

Tabelle1. Liste der polymorphen Proteinspots und Varianten in der cytosolischen Fraktion von Maus Gehirn: Kartierungsposition, Kopplungswahrscheinlichkeiten und genetische Abstände

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
E6_070	Acyl-coA-binding protein	SP P31786	9.93	6.96	mV131BS	A	1	<i>s. map</i>	64	≠ 2.5	D1Mit LOD 17.76 (0)
E6_047	Acyl-coA-binding protein	SP P31786	9.92	6.10	"	A	1	<i>s. map</i>	64	≠ 2.5	D1Mit LOD 17.76 (0)
B5_429	Acyl-coA dehydrogenase, long-chain specific	NCBI 1703064	45.08	6.55	mV244BS	A	1	<i>s. map</i> <sup>h</sup>	64	≠ 2.5	
D2_269	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.44	4.97	mV5BS	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_256	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.57	4.86	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_271	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.32	4.74	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_277	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.12	4.98	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_227	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.30	4.84	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_258	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.59	4.74	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_270	Astrocytic phosphoprotein PEA-15	NCBI 2498751	14.28	4.87	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
D2_278	Astrocytic phosphoprotein PEA-15 <sup>i</sup>		14.10	4.84	"	A	1	<i>Pea15</i> <sup>g</sup>	64	≠ 2.5	
B5_600	cDNA clone image: 334048 (5')	NCBI 1291927	38.56	6.46	mV242BS	A	1	<i>s. map</i>	64	≠ 2.5	
B2_238	Inositol polyphosphate-1-phosphatase	NCBI 6680457	49.92	5.00	aV172BS	A	1	<i>(Inpp1)</i> <sup>g</sup>	64	linked to chr	D1Mit234 LOD 4.82 (22.31)
B2_325			44.31	4.92	mV60BS	A	1		62	≠ 2.5	mV76BS LOD 18.66 (0)
B2_326			44.15	5.01	mV61BS	A	1		64	≠ 2.5	mV76BS LOD 19.27 (0)
B2_271			47.40	4.84	mV76BS	A	1		64	≠ 2.5	
B2_272			47.40	4.87	"	A	1		64	≠ 2.5	
B2_276			47.15	4.99	"	A	1		64	≠ 2.5	
B2_274			47.24	4.95	"	A	1		64	≠ 2.5	
B2_273			47.24	4.91	"	A	1		64	≠ 2.5	
D5_009			22.33	6.26	mV184BS	A	1		29	linked to chr	mV76BS LOD 4.29 (12.06) D1Mit234 LOD 2.58 (16.82)
C5_335			25.20	6.40	mV211BS	A	1		23	linked to chr	mV76BS LOD 3.71 (10.03)
C5_343			25.12	6.40	"	A	1		23	linked to chr	mV76BS LOD 3.71 (10.03)
C4_343			23.91	6.08	mV362BS	A	1		62	≠ 2.5	
C6_385			28.87	6.95	paV291BS	A	1		58	≠ 2.5	
B4_063			62.88	6.09	paV498BS	A	1		56	interval (2.2)	D1Mit234 LOD 11.17 (2.33)
C4_231	Antithrombin-III-precursor	SP P32261	27.15	6.00			1	<i>At3</i>			
C6_074	ATP synthase gamma chain, mitochondrial	NCBI 728931	33.09	7.32	mV233BS	A	2	<i>s. map</i>	64	≠ 2.5	
B6_004	Carnitine acetyltransferase	NCBI 6681009	67.62	6.84	mV283BS	A	2	<i>Crat</i> <sup>g</sup>	63	≠ 2.5	
D5_002	cDNA clone image: 400521 (5')	NCBI 1387530	22.33	6.48	mV185BS	A	2	<i>s. map</i>	64	≠ 2.5	
C2_082	E-1 enzyme	NCBI 6523813	33.00	4.87	mV349BS	A	2	<i>s. map</i>	64	interval (≠ 2.5)	bir39j10 LOD 18.06 (0)
B3_326	Glutathione synthetase type A1	NCBI 1016285	50.73	5.52	mV72BS	A	2	<i>s. map</i>	62	interval (≠ 2.5)	bir39j10 LOD 17.46 (0)
B4_591	Uroporphyrinogen decarboxylase	NCBI 2501645	38.90	6.03	paV120BS	A	2	<i>s. map</i> <sup>h</sup>	56	≠ 2.5	
B2_037			70.20	4.75	mV92BS	A	2		53	≠ 2.5	
B2_035			70.40	4.79	"	A	2		53	≠ 2.5	
B6_013			66.51	6.82	mV284BS	A	2		60	linked to chr	mV283BS LOD 5.65 (22.84)
B2_066			64.75	4.71	mV312BS	A	2		28	linked to chr	mV233BS LOD 3.44 (16.82)
B4_588			53.91	5.67	mV359BS	A	2		63	interval (≠ 2.5)	mbacr25p12 LOD 14.09 (1.89)
C4_345			35.49	5.99	paV105BS	A	2		52	interval (≠ 2.5)	D2Nds3 LOD 8.73 (8.91)
C3_032			34.89	5.46	paV113BS	A	2		63	interval (≠ 2.5)	mV233BS LOD 13.73 (5.00)
B3_102			62.54	5.29	paV179BS	A	2		58	≠ 2.5	
A3_161			103.57	5.36	paV184BS	A	2		59	≠ 2.5	
C5_010			35.68	6.28	paV396BS	A	2		64	interval (≠ 2.5)	D2Nds3 LOD 15.56 (1.72)
B5_392			47.19	6.57	paV466BS	A	2		57	interval (≠ 2.5)	bir39j10 LOD 15.95 (0)
B6_226	Creatine kinase, ubiquitous mitochondrial	SP P30275	47.50	6.98			2	<i>Ckmt1</i>			
B6_248	Creatine kinase, ubiquitous mitochondrial	SP P30275	47.27	6.98			2	<i>Ckmt1</i>			

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A4_171	DNA Topoisomerase I	SP Q04750	78.40	6.04			2	<i>Top1</i>			
B4_503	Dynamamin-1	SP P39053	38.82	6.07			2	<i>Dnm</i>			
B7_019	Elongation factor 1-alpha 2	SP P10126	51.89	7.80			2	<i>Eef1a2</i>			
B7_035	Elongation factor 1-alpha 2	SP P10126	51.98	7.74			2	<i>Eef1a2</i>			
B7_036	Elongation factor 1-alpha 2	SP P10126	52.08	7.64			2	<i>Eef1a2</i>			
D5_080	Gelsolin	SP P06396	17.13	6.21			2	<i>Gsn</i>			
A3_343	78 kD glucose regulated protein	SP P20029	77.20	5.07			2	<i>Grp78</i>			
B4_099	Probable protein disulfide isomerase er-60	SP P27773	59.73	5.85			2	<i>Grp58 (Erp60)</i>			
B5_505	Alcohol dehydrogenase, class 3	SP P28474	41.33	6.37	mV146BS	A	3	<i>s map</i>	64	≠ 2.5	
C2_049	Annexin V	SP P48036	34.18	4.91	mV27BS	A	3	<i>Anx5<sup>g</sup></i>	64	≠ 2.5	
C5_192	Carbonic anhydrase I	NCBI 1345656	29.03	6.60	paV255BS	A	3	<i>(Car1)<sup>g</sup></i>	44	linked to chr	D3Mit61 LOD 4.24 (18.97) D3Mit1 LOD 3.97 (9.55)
C5_151	Carbonic anhydrase II	SP P00920	29.60	6.67	mV138BS	A	3 / 1	<i>Car2<sup>g</sup></i>	64	interval (≠ 2.5)	D3Mit61 LOD 10.06 (9.46) D3Mit1 LOD 8.56 (2.94)
A5_009	Carbonic anhydrase II <sup>l</sup>		192.29	6.68	mV285BS	A	3 / 1	<i>Car2<sup>g</sup></i>	60	interval (≠ 2.5)	D3Mit61 LOD 9.02 (10.24) D3Mit1 LOD 7.70 (3.23)
A5_013	Carbonic anhydrase II <sup>l</sup>		186.51	6.67	"	A	3 / 1	<i>Car2<sup>g</sup></i>	60	interval (≠ 2.5)	D3Mit61 LOD 9.02 (10.24) D3Mit1 LOD 7.70 (3.23)
A5_017	Carbonic anhydrase II	SP P00920	181.69	6.67	"	A	3 / 1	<i>Car2<sup>g</sup></i>	60	interval (≠ 2.5)	D3Mit61 LOD 9.02 (10.24) D3Mit1 LOD 7.70 (3.23)
A5_021	Carbonic anhydrase II <sup>l</sup>		175.90	6.67	"	A	3 / 1	<i>Car2<sup>g</sup></i>	60	interval (≠ 2.5)	D3Mit61 LOD 9.02 (10.24) D3Mit1 LOD 7.70 (3.23)
C5_271	Carbonic anhydrase II	SP P00920	26.86	6.63	mV134BS	A	3 / 2	<i>s. map<sup>h</sup></i>	62	linked to chr	mV138BS LOD 3.77 (33.97) mV174BS LOD 4.24 (9.12) mV285BS LOD 4.06 (29.74)
D5_076	Carbonic anhydrase II	NCBI 192343	17.31	6.47	paV227BS	A	3 / 3	<i>s. map<sup>h</sup></i>	22	interval (≠ 2.5)	D3Mit1 LOD 6.02 (0)
B5_440	40kD Peptidyl-prolyl cis-trans isomerase (Cyclophilin 40)	SP Q08752	44.45	6.71	mV148BS	A	3	<i>s. map</i>	64	≠ 2.5	
C3_213	Glutamate cysteine ligase	NCBI 6680019	29.44	5.49	mV33BS	A	3	<i>Glcir<sup>g</sup></i>	56	≠ 2.5	
D4_125	Glutathione S-transferase GT 8.7	NCBI 121716	15.52	6.00	mV9BS	A	3 / 1	<i>s. map</i>	56	≠ 2.5	mV139BS LOD 16.86 (0)
C6_217	Glutathione S-transferase GT 8.7	SP P10649	28.23	6.97	mV139BS	A	3 / 1	<i>s. map</i>	64	≠ 2.5	
C5_243	Glutathione S-transferase GT 8.7	NCBI 121716	27.80	6.64	mV210BS	A	3 / 1	<i>s. map</i>	17	interval (≠ 2.5)	mV148BS, paV153BS, mbacr11j21, mV139BS, mV146BS LOD 5.12 (0)
C6_224	Glutathione S-transferase GT 8.7	SP P10649	28.20	6.76	mV215BS	A	3 / 1	<i>s. map</i>	64	≠ 2.5	mV139BS LOD 19.27 (0)
E4_015	Glutathione S-transferase GT 8.7	NCBI 121716	13.13	5.68	mV12BS	A	3 / 2	<i>s. map</i>	49	linked to chr	mV148BS LOD 5.28 (19.77) mV148BS, paV153BS, mbacr12j22, mbacr11j21, mV139BS, mV146BS LOD 3.20 (11.16)
C6_058	Glutathione S-transferase GT 8.7	NCBI 121716	28.26	7.23	paV299BS	A	3 / 3	<i>s. map</i>	20	linked to chr	
E7_009	Hemoglobin delta chain	NCBI 122717	12.80	7.53	mV174BS	A	3	<i>s. map</i>	24	interval (≠ 2.5)	D3Mit1 LOD 5.12 (0)
B6_420	Quinone oxidoreductase	SP P47199	39.05	6.97	mV262BS	A	3	<i>s. map</i>	52	linked to chr	D3Mit19 LOD 3.38 (19.47) mV146BS, bir51p6 LOD 5.25 (21.24)
B4_228	Tubulin alpha-2 chain	NCBI 135412	53.91	5.85	paV153BS	A	3	<i>s. map<sup>h</sup></i>	61	≠ 2.5	
B3_596	Tubulin beta-4 chain	NCBI 91858	38.23	5.38	paV129BS	A	3	<i>s. map<sup>h</sup></i>	63	≠ 2.5	
B5_657			36.87	6.11	mV222BS	A	3		61	≠ 2.5	
C2_056			33.88	5.05	mV350BS	A	3		35	≠ 2.5	mV27BS LOD 10.54 (0)
E1_020			9.50	4.39	aV3BS	A	3		62	≠ 2.5	mbacr12j22 LOD 15.65 (0)
C5_388			24.91	6.58	paV244BS	A	3		27	linked to chr	mV146BS LOD 4.04 (12.57)
C7_176			25.68	7.65	paV386BS	A	3		64	≠ 2.5	mbacr12j22 LOD 16.26 (0)
B5_704			37.00	6.21	paV397BS	A	3		52	interval (2.3)	mV222BS LOD 9.0 (8.72)
B3_279	ATP synthase beta chain, mitochondrial	SP P10719					3	<i>Atp5b</i>			
B2_200	ATP synthase beta chain, mitochondrial	SP P10719					3	<i>Atp5b</i>			
A5_071	Aconitase 1 <sup>l</sup>		102.31	6.31	mV287BS	A	4	<i>Aco1<sup>g</sup></i>	64	≠ 2.5	mbacr21j14 LOD 19.27 (0)

