

Table A List of polymorphic proteins detected in the mouse brain supernatant fraction by 2D-electrophoresis and comparison of two mouse species (*Mus musculus*/C57BL/6 and *Mus spretus*)

2-DE Spot-No ^a	Name ^b	PROTEINS				GENES				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
E6_070	diazepam binding inhibitor	SP P31786	9.93	6.96	61.01	mV131BS	A	1 ^g	<i>Dbi</i>	64	≥ 2.5	<i>D1Mit</i> LOD 17.76 (0)
E6_047	diazepam binding inhibitor	SP P31786	9.92	6.10	72.71	"	A	1 ^g	<i>Dbi</i>	64	≥ 2.5	<i>D1Mit</i> LOD 17.76 (0)
B5_429	modifier of Acyl-coA dehydrogenase, long-chain specific	NCBI 1703064	45.08	6.55	84.11	mV244BS	A	1 ^g	<i>Acadlm</i>	64	≥ 2.5	
D2_269	phosphoprotein enriched in astrocytes 15 ⁱ		14.44	4.97	23.79	mV5BS	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_256	phosphoprotein enriched in astrocytes 15 ⁱ		14.57	4.86	94.43	"	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_271	phosphoprotein enriched in astrocytes 15 ⁱ		14.32	4.74	155.11	"	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_277	phosphoprotein enriched in astrocytes 15 ⁱ		14.12	4.98	72.25	"	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_227	phosphoprotein enriched in astrocytes 15 ⁱ		14.30	4.84	20.77	"	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_258	phosphoprotein enriched in astrocytes 15 ⁱ		14.59	4.74	72.22	"	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_270	phosphoprotein enriched in astrocytes 15 ⁱ	NCBI 2498751	14.28	4.87	234.90	"	A	1	<i>Pea15</i>	64	≥ 2.5	
D2_278	phosphoprotein enriched in astrocytes 15 ⁱ		14.10	4.84	38.44	"	A	1	<i>Pea15</i>	64	≥ 2.5	
B5_600	RIKEN cDNA 0610033B02 gene	NCBI 1291927	38.56	6.46	46.95	mV242BS	A	1 ^g	<i>0610033B02Rik</i>	64	≥ 2.5	
B2_238	inositol polyphosphate-1-phosphatase	NCBI 6680457	49.92	5.00	124.72	aV172BS	A	1	<i>Inpp1</i>	64	linked to chr	<i>D1Mit234</i> LOD 4.82 (22.31)
B2_271	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ		47.40	4.84	30.06	mV76BS	A	1 ^g	<i>Ppp1r7</i>	64	≥ 2.5	
B2_272	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ		47.40	4.87	35.40	"	A	1 ^g	<i>Ppp1r7</i>	64	≥ 2.5	
B2_276	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ		47.15	4.99	48.15	"	A	1 ^g	<i>Ppp1r7</i>	64	≥ 2.5	
B2_274	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ		47.24	4.95	49.35	"	A	1 ^g	<i>Ppp1r7</i>	64	≥ 2.5	
B2_273	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ	NCBI 12655852	47.24	4.91	87.47	"	A	1 ^g	<i>Ppp1r7</i>	64	≥ 2.5	
B2_325	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ		44.31	4.92	33.74	mV60BS	A	1 ^g	<i>Ppp1r7</i>	62	≥ 2.5	<i>Ppp1r7</i> (mV76BS) LOD 18.66 (0)
B2_326	protein phosphatase 1, regulatory (inhibitor) subunit 7 ⁱ		44.15	5.01	24.92	mV61BS	A	1 ^g	<i>Ppp1r7</i>	64	≥ 2.5	<i>Ppp1r7</i> (mV76BS) LOD 19.27 (0)
D5_009			22.33	6.26	12.32	mV184BS	A	1	<i>mV184BS</i>	29	linked to chr	<i>Ppp1r7</i> (mV76BS) LOD 4.29 (12.06) <i>D1Mit234</i> LOD 2.58 (16.82)
C5_335			25.20	6.40	11.33	mV211BS	A	1	<i>mV211BS</i>	23	linked to chr	<i>Ppp1r7</i> (mV76BS) LOD 3.71 (10.03)
C5_343			25.12	6.40	28.46	"	A	1	<i>mV211BS</i>	23	linked to chr	<i>Ppp1r7</i> (mV76BS) LOD 3.71 (10.03)
C4_343			23.91	6.08	19.32	mV362BS	A	1	<i>mV362BS</i>	62	≥ 2.5	
C6_385			28.87	6.95	27.03	paV291BS	A	1	<i>paV291BS</i>	58	≥ 2.5	
B4_063			62.88	6.09	85.14	paV498BS	A	1	<i>paV498BS</i>	56	interval (2.2)	<i>D1Mit234</i> LOD 11.17 (2.33)
C4_231	serin (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1	SP P32261	27.15	6.00	500.63			1	<i>Serpinc1</i>			
C6_074	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	NCBI 728931	33.09	7.32	39.08	mV233BS	A	2 ^g	<i>Atp5c1</i>	64	≥ 2.5	
B6_004	carnitine acetyltransferase	NCBI 6681009	67.62	6.84	22.24	mV283BS	A	2	<i>Crat</i>	63	≥ 2.5	
C4_345	modifier 1 of glutamate dehydrogenase	NCBI 1283647	35.49	5.99	20.21	paV105BS	A	2 ^g	<i>Gludm1</i>	52	interval (≥ 2.5)	<i>D2Nds3</i> LOD 8.73 (8.91)
D5_002	RIKEN cDNA 1700037H04 gene	NCBI 1387530	22.33	6.48	30.23	mV185BS	A	2 ^g	<i>1700037H04Rik</i>	64	≥ 2.5	
C2_082	e-1 enzyme	NCBI 6523813	33.00	4.87	29.28	mV349BS	A	2 ^{g,k}	<i>Masa-pending</i>	64	interval (≥ 2.5)	<i>D2Irs4</i> LOD 18.06 (0)
B3_326	glutathione synthetase	NCBI 1016285	50.73	5.52	38.18	mV72BS	A	2 ^g	<i>Gss</i>	62	interval (≥ 2.5)	<i>D2Irs4</i> LOD 17.46 (0)
B4_591	modifier of uroporphyrinogen decarboxylase	NCBI 2501645	38.90	6.03	9.81	paV120BS	A	2 ^g	<i>Urodm</i>	56	≥ 2.5	
B2_037			70.20	4.75	13.31	mV92BS	A	2	<i>mV92BS</i>	53	≥ 2.5	
B2_035			70.40	4.79	36.82	"	A	2	<i>mV92BS</i>	53	≥ 2.5	
B6_013			66.51	6.82	16.75	mV284BS	A	2	<i>mV284BS</i>	60	linked to chr	<i>Crat</i> (mV283BS) LOD 5.65 (22.84)
B2_066			64.75	4.71	30.30	mV312BS	A	2	<i>mV312BS</i>	28	linked to chr	<i>Atp5c1</i> (mV233BS) LOD 3.44 (16.82)
B4_588			53.91	5.67	51.40	mV359BS	A	2	<i>mV359BS</i>	63	interval (≥ 2.5)	<i>D2Irs2</i> LOD 14.09 (1.89)
C3_032			34.89	5.46	44.71	paV113BS	A	2	<i>paV113BS</i>	63	interval (≥ 2.5)	<i>Atp5c1</i> (mV233BS) LOD 13.73 (5.00)
B3_102			62.54	5.29	27.17	paV179BS	A	2	<i>paV179BS</i>	58	≥ 2.5	
A3_161			103.57	5.36	30.01	paV184BS	A	2	<i>paV184BS</i>	59	≥ 2.5	
C5_010			35.68	6.28	90.48	paV396BS	A	2	<i>paV396BS</i>	64	interval (≥ 2.5)	<i>D2Nds3</i> LOD 15.56 (1.72)
B5_392			47.19	6.57	30.04	paV466BS	A	2	<i>paV466BS</i>	57	interval (≥ 2.5)	<i>D2Irs4</i> LOD 15.95 (0)
B6_226	creatine kinase, mitochondrial 1, ubiquitous	SP P30275	47.50	6.98	157.72			2	<i>Ckmt1</i>			
B6_248	creatine kinase, mitochondrial 1, ubiquitous	SP P30275	47.27	6.98	45.68			2	<i>Ckmt1</i>			
A4_171	topoisomerase (DNA) I	SP Q04750	78.40	6.04	97.61			2	<i>Top1</i>			
B4_503	dynamain	SP P39053	38.82	6.07	175.20			2	<i>Dnm</i>			

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B7_019	eukaryotic translation elongation factor 1 alpha 2	SP P27706	51.89	7.80	823.77			2	<i>Eef1a2</i>			
B7_035	eukaryotic translation elongation factor 1 alpha 2	SP P27706	51.98	7.74	360.53			2	<i>Eef1a2</i>			
B7_036	eukaryotic translation elongation factor 1 alpha 2	SP P27706	52.08	7.64	84.50			2	<i>Eef1a2</i>			
D5_080	geisolin	SP P06396	17.13	6.21	200.62			2	<i>Gsn</i>			
A3_343	heat shock 70kD protein 5 (glucose-regulated protein, 78kD)	SP P20029	77.20	5.07	179.87			2	<i>Hspa5</i>			
B4_099	glucose regulated protein, 58 kDa	SP P27773	59.73	5.85	237.64			2	<i>Grp58</i>			
B5_505	alcohol dehydrogenase 5	SP P28474	41.33	6.37	325.05	mV146BS	A	3 ^h	<i>Adh5</i>	64	≥ 2.5	
C2_049	annexin A5	SP P48036	34.18	4.91	152.10	mV27BS	A	3	<i>Anxa5</i>	64	≥ 2.5	
C5_388	modifier 1 of peroxiredoxin 5	NCBI 6671549	24.91	6.58	22.56	paV244BS	A	3 ^g	<i>Prdx5m1</i>	27	linked to chr	<i>Adh5</i> (mV146BS) LOD 4.04 (12.57)
C5_192	carbonic anhydrase 1	NCBI 1345656	29.03	6.60	160.67	paV255BS	A	3	<i>Car1</i>	44	linked to chr	<i>D3Mit61</i> LOD 4.24 (18.97) <i>D3Mit1</i> LOD 3.97 (9.55)
C5_151	carbonic anhydrase 2	SP P00920	29.60	6.67	649.88	mV138BS	A	3	<i>Car2</i>	64	interval (≥ 2.5)	<i>D3Mit61</i> LOD 10.06 (9.46) <i>D3Mit1</i> LOD 8.56 (2.94)
A5_009	carbonic anhydrase 2 ⁱ		192.29	6.68	4.59	mV285BS	A	3	<i>Car2</i>	60	interval (≥ 2.5)	<i>D3Mit61</i> LOD 9.02 (10.24) <i>D3Mit1</i> LOD 7.70 (3.23)
A5_013	carbonic anhydrase 2 ⁱ		186.51	6.67	5.77	"	A	3	<i>Car2</i>	60	interval (≥ 2.5)	<i>D3Mit61</i> LOD 9.02 (10.24) <i>D3Mit1</i> LOD 7.70 (3.23)
A5_017	carbonic anhydrase 2	SP P00920	181.69	6.67	33.08	"	A	3	<i>Car2</i>	60	interval (≥ 2.5)	<i>D3Mit61</i> LOD 9.02 (10.24) <i>D3Mit1</i> LOD 7.70 (3.23)
A5_021	carbonic anhydrase 2 ⁱ		175.90	6.67	9.77	"	A	3	<i>Car2</i>	60	interval (≥ 2.5)	<i>D3Mit61</i> LOD 9.02 (10.24) <i>D3Mit1</i> LOD 7.70 (3.23)
C5_271	modifier 1 of carbonic anhydrase 2	SP P00920	26.86	6.63	103.67	mV134BS	A	3 ^g	<i>Car2m1</i>	62	linked to chr	<i>Car2</i> (mV138BS) LOD 3.77 (33.97) <i>Hbbm</i> (mV174BS) LOD 4.24 (9.12) <i>Car2</i> (mV285BS) LOD 4.06 (29.74)
D5_076	modifier 2 of carbonic anhydrase 2	NCBI 192343	17.31	6.47	23.90	paV227BS	A	3 ^g	<i>Car2m2-pending</i>	22	interval (≥ 2.5)	<i>D3Mit1</i> LOD 6.02 (0)
B5_440	peptidylprolyl isomerase D-like (cyclophilin 40)	SP Q08752	44.45	6.71	325.70	mV148BS	A	3 ^g	<i>Ppidl</i>	64	≥ 2.5	
C3_213	glutamate-cysteine ligase, modifier subunit	NCBI 6680019	29.44	5.49	49.04	mV33BS	A	3	<i>Gclm</i>	56	≥ 2.5	
D4_125	glutathione S-transferase, mu 1	NCBI 121716	15.52	6.00	49.46	mV9BS	A	3 ^g	<i>Gstm1</i>	56	≥ 2.5	<i>Gstm1</i> (mV139BS) LOD 16.86 (0)
C6_217	glutathione S-transferase, mu 1	SP P10649	28.23	6.97	568.77	mV139BS	A	3 ^g	<i>Gstm1</i>	64	≥ 2.5	
C5_243	glutathione S-transferase, mu 1	NCBI 121716	27.80	6.64	59.36	mV210BS	A	3 ^g	<i>Gstm1</i>	17	interval (≥ 2.5)	<i>Ppidl</i> (mV148BS), <i>Tuba2m</i> (mV146BS), <i>D3Irs2</i> , <i>Gstm1</i> (paV153BS), <i>Adh5</i> (mV139BS) LOD 5.12 (0)
C6_224	glutathione S-transferase, mu 1	SP P10649	28.20	6.76	265.37	mV215BS	A	3 ^g	<i>Gstm1</i>	64	≥ 2.5	<i>Gstm1</i> (mV139BS) LOD 19.27 (0)
E4_015	modifier 1 of glutathione S-transferase, mu 1	NCBI 121716	13.13	5.68	27.29	mV12BS	A	3 ^g	<i>Gstm1m1</i>	49	linked to chr	<i>Ppidl</i> (mV148BS) LOD 5.28 (19.77)
C6_058	modifier 2 of glutathione S-transferase, mu 1	NCBI 121716	28.26	7.23	10.88	paV299BS	A	3 ^g	<i>Gstm1m2</i>	20	linked to chr	<i>Ppidl</i> (mV148BS), <i>Tuba2m</i> (paV153BS), <i>D3Irs1</i> , <i>D3Irs2</i> , <i>Gstm1</i> (mV139BS), <i>Adh5</i> (mV146BS) LOD 3.20 (11.16)
E7_009	modifier of hemoglobin beta chain complex	NCBI 122717	12.80	7.53	29.38	mV174BS	A	3 ^g	<i>Hbbm</i>	24	interval (≥ 2.5)	<i>D3Mit1</i> LOD 5.12 (0)
B6_420	crystallin, zeta (quinone reductase)	SP P47199	39.05	6.97	127.62	mV262BS	A	3 ^g	<i>Cryz</i>	52	linked to chr	<i>D3Mit19</i> LOD 3.38 (19.47) <i>Adh5</i> (mV146BS), <i>D3Irs4</i> LOD 5.25 (21.24)
C7_176	modifier of cathepsin H	NCBI 12856980	25.68	7.65	69.37	paV386BS	A	3 ^g	<i>Ctshn</i>	64	≥ 2.5	<i>D3Irs1</i> LOD 16.26 (0)
B4_228	modifier of tubulin, alpha 2	NCBI 135412	53.91	5.85	66.41	paV153BS	A	3 ^g	<i>Tuba2m</i>	61	≥ 2.5	
B3_596	modifier of tubulin, beta 4	NCBI 91858	38.23	5.38	34.20	paV129BS	A	3 ^g	<i>Tubb4m</i>	63	≥ 2.5	
B5_657			36.87	6.11	51.81	mV222BS	A	3	<i>mV222BS</i>	61	≥ 2.5	
C2_056			33.88	5.05	34.52	mV350BS	A	3	<i>mV350BS</i>	35	≥ 2.5	<i>Anxa5</i> (mV27BS) LOD 10.54 (0)
E1_020			9.50	4.39	30.63	aV3BS	A	3	<i>aV3BS</i>	62	≥ 2.5	<i>D3Irs1</i> LOD 15.65 (0)
B5_704			37.00	6.21	19.54	paV397BS	A	3	<i>paV397BS</i>	52	interval (2.3)	<i>mV222BS</i> (mV222BS) LOD 9.0 (8.72)
B3_279	ATP synthase, H ⁺ transporting mitochondrial F1 complex, beta subunit	SP P10719						3	<i>Atp5b</i>			
B2_200	ATP synthase, H ⁺ transporting mitochondrial F1 complex, beta subunit	SP P10719						3	<i>Atp5b</i>			
A5_071	aconitase 1 ⁱ		102.31	6.31	40.71	mV287BS	A	4	<i>Aco1</i>	64	≥ 2.5	<i>D4Irs2</i> LOD 19.27 (0)
A5_069	aconitase 1	NCBI 124899	102.31	6.37	59.30	"	A	4	<i>Aco1</i>	64	≥ 2.5	<i>D4Irs2</i> LOD 19.27 (0)
B5_703	glyoxylate reductase/hydroxypyruvate reductase	NCBI 3732528	39.67	6.37	65.40	mV241BS	A	4 ^g	<i>Grhpr</i>	64	≥ 2.5	
B5_551	glyoxylate reductase/hydroxypyruvate reductase	NCBI 3732528	39.55	6.37	29.94	"	A	4 ^g	<i>Grhpr</i>	64	≥ 2.5	
C3_074	RIKEN cDNA clone 2600015J22	NCBI 7045955	33.33	5.07	129.06	mV30BS	A	4 ^g	<i>2600015J22Rik</i>	64	≥ 2.5	<i>2600015J22Rik</i> (mV120BS) LOD 19.27 (0)

