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Mouse Chromosome 11

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Introduction

A consensus map of Chromosome 11 (Chr 11) was constructed from data from several multilocus genetic crosses as a foundation (Buchberg et al. 1989). The first update to the map included 20 new loci (Buchberg et al. 1991). In the second update reported here, over 100 new loci have been placed on the map. The largest class of new markers are anonymous sequences that can be typed by PCR (Miller et al. 1992). This report is to be used as a guide, to assist the readers in locating the primary resources relevant to their area of interest on Chr 11. Readers should give great attention to the primary data because substantial error in the consensus map is often unavoidable in cases where loci have not been mapped relative to one another. For example, the localization of microsatellite markers on well-characterized interspecific backcross panels will improve the accuracy of their integration into the consensus map (Buchberg et al. 1988; Miller et al. 1992). Similarly, the position of mutant loci relative to molecular markers has been determined in only a few cases, including *wr, df, spd, Tr,* and *Re* (Buchberg et al. 1988; Buckwalter et al. 1991, 1993; Kaupmann et al. 1992; Nadeau et al. 1990). Thus, most of the mutants on Chr 11 can be placed only approximately relative to molecular markers. An exciting development for Chr 11 this year was the identification of the lesion responsible for a classical mutation. *Tr* (trembler) was shown to be a defect in a peripheral myelin protein (*Pmp-22*) (Suter et al. 1992a, 1992b).

Locus list

Over 260 loci are now assigned to Chr 11 (Table 1). The new gene assignments include several kinases [the beta subunit of calmodulin kinase II (*Camk2b*), a creatine kinase (*Ck-rs5*), an FMS-like tyrosine kinase (*Flt-4*), and glucokinase (*Gk*)]; several receptors and transporters [the gamma-2 subunit of the $GABA_A$ receptor (*Gabrg-2*), a glutamate receptor (*Glr-1*), an insulin-responsive glucose transporter (*Glut-4*), serotonin transporter (*Htt*)]; and a variety of other genes including apolipoprotein H (*Apoh*), dopa decarboxylase (*Ddc*), connexin 45 (*Gja-7*), a guanine nucleotide binding protein (*Gna-l3*), two integrin genes (*Gp3a, Gp2b*), sequences related to histone 2b and high mobility group proteins (*Hist2b-rs1, Hmg14-rs4*), an additional gene in the keratin complex (*Krt-1.14*), a mesenchyme homeobox localized near the *Hox-2* cluster (*Mox-1*), a P40-related sequence (*P40-rs5*), a ras-related gene (*Rab-1*), a guanylate cyclase activator (*Rcvrn*), a ribosomal RNA gene cluster and ribosomal protein related sequence (*Rnr11, Rpl18-rs*), a β-spectrin gene (*Spnb-2*), a T-cell transcription factor (*Tcf-1*), a protease inhibitor (*Timp-2*), and topoisomerase II (*Top-2*).

Consensus map

A consensus map has been constructed (Buchberg et al. 1991) and updated (Fig. 1). Every effort has been made to include loci on the consensus map; however, loci were placed at the bottom of the map if they were mapped only in two-point linkages or solely by in situ hybridization, or assigned on the basis of analysis of somatic cell hybrids. One locus previously assigned to Chr 11 has been localized: *Anx-6* (formerly *Cabm*; Buckwalter and Camper 1992). Gene order is certain only for loci that have been mapped relative to one another in the same cross (Table 2). Gene order is ambiguous for some loci mapped by analysis of RI strain data, although RI strains suggest a gene order in some cases where it could not be determined in backcrosses (Table 4). The placement of several loci has been modified in this update, reflecting an improved knowledge of gene order. For example, the locations of *Rnula-1* and *AntP91a* on the consensus map have been significantly changed. Additionally, the positions

*Chair of Committee for Mouse Chromosome 11

Table 1. Locus list for mouse Chr 11.

New	Symbol	Name	A	M (cM)	T	Method	H. symbol	H. location	References
	Ace	angiotensin converting enzyme, (***D11Mit13***)		62	D	L	ACE1	17q23	71, 170
	Acrb	acetylcholine receptor beta (***Achr-2, D11Mit29, D11Mit31***)	1	42	D	L	CHRNB	17p12-p11	109, 18
	Achr-2	***See Acrb***							
	Adra-1	adrenergic receptor, alpha-1	1	19	D	S,L	ADRA1	5q32-q34	275
	Ahd-4	aldehyde dehydrogenase-4		33	B	L	ALDH3	17	168, 225
	Ahd-6	aldehyde dehydrogenase-6		26	B	L			220
	Akv-4	***See Emv-14***							
	Al	alopecia		52	V	L			68
	Amog	***See Atp1b2***							
	AntP91a	tumor-specific transplantation antigen (***D11Mit14***)		57	D	L			71
*	*Anx-6*	annexin-6 (formerly calcium binding membrane (*Cabm*) and *p68*		19	D	L	ANX-6	5q32-34	61, 42
*	*Apoh*	apolipoprotein H (beta-2-glycoprotein-1)		62	D	L, I	APOH	17q23-qter	198
	Asgr-1	asialoglycoprotein receptor-1		37	D	L	ASGR1	17p13-p11	224, 223
	Asgr-2	asialoglycoprotein receptor-2		37	D	L	ASGR2	17p	224, 118
	Atp1b2	Na,K-ATPase beta-2 (***Amog***)		41	D	S,L	ATP1B2	17p	204, 118
	Bda	bald-arthritic		58	V	L			83
	Brp8	brain protein-8 (provisional)		53	D	L			94
	Bsk	bare skin		58	V	L			160
	Cabm	formerly calcium binding protein, p68. See ***Anx-6***							
*	*Camk2b*	calmodulin kinase II, beta subunit		0	D	L, S			59, 136
	Chy	chylous ascites		26	B	L			161
*	*Ck-rs5*	creatine kinase, brain-related sequence5		17	D	L			50
	Cnp-1	cyclic nucleotide phosphodiesterase-1		59	D	L	CNP	17q21	19
	co	cocked		bt	V	L			207
	Cod	cerebellar outflow degeneration		75	V	L			196
	Cola-1	procollagen type I, alpha 1 (***Mov-13***)		56	D	I, L	COL1A1	17q21.3-q22	236, 256
	Cryb1	crystallin, beta polypeptide 1		46	D	L	CRYB1	17q11.1-q12	35, 274
	Csfg	colony stimulating factor, granulocyte		57	D	L	CSF3	17q11.2-q12	32, 258
	Csfgm	colony stimulating factor, granulocyte macrophage	1	29	D	S,L,P	CSF2	5q23-q31	95, 208
	Csfmu	colony stimulating factor, multi (contains ***Il-3***)		29	B	L			122, 120
	D11Bay1	DNA segment, Chr 11, Baylor-1		bt	D	S	D17S28	17p13.3	153
	D11Bay2	DNA segment, Chr 11, Baylor-2		45	D	S,L	D17S5	17p13.3	153
*	*D11Bir1*	DNA segment, Chr 11, Birkenmeier-1		53	D	L			22
*	*D11Byu1*	DNA segment, Chr 11, Brigham Young University-1		5	D	L			273
*	*D11Byu2*	DNA segment, Chr 11, Brigham Young University-2		17	D	L			273
*	*D11Byu3*	DNA segment, Chr 11, Brigham Young University-3		15	D	L			273
*	*D11Byu4*	DNA segment, Chr 11, Brigham Young University-4		15	D	L			273
*	*D11Cph1*	DNA segment, Chr 11, CEPH-1 (ex 3-2-20-P1)		30	D	L			135
*	*D11Cph2*	DNA segment, Chr 11, CEPH-2 (ex 3-2-21-P2)		30	D	L			135
*	*D11Cph3*	DNA segment, Chr 11, CEPH-3 (ex 6-1-3-P1)		30	D	L			135
*	*D11Cph4*	DNA segment, Chr 11, CEPH-4 (ex 10-1-10-P1)		30	D	L			135
*	*D11Dcw38*	DNA segment, Chr 11, D.C.Ward-38		bt	D	I			26
	D11H4S10	DNA segment, Chr 11, **formerly human D4S10h**		31	D	L	D4S10	4p16.3-p16.2	49
*	*D11Ham1*	DNA segment, Chr 11, Hamburg-1		bt	D	I			106
	D11Jkn1e	DNA segment, Chr 11, Jackson-1, expressed		75	D	L			125
*	*D11Jp1*	DNA segment, Chr 11, Japan-1		35	D	L			145
	D11Leh1	DNA segment, Chr 11, Lehrach-1		39	D	L			55
	D11Leh2	DNA segment, Chr 11, Lehrach-2		59	D	L			55
*	*D11Ler1*	DNA segment, Chr 11, Le-Roy-1		4	D	L			152
*	*D11Ler2*	DNA segment, Chr 11, Le-Roy-2		6	D	L			152
*	*D11Ler3*	DNA segment, Chr 11, Le-Roy-3		19	D	L			152
*	*D11Mc1*	DNA segment, Chr 11, McClelland-1		42	D	L			264
	D11Mit1	DNA segment, Chr 11, MIT-1		4	D	L			71
	D11Mit2	DNA segment, Chr 11, MIT-2		5	D	L			71
	D11Mit4	DNA segment, Chr 11, MIT-4		37	D	L			71
	D11Mit5	DNA segment, Chr 11, MIT-5	2	36	D	L			71
	D11Mit7	DNA segment, Chr 11, MIT-7		44	D	L			71
	D11Mit8	DNA segment, Chr 11, MIT-8	2	46	D	L			71
	D11Mit10	DNA segment, Chr 11, MIT-10		64	D	L			71
	D11Mit11	DNA segment, Chr 11, MIT-11		69	D	L			71
	D11Mit12	DNA segment, Chr 11, MIT-12	1	71	D	L			71
*	*D11Mit13*	DNA segment, Chr 11, MIT-13 ***See Ace***		62	D	L			183
*	*D11Mit14*	DNA segment, Chr 11, MIT-14 ***See AntP91a***		58	D	L			183
*	*D11Mit15*	DNA segment, Chr 11, MIT-15 ***See Glut-4***		39	D	L			183
*	*D11Mit16*	DNA segment, Chr 11, MIT-16 ***See Lif***	1	4	D	L			183
*	*D11Mit19*	DNA segment, Chr 11, MIT-19		11	D	L			183
*	*D11Mit20*	DNA segment, Chr 11, MIT-20		15	D	L			183
*	*D11Mit21*	DNA segment, Chr 11, MIT-21		15	D	L			183
*	*D11Mit22*	DNA segment, Chr 11, MIT-22		18	D	L			183
*	*D11Mit23*	DNA segment, Chr 11, MIT-23		22	D	L			183
*	*D11Mit24*	DNA segment, Chr 11, MIT-24		22	D	L			183
*	*D11Mit25*	DNA segment, Chr 11, MIT-25		22	D	L			183
*	*D11Mit26*	DNA segment, Chr 11, MIT-26		31	D	L			183
*	*D11Mit27*	DNA segment, Chr 11, MIT-27		36	D	L			183
*	*D11Mit28*	DNA segment, Chr 11, MIT-28		37	D	L			183
*	*D11Mit29*	DNA segment, Chr 11, MIT-29 ***See Acrb***	1	42	D	L			183
*	*D11Mit30*	DNA segment, Chr 11, MIT-30		42	D	L			183
*	*D11Mit31*	DNA segment, Chr 11, MIT-31 ***See Acrb***	1	42	D	L			183
*	*D11Mit32*	DNA segment, Chr 11, MIT-32		42	D	L			183
*	*D11Mit33*	DNA segment, Chr 11, MIT-33		42	D	L			183
*	*D11Mit34*	DNA segment, Chr 11, MIT-34		42	D	L			183
*	*D11Mit35*	DNA segment, Chr 11, MIT-35 ***See Mip1a***		48	D	L			183
*	*D11Mit36*	DNA segment, Chr 11, MIT-36		49	D	L			183

