

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 wellcharacterized 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 rasrelated 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	Sumbal	Nama		MAN	T	M-4 3	LI	H les	D.f.
INCW	Symbol		<u>A</u>	M (CM)	<u></u>	Method	H. symbol	H. location	Keterences
	ACE	angiotensin converting enzyme, (D11M#13)		62	D	L	ACE1	1/qZ3	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	В	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
*	Алх-б	annexin-6 (formerly calcium binding membrane (Cabm) and p68		19	Ď	ĩ	ANX-6	5032-34	61 42
*	Apoh	apolipoprotein H (beta-2-glycoprotein-1)		62	ñ	ĩт	APOH	17023 ater	108
	Asor-1	asialoglycoprotein recentor-1		37	ñ	L, 1 T	ASCDI	17012 -11	170
	Aser-2	asialoglyconnein recentor-2		37	ñ	L I	ASCRI	17-	224, 223
	Atp1b2	Na K-ATPase beta-2 (Amor)		41	ň	S I	ATDIDO	170	224,110
	Rda	hald-arthritic		50	v	з, с т	AIFIDZ	тp	204, 118
	Brng	hrsin protein_8 (provisional)		52	'n				8.3
	Reb	have skin		59	U V				94
	Cahm	formarly colour hinding partoin a 69 Sec. And C		20	v	L			160
*	Combat	Tormeny calcium binding protein, pos. See Anx-o		•	-				
	Came20	calmodulin kinase II, beta subunit		0	D	L, S			59, 136
	Chy	chylous ascites		26	B	L			161
-	CK-rss	creaune kinase, brain-related sequence)		17	D	L			50
	Cnp-1	cyclic nucleotide phosphodiesterase-1		59	D	L	CNP	17q21	19
	60	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	17g21.3-g22	236, 256
	Crybl	crystallin, beta polypeptide 1		46	D	Ĺ	CRYB1	17011.1-012	35. 274
	Csfg	colony stimulating factor, granulocyte		57	Ď	Ĺ	CSF3	17a11.2-a12	32, 258
	Csfgm	colony stimulating factor, granulocyte macrophage	1	29	Ď	S.L.P	CSF2	5023-031	95 208
	Csfmu	colony stimulating factor, multi (contains II-3)	•	29	Ř	L	W	adan dar	122 120
	DÌlBayl	DNA segment, Chr 11, Baylor-1		ht	ñ	ŝ	D17578	17013 2	152
	D11Bay2	DNA segment, Chr 11, Baylor-2		45	ñ	ŝī	D1795	17-12.2	153
*	DIIBirl	DNA segment. Chr 11. Birkenmeier-1		53	ň	з,с I	<i>C</i> (1)	1/11.3	133
*	DIIBvul	DNA segment, Chr 11, Brigham Young University 1		5	ř	ь Т			22
*	DIIB	DNA segment Chr 11 Brigham Young University 2		17	ע ח	L T			213
*	DIIRwa	DNA segment Chr 11 Brigham Young University 2		17	5	L			273
*	DIIRvud	DNA segment Chr 11 Brigham Young University-3		15	U U				2/3
*	DIIColi	DNA segment Chr 11 (EDIT 1 (- 2.0.00 DIV		10	D	L			273
*	DIICHI	DNA segment $Chr 11$ (CEDI 2 (2 2 21 D)		JU	D	L			135
*	DIICPAL	DNA segment $Che 11$ (CEPH-2 (CX 3-2-21-FZ)		30	D	L			135
*	DICPRS	DNA segment, Chr 11, CEPH-3 (ex 6-1-3-P1)		30	D	L			135
*	DIICPH4	DNA segment, Chr 11, CEPH-4 (ex 10-1-10-P1)		30	D	L			135
-	DINCWS	DNA segment, Unr 11, D.C. Ward-38		bt	D	I			26
÷	DI IH4SIU	DINA segment, Chr 11, formerly human D4S10h		31	Ð	L	D4S10	4р16.3-р16.2	49
-	DIIHaml	DNA segment, Chr 11, Hamburg-1		bt	D	I		- •	106
-	Diljknie	DNA segment, Chr 11, Jackson-1, expressed		75	D	L			125
Ŧ	DIIJpl	DNA segment, Chr 11, Japan-1		35	D	L			145
	DIILehl	DNA segment, Chr 11, Lehrach-1		39	Ð	L			55
	DIILeh2	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	Ē			152
*	DIIMcl	DNA segment, Chr 11, McClelland-1		42	$\vec{\mathbf{p}}$	ī			264
	DIIMitl	DNA segment, Chr 11, MIT-1		4	Ď	Ē			71
	D11Mit2	DNA segment, Chr 11, MIT-2		5	$\tilde{\mathbf{p}}$	ī			71
	D11Mit4	DNA segment, Chr 11, MIT-4		37	ñ	ĩ			71
	D11Mit5	DNA segment, Chr 11, MIT-5	2	36	ñ	ĩ			71
	D11Mit7	DNA segment, Chr 11, MIT-7	~	44	ñ	ĩ			71
	D11Mit8	DNA segment, Chr 11, MIT-8	2	46	ň	ř			71
	D11Mit10	DNA segment, Chr 11, MIT-10	4	64	ň	г Г			/1
	DIIMull	DNA segment. Chr 11, MIT-11		60	D D	L I			/1
	D11Mit12	DNA segment. Chr 11, MIT-12	,	71	D D	L T			/1
*	D11Mit13	DNA segment Chr 11 MIT-13 See Ace	1	/1 60	L L				71
*	DIIMin14	DNA segment Chr 11 MIT-14 See Aut D01.		02 50	D D	L			183
*	D11Mit15	DNA segment Chr 11 MTT-15 Can Cline 4		20	D D	L			183
*	DIIMinis	DNA segment Chr 11 MTT 16 5-5 7:6		39	D	L			183
*	D11M410	DNA comment Chr 11 MTT 10	1	4	D	L			183
*	DIIMIO	DNA segment, Chr 11, MII-19		11	D	L			183
*	DIIMENI	DNA segment Chr 11, MIT-20		15	D	L			183
*	DIIMIO	DNA segment Che 11 MIT-21		15	D	L			183