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A5_069	Aconitase 1	NCBI 124899	102.31	6.37	"	A	4	<i>Aco1<sup>g</sup></i>	64	≠ 2.5	mbacr21j14 LOD 19.27 (0)
B5_703	cDNA clone image: 1450561 (5')	NCBI 3732528	39.67	6.37	mV241BS	A	4	<i>s. map</i>	64	≠ 2.5	
B5_551	cDNA clone image: 1450561 (5')	NCBI 3732528	39.65	6.37	"	A	4	<i>s. map</i>	64	≠ 2.5	
C3_074	cDNA clone image: 2922806 (5')	NCBI 7045955	33.33	5.07	mV30BS	A	4	<i>s. map</i>	64	≠ 2.5	mV120BS LOD 19.27 (0)
C2_394	cDNA clone image: 2922806 (5')	NCBI 7045955	33.54	5.01	mV31BS	A	4	<i>s. map</i>	64	≠ 2.5	mV120BS LOD 19.27 (0)
C2_066	cDNA clone image: 2922806 (5')	NCBI 7045955	33.46	5.01	"	A	4	<i>s. map</i>	64	≠ 2.5	mV120BS LOD 19.27 (0)
C2_074	cDNA clone image: 2922806 (5')	NCBI 7045955	33.25	4.99	"	A	4	<i>s. map</i>	64	≠ 2.5	mV120BS LOD 19.27 (0)
C2_393	cDNA clone image: 2922806 (5')	NCBI 7045955	33.33	4.99	"	A	4	<i>s. map</i>	64	≠ 2.5	mV120BS LOD 19.27 (0)
C3_076	cDNA clone image: 2922806 (5')		33.33	5.13	mV36BS	A	4	<i>s. map</i>	64	≠ 2.5	mV120BS LOD 19.27 (0)
C3_102	cDNA clone image: 2922806 (5')	NCBI 7045955	32.66	5.13	mV120BS	A	4	<i>s. map</i>	64	≠ 2.5	
B5_691	Delta-1-pyrroline-5-carboxylate dehydrogenase (similar to cDNA clone)	NCBI 1656546	69.21	6.57	paV492BS	A	4	<i>s. map</i>	56	2.0	
B5_694	Dynamin-1	NCBI 729381	62.22	6.32	paV509BS	A	4	<i>s. map<sup>h</sup></i>	57	≠ 2.5	mV365BS LOD 17.16 (0)
B5_544	N-acetylneuraminic acid phosphate synthase	NCBI 9507063	39.88	6.66	mV259BS	A	4	<i>s. map</i>	64	interval (≠ 2.5)	mbacr19c7 LOD 18.66 (0)
B5_699	N-acetylneuraminic acid phosphate synthase	NCBI 9507063	40.70	6.59	paV412BS	A	4	<i>s. map</i>	62	interval (≠ 2.5)	mbacr19c7 LOD 18.06 (0)
D3_008	Sorcin	NCBI 134734	23.11	5.05	mV19BS	A	4	<i>s. map<sup>h</sup></i>	64	interval (≠ 2.5)	D4Nds16 LOD 14.09 (1.89)
D2_012	Sorcin <sup>i</sup>		22.79	4.96	mV20BS	A	4	<i>s. map<sup>h</sup></i>	64	interval (≠ 2.5)	D4Nds16 LOD 14.09 (1.89)
C5_119	Zinc finger protein, C3HC4 type (similar to cDNA clone)	NCBI 6631587	31.40	6.35	mV365BS	A	4	<i>s. map</i>	64	≠ 2.5	
C5_124	Zinc finger protein, C3HC4 type (similar to cDNA clone)	NCBI 6631587	31.32	6.35	"	A	4	<i>s. map</i>	64	≠ 2.5	
C7_125			27.48	7.65	mV196BS	A	4		24	linked to chr	mV120BS LOD 3.30 (14.38)
A6_081			69.05	7.01	mV280BS	A	4		55	interval (≠ 2.5)	D4Mit52 LOD 10.40 (6.26)
A5_127			89.78	6.43	mV289BS	A	4		24	interval (≠ 2.5)	mbacr23i4 LOD 6.62 (0) mbacr21j14 LOD 7.22 (0)
C6_075			33.05	7.17	aV381BS	A	4		58	linked to chr	mbacr23i4 LOD 6.88 (16.82)
B5_607			38.23	6.16	paV399BS	A	4		53	≠ 2.5	mV241BS LOD 15.95 (0)
B3_586	α-Enolase	SP P17182	38.35	5.54	aV353BS	C					
B4_433	α-Enolase	SP P17182	41.95	6.06			4	<i>Eno1</i>			
B4_521	α-Enolase	SP P17182	38.27	5.66			4	<i>Eno1</i>			
B5_317	α-Enolase	SP P17182	49.53	6.14			4	<i>Eno1</i>			
B3_542	α-Enolase	SP P17182	39.66	5.55			4	<i>Eno1</i>			
C5_229	GTP-binding nuclear protein RAN	SP P28746	27.94	6.69			4	<i>Tlr4 (Lps)</i>			
B3_384	SH3 domain-containing protein SH3P4	EMBL U58886	48.46	5.21			4	<i>Sh3d2a</i>			
D3_115	Stathmin (Phosphoprotein 19)	SP P54227	18.11	5.57			4	<i>Lag</i>			
D4_080	Stathmin (Phosphoprotein 19)	SP P54227	17.84	5.80			4	<i>Lag</i>			
B4_596	Acyl-coA dehydrogenase, short-chain specific	NCBI 584714	39.58	6.09	aV400BS	A	5	<i>Acads<sup>g</sup></i>	62	≠ 2.5	
B3_640	Annexin III	EMBL AJ001633	36.58	5.57	paV110BS	A	5	<i>Anx3<sup>g</sup></i>	64	≠ 2.5	
B3_511	COP9 complex subunit 4	NCBI 3309170	41.06	5.60	mV45BS	A	5	<i>s. map</i>	64	≠ 2.5	
B3_519	COP9 complex subunit 4	NCBI 3309170	40.49	5.60	"	A	5	<i>s. map</i>	64	≠ 2.5	
B3_531	COP9 complex subunit 4	NCBI 3309170	40.33	5.60	"	A	5	<i>s. map</i>	64	≠ 2.5	
B5_047	Coronin-3	NCBI 4895041	64.60	6.51	paV494BS	A	5	<i>s. map</i>	52	interval (≠ 2.5)	aV400BS LOD 10.40 (6.26)
B5_057	Coronin-3'		64.13	6.51	"	A	5	<i>s. map</i>	52	interval (≠ 2.5)	aV400BS LOD 10.40 (6.26)
C6_160	Dihydrolipoamide acetyltransferase (similar to cDNA clone)	NCBI 1284324	29.84	6.93	mV217BS	A	5	<i>s. map</i>	40	≠ 2.5	mbacr3e9 LOD 12.04 (0)
C4_164	Endoplasmic reticulum protein 29	NCBI 2507015	29.10	5.83	mV128BS	A	5	<i>s. map</i>	64	interval (≠ 2.5)	mbacr27o9, mV35BS LOD 17.03 (1.59)
B5_128	Leucine aminopeptidase	NCBI 4335941	58.87	6.45	mV298BS	A	5	<i>s. map</i>	57	≠ 2.5	mbacr14f5 LOD 17.16 (0)
C4_127	26S proteasome regulatory subunit P27 (similar to cDNA clone)	NCBI 7066625	30.51	6.05	mV35BS	A	5	<i>s. map</i>	64	≠ 2.5	
E4_053	Quinoid dihydropteridene reductase <sup>i</sup>		10.95	6.02	mV14BS	A	5	<i>Qdpr<sup>g</sup></i>	32	≠ 2.5	mbacr14f5 LOD 9.63 (0)
C5_167	Quinoid dihydropteridene reductase	SP P11348	29.44	6.49	mV137BS	A	5	<i>Qdpr<sup>g</sup></i>	64	≠ 2.5	mbacr14f5 LOD 19.27 (0)
D6_144	Quinoid dihydropteridene reductase <sup>i</sup>		14.50	6.94	mV160BS	A	5	<i>Qdpr<sup>g</sup></i>	53	≠ 2.5	mbacr14f5 LOD 15.95 (0)

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	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
A4_199	Serum albumin	SP P07724	72.00	5.67	mV83BS	A	5 / 1	<i>Alb1</i> <sup>g</sup>	64	≈ 2.5	
A4_210	Serum albumin <sup>i</sup>		73.00	5.62	"	A	5 / 1	<i>Alb1</i> <sup>g</sup>	64	≈ 2.5	
C4_215	Serum albumin	NCBI 5915682	27.61	6.05	paV52BS	A	5 / 2	<i>s. map</i> <sup>h</sup>	63	interval (≈ 2.5)	mV83BS LOD 13.73 (5.5) mV45BS LOD 12.49 (6.79)
B5_012	T-complex protein 1, zeta subunit	NCBI 549061	67.14	6.24	mV299BS	A	5	<i>s. map</i>	64	≈ 2.5	
B5_031	T-complex protein 1, zeta subunit <sup>i</sup>		66.03	6.24	"	A	5	<i>s. map</i>	64	≈ 2.5	
E5_002			13.89	6.28	mV157BS	A	5		60	≈ 2.5	mV83BS LOD 18.06 (0)
B4_336			48.13	6.05	mV236BS	A	5		61	interval (≈ 2.5)	mV83BS LOD 10.85 (8.95)
B6_382			40.31	6.81	mV260BS	A	5		64	≈ 2.5	mV45BS LOD 19.27 (0)
B4_593			36.88	5.70	paV109BS	A	5		56	interval (≈ 2.5)	paV110BS, mV45BS LOD 10.60 (7.71)
C5_286			26.46	6.30	paV247BS	A	5		36	linked to chr	D5Nds6 LOD 3.35 (21.77)
C5_382			28.47	6.50	paV258BS	A	5		60	linked to chr	bir39m21 LOD 4.82 (26.11)
C6_383			29.65	6.94	paV294BS	A	5		56	linked to chr	mbacr3e9, mbacr32a11 LOD 4.22 (27.98)
C3_419	Phosphatidylethanolamine-binding protein	EMBL U43206	24.60	5.10	aV102BS	B					
B6_451	Malate dehydrogenase, mitochondrial	SP P08249	37.38	7.18			5	<i>Mor1</i>			
C3_317	Ubiquitin carboxyl-terminal hydrolase L1	SP Q00981	27.26	5.16			5	<i>Uchl1</i>			
C3_314	Ubiquitin carboxyl-terminal hydrolase L1	SP Q00981	27.42	5.29			5	<i>Uchl1</i>			
B6_209	Acyl-coA thioesterase	NCBI 5102774	48.98	6.84	paV440BS	A	6	<i>s. map</i>	62	≈ 2.5	
B6_212	Acyl-coA thioesterase <sup>i</sup>		48.91	6.74	mV369BS	A	6	<i>s. map</i>	58	≈ 2.5	paV440BS LOD 16.86 (0)
B5_702	Fructose-bisphosphate aldolase A (muscle)	NCBI 553861	37.12	6.66	paV398BS	A	6	<i>s. map</i>	64	interval (≈ 2.5)	mV286BS, D6Mit47 LOD 13.97 (3.51)
B5_651	Fructose-bisphosphate aldolase A (muscle) <sup>i</sup>		37.04	6.66	"	A	6	<i>s. map</i>	64	interval (≈ 2.5)	mV286BS, D6Mit47 LOD 13.97 (3.51)
B6_318	Fructose-bisphosphate aldolase A (muscle)	SP P05064	43.13	7.07	aV574BS	C					
B6_308	Fructose-bisphosphate aldolase A (muscle)	SP P05064	43.36	7.05							
B6_328	Fructose-bisphosphate aldolase A (muscle)	SP P05064	43.13	7.05							
B6_309	Fructose-bisphosphate aldolase A (muscle)	SP P05064	43.13	7.14							
C4_285	γ-Enolase <sup>i</sup>		25.24	5.73	mV21BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	62	≈ 2.5	mV73BS LOD 18.66 (0)
C3_254	γ-Enolase <sup>i</sup>		28.64	5.56	mV34BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	52	≈ 2.5	mV73BS LOD 15.65 (0)
B3_402	γ-Enolase <sup>i</sup>		47.48	5.12	mV39BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	57	≈ 2.5	mV73BS LOD 17.16 (0)
B3_411	γ-Enolase <sup>i</sup>		47.32	5.06	mV40BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	56	≈ 2.5	mV73BS LOD 17.16 (0)
B3_483	γ-Enolase <sup>i</sup>		42.68	5.23	mV49BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	58	≈ 2.5	mV73BS LOD 17.46 (0)
B3_507	γ-Enolase <sup>i</sup>		41.22	5.15	mV51BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B2_378	γ-Enolase <sup>i</sup>		40.57	5.04	mV52BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B2_384	γ-Enolase <sup>i</sup>		40.65	5.02	"	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B3_527	γ-Enolase <sup>i</sup>		40.41	5.06	"	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B3_522	γ-Enolase	SP P17183	40.41	5.08	"	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B2_423	γ-Enolase	SP P17183	38.90	4.96	mV54BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B2_415	γ-Enolase	SP P17183	39.07	4.89	mV55BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B2_485	γ-Enolase <sup>i</sup>		37.17	4.88	mV58BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	63	≈ 2.5	mV73BS LOD 18.96 (0)
B2_460	γ-Enolase <sup>i</sup>		37.93	4.92	mV59BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	mV73BS LOD 19.27 (0)
B2_250	γ-Enolase <sup>i</sup>		48.94	5.03	mV73BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	D6Mit24 LOD 17.76 (0)
B2_249	γ-Enolase <sup>i</sup>		49.19	4.96	"	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	D6Mit24 LOD 17.76 (0)
B3_359	γ-Enolase	SP P17183	48.62	5.08	"	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	D6Mit24 LOD 17.76 (0)
B3_370	γ-Enolase <sup>i</sup>		48.78	5.10	"	A	6 / 1	<i>Eno2</i> <sup>g</sup>	64	≈ 2.5	D6Mit24 LOD 17.76 (0)
B3_300	γ-Enolase <sup>i</sup>		47.72	5.05	mV74BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	61	≈ 2.5	mV73BS LOD 18.36 (0)
B2_259	γ-Enolase <sup>i</sup>		48.29	5.00	mV75BS	A	6 / 1	( <i>Eno2</i> ) <sup>g</sup>	39	interval (≈ 2.5)	mV73BS, mV29BS LOD 11.74 (0)
B2_387	γ-Enolase <sup>i</sup>		40.16	4.97	mV129BS	A	6 / 1	<i>Eno2</i> <sup>g</sup>	56	≈ 2.5	mV73BS LOD 16.86 (0)
C3_006	γ-Enolase	NCBI 119348	35.86	5.07	mV57BS	A	6 / 2	<i>s. map</i> <sup>h</sup>	57	linked to chr	
B2_309	γ-Enolase	NCBI 119348	45.28	4.86	mV364BS	A	6 / 3	<i>s. map</i> <sup>h</sup>	29	linked to chr	mV232BS, mV141BS, mV73BS, mV29 BS LOD 4.54 (11.59)
C2_003	γ-Enolase	SP P17183	35.86	5.03			6	<i>Eno2</i>			

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	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
C7_095	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		28.39	7.98	mV141BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	63	≠ 2.5	mV73BS LOD 18.96 (0)
C7_107	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		28.15	7.99	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	63	≠ 2.5	mV73BS LOD 18.96 (0)
B5_660	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	SP P16858	36.71	6.55	mV143BS	A	6 / 1	( <i>Gapd</i> ) <sup>g</sup>	62	interval (≠ 2.5)	mV73BS LOD 14.83 (3.33)
B5_618	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		38.15	6.64	mV145BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	64	≠ 2.5	D6Mit24 LOD 17.76 (0)
B5_611	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	SP P16858	38.19	6.72	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	64	≠ 2.5	D6Mit24 LOD 17.76 (0)
B6_448	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	SP P16858	38.07	6.80	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	64	≠ 2.5	D6Mit24 LOD 17.76 (0)
B6_442	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	SP P16858	38.11	6.95	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	64	≠ 2.5	D6Mit24 LOD 17.76 (0)
B6_436	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	SP P16858	38.07	7.00	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	64	≠ 2.5	D6Mit24 LOD 17.76 (0)
C8_016	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		29.33	8.34	mV152BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	63	≠ 2.5	mV73BS LOD 18.96 (0)
C8_014	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		29.46	8.31	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	63	≠ 2.5	mV73BS LOD 18.96 (0)
C8_013	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		29.60	8.30	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	63	≠ 2.5	mV73BS LOD 18.96 (0)
D7_091	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		14.33	7.81	mV179BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	62	≠ 2.5	mV73BS LOD 18.66 (0)
D7_078	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		15.47	7.77	mV180BS	A	6 / 1	( <i>Gapd</i> ) <sup>g</sup>	16	interval (≠ 2.5)	mV73BS, mV29BS LOD 4.82 (0)
D7_080	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		15.30	7.80	"	A	6 / 1	( <i>Gapd</i> ) <sup>g</sup>	16	interval (≠ 2.5)	mV73BS, mV29BS LOD 4.82 (0)
C8_019	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		28.93	8.39	mV202BS	A	6 / 1	( <i>Gapd</i> ) <sup>g</sup>	30	interval (≠ 2.5)	mV73BS, mV29BS LOD 9.03 (0)
C7_129	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		27.16	8.30	mV203BS	A	6 / 1	( <i>Gapd</i> ) <sup>g</sup>	30	interval (≠ 2.5)	mV73BS, mV29BS LOD 9.03 (0)
C7_140	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		26.92	8.11	mV204BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	59	≠ 2.5	mV73BS LOD 17.76 (0)
C7_003	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		35.56	7.44	mV232BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	62	≠ 2.5	mV73BS LOD 18.66 (0)
C7_007	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		34.98	7.43	"	A	6 / 1	<i>Gapd</i> <sup>g</sup>	62	≠ 2.5	mV73BS LOD 18.66 (0)
B6_430	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>		38.68	6.90	paV431BS	A	6 / 1	<i>Gapd</i> <sup>g</sup>	64	≠ 2.5	mV73BS LOD 19.27 (0)
B5_612	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	NCBI 120707	38.31	6.55	paV408BS	A	6 / 2	<i>s. map</i> <sup>h</sup>	62	linked to chr	mV29BS LOD 9.28 (10.03)
B6_476	Glyceraldehyde 3-phosphate dehydrogenase <sup>l</sup>	NCBI 120707	36.95	6.91	paV425BS	A	6 / 3	<i>s. map</i> <sup>h</sup>	32	linked to chr	mV29BS, paV431BS LOD 5.31 (10.38)
B4_385	GTP-specific succinyl-coA synthetase beta subunit	NCBI 3766203	44.80	5.64	mV355BS	A	6	<i>s. map</i>	64	≠ 2.5	
B4_400	GTP-specific succinyl-coA synthetase beta subunit	NCBI 3766203	43.98	5.64	"	A	6	<i>s. map</i>	64	≠ 2.5	
E6_014	Hemoglobin epsilon-γ2 chain	NCBI 122728	12.34	6.93	mV158BS	A	6	<i>s. map</i> <sup>h</sup>	15	linked to chr	mV64BS, mV200BS, mV232BS, D6Mit24, mV141BS, mV73BS, mV29BS, D6Mit14 LOD > 3.6
E1_026	L-Lactate dehydrogenase H chain <sup>l</sup>		9.12	4.41	mV1BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
E2_078	L-Lactate dehydrogenase H chain <sup>l</sup>		19.84	4.58	mV2BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
E2_065	L-Lactate dehydrogenase H chain <sup>l</sup>		20.24	4.50	mV3BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C4_337	L-Lactate dehydrogenase H chain <sup>l</sup>		33.25	5.68	mV24BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C4_050	L-Lactate dehydrogenase H chain <sup>l</sup>		33.16	5.68	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C4_021	L-Lactate dehydrogenase H chain <sup>l</sup>		34.81	5.66	mV25BS	A	6	<i>Ldh2</i> <sup>g</sup>	63	≠ 2.5	mV42BS LOD 18.96 (0)
C4_336	L-Lactate dehydrogenase H chain <sup>l</sup>		35.44	5.81	mV26BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C4_005	L-Lactate dehydrogenase H chain <sup>l</sup>		35.36	5.81	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
B3_671	L-Lactate dehydrogenase H chain <sup>l</sup>		37.30	5.56	mV42BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	
B3_620	L-Lactate dehydrogenase H chain <sup>l</sup>		37.22	5.56	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	
B4_595	L-Lactate dehydrogenase H chain	SP P16125	37.22	5.66	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	
B4_547	L-Lactate dehydrogenase H chain	SP P16125	37.13	5.66	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	
B4_592	L-Lactate dehydrogenase H chain <sup>l</sup>		36.58	5.67	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	
B4_594	L-Lactate dehydrogenase H chain <sup>l</sup>		35.95	5.67	"	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	
C3_290	L-Lactate dehydrogenase H chain <sup>l</sup>		27.90	5.40	mV117BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C3_458	L-Lactate dehydrogenase H chain <sup>l</sup>		28.54	5.52	mV118BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C3_274	L-Lactate dehydrogenase H chain <sup>l</sup>		28.30	5.53	mV122BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
E3_064	L-Lactate dehydrogenase H chain <sup>l</sup>		10.99	5.24	paV7BS	A	6	<i>Ldh2</i> <sup>g</sup>	63	≠ 2.5	mV42BS LOD 18.96 (0)
E3_045	L-Lactate dehydrogenase H chain <sup>l</sup>		11.96	5.55	paV9BS	A	6	<i>Ldh2</i> <sup>g</sup>	63	≠ 2.5	mV42BS LOD 18.96 (0)
D4_102	L-Lactate dehydrogenase H chain <sup>l</sup>		16.73	6.04	paV17BS	A	6	<i>Ldh2</i> <sup>g</sup>	60	≠ 2.5	mV42BS LOD 18.06 (0)
D4_159	L-Lactate dehydrogenase H chain <sup>l</sup>		14.77	5.72	paV35BS	A	6	<i>Ldh2</i> <sup>g</sup>	64	≠ 2.5	mV42BS LOD 19.27 (0)
C4_084	L-Lactate dehydrogenase H chain	NCBI 126042	31.98	5.96	paV81BS	A	6	<i>Ldh2</i> <sup>g</sup>	62	≠ 2.5	mV42BS LOD 18.66 (0)