Continued on next page

Table 1. *Continued.*

*	*D11Mit37*	DNA segment, Chr 11, MIT-37		49	D	L			183
*	*D11Mit38*	DNA segment, Chr 11, MIT-38		50	D	L			183
*	*D11Mit39*	DNA segment, Chr 11, MIT-39		50	D	L			183
*	*D11Mit40*	DNA segment, Chr 11, MIT-40		44	D	L			183
*	*D11Mit41*	DNA segment, Chr 11, MIT-41		52	D	L			183
*	*D11Mit42*	DNA segment, Chr 11, MIT-42		71	D	L			183
*	*D11Mit48*	DNA segment, Chr 11, MIT-48		76	D	L			183
*	*D11Mit49*	DNA segment, Chr 11, MIT-49		76	D	L			183
*	*D11Mit50*	DNA segment, Chr 11, MIT-50		67	D	L			183
*	*D11Mit51*	DNA segment, Chr 11, MIT-51		14	D	L			183
*	*D11Mit52*	DNA segment, Chr 11, MIT-52		61	D	L			183
*	*D11Mit53*	DNA segment, Chr 11, MIT-53		13	D	L			183
*	*D11Mit54*	DNA segment, Chr 11, MIT-54		56	D	L			183
*	*D11Mit56*	DNA segment, Chr 11, MIT-56		49	D	L			183
*	*D11Mit58*	DNA segment, Chr 11, MIT-58 ***See Myla***	2	64	D	L			183
*	*D11Mit59*	DNA segment, Chr 11, MIT-59		58	D	L			183
*	*D11Mit60*	DNA segment, Chr 11, MIT-60		42	D	L			183
*	*D11Mit61*	DNA segment, Chr 11, MIT-61		71	D	L			183
*	*D11Mit62*	DNA segment, Chr 11, MIT-62		4	D	L			183
*	*D11Mit63*	DNA segment, Chr 11, MIT-63		5	D	L			183
*	*D11Mit64*	DNA segment, Chr 11, MIT-64		22	D	L			183
*	*D11Mit65*	DNA segment, Chr 11, MIT-65		44	D	L			183
*	*D11Mit66*	DNA segment, Chr 11, MIT-66		49	D	L			183
*	*D11Mit67*	DNA segment, Chr 11, MIT-67		57	D	L			183
*	*D11Mit68*	DNA segment, Chr 11, MIT-68		47	D	L			183
*	*D11Mit69*	DNA segment, Chr 11, MIT-69		80	D	L			183
*	*D11Mit70*	DNA segment, Chr 11, MIT-70		54	D	L			183
	D11Nds1	DNA segment, Chr 11, Nuffield Depart. of Surgery-1		45	D	L			52
	D11Nds2	DNA segment, Chr 11, Nuffield Depart. of Surgery-2		66	D	L			52
*	*D11Nds3*	DNA segment, Chr 11, Nuffield Depart. of Surgery-3		27	D	L			53
*	*D11Nds7*	DNA segment, Chr 11, Nuffield Depart. of Surgery-7 ***See Gfap***		62	D	L			71
*	*D11Nds9*	DNA segment, Chr 11, Nuffield Depart. of Surgery-9 ***See Il-5***		28	D	L			71
	D11Pas1	DNA segment, Chr 11, Pasteur-1		59	D	L			234
	D11Pas2	DNA segment, Chr 11, Pasteur-2		54	D	L			105
*	*D11Pas5*	DNA segment, Chr 11, Pasteur-5		43	D	L			13
*	*D11Pas6*	DNA segment, Chr 11, Pasteur-6		37	D	L			13
	D11Sel1	DNA segment, Chr 11, Seldin-1		23	D	L			201
*	*D11Sel2*	DNA segment, Chr 11, Seldin-2		73	D	L			233
*	*D11Sel3*	DNA segment, Chr 11, Seldin-3		74	D	L			233
*	*D11Sel4*	DNA segment, Chr 11, Seldin-4		43	D	L			233
	D11Was70	DNA segment, Chr 11, University of Washington-70		bt	D	I			72
	D4S10h	DNA segment, Chr 11, human D4S10 ***See D11H4S10***		31	D	L			
*	*Ddc*	dopa decarboxylase		bt	D	I	DDC	7p11	31
	df	Ames dwarf		25	V	L			14
	Dlb-1	dolichos lectin binding-1		55	B	L			209
	Edp-1	endothelial cell derived protein		38	D	L	EDP	17q22-q23	40
	Eif4al	eukaryotic initiation factor-4AI		39	D	L			197
	Empb3	erythrocyte membrane protein band 3		61	D	L	EPB3	17q21-q22	159, 235
	Emv-14	endogenous ecotropic MuLV-14 (***Akv-4, Akv-2J***)		38	D	L			130
	Emv-28	endogenous ecotropic MuLV-28		54	D	L			253
	Emv-30	endogenous ecotropic MuLV-30		11	D	L			215
	Emv-33	endogenous ecotropic MuLV-33 (***Bbv***)		69	D	L			148
	Erba	avian erythroblastosis oncogene A, thyroid hormone receptor		57	D	S,L	THRA1	17q11.2-q21	67, 186
	Erbb	avian erythroblastosis oncogene B, epidermal growth factor receptor	1	10	D	S,L,I	EGFR	7p14-p12.2	276, 239
	Erbb-2	avian erythroblastosis oncogene B-2		57	D	L	ERBB2	17p11.2-q12	32, 210
	Es-3	esterase-3 (***Ee-2***)		75	B	L			212, 206
	Evi-2	ecotropic viral integration site-2		46	D	L	EVI2A	17q11.2	32
*	*Flt-4*	FMS-like tyrosine kinase-4		bt	D	I	FLT4	5q34-q35	92
	Gaa	Acid alpha glucosidase		75	D	L	GAA	17q23	166, 165
	Gabra1	GABA receptor, subunit alpha-1		19	D	L	GABRA1	5q34-q35	140, 37
*	*Gabrg-2*	GABA-A receptor, subunit gamma-2		29	D	L	GABRG2	5q34-q35	41
	Gas-3	growth arrest specific-3 ***See Pmp-22, Tr***		33	D	L			51
	Gfap	glial fibrillary acidic protein,(***D11Nds7***)		62	D	L	GFAP	17q21	19, 25
	Gh	growth hormone		66	D	S,L	GH1	17q22-24	126, 274
*	*Gja-7*	gap junction membrane channel protein alpha-7 (connexin45)		bt	D	S			226
*	*Gk*	glucokinase		4	B	L	GCK	7p	156
	Glk	galactokinase		78	B	S	GALK	17q	185, 274
*	*Glns-ps1*	glutamine synthetase pseudogene-1		12	D	L	GLUL		159,
*	*Glr-1*	glutamate receptor-1		31	D	L	GLR1	5q33	42
*	*Glut-4*	glucose transporter, insulin responsive, (***D11Mit15***)		39	D	L	GLUT4	17p13	112, 117
*	*Gna-13*	guanine nucleotide-binding protein alpha-13		68	D	L			268
*	*Gp3a*	glycoprotein 3a, alpha IIIa integrin		68	D	L	ITGB3	17q21.32	233
*	*Gp2b*	glycoprotein 2b, alpha IIB integrin		68	D	L	ITGA2B	17q21.32	233
*	*Gtbp*	***see Rab-1***		12	D	L			152
	H(js)	histocompatibility(***js***)(provisional)		bt	B	L			8
	H(lt)	histocompatibility(***lt***)(provisional)		bt	B	L			8
	H(tn)	histocompatibility(***tn***) (provisional)		bt	B	L			8
	Hba	hemoglobin α-chain complex		17	B	L	HBA	16p13.3	211, 38
	Hba-x	hemoglobin X (alpha-like embryonic chain in Hba complex)		17	B	L			266
*	*Hcl1*	Heterochromatin satellite-11		0	D	L, I			169, 128
*	*Hist2b-rs1*	Histone 2b related sequence-1		32	D	L			143
*	*Hmg14-rs4*	high-mobility-group protein 14-related sequence-4		60	D	L			131
	HoxB	homeo box-2 cluster ***formerly Hox-2***	1	56	D	S,L	HOX2	17q21-q22	134,157, 227
	Hox-B1	homeo box-2 cluster, gene 1		56	D	L,P, I			158