*	DIIMUZZ	DNA segment, Chr 11, M11-22		18	D	L			183
*	DIDUCT	DNA segment, Chr 11, M11-23		22	D	L			183
*	DUMIZ4	DNA segment, Chr 11, MIT-24		22	D	L			183
*	DIIMUZS	DNA segment, Chr 11, MIT-25		22	D	L			183
-	D11Mit26	DNA segment, Chr 11, MIT-26		31	D	L			183
-	DIIMit27	DNA segment, Chr 11, MIT-27		36	D	L			183
	DIIMi28	DNA segment, Chr 11, MIT-28		37	D	L			183
*	D11Mit29	DNA segment, Chr 11, MIT-29 See Acrb	1	42	D	Ĺ			183
*	DIIMit30	DNA segment, Chr 11, MIT-30	· · ·	42	D	Ĺ			183
*	DIIMit31	DNA segment, Chr 11, MIT-31 See Acrb	1	42	Ď	Ĺ			183
*	D11Mit32	DNA segment, Chr 11, MIT-32	-	42	Ď	Ē			192
*	DIIMit33	DNA segment, Chr 11, MIT-33		42	กั	ĩ			162
*	D11Mit34	DNA segment, Chr 11, MIT-34		42	ň	ĩ			163
*	D11Mit35	DNA segment, Chr 11, MIT-35 See Min1a		48	ň	ř			183
*	DIIMit36	DNA segment, Chr 11, MIT-36		40	л Л	г т			183
				**7	D	L			183

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			1444					
*	D11Mir37	DNA segment Chr 11 MIT-37	40	D	т			1.07
•	DING	DNA sognitati, Cii 11, Mil-57	47	2	L V			185
	DIIMIGO	DNA segment, Chr 11, MIT-38	50	D	L			183
*	D11Mit39	DNA segment, Chr 11, MIT-39	50	D	L			183
*	D11Mii40	DNA segment, Chr 11, MIT-40	44	D	T.			183
	DINGAL	DNI - Chall MT 41		2	L			165
•	DIIMIHI	DNA segment, Chr II, MII-41	52	D	L			183
*	D11Mit42	DNA segment, Chr 11, MIT-42	71	D	L			183
*	DIIMida	DNA segment Chr 11 MTT-48	76	n	T			192
	DIIIIIIII		70	2	L			105
*	DIIMii49	DNA segment, Chr 11, MIT-49	76	D	L			183
*	D11Mit50	DNA segment, Chr 11, MIT-50	67	D	L			183
*	D11Mir51	DNA segment Chr.11 MTL-51	14	n	T			192
	DIIMAJI	Divis segment, cin 11, MIT-51	14	2	L			105
*	DIIMid2	DNA segment, Chr 11, MIT-52	61	D	L			183
*	D11MitS3	DNA segment, Chr 11, MIT-53	13	D	L			183
*	DIIMitSA	DNA request Chr 11 MIT-54	56	n	T			193
	DIIMMOT		50	2	L T			105
*	DIIMiDO	DNA segment, Chr II, MII-56	49	D	L			183
*	D11Mit58	DNA segment, Chr 11, MIT-58 See Myla	2 64	D	L			183
*	D11Mir50	DNA comment Che 11 MIT 50	58	- D	T			192
*	DIIMIOY	DNA segment, Chr 11, MIT-39	20		L			185
*	D11Mit60	DNA segment, Chr 11, MIT-60	42	D	L			183
*	D11Mit61	DNA segment, Chr 11 MIT-61	71	D	L			183
•	DINK	DNA segment (he 11 MTE ()		5	Ť			100
Ŧ	DIIMIIOZ	DNA segment, Chr II, MII-02	4	D	L			185
*	D11Mit63	DNA segment, Chr 11, MIT-63	5	D	L			183
*	DIIMinA	DNA segment Chr 11 MIT-64	22	n	T			192
	DIIMMO	Dive segment, clif 11, MIT-04	22	5				105
*	DIIMuos	DNA segment, Chr 11, MIT-65	44	D	L			183
*	D11Mit66	DNA segment, Chr 11, MIT-66	49	D	L			183
*	D1114:47	DNA comment Cha 11 MTT 67	57	n	T			192
-	DIIMU0/	Dive southern, Chi 11, Mil 1-0/	51	U L	ь			103
*	D11Mit68	DNA segment, Chr 11, MIT-68	47	D	L			183
*	D11Mit69	DNA segment, Chr 11, MIT-69	80	D	Ľ.			183
*	D1114:220	DNA segment Cha 11 MTT 70	E A	5	Ť			192
Ŧ	DIIMU/U	DIAA segment, Chr 11, MII-/U	54	D	L			165
	DIINdsl	DNA segment, Chr 11, Nuffield Depart. of Surgery-1	45	D	L			52
	DIINAN	DNA segment Chr 11 Nuffield Denart of Summer 2	66	D	T.			52
*	DINKSZ	Dive sources, Chi 11, Further Deput. of Surgery-2	~	L L	1. T			50
*	DIINds3	DNA segment, Chr 11, Nutfield Depart. of Surgery-3	27	D	L			53
*	DIINds7	DNA segment, Chr 11, Nuffield Denart, of Surgery-7 See Gfan	62	D	L			71
	DINLO	DNA assure (ha 11 Nuffeld Denort of Susanni 0 See 115	20	ñ	T			71
Ŧ	DIINasy	DIVA segment, Chr 11, Nutifield Depart. of Surgery-9 See 11-5	28	D	L			/1
	DIIPasl	DNA segment, Chr 11, Pasteur-1	59	D	L			234
	D11Pas2	DNA segment Chr 11 Pasteur-2	54	D	T.			105
		DNA CI 11 D C	40	5	1			105
•	DIIPass	DNA segment, Chr II, Pasteur-5	45	D	L			13
*	DIIPas6	DNA segment, Chr 11, Pasteur-6	37	Ð	L			13
	D115.11	DNA segment Chr 11 Seldin-1	23	D	T			201
4	DIIGEN		20	5	1.			201
*	DIISel2	DNA segment, Chr 11, Seldin-2	73	D	L			233
*	DIISel3	DNA segment, Chr 11, Seldin-3	74	D	L			233
*	D115-14	DNA comment Chr. 11 Saldin A	12	n	T			222
	DIIJer	DIAA Segment, Chi 11, Selum-4		2	ь •			233
	DI IWas70	DNA segment Chr 11 University of Washington 70	ht		1			72
		Diverse and a children of the astrony of the astrong con-10	0.	~	-			
	D4510h	DNA segment Chr 11 human D4S10 See D11H4S10	31	Ď	Ī.			