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C4_120	L-Lactate dehydrogenase H chain	NCBI 126042	30.72	5.97	paV198BS	A	6	(Ldh2) <sup>g</sup>	22	interval (≠ 2.5)	mV42BS, av6BS LOD 6.62
D5_019	L-Lactate dehydrogenase H chain	NCBI 6678674	21.13	6.28	paV228BS	A	6	(Ldh2) <sup>g</sup>	63	interval (≠ 2.5)	mV42BS LOD 16.73 (1.61)
D5_128	L-Lactate dehydrogenase H chain	NCBI 6678674	20.99	6.28	"	A	6	(Ldh2) <sup>g</sup>	63	interval (≠ 2.5)	mV42BS LOD 16.73 (1.61)
C5_369	L-Lactate dehydrogenase H chain <sup>i</sup>		23.81	6.60	paV237BS	A	6	Ldh2 <sup>g</sup>	46	≠ 2.5	mV42BS LOD 13.85 (0)
C5_371	L-Lactate dehydrogenase H chain <sup>i</sup>		23.75	6.60	"	A	6	Ldh2 <sup>g</sup>	46	≠ 2.5	mV42BS LOD 13.85 (0)
A5_054	p100 co-activator	NCBI 6009521	108.85	6.48	mV286BS	A	6	s. map	59	≠ 2.5	
A5_056	p100 co-activator <sup>j</sup>		108.85	6.45	"	A	6	s. map	59	≠ 2.5	
A5_057	p100 co-activator <sup>j</sup>		108.85	6.43	"	A	6	s. map	59	≠ 2.5	
B7_152	Succinyl-coA ligase alpha-chain, mitochondrial <sup>k</sup>		37.70	8.30	mV200BS	A	6	s. map	64	≠ 2.5	
B7_150	Succinyl-coA ligase alpha-chain, mitochondrial <sup>k</sup>		37.74	8.24	"	A	6	s. map	64	≠ 2.5	
B7_153	Succinyl-coA ligase alpha-chain, mitochondrial <sup>k</sup>		37.53	8.12	"	A	6	s. map	64	≠ 2.5	
B8_010	Succinyl-coA ligase alpha-chain, mitochondrial <sup>k</sup>		37.82	8.44	"	A	6	s. map	64	≠ 2.5	
B8_009	Succinyl-coA ligase alpha-chain, mitochondrial <sup>k</sup>		37.82	8.40	"	A	6	s. map	64	≠ 2.5	
B8_008	Succinyl-coA ligase alpha-chain, mitochondrial <sup>k</sup>	SP P13086	37.65	8.36	"	A	6	s. map	64	≠ 2.5	
C3_115			32.41	5.07	mV29BS	A	6		64		2.1
B2_198			53.45	4.72	mV77BS	A	6		64	≠ 2.5	
B2_194			53.36	4.69	"	A	6		64	≠ 2.5	
B2_359			41.79	4.92	mV116BS	A	6		64	interval (≠ 2.5)	mV73BS LOD 15.40 (3.23)
D1_017			20.32	4.22	mV119BS	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_018			20.24	4.27	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_080			19.89	4.22	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_077			19.57	4.24	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_075			20.35	4.25	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_019			20.19	4.23	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_081			19.91	4.20	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_079			19.59	4.23	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_015			20.35	4.26	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_021			19.84	4.27	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_026			19.62	4.27	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_082			19.59	4.21	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_014			20.37	4.29	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_070			19.86	4.26	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_027			19.62	4.26	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_076			19.46	4.27	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_020			19.95	4.29	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_022			19.89	4.23	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D1_078			19.64	4.24	"	A	6		62	≠ 2.5	mV73BS LOD 18.66 (0)
D6_057			19.60	7.30	mV132BS	A	6		64	≠ 2.5	mV73BS LOD 19.27 (0)
D6_060			19.32	7.31	"	A	6		64	≠ 2.5	mV73BS LOD 19.27 (0)
D6_021			21.69	7.38	mV133BS	A	6		64	≠ 2.5	mV73BS LOD 19.27 (0)
E5_074			11.90	6.21	mV156BS	A	6		51	interval (≠ 2.5)	mV42BS LOD 8.25 (10.91)
D6_072			18.12	7.33	mV175BS	A	6		18	interval (≠ 2.5)	mV73BS, mV29BS LOD 5.42 (0)
C6_302			26.22	7.05	mV192BS	A	6		57	interval (≠ 2.5)	mV73BS LOD 10.87 (7.56)
D6_001			23.22	7.06	mV194BS	A	6		12	interval (≠ 2.5)	D6Mit24 LOD 3.01 (0) mV29BS LOD 3.61 (0)
C6_357			24.32	7.30	mV195BS	A	6		26	interval (≠ 2.5)	mV73BS, mV29BS LOD 7.83 (0)
C7_164			26.14	7.43	mV197BS	A	6		61	≠ 2.5	
C7_185			25.12	7.85	mV199BS	A	6		33	linked to chr	mV232BS, mV141BS, mV73BS, mV29BS LOD 4.64 (13.88)
C7_046			30.78	7.93	mV201BS	A	6		17	interval (2.4)	mV200BS LOD 3.47 (0)
E4_050			11.15	5.86	av6BS	A	6		63	2.3	
C4_340			26.28	5.61	paV41BS	A	6		48	interval (≠ 2.5)	mV77BS LOD 12.34 (2.13)

2-DE Spot-No <sup>a</sup>	Proteinspots				Varianten			GENE MAPPING			
	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
D6_160			17.00	6.74	paV220BS	A	6		52	interval (± 2.5)	mV42BS LOD 7.58 (13.12)
E6_033			11.15	7.02	paV223BS	A	6		41	linked to chr	mV29BS LOD 3.55 (24.73)
C4_344			29.76	6.09	aV253BS	A	6		53	interval (± 2.5)	aV6BS LOD 8.50 (10.68)
C4_157			29.26	6.09	"	A	6		53	interval (± 2.5)	aV6BS LOD 8.50 (10.68)
C5_378			32.72	6.26	paV266BS	A	6		54	interval (± 2.5)	mV42BS LOD 14.09 (1.89)
C5_377			31.40	6.26	"	A	6		54	interval (± 2.5)	mV42BS LOD 14.09 (1.89)
C5_250	Triosephosphate isomerase	SP P17751	27.37	6.56			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			6	<i>Tpi</i>			
B6_513	E-stop protein	NCBI 3287265	58.49	7.15	mV276BS	A	7	<i>s. map</i>	64	± 2.5	
B6_066	E-stop protein	NCBI 3287265	58.30	7.15	"	A	7	<i>s. map</i>	64	± 2.5	
B6_010	E-stop protein <sup>l</sup>		66.98	7.31	mV279BS	A	7	<i>s. map</i>	62	± 2.5	mV276BS LOD 18.66 (0)
B5_464	Fructose-bisphosphate aldolase C (brain)	SP P09117	43.20	6.49	paV419BS	A	7	<i>s. map<sup>h</sup></i>	49	1.9	
B5_701	Fumarylacetoacetase	NCBI 544273	42.73	6.70	paV417BS	A	7	<i>Fah<sup>g</sup></i>	39	interval (± 2.5)	mV276BS LOD 8.31 (5.41)
C6_001	Glucose-6-phosphate isomerase	NCBI 120741	35.88	7.17	mV144BS	A	7	<i>Gpi1<sup>g</sup></i>	60	± 2.5	D7Nds5 LOD 16.56 (0)
C6_003	Glucose-6-phosphate isomerase	NCBI 120741	35.80	7.16	"	A	7	<i>Gpi1<sup>g</sup></i>	60	± 2.5	D7Nds5 LOD 16.56 (0)
D7_040	Glucose-6-phosphate isomerase <sup>l</sup>		18.06	8.26	mV178BS	A	7	<i>Gpi1<sup>g</sup></i>	44	± 2.5	D7Nds5 LOD 12.34 (0)
D7_048	Glucose-6-phosphate isomerase <sup>l</sup>		17.51	8.29	"	A	7	<i>Gpi1<sup>g</sup></i>	44	± 2.5	D7Nds5 LOD 12.34 (0)
C8_054	Glucose-6-phosphate isomerase <sup>l</sup>		23.99	8.56	mV206BS	A	7	<i>Gpi1<sup>g</sup></i>	62	± 2.5	D7Nds5 LOD 17.16 (0)
C8_052	Glucose-6-phosphate isomerase <sup>l</sup>		24.80	8.49	"	A	7	<i>Gpi1<sup>g</sup></i>	62	± 2.5	D7Nds5 LOD 17.16 (0)
B6_312	Glucose-6-phosphate isomerase	NCBI 120741	43.75	7.33	mV263BS	A	7	<i>Gpi1<sup>g</sup></i>	53	± 2.5	D7Nds5 LOD 14.75 (0)
B6_295	Glucose-6-phosphate isomerase <sup>l</sup>		44.77	7.32	"	A	7	<i>Gpi1<sup>g</sup></i>	53	± 2.5	D7Nds5 LOD 14.75 (0)
B6_096	Glucose-6-phosphate isomerase	NCBI 120741	55.75	6.98	mV274BS	A	7	<i>Gpi1<sup>g</sup></i>	63	± 2.5	D7Nds5 LOD 17.46 (0)
B3_624	MU-crystallin homolog	NCBI 3913376	37.22	5.46	mV43BS	A	7	<i>Crym<sup>g</sup></i>	64	± 2.5	
B3_621	MU-crystallin homolog <sup>l</sup>		37.30	5.36	paV160BS	A	7	<i>Crym<sup>g</sup></i>	56	± 2.5	mV43BS LOD 16.86 (0)
B4_233	Ornithine aminotransferase	SP P29758	47.80	5.90	mV343BS	A	7	<i>Oat<sup>g</sup></i>	58	± 2.5	
B4_340	Ornithine aminotransferase	SP P29758	47.64	5.90	"	A	7	<i>Oat<sup>g</sup></i>	58	± 2.5	
B3_525	PKCq-interacting protein PICOT	NCBI 6840949	40.33	5.53	mV47BS	A	7	<i>s. map</i>	62	± 2.5	
B3_550	Sumo-1 activating enzyme (similar to human)	NCBI 5689242	39.49	5.26	mV357BS	A	7	<i>s. map</i>	64	± 2.5	
B2_038			69.66	4.83	mV94BS	A	7		64	± 2.5	
B2_520			70.20	4.80	"	A	7		64	± 2.5	
A2_159			85.41	4.71	mV102BS	A	7		64	± 2.5	
A2_121			91.85	4.63	"	A	7		64	± 2.5	
A2_125			91.11	4.67	"	A	7		64	± 2.5	
A2_147			88.92	4.62	"	A	7		64	± 2.5	
A2_146			88.65	4.68	"	A	7		64	± 2.5	
A2_153			87.57	4.68	"	A	7		64	± 2.5	
C6_112			31.23	7.26	mV235BS	A	7		44	interval (± 2.5)	D7Nds5 LOD 12.04 (0)
E2_040			11.91	4.65	mV304BS	A	7		49	linked to chr	mV47BS LOD 6.35 (14.74)
B2_090			60.51	4.88	mV311BS	A	7		62	interval (± 2.5)	D7Nds5 LOD 14.97 (1.79)
B2_523			47.40	4.65	mV352BS	A	7		64	± 2.5	
D2_284			22.21	4.83	paV26BS	A	7		64	linked to chr	paV78BS LOD 6.29 (21.48)
C3_253			28.78	5.08	paV78BS	A	7		63	± 2.5	mV43BS LOD 18.96 (0)
C3_462			28.48	5.09	"	A	7		63	± 2.5	mV43BS LOD 8.96 (0)
C3_457			31.69	5.06	paV94BS	A	7		61	linked to chr	mV343BS LOD 10.33 (7.86)
C3_149	Apolipoprotein E	SP P08226	31.31	5.53	aV345BS	C					
E6_010	Hemoglobin beta-1 chain	SP P02088	12.38	7.34			7	<i>Hbb-b1</i>			
C5_001	L-Lactate dehydrogenase M chain	SP P06151	35.31	6.59			7	<i>Ldh1</i>			
D2_113	Olfactory marker protein	EMBL U01213	18.56	4.93			7	<i>Omp</i>			
B5_199	Glutamate dehydrogenase	NCBI 6980956	55.94	6.65	mV271BS	A	8	<i>s. map<sup>h</sup></i>	54	linked to chr	mbacr28o8 LOD 5.74 (13.98)
B6_088	Glutathione reductase	SP P47791	56.32	6.73	mV269BS	A	8	<i>Gr1<sup>g</sup></i>	64	interval (± 2.5)	D8Mit4 LOD 12.26 (3.92)