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Table 1. *Continued.*

	Hox-B2	homeo box-2 cluster, gene 2		56	D	P,L			158
	Hox-B3	homeo box-2 cluster, gene 3		56	D	L,I,P			190
	Hox-B4	homeo box-2 cluster, gene 4		56	D	P			73
	Hox-B5	homeo box-2 cluster, gene 5		56	D	P			73
	Hox-B6	homeo box-2 cluster, gene 6		56	D	L,P			158
	Hox-B7	homeo box-2 cluster, gene 7		56	D	P			73
	Hox-B8	homeo box-2 cluster, gene 8		56	D	P			96
	Hsp86-ps1	heat shock protein, 86 kDa-2 (***Hsp86-2***)		46	D	S,L			188
*	*Htt*	serotonin (5-hydroxytrptamine) transporter		44	D	L			99
	Idd4	insulin-dependent diabetes susceptibility-4		44	B	L			255
	Il-3	interleukin-3 (contained in ***Csfmu***)		29	D	I,S,L,P	IL3	5q23-q31	187, 120
	Il-4	interleukin-4		28	D	L,S	IL4	5q31	58, 246
	Il-5	interleukin-5, (***D11Nds9***)		28	D	S,I,L	IL5	5q23-q31	154,262, 245
	Int-4	***See Wnt-3***							
	Int-4A	***See Wnt-3A***							
	Irf-1	interferon regulatory factor-1		29	D	L	IRF1	5q23-q31	41, 124
	js	Jackson shaker		77	V	L			70
	Krt-1	keratin gene complex-1		58	D	S,L	KRT15	17q21-q22	181, 11
	Krt-1.10	keratin gene complex-1, gene 10		58	D	L	KRT10	17q21-q22	194
*	*Krt-1.14*	keratin gene complex-1, gene 14		58	D	I	KRT14	17q12-q21	54
	Lif	leukemia inhibitory factor (***D11Mit16***)	1	0	D	S,I,L	LIF	22q11.1-q13.1	240,144, 247
	lt	lustrous		bt	V	L			69
	Mgat-1	UDP-*N*-acetylglucosamine:a-3-D-mannoside b-1,2-*N*-acetylglucosaminyltransferase I		31	D	L	GLCT1	5	147, 121
	Mip1a	macrophage inflammatory protein-1 a ***See D11Mit35***		48	D	L	SCYA3	17q11-q21	270, 123
	Mip1b	macrophage inflammatory protein-1 b		48	D	L	SCYA4	17q11-q21	270, 123
	Mmv-8	MCF endogenous virus-8		bt	D	S			113
	Mmv-11	MCF endogenous virus-11		bt	D	S			113
	Mmv-13	MCF endogenous virus-13		bt	D	S			113
*	*Mmv-16*	MCF endogenous virus-16		48	D	L			86
*	*Mmv-17*	MCF endogenous virus-17		59	D	L			86
	Mov-9	Moloney leukemia virus-9		45	D	I,L			127
	Mov-13	***see Cola-1***							
*	*Mox-1*	mesenchyme homeobox-1		58	D	L, S			43
	Mpmv-2	modified polytropic murine leukemia virus-2		53	D	L			89
	Mpmv-4	modified polytropic murine leukemia virus-4(***Xmmv-3***)		48	D	L			88
	Mpmv-8	modified polytropic murine leukemia virus-8		63	D	L			89
	Mpmv-15	modified polytropic murine leukemia virus-15		72	D	L			89
	Mpmv-18	modified polytropic murine leukemia virus-18		11	D	L			89
	Mpo	myeloperoxidase	1	51	D	S,I,L	MPO	17q21.2-q23	33, 260
	Mtv-3	mammary tumor virus-3		72	D	L			200
*	*Mtv-45*	mammary tumor virus-45		bt					
	Myhs	myosin heavy chain, skeletal muscle		35	D	S,L	MYH	17p12-p13	56, 76
	Myhs-e	myosin heavy chain, skeletal muscle, embryonic		35	D	S,L,P			155
	Myhs-f2	myosin heavy chain, skeletal muscle, adult fast-2		35	D	S,L,I,P			155
	Myhs-p	myosin heavy chain, skeletal muscle, perinatal		35	D	S,L,P			155
	Myla	myosin light chain, alkali, cardiac atria ***See D11Mit58***	2	64	D	L	MYL4	17q	217, 231
	Nf-1	Neurofibromatosis type 1		46	D	L	NF1	17q11.2	35, 10, 232
	Nfh	neurofilament, heavy polypeptide		4	D	I	NFH	22q12.1-q13.1	173, 172
	Ngfr	nerve growth factor receptor		56	D	L	NGFR	17q21-q22	33, 119
	nu	nude		45	V	L			84
	oe	open eyelids		46	V	L			163
	Om	Ova produced substance responsible fot DDK syndrome		48	V	L			9,
*	*P40-rs5*	P40-related sequence 5		17	D	L			75
	P4hb	procollagen-proline, 2-oxoglutarate 4-dioxygenase, b polypeptide, (***Thbp***)	2	80	D	C,L	P4HB	17q25	35, 205
	Pad-1	MMTV LTR integration site		23	D	L			33
	Pdeg	cGMP-phosphodiesterase γ		bt	D	S	PDEG	17	60, 146, 257
*	*Pfn*	Profilin		bt	D	I	PFN	17p13.3	189a
*	*Phb*	Prohibitin		bt	D	I	PHB	17q21	189a
	Pkca	protein kinase C α		68	D	S,L	PRKCA	17q22-q24	33, 242
*	*Pmp-22*	peripheral myelin protein, 22kDa (*Tr*)		33	D	S,L	PMP22	17p11.1	243
	Pmv-2	polytropic murine virus-2		5	D	L			88
	Pmv-22	polytropic murine virus-22		8	D	L			88
	Pmv-46	polytropic murine virus-46		12	D	L			88
	Pmv-56	polytropic murine virus-56		64	D	L			88
*	*Pmv-58*	polytropic murine virus-58		14	D	L			86
*	*Rab-1*	Ras related gene member, mouse homolog of yeast YPT1***See Gtbp***		12	D	L			267
	Rara	retionic acid receptor, alpha		55	D	I, L	RARA	17q21.1	171
*	*Rcvrn*	recoverin (guanylate cyclase activator)		35	D	L	RCVRN	17	178
	Re	rex		58	V	L			81
	Rel	reticuloendotheliosis oncogene		14	D	S,L	REL	2p13-p12	30
*	*Rnr11*	ribosomal RNA gene cluster		2	D	L,I			132
	Rnu1a-1	U1a1 small nuclear RNA		51	D	S,L			182
	Rnu3b	U3B small nuclear RNA complex		bt	D	I			174
	Rnu3b-1	U3B small nuclear RNA-1		bt	D	I,P			174
	Rnu3b-2	U3B small nuclear RNA-2		bt	D	I,P			174
	Rnu3b-3	U3B small nuclear RNA-3		bt	D	I,P			174
	Rnu3b-4	U3B small nuclear RNA-4		bt	D	I,P			174
*	*Rpl18-rs*	ribosomal protein 18 related sequence		4	D	L			233
	Rpo2-1	RNA polymerase II-1		37	D	S,L	POLR2	17p13.1	15, 44
	Scn4a	sodium channel a subunit, skeletal muscle		63	D	L	SCN4A	17q23.1-q25	193, 93
	sh-2	shaker-2		32	V	L			74
	Shbg	sex hormone binding globulin		35	D	S,L	SHBG	17p13-p12	133, 20

Continued on next page

Table 1. *Continued.*

	shm	shambling		bt	V	L			97
	Sigje	small inducible gene JE (provisional)		48	D	S	SCYA2	17q11.2-q21.1	238, 179
	Sparc	secreted acidic cysteine rich glycoprotein (***osteonectin***)		30	D	L,I	SPARC	5q31-q33	167, 249
	spd	spasmodic		29	V	L			151
*	*Spnb-2*	beta-spectrin-2, non-erythrocytic		13	D	L	SPTBN1	2p	24
	Syb-2	synaptobrevin-2		bt	D	S	SYB2	17pter-p12	5
*	*Tell1p*	telomeric segment, Chr 11, p arm		bt	D	I			27
*	*Tell1q*	telomeric segment, Chr 11, q arm		bt	D	I			27
	Tca-3	T-cell activation family-3		48	D	L	SCYA1	17	270, 184
*	*Tcf-1*	T cell transcription factor-1		29	D	L	TCF7	5q31.1	233
	Tcf-2	Transcription factor 2, hepatocyte nuclear factor -1 beta (***D11Pas3, vHnf-1***)		44	D	S	TCF2	17cen-q21.3	105, 1
	Tcn-2	transcobalamin-2		2	B	L	TCN2	22q11.2-qter	90, 6
*	*Thbp*	thyroid hormone binding protein ***See P4hb***	2	80	D	L	P4HB	17q25	
	ti	tipsy		42	V	L			228
*	*Timp-2*	tissue inhibitor of metalloproteinase-2		74	D	L	TIMP2	17q25	241
	Tk-1	thymidine kinase-1		78	BD	S,C,I,L	TK1	17q23-q25	149,193, 141
	tn	teetering		79	V	L			180
*	*Top-2*	topoisomerase (DNA) II alpha		48	D	L	TOP2	17q21-q22	233
	Tr	trembler ***(Gas-3, Pmp-22)***		33	V	L			82
	Trp53	transformation-related protein 53		39	D	S,L,I	TP53	17p13.1	277, 57, 177
	Ts	tail-short		68	V	L			189
	Tse-1	tissue specific extinction-1, of TAT		bt	B	S	TSE1	17q23-q24	141,
	Umph-2	uridine monophosphatase-2		bt	B	S	UMPH2	17q23.2-q25.3	248, 269,
	vb	vibrator		32	V	L			263, 150
	Vpp-1	vacuolar (endomembrane) proton pump subunit-1 (116kDa)		bt	D	S	VPP1	17q21-qter	203
	vt	vestigial-tail		24	V	L			110
	wa-2	waved-2		7	V	L			139
	Wnt-3	wingless-related MMTV integration site-3 ***(Int-4)***		62	D	L	WNT3	17q21-q22	33, 216
	Wnt-3A	wingless-related MMTV integration site-3A ***(Int-4A)***		bt	D				199
	wr	wobbler		12	V	L			137
*	*Xmmv-77*	xenotropic MCF leukemia virus-77		52	D	L			86
	Xmv-4	xenotropic murine leukemia virus-4		bt	D	S			113
	Xmv-5	xenotropic murine leukemia virus-5		bt	D	S			113
	Xmv-20	xenotropic murine leukemia virus-20		54	D	L			87
	Xmv-42	xenotropic murine leukemia virus-42		53	D	L			87
*	*Xmv-47*	xenotropic murine leukemia virus-47		15	D	L			86
*	*Xmv-49*	xenotropic murine leukemia virus-49		56	D	L			86
	Xmv-63	xenotropic murine leukemia virus-63		3	D	L			85
	Zfp-2	zinc finger protein-2		45	D	S,L			195
	Zfp-3	zinc finger protein-3 ***(Fnp-1)***		42	D	R,L	ZFP3	17pter-p12	7

Loci preceded by an asterisk were added to last year's list (34). The gene name is presented along with alternate or archaic locus designations (if any). Recommended anchor loci are indicated, and the approximate map position of each locus relative to the centromere is given in cM. In the "T" column, the locus is described as a DNA sequence (D), a biochemical, protein, or immunological phenotype (B), or a visible phenotype (V). In the "Method" column, I = in situ hybridization, S = somatic cell genetics, R = radiation hybrid analysis, L = linkage analysis, C = cytogenetic analysis, D = deletion analysis, and P = physical mapping. Also presented are the human gene symbols and human gene locations. Original references describing the human and mouse gene characterization and map locations are listed. More complete descriptions of some genes can be found in Green (98).

of many loci distal to *Erbb* have been shifted proximal in comparison with last year's report.

Multilocus crosses

The multilocus backcrosses used to build a foundation for the consensus map (Table 2, cross A, B, C, and F) report linkages and genetic distances that are consistent with each other (Table 3). In this update, twelve new multilocus backcrosses have been included, bringing the total number of genetic crosses covered in the report to 48. The data presented in the new multilocus crosses are consistent with the previous data.