	D4S10h	DNA segment, Chr 11, human D4S10 See D11H4S10	31	Ď	Ĺ	DDC	7.11	21
*	D4S10h Ddc	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase	31 5t	D D	L I	DDC	7p11	31
*	D4S10h Ddc df	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf	31 bt 25	D D V	L I L	DDC	7p11	31 14
*	D4S10h Ddc df Dlb-1	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding.1	31 bt 25 55	D D V B	L I L	DDC	7p11	31 14 209
*	D4S10h Ddc df Dlb-1	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1	31 bt 25 55	D D V B	L I L L	DDC	7p11	31 14 209
*	D4S10h Ddc df Dlb-1 Edp-1	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein	31 bt 25 55 38	D D V B D	L I L L L	DDC EDP	7p11 17q22-q23	31 14 209 40
*	D4S10h Dac af Dlb-1 Edp-1 Eif4al	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukarvotic initiation factor-4AI	31 bt 25 55 38 39	D D V B D D	L I L L L L	DDC EDP	7p11 17q22-q23	31 14 209 40 197
*	D4S10h Dac af Dlb-1 Edp-1 Eif4a1 Emph3	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erstbroccta membrana protein band 3	31 bt 25 55 38 39 61	D D V B D D D	L I L L L L	DDC EDP	7p11 17q22-q23	31 14 209 40 197 159 235
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3	31 bt 25 55 38 39 61		L I L L L L L	DDC EDP EPB3	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-14	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J)	31 bt 25 38 39 61 38	D D V B D D D D D D	L I L L L L L L	DDC EDP EPB3	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235 130
*	D4S10h Ddc df Dlb-1 Eig4a1 Empb3 Emv-14 Emv-28	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28	31 bt 25 55 38 39 61 38 54			DDC EDP EPB3	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235 130 253
*	D4S10h Ddc df Dlb-1 Edp-1 Elf4al Empb3 Emv-14 Emv-28 Emv-28	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous costropic MuLV-28 endogenous costropic MuLV-28	31 bt 25 55 38 39 61 38 54	2 D D V B D D D D D D D D	L I L L L L L L L	DDC EDP EPB3	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235 130 253 215
*	D4S10h Ddc df Dlb-1 Edp-1 EiqP-1 Empb3 Emp-14 Emv-28 Emv-28 Emv-30	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28	31 bt 25 55 38 39 61 38 54 11		L I L L L L L L L	DDC EDP EPB3	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235 130 253 215
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-30 Emv-33	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 (Bbv)	51 51 55 38 39 61 38 54 11 69	D D V B D D D D D D D D D D	L I L L L L L L L L L	DDC EDP EPB3	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235 130 253 215 148
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Frba	DNA segment, Chi 11, human D4S10 See D11II4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncosene A, thyroid hormone receptor	31 bt 25 55 38 39 61 38 54 11 69 57		L I L L L L L L L L L L L	DDC EDP EPB3 THRA1	7p11 17q22-q23 17q21-q22	31 14 209 40 197 159, 235 130 253 215 148 67, 186
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-28 Emv-30 Emv-33 Erba Erba	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30	31 bt 25 55 38 39 61 38 54 11 69 57	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L S,L	DDC EDP EPB3	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-12.2	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erba Erbb	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncogene B, epidermal growth factor receptor	31 bt 25 55 38 39 61 38 54 11 69 57 1 10		L I L L L L L L L L L S,L,I	DDC EDP EPB3 THRA1 EGFR	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239
*	D4S10h Ddc df D1b-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erba Erbb Erbb-2	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30	31 bt 25 55 38 39 61 38 54 11 69 57 1 10 57	D D V B D D D D D D D D D D D D D D D D	L I L L L L L L L L S,L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-30 Emv-33 Erba Erbb Erbb-2 Ers-3	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 (Bbv) avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 estersae-3 (Ke-2)	31 bt 25 55 38 39 61 38 54 11 69 57 1 10 57 75		L I L L L L L L L S,L S,L,I L L	DDC EDP EPB3 THRA1 EGFR ERBB2	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erba Erbb Erbb Erbb-2 Es-3 Es-3	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (E=2)	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 57 1	0 0 V B 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erba Erbb Erbb Erbb-2 Es-3 Evi-2	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 esterase-3 (<i>Ee-2</i>) ecotropic viral integration site-2	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 75 46		L I L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVIZA	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32
*	D4S10h Ddc: df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Eta Erbb Erbb Erbb Erbb Erbb Erbb Erbb-2 Es-3 Evi-2 Flt-4	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (Ee-2) ecotropic viral integration site-2 FMS-like tyrosine kinase-4	51 bt 25 55 38 39 61 38 54 11 69 57 1 10 57 57 1 10 57 57 46 bt		L I L L L L L L L L L L L L L L I	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92
*	D4S10h Ddc df Dib-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erba Erbb Erbb-2 Es-3 Evi-2 Fit-4 Gaa	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75		L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA	7p11 17q22-q23 17q21-q22 17q11.2-q22 17p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165
*	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Emv-30 Emv-33 Emv-30 Emv-30 Emv-33 Ev-33 Ev-33 Ev-5 Ev-5 Ev-2 Flt-4 Gaa Galant	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 ($Akv-4$, $Akv-2J$) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 estorase endogenous ecotropic MuLV-30 estorase (MuLV-30 endogenous ecotropic MuLV-30 estorase (MuLV-30 endogenous ecotropic MuLV-30 estorase (MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 estorase (MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30	51 52 55 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 46 bt	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GAPA1	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37
*	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-28 Emv-28 Emv-30 Emv-30 Emv-33 Erba Erbb Erbb Erbb-2 Es-3 Evi-2 Flt-4 Gaa Gabral	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-32 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (Ee-2) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19		L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRA1	7p11 17q22-q23 17q21-q22 17q11-2-q22 17p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37
*	D4S10h Ddc đ Dlb-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-30 Emv-30 Emv-33 Eta Erbb Erbb-2 Es-3 Evi-2 Flt-4 Gata Gabrg-2	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 ecotropic Visit MuLV-30 ecotropic Visit MuLV-30 ecotropic	31 bt 25 55 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29	00000000000000000000000000000000000000	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GABA GABRA1 GABRG2	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41
*	D4S10h Ddc: df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-30 Emv-33 Erbb Erbb Erbb Erbb Erbb Erbb-2 Es-3 Evi-2 Flu-4 Gaa Gabra1 Gabra2 Gabra3	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (Ee-2) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit gamma-2 growth arrest specific-3 See Pmu-22. Tr	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29 33	00780000000080000000000000000000000000	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 5q34-q35 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51