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C2_394	RIKEN cDNA clone 2600015J22	NCBI 7045955	33.54	5.01	36.61	mV31BS	A	4 ^g	2600015J22Rik	64	≥ 2.5	2600015J22Rik (mV120BS) LOD 19.27 (0)
C2_066	RIKEN cDNA clone 2600015J22	NCBI 7045955	33.46	5.01	39.45	"	A	4 ^g	2600015J22Rik	64	≥ 2.5	2600015J22Rik (mV120BS) LOD 19.27 (0)
C2_074	RIKEN cDNA clone 2600015J22	NCBI 7045955	33.25	4.99	27.35	"	A	4 ^g	2600015J22Rik	64	≥ 2.5	2600015J22Rik (mV120BS) LOD 19.27 (0)
C2_393	RIKEN cDNA clone 2600015J22	NCBI 7045955	33.33	4.99	23.39	"	A	4 ^g	2600015J22Rik	64	≥ 2.5	2600015J22Rik (mV120BS) LOD 19.27 (0)
C3_076	RIKEN cDNA clone 2600015J22 ⁱ		33.33	5.13	46.37	mV36BS	A	4 ^g	2600015J22Rik	64	≥ 2.5	2600015J22Rik (mV120BS) LOD 19.27 (0)
C3_102	RIKEN cDNA clone 2600015J22	NCBI 7045955	32.66	5.13	116.57	mV120BS	A	4 ^g	2600015J22Rik	64	≥ 2.5	
B5_691	aldehyde dehydrogenase 4 family, member A1	NCBI 1656546	69.21	6.57	18.73	paV492BS	A	4 ^g	<i>Aldh4a1</i>	56	2.0	
B5_694	modifier of dynamin	NCBI 729381	62.22	6.32	18.14	paV509BS	A	4 ^g	<i>Dnmm</i>	57	≥ 2.5	2810435D12Rik (mV365BS) LOD 17.16 (0)
B5_544	sialic acid synthase	NCBI 9507063	39.88	6.66	65.56	mV259BS	A	4 ^g	<i>Sas</i>	64	interval (≥ 2.5)	<i>D4Irs3</i> LOD 18.66 (0)
B5_699	sialic acid synthase	NCBI 9507063	40.70	6.59	25.44	paV412BS	A	4 ^g	<i>Sas</i>	62	interval (≥ 2.5)	<i>D4Irs3</i> LOD 18.06 (0)
D3_008	modifier of Sorcin	NCBI 134734	23.11	5.05	60.40	mV19BS	A	4 ^g	<i>Srim</i>	64	interval (≥ 2.5)	<i>D4Nds16</i> LOD 14.09 (1.89)
D2_012	modifier of Sorcin ⁱ		22.79	4.96	17.85	mV20BS	A	4 ^g	<i>Srim</i>	64	interval (≥ 2.5)	<i>D4Nds16</i> LOD 14.09 (1.89)
C5_119	RIKEN cDNA clone 2810435D12	NCBI 6631587	31.40	6.35	32.59	mV365BS	A	4 ^g	2810435D12Rik	64	≥ 2.5	
C5_124	RIKEN cDNA clone 2810435D12	NCBI 6631587	31.32	6.35	32.69	"	A	4 ^g	2810435D12Rik	64	≥ 2.5	
C7_125			27.48	7.65	17.89	mV196BS	A	4	<i>mV196BS</i>	24	linked to chr	2600015J22Rik (mV120BS) LOD 3.30 (14.38)
A6_081			69.05	7.01	8.11	mV280BS	A	4	<i>mV280BS</i>	55	interval (≥ 2.5)	<i>D4Mit52</i> LOD 10.40 (6.26)
A5_127			89.78	6.43	17.63	mV289BS	A	4	<i>mV289BS</i>	24	interval (≥ 2.5)	<i>D4Irs1</i> LOD 6.62 (0) <i>D4Irs2</i> LOD 7.22 (0) <i>D4Irs1</i> LOD 6.88 (16.82)
C6_075			33.05	7.17	6.90	aV381BS	A	4	<i>aV381BS</i>	58	linked to chr	
B5_607			38.23	6.16	71.22	paV399BS	A	4	<i>paV399BS</i>	53	≥ 2.5	<i>Ghrpr</i> (mV241BS) LOD 15.95 (0)
B3_586	enolase 1, alpha non-neuron	SP P17182	38.35	5.54	286.90	aV353BS	C	4 ^j	<i>Eno1</i>			
B4_433	enolase 1, alpha non-neuron	SP P17182	41.95	6.06	298.77			4	<i>Eno1</i>			
B4_521	enolase 1, alpha non-neuron	SP P17182	38.27	5.66	489.83			4	<i>Eno1</i>			
B5_317	enolase 1, alpha non-neuron	SP P17182	49.53	6.14				4	<i>Eno1</i>			
B3_542	enolase 1, alpha non-neuron	SP P17182	39.66	5.55	263.94			4	<i>Eno1</i>			
C5_229	RAN, member RAS oncogene family	SP P28746	27.94	6.69	204.24			4	<i>Ran</i>			
B3_484	SH3 domain protein 2A	EMBL U58886	48.46	5.21	18.01			4	<i>Sh3d2a</i>			
D3_115	leukemia-associated gene	SP P54227	18.11	5.57	217.39			4	<i>Lag</i>			
D4_080	leukemia-associated gene	SP P54227	17.84	5.80	207.78			4	<i>Lag</i>			
C6_345	peroxiredoxin 1	SP P35700	24.93	6.84	490.80			4	<i>Prdx1</i>			
B4_596	acyl-coA dehydrogenase, short-chain	NCBI 584714	39.58	6.09	69.60	aV400BS	A	5	<i>Acads</i>	62	≥ 2.5	
B3_640	annexin A3	EMBL AJ001633	36.58	5.57	49.51	paV110BS	A	5	<i>Anxa3</i>	64	≥ 2.5	
B3_511	COP9 (constitutive photomorphogenic) homolog, subunit 4 (A. thaliana)	NCBI 3309170	41.06	5.60	9.99	mV45BS	A	5 ^g	<i>Cops4</i>	64	≥ 2.5	
B3_519	COP9 (constitutive photomorphogenic) homolog, subunit 4 (A. thaliana)	NCBI 3309170	40.49	5.60	26.38	"	A	5 ^g	<i>Cops4</i>	64	≥ 2.5	
B3_531	COP9 (constitutive photomorphogenic) homolog, subunit 4 (A. thaliana)	NCBI 3309170	40.33	5.60	27.64	"	A	5 ^g	<i>Cops4</i>	64	≥ 2.5	
B5_047	coronin, actin binding protein 1C	NCBI 4895041	64.60	6.51	21.99	paV494BS	A	5 ^g	<i>Coro1c</i>	52	interval (≥ 2.5)	<i>Acads</i> (aV400BS) LOD 10.40 (6.26)
B5_057	coronin, actin binding protein 1C ⁱ		64.13	6.51	58.39	"	A	5 ^g	<i>Coro1c</i>	52	interval (≥ 2.5)	<i>Acads</i> (aV400BS) LOD 10.40 (6.26)
C6_160	RIKEN cDNA 1110054D16 gene	NCBI 1284324	29.84	6.93	30.17	mV217BS	A	5 ^g	1110054D16Rik	40	≥ 2.5	<i>D5Irs7</i> LOD 12.04 (0)
C4_164	Endoplasmic reticulum protein 29	NCBI 2507015	29.10	5.83	99.41	mV128BS	A	5 ^g	<i>Erp29</i>	64	interval (≥ 2.5)	<i>D5Irs6</i> , <i>Psmid9</i> (mV35BS) LOD 17.03 (1.59)
B5_128	RIKEN cDNA 2410015L10 gene	NCBI 4335941	58.87	6.45	118.48	mV298BS	A	5 ^g	2410015L10Rik	57	≥ 2.5	<i>D5Irs3</i> LOD 17.16 (0)
C4_127	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	NCBI 7066625	30.51	6.05	55.46	mV35BS	A	5 ^g	<i>Psmid9</i>	64	≥ 2.5	
E4_053	quininoid dihydropteridene reductase ⁱ		10.95	6.02	6.07	mV14BS	A	5	<i>Qdpr</i>	32	≥ 2.5	<i>D5Irs3</i> LOD 9.63 (0)
C5_167	quininoid dihydropteridene reductase	SP P11348	29.44	6.49	583.88	mV137BS	A	5	<i>Qdpr</i>	64	≥ 2.5	<i>D5Irs3</i> LOD 19.27 (0)
D6_144	quininoid dihydropteridene reductase ⁱ		14.50	6.94	10.54	mV160BS	A	5	<i>Qdpr</i>	53	≥ 2.5	<i>D5Irs3</i> LOD 15.95 (0)
A4_199	serum albumin variant	SP P07724	72.00	5.67		mV83BS	A	5	<i>Alb1</i>	64	≥ 2.5	
A4_210	serum albumin variant ⁱ		73.00	5.62	171.28	"	A	5	<i>Alb1</i>	64	≥ 2.5	
C4_215	modifier 1 of serum albumin variant	NCBI 5915682	27.61	6.05	193.24	paV52BS	A	5 ^g	<i>Alb1m1</i>	63	interval (≥ 2.5)	<i>Alb1</i> (mV83BS) LOD 13.73 (5.5) <i>Cops4</i> (mV45BS) LOD 12.49 (6.79)
B5_012	chaperonin subunit 6a (zeta)	NCBI 549061	67.14	6.24	70.85	mV299BS	A	5 ^h	<i>Cct6a</i>	64	≥ 2.5	
B5_031	chaperonin subunit 6a (zeta) ⁱ		66.03	6.24	35.27	"	A	5 ^h	<i>Cct6a</i>	64	≥ 2.5	
E5_002			13.89	6.28	15.61	mV157BS	A	5	<i>mV157BS</i>	60	≥ 2.5	<i>Alb1</i> (mV83BS) LOD 18.06 (0)

2-DE Spot-No ^a	PROTEINS					GENES				GENE MAPPING		
	Name ^b	Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
B4_336			48.13	6.05	62.92	mV236BS	A	5	mV236BS	61	interval (≥ 2.5)	<i>Alb1</i> (mV83BS) LOD 10.85 (8.95)
B6_382			40.31	6.81	59.26	mV260BS	A	5	mV260BS	64	≥ 2.5	<i>Cops4</i> (mV45BS) LOD 19.27 (0)
B4_593			36.88	5.70	24.87	paV109BS	A	5	paV109BS	56	interval (≥ 2.5)	<i>Anxa3</i> (paV110BS), <i>Cops4</i> (mV45BS) LOD 10.60 (7.71)
C5_286			26.46	6.30	40.59	paV247BS	A	5	paV247BS	36	linked to chr	<i>D5Nds6</i> LOD 3.35 (21.77)
C5_382			28.47	6.50	31.61	paV258BS	A	5	paV258BS	60	linked to chr	<i>D5Irs5</i> LOD 4.82 (26.11)
C6_383			29.65	6.94	11.00	paV294BS	A	5	paV294BS	56	linked to chr	<i>D5Irs7</i> , <i>D5Irs8</i> LOD 4.22 (27.98)
B6_451	malate dehydrogenase, mitochondrial	SP P08249	37.38	7.18	873.07			5	<i>Mor1</i>			
C3_317	ubiquitin carboxyl-terminal hydrolase L1	SP Q00981	27.26	5.16	567.58			5	<i>Uchl1</i>			
C3_314	ubiquitin carboxyl-terminal hydrolase L1	SP Q00981	27.42	5.29	697.53			5	<i>Uchl1</i>			
B6_209	acyl-Coenzyme A thioesterase 2, mitochondrial	NCBI 5102774	48.98	6.84	45.45	paV440BS	A	6 ^g	<i>Acate2-pending</i>	62	≥ 2.5	
B6_212	acyl-Coenzyme A thioesterase 2, mitochondrial ^l		48.91	6.74	54.63	mV369BS	A	6 ^g	<i>Acate2-pending</i>	58	≥ 2.5	<i>Acate2-pending</i> (paV440BS) LOD 16.86 (0)
B5_702	aldolase 1, A isoform	NCBI 553861	37.12	6.66	52.73	paV398BS	A	6 ^g	<i>Aldo1</i>	64	interval (≥ 2.5)	<i>Snd1-pending</i> (mV286BS), <i>D6Mit47</i> LOD 13.97 (3.51)
B5_651	aldolase 1, A isoform ^l		37.04	6.66	51.47	"	A	6 ^g	<i>Aldo1</i>	64	interval (≥ 2.5)	<i>Snd1-pending</i> (mV286BS), <i>D6Mit47</i> LOD 13.97 (3.51)
B6_318	aldolase 1, A isoform	SP P05064	43.13	7.07	359.44	aV574BS	C					
B6_308	aldolase 1, A isoform	SP P05064	43.36	7.05	293.87							
B6_328	aldolase 1, A isoform	SP P05064	43.13	7.05	374.82							
B6_309	aldolase 1, A isoform	SP P05064	43.13	7.14	826.70							
C4_285	enolase 2, gamma neuronal ^l		25.24	5.73	33.44	mV21BS	A	6	<i>Eno2</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
C3_254	enolase 2, gamma neuronal ^l		28.64	5.56	34.72	mV34BS	A	6	<i>Eno2</i>	52	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 15.65 (0)
B3_402	enolase 2, gamma neuronal ^l		47.48	5.12	38.12	mV39BS	A	6	<i>Eno2</i>	57	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 17.16 (0)
B3_411	enolase 2, gamma neuronal ^l		47.32	5.06	67.77	mV40BS	A	6	<i>Eno2</i>	56	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 17.16 (0)
B3_483	enolase 2, gamma neuronal ^l		42.68	5.23	34.57	mV49BS	A	6	<i>Eno2</i>	58	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 17.46 (0)
B3_507	enolase 2, gamma neuronal ^l		41.22	5.15	54.26	mV51BS	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B2_378	enolase 2, gamma neuronal ^l		40.57	5.04	23.36	mV52BS	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B2_384	enolase 2, gamma neuronal ^l		40.65	5.02	12.01	"	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B3_527	enolase 2, gamma neuronal ^l		40.41	5.06	15.36	"	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B3_522	enolase 2, gamma neuronal	SP P17183	40.41	5.08	196.27	"	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B2_423	enolase 2, gamma neuronal	SP P17183	38.90	4.96	158.93	mV54BS	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B2_415	enolase 2, gamma neuronal	SP P17183	39.07	4.89	208.66	mV55BS	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B2_485	enolase 2, gamma neuronal ^l		37.17	4.88	44.80	mV58BS	A	6	<i>Eno2</i>	63	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
B2_460	enolase 2, gamma neuronal ^l		37.93	4.92	92.33	mV59BS	A	6	<i>Eno2</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B2_250	enolase 2, gamma neuronal ^l		48.94	5.03	410.64	mV73BS	A	6	<i>Eno2</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B2_249	enolase 2, gamma neuronal ^l		49.19	4.96	215.90	"	A	6	<i>Eno2</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B3_359	enolase 2, gamma neuronal	SP P17183	48.62	5.08	747.28	"	A	6	<i>Eno2</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B3_370	enolase 2, gamma neuronal ^l		48.78	5.10	244.45	"	A	6	<i>Eno2</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B3_300	enolase 2, gamma neuronal ^l		47.72	5.05	18.40	mV74BS	A	6	<i>Eno2</i>	61	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.36 (0)
B2_259	enolase 2, gamma neuronal ^l		48.29	5.00	31.81	mV75BS	A	6	<i>Eno2</i>	39	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 11.74 (0)
B2_387	enolase 2, gamma neuronal ^l		40.16	4.97	20.79	mV129BS	A	6	<i>Eno2</i>	56	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 16.86 (0)
C2_003	enolase 2, gamma neuronal	SP P17183	35.86	5.03	204.27	"	A	6	<i>Eno2</i>			
C3_006	modifier 1 of enolase 2, gamma neuronal	NCBI 119348	35.86	5.07	35.43	mV57BS	A	6 ^g	<i>Eno2m1</i>	57	linked to chr	
B2_309	modifier 2 of enolase 2, gamma neuronal	NCBI 119348	45.28	4.86	59.19	mV364BS	A	6 ^g	<i>Eno2m2</i>	29	linked to chr	<i>Gapd</i> (mV232BS), <i>Gapd</i> (mV141BS), <i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 4.54 (11.59)
C7_095	glyceraldehyde-3-phosphate dehydrogenase ^l		28.39	7.98	141.97	mV141BS	A	6	<i>Gapd</i>	63	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
C7_107	glyceraldehyde-3-phosphate dehydrogenase ^l		28.15	7.99	34.29	"	A	6	<i>Gapd</i>	63	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
B5_660	glyceraldehyde-3-phosphate dehydrogenase	SP P16858	36.71	6.55	308.57	mV143BS	A	6	<i>Gapd</i>	62	interval (≥ 2.5)	<i>Eno2</i> (mV73BS) LOD 14.83 (3.33)
B5_618	glyceraldehyde-3-phosphate dehydrogenase ^l		38.15	6.64	147.83	mV145BS	A	6	<i>Gapd</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B5_611	glyceraldehyde-3-phosphate dehydrogenase	SP P16858	38.19	6.72	271.73	"	A	6	<i>Gapd</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B6_448	glyceraldehyde-3-phosphate dehydrogenase	SP P16858	38.07	6.80	513.13	"	A	6	<i>Gapd</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B6_442	glyceraldehyde-3-phosphate dehydrogenase	SP P16858	38.11	6.95		"	A	6	<i>Gapd</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
B6_436	glyceraldehyde-3-phosphate dehydrogenase	SP P16858	38.07	7.00		"	A	6	<i>Gapd</i>	64	≥ 2.5	<i>D6Mit24</i> LOD 17.76 (0)
C8_016	glyceraldehyde-3-phosphate dehydrogenase ^l		29.33	8.34	83.28	mV152BS	A	6	<i>Gapd</i>	63	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
C8_014	glyceraldehyde-3-phosphate dehydrogenase ^l		29.46	8.31	91.69	"	A	6	<i>Gapd</i>	63	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
C8_013	glyceraldehyde-3-phosphate dehydrogenase ^l		29.60	8.30	18.25	"	A	6	<i>Gapd</i>	63	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
D7_091	glyceraldehyde-3-phosphate dehydrogenase ^l		14.33	7.81	71.62	mV179BS	A	6	<i>Gapd</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.96 (0)
D7_078	glyceraldehyde-3-phosphate dehydrogenase ^l		15.47	7.77	15.18	mV180BS	A	6	<i>Gapd</i>	16	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 4.82 (0)