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
B3_502	Histone deacetylase 1	NCBI 2347180	41.54	5.11	paV133BS	A	8	<i>s. map</i> <sup>h</sup>	58	interval (± 2.5)	Acta1 LOD 12.26 (3.92)
C6_154	NAD(P)H dehydrogenase 1, quinone	SP Q64669	29.97	7.10	mV219BS	A	8	<i>Dia4</i> <sup>g</sup>	64	± 2.5	mbacr10i4 LOD 18.06 (0)
C6_198	Proline synthetase associated	NCBI 4126980	28.87	6.93	paV292BS	A	8	<i>s. map</i>	64	± 2.5	
C6_384	Proline synthetase associated <sup>i</sup>		29.57	6.91	paV293BS	A	8	<i>s. map</i>	56	± 2.5	paV292BS LOD 16.86 (0)
B2_385			40.41	4.67	mV63BS	A	8		60	2.1	mV272BS LOD 18.06 (0)
B1_027			54.45	4.39	mV78BS	A	8		43	± 2.5	mV272BS LOD 12.94 (0)
B1_006			53.55	4.39	"	A	8		43	± 2.5	mV272BS LOD 12.94 (0)
E8_014			12.41	8.40	mV181BS	A	8		10	linked to chr	mV272BS LOD 3.01 (0)
B6_059			58.87	6.84	mV272BS	A	8		64	± 2.5	
B1_024			59.09	4.45	mV315BS	A	8		28	linked to chr	mV272BS LOD 4.29 (12.06)
B1_005			58.18	4.45	"	A	8		28	linked to chr	mV272BS LOD 4.29 (12.06)
C1_025			35.06	4.09	paV116BS	A	8		20	linked to chr	mbacr10i4 LOD 3.74 (5.89)
C1_024			34.68	4.10	"	A	8		20	linked to chr	mbacr10i4 LOD 3.74 (5.89)
C1_026			34.89	4.07	"	A	8		20	linked to chr	mbacr10i4 LOD 3.74 (5.89)
B3_293			52.27	5.36	paV165BS	A	8		62	interval (± 2.5)	mV272BS LOD 14.83 (3.33)
B3_665			64.75	5.52	paV180BS	A	8		60	linked to chr	paV292BS LOD 3.41 (34.66) D8Mit4 LOD 3.61 (28.99) bir38b16 LOD 3.54 (32.96) mV272BS LOD 3.91 (31.43)
C6_382			29.14	6.77	paV288BS	A	8		58	± 2.5	paV292BS LOD 17.46 (0)
C6_381			28.95	6.77	"	A	8		58	± 2.5	paV292BS LOD 17.46 (0)
C6_180			29.28	7.07	paV300BS	A	8		63	± 2.5	paV292BS LOD 18.96 (0)
B1_001	Calreticulin	SP P14211	17.00	4.45	aV373BS	C					
B7_125	Aspartate aminotransferase, mitochondrial	SP P05202	40.39	7.55			8	<i>Got2</i>			
B7_128	Aspartate aminotransferase, mitochondrial	SP P05202	40.39	7.45			8	<i>Got2</i>			
C6_345	Osteoblast specific factor 3	SP P35700	24.93	6.84			8	<i>Paga</i>			
B5_463	Acetyl-coA acetyltransferase, mitochondrial <sup>i</sup>		43.20	6.54	mV147BS	A	9	<i>Acat1</i> <sup>g</sup>	64	± 2.5	
B5_461	Acetyl-coA acetyltransferase, mitochondrial	SP P17764	43.28	6.69	"	A	9	<i>Acat1</i> <sup>g</sup>	64	± 2.5	
C6_362	alpha-B-crystallin	EMBL M73741	24.10	6.88	aV274BS	A	9	<i>(Crya2)</i> <sup>g</sup>	64	linked to chr	mV110BS LOD 5.43 (24.48)
C3_460	Apolipoprotein A-I	NCBI 2145139	25.40	5.38	mV348BS	A	9	<i>Apoa1</i> <sup>g</sup>	64	± 2.5	
B3_486	Apolipoprotein A-IV	NCBI 1703331	42.20	5.19	mV50BS	A	9	<i>Apoa4</i> <sup>g</sup>	64	± 2.5	sV348BS LOD 18.66 (0)
A3_035	Glucose regulated protein 170K	NCBI 2137069	180.69	5.24	mV110BS	A	9	<i>s. map</i>	64	± 2.5	
A3_036	Glucose regulated protein 170K	NCBI 2137069	179.77	5.22	"	A	9	<i>s. map</i>	64	± 2.5	
A3_037	Glucose regulated protein 170K	NCBI 2137069	178.85	5.20	"	A	9	<i>s. map</i>	64	± 2.5	
A3_040	Glucose regulated protein 170K <sup>i</sup>		178.85	5.18	"	A	9	<i>s. map</i>	64	± 2.5	
A3_042	Glucose regulated protein 170K <sup>i</sup>		178.85	5.16	"	A	9	<i>s. map</i>	64	± 2.5	
A3_047	Glucose regulated protein 170K <sup>i</sup>		170.57	5.11	mV111BS	A	9	<i>s. map</i>	63	± 2.5	mV110BS LOD 18.36 (0)
A3_049	Glucose regulated protein 170K <sup>i</sup>		169.66	5.09	"	A	9	<i>s. map</i>	63	± 2.5	mV110BS LOD 18.36 (0)
A3_051	Glucose regulated protein 170K <sup>i</sup>		168.74	5.07	"	A	9	<i>s. map</i>	63	± 2.5	mV110BS LOD 18.36 (0)
A3_052	Glucose regulated protein 170K <sup>i</sup>		168.74	5.06	"	A	9	<i>s. map</i>	63	± 2.5	mV110BS LOD 18.36 (0)
A3_054	Glucose regulated protein 170K <sup>i</sup>		167.82	5.05	"	A	9	<i>s. map</i>	63	± 2.5	mV110BS LOD 18.36 (0)
A3_064	Glucose regulated protein 170K <sup>i</sup>		154.94	5.08	mV112BS	A	9	<i>s. map</i>	55	interval (± 2.5)	mV110BS LOD 15.95 (0) D9Nds10 LOD 14.75 (0)
A3_065	Glucose regulated protein 170K <sup>i</sup>		154.02	5.07	"	A	9	<i>s. map</i>	55	interval (± 2.5)	mV110BS LOD 15.95 (0) D9Nds10 LOD 14.75 (0)
A3_067	Glucose regulated protein 170K <sup>i</sup>		151.26	5.05	"	A	9	<i>s. map</i>	55	interval (± 2.5)	mV110BS LOD 15.95 (0) D9Nds10 LOD 14.75 (0)
C5_006	Heat shock protein cognate 70	NCBI 123651	35.76	6.12	mV223BS	A	9	<i>(Hsc70)</i> <sup>g</sup>	60	linked to chr	mV6BS LOD 5.88 (21.14)
B3_001	Heat shock protein cognate 70	EMBL U73744	69.15	5.34			9	<i>Hsc70</i>			
B3_003	Heat shock protein cognate 70	EMBL U73744	68.98	5.38			9	<i>Hsc70</i>			
B4_278	Heat shock protein cognate 70	SP P08109	51.00	5.75			9	<i>Hsc70</i>			
B5_021	NADP-dependent malic enzyme	NCBI 126738	66.51	6.47	mV296BS	A	9 / 1	<i>Mod1</i> <sup>g</sup>	64	± 2.5	



2-DE Spot-No <sup>a</sup>	Proteinspots				Varianten				GENE MAPPING		
	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
C5_381	NADP-dependent malic enzyme	NCBI 126738	31.85	6.59	paV271BS	A	9 / 2	<i>s. map</i> <sup>h</sup>	35	interval (± 2.5)	mV28BS, mV296BS LOD 7.21 (6.07) mbacr1k4 LOD 6.11 (6.91)
C2_047	Topomyosin alpha chain, brain-3	NCBI 136104	34.26	4.78	mV28BS	A	9	<i>s. map</i>	64	± 2.5	
C2_170	Topomyosin alpha chain, brain-3	NCBI 136104	29.87	4.79	mV38BS	A	9	<i>s. map</i>	64	± 2.5	mV28BS LOD 18.66 (0)
A5_135	Serotransferrin (similar to cDNA clone)	NCBI 1446473	87.78	6.46	mV291BS	A	9	<i>Trf</i> <sup>g</sup>	59	± 2.5	D9Mit24 LOD 15.65 (0)
A5_150	Serotransferrin (similar to cDNA clone)	NCBI 1446473	87.33	6.46	"	A	9	<i>Trf</i> <sup>g</sup>	59	± 2.5	D9Mit24 LOD 15.65 (0)
C6_326	Smooth muscle protein 22-alpha	NCBI 1351075	25.47	6.96	mV190BS	A	9	<i>Tagln</i> <sup>g</sup>	57	interval (± 2.5)	mV110BS, sV348BS LOD 16.56 (0) D9Nds10 LOD 15.65 (0)
D4_156	Spermatid specific heat shock protein 70	NCBI 3461872	13.85	5.61	mV6BS	A	9	<i>s. map</i> <sup>h</sup>	64	± 2.5	
B4_432			42.20	5.84	mV41BS	A	9		64	± 2.5	mV368BS LOD 18.66 (0)
B2_388			40.16	4.52	mV70BS	A	9		57	interval (± 2.5)	mbacr9k13, mV6BS LOD 16.56 (0)
B2_393			39.92	4.48	"	A	9		57	interval (± 2.5)	mbacr9k13, mV6BS LOD 16.56 (0)
B2_182			54.18	5.01	mV79BS	A	9		59	± 2.5	D9Mit24 LOD 15.95 (0)
B2_104			59.64	4.77	mV88BS	A	9		52	interval (± 2.5)	sV348BS LOD 14.09 (1.89)
A2_109			102.14	4.68	mV103BS	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_219			105.36	4.76	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_220			104.29	4.77	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_095			103.21	4.77	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_217			105.00	4.74	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_218			103.21	4.75	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_098			102.14	4.75	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_216			103.57	4.72	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_215			102.50	4.72	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_105			101.79	4.72	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_214			102.86	4.70	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A2_107			101.79	4.70	"	A	9		58	interval (2.2)	mV110BS LOD 11.78 (5.67)
A6_056			76.28	7.09	mV281BS	A	9		60	± 2.5	
B6_294			44.69	7.35	mV368BS	A	9		64	± 2.5	
B4_590			40.73	6.04	paV119BS	A	9		49	± 2.5	
D5_131			16.16	6.28	paV234BS	A	9		57	interval (± 2.5)	sV348BS, mV147BS LOD 11.50 (5.78)
B5_073	Pyruvate kinase, isozyme M2	SP P52480	61.75	6.68			9	<i>Pk3</i>			
B5_092	Pyruvate kinase, isozyme M2	SP P52480	59.91	6.55			9	<i>Pk3</i>			
E4_079	D-dopachrome tautomerase	NCBI 6753618	12.21	6.07	mV4BS	A	10	<i>Ddt</i> <sup>g</sup>	64	interval (± 2.5)	D10Mit20 LOD 14.45 (0)
A2_097	Endoplasmin	SP P08113	105.71	4.86	mV104BS	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_087	Endoplasmin	SP P08113	106.79	4.83	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_091	Endoplasmin	SP P08113	106.43	4.86	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_094	Endoplasmin	SP P08113	106.07	4.83	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_086	Endoplasmin	SP P08113	107.14	4.84	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_092	Endoplasmin	SP P08113	106.43	4.84	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_088	Endoplasmin	SP P08113	106.43	4.89	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_082	Endoplasmin	SP P08113	107.14	4.88	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_090	Endoplasmin	SP P08113	106.43	4.88	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_096	Endoplasmin	SP P08113	105.71	4.88	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_084	Endoplasmin	SP P08113	107.50	4.87	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_089	Endoplasmin	SP P08113	106.79	4.87	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_093	Endoplasmin	SP P08113	106.07	4.87	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_085	Endoplasmin	SP P08113	107.14	4.86	"	A	10	<i>Tra1</i> <sup>g</sup>	64	2.2	
A2_210	H-2 class I histocompatibility antigen, D-P alpha chain	NCBI 122130	75.20	4.94	mV97BS	A	10	<i>s. map</i> <sup>h</sup>	36	linked to chr	mV104BS LOD 7.48 (5.89)
C6_265	KNP-I alpha protein <sup>i</sup>		27.08	7.09	mV366BS	A	10	<i>s. map</i>	64	interval (± 2.5)	D10Mit20 LOD 14.45 (0)
C6_271	KNP-I alpha protein	NCBI 2250700	27.02	7.09	"	A	10	<i>s. map</i>	64	interval (± 2.5)	D10Mit20 LOD 14.45 (0)

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
C6_273	KNP-I alpha protein <sup>l</sup>		26.89	7.10	"	A	10	<i>s. map</i>	64	interval (± 2.5)	D10Mit20 LOD 14.45 (0)
C6_260	KNP-I alpha protein	NCBI 2250700	27.16	7.23	mV367BS	A	10	<i>s. map</i>	64	interval (± 2.5)	D10Mit20 LOD 14.45 (0)
E3_073			10.36	5.40	mV11BS	A	10		63	± 2.5	
B2_506			36.41	4.76	mV65BS	A	10		28	linked to chr	mV104BS LOD 3.44 (16.82)
A3_031			181.61	5.50	mV114BS	A	10		61	2.1	
A3_032			181.61	5.49	"	A	10		61	2.1	
A3_033			181.61	5.48	"	A	10		61	2.1	
A3_034			182.53	5.46	"	A	10		61	2.1	
A4_232			90.00	6.01	mV115BS	A	10		14	interval (± 2.5)	D10Mit24 LOD 4.21 (0)
C5_034			34.65	6.33	mV226BS	A	10		64	± 2.5	
C5_044			34.53	6.33	"	A	10		64	± 2.5	
C6_081			32.67	6.89	mV239BS	A	10		62	interval (± 2.5)	bir51f7 LOD 9.34 (11.37) D10Mit20 LOD 9.30 (6.83) D10Mit7 LOD 8.47 (9.12) mV104BS LOD 10.10 (10.46)
C4_338			28.75	5.61	paV65BS	A	10		52	linked to chr	mV104BS LOD 6.77 (19.47)
C6_277			26.78	6.93	paV276BS	A	10		47	± 2.5	
A2_207	Heat shock protein 110 kDa <sup>l</sup>		75.60	4.90	mV93BS	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_225	Heat shock protein 110 kDa <sup>l</sup>		76.00	4.88	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_206	Heat shock protein 110 kDa <sup>l</sup>		75.80	4.88	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_204	Heat shock protein 110 kDa <sup>l</sup>		76.00	4.86	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_224	Heat shock protein 110 kDa <sup>l</sup>		76.20	4.85	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_015	Heat shock protein 110 kDa <sup>l</sup>		72.00	4.93	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_003	Heat shock protein 110 kDa <sup>l</sup>		72.40	4.90	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_013	Heat shock protein 110 kDa <sup>l</sup>		72.40	4.88	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_001	Heat shock protein 110 kDa <sup>l</sup>		72.60	4.87	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_007	Heat shock protein 110 kDa <sup>l</sup>		72.40	4.87	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_046	Heat shock protein 110 kDa <sup>l</sup>		67.97	4.79	mV96BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_055	Heat shock protein 110 kDa <sup>l</sup>		67.29	4.79	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_051	Heat shock protein 110 kDa <sup>l</sup>		67.46	4.81	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_048	Heat shock protein 110 kDa <sup>l</sup>		68.14	4.81	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_050	Heat shock protein 110 kDa <sup>l</sup>		67.29	4.82	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_049	Heat shock protein 110 kDa <sup>l</sup>		67.63	4.84	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_123	Heat shock protein 110 kDa <sup>l</sup>		89.46	4.96	mV98BS	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_141	Heat shock protein 110 kDa <sup>l</sup>		89.73	4.94	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_140	Heat shock protein 110 kDa <sup>l</sup>		89.73	4.91	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_155	Heat shock protein 110 kDa <sup>l</sup>		85.68	4.96	mV99BS	A	11	<i>s. map</i>	58	interval (± 2.5)	D11Nds19 LOD 12.54 (3.85)
A2_156	Heat shock protein 110 kDa <sup>l</sup>		85.68	4.93	"	A	11	<i>s. map</i>	58	interval (± 2.5)	D11Nds19 LOD 12.54 (3.85)
A2_164	Heat shock protein 110 kDa <sup>l</sup>		84.59	5.03	mV100BS	A	11	<i>s. map</i>	53	interval (± 2.5)	D11Nds19 LOD 11.12 (4.26)
A2_165	Heat shock protein 110 kDa <sup>l</sup>		84.59	5.00	"	A	11	<i>s. map</i>	53	interval (± 2.5)	D11Nds19 LOD 11.12 (4.26)
A2_173	Heat shock protein 110 kDa <sup>l</sup>		82.43	4.99	mV101BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_174	Heat shock protein 110 kDa <sup>l</sup>		82.43	4.96	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_173	Heat shock protein 110 kDa <sup>l</sup>		101.07	5.10	mV106BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_166	Heat shock protein 110 kDa <sup>l</sup>		101.43	5.13	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_165	Heat shock protein 110 kDa <sup>l</sup>		101.79	5.16	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_149	Heat shock protein 110 kDa <sup>l</sup>		105.71	5.15	mV107BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_151	Heat shock protein 110 kDa <sup>l</sup>		105.71	5.13	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_153	Heat shock protein 110 kDa <sup>l</sup>		105.71	5.10	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_150	Heat shock protein 110 kDa <sup>l</sup>		105.71	5.21	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_148	Heat shock protein 110 kDa <sup>l</sup>		105.71	5.18	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_146	Heat shock protein 110 kDa <sup>l</sup>		106.76	5.33	mV108BS	A	11	<i>s. map</i>	53	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)

