Q8C2Q8	IPI00750074	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	2.7	2.5	1.9	2.6	2.4	4.94	2.76	0.47	1.90	1.27	+	+
B_87	Q8QZV3	IPI00331692	Dci	Dodecenoyl-Coenzyme A delta isomerase	34.5	12.1	3.2	3.6	21.6	5.49	0.89	0.07	1.28	1.72	+	
B_72	Q91W85	IPI00331251	Acads	Acyl-Coenzyme A dehydrogenase, short chain	12.8	16.5	3.2	11.3	1.8	6.59	0.81	0.20	0.66	0.63	+	
A_138	Q91W85	IPI00331251	Acads	Acyl-Coenzyme A dehydrogenase, short chain	13.6	33.9	6.6	11.8	2.9						+	
B_36	SCOT	IPI00132653	Oxct1	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	1.6	4.0	1.1	40.1	28.0						+	
A_129	SUCB1	IPI00261627	Sucba2	Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial	9.1	5.9	3.3	8.8	4.9	3.70	1.74	0.89	1.21	0.59	+	
B_91	UCRI	IPI00133240	Uqcrrf1	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial	29.9	11.7	3.5	4.9	9.7	6.14	4.65	0.87	1.43	2.18	+	
A_118	UQCR1	IPI00111885	Uqcrc1	Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial	23.5	45.0	4.7	6.9	27.8	14.48	2.16	1.79	0.73	1.14	+	+
A_115	UQCR1	IPI00111885	Uqcrc1	Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial	11.1	20.1	2.8	4.6	21.9	9.50	2.75	2.63	1.71	1.18	+	+
B_57	UQCR2	IPI00119138	Uqcrc2	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial	26.1	4.6	1.5	44.8	2.6	4.48	0.23	0.69	1.81	1.04	+	+
B_56	UQCR2	IPI00119138	Uqcrc2	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial	18.7	8.5	1.8	50.4	2.5	5.07	1.06	0.77	2.39	2.80	+	+
B_77	ANXA2	IPI00468203	Anxa2	Annexin A2	10.8	6.6	5.2	7.8	5.0	2.14	0.21	2.54	1.60	0.83	+	+
A_93	COR1A	IPI00323600	Coro1a	Coronin-1A	3.3	2.3	1.4	0.1	0.3						+	+
A_102	DESM	IPI00130102	Des	Desmin	12.9	2.0	4.2	20.7	5.2	1.72	0.39	0.26	0.63	0.21	+	+
A_100	DESM	IPI00130102	Des	Desmin	3.8	2.6	2.5	5.9	2.5	1.51	1.19	1.35	1.78	0.59	+	
A_107	DESM	IPI00130102	Des	Desmin	19.6	3.2	4.8	44.2	4.8						+	
A_46	DNM1L	IPI00172221	Dnm1l	Isoform 3 of Dynamin-1-like protein	0.7	0.8	0.7	0.2	20.2						+	+
B_78	FHL2	IPI00118205	Fhl2	Four and a half LIM domains protein 2	6.8	6.3	4.9	7.0	2.8	17.98	2.43	0.94	2.75	1.27	+	

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A_62	ALBU	IPI00131695	Alb1	Serum albumin	75.4	76.2	3.2	27.0	13.5	7.10	1.52	0.56	3.83	0.57	+
A_67	ALBU	IPI00131695	Alb1	Serum albumin	570.3	707.0	89.4	63558.5	583.2						+
B_21	TRFE	IPI00139788	Trf	Serotransferrin	13.1	25.0	1.1	5.9	24.1	82.13	0.63	8.75	71.13	34.00	+
B_20	TRFE	IPI00139788	Trf	Serotransferrin	25.3	27.0	1.4	6.8	21.4						+
A_40	TRFE	IPI00139788	Trf	Serotransferrin	139.4	60.9	3.8	17.6	107.9						+
A_37	TRFE	IPI00139788	Trf	Serotransferrin	47.6	20.5	3.1	7.4	455.1						+
A_38	TRFE	IPI00139788	Trf	Serotransferrin	34.2	26.8	11.6	8.6	473.2						+