2-DE Spot-No ^a	PROTEINS				GENES			GENE MAPPING				
	Name ^b	Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
D7_080	glyceraldehyde-3-phosphate dehydrogenase ¹		15.30	7.80	4.90	"	A	6	<i>Gapd</i>	16	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 4.82 (0)
C8_019	glyceraldehyde-3-phosphate dehydrogenase ¹		28.93	8.39	26.34	mV202BS	A	6	<i>Gapd</i>	30	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 9.03 (0)
C7_129	glyceraldehyde-3-phosphate dehydrogenase ¹		27.16	8.30	19.36	mV203BS	A	6	<i>Gapd</i>	30	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 9.03 (0)
C7_140	glyceraldehyde-3-phosphate dehydrogenase ¹		26.92	8.11	75.01	mV204BS	A	6	<i>Gapd</i>	59	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 17.76 (0)
C7_003	glyceraldehyde-3-phosphate dehydrogenase ¹		35.56	7.44	33.38	mV232BS	A	6	<i>Gapd</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
C7_007	glyceraldehyde-3-phosphate dehydrogenase ¹		34.98	7.43	24.25	"	A	6	<i>Gapd</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
B6_430	glyceraldehyde-3-phosphate dehydrogenase ¹		38.68	6.90	77.47	paV431BS	A	6	<i>Gapd</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
B5_612	modifier 1 of glyceraldehyde 3-phosphate dehydrogenase	NCBI 120707	38.31	6.55	51.03	paV408BS	A	6 ^g	<i>Gapdm1</i>	62	linked to chr	<i>mV29BS</i> LOD 9.28 (10.03)
B6_476	modifier 2 of glyceraldehyde 3-phosphate dehydrogenase	NCBI 120707	36.95	6.91	64.02	paV425BS	A	6 ^g	<i>Gapdm2</i>	32	linked to chr	<i>mV29BS</i> , <i>Gapd</i> (paV431BS) LOD 5.31 (10.38)
B4_385	succinate-Coenzyme A ligase, GDP forming, beta subunit	NCBI 3766203	44.80	5.64	48.02	mV355BS	A	6 ^g	<i>Suc1g2</i>	64	≥ 2.5	
B4_400	succinate-Coenzyme A ligase, GDP forming, beta subunit	NCBI 3766203	43.98	5.64	60.66	"	A	6 ^g	<i>Suc1g2</i>	64	≥ 2.5	
E6_014	modifier of hemoglobin Y, beta-like embryonic chain	NCBI 122728	12.34	6.93	131.49	mV158BS	A	6 ^g	<i>Hbb-ym</i>	15	linked to chr	<i>Suc1g1</i> (mV200BS), <i>Gapd</i> (mV232BS), <i>D6Mit24</i> , <i>Gapd</i> (mV141BS), <i>Eno2</i> (mV73BS), <i>mV29BS</i> , <i>D6Mit14</i> LOD > 3.6
E1_026	lactate dehydrogenase2, B chain ¹		9.12	4.41	67.38	mV1BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
E2_078	lactate dehydrogenase2, B chain ¹		19.84	4.58	38.03	mV2BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
E2_065	lactate dehydrogenase2, B chain ¹		20.24	4.50	180.42	mV3BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C4_337	lactate dehydrogenase2, B chain ¹		33.25	5.68	76.10	mV24BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C4_050	lactate dehydrogenase2, B chain ¹		33.16	5.68	27.99	"	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C4_021	lactate dehydrogenase2, B chain ¹		34.81	5.66	123.11	mV25BS	A	6	<i>Ldh2</i>	63	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 18.96 (0)
C4_336	lactate dehydrogenase2, B chain ¹		35.44	5.81	52.39	mV26BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C4_005	lactate dehydrogenase2, B chain ¹		35.36	5.81	48.51	"	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
B3_671	lactate dehydrogenase2, B chain ¹		37.30	5.56	141.73	mV42BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
B3_620	lactate dehydrogenase2, B chain ¹		37.22	5.56	204.52	"	A	6	<i>Ldh2</i>	64	≥ 2.5	
B4_595	lactate dehydrogenase2, B chain ¹	SP P16125	37.22	5.66	471.74	"	A	6	<i>Ldh2</i>	64	≥ 2.5	
B4_547	lactate dehydrogenase2, B chain ¹	SP P16125	37.13	5.66	415.39	"	A	6	<i>Ldh2</i>	64	≥ 2.5	
B4_592	lactate dehydrogenase2, B chain ¹		36.58	5.67	36.27	"	A	6	<i>Ldh2</i>	64	≥ 2.5	
B4_594	lactate dehydrogenase2, B chain ¹		35.95	5.67	54.54	"	A	6	<i>Ldh2</i>	64	≥ 2.5	
C3_290	lactate dehydrogenase2, B chain ¹		27.90	5.40	65.32	mV117BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C3_458	lactate dehydrogenase2, B chain ¹		28.54	5.52	34.18	mV118BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C3_274	lactate dehydrogenase2, B chain ¹		28.30	5.53	63.74	mV122BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
E3_064	lactate dehydrogenase2, B chain ¹		10.99	5.24	44.77	paV7BS	A	6	<i>Ldh2</i>	63	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 18.96 (0)
E3_045	lactate dehydrogenase2, B chain ¹		11.96	5.55	35.10	paV9BS	A	6	<i>Ldh2</i>	63	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 18.96 (0)
D4_102	lactate dehydrogenase2, B chain ¹		16.73	6.04	42.01	paV17BS	A	6	<i>Ldh2</i>	60	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 18.06 (0)
D4_159	lactate dehydrogenase2, B chain ¹		14.77	5.72	9.74	paV35BS	A	6	<i>Ldh2</i>	64	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 19.27 (0)
C4_084	lactate dehydrogenase2, B chain ¹	NCBI 126042	31.98	5.96	51.67	paV81BS	A	6	<i>Ldh2</i>	62	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 18.66 (0)
C4_120	lactate dehydrogenase2, B chain ¹	NCBI 126042	30.72	5.97	50.53	paV198BS	A	6	<i>Ldh2</i>	22	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS), <i>aV6BS</i> LOD 6.62
D5_019	lactate dehydrogenase2, B chain ¹	NCBI 6678674	21.13	6.28	89.06	paV228BS	A	6	<i>Ldh2</i>	63	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS) LOD 16.73 (1.61)
D5_128	lactate dehydrogenase2, B chain ¹	NCBI 6678674	20.99	6.28	87.70	"	A	6	<i>Ldh2</i>	63	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS) LOD 16.73 (1.61)
C5_369	lactate dehydrogenase2, B chain ¹		23.81	6.60	17.39	paV237BS	A	6	<i>Ldh2</i>	46	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 13.85 (0)
C5_371	lactate dehydrogenase2, B chain ¹		23.75	6.60	19.88	"	A	6	<i>Ldh2</i>	46	≥ 2.5	<i>Ldh2</i> (mV42BS) LOD 13.85 (0)
A5_054	staphylococcal nuclease domain containing 1	NCBI 6009521	108.85	6.48	18.87	mV286BS	A	6 ^g	<i>Snd1-pending</i>	59	≥ 2.5	
A5_056	staphylococcal nuclease domain containing 1 ¹		108.85	6.45	10.12	"	A	6 ^g	<i>Snd1-pending</i>	59	≥ 2.5	
A5_057	staphylococcal nuclease domain containing 1 ¹		108.85	6.43	7.40	"	A	6 ^g	<i>Snd1-pending</i>	59	≥ 2.5	
B7_152	succinate-Coenzyme A ligase, GDP forming, alpha subunit ¹		37.70	8.30	114.89	mV200BS	A	6 ^g	<i>Suc1g1</i>	64	≥ 2.5	
B7_150	succinate-Coenzyme A ligase, GDP forming, alpha subunit ¹		37.74	8.24	48.12	"	A	6 ^g	<i>Suc1g1</i>	64	≥ 2.5	
B7_153	succinate-Coenzyme A ligase, GDP forming, alpha subunit ¹		37.53	8.12	30.34	"	A	6 ^g	<i>Suc1g1</i>	64	≥ 2.5	
B8_010	succinate-Coenzyme A ligase, GDP forming, alpha subunit ¹		37.82	8.44	6.29	"	A	6 ^g	<i>Suc1g1</i>	64	≥ 2.5	
B8_009	succinate-Coenzyme A ligase, GDP forming, alpha subunit ¹		37.82	8.40	18.58	"	A	6 ^g	<i>Suc1g1</i>	64	≥ 2.5	
B8_008	succinate-Coenzyme A ligase, GDP forming, alpha subunit	SP P13086	37.65	8.36	361.49	"	A	6 ^g	<i>Suc1g1</i>	64	≥ 2.5	

2-DE Spot-No ^a	Name ^b	PROTEINS				GENES			GENE MAPPING			
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
C6_357	triosephosphate isomerase	NCBI 1864018	24.32	7.30	23.71	mV195BS	A	6	<i>Tpi</i>	26	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 7.83 (0)
D6_001	triosephosphate isomerase ^l		23.22	7.06	6.15	mV194BS	A	6	<i>Tpi</i>	12	interval (≥ 2.5)	<i>D6Mit24</i> LOD 3.01 (0) <i>mV29BS</i> LOD 3.61 (0)
C5_250	triosephosphate isomerase	SP P17751	27.37	6.56	918.95			6	<i>Tpi</i>			
C5_254	triosephosphate isomerase	SP P17751	27.37	6.37				6	<i>Tpi</i>			
C5_264	triosephosphate isomerase	SP P17751	27.24	6.32	225.83			6	<i>Tpi</i>			
C3_115			32.41	5.07	35.95	mV29BS	A	6	<i>mV29BS</i>	64	2.1	
B2_198			53.45	4.72	274.31	mV77BS	A	6	<i>mV77BS</i>	64	≥ 2.5	
B2_194			53.36	4.69	98.05	"	A	6	<i>mV77BS</i>	64	≥ 2.5	
B2_359			41.79	4.92	16.72	mV116BS	A	6	<i>mV116BS</i>	64	interval (≥ 2.5)	<i>Eno2</i> (mV73BS) LOD 15.40 (3.23)
D1_017			20.32	4.22	16.19	mV119BS	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_018			20.24	4.27	26.67	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_080			19.89	4.22	9.58	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_077			19.57	4.24	5.04	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_075			20.35	4.25	9.74	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_019			20.19	4.23	9.47	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_081			19.91	4.20	5.84	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_079			19.59	4.23	5.71	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_015			20.35	4.26	16.63	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_021			19.84	4.27	10.84	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_026			19.62	4.27	40.22	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_082			19.59	4.21	6.30	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_014			20.37	4.29	45.23	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_070			19.86	4.26	3.88	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_027			19.62	4.26	17.72	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_076			19.46	4.27	8.69	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_020			19.95	4.29	20.24	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_022			19.89	4.23	17.21	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D1_078			19.64	4.24	6.70	"	A	6	<i>mV119BS</i>	62	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 18.66 (0)
D6_057			19.60	7.30	126.10	mV132BS	A	6	<i>mV132BS</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
D6_060			19.32	7.31	59.38	"	A	6	<i>mV132BS</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
D6_021			21.69	7.38	34.16	mV133BS	A	6	<i>mV133BS</i>	64	≥ 2.5	<i>Eno2</i> (mV73BS) LOD 19.27 (0)
E5_074			11.90	6.21	14.74	mV156BS	A	6	<i>mV156BS</i>	51	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS) LOD 8.25 (10.91)
D6_072			18.12	7.33	37.25	mV175BS	A	6	<i>mV175BS</i>	18	interval (≥ 2.5)	<i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 5.42 (0)
C6_302			26.22	7.05	26.59	mV192BS	A	6	<i>mV192BS</i>	57	interval (≥ 2.5)	<i>Eno2</i> (mV73BS) LOD 10.87 (7.56)
C7_164			26.14	7.43	28.93	mV197BS	A	6	<i>mV197BS</i>	61	≥ 2.5	
C7_185			25.12	7.85	19.26	mV199BS	A	6	<i>mV199BS</i>	33	linked to chr	<i>Gapd</i> (mV232BS), <i>Gapd</i> (mV141BS), <i>Eno2</i> (mV73BS), <i>mV29BS</i> LOD 4.64 (13.88)
C7_046			30.78	7.93	10.28	mV201BS	A	6	<i>mV201BS</i>	17	interval (2.4)	<i>Suclg1</i> (mV200BS) LOD 3.47 (0)
E4_050			11.15	5.86	29.82	aV6BS	A	6	<i>aV6BS</i>	63	2.3	
C4_340			26.28	5.61	19.21	paV41BS	A	6	<i>paV41BS</i>	48	interval (≥ 2.5)	<i>mV77BS</i> LOD 12.34 (2.13)
D6_160			17.00	6.74	18.65	paV220BS	A	6	<i>paV220BS</i>	52	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS) LOD 7.58 (13.12)
E6_033			11.15	7.02	14.26	paV223BS	A	6	<i>paV223BS</i>	41	linked to chr	<i>mV29BS</i> LOD 3.55 (24.73)
C4_344			29.76	6.09	10.50	aV253BS	A	6	<i>aV253BS</i>	53	interval (≥ 2.5)	<i>aV6BS</i> LOD 8.50 (10.68)
C4_157			29.26	6.09	35.99	"	A	6	<i>aV253BS</i>	53	interval (≥ 2.5)	<i>aV6BS</i> LOD 8.50 (10.68)
C5_378			32.72	6.26	17.09	paV266BS	A	6	<i>paV266BS</i>	54	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS) LOD 14.09 (1.89)
C5_377			31.40	6.26	19.20	"	A	6	<i>paV266BS</i>	54	interval (≥ 2.5)	<i>Ldh2</i> (mV42BS) LOD 14.09 (1.89)
B6_513	microtubule-associated protein 6	NCBI 1588595	58.49	7.15	13.70	mV276BS	A	7 ^h	<i>Mtap6</i>	64	≥ 2.5	
B6_066	microtubule-associated protein 6	NCBI 1588595	58.30	7.15	7.32	"	A	7 ^h	<i>Mtap6</i>	64	≥ 2.5	
B6_010	microtubule-associated protein 6 ⁱ		66.98	7.31	11.11	mV279BS	A	7 ^h	<i>Mtap6</i>	62	≥ 2.5	<i>Mtap6</i> (mV276BS) LOD 18.66 (0)
B5_464	modifier of aldolase 3, C isoform	SP P09117	43.20	6.49	85.22	paV419BS	A	7 ^d	<i>Aldo3m</i>	49	1.9	
B5_701	fumarylacetoacetate hydrolase	NCBI 544273	42.73	6.70	15.55	paV417BS	A	7	<i>Fah</i>	39	interval (≥ 2.5)	<i>Mtap6</i> (mV276BS) LOD 8.31 (5.41)
C6_001	glucose phosphate isomerase 1 complex	NCBI 120741	35.88	7.17	51.62	mV144BS	A	7	<i>Gpi1</i>	60	≥ 2.5	<i>D7Nds5</i> LOD 16.56 (0)
C6_003	glucose phosphate isomerase 1 complex	NCBI 120741	35.80	7.16	67.04	"	A	7	<i>Gpi1</i>	60	≥ 2.5	<i>D7Nds5</i> LOD 16.56 (0)
D7_040	glucose phosphate isomerase 1 complex ^l		18.06	8.26	9.23	mV178BS	A	7	<i>Gpi1</i>	44	≥ 2.5	<i>D7Nds5</i> LOD 12.34 (0)
D7_048	glucose phosphate isomerase 1 complex ^l		17.51	8.29	23.44	"	A	7	<i>Gpi1</i>	44	≥ 2.5	<i>D7Nds5</i> LOD 12.34 (0)
C8_054	glucose phosphate isomerase 1 complex ^l		23.99	8.56	17.09	mV206BS	A	7	<i>Gpi1</i>	62	≥ 2.5	<i>D7Nds5</i> LOD 17.16 (0)
C8_052	glucose phosphate isomerase 1 complex ^l		24.80	8.49	17.81	"	A	7	<i>Gpi1</i>	62	≥ 2.5	<i>D7Nds5</i> LOD 17.16 (0)