*	D4S10h Ddc df Dib-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-30 Emv-30 Emv-33 Eta Erbb Erbb Erbb-2 Es-3 Evi-2 Fil-4 Gabra1 Gabra2 Gabra2 Gabra2 Gabra2 Gabra2 Gabra3 Cfm	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 esterase-3 (<i>Ee-2</i>) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit agmma-2 growth arrest specific-3 See Pmp-22, Tr	51 55 55 38 39 61 38 54 11 69 57 10 57 75 46 bt 75 19 29 33 62	00080000000008000000000000000000000000	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GEAD	7p11 17q22-q23 17q21-q22 17q11.2-q22 17p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 5q34-q35 5q34-q35 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19 25
* *	D4S10h Ddc: df Dlb-1 Edp-1 Eif4al Empb3 Emv-28 Emv-28 Emv-30 Emv-33 Eta Erbb Erbb Erbb Erbb Erbb Erbb Erbb Erb	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (<i>Ee-2</i>) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit gamma-2 growth arrest specific-3 See Pmp-22, Tr glial fibrillary acidic protein,(D11Nds7)	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29 33 62		L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 5q34-q35 5q34-q35	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 51 25 25 25 25 25 25 25 25 25 25
* *	D4S10h Ddc df Dib-1 Edp-1 Eif4a1 Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erba Erbb-2 Erbb-2 Es-3 Evi-2 Fit-4 Gaa Gabra1 Gabrg-2 Gas-3 Gfap Gh	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30	51 bt 25 55 38 39 61 38 57 61 57 57 1 10 57 75 46 bt 75 19 29 33 62 66	0 0 V 8 0 0 0 0 0 0 0 0 0 8 0 0 0 0 0 0	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRA1 GABRG2 GFAP GH1	7p11 17q22-q23 17q21-q22 17q11-2-q22 17p14-p12-2 17p14-p12-2 17p11-2-q12 17q11-2 5q34-q35 17q23 5q34-q35 5q34-q35 5q34-q35 17q21 17q22-24	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274
* * *	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-2 Edp-2 Edp-2 Edp-2 Erbb Erbb Erbb Erbb Erbb Erbb-2 Es-3 Evi-2 Flu-4 Gabral Gabral Gabral Gabra-2 Gas-3 Gfap Gh Gia-7	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 ecotropic Visit Hatter and ecotropic MuLV-30 ecotropic Visit Hatter ecotropic Visit Hatter ecotropic Visit Hatter e	51 52 55 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29 33 62 bt 66 bt	0 0 V B 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRA1 GABRG2 GFAP GH1	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 5q34-q35 5q34-q35 17q21 17q22-24	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226
* * *	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-28 Emv-28 Emv-30 Emv-30 Emv-33 Erba Erbb Erbb Erbb-2 Es-3 Evi-2 Flt-4 Gaa Gabral Gabra2 Gabra3 Gfap Gh Gja7 Gck	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-32 esterase-3 (<i>Bev</i>) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (<i>Ee-2</i>) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit alpha-1 growth arrest specific-3 See Pmp-22, Tr gial fibrillary acidic protein,(D11Nds7) growth hormone gap junction membrane channel protein alpha-7 (connexin45) ebuchingen	51 55 55 38 39 61 38 54 11 69 57 10 57 75 46 57 19 29 33 62 66 bt	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK	7p11 17q22-q23 17q21-q22 17q11-2-q22 17p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 255 146 150 150 150 150 150 150 150 150
* * *	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Emv-30 Emv-30 Emv-30 Emv-30 Emv-30 Emv-30 Emv-33 Ev-33 Ev-3 Ev-3 Ev-3 Ev-3 Ev-2 Flt-4 Gaa Gabrg-2 Gas-3 Gfap Gh Gja-7 Gk	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30 ecotropic Visit integration site-2 growth arest specific-3 See Pmp-22, Tr glial fibril	51 52 55 38 39 61 38 54 11 69 57 10 57 46 bt 75 46 bt 75 19 29 33 62 66 bt 4 	00000000000000000000000000000000000000	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRA1 GABRA1 GABRG2 GFAP GH1 GCK CUX	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 5q34-q35 17q21 17q22-24 7p	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 156 157 156 157 126 157 126 157 126 157 157 157 157 157 157 157 157
* * *	D4S10h Ddc: df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-30 Emv-33 Erbb Erbb Erbb Erbb Erbb-2 Es-3 Evi-2 Flu-4 Gaar Gabral Gabrg-2 Gas-3 Gfap Gh Gja-7 Gk Glk	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-230 (Bev) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (E-2) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA-receptor, subunit alpha-1 GABA-A receptor, subunit alpha-1 growth arrest specific-3 See Pmp-22, Tr glial fibrillary acidic protein,(D11Nds7) growth homone gap junction membrane channel protein alpha-7 (connexin45) glucokinase galactokinase	31 bt 25 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29 33 62 66 bt 4 78	0 0 V 8 0 0 0 0 0 0 0 0 0 8 0 0 0 0 0 0	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK GALK	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 5q34-q35 17q21 17q22-24 7p 17q	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 19, 25 126, 274 226 156 185, 274
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* * * ** ****	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-28 Emv-28 Emv-30 Emv-33 Erba Erbb Erbb Erbb-2 Es-3 Evi-2 Flt-4 Gaa Gabral Gabral Gabrg-2 Gas-3 Gfap Gh Gik Gik Gins-ps1 Gib-1 Giu-4 Gna-13 Gp3a Gp2b Gibp H(lu) H(lu) H(lu)	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-29 endogenous ecotropic MuLV-30 endogenous ecotropic multi-3 giveorotin stepsonsite, (D11Mit15) guanine nucleotide-binding protein alpha-13 glycoprotein 3a, alpha IIB integrin see Rab-1 histocompatibility(s)(provisional) histocompatibility(s)(provisional) histocompatibility(s) (provisional)	1 10 57 55 38 39 61 38 54 11 69 57 75 46 bt 57 75 46 bt 57 75 46 bt 4 78 12 31 39 68 68 68 12 bt bt 57 51 57 55 55 55 55 55 55 55 55 55 55 55 55	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 ITGB3 ITGA2B	7p11 17q22-q23 17q21-q22 17q11-2-q12 17p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 17q21.32	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 156 185, 274 159, 42 112, 117 268 233 233 152 8 8 8 8 8 8
* * * ** *****	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Emv-28 Emv-28 Emv-30 Emv-33 Erbo Erbb Erbb Erbb Erbb Erbb Erbb Erbb	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 (Bbv) avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (<i>Ee-2</i>) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit gamma-2 growth arrest specific-3 See Pmp-22, Tr glial fibrillary acidic protein,(D11Nds7) growth homone gap junction membrane channel protein alpha-7 (connexin45) glucokinase galactokinase glutamine synthetase pseudogene-1 glutamate receptor-1 glucose transporter, insulin responsive, (D11Mit15) guanine nucleotide-binding protein alpha-13 glycoprotein 2a, alpha IIB integrin see Rab-1 histocompatibility(<i>is</i>)(provisional) histocompatibility(<i>is</i>)(provisional) histocompatibility(<i>in</i>) (provisional) histocompatibility(<i>in</i>) (provisional)	51 55 55 55 39 61 38 39 61 38 57 1 1 57 75 46 bt 75 19 29 33 62 66 bt 4 78 12 31 39 68 68 68 68 68 61 51 51 51 51 51 55 55 55 55 5	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 ITGB3 ITGA2B	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 17q21.32	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 185, 274 159, 42 112, 117 268 233 152 8 8 8 8 211, 38