RI strain data

Twenty new entries have been made into the recombinant inbred strain resources (Table 4). Some of these entries are for loci that have been previously ordered in another set of RI strains or by another mapping method. However, thirteen of these entries represent the first report of the localization. Six were endogenous viral loci, five were anonymous loci typed by PCR, and two were genes.

Cytogenetics

Twenty-nine loci have been mapped cytogenetically to Chr 11 (Table 5). These physical locations (Table 5) are consistent with the relative order presented in the consensus linkage map (Fig. 1). The chromosomal variants involving Chr 11 include ten Robertsonian fusions, nine translocations, and two inversions (Table 6).

Comparative maps

Mouse Chr 11 contains genes whose human homologs map to human Chrs 2, 4, 5, 7, 16, 17, and 22; this suggests that Chr 11 may bear at least seven homology segments (Nadeau 1989).

The most extensive region of synteny homology is observed between mouse Chr 11 and human Chr 17. It comprises more than half of mouse Chr 11, extending

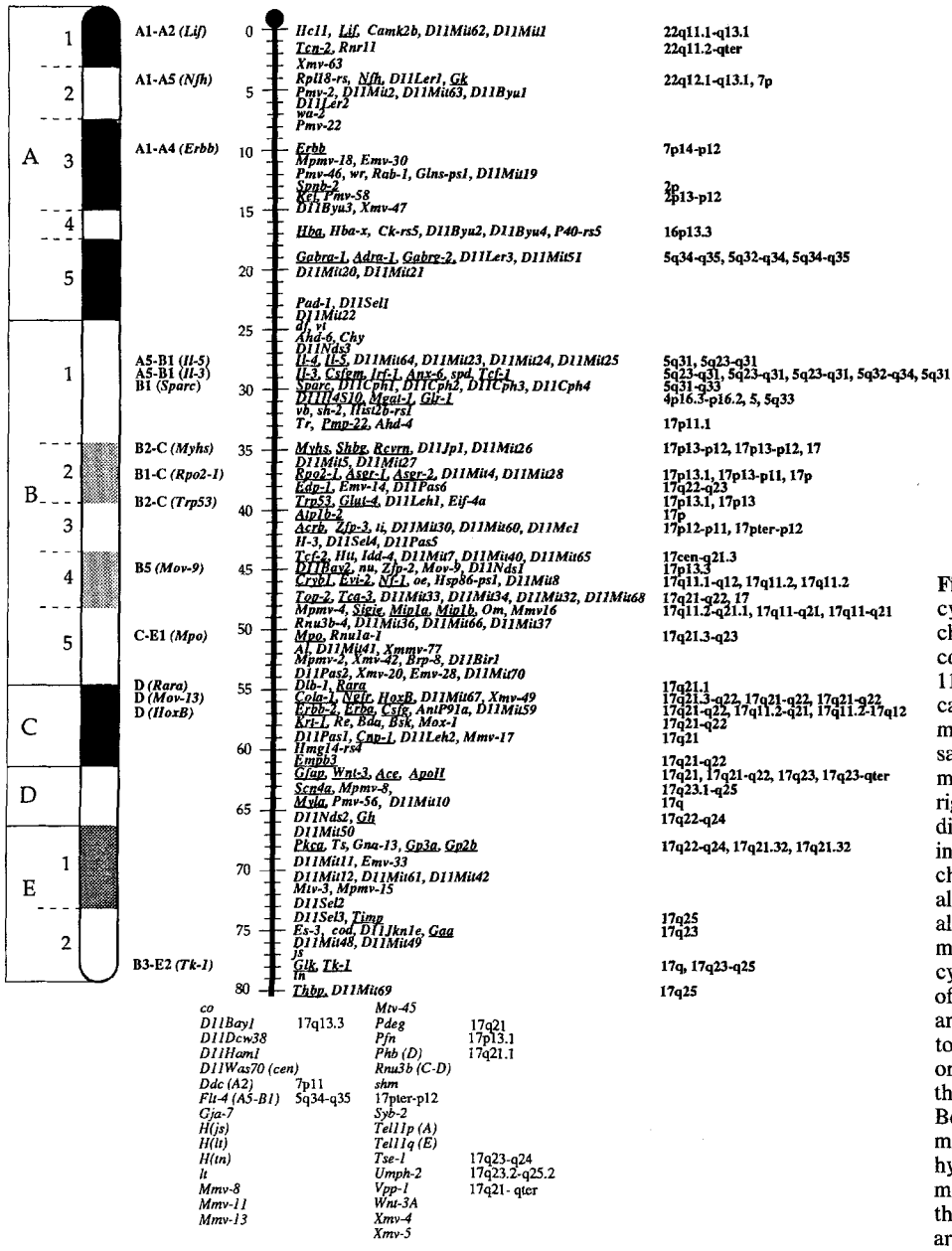


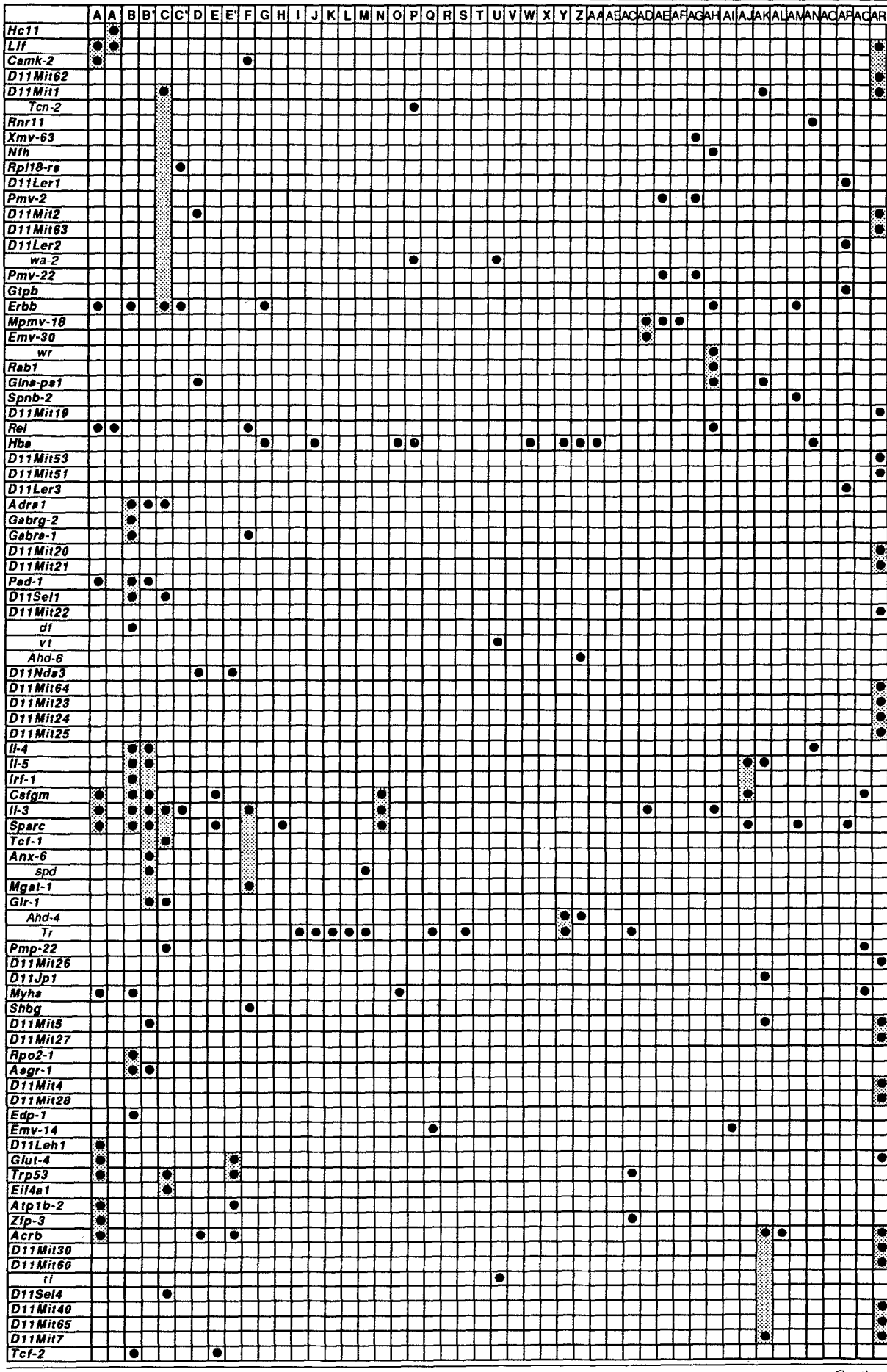
Fig. 1. Consensus linkage and cytogenetic map of mouse Chr 11. The chromosome on the right represents the consensus linkage map of mouse Chr 11, and it is likely to be inaccurate in cases where genes have not been mapped relative to one another in the same cross. The genes mapping to mouse Chr 11 are presented on the right of the chromosome, and the distance from the centromere is indicated on the left of the chromosome. Genes that are listed along the left of the chromosome have also been localized on the cytogenetic map (on the left of the figure), with the cytogenetic location shown to the left of the chromosome (Table 5). Loci that are **underlined** have also been localized to human chromosomes; their locations on human chromosomes are shown to the right of the chromosome (Table 1). Below the chromosome are those loci mapping to Chr 11 by somatic cell hybrid analysis, in situ hybridization methods, or two-point genetic analysis; their cytogenetic and human location are shown.

from the medial region to the telomere. This region of Chr 11 was previously known to contain 43 genes reported to map to human Chr 17, and this year nine additional genes were localized to this region. These include *Apoh, Glut-4, Gp3a, Gp2b, Krt-1.10, Pmp-22, Rcvrn, Timp-2,* and *Top-2*. The majority of the genes located in the distal half of mouse Chr 11 appear to comprise distinct conserved linkage groups; that is, genes whose homologs are located on human Chr 17q are clustered, and those whose homologs are localized to human Chr 17p are clustered. The locations of the exceptions, *Edp-1* and *Tcf-2,* will most likely be altered once they are mapped with respect to additional genes.

The only other extensive region of synteny homology is the medial region of mouse Chr 11 and human chromosome 5q23-35. The five genes localized this year that extended this previously recognized conservation are *Anx-6, Flt-4, Gabrg-2, Glr-1,* and *Tcf-1*. This brings the total number of genes in this synteny group to 13; however, many genes from human Chr 5q map to other mouse chromosomes, particularly mouse Chr 18. Thus, it is not possible to accurately predict the location of the murine homologs of human 5q genes.