2-DE Spot-No ^a	PROTEINS				GENES				GENE MAPPING			
	Name ^b	Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
B6_312	glucose phosphate isomerase 1 complex	NCBI 120741	43.75	7.33	65.18	mV263BS	A	7	<i>Gpi1</i>	53	≥ 2.5	<i>D7Nds5</i> LOD 14.75 (0)
B6_295	glucose phosphate isomerase 1 complex ¹		44.77	7.32	9.98	"	A	7	<i>Gpi1</i>	53	≥ 2.5	<i>D7Nds5</i> LOD 14.75 (0)
B6_096	glucose phosphate isomerase 1 complex	NCBI 120741	55.75	6.98	64.07	mV274BS	A	7	<i>Gpi1</i>	63	≥ 2.5	<i>D7Nds5</i> LOD 17.46 (0)
B3_624	crystallin, mu	NCBI 3913376	37.22	5.46	200.29	mV43BS	A	7	<i>Crym</i>	64	≥ 2.5	
B3_621	crystallin, mu ¹		37.30	5.36	56.02	paV160BS	A	7	<i>Crym</i>	56	≥ 2.5	<i>Crym</i> (mV43BS) LOD 16.86 (0)
B4_233	ornithine aminotransferase	SP P29758	47.80	5.90	37.44	mV343BS	A	7	<i>Oat</i>	58	≥ 2.5	
B4_340	ornithine aminotransferase	SP P29758	47.64	5.90	55.42	"	A	7	<i>Oat</i>	58	≥ 2.5	
B3_525	thioredoxin-like 2	NCBI 6840949	40.33	5.53	101.76	mV47BS	A	7 ^g	<i>Txn12</i>	62	≥ 2.5	
B3_550	ubiquitin-like 1 (sentrin) activating enzyme E1A	NCBI 5689242	39.49	5.26	44.54	mV357BS	A	7 ^g	<i>Uble1a</i>	64	≥ 2.5	
B2_038			69.66	4.83	17.14	mV94BS	A	7	<i>mV94BS</i>	64	≥ 2.5	
B2_520			70.20	4.80	13.78	"	A	7	<i>mV94BS</i>	64	≥ 2.5	
A2_159			85.41	4.71	46.22	mV102BS	A	7	<i>mV102BS</i>	64	≥ 2.5	
A2_121			91.85	4.63	99.89	"	A	7	<i>mV102BS</i>	64	≥ 2.5	
A2_125			91.11	4.67	49.42	"	A	7	<i>mV102BS</i>	64	≥ 2.5	
A2_147			88.92	4.62	77.61	"	A	7	<i>mV102BS</i>	64	≥ 2.5	
A2_146			88.65	4.68	60.90	"	A	7	<i>mV102BS</i>	64	≥ 2.5	
A2_153			87.57	4.68	10.41	"	A	7	<i>mV102BS</i>	64	≥ 2.5	
C6_112			31.23	7.26	21.66	mV235BS	A	7	<i>mV235BS</i>	44	interval (≥ 2.5)	<i>D7Nds5</i> LOD 12.04 (0)
E2_040			11.91	4.65	8.51	mV304BS	A	7	<i>mV304BS</i>	49	linked to chr	<i>Txn12</i> (mV47BS) LOD 6.35 (14.74)
B2_090			60.51	4.88	31.67	mV311BS	A	7	<i>mV311BS</i>	62	interval (≥ 2.5)	<i>D7Nds5</i> LOD 14.97 (1.79)
B2_523			47.40	4.65	12.15	mV352BS	A	7	<i>mV352BS</i>	64	≥ 2.5	
D2_284			22.21	4.83	6.50	paV26BS	A	7	<i>paV26BS</i>	64	linked to chr	<i>paV78BS</i> LOD 6.29 (21.48)
C3_253			28.78	5.08	27.52	paV78BS	A	7	<i>paV78BS</i>	63	≥ 2.5	<i>Crym</i> (mV43BS) LOD 18.96 (0)
C3_462			28.48	5.09	35.37	"	A	7	<i>paV78BS</i>	63	≥ 2.5	<i>Crym</i> (mV43BS) LOD 18.96 (0)
C3_457			31.69	5.06	12.72	paV94BS	A	7	<i>paV94BS</i>	61	linked to chr	<i>Oat</i> (mV343BS) LOD 10.33 (7.86)
C3_149	apolipoprotein E	SP P08226	31.31	5.53	54.45	aV345BS	C	7 ^j	<i>ApoE</i>			
E6_010	hemoglobin, beta adult major chain	SP P02088	12.38	7.34			7		<i>Hbb-b1</i>			
C5_001	lactate dehydrogenase 1, A chain	SP P06151	35.31	6.59	565.57		7		<i>Ldh1</i>			
D2_113	olfactory marker protein	EMBL U01213	18.56	4.93	232.69		7		<i>Omp</i>			
B5_199	modifier 2 of glutamate dehydrogenase	NCBI 6980956	55.94	6.65	36.96	mV271BS	A	8 ^g	<i>Gludm2</i>	54	linked to chr	<i>D8Irs2</i> LOD 5.74 (13.98)
B6_088	glutathione reductase 1	SP P47791	56.32	6.73	107.86	mV269BS	A	8	<i>Gsr</i>	64	interval (≥ 2.5)	<i>D8Mit4</i> LOD 12.26 (3.92)
B3_502	modifier of histone deacetylase 1	NCBI 2347180	41.54	5.11	26.70	paV133BS	A	8 ^g	<i>Hdac1m</i>	58	interval (≥ 2.5)	<i>Acta1</i> LOD 12.26 (3.92)
B3_293	RIKEN cDNA 1300017C10 gene	NCBI 9624498	52.27	5.36	32.90	paV165BS	A	8 ^g	<i>1300017C10Rik</i>	62	interval (≥ 2.5)	<i>mV272BS</i> LOD 14.83 (3.33)
C6_154	diaphorase 4 (NADH/NADPH)	SP Q64669	29.97	7.10	67.04	mV219BS	A	8	<i>Dia4</i>	64	≥ 2.5	<i>D8Irs3</i> LOD 18.06 (0)
C6_198	proline synthetase co-transcribed	NCBI 4126980	28.87	6.93	101.45	paV292BS	A	8 ^g	<i>Prosc</i>	64	≥ 2.5	
C6_384	proline synthetase co-transcribed ¹		29.57	6.91	13.01	paV293BS	A	8 ^g	<i>Prosc</i>	56	≥ 2.5	<i>Prosc</i> (paV292BS) LOD 16.86 (0)
B2_385			40.41	4.67	34.07	mV63BS	A	8	<i>mV63BS</i>	60	2.1	<i>mV272BS</i> LOD 18.06 (0)
B1_027			54.45	4.39	21.02	mV78BS	A	8	<i>mV78BS</i>	43	≥ 2.5	<i>mV272BS</i> LOD 12.94 (0)
B1_006			53.55	4.39	67.84	"	A	8	<i>mV78BS</i>	43	≥ 2.5	<i>mV272BS</i> LOD 12.94 (0)
E8_014			12.41	8.40	12.05	mV181BS	A	8	<i>mV181BS</i>	10	linked to chr	<i>mV272BS</i> LOD 3.01 (0)
B6_059			58.87	6.84	34.11	mV272BS	A	8	<i>mV272BS</i>	64	≥ 2.5	
B1_024			59.09	4.45	37.09	mV315BS	A	8	<i>mV315BS</i>	28	linked to chr	<i>mV272BS</i> LOD 4.29 (12.06)
B1_005			58.18	4.45	19.10	"	A	8	<i>mV315BS</i>	28	linked to chr	<i>mV272BS</i> LOD 4.29 (12.06)
C1_025			35.06	4.09	11.43	paV116BS	A	8	<i>paV116BS</i>	20	linked to chr	<i>D8Irs3</i> LOD 3.74 (5.89)
C1_024			34.68	4.10	12.31	"	A	8	<i>paV116BS</i>	20	linked to chr	<i>D8Irs3</i> LOD 3.74 (5.89)
C1_026			34.89	4.07	9.81	"	A	8	<i>paV116BS</i>	20	linked to chr	<i>D8Irs3</i> LOD 3.74 (5.89)
B3_665			64.75	5.52	14.94	paV180BS	A	8	<i>paV180BS</i>	60	linked to chr	<i>Prosc</i> (paV292BS) LOD 3.41 (34.66) <i>D8Mit4</i> LOD 3.61 (28.99) <i>D8Irs1</i> LOD 3.54 (32.96) <i>mV272BS</i> LOD 3.91 (31.43)
C6_382			29.14	6.77	16.10	paV288BS	A	8	<i>paV288BS</i>	58	≥ 2.5	<i>Prosc</i> (paV292BS) LOD 17.46 (0)
C6_381			28.95	6.77	10.32	"	A	8	<i>paV288BS</i>	58	≥ 2.5	<i>Prosc</i> (paV292BS) LOD 17.46 (0)
C6_180			29.28	7.07	40.96	paV300BS	A	8	<i>paV300BS</i>	63	≥ 2.5	<i>Prosc</i> (paV292BS) LOD 18.96 (0)
B1_001	calreticulin	SP P14211	17.00	4.45	839.88	aV373BS	C	8 ^j	<i>Calr</i>			
B7_125	glutamate oxaloacetate transaminase 2, mitochondrial	SP P05202	40.39	7.55	496.64		8		<i>Got2</i>			
B7_128	glutamate oxaloacetate transaminase 2, mitochondrial	SP P05202	40.39	7.45	263.34		8		<i>Got2</i>			
B5_463	acetyl-coA acetyltransferase 1 ¹		43.20	6.54	223.83	mV147BS	A	9	<i>Acat1</i>	64	≥ 2.5	

2-DE Spot-No ^a	Name ^b	PROTEINS				GENES				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
B5_461	acetyl-coA acetyltransferase 1	SP P17764	43.28	6.69	346.75	"	A	9	<i>Acat1</i>	64	≥ 2.5	
C6_362	crystallin, alpha B	EMBL M73741	24.10	6.88	87.53	aV274BS	A	9	<i>Cryab</i>	64	linked to chr	<i>Cab140</i> (mV110BS) LOD 5.43 (24.48)
C3_460	apolipoprotein A-I	NCBI 2145139	25.40	5.38	10.29	mV348BS	A	9	<i>Apoa1</i>	64	≥ 2.5	
B3_486	apolipoprotein A-IV	NCBI 1703331	42.20	5.19	55.44	mV50BS	A	9	<i>Apoa4</i>	64	≥ 2.5	<i>Apoa1</i> (mV348BS) LOD 18.66 (0)
A3_035	calcium binding protein, 140 kDa	NCBI 2137069	180.69	5.24	33.93	mV110BS	A	9 ^g	<i>Cab140</i>	64	≥ 2.5	
A3_036	calcium binding protein, 140 kDa	NCBI 2137069	179.77	5.22	44.33	"	A	9 ^g	<i>Cab140</i>	64	≥ 2.5	
A3_037	calcium binding protein, 140 kDa	NCBI 2137069	178.85	5.20	42.45	"	A	9 ^g	<i>Cab140</i>	64	≥ 2.5	
A3_040	calcium binding protein, 140 kDa ^l		178.85	5.18	31.92	"	A	9 ^g	<i>Cab140</i>	64	≥ 2.5	
A3_042	calcium binding protein, 140 kDa ^l		178.85	5.16	16.79	"	A	9 ^g	<i>Cab140</i>	64	≥ 2.5	
A3_047	calcium binding protein, 140 kDa ^l		170.57	5.11	23.44	mV111BS	A	9 ^g	<i>Cab140</i>	63	≥ 2.5	<i>Cab140</i> (mV110BS) LOD 18.36 (0)
A3_049	calcium binding protein, 140 kDa ^l		169.66	5.09	27.66	"	A	9 ^g	<i>Cab140</i>	63	≥ 2.5	<i>Cab140</i> (mV110BS) LOD 18.36 (0)
A3_051	calcium binding protein, 140 kDa ^l		168.74	5.07	22.92	"	A	9 ^g	<i>Cab140</i>	63	≥ 2.5	<i>Cab140</i> (mV110BS) LOD 18.36 (0)
A3_052	calcium binding protein, 140 kDa ^l		168.74	5.06	15.37	"	A	9 ^g	<i>Cab140</i>	63	≥ 2.5	<i>Cab140</i> (mV110BS) LOD 18.36 (0)
A3_054	calcium binding protein, 140 kDa ^l		167.82	5.05	10.42	"	A	9 ^g	<i>Cab140</i>	63	≥ 2.5	<i>Cab140</i> (mV110BS) LOD 18.36 (0)
A3_064	calcium binding protein, 140 kDa ^l		154.94	5.08	16.44	mV112BS	A	9 ^g	<i>Cab140</i>	55	interval (≥ 2.5)	<i>Cab140</i> (mV110BS) LOD 15.95 (0) <i>D9Nds10</i> LOD 14.75 (0)
A3_065	calcium binding protein, 140 kDa ^l		154.02	5.07	19.45	"	A	9 ^g	<i>Cab140</i>	55	interval (≥ 2.5)	<i>Cab140</i> (mV110BS) LOD 15.95 (0) <i>D9Nds10</i> LOD 14.75 (0)
A3_067	calcium binding protein, 140 kDa ^l		151.26	5.05	12.16	"	A	9 ^g	<i>Cab140</i>	55	interval (≥ 2.5)	<i>Cab140</i> (mV110BS) LOD 15.95 (0) <i>D9Nds10</i> LOD 14.75 (0)
C5_006	heat shock 70kD protein 8	NCBI 123651	35.76	6.12	42.31	mV223BS	A	9	<i>Hspa8</i>	60	linked to chr	<i>Hspa11m</i> (mV6BS) LOD 5.88 (21.14)
B3_001	heat shock 70kD protein 8	EMBL U73744	69.15	5.34	500.71			9	<i>Hspa8</i>			
B3_003	heat shock 70kD protein 8	EMBL U73744	68.98	5.38	398.64			9	<i>Hspa8</i>			
B4_278	heat shock 70kD protein 8	SP P08109	51.00	5.75	123.81			9	<i>Hspa8</i>			
B5_021	malic enzyme, supernatant	NCBI 126738	66.51	6.47	114.99	mV296BS	A	9	<i>Mod1</i>	64	≥ 2.5	
C5_381	modifier of malic enzyme, supernatant	NCBI 126738	31.85	6.59	11.88	paV271BS	A	9 ^g	<i>Mod1m</i>	35	interval (≥ 2.5)	<i>Tpm1</i> (mV28BS), <i>Mod1</i> (mV296BS) LOD 7.21 (6.07) <i>D9Irs5</i> LOD 6.11 (6.91)
C2_047	tropomyosin 1, alpha	NCBI 136104	34.26	4.78	69.59	mV28BS	A	9	<i>Tpm1</i>	64	≥ 2.5	
C2_170	tropomyosin 1, alpha	NCBI 136104	29.87	4.79	103.47	mV38BS	A	9	<i>Tpm1</i>	64	≥ 2.5	<i>Tpm1</i> (mV28BS) LOD 18.66 (0)
A5_135	transferrin	NCBI 1446473	87.78	6.46	28.13	mV291BS	A	9	<i>Trf</i>	59	≥ 2.5	<i>D9Mit24</i> LOD 15.65 (0)
A5_150	transferrin	NCBI 1446473	87.33	6.46	48.11	"	A	9	<i>Trf</i>	59	≥ 2.5	<i>D9Mit24</i> LOD 15.65 (0)
C6_326	transgelin	NCBI 1351075	25.47	6.96	79.14	mV190BS	A	9	<i>Tagln</i>	57	interval (≥ 2.5)	<i>Cab140</i> (mV110BS), <i>Apoa1</i> (mV348BS) LOD 16.56 (0) <i>D9Nds10</i> LOD 15.65 (0)
D4_156	modifier of heat shock 70kD protein-like 1	NCBI 3461872	13.85	5.61	64.13	mV6BS	A	9 ^g	<i>Hspa11m</i>	64	≥ 2.5	
B4_432			42.20	5.84	58.81	mV41BS	A	9	<i>mV41BS</i>	64	≥ 2.5	<i>mV368BS</i> LOD 18.66 (0)
B2_388			40.16	4.52	11.75	mV70BS	A	9	<i>mV70BS</i>	57	interval (≥ 2.5)	<i>D9Irs2</i> , mV6BS LOD 16.56 (0)
B2_393			39.92	4.48	13.94	"	A	9	<i>mV70BS</i>	57	interval (≥ 2.5)	<i>mbacr9k13</i> , <i>Hspa11m</i> (mV6BS) LOD 16.56 (0)
B2_182			54.18	5.01	82.15	mV79BS	A	9	<i>mV79BS</i>	59	≥ 2.5	<i>D9Mit24</i> LOD 15.95 (0)
B2_104			59.64	4.77	17.22	mV88BS	A	9	<i>mV88BS</i>	52	interval (≥ 2.5)	<i>Apoa1</i> (mV348BS) LOD 14.09 (1.89)
A2_109			102.14	4.68	16.21	mV103BS	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_219			105.36	4.76	10.27	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_220			104.29	4.77	12.66	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_095			103.21	4.77	10.12	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_217			105.00	4.74	8.19	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_218			103.21	4.75	22.56	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_098			102.14	4.75	11.59	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_216			103.57	4.72	9.17	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_215			102.50	4.72	8.80	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_105			101.79	4.72	11.70	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_214			102.86	4.70	11.02	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A2_107			101.79	4.70	12.30	"	A	9	<i>mV103BS</i>	58	interval (2.2)	<i>Cab140</i> (mV110BS) LOD 11.78 (5.67)
A6_056			76.28	7.09	14.77	mV281BS	A	9	<i>mV281BS</i>	60	≥ 2.5	
B6_294			44.69	7.35	13.81	mV368BS	A	9	<i>mV368BS</i>	64	≥ 2.5	
B4_590			40.73	6.04	11.65	paV119BS	A	9	<i>paV119BS</i>	49	≥ 2.5	