* * * ** ****	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-28 Emv-28 Emv-30 Emv-33 Erbb Erbb Erbb Erbb-2 Es-3 Evic2 Flt-4 Gaa Gabral Gabrg-2 Gas-3 Gfap Gh Gja7 Gk Gik Glk Glns-ps1 Gik-1 Giu-4 Gma-13 Gp3a Gp2b Gtbp H(is) H(in) H(in) Hbax	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-23 endogenous ecotropic MuLV-30 endogenous ecotropic multor growth arrest specific-3 <i>See Pmp-22</i> , <i>Tr</i> glial fibrillary acidic protein,(<i>D11Nds7</i>) growth homone gap junction membrane channel protein alpha-7 (connexin45) glucokinase glutamine synthetase pseudogene-1 glutamate receptor-1 glucose transporter, insulin responsive, (<i>D11Mit15</i>) guanine mucleotide-binding protein alpha-13 glycoprotein 3a, alpha IIIa integrin see Rab-1 histocompatibility(<i>b</i>)(provisional) histocompatibility(<i>b</i>)(provisional) histocompatibility(<i>b</i>)(provisional) histocompatibility(<i>b</i>)(provisional) hemoglobin X (alpha-like embryonic chain in Hba complex)	1 10 57 55 38 39 61 38 54 11 69 57 75 46 bt 57 75 46 bt 57 19 29 33 62 66 bt 4 78 12 31 39 68 68 68 12 bt bt 17 17	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 ITGB3 ITGA2B HBA	7p11 17q22-q23 17q21-q22 17q11-2-q12 17p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 17q21.32 17q21.32	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 185, 274 159, 42 112, 117 268 233 233 152 8 8 8 8 8 8 8 8 8 8 8 8 8
* * * ** *****	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Edp-1 Emv-28 Emv-30 Emv-33 Eva Emv-30 Emv-33 Evba Erbb Erbb Erbb Erbb Erbb Erbb-2 Es-3 Evi-2 Fl-4 Gaa Gabral Gabral Gabral Gabra Gia-7 Gik Glk Glns-ps1 Giu-4 Gna-13 Gp2b Gibp H(is) H(in) Hba Hba-x Hc1!	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-30	31 bt 25 55 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29 33 62 bt 4 78 12 31 39 68 68 68 12 bt bt 17 17 10	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRA1 GABRA2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 ITGB3 ITGA2B HBA	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 17q21.32	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 156 185, 274 159, 42 112, 117 268 233 233 152 8 8 8 211, 38 266 169 128
* * * ******* *.	D4S10h Ddc: df Dlb-1 Edp-1 Eif4al Empb3 Emv-14 Emv-28 Emv-30 Emv-33 Erbb Erbb Erbb Erbb-2 Es-3 Evic2 Flu-4 Gaar Gabral Gabrg-2 Gas-3 Gfap Gh Gja-7 Gk Glk Glk Glns-ps1 Glv-1 Glu-13 Gp3a Gp2b Gtbp H(js) H(js) H(in) Hba-x Hc11	DNA segment, Chr 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-230 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (Ee-2) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit gamma-2 growth arrest specific-3 See Pmp-22, Tr glial fibrillary acidic protein,(D11Nds7) growth homone gap junction membrane channel protein alpha-7 (connexin45) glucokinase galactokinase glutamine synthetase pseudogene-1 glucose transporter, insulin responsive, (D11Mit15) guarnien encleotide-binding protein alpha-13 glycoprotein 3a, alpha IIIa integrin see Rab-1 histocompatibility(<i>is</i>)(provisional) histocompatibility(<i>in</i>) (provisional) histocompatibility(<i></i>	1 10 57 55 38 39 61 38 57 1 10 57 75 46 bt 75 19 29 33 62 66 bt 4 78 12 31 39 68 68 68 12 bt bt 17 17 0	00V80000000088000000088000000088888000000	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 TTGB3 TTGA2B HBA	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 17q21.32 16p13.3	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 19, 25 126, 274 256 185, 274 159, 42 112, 117 268 233 233 152 8 8 8 211, 38 266 169, 128 129 129 129 129 128 129 129 129 129 129 129 120 120 120 120 120 120 120 120
* * * ** ***** **	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Edp-1 Emv-28 Emv-30 Emv-33 Emv-30 Emv-33 Ev-3 Ev-3 Ev-3 Ev-3 Ev-3 Ev-3 Ev-3	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-30 endogenous ecotropic multi-30 endogenous ecotropic matcher exit erythroblastosis oncogene B, epidermal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (<i>Ee-2</i>) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit gamma-2 growth homone gap junction membrane channel protein alpha-7 (connexin45) glucokinase galactokinase galactokinase glutarnine synthetase pseudogene-1 glutose transporter, insulin responsive, (D11Mit15) guanine nucleotide-binding protein alpha-13 glycoprotein 3a, alpha IIIa integrin glycoprotein 2b, alpha IIB integrin glycoprotein 2b, alpha IIB integrin see Rab-1 histocompatibility(<i>in</i>) (provisional) histocompatibility(<i>in</i>) (provisional) hemoglobin α chain complex hemoglobin α chain complex hemoglobin α chain complex hemoglobin α chain in stellite-11 Histone 2b related sequence-1	31 bt 25 55 38 39 61 38 54 11 69 57 1 10 57 75 46 bt 75 19 29 33 626 bt 4 78 12 31 39 68 68 68 12 bt bt 17 10 32	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRA1 GABRA1 GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 TTGB3 TTGA2B	7p11 17q22-q23 17q21-q22 17q11.2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 5q34-q35 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 17q21.32 17q21.32	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 129, 25 126, 274 159, 42 112, 117 268 233 233 152 8 8 8 211, 38 266 169, 128 143
* * * ** ****** ***	D4S10h Ddc: df Dlb-1 Edp-1 Eif4a1 Empb3 Emv-28 Emv-30 Emv-33 Erbb Erbb Erbb Erbb-2 Es-3 Evi-2 Flu-4 Gaa Gabra1 Gabrg-2 Gas-3 Gfap Gh Gja-7 Gk Glus-ps1 Glu-4 Gins-ps1 Glu-4 Gins-ps1 Glu-4 Gins-ps1 Glu-4 Gins-ps1 Glu-4 Gins-ps1 Glu-1 Glu-4 Gins-ps1 H(u) H(u) H(u) H(u) H(u) H(u) H(u) H(u)	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncogene A, thyroid hormone receptor avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (E-2) ecotropic viral integration site-2 FMS-like tryosine kinase-4 Acid alpha glucosidase GABA-receptor, subunit alpha-1 GABA-A receptor, subunit ganma-2 growth arrest specific-3 See Pmp-22, Tr glial fibrillary acidic protein,(D11Nds7) growth hormone gap junction membrane channel protein alpha-7 (connexin45) glucokinase glutamine synthetase pseudogene-1 glutamate receptor-1 glucose transporter, insulin responsive, (D11Mit15) guanine nucleotide-binding protein alpha-13 glycoprotein 3a, alpha IIIa integrin glycoprotein 3a, alpha IIIa integrin glycoprotein 3a, alpha IIIa integrin see Rab-1 histocompatibility(<i>i</i>)(provisional) histocompatibility(<i>i</i>)(provisional) histocompa	1 10 57 55 38 39 61 38 57 10 57 75 46 bt 57 75 46 bt 57 19 29 33 62 66 bt 4 78 12 31 88 68 68 68 12 bt bt 57 17 0 32 60	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 TTGB3 TTGA2B	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 16p13.3	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 19, 25 126, 274 256 185, 274 159, 42 112, 117 268 233 233 152 8 8 8 8 8 8 211, 38 266 169, 128 131