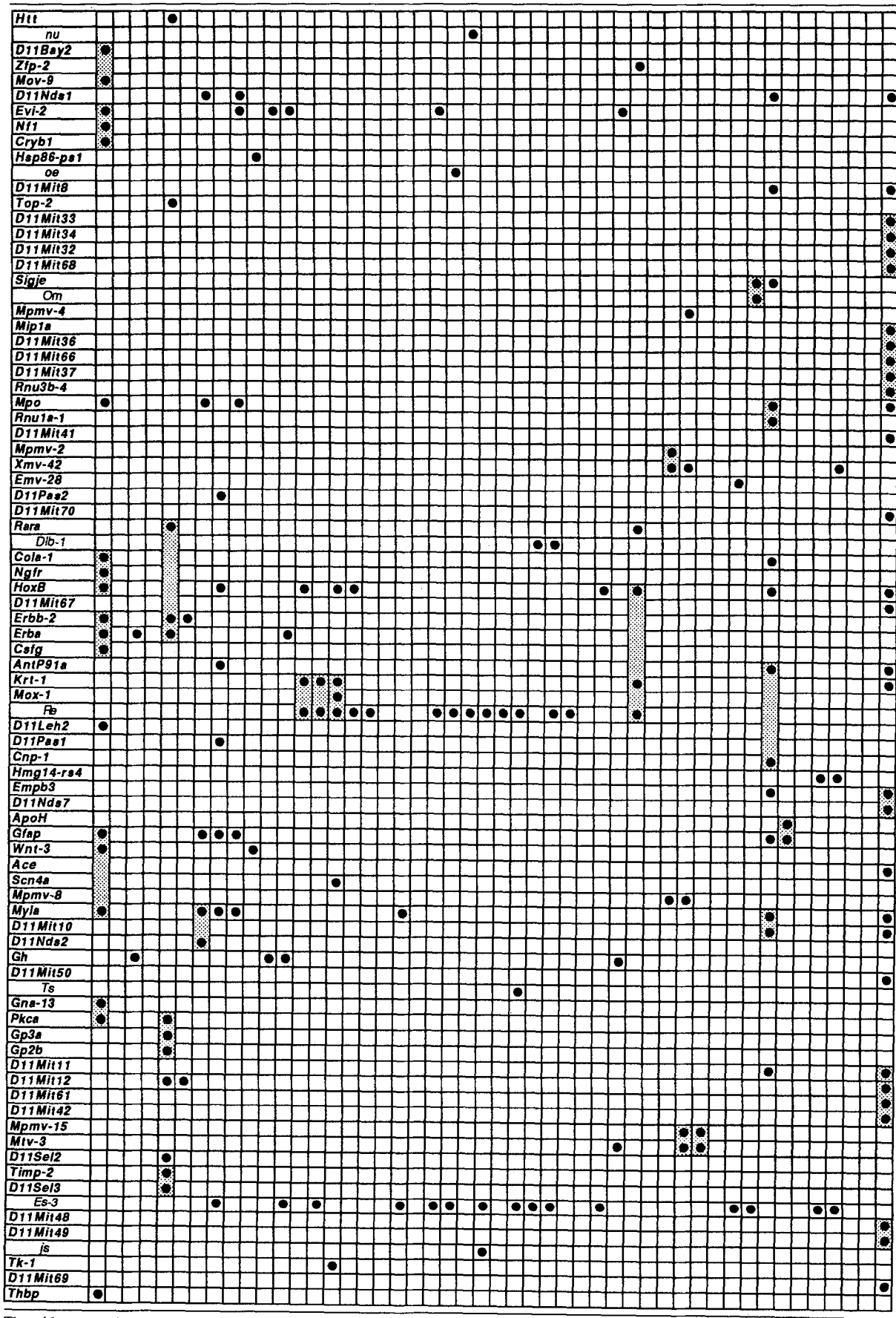
The only locus from human Chr 4 that has been mapped to mouse Chr 11 is D11H4S10. Based on the fact that D11H4S10 is an anonymous human sequence and genes neighboring D11H4S10 in humans are linked on a different mouse chromosome, it seems possible that D11H4S10 may be hybridizing to a related, but different sequence in the mouse genome. Therefore,

Table 2. Order list.



Continued on next page

Table 2. *Continued.*



The table summarizes the proposed order for loci mapped in multilocus genetic crosses. The order is from proximal to distal. Each column represents the order information obtained from a single multilocus cross. The black dot indicates the loci mapped in each cross. The open, shaded regions containing black dots indicate that order could not be determined in that specific cross for those markers indicated. Loci typed by molecular probes are indicated in bold and left-justified. Mutant or biochemical markers are in plain text and center-justified. Each cross is represented by a letter at the top of each column and is cross-referenced in Table 3.

Table 3. This table presents the gene order (proximal to distal) and recombination distance (cM ± standard error) for the multilocus crosses presented in Table 2. References are shown in bold for each cross. An asterisk indicates that the standard error was not included with the submitted data.

A. (*Camk2b, Lif*)-3.8±1.6-*Erbb*-3.8±1.5-*Rel*-15.0±2.9-*Pad-1*-6.7±2.2-(*Il-3, Csfgm, Sparc*)-5.6±2.4-*Myhs*-4.8±1.8-(*Acrb, Atp1b2, Trp53, Zfp-3, Glut-4, D11Lehl*)-2.1±1.2-(*D11Bay2, Mov-9*)-0.7±0.7-(*Cryb1, Evi-2, Nf-1*)-5.6±2.7-*Mpo*-6.3±2.0-(*Cola-1, Ngfr, HoxB*)-0.7±0.7-(*Erbb-2, Erba, Csfg*)-1.7±1.6-*D11Leh2*-3.5±2.4-(*Gfap, Wnt-3, Myla*)-3.2±1.4-(*Pkca, Gna-13*)-11.1±2.5-*P4hb*. **33, 35, 7, 55, 112, 136, 268**

A. (*Cenl1, Lif*)-12.6±3.4-*Rel* **128**

B. *Erbb*-14.5±3.3-(*Adral, Gabra-1*)-3.4±1.7-(*Pad-1, D11Sel1*)-0.9±0.9-*df*-2.6±1.5-(*Il-3, Csfgm, Irf-1, Il-5, Il-4, Sparc*)-2.6±1.5-*Myhs*-1.7±1.2-(*Rpo-2, Asgr*)-0.9±0.9-*Edp-1*-5.8±2.5-*Tcf-2*-16.3±4.0-*Erba*-4.3±1.9-*Gh*. **40, 42a**

B. *Adra-1*-3.8±21-*Pad-1*-6.3±2.7-(*Anx-6, Csfgm, Glr-1, Il-3, Il-4, Il-5, Sparc, spd*)-9.1±2.4-*D11Mit5*-2.2±1.5-*Asgr-1*. **42**

C.* (*D11Mit1, Erbb*)-15.4-*Adra1*-6.1-*D11Sel1*-2.7-(*Il-3, Tcf-1*)-1.9-*Glr-1*-5.3-*Pmp-22*-4.4-(*Eif4a1, Trp53*)-0.9-*D11Sel4*-0.9-*Htt*-3.2-*Top-2*-0.9-(*Erba, Erbb2, Rara*)-6.1-(*Pkca, Gp3a, Gp2b*)-1.2-*D11Mit12*-2.3-D11Sel2-0.9-(*Timp-2, D11Sel3*) **201, 202, 51, 241, 233, 197**

C.* *Rpl18-rs*-6.9-*Erbb*-37.4-*Il3*-20.7-*Erbb2*-16.2-*D11Mit12* **233**

D. *D11Mit2*-9.5±4.5-*Glns*-16.3±2.1-*D11Nds3*-12.7±1.5-*Acrb*-4.9±0.9-*D11Nds1*-5.9±1.2-*Mpo*-13.7±1.7-*Gfap*-3.4±1.1-(*Myla., D11Nds2*) **255, 176**

E. *D11Pas3*-21.4±10.9-*Sparc*-3.4±2.4-*Csfgm*-28.8±5.9-*D11Pas2*-2.3±2.3-*HoxB*-1.9±1.9-*D11Pas1*-1.4±1.4-*Gfap*-7.3±3.1-*Myla*-5.8±2.8-*Es-3* **105**

E. *D11Nds3*-16.5±4.2-(*Glut-4, Trp53*)-1.4±.08-*Atp1b2*-0.5±0.5-*Acrb*-0.9±0.6-*D11Nds1*-1.4±0.8-*Evi-2*-4.3±1.4-*Mpo*-14.3±4.1-*Gfap*-6.5±3.1-*Myla* **176**

F. *Camk2b*-8.0±2.9-*Rel*-9.8±3.3-*Gabra-1*-3.3±2.3-(*Il-3, Mgat-1*)-8.9 ± 3.8-*Shbg*-11.6±3.9-*Hsp86-ps1*-17.4±4.6-*Wnt-3*. **133, 140, 188, 213, 59**

G. *Erbb*-9.5±3.7-*Hba*-20.6±5.1-*Evi-2*-25.4±5.5-*Gh*. **77, 78**

H. *Sparc*-16.7±4.2-*Evi-2*-9.0±3.2-*Erba*-2.6±1.8-*Gh*-19.2±4.5-*Es-3*. **78**

I. *Tr*-21.3±4.7-*HoxB*-1.3±1.3-(*Krt-1, Re*). **194**

J. *Hba*-20.3±4.5-*Tr*-27.7±3.6-(*Krt-1, Re*)-13.9±3.9-*Es-3*. **194**

K. *Tr*-21.2±5.0-*HoxB*-1.5±1.5-(*Krt-1, Re, Mox-1*)-2.6±1.8-*Scn4a*-12.8±3.8-*Tk-1*. **43, 194, 193**

L. *Tr*-20.6±4.7-*HoxB*-1.4±1.4-*Re*. **107**

M. *spd*-2.5±1.2-*Tr*-25.3±3.4-*Re*. **151**

N. (*Il-3, Csfgm, Sparc*). **12**

O. *Hba*-32.2±8.4-*Myhs*-26.2±6.8-*Myla*-8.1±4.5-*Es-3*. **265, 217**

P. *Tcn-2*-6.9±2.2-*wa-2*-12.3±2.9-*Hba*. **91**

Q. *Tr*-4.1±2.8-*Akv-4*-12.2±4.7-*Evi-2*-24.5±6.1-*Re*-10.2±4.3-*Es-3*. **254, 32**

R. *oe*-13.3±6.2-*Re*-20.0±7.3-*Es-3*. **21**

S. *Tr*-7.4±3.6-*nu*-11.1±4.3-*Re*. **84**

T. *Re*-13.3±6.2-*Es-3*-3.3±3.3-*js*. **219**

U. *wa-2*-22.2±1.7-*vt*-8.9±1.2-*ti*-20.2±1.5-*Re*. **228**

V. *Re*-8.6±3.7-*Ts*-5.2±2.2-*Es-3*. **250**

W *Hba*-40.5 ± 4.56 -*Dlb-1*-28.4± 4.2-*Es-3*. **259**

X. *Dlb-1*-2.3±1.3-*Re*-20.3±3.5-*Es-3*. **259**

Y. *Hba*-20.4±2.9-(*Ahd-4, Tr*)-26.3±3.2-*Re*. **114**

Z. *Hba*-13.8±3.9-*Ahd-6*-7.5±2.9-*Ahd-4*. **115**

AA. *Hba*-29.6±4.6-*HoxB*-23.5±4.3-*Es-3*. **261**

AB. *Evi-2*-27.0±7.3-*Gh*-5.4±3.7-*Es-3*. **77**

AC. *Tr*-4.7±3.2-*Trp53*-1.6±1.6-*Zfp-3*-8.1±3.5-*Zfp-2*-30.6±5.9-*Rara*-32.±2.2- (*HoxB, Krt-1,Re*). **195**