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	Name ^b	Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
D5_131			16.16	6.28	9.09	paV234BS	A	9	paV234BS	57	interval (≥ 2.5)	<i>Apoa1</i> (mV348BS), <i>Acat1</i> (mV147BS) LOD 11.50 (5.78)
B5_073	pyruvate kinase 3	SP P52480	61.75	6.68	287.14			9	<i>PK3</i>			
B5_092	pyruvate kinase 3	SP P52480	59.91	6.55	927.83			9	<i>PK3</i>			
E4_079	D-dopachrome tautomerase	NCBI 6753618	12.21	6.07	219.79	mV4BS	A	10	<i>Ddt</i>	64	interval (≥ 2.5)	<i>D10Mit20</i> LOD 14.45 (0)
A2_097	tumor rejection antigen gp96	SP P08113	105.71	4.86	8.51	mV104BS	A	10	<i>Tra1</i>	64	2.2	
A2_087	tumor rejection antigen gp96	SP P08113	106.79	4.83	16.22	"	A	10	<i>Tra1</i>	64	2.2	
A2_091	tumor rejection antigen gp96	SP P08113	106.43	4.86	6.23	"	A	10	<i>Tra1</i>	64	2.2	
A2_094	tumor rejection antigen gp96	SP P08113	106.07	4.83	11.43	"	A	10	<i>Tra1</i>	64	2.2	
A2_086	tumor rejection antigen gp96	SP P08113	107.14	4.84	14.62	"	A	10	<i>Tra1</i>	64	2.2	
A2_092	tumor rejection antigen gp96	SP P08113	106.43	4.84	20.25	"	A	10	<i>Tra1</i>	64	2.2	
A2_088	tumor rejection antigen gp96	SP P08113	106.43	4.89	29.54	"	A	10	<i>Tra1</i>	64	2.2	
A2_082	tumor rejection antigen gp96	SP P08113	107.14	4.88	46.84	"	A	10	<i>Tra1</i>	64	2.2	
A2_090	tumor rejection antigen gp96	SP P08113	106.43	4.88	10.18	"	A	10	<i>Tra1</i>	64	2.2	
A2_096	tumor rejection antigen gp96	SP P08113	105.71	4.88	28.14	"	A	10	<i>Tra1</i>	64	2.2	
A2_084	tumor rejection antigen gp96	SP P08113	107.50	4.87	20.94	"	A	10	<i>Tra1</i>	64	2.2	
A2_089	tumor rejection antigen gp96	SP P08113	106.79	4.87	9.22	"	A	10	<i>Tra1</i>	64	2.2	
A2_093	tumor rejection antigen gp96	SP P08113	106.07	4.87	35.49	"	A	10	<i>Tra1</i>	64	2.2	
A2_085	tumor rejection antigen gp96	SP P08113	107.14	4.86	18.77	"	A	10	<i>Tra1</i>	64	2.2	
A2_210	modifier of histocompatibility 2, D region locus 1	NCBI 122130	75.20	4.94	34.84	mV97BS	A	10 ^g	<i>H2-d1m</i>	36	linked to chr	<i>Tra1</i> (mV104BS) LOD 7.48 (5.89)
C6_265	DNA segment, Chr 10, Johns Hopkins University 81 expressed ^d		27.08	7.09	66.21	mV366BS	A	10	<i>D10Jhu81e</i>	64	interval (≥ 2.5)	<i>D10Mit20</i> LOD 14.45 (0)
C6_271	DNA segment, Chr 10, Johns Hopkins University 81 expressed ^d	NCBI 2250700	27.02	7.09	73.89	"	A	10	<i>D10Jhu81e</i>	64	interval (≥ 2.5)	<i>D10Mit20</i> LOD 14.45 (0)
C6_273	DNA segment, Chr 10, Johns Hopkins University 81 expressed ^d		26.89	7.10	69.23	"	A	10	<i>D10Jhu81e</i>	64	interval (≥ 2.5)	<i>D10Mit20</i> LOD 14.45 (0)
C6_260	DNA segment, Chr 10, Johns Hopkins University 81 expressed ^d	NCBI 2250700	27.16	7.23	236.85	mV367BS	A	10	<i>D10Jhu81e</i>	64	interval (≥ 2.5)	<i>D10Mit20</i> LOD 14.45 (0)
E3_073			10.36	5.40	50.92	mV11BS	A	10	<i>mV11BS</i>	63	≥ 2.5	
B2_506			36.41	4.76	34.24	mV65BS	A	10	<i>mV65BS</i>	28	linked to chr	<i>Tra1</i> (mV104BS) LOD 3.44 (16.82)
A3_031			181.61	5.50	19.19	mV114BS	A	10	<i>mV114BS</i>	61	2.1	
A3_032			181.61	5.49	11.94	"	A	10	<i>mV114BS</i>	61	2.1	
A3_033			181.61	5.48	13.82	"	A	10	<i>mV114BS</i>	61	2.1	
A3_034			182.53	5.46	13.81	"	A	10	<i>mV114BS</i>	61	2.1	
A4_232			90.00	6.01	14.44	mV115BS	A	10	<i>mV115BS</i>	14	interval (≥ 2.5)	<i>D10Mit24</i> LOD 4.21 (0)
C5_034			34.65	6.33	38.21	mV226BS	A	10	<i>mV226BS</i>	64	≥ 2.5	
C5_044			34.53	6.33	23.95	"	A	10	<i>mV226BS</i>	64	≥ 2.5	
C6_081			32.67	6.89	6.96	mV239BS	A	10	<i>mV239BS</i>	62	interval (≥ 2.5)	<i>D10Irs2</i> LOD 9.34 (11.37) <i>D10Mit20</i> LOD 9.30 (6.83) <i>D10Mit7</i> LOD 8.47 (9.12) <i>Tra1</i> (mV104BS) LOD 10.10 (10.46)
C4_338			28.75	5.61	10.67	paV65BS	A	10	<i>paV65BS</i>	52	linked to chr	<i>Tra1</i> (mV104BS) LOD 6.77 (19.47)
C6_277			26.78	6.93	31.61	paV276BS	A	10	<i>paV276BS</i>	47	≥ 2.5	
A2_207	heat shock 70 kDa protein 4 ⁱ		75.60	4.90	28.77	mV93BS	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_225	heat shock 70 kDa protein 4 ⁱ		76.00	4.88	29.81	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_206	heat shock 70 kDa protein 4 ⁱ		75.80	4.88	15.35	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_204	heat shock 70 kDa protein 4 ⁱ		76.00	4.86	23.06	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_224	heat shock 70 kDa protein 4 ⁱ		76.20	4.85	21.42	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_015	heat shock 70 kDa protein 4 ⁱ		72.00	4.93	26.04	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_003	heat shock 70 kDa protein 4 ⁱ		72.40	4.90	38.00	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_013	heat shock 70 kDa protein 4 ⁱ		72.40	4.88	11.86	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_001	heat shock 70 kDa protein 4 ⁱ		72.60	4.87	13.10	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_007	heat shock 70 kDa protein 4 ⁱ		72.40	4.87	24.33	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_046	heat shock 70 kDa protein 4 ⁱ		67.97	4.79	12.69	mV96BS	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_055	heat shock 70 kDa protein 4 ⁱ		67.29	4.79	11.79	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_051	heat shock 70 kDa protein 4 ⁱ		67.46	4.81	11.78	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_048	heat shock 70 kDa protein 4 ⁱ		68.14	4.81	7.84	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_050	heat shock 70 kDa protein 4 ⁱ		67.29	4.82	33.76	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_049	heat shock 70 kDa protein 4 ⁱ		67.63	4.84	29.84	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)

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A2_123	heat shock 70 kDa protein 4 ^l		89.46	4.96	22.64	mV98BS	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_141	heat shock 70 kDa protein 4 ^l		89.73	4.94	42.86	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_140	heat shock 70 kDa protein 4 ^l		89.73	4.91	33.54	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_155	heat shock 70 kDa protein 4 ^l		85.68	4.96	21.04	mV99BS	A	11	<i>Hspa4</i>	58	interval (≥ 2.5)	<i>D11Nds19</i> LOD 12.54 (3.85)
A2_156	heat shock 70 kDa protein 4 ^l		85.68	4.93	31.26	"	A	11	<i>Hspa4</i>	58	interval (≥ 2.5)	<i>D11Nds19</i> LOD 12.54 (3.85)
A2_164	heat shock 70 kDa protein 4 ^l		84.59	5.03	36.68	mV100BS	A	11	<i>Hspa4</i>	53	interval (≥ 2.5)	<i>D11Nds19</i> LOD 11.12 (4.26)
A2_165	heat shock 70 kDa protein 4 ^l		84.59	5.00	26.50	"	A	11	<i>Hspa4</i>	53	interval (≥ 2.5)	<i>D11Nds19</i> LOD 11.12 (4.26)
A2_173	heat shock 70 kDa protein 4 ^l		82.43	4.99	25.03	mV101BS	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_174	heat shock 70 kDa protein 4 ^l		82.43	4.96	27.16	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_173	heat shock 70 kDa protein 4 ^l		101.07	5.10	16.69	mV106BS	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_166	heat shock 70 kDa protein 4 ^l		101.43	5.13	25.31	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_165	heat shock 70 kDa protein 4 ^l		101.79	5.16	32.04	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_149	heat shock 70 kDa protein 4 ^l		105.71	5.15	35.83	mV107BS	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_151	heat shock 70 kDa protein 4 ^l		105.71	5.13	21.70	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_153	heat shock 70 kDa protein 4 ^l		105.71	5.10	16.65	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_150	heat shock 70 kDa protein 4 ^l		105.71	5.21	57.50	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_148	heat shock 70 kDa protein 4 ^l		105.71	5.18	62.14	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_146	heat shock 70 kDa protein 4 ^l		106.76	5.33	47.91	mV108BS	A	11	<i>Hspa4</i>	53	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_144	heat shock 70 kDa protein 4 ^l		106.43	5.30	56.07	"	A	11	<i>Hspa4</i>	53	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_140	heat shock 70 kDa protein 4 ^l		106.07	5.27	33.59	"	A	11	<i>Hspa4</i>	53	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_111	heat shock 70 kDa protein 4 ^l		118.95	5.31	27.77	mV109BS	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_110	heat shock 70 kDa protein 4 ^l		119.47	5.28	25.22	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_092	heat shock 70 kDa protein 4	EMBL D85904	119.47	5.25	115.47	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_077	heat shock 70 kDa protein 4	EMBL D85904	120.00	5.23	249.70	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_084	heat shock 70 kDa protein 4	EMBL D85904	120.00	5.20	224.57	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_086	heat shock 70 kDa protein 4	EMBL D85904	120.00	5.18	162.91	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_109	heat shock 70 kDa protein 4	EMBL D85904	120.00	5.16	71.76	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B2_158	heat shock 70 kDa protein 4 ^l		55.50	4.67	22.57	mV314BS	A	11	<i>Hspa4</i>	29	interval (≥ 2.5)	<i>D11Nds19</i> LOD 6.27 (3.85)
B2_157	heat shock 70 kDa protein 4 ^l		55.64	4.70	23.64	"	A	11	<i>Hspa4</i>	29	interval (≥ 2.5)	<i>D11Nds19</i> LOD 6.27 (3.85)
A2_120	heat shock 70 kDa protein 4 ^l		93.33	5.05	25.81	mV316BS	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_223	heat shock 70 kDa protein 4 ^l		92.96	5.08	32.47	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A3_227	heat shock 70 kDa protein 4 ^l		92.59	5.11	24.65	"	A	11	<i>Hspa4</i>	63	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_222	heat shock 70 kDa protein 4 ^l		89.46	4.89	18.42	mV372BS	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_148	heat shock 70 kDa protein 4 ^l		88.92	4.89	20.93	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_221	heat shock 70 kDa protein 4 ^l		89.73	4.87	5.43	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
A2_142	heat shock 70 kDa protein 4 ^l		89.19	4.87	17.83	"	A	11	<i>Hspa4</i>	64	interval (≥ 2.5)	<i>D11Nds19</i> LOD 13.97 (3.51)
B5_046	modifier of collapsin response mediator protein 1	NCBI 3122030	64.44	6.53	37.85	paV493BS	A	11 ^g	<i>Crmp1m</i>	60	≥ 2.5	<i>D11rs2</i> LOD 18.06 (0)
B5_065	modifier of dihydropyrimidinase like 4	NCBI 3122037	63.65	6.26	49.19	paV507BS	A	11 ^g	<i>Dpysl4m</i>	60	interval (≥ 2.5)	<i>paV496BS</i> LOD 14.39 (1.85)
B5_695	TU translation elongation factor, mitochondrial	NCBI 1706611	46.56	6.33	30.11	paV468BS	A	11 ^g	<i>Tufm</i>	61	interval (≥ 2.5)	<i>D11Mit16</i> LOD 6.60 (14.38)
D6_120	aldolase 3, C isoform	NCBI 2118269	15.63	6.92	29.22	mV159BS	A	11	<i>Aldo3</i>	42	interval (≥ 2.5)	<i>D11Mit31</i> LOD 7.70 (3.23) <i>Srr</i> (paV189BS) LOD 7.99 (3.13) <i>2700085E05Rik</i> (mV351BS) LOD 8.28 (3.03)
B5_467	aldolase 3, C isoform	SP P09117	43.28	6.47	362.44			11	<i>Aldo3</i>			
B5_490	aldolase 3, C isoform	SP P09117	42.42	6.48	372.76			11	<i>Aldo3</i>			
B5_040	RIKEN cDNA 1300003G02 gene	NCBI 1864372	65.24	6.40	18.47	mV300BS	A	11 ^g	<i>1300003G02Rik</i>	64	interval (≥ 2.5)	<i>D11rs2</i> LOD 15.40 (3.23)
A2_007	neurofilament, heavy polypeptide	NCBI 128127		4.86	245.35	paV190BS	A	11	<i>Nfh</i>	57	interval (≥ 2.5)	<i>D11Mit16</i> LOD 12.05 (2.17)
A2_009	neurofilament, heavy polypeptide ^l			4.77	163.67	"	A	11	<i>Nfh</i>	57	interval (≥ 2.5)	<i>D11Mit16</i> LOD 12.05 (2.17)
A2_011	neurofilament, heavy polypeptide ^l		193.56	4.68	74.70	"	A	11	<i>Nfh</i>	57	interval (≥ 2.5)	<i>D11Mit16</i> LOD 12.05 (2.17)
A2_014	neurofilament, heavy polypeptide ^l		178.85	4.61	340.83	"	A	11	<i>Nfh</i>	57	interval (≥ 2.5)	<i>D11Mit16</i> LOD 12.05 (2.17)
C6_186	phosphoglycerate mutase 2	NCBI 6093745	29.17	7.16	51.13	aV380BS	A	11 ^h	<i>Pgam2</i>	63	interval (≥ 2.5)	<i>D11Mit16</i> LOD 10.12 (6.39)
B2_464	prolyl 4-hydroxylase, beta polypeptide	NCBI 202547	37.97	4.82	39.12	mV130BS	A	11	<i>P4hb</i>	64	interval (≥ 2.5)	<i>D11Mit11</i> LOD 4.22 (27.98)
B2_458	prolyl 4-hydroxylase, beta polypeptide	NCBI 202547	38.19	4.80	19.72	"	A	11	<i>P4hb</i>	64	interval (≥ 2.5)	<i>D11Mit11</i> LOD 4.22 (27.98)
B2_150	modifier of prolyl 4-hydroxylase, beta polypeptide ^l		56.36	4.89	76.16	mV86BS	A	11 ^g	<i>P4hbm</i>	64	interval (≥ 2.5)	<i>D11Mit11</i> LOD 7.69 (14.38)
B2_146	modifier of prolyl 4-hydroxylase, beta polypeptide	NCBI 129729	56.55	4.86	175.31	"	A	11 ^g	<i>P4hbm</i>	64	interval (≥ 2.5)	<i>D11Mit11</i> LOD 7.69 (14.38)
B2_147	modifier of prolyl 4-hydroxylase, beta polypeptide ^l		56.64	4.83	85.48	"	A	11 ^g	<i>P4hbm</i>	64	interval (≥ 2.5)	<i>D11Mit11</i> LOD 7.69 (14.38)
C5_165	pyridoxine 5'-phosphate oxidase	NCBI 3237304	29.65	6.12	92.53	mV209BS	A	11 ^{g,k}	<i>Ppo-pending</i>	64	≥ 2.5	
B5_692	modifier of pyruvate kinase 3	NCBI 2506796	61.43	6.49	79.38	paV495BS	A	11 ^g	<i>Pk3m</i>	54	interval (≥ 2.5)	<i>paV496BS</i> LOD 10.84 (4.35)