* * * * ****** ***	D4S10h Ddc df Dlb-1 Edp-1 Eif4al Empb3 Emv-28 Emv-28 Emv-30 Emv-33 Erba Erbb Erbb-2 Erbb-2 Es-3 Evi-2 Flt-4 Gaa Gabral Gabral Gabral Gabra Gfap Gh Gik Gik Gik-1 Giu-4 Gma-13 Gp3a Gp2b Gibp H(is) H(i	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-29 endogenous ecotropic MuLV-30 endogenous ecotropic managenetic factor receptor avian erythroblastosis oncogene B, epidermal growth factor receptor growth arrest specific-3 <i>See Pmp-22</i> , Tr glial fibrillary acidic protein,(<i>D11Nds7</i>) growth hormone gap junction membrane channel protein alpha-7 (connexin45) glucokinase galactokinase galactokinase glutamine synthetase pseudogene-1 glutamate receptor-1 glucose transporter, insulin responsive, (<i>D11Mit15</i>) guanine nucleotide-binding protein alpha-13 glycoprotein 3a, alpha IIIa integrin see Rab-1 histocompatibility(<i>is</i>)(provisional) histocompatibility(<i>is</i>)(provisional) histocompatibility(<i>is</i>)(provisional) heterochromatin satellite-11 Histone 2b related sequence-1 high-mobility-group protein 14-related sequence-4 hormeo how-2 cluster foremerie Marv-2	1 10 57 55 38 39 61 38 54 11 69 57 75 46 bt 19 29 33 66 bt 4 78 12 31 39 68 68 12 bt bt 17 10 32 66 17 10 10 10 10 10 10 10 10 10 10	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EVI2A FLT4 GAA GABRA1 GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 ITGB3 ITGA2B HBA	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17p13 17q21.32 17q21.32 16p13.3	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 156 185, 274 159, 42 112, 117 268 233 233 152 8 8 8 8 211, 38 266 169, 128 143 131 134, 157, 227
* * * ** ***** ***	D4S10h Ddc: df Dlb-1 Edp-1 Edp-1 Edp-1 Edp-1 Emv-28 Emv-28 Emv-30 Emv-33 Eta Erbb Erbb Erbb Erbb Erbb Erbb Erbb Erb	DNA segment, Chi 11, human D4S10 See D11H4S10 dopa decarboxylase Ames dwarf dolichos lectin binding-1 endothelial cell derived protein eukaryotic initiation factor-4AI erythrocyte membrane protein band 3 endogenous ecotropic MuLV-14 (Akv-4, Akv-2J) endogenous ecotropic MuLV-28 endogenous ecotropic MuLV-30 endogenous ecotropic MuLV-33 (Bbv) avian erythroblastosis oncogene B, epidemal growth factor receptor avian erythroblastosis oncogene B-2 esterase-3 (Ee-2) ecotropic viral integration site-2 FMS-like tyrosine kinase-4 Acid alpha glucosidase GABA receptor, subunit alpha-1 GABA-A receptor, subunit gamma-2 growth arrest specific-3 See Pmp-22, Tr glial fibrillary acidic protein,(D11Nds7) growth homone gap junction membrane channel protein alpha-7 (connexin45) glucokinase glatataine synthetase pseudogene-1 glutamate receptor-1 glucose transporter, insulin responsive, (D11Mit15) guanine nucleotide-binding protein alpha-13 glycoprotein 2a, alpha IIB integrin see Rab-1 histocompatibility(is)(provisional) hist	31 bt 25 55 38 39 61 38 57 11 69 57 11 57 75 46 bt 75 19 29 33 62 66 bt 4 78 12 31 39 68 68 68 68 68 61 bt bt bt bt 17 70 32 60 1 55 32 61 10 57 55 10 5 55 10 55 55 10 55 55 10 55 55 10 55 55 10 55 55 55 10 55 10 55 55 10 55 55 10 55 55 10 55 55 10 55 55 10 55 55 10 55 55 55 10 55 55 55 10 55 55 55 10 55 55 55 10 55 55 55 10 55 55 55 10 55 55 55 55 55 55 55 55 55 55 55 55 55	, , , , , , , , , , , , , , , , , , ,	L I L L L L L L L L L L L L L L L L L L	DDC EDP EPB3 THRA1 EGFR ERBB2 EV12A FLT4 GAA GABRG2 GFAP GH1 GCK GALK GLUL GLR1 GLUT4 ITGB3 ITGA2B HBA HOX2	7p11 17q22-q23 17q21-q22 17q11-2-q21 7p14-p12.2 17p11.2-q12 17q11.2 5q34-q35 17q23 5q34-q35 17q21 17q22-24 7p 17q 5q33 17q21.32 17q21.32 16p13.3	31 14 209 40 197 159, 235 130 253 215 148 67, 186 276, 239 32, 210 212, 206 32 92 166, 165 140, 37 41 51 19, 25 126, 274 226 156 185, 274 159, 42 112, 117 268 233 152 8 8 8 211, 38 266 169, 128 143 131 134, 157, 227 158 209 209 209 215 209 215 209 215 215 215 215 215 215 215 215

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Table 1. Continued.

	Hox-R2	homen hor.? cluster nene?		56	D	DI			159
	Ucr D2	homes has 2 shutter and 2		50	20	F,L I I D			158
	IIUA-DJ	nomeo box-2 cluster, gene 3		20	D	L,1,P			190
	HOX-B4	homeo box-2 cluster, gene 4		56	D	Р			73
	Hox-B5	homeo box-2 cluster, gene 5		56	D	Р			73
	Hox-B6	homeo box-2 cluster, gene 6		56	D	L.P			158
	Hox-B7	homeo box-2 cluster, gene 7		56	Ď	-,- P			73
	Hox-B8	homen hox-2 cluster gene 8		56	ñ	Ď			00
	Hangh nel	hast shock matrin 86 kDo 7 (Man 86 2)		50	5	r o t			90
	115000-051	near snock protein, so ki/a-2 (11 spso-2)		46	D	5,1			188
-	HU	serotonin (3-hydroxytrptamine) transporter		44	D	L			99
	ldd-4	insulin-dependent diabetes susceptibility-4		44	В	L			255
	II-3	interleukin-3 (contained in Csfmu)		29	D	LS.L.P	П.3	5023-031	187 120
	11-4	interleukin-4		28	ñ	T S	Π.4	5-21	58 746
	11-5	interleukin-5 (DIINdeQ)		20	ň	6 T T	115	5-02-21	154.000 045
		monoukin-5, (Diffees)		20	U	3,1,1	шэ	5q23-q31	154,262, 245
	Int-4	See Whi-3							
	Int-4A	See Wat-3A							
	lrf-1	interferon regulatory factor-1		29	D	L	IRF1	5a23-a31	41, 124
	is	Jackson shaker		77	v	T.		· T 1	70
	Krt.l	kentin gene complex.		58	'n	ŝī	KDT15	17-01-00	191 11
	R 1 10	kontin sere complex 1 sere 10		50		3,L. T	KNT10	17421-422	101, 11
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Ŧ	Krt-1.14	keratin gene complex-1, gene 14		58	D	i	KRT14	17q12-q21	54
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	Mmv-13	MCF endogenous virus-13		bt	D	S			113
*	Mmv-16	MCF endogenous virus-16		48	D	T.			86
*	Mmv-17	MCF endogenous virus-17		50	ñ	ĩ			96
	Mong	Meleneu leukemie viewe 0		15	2				80
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	Mpmv-4	modified polytropic murine leukemia virus-4(Xmmv-3)		48	D	L			88
	Mpmy-8	modified polytropic murine leukemia virus-8		63	n	ĩ			80
	Momy-15	modified polytropic murine leukemia vinus 15		70	Б Б	L T			07
	Manual 10	modified polytopic multile leakening vitus-15		12	U D	L L			89
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*	Mtv-45	mammary tumor virus-45		bt					
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	Muha 12	myosin hoavy chain, account muscle, enotyonic		35	2	3,L,P			100
	Myns-j2	myosin neavy chain, skeletal muscle, adult last-2		35	U	S,L,I,P			155
	myns-p	myosin heavy chain, skeletal muscle, perinatal		35	D	S,L,P			155
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	0m	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.	2	80	D	C.L	P4HB	17625	35 205
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*	Pf.	Denfilin		DL L	ň	3	PDEG	17	00, 146, 257
*	DLL			DL	D	1	PFN	17p13.3	189a
	CRD DL	Prontonum		bt	D	1	PHB	17q21	189a
	rnca	protein kinase C a		68	D	S,L	PRKCA	17q22-q24	33, 242
*	Pmp-22	peripheral myelin protein, 22kDa (Tr)		33	D	S,L	PMP22	17011.1	243
	Pmv-2	polytropic murine virus-2		5	D	L			88
	Pmv-22	polytropic murine virus-22		8	ñ	Ĩ.			99
	Pmv-46	polytropic murine vinis-46		12	5	ĩ			90
	Pmy-56	nolytronic murine vine-56		14	ň	L			55
*	D	poryaopie mutue vitus-JO		04	D	L			88
*	rmv-38	polytropic murine virus-38		14	D	L			86
*	Kab-I	Kas related gene member, mouse homolog of yeast YPT1See Gibp		12	D	L			267
	Rana	retionic acid receptor, alpha		55	D	LL	RARA	17021 1	171
*	Revrn	recoverin (guanylate cyclase activator)		35	ñ	ī,	ROVEN	17	179
	Re	rex		58	v	Ť	AC TRIV	11	1/0
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*	Revil	ribosomal DNA cana aluster		14	D	5,L	REL	2p13-p12	30
-	ANULL David s	Those that KINA gene cluster		2	D	L,I			132
	KNUIA-1	Ulai small nuclear KNA		51	D	S,L			182
	Knu3b	U3B small nuclear RNA complex		bt	D	I			174
	Rnu3b-1	U3B small nuclear RNA-1		bt	ñ	L.P.			174
	Rnu3b-2	U3B small nuclear RNA-2		51 1.1	2	1,1 1 D			1/4
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*	Pol19	where we have the start of the		bt	D	1,P			174
	Aprilo-FS	noosomal protein 18 related sequence		4	D	L			233
	Kp02-1	RNA polymerase II-1		37	D	S,L	POLR2	17p13.1	15.44
	Scn4a	sodium channel a subunit, skeletal muscle		63	D	L	SCN4A	17023 1-025	103 02
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	sh-2	shaker-2			•••				74
	sh-2 Shbo	shaker-2 sex hormone hinding globulin		32	v r		0110-0		74
	sh-2 Shbg	shaker-2 sex hormone binding globulin		32 35	D	S,L	SHBG	17р13-р12	74 133, 20

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Table 1. Continued.