AD. (*Mpmv-18, Emv-30*)-25.0±7.2-*Il-3*. **215**

AE. *Pmv-2*-3.3±3.3-*Pmv-22*-3.7±3.6-*Mpmv-18*-51.8±9.6-(*Mpmv-2, Xmv-42*)-9.4±5.2-*Mpmv-8*. **89**

AF. *Mpmv-18*-32.1±6.2-*Mpmv-4*-3.5±2.4-*Xmv-42*-14.0±4.6-*Mpmv-8*-15.8±4.8-(*Mpmv-15, Mtv-3*). **89**

AG. *Xmv-63*-8.2±3.5-*Pmv-2*-4.5±3.2-*Pmv-22*-53.5±7.6-(*Mpmv-15, Mtv-3*). **89**

AH. *Nfh*-5.6±3.1-*Erbb*-1.1±1.1-(*Rabl, Glns-ps1, wr*)-2.2±1.6-*Rel*-4.4±2.1-*Hba*-17.8±4.0-*Il-3*. **138**

AI. *Emv-14*- 23±9 -*Emv-28* - 23±9 - *Es-3*. **253**

AJ. (*Il-5, Csfgm*)-4.7±3.2-*Sparc*-30.2±7.0-(*Om, Sigje*)-20.9±6.2-*Es-3*. **9**

AK. *D11Mit1*-11.4±1.9-*Glns*-26.2±2.8-*Il-5*-2.7±1.0-*D11Jp1*-1.6±0.8-*D11Mit5*-3.5±1.2-*D11Nds1*-0.4±0.4-(*D11Mit7, Acrb*)-2.0±0.9-*D11Mit8*-1.2±0.7-*Sigje*-1.5±0.8-(*Mpo, Rnu1a-1*)-3.1±1.1-*Cola1*-1.5±0.8-*HoxB*-2.4±1.0-(*Antp91A, Cnp-1*)-5.1±1.4-*Empb3*-0.4±0.4-*Gfap*-2.0±0.9-(*D11Mit10, Myla*)-5.5±1.4-*D11Mit11* **145**

AL. *Acrb*-18±5.4-(*Gp2b, Gfap*). **198**

AM. *Erbb*-2.6±1.8-*Spnb-2*-17.9±4.4-*Sparc*. **24**

AN. *Rnr11*-19.9±3.4-*Hba*-13.8±2.9-*Il-4*-33.6±4.0-*Hmg14-rs4*-11.4±2.7-*Es-3* **131, 132**

AO. *Xmv-42*-13.4±2.9-*Hmg14-rs4*-11.3±2.7-*Es-3* **131**

AP.* *D11Ler1-2-D11Ler2-2-Gtbp*-17-*D11Ler3*-10-*Sparc* **152**

AQ. *Csfgm*-4.4±2.1-*Pmp-22*-2.2±1.5-*Myhs* **243**

AR.* (*D11Mit1, D11Mit62, D11Mit16*)-2.0-(*D11Mit2, D11Mit63*)-7.3-*D11Mit19*-2.4-*D11Mit53*-1.9-*D11Mit51*-3.0-(*D11Mit20, D11Mit21*)-3.4-*D11Mit22*-2.2-(*D11Nds9, D11Mit64, D11Mit23, D11Mit24, D11Mit25*)-7.3-*D11Mit26*-4.7-(*D11Mit27, D11Mit5, D11Mit4, D11Mit28*)-1.1-(*D11Mit15, D11Mit29, D11Mit31, D11Mit30, D11Mit60*)-3.4-(*D11Nds1, D11Mit7, D11Mit65*)-2.2-(*D11Mit33, D11Mit8, D11Mit34, D11Mit32, D11Mit68*)-1.1-(*D11Mit35, D11Mit36, D11Mit66, D11Mit37, D11Mit56*)-1.1-(*D11Mit38, D11Mit39*)-3.4-*D11Mit41*-5.2-*D11Mit70*-8.8-*D11Mit54*-1.1-(*D11Mit67, D11Mit58*)-2.2-*D11Mit14*-1.1-*D11Mit59*-1.0-*D11Mit52*-0.1-*D11Nds7*-1.1-*D11Mit10*-1.1-*D11Mit13*-4.5-*D11Mit50*-2.2-*D11Mit11*-1.8-*D11Mit61*-0.9-(*D11Mit12, D11Mit42*)-5.8-(*D11Mit48, D11Mit49*)-2.8-*D11Mit69* **71, 183**

currently there is insufficient evidence to support the suggestion of synteny homology between mouse Chr 11 and human Chr 4.

In contrast, two other regions of putative synteny homology have been supported by gene localizations reported this year. In the previous chromosome report, *Erbb* was the only gene on mouse Chr 11 whose homolog mapped to human Chr 7. The recent localization of *Gk* to proximal Chr 11 suggests that a region of synteny homology might exist. Another gene, *Ddc*, from HSA 7p has recently been assigned to this region of mouse Chr 11 by in situ hybridization, providing further support for the suggestion of a human Chr 7p synteny homology region. Similarly, whereas *Rel* was formerly the only gene on mouse Chr 11 whose homolog mapped to human Chr 2, the localization of

Table 4. SDPs of Chr 11 loci in RI strains. Crossovers within a chromosome are underlined.

AKXD. A and D represent alleles derived from AKR/J and DBA/2J, respectively.

Locus	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	20	21	22	23	24	25	26	27	28	References
Pmv-2	D	A	A			A	A	D	A	D	D	D	D	D	A	A	A	A	D	D	D	D	A	A	D	A	D	88
Mpmv-18	A	A	D			A	A	A	A	D	A	A	D	D	D	A		A	D	D	D	D	A	A	A	A	D	89
Hba	A	D	D	A	D	A	A	A	A	D	A	A	D	D	A	D	A	A	D	D	A	A	D	A	A	A	D	49
Sparc	D	D	D			A	A	A	A			A	D	A	D			A	D	D		A		D				167
D11H4S10	D	D	D				A	A	A	D	D	A	D	A	D	D	D	A	D	D	D	A	D		A	A	D	49
Emv-14	A	A	D			A	A	D	A	D	D	A	A	A	D	D	D	A	D	D	D	A	A	D	A	A	D	129
Atpb-2		A	D			A	A	D		D	D	A	D	A	D	A		A	D	D	D	A	D	D	D	A	D	164
Acrb	D	A	D			A	A	D	A	D	D	A	D	A	D	A		A	D	D	D	A	D	D	D	A	D	108
Glut4	D	A	D			A	A	D	A	D	D	A	D	A	D	A		A	D	D	D	A	D	D	D	A	D	108
Evi-2	D	A	D	A	D	A	A	D	A	D	D	A	D	A	D	A	D	A	D	D	D	A	D	D	D	D	D	32
Xmv-20						A	A			D			D	A	D	A		A	A	D	D		A	D			87
Cola-1	D	A	D			A	A	D			D	D	D	A	D	A		D	A	D	D	A	D	A	D	D	D	4
HoxB	D	A	D			A	A	D	A	D	D	D	D	A	D	A	D	D	A	D	D	A	D	A	D	D	D	107
Cnp-1	D	A	D			A	A	D	A	D	D	D	D	A	D	A	D	A	A	D	D	A	D	D	D	D	D	19
Gfap	D	A	D			A	D	D	A	D	D	D	D	A	D	A	A	A	A	D	D	A	A	D	D	D	D	19
Gaa	A	D	A			D	D	D	A		D	D	D	A	A	A		A	A	D	D	A	A		D	D	D	166
Mpmv-15	A	D	A			A	D	D	A	D	D	D	D	A	A	A		A	A	D	D	A	A	D	D	D	D	89

BXD. B and D represent alleles derived from C57BL/6J and DBA/2J, respectively.