2-DE Spot-No <sup>a</sup>	Proteinspots				Varianten				GENE MAPPING		
	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
A3_144	Heat shock protein 110 kDa <sup>l</sup>		106.43	5.30	"	A	11	<i>s. map</i>	53	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_140	Heat shock protein 110 kDa <sup>l</sup>		106.07	5.27	"	A	11	<i>s. map</i>	53	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_111	Heat shock protein 110 kDa <sup>l</sup>		118.95	5.31	mV109BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_110	Heat shock protein 110 kDa <sup>l</sup>		119.47	5.28	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_092	Heat shock protein 110 kDa	EMBL D85904	119.47	5.25	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_077	Heat shock protein 110 kDa	EMBL D85904	120.00	5.23	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_084	Heat shock protein 110 kDa	EMBL D85904	120.00	5.20	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_086	Heat shock protein 110 kDa	EMBL D85904	120.00	5.18	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_109	Heat shock protein 110 kDa	EMBL D85904	120.00	5.16	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B2_158	Heat shock protein 110 kDa <sup>l</sup>		55.50	4.67	mV314BS	A	11	<i>s. map</i>	29	interval (± 2.5)	D11Nds19 LOD 6.27 (3.85)
B2_157	Heat shock protein 110 kDa <sup>l</sup>		55.64	4.70	"	A	11	<i>s. map</i>	29	interval (± 2.5)	D11Nds19 LOD 6.27 (3.85)
A2_120	Heat shock protein 110 kDa <sup>l</sup>		93.33	5.05	mV316BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_223	Heat shock protein 110 kDa <sup>l</sup>		92.96	5.08	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A3_227	Heat shock protein 110 kDa <sup>l</sup>		92.59	5.11	"	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_222	Heat shock protein 110 kDa <sup>l</sup>		89.46	4.89	mV372BS	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_148	Heat shock protein 110 kDa <sup>l</sup>		88.92	4.89	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_221	Heat shock protein 110 kDa <sup>l</sup>		89.73	4.87	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
A2_142	Heat shock protein 110 kDa <sup>l</sup>		89.19	4.87	"	A	11	<i>s. map</i>	64	interval (± 2.5)	D11Nds19 LOD 13.97 (3.51)
B5_046	Dihydropyrimidinase related protein-1	NCBI 3122030	64.44	6.53	paV493BS	A	11	<i>s. map<sup>h</sup></i>	60	± 2.5	bir42k5 LOD 18.06 (0)
B5_065	Dihydropyrimidinase related protein-4	NCBI 3122037	63.65	6.26	paV507BS	A	11	<i>s. map<sup>h</sup></i>	60	interval (± 2.5)	paV496BS LOD 14.39 (1.85)
B5_695	Elongation factor TU, mitochondrial	NCBI 1706611	46.56	6.33	paV468BS	A	11	<i>s. map</i>	61	interval (± 2.5)	D11Nds19 LOD 6.60 (14.38)
D6_120	Fructose-bisphosphate aldolase C (brain)	NCBI 2118269	15.63	6.92	mV159BS	A	11	Aldo3 <sup>g</sup>	42	interval (± 2.5)	D11Mit31 LOD 7.70 (3.23) paV189BS LOD 7.99 (3.13) mV351 LOD 8.28 (3.03)
B5_467	Fructose-bisphosphate aldolase C (brain)	SP P09117	43.28	6.47			11	<i>Aldo3</i>			
B5_490	Fructose-bisphosphate aldolase C (brain)	SP P09117	42.42	6.48			11	<i>Aldo3</i>			
B5_040	Hypothetical 32.1 kd protein (similar to cDNA clone)	NCBI 1864372	65.24	6.40	mV300BS	A	11	<i>s. map</i>	64	interval (± 2.5)	bir42k5 LOD 15.40 (3.23)
A2_007	Neurofilament triplet H protein	NCBI 128127		4.86	paV190BS	A	11	<i>Nfh<sup>g</sup></i>	57	interval (± 2.5)	D11Mit16 LOD 12.05 (2.17)
A2_009	Neurofilament triplet H protein <sup>l</sup>			4.77	"	A	11	<i>Nfh<sup>g</sup></i>	57	interval (± 2.5)	D11Mit16 LOD 12.05 (2.17)
A2_011	Neurofilament triplet H protein <sup>l</sup>		193.56	4.68	"	A	11	<i>Nfh<sup>g</sup></i>	57	interval (± 2.5)	D11Mit16 LOD 12.05 (2.17)
A2_014	Neurofilament triplet H protein <sup>l</sup>		178.85	4.61	"	A	11	<i>Nfh<sup>g</sup></i>	57	interval (± 2.5)	D11Mit16 LOD 12.05 (2.17)
C6_186	Phosphoglycerate mutase, muscle form	NCBI 6093745	29.17	7.16	aV380BS	A	11	<i>s. map</i>	63	interval (± 2.5)	D11Mit16 LOD 10.12 (6.39)
B2_464	Protein disulfide isomerase	NCBI 202547	37.97	4.82	mV130BS	A	11 / 1	( <i>P4hb</i> ) <sup>g</sup>	64	interval (± 2.5)	D11Mit11 LOD 4.22 (27.98)
B2_458	Protein disulfide isomerase	NCBI 202547	38.19	4.80	"	A	11 / 1	( <i>P4hb</i> ) <sup>g</sup>	64	interval (± 2.5)	D11Mit11 LOD 4.22 (27.98)
B2_150	Protein disulfide isomerase <sup>l</sup>		56.36	4.89	mV86BS	A	11 / 2	<i>s. map<sup>h</sup></i>	64	interval (± 2.5)	D11Mit11 LOD 7.69 (14.38)
B2_146	Protein disulfide isomerase	NCBI 129729	56.55	4.86	"	A	11 / 2	<i>s. map<sup>h</sup></i>	64	interval (± 2.5)	D11Mit11 LOD 7.69 (14.38)
B2_147	Protein disulfide isomerase <sup>l</sup>		56.64	4.83	"	A	11 / 2	<i>s. map<sup>h</sup></i>	64	interval (± 2.5)	D11Mit11 LOD 7.69 (14.38)
C5_165	Pyridoxine 5'-phosphate oxidase	NCBI 3237304	29.65	6.12	mV209BS	A	11	<i>s. map</i>	64	± 2.5	
B5_692	Pyruvate kinase, isozyme M2	NCBI 2506796	61.43	6.49	paV495BS	A	11	<i>s. map<sup>h</sup></i>	54	interval (± 2.5)	paV496BS LOD 10.84 (4.35)
B5_393	45kD Secretory protein	NCBI 5596963	46.88	6.19	mV237BS	A	11	<i>s. map</i>	64	interval (± 2.5)	mbacr27I20 LOD 8.79 (14.38)
B4_523	Serine racemase	NCBI 6448865	38.27	5.63	paV189BS	A	11	<i>s. map</i>	63	2.4	
B4_532	Serine racemase	NCBI 6448865	38.06	5.63	"	A	11	<i>s. map</i>	63	2.4	
C3_162	Serine/threonine-protein kinase kcialre (similar to cDNA clone)	NCBI 1285464	30.72	5.38	mV351BS	A	11	<i>s. map</i>	64	2.2	
B3_240			54.82	5.25	mV80BS	A	11		62	interval (± 2.5)	D11Mit16 LOD 12.63 (2.08)
C4_342			24.12	5.82	mV127BS	A	11		64	± 2.5	bir42k5 LOD 19.27 (0)
D5_129			17.35	6.21	mV168BS	A	11		48	linked to chr	paV189BS LOD 3.58 (27.72)
B2_521			54.36	4.94	mV309BS	A	11		33	interval (± 2.5)	bir42k5 LOD 4.64 (13.88) D11Mit11 LOD 4.15 (14.92)

2-DE Spot-No <sup>a</sup>	Proteinspots					Varianten			GENE MAPPING		
	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
B2_180			54.45	4.91	"	A	11		33	interval (≠ 2.5)	bir42k5 LOD 4.64 (13.88) D11Mit11 LOD 4.15 (14.92)
C2_137			31.27	4.75	mV322BS	A	11		55	interval (≠ 2.5)	D11Mit11 LOD 4.18 (24.14)
C2_328			25.61	5.04	paV95BS	A	11		61	linked to chr	mV351BS LOD 9.85 (10.95)
B6_412			39.26	7.29	paV432BS	A	11		63	interval (≠ 2.5)	D11Mit11 LOD 4.60 (25.54)
B5_066			63.65	6.17	paV496BS	A	11		58	≠ 2.5	
E7_015	Hemoglobin alpha-1 chain	SP P01942	12.14	7.68			11	<i>Hba-a1</i>			
C4_022	Malate dehydrogenase, cytoplasmic	SP P14152	34.35	5.88			11	<i>Mor2</i>			
C5_295	Malate dehydrogenase, cytoplasmic	SP P14152	26.09	6.45			11	<i>Mor2</i>			
C6_331	Peptidyl-prolyl cis-trans isomerase A	SP P17742	25.25	7.07			11	<i>Ppia</i>			
D6_091	Peptidyl-prolyl cis-trans isomerase A	SP P17742	17.46	6.76			11	<i>Ppia</i>			
D6_075	Peptidyl-prolyl cis-trans isomerase A	SP P17742	18.06	6.76			11	<i>Ppia</i>			
B4_589	Acyl-coA thioesterase long chain, mitochondrial	NCBI 6478480	45.37	6.07	paV118BS	A	12	<i>s. map</i>	61	interval (≠ 2.5)	mV48BS LOD 15.56 (1.72)
B5_167	Methylmalonate-semialdehyde dehydrogenase, acylating	NCBI 400269	56.60	6.33	paV463BS	A	12	<i>s. map</i>	64	≠ 2.5	
B5_428	Methylmalonate-semialdehyde dehydrogenase, acylating <sup>1</sup>		45.31	6.22	paV421BS	A	12	<i>s. map</i>	62	≠ 2.5	paV463BS LOD 18.66 (0)
B5_172	Methylmalonate-semialdehyde dehydrogenase, acylating	NCBI 400269	56.70	6.22	paV486BS	A	12	<i>s. map</i>	50	≠ 2.5	
B2_151	Tubulin beta-5 chain	NCBI 135471	56.64	5.03	aV174BS	A	12	<i>s. map</i>	56	interval (≠ 2.5)	paV175BS LOD 9.28 (10.03)
B2_121	Tubulin beta-5 chain	SP P05218	57.91	4.95			12	<i>Tubb5</i>			
B2_118	Tubulin beta-5 chain	SP P05218	58.00	4.98			12	<i>Tubb5</i>			
B3_513			41.06	5.34	mV48BS	A	12		62	≠ 2.5	paV463BS LOD 81.66 (0)
B2_117			58.36	4.83	mV310BS	A	12		57	interval (2.4)	paV175BS LOD 10.33 (7.86)
B2_111			58.64	4.77	"	A	12		57	interval (≠ 2.5)	paV175BS LOD 10.33 (7.86)
D3_223			14.35	5.47	paV18BS	A	12		49	linked to chr	D12Mit4 LOD 3.77 (25.54)
B3_207			56.27	5.05	aV173BS	A	12		61	interval (≠ 2.5)	D12Nds11 LOD 3.36 (33.79)
B2_137			57.36	4.97	paV175BS	A	12		61	≠ 2.5	
B2_138			57.36	4.95	"	A	12		61	≠ 2.5	
B2_134			57.45	4.91	paV176BS	A	12		58	≠ 2.5	paV175BS LOD 17.46 (0)
B2_133			57.64	4.91	"	A	12		58	≠ 2.5	paV175BS LOD 17.46 (0)
E6_071			11.68	6.78	paV225BS	A	12		45	interval (≠ 2.5)	D12Nds11 LOD 3.76 (23.98)
C3_058	Creatine kinase b chain	SP Q04447	34.09	5.22	aV348BS	C					
B3_423	Creatine kinase b chain	SP Q04447	46.42	5.53			12	<i>Ckb</i>			
B4_354	Creatine kinase b chain	SP Q04447	46.26	5.59			12	<i>Ckb</i>			
C2_189	Creatine kinase b chain	SP Q04447	29.18	4.89			12	<i>Ckb</i>			
C3_052	Creatine kinase b chain	SP Q04447	34.26	5.32			12	<i>Ckb</i>			
C3_135	Creatine kinase b chain	SP Q04447	31.73	5.19			12	<i>Ckb</i>			
C3_141	Creatine kinase b chain	SP Q04447	31.60	5.09			12	<i>Ckb</i>			
C6_023	Aldo-keto reductase	EMBL U68535	35.23	6.83	mV229BS	A	13	<i>s. map</i>	64	≠ 2.5	mV290BS LOD 19.27 (0)
C6_034	Aldo-keto reductase	EMBL U68535	34.98	6.83	"	A	13	<i>s. map</i>	64	≠ 2.5	mV290BS LOD 19.27 (0)
A3_098	Calpastatin <sup>1</sup>		129.20	5.14	mV113BS	A	13	<i>s. map</i>	64	≠ 2.5	
A3_101	Calpastatin <sup>1</sup>		129.20	5.11	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_093	Calpastatin <sup>1</sup>		132.87	5.11	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_089	Calpastatin	NCBI 6006275	136.55	5.11	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_083	Calpastatin <sup>1</sup>		141.15	5.11	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_397	Calpastatin <sup>1</sup>		129.20	5.10	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_094	Calpastatin <sup>1</sup>		133.79	5.09	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_090	Calpastatin	NCBI 6006275	136.55	5.09	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_080	Calpastatin <sup>1</sup>		141.15	5.08	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_076	Calpastatin <sup>1</sup>		146.67	5.08	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_095	Calpastatin <sup>1</sup>		133.79	5.07	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_091	Calpastatin	NCBI 6006275	137.47	5.06	"	A	13	<i>s. map</i>	64	≠ 2.5	