2-DE Spot-No ^a	Name ^b	PROTEINS				GENES				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
B5_393	45kD secretory protein	NCBI 5596693	46.88	6.19	121.35	mV237BS	A	11 ^{g,k}	<i>Sec-like2-pending</i>	64	interval (≥ 2.5)	<i>D11rs1</i> LOD 8.79 (14.38)
B4_523	serine racemase	NCBI 6448865	38.27	5.63	58.71	paV189BS	A	11 ^g	<i>Srr</i>	63	2.4	
B4_532	serine racemase	NCBI 6448865	38.06	5.63	83.17	"	A	11 ^g	<i>Srr</i>	63	2.4	
C3_162	RIKEN cDNA 2700085E05 gene	NCBI 1285464	30.72	5.38	177.59	mV351BS	A	11 ^g	<i>2700085E05Rik</i>	64	2.2	
B3_240			54.82	5.25	60.21	mV80BS	A	11	<i>mV80BS</i>	62	interval (≥ 2.5)	<i>D11Mit16</i> LOD 12.63 (2.08)
C4_342			24.12	5.82	79.47	mV127BS	A	11	<i>mV127BS</i>	64	≥ 2.5	<i>D11rs2</i> LOD 19.27 (0)
D5_129			17.35	6.21	15.46	mV168BS	A	11	<i>mV168BS</i>	48	linked to chr	<i>Srr</i> (paV189BS) LOD 3.58 (27.72)
B2_521			54.36	4.94	20.25	mV309BS	A	11	<i>mV309BS</i>	33	interval (≥ 2.5)	<i>D11rs2</i> LOD 4.64 (13.88) <i>D11Mit11</i> LOD 4.15 (14.92)
B2_180			54.45	4.91	46.60	"	A	11	<i>mV309BS</i>	33	interval (≥ 2.5)	<i>D11rs2</i> LOD 4.64 (13.88) <i>D11Mit11</i> LOD 4.15 (14.92)
C2_137			31.27	4.75	21.94	mV322BS	A	11	<i>mV322BS</i>	55	interval (≥ 2.5)	<i>D11Mit11</i> LOD 4.18 (24.14)
C2_328			25.61	5.04	31.82	paV95BS	A	11	<i>paV95BS</i>	61	linked to chr	<i>2700085E05Rik</i> (mV351BS) LOD 9.85 (10.95)
B6_412			39.26	7.29	21.31	paV432BS	A	11	<i>paV432BS</i>	63	interval (≥ 2.5)	<i>D11Mit11</i> LOD 4.60 (25.54)
B5_066			63.65	6.17	52.43	paV496BS	A	11	<i>paV496BS</i>	58	≥ 2.5	
E7_015	hemoglobin alpha, adult chain 1	SP P01942	12.14	7.68	24.52			11	<i>Hba-a1</i>			
C4_022	malate dehydrogenase, soluble	SP P14152	34.35	5.88	952.45			11	<i>Mor2</i>			
C5_295	malate dehydrogenase, soluble	SP P14152	26.09	6.45	200.57			11	<i>Mor2</i>			
D6_083	peptidylprolyl isomerase A	SP P17742	25.25	7.07	345.96			11	<i>Ppia</i>			
D6_091	peptidylprolyl isomerase A	SP P17742	17.46	6.76	169.28			11	<i>Ppia</i>			
D6_075	peptidylprolyl isomerase A	SP P17742	18.06	6.76	888.01			11	<i>Ppia</i>			
B4_589	acyl-coA thioesterase long chain, mitochondrial	NCBI 6478480	45.37	6.07	28.19	paV118BS	A	12 ^{g,k}	<i>Actm-pending</i>	61	interval (≥ 2.5)	<i>mV48BS</i> LOD 15.56 (1.72)
B5_167	methylmalonate-semialdehyde dehydrogenase	NCBI 400269	56.60	6.33	251.19	paV463BS	A	12	<i>Mmsdh</i>	64	≥ 2.5	
B5_428	methylmalonate-semialdehyde dehydrogenase ^l		45.31	6.22	69.89	paV421BS	A	12	<i>Mmsdh</i>	62	≥ 2.5	<i>Mmsdh</i> (paV463BS) LOD 18.66 (0)
B5_172	modifier of methylmalonate-semialdehyde dehydrogenase	NCBI 400269	56.70	6.22	83.57	paV486BS	A	12 ^g	<i>Mmsdhm</i>	50	≥ 2.5	
B2_151	modifier of tubulin, beta 5	NCBI 135471	56.64	5.03	37.67	aV174BS	A	12 ^g	<i>Tubb5m</i>	56	interval (≥ 2.5)	<i>paV175/176BS</i> LOD 9.28 (10.03)
B2_137	homologous tubulin beta-15 chain (rat)	NCBI 92930	57.36	4.97	84.89	paV175BS	A	12 ^g	<i>paV175/176BS</i>	61	≥ 2.5	
B2_138	homologous tubulin beta-15 chain (rat)	NCBI 92930	57.36	4.95	82.82	"	A	12 ^g	<i>paV175/176BS</i>	61	≥ 2.5	
B2_134	homologous tubulin beta-15 chain (rat) ^l		57.45	4.91	70.39	paV176BS	A	12 ^g	<i>paV175/176BS</i>	58	≥ 2.5	<i>paV175/176BS</i> LOD 17.46 (0)
B2_133	homologous tubulin beta-15 chain (rat) ^l		57.64	4.91	78.59	"	A	12 ^g	<i>paV175/176BS</i>	58	≥ 2.5	<i>paV175/176BS</i> LOD 17.46 (0)
B3_513			41.06	5.34	40.00	mV48BS	A	12	<i>mV48BS</i>	62	≥ 2.5	<i>Mmsdh</i> (paV463BS) LOD 81.66 (0)
B2_117			58.36	4.83	70.87	mV310BS	A	12	<i>mV310BS</i>	57	interval (2.4)	<i>paV175/176BS</i> LOD 10.33 (7.86)
B2_111			58.64	4.77	54.03	"	A	12	<i>mV310BS</i>	57	interval (≥ 2.5)	<i>paV175/176BS</i> LOD 10.33 (7.86)
D3_223			14.35	5.47	7.02	paV18BS	A	12	<i>paV18BS</i>	49	linked to chr	<i>D12Mit4</i> LOD 3.77 (25.54)
B3_207			56.27	5.05	64.04	aV173BS	A	12	<i>aV173BS</i>	61	interval (≥ 2.5)	<i>D12Nds11</i> LOD 3.36 (33.79)
E6_071			11.68	6.78	6.85	paV225BS	A	12	<i>paV225BS</i>	45	interval (≥ 2.5)	<i>D12Nds11</i> LOD 3.76 (23.98)
C3_058	creatine kinase, brain	SP Q04447	34.09	5.22	223.96	aV348BS	C	12 ^l	<i>Ckb</i>			
B3_423	creatine kinase, brain	SP Q04447	46.42	5.53				12	<i>Ckb</i>			
B4_354	creatine kinase, brain	SP Q04447	46.26	5.59	916.60			12	<i>Ckb</i>			
C2_189	creatine kinase, brain	SP Q04447	29.18	4.89	545.86			12	<i>Ckb</i>			
C3_052	creatine kinase, brain	SP Q04447	34.26	5.32	425.44			12	<i>Ckb</i>			
C3_135	creatine kinase, brain	SP Q04447	31.73	5.19	288.41			12	<i>Ckb</i>			
C3_141	creatine kinase, brain	SP Q04447	31.60	5.09	215.34			12	<i>Ckb</i>			
C6_023	aldo-keto reductase family 1, member E1	EMBL U68535	35.23	6.83	44.51	mV229BS	A	13 ^g	<i>Akr1e1</i>	64	≥ 2.5	<i>Pfkip</i> (mV290BS) LOD 19.27 (0)
C6_034	aldo-keto reductase family 1, member E1	EMBL U68535	34.98	6.83	10.44	"	A	13 ^g	<i>Akr1e1</i>	64	≥ 2.5	<i>Pfkip</i> (mV290BS) LOD 19.27 (0)
A3_098	calpastatin ^l		129.20	5.14	37.01	mV113BS	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_101	calpastatin ^l		129.20	5.11	20.15	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_093	calpastatin ^l		132.87	5.11	15.76	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_089	calpastatin	NCBI 6006275	136.55	5.11	9.65	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_083	calpastatin ^l		141.15	5.11	6.40	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_397	calpastatin ^l		129.20	5.10	8.68	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_094	calpastatin ^l		133.79	5.09	17.96	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_090	calpastatin	NCBI 6006275	136.55	5.09	8.90	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	

2-DE Spot-No ^a	PROTEINS					GENES			GENE MAPPING			
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A3_080	calpastatin ^l		141.15	5.08	13.95	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_076	calpastatin ^l		146.67	5.08	5.64	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_095	calpastatin ^l		133.79	5.07	8.84	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_091	calpastatin ^l	NCBI 6006275	137.47	5.06	7.60	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_081	calpastatin ^l		140.23	5.06	11.68	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
A3_078	calpastatin ^l		143.91	5.06	6.16	"	A	13 ^g	<i>Cast</i>	64	≥ 2.5	
E6_045	modifier of hemoglobin alpha, adult chain 1	NCBI 109958	10.04	7.03	85.87	paV224BS	A	13 ^g	<i>Hba-a1m</i>	64	≥ 2.5	
B4_169	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	NCBI 123333	56.45	5.75	54.24	paV157BS	A	13	<i>Hmgcs1</i>	63	≥ 2.5	
A5_147	phosphofructokinase, platelet	NCBI 4567052	87.11	6.26	97.94	mV290BS	A	13 ^g	<i>Pfkp</i>	64	≥ 2.5	<i>D13Mit56</i> LOD 10.06 (8.02)
B4_474	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1a	NCBI 12834891	39.87	5.86	106.27	aV124BS	A	13 ^g	<i>Serpnb1a</i>	64	≥ 2.5	
C6_392	modifier of transaldolase 1	NCBI 2851596	28.07	7.14	13.29	mV221BS	A	13 ^g	<i>Taldo1m</i>	50	≥ 2.5	<i>Serpnb1a</i> (aV124BS) LOD 15.05 (0)
A2_209	ubiquilin 1 ^l		75.00	4.61	75.22	mV91BS	A	13 ^g	<i>Ubqln1</i>	51	≥ 2.5	
A2_212	ubiquilin 1	NCBI 5733824	74.80	4.66	121.89	"	A	13 ^g	<i>Ubqln1</i>	51	≥ 2.5	
B2_014	ubiquilin 1 ^l		71.60	4.62	56.80	"	A	13 ^g	<i>Ubqln1</i>	51	≥ 2.5	
B2_019	ubiquilin 1	NCBI 5733824	71.60	4.66	131.98	"	A	13 ^g	<i>Ubqln1</i>	51	≥ 2.5	
E5_046	homologous ubiquitin (rabbit)	NCBI 346623	10.31	6.24	63.23	mV155BS	A	13 ^g	<i>mV155BS</i>	63	≥ 2.5	<i>Hba-a1m</i> (paV224BS) LOD 18.96 (0)
C6_226			28.15	7.30	59.53	mV140BS	A	13	<i>mV140BS</i>	63	≥ 2.5	<i>Serpnb1a</i> (aV124BS) LOD 18.96 (0)
E4_080			9.91	5.76	19.14	paV5BS	A	13	<i>paV5BS</i>	63	interval (≥ 2.5)	<i>Cast</i> (mV113BS) LOD 16.73 (1.61)
C4_221			27.58	6.06	116.95	paV50BS	A	13	<i>paV50BS</i>	61	1.7	<i>D13Mit56</i> LOD 8.50 (10.68)
C4_311			24.34	5.91	11.12	paV117BS	A	13	<i>paV117BS</i>	61	interval (≥ 2.5)	<i>Serpnb1a</i> (aV124BS) LOD 13.17 (5.18)
B4_490			39.28	5.75	61.32	paV125BS	A	13	<i>paV125BS</i>	64	≥ 2.5	<i>Serpnb1a</i> (aV124BS) LOD 19.27 (0)
C4_019			34.98	6.09	39.37	paV395BS	A	13	<i>paV395BS</i>	59	≥ 2.5	<i>D13Mit56</i> LOD 10.12 (6.39)
B5_458			43.75	6.27	69.03	paV420BS	A	13	<i>paV420BS</i>	64	interval (≥ 2.5)	<i>Serpnb1a</i> (aV124BS) LOD 17.03 (1.59)
B3_248	annexin A7	SP Q07076	54.36	5.11	173.22	paV171BS	A	14	<i>Anxa7</i>	62	≥ 2.5	
D5_073	fragile histidine triad gene	NCBI 6015152	17.59	6.38	21.86	paV231BS	A	14	<i>Fhit</i>	59	interval (≥ 2.5)	<i>D14Irs2</i> LOD 15.56 (1.72)
C4_114	dihydropyrimidinase-like 2	NCBI 3122040	30.93	5.76	52.82	paV86BS	A	14	<i>Dpysl2</i>	63	≥ 2.5	<i>D14Irs4</i> LOD 18.66 (0)
A4_216	dihydropyrimidinase-like 2	SP P47942	71.80	5.82	265.48			14	<i>Dpysl2</i>			
B4_018	dihydropyrimidinase-like 2	SP P47942	66.44	5.90	339.34			14	<i>Dpysl2</i>			
B4_022	dihydropyrimidinase-like 2	SP P47942	66.10	6.01	799.40			14	<i>Dpysl2</i>			
D3_092	glia maturation factor, beta	SP Q63228	18.76	5.16	232.97	mV8BS	A	14 ^g	<i>Gmfb</i>	63	interval (≥ 2.5)	<i>D14Irs4</i> LOD 16.44 (1.64)
A5_294	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	SP Q16822	72.79	6.20	63.88	mV301BS	A	14	<i>Pck2</i>	64	≥ 2.5	<i>D14Irs4</i> LOD 18.96 (0)
C5_387	RIKEN cDNA clone: 2310045J23	NCBI 12832275	26.84	6.46	13.23	paV250BS	A	14 ^g	<i>2310045J23Rik</i>	59	linked to chr	<i>D14Mit45</i> LOD 4.03 (28.67) <i>D14Nds7</i> LOD 4.60 (25.54)
B4_151	modifier of synapsin II	NCBI 3860049	57.55	5.99	59.01	mV358BS	A	14 ^g	<i>Syn2m</i>	59	2.3	
C2_163			30.08	4.76	20.02	mV321BS	A	14	<i>mV321BS</i>	57	interval (≥ 2.5)	<i>D14Irs4</i> LOD 13.11 (3.71)
D4_160			21.84	6.09	6.59	paV23BS	A	14	<i>paV23BS</i>	43	interval (≥ 2.5)	<i>D14Irs2</i> LOD 10.88 (2.38)
B3_666			52.45	5.13	26.14	paV170BS	A	14	<i>paV170BS</i>	64	linked to chr	<i>D14Irs2</i> LOD 5.85 (23.50)
B5_176	glutamate dehydrogenase	SP P26443	56.32	6.56	333.42			14	<i>Glud</i>			
B2_017	neurofilament, light polypeptide	SP P08551	71.40	4.79	37.04			14	<i>Nfl</i>			
A5_103	modifier 1 of aconitase 2, mitochondrial ^l		92.50	6.61	117.18	mV150BS	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A5_102	modifier 1 of aconitase 2, mitochondrial ^l		92.19	6.65	292.90	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A5_097	modifier 1 of aconitase 2, mitochondrial ^l	SP P16276	91.88	6.73	480.75	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_008	modifier 1 of aconitase 2, mitochondrial ^l	SP P16276	91.56	6.74	711.30	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_012	modifier 1 of aconitase 2, mitochondrial ^l		88.44	6.80	16.82	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_011	modifier 1 of aconitase 2, mitochondrial ^l		88.44	6.86	28.71	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_009	modifier 1 of aconitase 2, mitochondrial ^l		91.88	6.80	164.94	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_013	modifier 1 of aconitase 2, mitochondrial ^l		88.22	6.81	16.59	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_010	modifier 1 of aconitase 2, mitochondrial ^l		89.11	6.77	17.22	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_014	modifier 1 of aconitase 2, mitochondrial ^l		88.00	6.77	7.84	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
A6_015	modifier 1 of aconitase 2, mitochondrial ^l		87.11	6.76	4.51	"	A	15 ^g	<i>Aco2m1</i>	61	≥ 2.5	<i>D15Irs2</i> LOD 18.36 (0)
B6_220	modifier 1 of aconitase 2, mitochondrial ^l	SP P16276	48.36	7.12	41.26	mV248BS	A	15 ^g	<i>Aco2m1</i>	48	≥ 2.5	<i>D15Irs1</i> LOD 14.45 (0)
A5_219	modifier 1 of aconitase 2, mitochondrial ^l		80.00	6.66	24.83	mV292BS	A	15 ^g	<i>Aco2m1</i>	62	≥ 2.5	<i>D15Irs2</i> LOD 18.66 (0)