Locus	01	02	04	05	06	08	09	12	13	14	15	16	17	18	19	20	21	23	24	27	28	29	30	31	32	References
Pmv-22	B	B		B	D	B	D	B	B	D	D	B	B	D	B	D	B	B	B	D	B	D	D	D	B	D	D	88
D11Byu1	B	B		B	D	B	D	B	B	D	D	B	B	D	B	D	B	B	D	D	B	D	D	D	B	D	D	273
D11Mit2		B		B	D	B	D	B	B	D	D	B		D	B	D	B	B	D	D	B	D	D	D				71
Glns-ps1	B	D		B	D	B	D	B	B	D	D	D	B	D	B	D	B	B	D	D	B	D	D	D	D	D	D	159
D11Byu3	B	D		B	D	B	B	B	B	D	D	D	B	D	D	D	B	B	B	D	B	D	D	D	D	B	D	273
Hba	B	D		B	D	B	B	B	B	D	D	D	B	D	D	D	B	B	B	D	B	D	D	D	D			237
D11Byu2	B	D		B	D	B	B	B	B	D	D	D	B	D	D	D	B	B	B	D	B	D	D	D	D	D	D	273
D11Byu4	B	D		B	D	B	B	B	B	D	D	D	B	D	D	D	B	B	B	D	B	D	D	D	D	D	D	273
P40-rs5	D	D		B	D	B	B	B	B	D	D	D	B	D	D	D	B	B	B	D	B	D	D	D	D	D	D	75
Sparc	D	D		B	D	B	B	B	D	D	B	B	D	D	B	B	D	B	B	B	B	D	D	B	D	D	D	167
Il-5	D	D		B	D	B	B	B	D	D	D	B	D	B	B	B	D	B	B	B	B	B	D	D	B	D	D	270
D11H4S10	D	D		B	D	B	B	B	D	D	D	B	D	B	B	B	D	B	B	B	B	B	D	D	B	D	D	49
Hist2b-rs1	D	D		B	D	B	B	B	D	D	D	B	D	B	D	B	D	B	B	B	B	B	D	D	B	D		143
Rcvrn	B	D		B	D	B	B	B	B	D	B	B	D		D	B	D	B	B	B	B	B	D	D	B	D	D	178
D11Mit4		D		B	D	B	B	B	B	D	B	B	D	B	D	B	D	B	B	B	B	B	D	D				71
Glut-4	B	D		B	D	B	B	B	B	D	B	D	D	B	D	B	D	B	B	B	B	B	D	D	B	B	D	108,71
Asgr-1	B	D		B	D	B	B	B	B	D	B	D	D	B	D	B	D	B	B	B	B	B	D	D	B	B		224
Asgr-2	B	D		B	D	B	B	B	B	D	B	D	D	B	D	B	D	B	B	B	B	B	D	D	B	B		224
Acrb		D		B	D	B	B	B	B	D	B	D	D	B	D	B	D	B	B	B	B	B	D	D	B	B	D	108
Atp1b-2	B	D		B	D	B	B	B	B	D	B	D	D	B	D	B	D	B	B	B		B	D	D	B	B	D	164, 118
Zfp-3	B	D		B	D	B	B	B	B	D	B	D	D	B	D	B	D	B	B	B	B	B	D	D	B	B	D	7
D11Nds1	B	D		B	D	B	B	B	B	D	B	D	D		D	B	D	B	B	B	B	B	D	D	B	B	D	52
Mpmv-2	B	D		B	D	B	B	B	B	D	D	D	D	B	D	B	D	B	B	B	B	B	B	D	B	B	D	89
Brp-8	B	D		B	D	B	B	B	B	D	D	D	D	B				B		B			B	D	B		D	94
Tca-3	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	270
Xmmv-3	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	23
Mpmv-4	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	89
D11Bir1	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	22
Xmv-42	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	87
Mpo		D		D	B	B	D	B	D	B	D		D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	108
Mip1a	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	270
Mip1b	B	D		D	B	B	D	B	D	B	D	D	D	B	D	D	D	D	B	B	B	B	B	D	B	B	D	270
AntP91a		D		D	D	D	D	B	B	B	D	D	D	B	D	D	D	D	B	D	B	B	B	D				71
HoxB	B	D		D	D	D	D	B	B	B	D	D	D	B	D	D	D	D	B	D	B	D	B	D	D	B	D	159
Krt-1	B	D		D	D	D	D	B	B	B	D	D	D	B	D	D	D	D	B	D	B	B	B	B	D	B	D	181, 194
D11Nds2	D	D		D	D	D	D	B	B	B	D	D	B	D	D	D	D	D	B	D	B	B	B	B	D	B	D	108
Gfap	D	D		D	D	D	D	B	B	B	D	D	B	D	D	D	D	D	B	D	B	B	B	B	D	B	D	19, 159
Empb3	D	D		D	D		D	B	B	B	B	D	B	D	D	D	D	D	B	D	B	B	B	B	D	B	D	159
Myla	D	D		D	D	D	D	B	B	B	B	B	B	D	D	D	D	D	B	D	B	B	B	B	D	B	D	159
Mpmv-8	D	D		D	D	D	D	D	D	D	D	D	B	D	D	D	D	D	B	D	B	B	B	B	D	B	D	89
Es-3	D	D	D	B	D	D	D	B	D	D	B	D	D	B	B	D	D	D	B	D	D	D	B	B	D	B	D	252
D11Jkn1e	D	D		B	D	D	D	B	D		B	D	D	B	B			D		D	D		B	B	D		D	125
Tk-1	D	D		B	D	D	D	B	D	D	B	D	D	B	B	D	D	D	B	D	D	D	B	B	D	B	D	166
Gaa	D	D		B	D	D	D	B	D	D	B	D	D	B	B	D	D	D	B	B	D	D	B	B	D	B	D	166

AKXL. A and L represent alleles derived from AKR/J and C57L/J, respectively.

Locus	01	02	04	05	06	07	08	09	11	12	13	14	16	17	18	19	21	23	24	25	27	29	36	37	38	References
Pmv-22				A	L	A	L	A		L	L	A	A	A		L	A		L	A	A	A		A	A	88
Pmv-2					L	A	L	A		L	L	A	A	A		L	A		L	A	A	A		A	A	88
Erbb				A	L	L	L	A		L	L	A	A	A		L	A		L	A	A	A		L	A	237
Mpmv-18				A	L	L	L	A		L	A	A	A	A		L	L		L	A	L	A		A	A	89
Hba				A	L		L	A		L	A	A	A	A		L	L		L	A	L	L		L	A	237
Emv-14				A	A	A	A	L		L	A	A	L	A		A	L		A	L	L	L	L	A	A	254
Evi-2				A	A	A	A	L		L	L	A	L	A		A	L		A	L	L	A		A	A	32
Mpmv-2				A	A	A	A	L		L	L	A	L	A		A	L		A	L	L	A		A	A	89
Tca-3				A	A	A	A	L		L	L	A	L	A		A	L		A	L	L	L		A	A	270
Mpmv-4					A	A	A	L		L	L	A	A	A		A	L		A	L	L	L		A	A	89
Mip1a				A	A	A	A	L		L	L	A	A	A		A	L		A	L	L	L		A	A	270
Mip1b				A	A	A	A	L		L	L	A	A	A		A	L		A	L	L	L		A	A	270
Xmv-42				A	A	A	A	L		L	L	A	A	A		A	L		L	L	L	L		A	A	87
Xmv-20				A	A	A	A	L		L	L	A	A	A		A	L		L	L	A	A		A	A	87
HoxB				A	A	A	A	L		L	L	A	A	A		L	L		L	L	L	A		A	A	107
Cnp-1				A	A	A	A	L		L	L	A	L	A		L	L		L	A	L	L		A	A	19
Mpmv-8				A	A	L	L	L		L	L	A	L	A		L	L		L	A	L	L		A	L	89
Es-3	L	A	A	A	L	L	A	L	L	L	L	L	L	A	A	A	L	A	L	L	L	L	L	A	A	185
Gaa				A	L	L	A	L		L	L	L	L	A		A	L		L	L				A	L	166
Glk				A	L	A	A	L			A	L	L	A		A	L		L	L	L	L		A	L	185
Mpmv-15				A	L	L	A	L			A	L	L	A		A	L		A	L	L	L		A	L	89

Continued on next page

Table 4. *Continued.*

SWXL. S and L represent alleles derived from SWR/J and C57L/J, respectively.

Locus	0 4	0 7	1 2	1 4	1 5	1 6	1 7	References
Sparc	S	L	L	L		S	S	167
Ahd-4	S		L	L	S	S		114
Dlb-1	S	L	S	S	S	S	S	259
Gaa	L	S	S	S	L	S	S	166

OXA. O and A represent alleles derived from O20/A and AKR/FuRdA, respectively.

Locus	1 5	1 6	1 7	1 8	1 9	2 0	2 1	2 2	2 3	2 4	2 5	2 6	2 7	2 8	References
Il-5	O	O	A	A	A	A	O	O	A	O	A	A	A	O	270
Il-4	O	O	A	A	A	A	O	O	A	O	A	A	A	O	251
Il-3	O	O	A	A	A	A	O	O	A	O	A	A	A	O	251
Tca-3	A	A	O	A	A	A	O	O	A	O	A	A	A	A	270

BXH. B and H represent alleles derived from C57BL/6J and C3H/HeJ, respectively.

Locus	0 2	0 3	0 4	0 5	0 6	0 7	0 8	0 9	1 0	1 1	1 2	1 4	1 5	1 8	1 9	2 0	References
Pmv-22	H	H	H		H	B	B	B	B	H	B	H			H		88
Pmv-2	H	H	H		H	B	B	B	B	H	B	H			H		88
Hba	B	H	B	H	H	B	B	B	B	B	B	H		B	H	B	49
Sparc	B	H	B		H	H	H	B	B	B	B	B			H		167
D11H4S10	B	H	B		H	H	H	B	B	B	B	B			H		49
Mpmv-2	H	H	B		H	H	H	B	B	B	H	H			B		89
Mpmv-4	H	H	H		H	H	H	B	B	B	H	H			B		89
Xmv-42	H	H	H		H	H	H	B	B	B	B	H			B		87
Krt-1	B	H	H		H	H	H	B	B	H	B	H			B		194
Gfap	B	H	H		H	H	H	B	B	H	B	H			B		19
Myla			H		B	H	H	B	B	H	B	H			B		217
Mpmv-8	B	H	H		B	H	H	B	B	H	B	H			B		89
Es-3	B	B	H	H	B	H	H	B	B	H	B	B	B	B	B	B	185
Tk-1	B	B	H		B	H	H	B	B	H	B	B			B		166
Gaa	H	B	H		B	H	H	B	B	H	B	H			B		166
Glk	B	B	H	H	B	H	H	B	B	H	B	H		B	B		185

CXB. C and B represent alleles derived from BALB/cJ and C57BL/6J, respectively.

Locus	0 1	0 2	0 3	0 4	0 5	0 6	0 7	0 9	1 0	1 1	1 2	1 3	References
Pmv-22	C	C	B	B	B	B	C						88
Pmv-2	C	C	B	B	B	B	C						88
Erbb	C	B	B	C	B	B	C						237
Mpmv-18	C	B	B	C	B	B	C						89
Hba	C	B	B	C	B	B	C						221
Ck-rs5	C	B	B	C	B	B	C	C	B	C	C	B	50
Mpmv-2	C	B	C	C	B	C	C						89
Xmv-42	B	B	B	B	B	C	C						87
Mpmv-8	B	B	C	C	B	C	B						89
Gaa	B	B	B	C	C	C	B	C	C	B	C	C	166

AXB. A and B represent alleles derived from A/J and C57BL/6J, respectively.

Locus	0 1	0 2	0 3	0 4	0 5	0 6	0 7	0 8	0 9	1 0	1 1	1 2	1 3	1 4	1 5	1 7	1 8	1 9	2 0	2 1	2 2	2 3	2 4	2 5	References
Pmv-2	A	B	A	A	A	A	A	A	A	A	A	A	A				A		A	A	B	B	A	A	88
Pmv-22	A	B	A	A	A	A	A	A	A	A							A		A	A	B	B		A	88
Erbb	A	B	A	A		A	A	A		A	A	A		A	B		A			A					195a
Pmv-46	A	B	A	A	A	A	A	A	A	A	B	A	A	B			A		A	A	B	A		B	195a
Hba	B	B	A	A	A	A	A	A	B	A	A	B	B	B	B	A	A					A			158
Il-3	B	B	A	B	A	A	B	A	A	B	A		B	B	B		A	A	A			A	A		158
Mpmv-2	B	B	A	B	B	B	A	A	A	B	B	B	B	B			A		A	B	B	A	A	A	89
Myhs	B	B	A	B	A	A		A		B	B	A	B	B	A	A	A	B	A	A	B	A	A		158
Xmv-42	B	B	A	B	A	A	A	A	B	B	A	A	A	B			A		A	B	A	A	A	B	87
Mpmv-4	B	B	A	A	A	A	A	A	B	B	A	A	A	B			A		A	B	A	A	A	B	89
Hox-2.1	B	B	A	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	A	A		158
Hox 2.6	B	B	A	B	A	A	A	A	B	B	A	B	A	B	B	B	B	B	B	B	A	A	A		158
Mpmv-8	B	B	B	B	A	A	A	B	B	B	A	B	A	B			B		B	B	B	A	A	B	89
Pmv-56	B	B	B	B	A	A	B	B	B	A	B	A	B				B		B	B	A	A	A	B	88
Es-3	B	B	A	A	A	B	A	B	A	B	A	A	A	B	B	B	B	B	B	B		A	A		158

BXA. B and A represent alleles derived from C57BL/6J and A/J, respectively.