				_					
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	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
*	Tell 1 p	telomeric segment, Chr 11, p arm		bt	D	I		• •	27
*	Tell Iq	telomeric segment, Chr 11, q ann		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	В	L	TCN2	22a11.2-ater	90.6
*	Thbp	thyroid hormone binding protein See P4hb	2	80	D	L	P4HB	17925	
	ti	tipsv		42	v	L		T	228
*	Timp-2	tissue inhibitor of metalloproteinase-2		74	D	L	TIMP2	17a25	241
	Tk-1	thymidine kinase-1		78	BD	S,C,I,L	TK1	17a23-q25	149,193, 141
	tn	tectering		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	В	S	TSE1	17a23-a24	141.
	Umnh-2	uridine monophosphatase-2		bt	B	S	UMPH2	17a23.2-a25.3	248, 269,
	vb	vibrator		32	v	L			263.150
	Vnn-1	vacuolar (endomembrane) proton pump subunit-1 (116kDa)		bt	D	S	VPP1	17a21-oter	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	17g21-g22	33, 216
	Wnt-3A	wingless-related MMTV integration site-3A (Int-4A)		bt	D			• •	199
	w	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,

	A	A	В	B'	С	C.	D	Ε	E'	F	G	н	1	J	κ	L	М	N	0	P	Q	R	S	T	υN	/ w		(Y	Z	A۸	AE	AC	DA	EA	A	A-	A	AJ	AK	AL	AM	AN	۸d/	APA	dA	R
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Mirisia Kri-1 Mox-1 D11Leh2 D11Leh2 D11Pas1 Cnp-1 Hmg14-rs4 Empb3 D11Nds7 ApoH								•																				•	•																
Krt-1 Mox-1 Fe D11Leh2 D11Pse1 Cnp-1 Hmg14-rs4 Empb3 D11Nds7 ApoH Gfap								•																					•																
Minista Rotini Dilleh2 Dilleh2 Dilleh2 Cnp-1 Hmg14-rs4 Empb3 DilNds7 ApoH Gfap Wnt-3								•																																					
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Krt-1 Mox-1 Fe D11Leh2 D11Pas1 Cnp-1 Hmg14-rs4 Empb3 D11Nds7 ApoH Gfap Wnt-3 Ace								•																																					
Ministra Mox-1 Re D11Leh2 D11Pas1 Cnp-1 Hmg14-rs4 Empb3 D11N4s7 ApoH Gfap Wnt-3 Ace Scn4a																																													
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American Krt-1 Mox-1 D11Leh2 D11Leh2 D11Pas1 Cnp-1 Hmg14-rs4 Empb3 D11Nds7 ApoH Gfap Wnt-3 Acce Scn4a Myla D11Mit10 D11Nds2 Gh Ts Gna-13 Pkca Gn3a																																													
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Anir 3 ta Rrt-1 Mox-1 Ra D11Leh2 D11Pas1 Cnp-1 Hmg14-rs4 Empb3 D11Nds7 ApoH Gfap Wnt-3 Ace Scn4a Mpmv-8 Myla D11Nit50 Ts Gna-13 Pkca Gp3a Gp2b D11Mit12 D11Mit2																																													
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Artic - 1 Mox-1 Ro D11Leh2 D11Leh2 D11Pas1 Cnp-1 Hmg14-rs4 Empb3 D11Nds7 ApoH Gfap Wnt-3 Acce Scn4a Mpmv-8 Myla D11Nits0 D11Nits0 Ts Gna-13 Pkce Gp2b D11Mit11 D11Mit12 D11Mit12 D11Mit12 D11Mit12 D11Mit12																																													
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Artic - 1 Mox-1 Re D11Leh2 D11Pss1 Cnp-1 Hmg14-rs4 Empb3 D11N437 ApoH Gfap Wnt-3 Acce Scn4a Myla D11Nds2 Gh D11Nit50 Ts Gns-13 Pkca Gp2b D11Mit10 D11Mit50 Ts Gns-13 Pkca D11Mit50 Ts Gp2b D11Mit11 D11Mit12 D11Mit13 D11Mit142 Mpmv-15 Mit-3 D11Sel2 Timp-2																																													┿ ╸╸ ╸ ╸ ╸ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴ ╴
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Anno 10 Rri-1 Mox-1 Re D111Leh2 D111Res1 Cnp-1 Hmg14-rs4 Empb3 Emph3 D11Nds7 ApoH Gfap Wnt-3 Acce Scn4a Mynw-8 Myla D11Nits0 D11Nits0 Tis Gna-13 Pkca Gp2b D11Mit12 D11Mit12 D11Mit12 D11Mit2 D11Mit61 D11Mit62 Mprw-15 Mitv-3 D11Sel2 Timp-2 D11Sel3																																													
Ministra Riscond Riscond D11Pas1 Cnp-1 Hmg14-re4 Empb3 D11N487 ApoH Gfap Wnt-3 Acce Scn4a Mpmv-8 Myla D11Nds2 Gh D11Mit50 Ts Gna-13 Pkca Gp2b D11Mit11 D11Mit12 D11Mit130 Ts Gna-13 Pkca D11Mit11 D11Mit12 D11Mit13 D11Mit13 D11Mit14 D11Mit2 Mpmv-15 Mitv-3 D11Sei2 D11Sei3 Es-3 D11Mit-4																																													┿╋╋┿┿┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙┙
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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 centerjustified. 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.

- (Camk2b, Lif)-3.8±1.6-Erbb-3.8±1.5-Rel-15.0±2.9-Pad-1-6.7±2.2-(II-3, Csfgm, Sparc)-5.6±2.4-Myhs-4.8±1.8-(Acrb, Atp1b2, Trp53, Zfp-3. A. Glut-4, D11Leh1)-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, 33, 35, 7, 55, 112, 136, 268 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. (Cen11, Lif)-12.6±3.4-Rel 128 A
- Erbb-14.5±3.3-(Adra1, Gabra-1)-3.4±1.7-(Pad-1, D11Sel1)-0.9±0.9-df-2.6±1.5-(II-3, Csfgm, Irf-1, II-5, II-4, Sparc)-2.6±1.5-(Myhs-1.7±1.2-(Rpo-B. 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
- Adra-1-3.8±21-Pad-1-6.3±2.7-(Anx-6, Csfgm, Glr-1, 11-3, 11-4, 11-5, Sparc, spd)-9.1±2.4-D11Mit5-2.2±1.5-Asgr-1. 42 R.