2-DE Spot-No ^a	PROTEINS					GENES				GENE MAPPING		
	Name ^b	Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
A5_240	modifier 1 of aconitase 2, mitochondrial ^l		77.91	6.69	16.53	"	A	15 ^g	<i>Aco2m1</i>	62	≥ 2.5	<i>D15Irs2</i> LOD 18.66 (0)
A5_241	modifier 1 of aconitase 2, mitochondrial ^l		77.91	6.68	30.75	"	A	15 ^g	<i>Aco2m1</i>	62	≥ 2.5	<i>D15Irs2</i> LOD 18.66 (0)
A5_202	modifier 1 of aconitase 2, mitochondrial ^l	NCBI 5304852	82.22	6.65	56.32	"	A	15 ^g	<i>Aco2m1</i>	62	≥ 2.5	<i>D15Irs2</i> LOD 18.66 (0)
B5_038	modifier 2 of aconitase 2, mitochondrial	NCBI 3600098	65.08	6.69	45.99	mV297BS	A	15 ^g	<i>Aco2m2</i>	58	linked to chr	<i>D15Irs2</i> LOD 10.06 (9.46)
B5_063	modifier 2 of aconitase 2, mitochondrial	NCBI 3600098	63.49	6.63	77.77	"	A	15 ^g	<i>Aco2m2</i>	58	linked to chr	<i>D15Irs2</i> LOD 10.06 (9.46)
B5_263	adenylosuccinate lyase	NCBI 1709933	52.74	6.48	71.73	mV266BS	A	15	<i>Adsl</i>	64	≥ 2.5	<i>D15Irs2</i> LOD 19.27 (0)
B5_301	modifier of actin, alpha, cardiac	NCBI 627834	51.13	6.62	39.31	mV267BS	A	15 ^g	<i>Actc1m</i>	52	≥ 2.5	
C5_236	modifier of RAN, member RAS oncogene family	NCBI 131844	27.88	6.51	40.25	paV257BS	A	15 ^g	<i>Ranm</i>	32	interval (2.0)	<i>D15Irs1</i> LOD 6.38 (6.68)
C5_038	3-mercaptopyruvate sulfotransferase	SP P97532	34.61	6.18	58.21	mV363BS	A	15 ^g	<i>Mpst</i>	64	≥ 2.5	
B5_696	modifier of tissue specific transplantation antigen P35B	NCBI 387474	46.09	6.48	20.77	paV467BS	A	15 ^g	<i>Tstap35bm</i>	50	≥ 2.5	
C6_089	RIKEN cDNA clone: 1110058B13	NCBI 12833245	32.18	6.86	52.24	aV384BS	A	15 ^g	<i>1110058B13Rik</i>	36	interval (≥ 2.5)	<i>mV66BS</i> , <i>Mpst</i> (mV363BS) LOD 2.86
B5_124	3-oxoacid CoA transferase	NCBI 2492998	58.77	6.31	165.62	mV149BS	A	15 ^g	<i>Oxct</i>	64	≥ 2.5	<i>D15Mit11</i> LOD 17.76 (0)
B5_129	3-oxoacid CoA transferase	NCBI 2492998	58.87	6.42	256.96	"	A	15 ^g	<i>Oxct</i>	64	≥ 2.5	<i>D15Mit11</i> LOD 17.76 (0)
C2_032			34.89	4.98	20.47	mV66BS	A	15	<i>mV66BS</i>	64	≥ 2.5	
B2_525			38.06	4.94	10.11	mV68BS	A	15	<i>mV68BS</i>	57	≥ 2.5	
B2_517			36.24	5.02	32.87	mV67BS	A	15	<i>mV67BS</i>	64	≥ 2.5	<i>mV66BS</i> LOD 19.27 (0)
D8_016			18.37	8.36	27.05	mV177BS	A	15	<i>mV177BS</i>	37	interval (≥ 2.5)	<i>D15Irs2</i> LOD 9.14 (2.78)
B6_193			49.53	6.79	27.51	mV246BS	A	15	<i>mV246BS</i>	61	linked to chr	<i>D15Mit11</i> LOD 3.68 (31.21)
B5_335			49.38	6.66	54.91	mV293BS	A	15	<i>mV293BS</i>	59	≥ 2.5	<i>D15Mit11</i> LOD 16.56 (0)
C3_001			36.16	5.08	20.86	paV114BS	A	15	<i>paV114BS</i>	64	≥ 2.5	
B5_650	glycerol phosphate dehydrogenase 1, cytoplasmic adult	SP P13707	37.08	6.55	44.85			15	<i>Gdc1</i>			
C6_072	carbonyl reductase 1	SP P48758	33.09	6.93	173.67	mV142BS	A	16	<i>Cbr1</i>	64	interval (≥ 2.5)	<i>Mx1</i> LOD 13.40 (3.64)
C6_389	carbonyl reductase 1	SP P48758	34.12	6.74	102.01	mV153BS	A	16	<i>Cbr1</i>	64	interval (≥ 2.5)	<i>Mx1</i> LOD 13.40 (3.64)
C5_379	carbonyl reductase 1	SP P48758	35.06	6.54	82.86	mV154BS	A	16	<i>Cbr1</i>	64	interval (≥ 2.5)	<i>Mx1</i> LOD 13.40 (3.64)
C5_376	modifier 1 of carbonyl reductase 1	NCBI 3102770	31.48	6.14	15.59	paV264BS	A	16 ^g	<i>Cbr1m1</i>	63	interval (≥ 2.5)	<i>Mx1</i> LOD 10.60 (7.71)
C6_391	modifier 2 of carbonyl reductase 1	NCBI 1352256	33.13	7.11	13.29	paV385BS	A	16 ^g	<i>Cbr1m2</i>	63	interval (≥ 2.5)	<i>Mx1</i> LOD 10.60 (7.71)
C6_380	modifier 2 of carbonyl reductase 1	NCBI 1352256	33.09	7.11	12.44	"	A	16 ^g	<i>Cbr1m2</i>	63	interval (≥ 2.5)	<i>Mx1</i> LOD 10.60 (7.71)
C3_459	modifier of catechol O-methyltransferase	NCBI 5921831	25.61	5.30	32.68	paV47BS	A	16 ^g	<i>Comtm</i>	54	≥ 2.5	
C3_258	modifier of catechol O-methyltransferase	NCBI 5921831	26.22	5.11	28.77	paV48BS	A	16 ^g	<i>Comtm</i>	55	interval (≥ 2.5)	<i>Comtm</i> (paV47BS) LOD 14.75 (0)
C5_088	modifier of peroxisome proliferator activated receptor delta	NCBI 2137629	32.63	6.30	107.93	aV268BS	A	16 ^g	<i>Ppardm</i>	62	interval (≥ 2.5)	<i>Pprm1</i> LOD 10.87 (7.56)
C4_185	phosphomannomutase 2	NCBI 4105149	28.40	5.89	61.45	mV125BS	A	16 ^h	<i>Pmm2</i>	64	interval (≥ 2.5)	<i>Pprm1</i> LOD 11.41 (7.29)
A4_207	RIKEN cDNA clone: 2410002K23	NCBI 13385998	74.20	5.86	24.85	mV360BS	A	16 ^g	<i>2410002K23Rik</i>	62	interval (≥ 2.5)	<i>Pprm1</i> LOD 10.87 (7.56)
C6_059			33.91	7.37	4.17	mV234BS	A	16	<i>mV234BS</i>	64	≥ 2.5	<i>D16Irs1</i> LOD 17.16 (0)
E3_106			10.18	5.24	9.79	paV32BS	A	16	<i>paV32BS</i>	36	linked to chr	<i>Comtm</i> (paV47BS) LOD 4.15 (14.92)
B5_254			53.30	6.13	12.98	aV483BS	A	16	<i>aV483BS</i>	59	linked to chr	<i>D16Irs1</i> LOD 5.25 (21.24)
A5_288	transketolase	SP P40142	72.09	6.65	334.18			16	<i>Tkt</i>			
D3_200	RIKEN cDNA 2700094G22 gene	NCBI 5860834	14.62	5.17	72.78	mV347BS	A	17 ^g	<i>2700094G22Rik</i>	63	interval (≥ 2.5)	<i>D17Irs1</i> , <i>D17Irs2</i> LOD 18.96 (0)
B5_523	modifier of cytosolic acyl coenzyme A thioester hydrolase	SP Q64559	40.63	6.52	93.73	paV410BS	A	17 ^g	<i>Hbachm-pending</i>	35	≥ 2.5	<i>D17Mit25</i> LOD 9.90 (0)
B5_492	cytosolic acyl coenzyme A thioester hydrolase	EMBL U49694	42.11	6.62	9.52	aV415BS	C		<i>Hbach-pending</i>			
B6_339	cytosolic acyl coenzyme A thioester hydrolase	EMBL U49694	42.11	6.73	354.72				<i>Hbach-pending</i>			
C4_339	NADH dehydrogenase (ubiquinone) flavoprotein 2	NCBI 128867	26.14	5.63	13.89	paV45BS	A	17 ^g	<i>Ndufv2</i>	49	interval (≥ 2.5)	<i>D17Mit9</i> LOD 9.99 (4.65) <i>mV273BS</i> LOD 11.12 (4.26) <i>D17Irs4</i> LOD 10.84 (4.35)
C6_274	proteasome (prosome, macropain) subunit, beta type 1	SP O09061	26.86	6.98	79.67	mV191BS	A	17	<i>Psmb1</i>	64	2.2	
B5_519	acetyl-Coenzyme A acetyltransferase 2	NCBI 539926	40.70	6.64	178.94	paV413BS	A	17	<i>Acat2</i>	60	interval (≥ 2.5)	<i>D17Mit25</i> LOD 14.39 (1.85)
C6_192	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	NCBI 1169205	29.06	7.03	67.42	mV220BS	A	17 ^g	<i>Dci</i>	64	interval (≥ 2.5)	<i>D17Irs1</i> , <i>D17Irs2</i> LOD 19.27 (0)
C4_136	dimethylarginine dimethylaminohydrolase 2	NCBI 2183321	29.92	5.65	63.74	mV95BS	A	17 ^h	<i>Ddah2</i>	57	≥ 2.5	
B4_078			61.36	5.79	88.51	mV82BS	A	17	<i>mV82BS</i>	64	interval (≥ 2.5)	<i>D17Mit25</i> LOD 15.56 (1.72)
D2_259			14.62	4.89	50.45	mV126BS	A	17	<i>mV126BS</i>	64	interval (≥ 2.5)	<i>D17Irs1</i> , <i>D17Irs2</i> LOD 19.27 (0)
B6_064			58.77	6.96	24.43	mV273BS	A	17	<i>mV273BS</i>	64	2.4	
A5_100			93.75	6.33	26.95	mV288BS	A	17	<i>mV288BS</i>	57	2.4	

2-DE Spot-No ^a	PROTEINS					GENES			GENE MAPPING			
	Name ^b	Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
B6_362			40.78	6.88	31.23	paV433BS	A	17	paV433BS	59	interval (≥ 2.5)	D17Mit25 LOD 12.54 (3.85)
B6_371			40.55	6.75	30.01	aV438BS	A	17	aV438BS	55	interval (≥ 2.5)	D17Mit25 LOD 7.33 (13.41)
B4_072			62.20	6.07	18.03	paV500BS	A	17	paV500BS	58	≥ 2.5	
C3_358	glyoxylase 1 complex	SP Q04760	26.25	5.13	128.96			17	Glo1			
C6_331	superoxide dismutase 2, mitochondrial	EMBL Z18857	25.25	7.07	345.96			17	Sod2			
C6_338	superoxide dismutase 2, mitochondrial	EMBL Z18857	25.20	6.95	198.41			17	Sod2			
B2_121	tubulin, beta 5	SP P05218	57.91	4.95	209.06			17	Tubb5			
B2_118	tubulin, beta 5	SP P05218	58.00	4.98	228.24			17	Tubb5			
B7_120	ferrochelatase ^l		42.19	7.86	11.23	mV264BS	A	18	Fech	64	2.3	
B7_118	ferrochelatase	NCBI 193271	42.19	7.81	20.52	"	A	18	Fech	64	2.3	
B7_119	ferrochelatase	NCBI 193271	42.19	7.74	20.38	"	A	18	Fech	64	2.3	
B3_113	heat shock protein, 74 kDa, A ^l		61.19	5.22	34.72	mV84BS	A	18	Hspa9a	63	≥ 2.5	Hspa9a (mV56BS) LOD 18.96 (0)
B3_144	heat shock protein, 74 kDa, A	NCBI 1072476	59.09	5.22	69.38	"	A	18	Hspa9a	63	≥ 2.5	Hspa9a (mV56BS) LOD 18.96 (0)
B3_669	heat shock protein, 74 kDa, A ^l		41.22	5.13	22.38	mV56BS	A	18	Hspa9a	64	≥ 2.5	
B3_505	heat shock protein, 74 kDa, A ^l		40.89	5.13	13.34	"	A	18	Hspa9a	64	≥ 2.5	
B3_142	heat shock protein 74kD, A	NCBI 6754256	59.73	5.53	12.48	mV308BS	A	18	Hspa9a	53	interval (≥ 2.5)	Hspa9a (mV56BS) LOD 12.26 (3.92)
B3_123	heat shock protein 74kD, A	NCBI 6754256	60.17	5.53	9.63	"	A	18	Hspa9a	53	interval (≥ 2.5)	Hspa9a (mV56BS) LOD 12.26 (3.92)
A3_368	heat shock protein 74kD, A	SP P38647	74.00	5.47	246.81			18	Hspa9a			
B6_495	hydroxysteroid 17-beta dehydrogenase 4	NCBI 6680287	36.46	6.97	21.90	paV426BS	A	18 ^g	Hsd17b4	64	2.0	
D3_152	modifier of triosephosphate isomerase	SP P17751	16.24	5.54	138.66	aV19BS	A	18 ^g	Tpim	64	linked to chr	D18Nds1, D18Mit25 LOD 3.23 (35.51)
D3_222			15.09	5.30	44.70	mV7BS	A	18	mV7BS	64	≥ 2.5	mV10BS LOD 19.27 (0)
D3_192			15.05	5.53	16.92	mV10BS	A	18	mV10BS	64	≥ 2.5	
C4_081			32.19	5.82	118.10	mV23BS	A	18	mV23BS	64	≥ 2.5	mV10BS LOD 19.27 (0)
B3_168			58.27	5.18	31.32	mV85BS	A	18	mV85BS	44	linked to chr	Hspa9a (mV56BS) LOD 6.48 (12.89)
C3_146			31.43	5.51	56.29	mV123BS	A	18	mV123BS	64	≥ 2.5	mV10BS LOD 19.27 (0)
C4_123			30.59	5.71	53.06	mV124BS	A	18	mV124BS	64	≥ 2.5	mV10BS LOD 19.27 (0)
A6_026			85.11	6.99	11.74	mV282BS	A	18	mV282BS	64	interval (≥ 2.5)	Hsd17b4 (paV426BS) LOD 17.03 (1.59)
C2_077			33.21	4.53	20.59	paV104BS	A	18	paV104BS	41	1.9	
C5_322			25.52	6.22	13.98	paV240BS	A	18	paV240BS	59	≥ 2.5	
B6_084	aldehyde dehydrogenase family 1, subfamily A1	SP P24549	56.42	6.76	182.95	mV268BS	A	19	Aldh1a1	64	≥ 2.5	D19Ler1 LOD 14.75
B3_158	alpha-Internexin neuronal intermediate filament protein ^l		59.00	5.41	22.00	mV81BS	A	19 ^h	Ina	64	interval (≥ 2.5)	D19Nds1 LOD 12.63 (2.08)
B3_150	alpha-Internexin neuronal intermediate filament protein ^l		59.18	5.47	31.48	"	A	19 ^h	Ina	64	≥ 2.5	D19Nds1 LOD 12.63 (2.08)
B3_149	alpha-Internexin neuronal intermediate filament protein	NCBI 609535	59.09	5.52	56.70	"	A	19 ^h	Ina	64	≥ 2.5	D19Nds1 LOD 12.63 (2.08)
B4_137	alpha-Internexin neuronal intermediate filament protein	NCBI 6754348	58.36	5.61	35.06	aV163BS	A	19 ^h	Ina	63	1.9	
C3_456	modifier of creatine kinase, brain	NCBI 417208	33.50	5.24	8.17	paV141BS	A	19 ^g	Ckbm	58	interval (2.0)	Ina (aV163BS) LOD 8.33 (12.31)
C3_073	modifier of creatine kinase, brain	NCBI 417208	33.38	5.24	8.62	"	A	19 ^g	Ckbm	58	interval (2.0)	Ina (aV163BS) LOD 8.33 (12.31)
C4_224	modifier 2 of peroxiredoxin 5	NCBI 4139186	27.42	6.03	259.74	aV51BS	A	19 ^g	Prdx5m2	62	interval (≥ 2.5)	Fth LOD 9.58 (6.68)
C5_106	glutathione S-transferase omega 1	NCBI 6016174	32.02	6.37	94.89	aV269BS	A	19 ^h	Gsto1	63	interval (≥ 2.5)	D19Nds1 LOD 10.84 (4.35)
C3_453	glutathione S-transferase, pi 2	NCBI 576133	23.40	5.36	89.79	mV18BS	A	19	Gstp2	62	interval (≥ 2.5)	D19Irs1 LOD 15.85 (1.70)
C4_323	glutathione S-transferase, pi 2	NCBI 576133	23.94	5.62	36.00	mV53BS	A	19	Gstp2	23	interval (≥ 2.5)	D19Irs1 LOD 6.92
C5_330	glutathione S-transferase, pi 2	NCBI 576133	25.28	6.48	75.28	mV212BS	A	19	Gstp2	60	interval (≥ 2.5)	D19Irs1 LOD 15.27 (1.75)
D4_149	glutathione S-transferase, pi 2	NCBI 576133	14.26	6.03	48.17	mV13BS	A	19	Gstp2	47	interval (≥ 2.5)	D19Irs1 LOD 9.30 (6.83)
C5_360	glutathione S-transferase, pi 2	NCBI 576133	24.26	6.32	41.31	mV183BS	A	19	Gstp2	63	interval (≥ 2.5)	D19Irs1 14.54 (3.39)
C5_366	glutathione S-transferase, pi 2	NCBI 576133	24.16	6.32	22.62	"	A	19	Gstp2	63	interval (≥ 2.5)	D19Irs1 14.54 (3.39)
C6_296	glutathione S-transferase, pi 2	SP P19157	26.17	6.84	499.33			19	Gstp2			
B3_333	guanine deaminase	NCBI 5738216	50.27	5.46	136.26	mV71BS	A	19 ^g	Gda	64	≥ 2.5	D19Ler1 LOD 14.75
B3_383	guanine deaminase ^l		48.21	5.46	47.83	"	A	19 ^g	Gda	64	≥ 2.5	D19Ler1 LOD 14.75
C5_383	modifier 2 of serum albumin variant	NCBI 5915682	28.34	6.25	123.97	mV136BS	A	19 ^g	Alb1m2	57	interval (≥ 2.5)	Fth LOD 7.95 (7.71)
C5_384	modifier 2 of serum albumin variant	NCBI 5915682	28.18	6.25	53.71	"	A	19 ^g	Alb1m2	57	interval (≥ 2.5)	Fth LOD 7.95 (7.71)
B4_419			43.01	5.67	78.53	mV356BS	A	19	mV356BS	40	interval (≥ 2.5)	D19Nds1 LOD 4.80 (11.16)
D7_009			21.18	8.28	8.57	paV209BS	A	19	paV209BS	59	interval (≥ 2.5)	Fth LOD 10.56 (4.45)
C4_214			27.77	6.08	71.28	aV251BS	A	19	aV251BS	49	1.9	
C6_388			26.27	7.13	11.63	paV278BS	A	19	paV278BS	60	interval (≥ 2.5)	D19Irs1 LOD 15.27 (1.75)
D5_036	cofilin 1, non-muscle	SP P18760	19.34	6.51	732.74	aV518BS	C	19 ^l	Cfl1			