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
A3_081	Calpastatin <sup>l</sup>		140.23	5.06	"	A	13	<i>s. map</i>	64	≠ 2.5	
A3_078	Calpastatin <sup>l</sup>		143.91	5.06	"	A	13	<i>s. map</i>	64	≠ 2.5	
E6_045	Hemoglobin alpha-1 chain	NCBI 109958	10.04	7.03	paV224BS	A	13	<i>s. map<sup>h</sup></i>	64	≠ 2.5	
B4_169	Hydroxymethylglutaryl-coA synthase, cytoplasmic	NCBI 123333	56.45	5.75	paV157BS	A	13	<i>Hmgcs1<sup>g</sup></i>	63	≠ 2.5	
A5_147	Phosphofruktokinase-1 C isozyme	NCBI 4567052	87.11	6.26	mV290BS	A	13	<i>s. map</i>	64	≠ 2.5	D13Mit56 LOD 10.06 (8.02)
C6_392	Transaldolase	NCBI 2851596	28.07	7.14	mV221BS	A	13	<i>s. map<sup>h</sup></i>	50	≠ 2.5	aV124BS LOD 15.05 (0)
A2_209	Ubiquilin <sup>l</sup>		75.00	4.61	mV91BS	A	13	<i>s. map</i>	51	≠ 2.5	
A2_212	Ubiquilin <sup>l</sup>	NCBI 5733824	74.80	4.66	"	A	13	<i>s. map</i>	51	≠ 2.5	
B2_014	Ubiquilin <sup>l</sup>		71.60	4.62	"	A	13	<i>s. map</i>	51	≠ 2.5	
B2_019	Ubiquilin <sup>l</sup>	NCBI 5733824	71.60	4.66	"	A	13	<i>s. map</i>	51	≠ 2.5	
E5_046	Ubiquitin	NCBI 346623	10.31	6.24	mV155BS	A	13	<i>s. map</i>	63	≠ 2.5	paV224BS LOD 18.96 (0)
C6_226			28.15	7.30	mV140BS	A	13		63	≠ 2.5	aV124BS LOD 18.96 (0)
E4_080			9.91	5.76	paV5BS	A	13		63	interval (≠ 2.5)	sV113BS LOD 16.73 (1.61)
C4_221			27.58	6.06	paV50BS	A	13		61	1.7	D13Mit56 LOD 8.50 (10.68)
C4_311			24.34	5.91	paV117BS	A	13		61	interval (≠ 2.5)	aV124BS LOD 13.17 (5.18)
B4_474			39.87	5.86	aV124BS	A	13		64	≠ 2.5	
B4_490			39.28	5.75	paV125BS	A	13		64	≠ 2.5	aV124BS LOD 19.27 (0)
B4_179			56.27	5.67	aV161BS	A	13		64	linked to chr	paV157BS LOD 6.99 (19.10)
C4_019			34.98	6.09	paV395BS	A	13		59	≠ 2.5	D13Mit56 LOD 10.12 (6.39)
B5_458			43.75	6.27	paV420BS	A	13		64	interval (≠ 2.5)	aV124BS LOD 17.03 (1.59)
B3_248	Annexin VII	SP Q07076	54.36	5.11	paV171BS	A	14	<i>Anx7<sup>g</sup></i>	62	≠ 2.5	
D5_073	Bis(5'-adenosyl)-triphosphatase	NCBI 6015152	17.59	6.38	paV231BS	A	14	<i>Fhit<sup>g</sup></i>	59	interval (≠ 2.5)	mbacr19c16 LOD 15.56 (1.72)
C4_114	Dihydropyrimidinase related protein-2	NCBI 3122040	30.93	5.76	paV86BS	A	14	<i>Dpysl2<sup>g</sup></i>	63	≠ 2.5	mbacr11b5 LOD 18.66 (0)
A4_216	Dihydropyrimidinase related protein-2	SP P47942	71.80	5.82			14	<i>Dpysl2</i>			
B4_018	Dihydropyrimidinase related protein-2	SP P47942	66.44	5.90			14	<i>Dpysl2</i>			
B4_022	Dihydropyrimidinase related protein-2	SP P47942	66.10	6.01			14	<i>Dpysl2</i>			
D3_092	Glia maturation factor beta	SP Q63228	18.76	5.16	mV8BS	A	14	<i>s. map</i>	63	interval (≠ 2.5)	mbacr11b5 LOD 16.44 (1.64)
A5_294	Phosphoenolpyruvate carboxykinase, mitochondrial	SP Q16822	72.79	6.20	mV301BS	A	14	<i>s. map</i>	64	≠ 2.5	mbacr11b5 LOD 18.96 (0)
B4_151	Synapsin IIb	NCBI 3860049	57.55	5.99	mV358BS	A	14	<i>s. map<sup>h</sup></i>	59	2.3	
C2_163			30.08	4.76	mV321BS	A	14		57	interval (≠ 2.5)	mbacr11b5 LOD 13.11 (3.71)
D4_160			21.84	6.09	paV23BS	A	14		43	interval (≠ 2.5)	mbacr19c16 LOD 10.88 (2.38)
B3_666			52.45	5.13	paV170BS	A	14		64	linked to chr	mbacr19c16 LOD 5.85 (23.50)
C5_387			26.84	6.46	paV250BS	A	14		59	linked to chr	D14Mit45 LOD 4.03 (28.67) D14Nds7 LOD 4.60 (25.54)
B5_176	Glutamate dehydrogenase	SP P26443	56.32	6.56			14	<i>Glud</i>			
B2_017	Neurofilament triplet L protein	SP P08551	71.40	4.79			14	<i>Nfi</i>			
A5_103	Aconitase 2, mitochondrial <sup>l</sup>		92.50	6.61	mV150BS	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A5_102	Aconitase 2, mitochondrial <sup>l</sup>		92.19	6.65	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A5_097	Aconitase 2, mitochondrial	SP P16276	91.88	6.73	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_008	Aconitase 2, mitochondrial	SP P16276	91.56	6.74	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_012	Aconitase 2, mitochondrial <sup>l</sup>		88.44	6.80	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_011	Aconitase 2, mitochondrial <sup>l</sup>		88.44	6.86	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_009	Aconitase 2, mitochondrial <sup>l</sup>		91.88	6.80	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_013	Aconitase 2, mitochondrial <sup>l</sup>		88.22	6.81	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_010	Aconitase 2, mitochondrial <sup>l</sup>		89.11	6.77	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_014	Aconitase 2, mitochondrial <sup>l</sup>		88.00	6.77	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
A6_015	Aconitase 2, mitochondrial <sup>l</sup>		87.11	6.76	"	A	15 / 1	<i>s. map<sup>h</sup></i>	61	≠ 2.5	mbacr20n16 LOD 18.36 (0)
B6_220	Aconitase 2, mitochondrial	SP P16276	48.36	7.12	mV248BS	A	15 / 1	<i>s. map<sup>h</sup></i>	48	≠ 2.5	bir46p16 LOD 14.45 (0)
A5_219	Aconitase 2, mitochondrial <sup>l</sup>		80.00	6.66	mV292BS	A	15 / 1	<i>s. map<sup>h</sup></i>	62	≠ 2.5	mbacr20n16 LOD 18.66 (0)
A5_240	Aconitase 2, mitochondrial <sup>l</sup>		77.91	6.69	"	A	15 / 1	<i>s. map<sup>h</sup></i>	62	≠ 2.5	mbacr20n16 LOD 18.66 (0)

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	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
A5_241	Aconitase 2, mitochondrial		77.91	6.68	"	A	15 / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mbacr20n16 LOD 18.66 (0)
A5_202	Aconitase 2, mitochondrial	NCBI 5304852	82.22	6.65	"	A	15 / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mbacr20n16 LOD 18.66 (0)
B5_038	Aconitase 2, mitochondrial	NCBI 3600098	65.08	6.69	mV297BS	A	15 / 2	<i>s. map</i> <sup>h</sup>	58	linked to chr	mbacr20n16 LOD 10.06 (9.46)
B5_063	Aconitase 2, mitochondrial	NCBI 3600098	63.49	6.63	"	A	15 / 2	<i>s. map</i> <sup>h</sup>	58	linked to chr	mbacr20n16 LOD 10.06 (9.46)
B5_263	Adenylosuccinate lyase	NCBI 1709933	52.74	6.48	mV266BS	A	15	<i>s. map</i>	64	≠ 2.5	mbacr20n16 LOD 19.27 (0)
B5_301	alpha-Actin, cardiac	NCBI 627834	51.13	6.62	mV267BS	A	15	<i>s. map</i> <sup>h</sup>	52	≠ 2.5	
B2_525	γ-Enolase Epidermal keratin 10	NCBI 119348 NCBI 7638398	38.06	4.94	mV68BS	A	15	<i>s. map</i> <i>s. map</i>	57	≠ 2.5	
C5_236	GTP-binding nuclear protein RAN	NCBI 131844	27.88	6.51	paV257BS	A	15	<i>s. map</i> <sup>h</sup>	32	interval (2.0)	bir46p16 LOD 6.38 (6.68)
C5_038	3-Mercaptopyruvate sulfotransferase	SP P97532	34.61	6.18	mV363BS	A	15	<i>s. map</i>	64	≠ 2.5	
B5_696	MHC tum-transplantation antigen P35B	NCBI 387474	46.09	6.48	paV467BS	A	15	<i>s. map</i>	50	≠ 2.5	
B5_124	Succinyl-coA:3-ketoacid-coenzyme A transferase	NCBI 2492998	58.77	6.31	mV149BS	A	15	<i>s. map</i>	64	≠ 2.5	D15Mit11 LOD 17.76 (0)
B5_129	Succinyl-coA:3-ketoacid-coenzyme A transferase	NCBI 2492998	58.87	6.42	"	A	15	<i>s. map</i>	64	≠ 2.5	D15Mit11 LOD 17.76 (0)
C2_032			34.89	4.98	mV66BS	A	15		64	≠ 2.5	
B2_517			36.24	5.02	mV67BS	A	15		64	≠ 2.5	mV66BS LOD 19.27 (0)
D8_016			18.37	8.36	mV177BS	A	15		37	interval (≠ 2.5)	mbacr20n16 LOD 9.14 (2.78)
B6_193			49.53	6.79	mV246BS	A	15		61	linked to chr	D15Mit11 LOD 3.68 (31.21)
B5_335			49.38	6.66	mV293BS	A	15		59	≠ 2.5	D15Mit11 LOD 16.56 (0)
C3_001			36.16	5.08	paV114BS	A	15		64	≠ 2.5	
C6_089			32.18	6.86	aV384BS	A	15		36	interval (≠ 2.5)	mV66BS, mV363BS LOD 2.86
B5_650	Glycerol-3-phosphate dehydrogenase, cytoplasmic	SP P13707	37.08	6.55			15	<i>Gdc1</i>			
C6_072	Carbonyl reductase	SP P48758	33.09	6.93	mV142BS	A	16 / 1	( <i>Cbr</i> ) <sup>g</sup>	64	interval (≠ 2.5)	Mx1 LOD 13.40 (3.64)
C6_389	Carbonyl reductase	SP P48758	34.12	6.74	mV153BS	A	16 / 1	( <i>Cbr</i> ) <sup>g</sup>	64	interval (≠ 2.5)	Mx1 LOD 13.40 (3.64)
C5_379	Carbonyl reductase	SP P48758	35.06	6.54	mV154BS	A	16 / 1	( <i>Cbr</i> ) <sup>g</sup>	64	interval (≠ 2.5)	Mx1 LOD 13.40 (3.64)
C5_376	Carbonyl reductase	NCBI 3102770	31.48	6.14	paV264BS	A	16 / 2	<i>s. map</i> <sup>h</sup>	63	interval (≠ 2.5)	Mx1 LOD 10.60 (7.71)
C6_391	Carbonyl reductase	NCBI 1352256	33.13	7.11	paV385BS	A	16 / 3	<i>s. map</i> <sup>h</sup>	63	interval (≠ 2.5)	Mx1 LOD 10.60 (7.71)
C6_380	Carbonyl reductase	NCBI 1352256	33.09	7.11	"	A	16 / 3	<i>s. map</i> <sup>h</sup>	63	interval (≠ 2.5)	Mx1 LOD 10.60 (7.71)
C3_459	Catechol O-methyltransferase, membrane-bound form	NCBI 5921831	25.61	5.30	paV47BS	A	16	<i>s. map</i> <sup>h</sup>	54	≠ 2.5	
C3_258	Catechol O-methyltransferase, membrane-bound form	NCBI 5921831	26.22	5.11	paV48BS	A	16	<i>s. map</i> <sup>h</sup>	55	interval (≠ 2.5)	paV47BS LOD 14.75 (0)
C5_088	Peroxisome proliferator activated receptor delta	NCBI 2137629	32.63	6.30	aV268BS	A	16	<i>s. map</i> <sup>h</sup>	62	interval (≠ 2.5)	Prrm1 LOD 10.87 (7.56)
C4_185	Phosphomannomutase	NCBI 4105149	28.40	5.89	mV125BS	A	16	<i>s. map</i>	64	interval (≠ 2.5)	Prrm1 LOD 11.41 (7.29)
C6_059			33.91	7.37	mV234BS	A	16		64	≠ 2.5	mbacr10p3 LOD 17.16 (0)
A4_207			74.20	5.86	mV360BS	A	16		62	interval (≠ 2.5)	Prrm1 LOD 10.87 (7.56)
E3_106			10.18	5.24	paV32BS	A	16		36	linked to chr	paV47BS LOD 4.15 (14.92)
B5_254			53.30	6.13	aV483BS	A	16		59	linked to chr	mbacr10p3 LOD 5.25 (21.24)
A5_288	Transketolase	SP P40142	72.09	6.65			16	<i>Tkt</i>			
D3_200	cDNA clone image: 2182265 (5') similar to Brain acetylcholinesterase putative membrane acnchor	NCBI 5860834	14.62	5.17	mV347BS	A	17	<i>s. map</i>	63	interval (≠ 2.5)	bir42m17, cr9h7 LOD 18.96 (0)
B5_523	Cytosolic acyl coenzyme A thioester hydrolase	SP Q64559	40.63	6.52	paV410BS	A	17	<i>s. map</i>	35	≠ 2.5	D17Mit25 LOD 9.90 (0)
B6_339	Cytosolic acyl coenzyme A thioester hydrolase	EMBL U49694	42.11	6.73							
C6_274	Proteasome component C5	SP O09061	26.86	6.98	mV191BS	A	17	<i>Psmb1</i> <sup>g</sup>	64	2.2	
B5_519	T-complex protein 1x	NCBI 539926	40.70	6.64	paV413BS	A	17	<i>Tcp1-rs1</i> <sup>g</sup>	60	interval (≠ 2.5)	D17Mit25 LOD 14.39 (1.85)
C6_192	3,2-Trans-Enoyl-coA isomerase, mitochondrial	NCBI 1169205	29.06	7.03	mV220BS	A	17	<i>s. map</i>	64	interval (≠ 2.5)	bir42m17, cr9h7 LOD 19.27 (0)
C4_136	unknown protein	NCBI 2183321	29.92	5.65	mV95BS	A	17	<i>s. map</i>	57	≠ 2.5	
B4_078			61.36	5.79	mV82BS	A	17		64	interval (≠ 2.5)	D17Mit25 LOD 15.56 (1.72)
D2_259			14.62	4.89	mV126BS	A	17		64	interval (≠ 2.5)	bir42m17, cr9h7 LOD 19.27 (0)
B6_064			58.77	6.96	mV273BS	A	17		64	2.4	
A5_100			93.75	6.33	mV288BS	A	17		57	2.4	

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	Name <sup>b</sup>	Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
C4_339			26.14	5.63	paV45BS	A	17		49	interval (± 2.5)	D17Mit9 LOD 9.99 (4.65) mV273BS LOD 11.12 (4.26) cr16i7 LOD 10.84 (4.35)
B6_362			40.78	6.88	paV433BS	A	17		59	interval (± 2.5)	D17Mit25 LOD 12.54 (3.85)
B6_371			40.55	6.75	aV438BS	A	17		55	interval (± 2.5)	D17Mit25 LOD 7.33 (13.41)
B4_072			62.20	6.07	paV500BS	A	17		58	± 2.5	
C3_358	Lactoylglutathione lyase	SP Q04760	26.25	5.13			17	<i>Glo1</i>			
C6_331	Manganese superoxide dismutase, mitochondrial	EMBL Z18857	25.25	7.07			17	<i>Sod2</i>			
C6_338	Manganese superoxide dismutase, mitochondrial	EMBL Z18857	25.20	6.95			17	<i>Sod2</i>			
C3_146	Apolipoprotein E	NCBI 114041	31.43	5.51	mV123BS	A	18	<i>s. map<sup>h</sup></i>	64	± 2.5	mV10BS LOD 19.27 (0)
B3_113	dnaK-type molecular chaperone, mitochondrial <sup>l</sup>		61.19	5.22	mV84BS	A	18	<i>s. map</i>	63	± 2.5	mV56BS LOD 18.96 (0)
B3_144	dnaK-type molecular chaperone, mitochondrial	NCBI 1072476	59.09	5.22	"	A	18	<i>s. map</i>	63	± 2.5	mV56BS LOD 18.96 (0)
B3_669	dnaK-type molecular chaperone, mitochondrial <sup>l</sup>		41.22	5.13	mV56BS	A	18	<i>s. map</i>	64	± 2.5	
B3_505	dnaK-type molecular chaperone, mitochondrial <sup>l</sup>		40.89	5.13	"	A	18	<i>s. map</i>	64	± 2.5	
B7_120	Ferrochelataase <sup>l</sup>		42.19	7.86	mV264BS	A	18	<i>Fech<sup>g</sup></i>	64	2.3	
B7_118	Ferrochelataase	NCBI 193271	42.19	7.81	"	A	18	<i>Fech<sup>g</sup></i>	64	2.3	
B7_119	Ferrochelataase	NCBI 193271	42.19	7.74	"	A	18	<i>Fech<sup>g</sup></i>	64	2.3	
B3_142	Heat shock protein 74kD, A (Mitochondrial stress-70 protein)	NCBI 6754256	59.73	5.53	mV308BS	A	18	<i>Hspa74<sup>g</sup></i>	53	interval (± 2.5)	mV56BS LOD 12.26 (3.92)
B3_123	Heat shock protein 74kD, A (Mitochondrial stress-70 protein)	NCBI 6754256	60.17	5.53	"	A	18	<i>Hspa74<sup>g</sup></i>	53	interval (± 2.5)	mV56BS LOD 12.26 (3.92)
A3_368	Heat shock protein 74kD, A (Mitochondrial stress-70 protein)	SP P38647	74.00	5.47			18	<i>Hspa74</i>			
B6_495	Hydroxysteroid 17-beta dehydrogenase 4	NCBI 6680287	36.46	6.97	paV426BS	A	18	<i>s. map</i>	64	2.0	
D3_152	Triosephosphate isomerase	SP P17751	16.24	5.54	aV19BS	A	18	<i>s. map<sup>h</sup></i>	64	linked to chr	D18Nds1, D18Mit25 LOD 3.23 (35.51)
D3_222			15.09	5.30	mV7BS	A	18		64	± 2.5	mV10BS LOD 19.27 (0)
D3_192			15.05	5.53	mV10BS	A	18		64	± 2.5	
C4_081			32.19	5.82	mV23BS	A	18		64	± 2.5	mV10BS LOD 19.27 (0)
B3_168			58.27	5.18	mV85BS	A	18		44	linked to chr	mV56BS LOD 6.48 (12.89)
C4_123			30.59	5.71	mV124BS	A	18		64	± 2.5	mV10BS LOD 19.27 (0)
A6_026			85.11	6.99	mV282BS	A	18		64	interval (± 2.5)	paV426BS LOD 17.03 (1.59)
C2_077			33.21	4.53	paV104BS	A	18		41	1.9	
C5_322			25.52	6.22	paV240BS	A	18		59	± 2.5	
B6_084	Aldehyde dehydrogenase, cytosolic	SP P24549	56.42	6.76	mV268BS	A	19	<i>Aldh1<sup>g</sup></i>	64	± 2.5	D19Ler1 LOD 14.75
B3_158	α-Internexin neuronal intermediate filament protein <sup>l</sup>		59.00	5.41	mV81BS	A	19	<i>s. map</i>	64	interval (± 2.5)	D19Nds1 LOD 12.63 (2.08)
B3_150	α-Internexin neuronal intermediate filament protein <sup>l</sup>		59.18	5.47	"	A	19	<i>s. map</i>	64	± 2.5	D19Nds1 LOD 12.63 (2.08)
B3_149	α-Internexin neuronal intermediate filament protein	NCBI 609535	59.09	5.52	"	A	19	<i>s. map</i>	64	± 2.5	D19Nds1 LOD 12.63 (2.08)
C3_456	Creatine kinase b chain	NCBI 417208	33.50	5.24	paV141BS	A	19	<i>s. map<sup>h</sup></i>	58	interval (2.0)	aV163BS LOD 8.33 (12.31)
C3_073	Creatine kinase b chain	NCBI 417208	33.38	5.24	"	A	19	<i>s. map<sup>h</sup></i>	58	interval (2.0)	aV163BS LOD 8.33 (12.31)
C4_224	1-Cys peroxiredoxin protein	NCBI 4139186	27.42	6.03	aV51BS	A	19	<i>s. map</i>	62	interval (± 2.5)	Fth LOD 9.58 (6.68)
C5_106	Glutathione-S-transferase homolog	NCBI 6016174	32.02	6.37	aV269BS	A	19	<i>s. map</i>	63	interval (± 2.5)	D19Nds1 LOD 10.84 (4.35)
C3_453	Glutathione-S-transferase P1	NCBI 576133	23.40	5.36	mV18BS	A	19 / 1	<i>(Gstp2)<sup>g</sup></i>	62	interval (± 2.5)	bir51e8 LOD 15.85 (1.70)
C4_323	Glutathione-S-transferase P1	NCBI 576133	23.94	5.62	mV53BS	A	19 / 1	<i>(Gstp2)<sup>g</sup></i>	23	interval (± 2.5)	bir51e8 LOD 6.92
C5_330	Glutathione-S-transferase P1	NCBI 576133	25.28	6.48	mV212BS	A	19 / 1	<i>(Gstp2)<sup>g</sup></i>	60	interval (± 2.5)	bir51e8 LOD 15.27 (1.75)
D4_149	Glutathione-S-transferase P1	NCBI 576133	14.26	6.03	mV13BS	A	19 / 2	<i>s. map<sup>h</sup></i>	47	interval (± 2.5)	bir51e8 LOD 9.30 (6.83)
C5_360	Glutathione-S-transferase P1	NCBI 576133	24.26	6.32	mV183BS	A	19 / 3	<i>s. map<sup>h</sup></i>	63	interval (± 2.5)	bir51e8 LOD 14.54 (3.39)
C5_366	Glutathione-S-transferase P1	NCBI 576133	24.16	6.32	"	A	19 / 3	<i>s. map<sup>h</sup></i>	63	interval (± 2.5)	bir51e8 LOD 14.54 (3.39)
C6_296	Glutathione-S-transferase P1	SP P19157	26.17	6.84			19	<i>Gstp2</i>			
B3_333	Guanine deaminase	NCBI 5738216	50.27	5.46	mV71BS	A	19	<i>s. map</i>	64	± 2.5	D19Ler1 LOD 14.75