B_80	VDAC1	IPI00122549	Vdac1	Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel protein 1	6.6	1.3	1.3	3.5	2.8	4.03	0.61	0.65	2.95	2.00	+
B_94	VDAC1	IPI00122549	Vdac1	Isoform Mt-VDAC1 of Voltage-dependent anion-selective channel protein 1	8.6	2.4	1.5	4.8	27.0						+
B_47	ECHB	IPI00115607	Hadhb	Trifunctional enzyme subunit beta, mitochondrial	16.3	18.4	10.6	150.2	15.4	10.26	0.88	0.98	26.39	1.40	+
B_44	EF1A2	IPI00119667	Eef1a2	Elongation factor 1-alpha 2	62.2	87.0	76.8	44.1	2.1	3.61	0.98	2.33	16.17	10.10	+
B_34	EF1A2	IPI00119667	Eef1a2	Elongation factor 1-alpha 2	138.1	177.1	64.6	24.5	2.2						+
A_120	EF1G	IPI00318841	Eef1g	Elongation factor 1-gamma	9.2	11.2	0.9	3.4	2.9	9.50	6.15	0.78	0.79	0.56	+
B_16	EF2	IPI00466069	Eef2	Elongation factor 2	27.4	34.9	9.7	2.9	0.5						+
A_29	EF2	IPI00466069	Eef2	Elongation factor 2	18.9	33.6	2.7	1.0	4.2						+
A_28	EF2	IPI00466069	Eef2	Elongation factor 2	38.2	16.8	5.9	1.6	11.2						+
B_52	EFTU	IPI00274407	Tufm	Isoform 1 of Elongation factor Tu, mitochondrial	70.0	48.1	4.8	33.6	1.8	28.23	1.42	0.39	2.52	0.12	+
A_124	EFTU	IPI00274407	Tufm	Splice Isoform 1 of Elongation factor Tu, mitochondrial	82.1	79.0	3.0	41.2	3.0	16.41	3.09	1.01	1.68	0.46	+
A_90	PDIA3	IPI00230108	Pdia3	Protein disulfide isomerase associated 3	0.0	1.5	1.4	0.0	46.5						+
A_121	PRS7	IPI00270326	Psmc2	26S protease regulatory subunit 7	5.4	0.6	0.7	0.8	0.0						+
B_55	Q3TIT9	IPI00653158	Acaa2	Acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	14.3	2.1	1.4	3.4	2.3	5.33	0.83	0.53	1.74	1.34	+
A_43	Q3TLV2	IPI00387333	Tgm2	Transglutaminase 2, C polypeptide	23.4	165.8	19.1	1.1	2.8	21.77	3.29	2.03	0.14	0.03	+
A_106	SAM50	IPI00221608	Samm50	SAM50-like protein CGI-51 homolog	10.6	9.8	2.8	5.9	6.8						+
A_104	SAM50	IPI00221608	Samm50	Sorting and assembly machinery component 50 homolog	24.2	17.7	2.5	3.5	7.7						+
A_101	SYDC	IPI00122743	Dars	Aspartyl-tRNA synthetase	5.9	366.9	957.1	111.8	3.4						+
B_64	THIL	IPI00154054	Acat1	Acetyl-CoA acetyltransferase, mitochondrial	17.9	255.3	29.3	8.2	37.5	6.67	0.73	0.96	6.09	0.00	+
B_66	THIL	IPI00154054	Acat1	Acetyl-CoA acetyltransferase, mitochondrial	17.4	52.4	6.3	5.4	14.7				5.88	3.51	+
A_103	TRI72	IPI00462157	Trim72	similar to tripartite motif protein 50	1.8	2.0	2.2	2.2	54.1						+
B_40	SMYD1	IPI00118495	Smyd1	Smyd1 protein	0.7	11.2	204.6	4.0	2.1						+
A_104	SMYD1	IPI00118495	Smyd1	Smyd1 protein	24.2	17.7	2.5	3.5	7.7						+
B_70	AATC	IPI00230204	Got1	Aspartate aminotransferase, cytoplasmic	15.0	5.8	7.6	8.8	8.9	17.14	8.78	5.92	27.01	11.43	+
B_65	AATM	IPI00117312	Got2	Aspartate aminotransferase, mitochondrial	18.1	12.1	3.3	6.0	3.9	4.67	1.01	0.57	4.10	2.26	+
A_114	ALDH2	IPI00111218	Aldh2	Aldehyde dehydrogenase, mitochondrial	16.1	32.7	3.3	9.8	1.9	127.70	22.70	19.29	31.24	12.52	+