2-DE Spot-No ^a	Name ^b	PROTEINS			GENES				GENE MAPPING			
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
D5_042	cofilin 1, non-muscle	SP P18760	19.29	6.51	557.98	"	C	19 ^g	<i>Cfl1</i>			
B5_477	glutamate oxaloacetate transaminase 1, soluble	SP P05201	42.73	6.45	564.72			19	<i>Got1</i>			
C5_177	phosphoglycerate mutase 1	SP P18669	29.52	6.54	857.29			19	<i>Pgam1</i>			
C5_185	phosphoglycerate mutase 1	SP P18669	29.33	6.36	277.17			19	<i>Pgam1</i>			
C1_016	modifier 1 of heat shock 70kD protein 8 ⁱ		27.77	4.43	28.10	mV22BS	A	x ^g	<i>Hspa8m1</i>	62	≥ 2.5	<i>Hspa8m1</i> (mV90BS) LOD 18.66 (0)
C2_241	modifier 1 of heat shock 70kD protein 8 ⁱ		27.85	4.47	33.40	"	A	x ^g	<i>Hspa8m1</i>	62	≥ 2.5	<i>Hspa8m1</i> (mV90BS) LOD 18.66 (0)
C2_263	modifier 1 of heat shock 70kD protein 8 ⁱ		27.37	4.47	11.63	"	A	x ^g	<i>Hspa8m1</i>	62	≥ 2.5	<i>Hspa8m1</i> (mV90BS) LOD 18.66 (0)
C2_396	modifier 1 of heat shock 70kD protein 8 ⁱ		27.79	4.49	13.00	"	A	x ^g	<i>Hspa8m1</i>	62	≥ 2.5	<i>Hspa8m1</i> (mV90BS) LOD 18.66 (0)
C2_397	modifier 1 of heat shock 70kD protein 8 ⁱ		27.45	4.50	6.92	"	A	x ^g	<i>Hspa8m1</i>	62	≥ 2.5	<i>Hspa8m1</i> (mV90BS) LOD 18.66 (0)
B1_028	modifier 1 of heat shock 70kD protein 8	NCBI 123651	71.20	4.41	52.91	mV90BS	A	x ^g	<i>Hspa8m1</i>	64	2.1	
B1_031	modifier 1 of heat shock 70kD protein 8	NCBI 123651	70.80	4.39	27.52	"	A	x ^g	<i>Hspa8m1</i>	64	2.1	
B2_034	modifier 2 of heat shock 70kD protein 8 ⁱ		70.20	5.03	31.27	mV313BS	A	x ^g	<i>Hspa8m2</i>	29	interval (≥ 2.5)	<i>DXWas70</i> LOD 5.42 (4.35)
B2_045	modifier 2 of heat shock 70kD protein 8	NCBI 123651	68.31	5.03	30.24	"	A	x ^g	<i>Hspa8m2</i>	29	interval (≥ 2.5)	<i>DXWas70</i> LOD 5.42 (4.35)
B2_041	modifier 2 of heat shock 70kD protein 8 ⁱ		69.49	5.01	11.79	"	A	x ^g	<i>Hspa8m2</i>	29	interval (≥ 2.5)	<i>DXWas70</i> LOD 5.42 (4.35)
B2_025	modifier 2 of heat shock 70kD protein 8	NCBI 123651	70.40	5.00	57.84	"	A	x ^g	<i>Hspa8m2</i>	29	interval (≥ 2.5)	<i>DXWas70</i> LOD 5.42 (4.35)
B2_039	modifier 2 of heat shock 70kD protein 8 ⁱ		69.66	4.97	28.42	"	A	x ^g	<i>Hspa8m2</i>	29	interval (≥ 2.5)	<i>DXWas70</i> LOD 5.42 (4.35)
B3_029	modifier 2 of heat shock 70kD protein 8 ⁱ		67.63	5.06	14.87	"	A	x ^g	<i>Hspa8m2</i>	29	interval (≥ 2.5)	<i>DXWas70</i> LOD 5.42 (4.35)
C5_227	hypoxanthine guanine phosphoribosyl transferase	SP P00493	28.04	6.38	184.74	mV135BS	A	x	<i>Hprt</i>	64	interval (≥ 2.5)	<i>DXMit81x</i> LOD 11.95 (7.03)
C5_238	hypoxanthine guanine phosphoribosyl transferase ^j		27.99	6.38	170.59	"	A	x	<i>Hprt</i>	64	interval (≥ 2.5)	<i>DXMit81x</i> LOD 11.95 (7.03)
A3_187	grip-associated protein 1 (KIAA1167)	NCBI 6330176	98.52	5.16	48.88	mV105BS	A	x ^{g,k}	<i>Grasp1-pending</i>	64	≥ 2.5	<i>DXWas70</i> LOD 17.16 (0)
A3_188	grip-associated protein 1 (KIAA1167)	NCBI 6330176	98.89	5.14	30.89	"	A	x ^{g,k}	<i>Grasp1-pending</i>	64	≥ 2.5	<i>DXWas70</i> LOD 17.16 (0)
A3_185	grip-associated protein 1 (KIAA1167) ^j		99.26	5.11	12.74	"	A	x ^{g,k}	<i>Grasp1-pending</i>	64	≥ 2.5	<i>DXWas70</i> LOD 17.16 (0)
A3_180	grip-associated protein 1 (KIAA1167) ^j		99.26	5.09	9.66	"	A	x ^{g,k}	<i>Grasp1-pending</i>	64	≥ 2.5	<i>DXWas70</i> LOD 17.16 (0)
A3_191	grip-associated protein 1 (KIAA1167) ^j		99.26	5.07	16.44	"	A	x ^{g,k}	<i>Grasp1-pending</i>	64	≥ 2.5	<i>DXWas70</i> LOD 17.16 (0)
B6_206	serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	NCBI 2961472	49.14	6.91	40.55	mV247BS	A	x ^g	<i>Serpinf1</i>	64	interval (≥ 2.5)	<i>DXIrs1</i> LOD 12.49 (6.79)
A6_027	synapsin I	NCBI 6686018	84.89	7.42	26.74	sV151BS	A	x ^j	<i>Syn1</i>			
A6_024	synapsin I ^l		85.78	7.23	11.76	"	A	x ^j	<i>Syn1</i>			
A6_044	synapsin I ^l		81.56	7.30	13.97	"	A	x ^j	<i>Syn1</i>			
A6_022	synapsin I ^l		84.89	7.41	24.38	"	A	x ^j	<i>Syn1</i>			
A6_025	synapsin I ^l		85.56	7.22	10.13	"	A	x ^j	<i>Syn1</i>			
A6_043	synapsin I ^l		81.78	7.28	6.23	"	A	x ^j	<i>Syn1</i>			
A6_085	synapsin I ^l		85.56	7.41	8.13	"	A	x ^j	<i>Syn1</i>			
A6_020	synapsin I ^l		85.78	7.17	9.00	"	A	x ^j	<i>Syn1</i>			
A6_039	synapsin I ^l		82.22	7.24	7.18	"	A	x ^j	<i>Syn1</i>			
A6_023	synapsin I ^l		84.44	7.38	8.29	"	A	x ^j	<i>Syn1</i>			
A6_021	synapsin I ^l		86.00	7.13	10.22	"	A	x ^j	<i>Syn1</i>			
A6_038	synapsin I ^l		82.22	7.24	6.72	"	A	x ^j	<i>Syn1</i>			
A6_086	synapsin I ^l		85.11	7.37	16.05	"	A	x ^j	<i>Syn1</i>			
A6_017	synapsin I ^l		86.00	7.10	11.73	"	A	x ^j	<i>Syn1</i>			
A6_040	synapsin I ^l		82.44	7.19	5.94	"	A	x ^j	<i>Syn1</i>			
A6_087	synapsin I ^l		85.11	7.37	26.83	"	A	x ^j	<i>Syn1</i>			
A6_019	synapsin I ^l		85.33	7.32	19.81	"	A	x ^j	<i>Syn1</i>			
A6_018	synapsin I ^l		86.00	7.06	4.54	"	A	x ^j	<i>Syn1</i>			
A6_089	synapsin I ^l		85.56	7.31	17.30	"	A	x ^j	<i>Syn1</i>			
A6_016	synapsin I ^l		85.33	7.28	14.71	"	A	x ^j	<i>Syn1</i>			
A6_041	synapsin I ^l		81.33	7.38	24.11	"	A	x ^j	<i>Syn1</i>			
A6_088	synapsin I ^l		81.33	7.39	28.60	"	A	x ^j	<i>Syn1</i>			
A6_090	synapsin I ^l		85.56	7.27	16.52	"	A	x ^j	<i>Syn1</i>			

2-DE Spot-No ^a	Name ^b	PROTEINS			GENES			GENE MAPPING				
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins	Marker, LOD scores and distances (cM) for protein-map marker or protein-protein linkage
A6_042	synapsin I ^l		81.56	7.34	27.90	"	A	x ^j	<i>Syn1</i>			
A7_009	synapsin I ^l		84.67	7.58	6.53	"	A	x ^j	<i>Syn1</i>			
A7_011	synapsin I ^l	SP P09951	80.89	7.59	65.41	"	A	x ^j	<i>Syn1</i>			
A7_008	synapsin I ^l		84.67	7.52	28.91	"	A	x ^j	<i>Syn1</i>			
A7_015	synapsin I ^l		80.67	7.55	147.47	"	A	x ^j	<i>Syn1</i>			
A7_007	synapsin I ^l		84.67	7.46	40.95	"	A	x ^j	<i>Syn1</i>			
A7_012	synapsin I ^l		80.89	7.50	114.57	"	A	x ^j	<i>Syn1</i>			
A7_017	synapsin I ^l		80.89	7.83	12.49	"	A	x ^j	<i>Syn1</i>			
A7_016	synapsin I ^l		80.89	7.49	100.36	"	A	x ^j	<i>Syn1</i>			
A7_019	synapsin I ^l		80.44	7.73	18.34	"	A	x ^j	<i>Syn1</i>			
A7_010	synapsin I ^l		81.11	7.43	53.36	"	A	x ^j	<i>Syn1</i>			
A7_020	synapsin I ^l		80.67	7.66	34.54	"	A	x ^j	<i>Syn1</i>			
A7_013	synapsin I ^l		81.11	7.44	61.87	"	A	x ^j	<i>Syn1</i>			
A7_018	synapsin I ^l		80.67	7.70	73.22	"	A	x ^j	<i>Syn1</i>			
A7_014	synapsin I ^l		80.67	7.62	140.62	"	A	x ^j	<i>Syn1</i>			
E3_094			9.37	5.18	5.52	mV16BS	A	x	<i>mV16BS</i>	49	linked to chr	<i>Hspa8m1</i> (mV90BS) LOD 7.74 (11.41)
D7_001			22.47	7.79	13.70	mV176BS	A	x	<i>mV176BS</i>	52	interval (≥ 2.5)	<i>DXMit8</i> LOD 6.35 (14.74)
B6_204			49.30	6.82	12.29	mV245BS	A	x	<i>mV245BS</i>	61	interval (≥ 2.5)	<i>DXIrs1</i> LOD 8.68 (13.29)
B6_054			59.43	7.09	10.75	mV277BS	A	x	<i>mV277BS</i>	49	linked to chr	<i>DXMit8</i> LOD 3.19 (29.39)
B3_667			45.04	5.06	20.40	paV131BS	A	x	<i>paV131BS</i>	44	interval (2.2)	<i>DXMit54</i> LOD 7.83 (0)
B3_439			44.88	5.06	18.90	"	A	x	<i>paV131BS</i>	44	interval (2.2)	<i>DXMit54</i> LOD 7.83 (0)
B5_439	phosphoglycerate kinase 1	SP P09411	44.38	6.42				x	<i>Pgk1</i>			
D5_068	Nucleoside diphosphate kinase A	SP P15532	17.77	6.34	138.27	aV232BS	A					
D5_071	Nucleoside diphosphate kinase A	SP P15532	17.70	6.34	127.72	"	A					
D5_083	Nucleoside diphosphate kinase A	SP P15532	16.95	6.34	166.35	"	A					
D5_085	Nucleoside diphosphate kinase A	SP P15532	16.89	6.34	140.29	"	A					
D4_002						mV17BS	A					
C2_395						mV32BS	A					
C2_164						"	A					
C2_174						"	A					
C2_113						mV37BS	A					
B2_455						mV69BS	A					
B2_105						mV89BS	A					
B2_097						"	A					
B3_087						mV121BS	A					
B3_081						"	A					
B3_073						"	A					
D6_108						mV161BS	A					
D5_078						mV169BS	A					
E5_027						mV172BS	A					
E6_015						mV173BS	A					
E7_019						mV182BS	A					
C5_197						mV214BS	A					
C7_208						mV218BS	A					
C5_140						mV227BS	A					
B6_292						mV258BS	A					
B6_069						mV275BS	A					
A5_158						mV294BS	A					
A5_153						"	A					
A5_154						"	A					
D2_285						mV306BS	A					

2-DE Spot-No ^a	Name ^b	PROTEINS			GENES				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Spot volume ^c	Variant spots V-No ^d	Categories of genetic significance ^e	Chr. No ^f	Gene locus ^f	Number of B ₁ -animals	Log likelihood ratios for map orders of proteins
C1_006						mV361BS	A				
E3_020						aV10BS	A				
E4_012						aV11BS	A				
E2_098						paV16BS	A				
B3_668						paV134BS	A				
C3_301						paV191BS	A				
E7_020						aV202BS	A				
D5_070						paV229BS	A				
C5_346						aV242BS	A				
C5_086						aV261BS	A				
C7_138						aV387BS	A				
C7_052						aV394BS	A				

^a Spot numbers refer to the protein spots of the brain/supernatant 2-DE standard pattern.

^b Proteins were identified by mass spectrometry (see Methods).

^c Spot volumes (spot area x O.D. per pixel) were determined as described⁴⁸.

^d Numbers of variant spots indicate the type (m, pa, a) of genetic variation (V) and the running number of variant protein spots of brain supernatant (BS) proteins shown in the 2-DE standard pattern. mV: variation in electrophoretic mobility, paV: presence/absence variation, aV: spots varying in protein amount.

^e Categories: the polymorphism of proteins segregated in the B₁-generation (A), or showed a hybrid pattern in the F₁-generation, but no monogenic segregation in B₁ (B), or showed strain specificity, but no clearly interpretable F₁- and B₁-patterns (C).

^f The chromosome map is presented in Fig. A.

^g Gene locus of an identified protein newly mapped on mouse chromosomes. Note: The locus positions indicated without any superscript confirmed the known position given by the Mouse Genome Database (URL: <http://www.informatics.jax.org>).

^h Fine mapping of syntenic locus.

ⁱ Tentatively identified protein: A protein spot was considered as to be indirectly identified if identical in phenotype (e.g. same mm-distance and same shift direction of the two allelic spots) and mapping position with a directly identified spot.

^j Identified protein spot of variation category B/C variation. These categories of variation did not allow us to map the locus by our approach. The chromosomal position indicated refers to the Mouse Genome Database (URL: <http://www.informatics.jax.org>).

^k In this case '-pending' means that the gene name was taken from the corresponding human orthologue and is not approved for mouse yet.