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B3_383	Guanine deaminase <sup>1</sup>		48.21	5.46	"	A	19	<i>s. map</i>	64	≠ 2.5	D19Ler1 LOD 14.75
C5_383	Serum albumin	NCBI 5915682	28.34	6.25	mV136BS	A	19	<i>s. map</i> <sup>h</sup>	57	interval (≠ 2.5)	Fth LOD 7.95 (7.71)
C5_384	Serum albumin	NCBI 5915682	28.18	6.25	"	A	19	<i>s. map</i> <sup>h</sup>	57	interval (≠ 2.5)	Fth LOD 7.95 (7.71)
B4_419			43.01	5.67	mV356BS	A	19		40	interval (≠ 2.5)	D19Nds1 LOD 4.80 (11.16)
B4_137			58.36	5.61	aV163BS	A	19		63	1.9	
D7_009			21.18	8.28	paV209BS	A	19		59	interval (≠ 2.5)	Fth LOD 10.56 (4.45)
C4_214			27.77	6.08	aV251BS	A	19		49	1.9	
C6_388			26.27	7.13	paV278BS	A	19		60	interval (≠ 2.5)	bir51e8 LOD 15.27 (1.75)
D5_036	Cofilin, non-muscle isoform	SP P18760	19.34	6.51	aV518BS	C					
D5_042	Cofilin, non-muscle isoform	SP P18760	19.29	6.51	"	C					
B5_477	Aspartate aminotransferase, cytoplasmic	SP P05201	42.73	6.45			19	<i>Got1</i>			
C5_177	Phosphoglycerate mutase, brain form	SP P18669	29.52	6.54			19	<i>Pgam1</i>			
C5_185	Phosphoglycerate mutase, brain form	SP P18669	29.33	6.36			19	<i>Pgam1</i>			
C1_016	Heat shock protein cognate 70 <sup>i</sup>		27.77	4.43	mV22BS	A	x / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mV90BS LOD 18.66 (0)
C2_241	Heat shock protein cognate 70 <sup>i</sup>		27.85	4.47	"	A	x / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mV90BS LOD 18.66 (0)
C2_263	Heat shock protein cognate 70 <sup>i</sup>		27.37	4.47	"	A	x / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mV90BS LOD 18.66 (0)
C2_396	Heat shock protein cognate 70 <sup>i</sup>		27.79	4.49	"	A	x / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mV90BS LOD 18.66 (0)
C2_397	Heat shock protein cognate 70 <sup>i</sup>		27.45	4.50	"	A	x / 1	<i>s. map</i> <sup>h</sup>	62	≠ 2.5	mV90BS LOD 18.66 (0)
B1_028	Heat shock protein cognate 70	NCBI 123651	71.20	4.41	mV90BS	A	x / 1	<i>s. map</i> <sup>h</sup>	64	2.1	
B1_031	Heat shock protein cognate 70	NCBI 123651	70.80	4.39	"	A	x / 1	<i>s. map</i> <sup>h</sup>	64	2.1	
B2_034	Heat shock protein cognate 70 <sup>i</sup>		70.20	5.03	mV313BS	A	x / 2	<i>s. map</i> <sup>h</sup>	29	interval (≠ 2.5)	DXWas70 LOD 5.42 (4.35)
B2_045	Heat shock protein cognate 70	NCBI 123651	68.31	5.03	"	A	x / 2	<i>s. map</i> <sup>h</sup>	29	interval (≠ 2.5)	DXWas70 LOD 5.42 (4.35)
B2_041	Heat shock protein cognate 70 <sup>i</sup>		69.49	5.01	"	A	x / 2	<i>s. map</i> <sup>h</sup>	29	interval (≠ 2.5)	DXWas70 LOD 5.42 (4.35)
B2_025	Heat shock protein cognate 70	NCBI 123651	70.40	5.00	"	A	x / 2	<i>s. map</i> <sup>h</sup>	29	interval (≠ 2.5)	DXWas70 LOD 5.42 (4.35)
B2_039	Heat shock protein cognate 70 <sup>i</sup>		69.66	4.97	"	A	x / 2	<i>s. map</i> <sup>h</sup>	29	interval (≠ 2.5)	DXWas70 LOD 5.42 (4.35)
B3_029	Heat shock protein cognate 70 <sup>i</sup>		67.63	5.06	"	A	x / 2	<i>s. map</i> <sup>h</sup>	29	interval (≠ 2.5)	DXWas70 LOD 5.42 (4.35)
C5_227	Hypoxanthine-guanine phosphoribosyltransferase	SP P00493	28.04	6.38	mV135BS	A	x	<i>Hprt</i> <sup>g</sup>	64	interval (≠ 2.5)	DXMit81x LOD 11.95 (7.03)
C5_238	Hypoxanthine-guanine phosphoribosyltransferase <sup>1</sup>		27.99	6.38	"	A	x	<i>Hprt</i> <sup>g</sup>	64	interval (≠ 2.5)	DXMit81x LOD 11.95 (7.03)
A3_187	KIAA1167 protein	NCBI 6330176	98.52	5.16	mV105BS	A	x	<i>s. map</i>	64	≠ 2.5	DXWas70 LOD 17.16 (0)
A3_188	KIAA1167 protein	NCBI 6330176	98.89	5.14	"	A	x	<i>s. map</i>	64	≠ 2.5	DXWas70 LOD 17.16 (0)
A3_185	KIAA1167 protein <sup>1</sup>		99.26	5.11	"	A	x	<i>s. map</i>	64	≠ 2.5	DXWas70 LOD 17.16 (0)
A3_180	KIAA1167 protein <sup>1</sup>		99.26	5.09	"	A	x	<i>s. map</i>	64	≠ 2.5	DXWas70 LOD 17.16 (0)
A3_191	KIAA1167 protein <sup>1</sup>		99.26	5.07	"	A	x	<i>s. map</i>	64	≠ 2.5	DXWas70 LOD 17.16 (0)
B6_206	Pigment epithelium-derived factor	NCBI 2961472	49.14	6.91	mV247BS	A	x	<i>s. map</i>	64	interval (≠ 2.5)	bir38117 LOD 12.49 (6.79)
A6_027	Synapsin I	NCBI 6686018	84.89	7.42	sV151BS	A					
A6_024	Synapsin I <sup>1</sup>		85.78	7.23	"	A					
A6_044	Synapsin I <sup>1</sup>		81.56	7.30	"	A					
A6_022	Synapsin I <sup>1</sup>		84.89	7.41	"	A					
A6_025	Synapsin I <sup>1</sup>		85.56	7.22	"	A					
A6_043	Synapsin I <sup>1</sup>		81.78	7.28	"	A					
A6_085	Synapsin I <sup>1</sup>		85.56	7.41	"	A					
A6_020	Synapsin I <sup>1</sup>		85.78	7.17	"	A					
A6_039	Synapsin I <sup>1</sup>		82.22	7.24	"	A					
A6_023	Synapsin I <sup>1</sup>		84.44	7.38	"	A					
A6_021	Synapsin I <sup>1</sup>		86.00	7.13	"	A					
A6_038	Synapsin I <sup>1</sup>		82.22	7.24	"	A					
A6_086	Synapsin I <sup>1</sup>		85.11	7.37	"	A					
A6_017	Synapsin I <sup>1</sup>		86.00	7.10	"	A					
A6_040	Synapsin I <sup>1</sup>		82.44	7.19	"	A					



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A6_087	Synapsin I		85.11	7.37	"	A				
A6_019	Synapsin I		85.33	7.32	"	A				
A6_018	Synapsin I		86.00	7.06	"	A				
A6_089	Synapsin I		85.56	7.31	"	A				
A6_016	Synapsin I		85.33	7.28	"	A				
A6_041	Synapsin I		81.33	7.38	"	A				
A6_088	Synapsin I		81.33	7.39	"	A				
A6_090	Synapsin I		85.56	7.27	"	A				
A6_042	Synapsin I		81.56	7.34	"	A				
A7_009	Synapsin I		84.67	7.58	"	A				
A7_011	Synapsin I	SP P09951	80.89	7.59	"	A				
A7_008	Synapsin I		84.67	7.52	"	A				
A7_015	Synapsin I		80.67	7.55	"	A				
A7_007	Synapsin I		84.67	7.46	"	A				
A7_012	Synapsin I		80.89	7.50	"	A				
A7_017	Synapsin I		80.89	7.83	"	A				
A7_016	Synapsin I		80.89	7.49	"	A				
A7_019	Synapsin I		80.44	7.73	"	A				
A7_010	Synapsin I		81.11	7.43	"	A				
A7_020	Synapsin I		80.67	7.66	"	A				
A7_013	Synapsin I		81.11	7.44	"	A				
A7_018	Synapsin I		80.67	7.70	"	A				
A7_014	Synapsin I		80.67	7.62	"	A				
E3_094			9.37	5.18	mV16BS	A	x		49	linked to chr mV90BS LOD 7.74 (11.41)
D7_001			22.47	7.79	mV176BS	A	x		52	interval (± 2.5) DXMit8 LOD 6.35 (14.74)
B6_204			49.30	6.82	mV245BS	A	x		61	interval (± 2.5) bir38117 LOD 8.68 (13.29)
B6_054			59.43	7.09	mV277BS	A	x		49	linked to chr DXMit8 LOD 3.19 (29.39)
B3_667			45.04	5.06	paV131BS	A	x		44	interval (2.2) DXMit54 LOD 7.83 (0)
B3_439			44.88	5.06	"	A	x		44	interval (2.2) DXMit54 LOD 7.83 (0)
B5_439	Phosphoglycerate kinase I	SP P09411	44.38	6.42			x	<i>Pgk1</i>		
D5_068	Nucleoside diphosphate kinase A	SP P15532	17.77	6.34	aV232BS	A				
D5_071	Nucleoside diphosphate kinase A	SP P15532	17.70	6.34	"	A				
D5_083	Nucleoside diphosphate kinase A	SP P15532	16.95	6.34	"	A				
D5_085	Nucleoside diphosphate kinase A	SP P15532	16.89	6.34	"	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				

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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					
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					
B5_251	4-aminobutyrat aminotransferase, mitochondrial	SP P50554	53.02	6.68	aV464BS	B					
B6_130	4-aminobutyrat aminotransferase, mitochondrial	SP P50554	52.83	6.78							
D4_136					mV44BS	B					
B4_445					mV46BS	B					
C3_400					mV87BS	B					
D5_035					mV167BS	B					
D5_102					mV170BS	B					
D5_122					mV171BS	B					
E5_006					"	B					
C5_405					mV188BS	B					
C5_336					"	B					
C6_355					mV193BS	B					
C7_188					mV198BS	B					
C5_406					mV207BS	B					
C5_407					mV208BS	B					
C3_016					mV216BS	B					
B5_677					mV225BS	B					
B5_526					mV240BS	B					
B6_128					mV249BS	B					
B6_169					mV250BS	B					
B6_202					mV251BS	B					
B6_264					mV254BS	B					
B6_290					mV256BS	B					
B6_298					mV257BS	B					
B6_336					mV261BS	B					
B6_077					mV270BS	B					
B6_083					"	B					
B6_037					mV278BS	B					
B6_052					"	B					
A5_258					mV295BS	B					
E2_101					mV303BS	B					
B4_098					mV307BS	B					
C4_148					mV317BS	B					
C3_184					mV318BS	B					