B_76	ALDR	IPI00223757	Akr1b3	Aldose reductase	21.1	5.5	3.1	12.1	1.8	1.82	0.00	0.00	1.01	1.39	+
B_50	FUMH	IPI00129928	Fh1	Isoform Cytoplasmic of Fumarate hydratase, mitochondrial	42.0	21.6	12.7	5.5	3.2	4.00	0.44	0.51	3.87	1.76	+
B_48	FUMH	IPI00129928	Fh1	Isoform Cytoplasmic of Fumarate hydratase, mitochondrial	33.7	23.6	15.7	12.0	2.3	4.25	0.71	0.74	5.80	3.11	+
B_49	FUMH	IPI00129928	Fh1	Isoform Cytoplasmic of Fumarate hydratase, mitochondrial	63.9	53.6	18.8	4.2	2.9						+
A_16	Q9JHW2	IPI00119945	Nit2	Nit protein 2	15.0	6.2	5.4	978.5	39.9	7.17	1.15	3.05	11.84	3.24	+
A_150	Q9JHW2	IPI00119945	Nit2	Nit protein 2	0.2	4.6	0.8	0.8	0.5						+
B_43	Glud1*	IPI00753095	Glud1	similar to Glutamate dehydrogenase 1, mitochondrial (GDH) isoform	3.4	2.0	0.5	438.5	2.1						+
A_83	2AAA	IPI00310091	Ppp2r1a	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	22.4	75.3	2.7	4.3	1.9						+
A_140	ARHL1	IPI00221629	Adprhl1	ADP-ribosylhydrolase like 1	3.8	4.7	3.4	3.5	3.5						+
A_147	CLYBL	IPI00153903	Clybl	Citrate lyase beta subunit	1.6	28.7	13.3	2.6	0.2						+
B_81	CLYBL	IPI00153903	Clybl	Citrate lyase beta subunit	3.8	23.0	5.3	2.2	0.4						+
B_93	ES1	IPI00133284	D10Jhu81e	ES1 protein homolog, mitochondrial	48.3	33.3	17.0	24.6	2.1	5.49	1.25	0.00	0.59	0.29	+
B_99	H2B1K	IPI00265768	Hist1h2bk	Histone H2B type 1-K	55.7	8.6	4.1	1.4	0.9						+
A_63	IMMT	IPI00228150	Immt	Isoform 2 of Mitochondrial inner membrane protein	44.2	26.4	10.6	9.9	3.0	4.21	2.77	2.06	23.80	1.94	+
A_64	IMMT	IPI00228150	Immt	Inner membrane protein, mitochondrial	5.7	1.1	0.7	0.0	0.0						+
B_24	IMMT	IPI00228150	Immt	Isoform 2 of Mitochondrial inner membrane protein	19.8	11.5	5.6	2.5	1.8						+
A_130	Q3T9C9	IPI00653566	Acot2	Mitochondrial acyl-CoA thioesterase 1	22.6	8.4	2.3	3.7	1.6	12.53	1.85	0.57	0.60	4.02	+
A_147	Q9DCJ6	IPI00620329	Clybl	Hypothetical malate synthase G structure containing protein	1.6	28.7	13.3	2.6	0.2						+
A_72	#NV	IPI00753407		similar to heat shock protein 8	24.0	28.0	3.7	1044.2	22.5	25.06	2.05	0.97	2.56	0.52	
A_80	#NV	IPI00122737		222 kDa protein	4.9	2.0	1.7	794.8	38.5	3.81	0.53	0.15	0.90	0.61	
A_61	#NV	IPI00753407		similar to heat shock protein 8	12.3	8.9	2.9	1474.3	11.7						
A_58	#NV	IPI00480560		71 kDa protein	20.0	11.0	6.0	2518.0	20.2						
Mean value across all Western Blot signals per time point					25.6	31.1	14.7	636.4	41.1	22.0	4.3	7.1	12.3	4.7	

#	
1	Energy metabolism
2	Cell structure and associated proteins
3	Immunity
4	Cell cycle
5	Signal transduction
6	Intracellular protein traffic
7	Transport
8	Protein metabolism and modification
9	Nucleoside, nucleotide and nucleic acid metabolism
10	Other process
11	Biological process unclassified