Locus	0 1	0 2	0 3	0 4	0 5	0 6	0 7	0 8	0 9	1 0	1 1	1 1	1 2	1 3	1 4	1 6	1 7	1 8	1 9	2 0	2 1	2 2	2 3	2 4	2 5	References
Pmv-2	A	B		A		B	A	B	A	A	B	B	B	B	A		B	A	A	A		A	A	A	A	88
Pmv-22	A	B		A		B	A	B	A	A	B	B	B	B	A		A	A	B	A		A	A	A	A	88
Erbb			B	A	A		A	A			B															195a
Pmv-46	A	B		A		A	A	A	A	A	B	A	A	A	A		A	A	A	A	A	A	A	A	A	88
Hba	A			A				A			B	A	A	A	A	A	A	A	A	B			A			158
Il-3	A	B	B	B		A	A		B		B		A	A				A	B			A		A		158
Mpmv-2	A	B		B		B	A	B	B	A	A	A	B	A			B	A		B		A	A	A	B	89
Myhs	A	B		B		B	A	B	B	A	B	B	B	A	A	A	B	A	B			A		A		158
Xmv-42	B	B		B		B	A	A	B	A	A	B	B	B			A	A	B	A		A	B	A	B	87
Mpmv-4	B	B		B		B	A	A	B	A	A	B	B	B			A	A		A		A	B	A	A	89
Hox-2.1	B	B	A	B		B	A	A	B	A		B	B	B	A			A	A	A			B			158
Hox-2.6	B	B		B		B	A	A	B	A	A	B	B	B	A	A	A	A	A	A		A		B		158
Hox-2.3	B	B	B	B		B	A	A	B		A	B	B	B	A	A	A	A	A	A		A		B		158
Mpmv-8	B	B		B		A	A	A	B	A	A	B	B	B			A	A	A	A	A	B	A			89
Pmv-56	B	B		B		A	A	A	B	A	A	B	B	B			B	A	A	A		A	A	B	A	88
Es-3	B	A	B	B		B	A	A	B		A		B	A	A		A	A	A	A		B		B		158

CXS. C and S represent alleles derived from BALB/cHeA and STS/A, respectively.

Locus	0 1	0 2	0 3	0 4	0 5	0 6	0 7	0 8	0 9	1 0	1 1	1 2	1 3	1 4	References
Tcn-2	C	S	S	C	S	C	S	C	C	S	C	C	C	S	91
Hba	C	S	C	C	C	S	S	C	C	S	C	C	C	S	91
Il-5	C	C	C	C	C	S	S	C	S	S	C	C	C	S	270
Il-4	C	C	C	C	C	S	S	C	S	S	C	C	C	S	58
Il-3	C	C	C	C	S	S	S	C	S	S	C	S	C	S	58
Dlb-1	C	C	C	S	S	S	S	C	S	S	S	S	C	S	111
HoxB	C	C	S	S	S	S	S	C	S	S	S	S	C	S	270
Tca-3	C	C	S	S	S	S	S	C	S	C	S	S	C	S	270
Rnu1a-1	C	C	S	S	S	S	S	C	S	C	S	S	C	S	182
Sigje	C	C	S	C	S	S	S	C	S	C	S	S	S	S	270
Mtv-3	C	C	S	C	S	S	C	S	C	S	S	S	C	S	111
Es-3	C	S	S	C	S	C	S	C	S	S	S	S	C	S	91

NXSM. N and S represent alleles derived from NZB/B1NRe and SM/J, respectively.

Locus	A	C	D	E	F	I	L	N	P	Q	T 1	T 2	U	V	W	X	Z	References
Tcn-2	S	S	N	S	S	S	N	N	S	N	S	S	S	N	S	S	N	77
Pmv-2	S	S	N	S	S	S	N	N	S	N	S	S	S	N	S	S	N	86
Erbb	S	S	S	S	S	S	N	N	S	S	S	S	S	S	S	S	N	77
Pmv-58	S	S	N	S	S	S	N	N	S	S	S	S	S	N	S	S	N	86
Xmv-47	S	N	N	S	S	S	N	N	S	S	S	S	S	N	S	S	N	86
Hba	N	N	N	S	S	S	N	N	S	S	S	S	S	N	S	S	N	77
Evi-2	S	N	N	S	N	S	N	N	N	S	N	N	S	S	S	N	N	77
Mpmv-4	S	N	N	S	N	S	N	N	N	S	N	N	S	S	S	N	N	86
Mmv-16	S	N	N	S	N	S	N	N	N	S	N	N	S	S	S	N	N	86
Xmmv-77	S	N	N	S	N	S	S	N	N	S	N	N	S	S	S	N	N	86
Xmv-49	S	N	N	S	N	S	S	N	N	S	S	S	S	S	S	N	N	86
Mmv-17	S	N	N	S	N	S	N	N	N	S	S	S	S	S	S	N	N	86
Mpmv-8	S	N	N	S	N	S	N	N	N	N	S	S	S	S	S	N	N	86
Gh	S	N	N	S	N	S	N	N	N	N	S	S	S	N	S	N	N	77
Mpmv-15	S	N	N	S	N	S	N	N	N	S	S	S	S	N	S	N	N	86
Mtv-3	S	N	N	S	N	S	N	N	N	S	S	S	S	N	S	N	N	77

Table 5. Cytogenetic location of genes on mouse Chr 11.

Locus	Band location	Reference
Apoh	A5-B1	198
Cola-1	D	192
Ddc	A2	31
D11Was70	Chr11	72
Erbb	A1-A4	191
Flt-4	A5-B1	92
HoxB	D	190
Il-3	A5-B1	262
Il-5	A5-B1	262
Krt-1.14	D	54
Lif	A1-A2	144
Mov-9	B5	192
Mpo	C-E	218
Myhs-f	B2-C	191
Nfh	A1-A5	173
Pfn	11	189a
Phb	D	189a
Rara	D	171
Rnu3b	C-D	175
Rnu3b-1	C-D	175
Rnu3b-2	C-D	175
Rnu3b-3	C-D	175
Rnu3b-4	C-D	175
Rpo2-1	B1-C	214
Sparc	B1	167
Tel11p	A	27
Tel11q	E	27
Tk-1	B3-E2	116
Trp53	B2-C	191

Spnb-2 to the vicinity of *Rel* suggests the possibility that other genes from HSA 2 may map to proximal Chr 11.

Some genes recently mapped to mouse Chr 11 have not been assigned to human chromosomes. The observed evolutionary conservation of chromosomal assignments of genes makes some predictions possible. The high degree of homology between mouse Chr 11 and human Chr 17 strongly supports the suggestion that *Gna-13, Hmg14-rs4, Htt,* and *Mox-1* will map to human 17. *Tr* (*Pmp-22, Gas-3*) currently defines the most proximal locus from HSA 17 on mouse Chr 11. The assignment of *Hist2b-rs1* to either human Chr 17 or human Chr 5 might help to more precisely define the boundary between these two synteny homology groups on Chr 11.

It is more difficult to predict with certainty the human chromosome assignment of genes mapped to proximal mouse Chr 11 because this region contains genes that map to human Chrs 22, 7, 2, 16, and 5. Three genes from HSA 22—*Tcn-2, Lif,* and *Nfh*—map on proximal mouse Chr 11 near the centromere. This suggests that three genes recently localized to this region, *Camk2b, Rnr11,* and *Rpl18-rs,* might map to human Chr 22. As the human chromosome assignments of *Ck-rs5, Glns-ps1, P40-rs5,* and *Rab-1* are completed, the extent of evolutionary conservation on proximal mouse Chr 11 may be clarified.

Table 6. List of variant chromosomes involving mouse Chr 11. NA = not applicable.

Variant name	Breakpoint	References
Robertsonian fusions		
Rb(1.11)2Mpl	NA	222
Rb(4.11)12Rma	NA	46
Rb(9.11)14Tu	NA	3, 28,29
Rb(10.11)8Bnr	NA	104, 46
Rb(10.11)5Rma	NA	45, 46, 100
Rb(11.13)4Bnr	NA	278, 102, 103, 101
Rb(11.13)6Lub	NA	100, 271, 272
Rb(11.13)6Tu	NA	3
Rb(11.14)1Dn	NA	64
Rb(11.16)2H	NA	162
Translocations		
T(X;11)38H	XA1, 11E1	230, 80, 229, 16
T(2;11)4Dn	2D,11B5	63
T(2;11)30H	2H1,11B1	47,16, 48
T(3;11)16Ad	3F1,11B5	63
T(5;11)17Ad	5B,11B1	63
T(9;11) 9Ad	9B1,11D	2
T(11;16)53Dn	11D,16A	63
T(11;17)39Dn	11D,17A2	63
T(11;19)42H	11D, 19B	230, 79, 17, 142
Chromosomal inversions		
In(11)2Dn	11A4, 11B1	62
In(11)20Rk	11A2, 11D	66, 65

Reference mapping loci

In the previous report, we proposed the use of eleven anchor loci to provide a means of cross-referencing maps. Primary anchor loci were chosen from well-spaced loci whose chromosomal location had been confirmed in independent crosses. In order to provide adequate coverage of the chromosome, we proposed several secondary anchor loci that had not been as extensively mapped. *Glns* has been removed as an anchor locus because of its identification as a pseudogene and hence might not be present in all strains. This year we are suggesting the addition of two anchor loci, *D11Mit5* and *D11Mit12*. The following gene order and distances (cM) as estimated from the consensus map are:

Lif (*D11Mit16*)–10–*Erbb*–9–*Adra-1*–10–*Csfgm* –7–*D11Mit5*–6–*Acrb* (*D11Mit29, D11Mit31*)–4– *D11Mit8*–4–*Mpo*–5–*HoxB*–8–*Myla* (*D11Mit58*) –6–*D11Mit12*–9–*Thbp* (*P4hb*).

These anchor loci span the entire 80 cM of Chr 11. Researchers involved in placing markers on mouse Chr 11 are encouraged to include these loci in their analyses.

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