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
C3_260					mV319BS	B				
D2_010					mV320BS	B				
C2_054					mV323BS	B				
A3_053					mV324BS	B				
A3_055					"	B				
A2_039					mV325BS	B				
A2_041					"	B				
A2_042					"	B				
B3_364					mV345BS	B				
B4_102					mV353BS	B				
B4_117					"	B				
B2_474					mV354BS	B				
B2_490					"	B				
C2_165					mV370BS	B				
E3_105					paV1BS	B				
D3_102					aV2BS	B				
D3_117					"	B				
E4_074					aV4BS	B				
E3_046					aV8BS	B				
D3_216					aV12BS	B				
D3_210					"	B				
E3_005					aV13BS	B				
C2_398					paV14BS	B				
E2_030					paV15BS	B				
D2_289					paV20BS	B				
D2_287					paV21BS	B				
D4_021					paV24BS	B				
D3_031					aV25BS	B				
D3_052					"	B				
D2_018					aV27BS	B				
C4_353					paV30BS	B				
C4_354					paV31BS	B				
E3_059					aV33BS	B				
E2_048					paV34BS	B				
D3_225					paV36BS	B				
C4_260					aV37BS	B				
C4_355					"	B				
C4_302					aV38BS	B				
C4_296					aV39BS	B				
C4_230					aV40BS	B				
C4_240					"	B				
C4_254					"	B				
C4_268					paV42BS	B				
C4_269					"	B				
C3_468					paV43BS	B				
C3_438					aV44BS	B				
C3_413					aV46BS	B				
C2_171					aV49BS	B				
C4_207					aV55BS	B				
C4_162					aV56BS	B				
C4_196					paV61BS	B				
C4_204					paV62BS	B				
C4_160					paV64BS	B				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
C4_169					"	B				
C3_289					aV66BS	B				
C3_300					aV67BS	B				
C3_221					aV69BS	B				
C3_247					aV70BS	B				
C3_241					aV71BS	B				
C3_297					aV72BS	B				
C3_315					aV74BS	B				
C3_469					aV75BS	B				
C3_471					paV76BS	B				
C3_470					"	B				
C3_216					aV77BS	B				
C2_282					aV79BS	B				
C1_014					aV80BS	B				
C1_011					"	B				
C1_013					"	B				
C1_015					"	B				
C1_017					"	B				
C4_069					aV82BS	B				
C4_108					aV83BS	B				
C4_352					paV84BS	B				
C3_170					paV90BS	B				
C3_075					aV92BS	B				
C3_099					aV93BS	B				
C3_066					aV96BS	B				
C3_467					paV97BS	B				
C2_185					paV98BS	B				
C2_127					aV99BS	B				
C2_143					aV100BS	B				
C3_466					paV101BS	B				
C2_096					paV103BS	B				
B4_582					aV106BS	B				
B4_545					aV107BS	B				
B4_531					paV108BS	B				
B3_658					aV111BS	B				
C3_021					aV112BS	B				
B4_605					paV121BS	B				
B4_373					paV122BS	B				
B4_489					aV126BS	B				
B2_482					aV127BS	B				
B2_406					aV128BS	B				
B3_529					aV132BS	B				
B2_302					paV135BS	B				
B2_371					aV136BS	B				
B2_350					aV137BS	B				
B3_405					aV142BS	B				
B3_406					"	B				
B3_675					paV143BS	B				
B4_111					aV144BS	B				
B3_553					paV145BS	B				
C3_070					aV148BS	B				
C4_046					aV150BS	B				
B4_160					aV151BS	B				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
B4_317					aV155BS	B				
B4_165					aV156BS	B				
C4_003					aV158BS	B				
C4_014					"	B				
B4_262					aV159BS	B				
B4_162					aV162BS	B				
B3_678					paV164BS	B				
B3_214					aV166BS	B				
B3_281					paV167BS	B				
B3_677					paV169BS	B				
B3_676					paV169BS	B				
B3_118					paV177BS	B				
B3_674					paV178BS	B				
A3_394					aV181BS	B				
B3_010					"	B				
B3_030					"	B				
B4_606					paV182BS	B				
A3_137					aV183BS	B				
A3_128					"	B				
A3_125					"	B				
A4_047					"	B				
A4_043					"	B				
A4_044					"	B				
A3_309					aV185BS	B				
A3_312					"	B				
A3_344					paV186BS	B				
A3_396					paV188BS	B				
B4_395					aV192BS	B				
B4_378					aV193BS	B				
B1_032					paV194BS	B				
B2_175					paV195BS	B				
B2-189					"	B				
B2_534					paV196BS	B				
B2_535					"	B				
B2_536					"	B				
B2_533					paV197BS	B				
E8_047					paV199BS	B				
E8_016					aV200BS	B				
E8_009					aV201BS	B				
D7_096					aV203BS	B				
D7_061					aV204BS	B				
D7_050					aV205BS	B				
D7_045					aV206BS	B				
D7_102					paV207BS	B				
D7_101					paV208BS	B				
D6_066					paV210BS	B				
D6_164					paV211BS	B				
D6_165					paV212BS	B				
D6_142					paV213BS	B				
D6_143					aV214BS	B				
D6_154					aV215BS	B				
D6_163					paV216BS	B				
D6_161					paV217BS	B				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
D6_162					paV217BS	B				
D6_034					aV218BS	B				
D5_024					aV219BS	B				
D6_119					aV221BS	B				
D6_166					paV222BS	B				
D6_167					"	B				
E5_028					aV226BS	B				
D5_018					aV230BS	B				
D5_133					paV233BS	B				
D5_132					"	B				
D5_134					paV235BS	B				
E5_076					paV236BS	B				
E5_022					aV238BS	B				
C5_368					aV239BS	B				
C5_372					"	B				
C5_320					aV241BS	B				
C5_397					paV243BS	B				
C5_313					aV245BS	B				
C5_398					"	B				
C5_291					paV246BS	B				
C5_404					paV248BS	B				
C5_410					paV249BS	B				
C5_263					paV252BS	B				
C5_403					paV254BS	B				
C5_261					aV256BS	B				
C5_147					aV259BS	B				
C5_161					"	B				
C5_205					aV260BS	B				
C5_216					"	B				
C5_090					aV262BS	B				
C5_396					aV263BS	B				
C5_395					paV265BS	B				
C5_408					paV267BS	B				
C5_402					"	B				
C5_401					paV270BS	B				
C5_399					paV272BS	B				
C6_368					aV273BS	B				
C6_282					aV275BS	B				
C6_405					paV279BS	B				
C6_400					paV280BS	B				
C6_254					paV281BS	B				
C6_257					aV282BS	B				
C6_249					"	B				
C6_403					paV283BS	B				
C6_245					aV284BS	B				
C6_390					aV285BS	B				
C6_399					paV286BS	B				
C6_398					paV287BS	B				
C5_400					paV289BS	B				
C6_211					aV290BS	B				
C6_212					"	B				
C6_401					paV295BS	B				
C6_402					paV296BS	B				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
C6_404					paV297BS	B				
C6_221					paV298BS	B				
C6_101					paV377BS	B				
C6_146					aV378BS	B				
C6_125					aV379BS	B				
C6_397					paV382BS	B				
C6_066					paV383BS	B				
C7_128					aV388BS	B				
C7_210					paV389BS	B				
C7_159					aV390BS	B				
C7_122					paV391BS	B				
C7_209					paV392BS	B				
C7_097					aV393BS	B				
B5_549					paV401BS	B				
B5_566					aV402BS	B				
B5_719					aV403BS	B				
B5_620					aV404BS	B				
B5_630					aV404BS	B				
B5_565					aV405BS	B				
B5_720					aV406BS	B				
B5_619					aV407BS	B				
B5_627					"	B				
B5_590					aV409BS	B				
B5_604					"	B				
B5_617					aV409BS	B				
B5_494					aV414BS	B				
B5_717					paV416BS	B				
B5_718					"	B				
B5_716					paV418BS	B				
B6_505					paV422BS	B				
B6_500					paV423BS	B				
C6_008					paV424BS	B				
B6_439					aV427BS	B				
B6_428					paV428BS	B				
B6_524					paV429BS	B				
B6_523					paV430BS	B				
B6_296					paV434BS	B				
B6_525					paV435BS	B				
B6_374					aV436BS	B				
B6_356					aV437BS	B				
B6_522					paV439BS	B				
B6_180					paV441BS	B				
B6_108					paV442BS	B				
B6_157					paV443BS	B				
B6_518					paV444BS	B				
B6_519					paV445BS	B				
B6_184					aV446BS	B				
B6_196					paV447BS	B				
B6_242					aV448BS	B				
B6_230					aV449BS	B				
B6_520					paV450BS	B				
B6_521					"	B				
A5_350					paV451BS	B				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
A5_255					paV452BS	B				
A5_313					aV453BS	B				
A5_292					aV454BS	B				
A5_289					"	B				
A5_278					aV455BS	B				
A5_275					"	B				
A5_233					aV456BS	B				
A5_215					aV457BS	B				
A5_349					paV458BS	B				
A5_351					paV459BS	B				
A5_093					aV460BS	B				
A5_099					aV461BS	B				
A5_109					aV462BS	B				
B5_398					paV469BS	B				
B5_715					paV470BS	B				
B5_714					paV471BS	B				
B5_361					paV472BS	B				
B5_285					paV473BS	B				
B5_229					paV474BS	B				
B5_249					aV475BS	B				
B5_255					aV476BS	B				
B5_239					aV477BS	B				
B5_222					aV478BS	B				
B5_237					aV479BS	B				
B5_319					aV480BS	B				
B5_223					aV481BS	B				
B5_308					aV482BS	B				
B5_210					aV484BS	B				
B4_189					paV485BS	B				
B5_165					aV487BS	B				
B5_121					paV488BS	B				
B5_713					paV489BS	B				
B6_526					paV490BS	B				
B6_016					paV491BS	B				
B4_115					aV497BS	B				
B4_604					aV499BS	B				
B5_005					aV501BS	B				
A5_352					paV502BS	B				
A5_342					paV503BS	B				
B5_141					paV504BS	B				
B5_084					aV506BS	B				
B5_085					aV506BS	B				
B5_022					paV508BS	B				
B5_083					paV510BS	B				
B5_492	Cytosolic acyl coenzyme A thioester hydrolase	EMBL U49694			aV415BS	C				
D6_073					mV162BS	C				
D6_124					mV163BS	C				
E6_004					mV164BS	C				
E6_020					mV165BS	C				
D4_074					mV166BS	C				
D5_059					mV186BS	C				
D5_130					mV187BS	C				
C5_367					mV189BS	C				



2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
C7_141					mV205BS	C				
C5_166					mV213BS	C				
C4_054					mV224BS	C				
C4_060					mV224BS	C				
C5_050					mV228BS	C				
B6_498					mV230BS	C				
C6_002					mV231BS	C				
C6_019					mV231BS	C				
C6_024					mV231BS	C				
C6_009					mV231BS	C				
C6_022					mV231BS	C				
C6_029					mV231BS	C				
B5_623					mV243BS	C				
B6_171					mV252BS	C				
B6_174					mV252BS	C				
B6_246					mV253BS	C				
B6_260					mV255BS	C				
D4_142					mV302BS	C				
E2_047					mV305BS	C				
B6_387					mV326BS	C				
B6_492					mV327BS	C				
D3_199					mV328BS	C				
D1_052					mV329BS	C				
D3_224					mV330BS	C				
C4_327					mV331BS	C				
C3_402					mV333BS	C				
C3_306					mV334BS	C				
C4_197					mV335BS	C				
C4_116					mV336BS	C				
C3_158					mV337BS	C				
C3_472					mV338BS	C				
C3_464					mV339BS	C				
D3_006					mV340BS	C				
D3_030					"	C				
C3_194					mV341BS	C				
C3_202					"	C				
B4_476					mV342BS	C				
B3_355					mV344BS	C				
B3_257					mV346BS	C				
B5_280					mV371BS	C				
C2_023					aV115BS	C				
B4_347					paV123BS	C				
B4_337					"	C				
B2_392					aV139BS	C				
B2_403					"	C				
B2_397					"	C				
B2_410					"	C				
B4_173					aV146BS	C				
B4_174					"	C				
B4_195					aV147BS	C				
B4_131					aV149BS	C				
B4_086					aV154BS	C				
B3_673					paV168BS	C				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
E4_054					aV301BS	C				
D4_116					aV302BS	C				
D4_143					aV303BS	C				
D4_139					aV304BS	C				
D4_161					paV305BS	C				
D4_133					paV306BS	C				
D4_152					paV307BS	C				
E4_081					aV308BS	C				
D3_085					aV309BS	C				
D3_077					aV310BS	C				
D3_169					aV311BS	C				
D3_185					aV312BS	C				
D3_180					paV313BS	C				
E3_076					aV314BS	C				
D2_168					aV315BS	C				
D2_102					paV316BS	C				
D2_177					aV317BS	C				
D2_220					aV318BS	C				
E2_100					aV319BS	C				
E2_099					paV320BS	C				
D2_286					paV321BS	C				
D1_035					aV322BS	C				
E2_062					aV323BS	C				
D4_052					aV324BS	C				
D2_020					aV326BS	C				
C1_029					aV327BS	C				
C2_327					aV329BS	C				
C2_286					aV330BS	C				
C2_297					aV330BS	C				
C2_300					aV330BS	C				
C3_310					aV331BS	C				
C3_296					aV332BS	C				
C4_350					paV333BS	C				
C2_216					aV334BS	C				
C2_195					aV335BS	C				
C2_175					aV336BS	C				
C4_181					aV337BS	C				
C4_155					paV338BS	C				
C4_152					paV339BS	C				
C2_138					paV340BS	C				
C2_156					paV341BS	C				
C2_087					paV342BS	C				
C3_463					paV343BS	C				
C3_154					paV344BS	C				
C3_163					"	C				
C3_172					"	C				
C4_351					aV346BS	C				
C4_118					aV347BS	C				
C4_059					aV349BS	C				
C4_063					"	C				
C4_040					aV350BS	C				
C4_047					"	C				
B3_619					aV351BS	C				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
B4_602					paV352BS	C				
B2_257					aV354BS	C				
B2_258					"	C				
B2_237					aV355BS	C				
B3_401					aV356BS	C				
B3_672					paV357BS	C				
B3_336					paV358BS	C				
B2_527					paV359BS	C				
B4_603					paV360BS	C				
B4_600					paV361BS	C				
B4_599					aV362BS	C				
B4_601					paV363BS	C				
B3_288					paV364BS	C				
B2_125					paV365BS	C				
B2_093					paV366BS	C				
B2_108					paV367BS	C				
B2_528					paV368BS	C				
B2_529					paV369BS	C				
B2_531					paV370BS	C				
B2_532					paV371BS	C				
B2_530					paV372BS	C				
B2_526					paV374BS	C				
C3_465					paV375BS	C				
D2_028					aV376BS	C				
B5_346					aV465BS	C				
E7_063					paV511BS	C				
E8_035					aV512BS	C				
E6_074					paV513BS	C				
D7_070					aV514BS	C				
D5_111					aV515BS	C				
D5_098					aV516BS	C				
D5_051					aV517BS	C				
D5_066					aV519BS	C				
D6_043					aV520BS	C				
C5_394					aV521BS	C				
C5_361					aV522BS	C				
C5_365					aV522BS	C				
C5_329					aV523BS	C				
C5_344					aV524BS	C				
C5_340					aV525BS	C				
C5_312					aV526BS	C				
C6_341					aV527BS	C				
C6_289					aV528BS	C				
C6_335					aV529BS	C				
C6_293					aV530BS	C				
C7_155					paV531BS	C				
C7_123					paV532BS	C				
C5_391					paV533BS	C				
C5_392					"	C				
C5_393					"	C				
C5_204					aV536BS	C				
C5_172					aV537BS	C				
C6_395					paV538BS	C				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten			GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten
C6_199					aV539BS	C				
C6_195					aV540BS	C				
C6_394					paV541BS	C				
C6_393					paV542BS	C				
C6_386					paV543BS	C				
C6_140					aV544BS	C				
C6_144					"	C				
C5_389					paV545BS	C				
C5_390					aV546BS	C				
B5_673					aV547BS	C				
B5_712					paV548BS	C				
B5_631					aV549BS	C				
B5_652					"	C				
B5_582					aV550BS	C				
B6_516					aV551BS	C				
B6_517					paV552BS	C				
C6_014					aV553BS	C				
B7_174					paV554BS	C				
C7_014					aV555BS	C				
B4_598					paV556BS	C				
B5_710					paV557BS	C				
B5_571					aV558BS	C				
B5_711					paV559BS	C				
B5_538					aV560BS	C				
B5_529					aV561BS	C				
B5_537					aV562BS	C				
B5_568					aV563BS	C				
B5_455					aV565BS	C				
B5_402					aV566BS	C				
B5_722					paV567BS	C				
B5_371					paV568BS	C				
B5_385					aV569BS	C				
B5_384					aV570BS	C				
B6_345					aV571BS	C				
B6_514					paV572BS	C				
B6_515					paV573BS	C				
B6_274					aV575BS	C				
B6_380					aV576BS	C				
B5_708					aV577BS	C				
B5_266					paV578BS	C				
B5_204					paV579BS	C				
B5_187					aV580BS	C				
B5_709					paV581BS	C				
B5_107					paV582BS	C				
B5_098					paV584BS	C				
B5_097					aV585BS	C				
B5_247					aV586BS	C				
B5_259					aV587BS	C				
B5_707					paV589BS	C				
B5_162					paV590BS	C				
B5_705					paV591BS	C				
B6_055					aV592BS	C				
B6_053					aV593BS	C				

2-DE Spot-No <sup>a</sup>	Name <sup>b</sup>	Proteinspots			Varianten				GENE MAPPING		
		Accession	Mr (kDa) (gel)	pI (gel)	Varianten-No <sup>d</sup>	Kategorien genetischer Signifikanz <sup>e</sup>	Chr. No / position <sup>f</sup>	Gen- Locus	Zahl der B <sub>1</sub> -Tiere	Log likelihood ratios fuer die Reihenfolge der Varianten	LOD score and genet. Abstand (cM) der Variante zur Position eines Markers/einer Variante
B6_044					paV594BS	C					
B5_019					aV595BS	C					
A5_296					aV596BS	C					
A6_071					aV597BS	C					
A5_196					aV598BS	C					
A5_346					paV599BS	C					
A5_347					aV600BS	C					
A5_348					paV601BS	C					
C3_377					paV602BS	C					