- (D11Mill, Erbb)-15.4-Adra1-6.1-D11Sel1-2.7-(11-3, 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-C.* (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 Rpl18-rs-6.9-Erbb-37.4-113-20.7-Erbb2-16.2-D11Mit12 C.* 233
- $D11Mil2 = 9.5 \pm 4.5 Glns 16.3 \pm 2.1 D11Nds3 12.7 \pm 1.5 Acrb 4.9 \pm 0.9 D11Nds1 5.9 \pm 1.2 Mpo 13.7 \pm 1.7 Gfap 3.4 \pm 1.1 (Myla., D11Nds2) 0.9 \pm 0.9 D11Nds2 0.9 \pm 0.9 D11Nds2 0.9 \pm 0.9 D11Nds2 0.9 \pm 0.9 \pm 0.9 D11Nds2 0.9 \pm$ 255. D. 176
- E. 105
- $D11Nds3-16.5\pm4.2-(Glu1.4, Trp53)-1.4\pm.08-Atp1b2-0.5\pm0.5-Acrb-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-Gfap-6.5\pm3.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-Gfap-6.5\pm3.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-Gfap-6.5\pm3.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-Gfap-6.5\pm3.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.6-D11Nds1-1.4\pm0.8-Evi-2-4.3\pm1.4-Mpo-14.3\pm4.1-0.9\pm0.8\pm0.8-10-0.9\pm0.8-10-0.8-10-0.9\pm0.8-10-0.9\pm0.8-10-0.9\pm0.8-10-0.9\pm0.8-10-0.9\pm0.8-10-0.9\pm0.8-10-0.8-10-0.9\pm0.8-10-0.8$ E. 176 Myla

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- Camk2b-8.0±2.9-Rel-9.8±3.3-Gabra-1-3.3±2.3-(11-3, Mgat-1)-8.9 ± 3.8-Shbg-11.6±3.9-Hsp86-ps1-17.4±4.6-Wnt-3. 133, 140, 188, 213, F. 59
- Erbb-9.5±3.7-Hba-20.6±5.1-Evi-2-25.4±5.5-Gh. 77. 78 G
- Sparc-16.7±4.2-Evi-2-9.0±3.2-Erba-2.6±1.8-Gh-19.2±4.5-Es-3. 78 H.
- Tr-21.3±4.7-HoxB-1.3±1.3-(Krt-1, Re). 194 I.
- Hba-20.3±4.5-Tr-27.7±3.6-(Krt-1, Re)-13.9±3.9-Es-3. J.
- 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 K.
- Tr-20.6±4.7-HoxB-1.4±1.4-Re. 107 L
- spd-2.5±1.2-Tr-25.3±3.4-Re. M 151
- N. (II-3, Csfgm, Sparc).
- 12 Hba-32.2±8.4-Myhs-26.2±6.8-Myla-8.1±4.5-Es-3. 265, 217 0.
- Ρ. Tcn-2-6.9±2.2-wa-2-12.3±2.9-Hba. 91
- 254, 32 $Tr-4.1\pm 2.8-Akv-4-12.2\pm 4.7-Evi-2-24.5\pm 6.1-Re-10.2\pm 4.3-Es-3.$ Q.
- 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
- wa-2-22.2±1.7-vt-8.9±1.2-ti-20.2±1.5-Re. 228 U.
- ٧. 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. Y. Dlb-1-2.3±1.3-Re-20.3±3.5-Es-3. 259
- Hba-20.4±2.9-(Ahd-4, Tr)-26.3±3.2-Re. 114 115
- Z. Hba-13.8±3.9-Ahd-6-7.5±2.9-Ahd-4. 261
- Hba-29.6±4.6-HoxB-23.5±4.3-Es-3. AA.
- Evi-2-27.0±7.3-Gh-5.4±3.7-Es-3. 77 AB.
- 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 AC.
- (Mpmv-18, Emv-30)-25.0±7.2-11-3. 215 AD.
- 89 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. AE. 89
- 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). AF.
- Xmv-63-8.2±3.5-Pmv-2-4.5±3.2-Pmv-22-53.5±7.6-(Mpmv-15, Mtv-3). 89 AG.
- Nfh-5.6±3.1-Erbb-1.1±1.1-(Rab1, Gins-ps1, wr)-2.2±1.6-Rel-4.4±2.1-Hba-17.8±4.0-II-3. 138 AH.
- 253 Emv-14-23±9-Emv-28-23±9-Es-3. AI.
- (11-5, Csfgm)-4.7±3.2-Sparc-30.2±7.0-(Om, Sigje)-20.9±6.2-Es-3. AJ.
- D11MitI-11.4±1.9-Glns-26.2±2.8-II-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-AK. $1.2 \pm 0.7 - Sigje - 1.5 \pm 0.8 - (Mpo, Rnu1a - 1) - 3.1 \pm 1.1 - Cola1 - 1.5 \pm 0.8 - Hox B - 2.4 \pm 1.0 - (Antp91A, Cnp - 1) - 5.1 \pm 1.4 - Empb3 - 0.4 \pm 0.4 - Gfap - 2.0 \pm 0.9 - 0.4 \pm 0.4 - Gfap - 2.0 \pm 0.9 - 0.4 \pm 0.4 - Gfap - 2.0 \pm 0.9 - 0.4 \pm 0.4 \pm 0.4 - 0.4 \pm 0$ (D11Mit10, Myla)-5.5±1.4-D11Mit11 145
- Acrb-18±5.4-(Gp2b, Gfap). 198 AL
- AM. Erbb-2.6±1.8-Spnb-2-17.9±4.4-Sparc. 24 AN. Rnr11-19.9±3.4-Hba-13.8±2.9-11-4-33.6±4.0-Hmg14-rs4-11.4±2.7-Es-3 131, 132
- 131
- AO. Xmv-42-13.4±2.9-Hmg14-rs4-11.3±2.7-Es-3
- 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-D11Mit13-4.5-71, 183 D11Mit50-2.2-D11Mit11-1.8-D11Mit61-0.9-(D11Mit12, D11Mit42)-5.8-(D11Mit48, D11Mit49)-2.8-D11Mit69

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 a	nd D represent alleles derived from AKR/J and DBA/2J, respectively.
Durin 2	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 0 1 2 3 4 5 6 7 8 D 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 0 1 2 3 4 5 6 7 8
Pmv-2 Mpmv-18 Hba Sparc D11H4S10 Emv-14 Atpb-2	D A A A D D D A A A D D D A A D D D A A D D D A A D D D D A A D D D D A A D D D D A A D D S8 A D D A A D D D D A A D D D A A D D D A A D D D A A D D D D A A D D D D A A D
Acrb Glut4 Evi-2 Xmv-20	D A D A A D A D D A D A D A A A D D D A D D A D 108 D A D A A D A D D A D A D A D A D A D D D A D D D A D 108 D A D A D A A D A D A D A D A D A D A D
Cola-1 HoxB Cnp-1 Gfap Gan	D A D A A D D D D A D A D A D D D D A D A D A D D D 4 D A D A A D A D D D D D A D A D <u>A</u> D D A D A D <u>A</u> D D D 107 D A D A <u>A</u> D A D D D D D A D A <u>D</u> A A D D A <u>D</u> D D D D 19 D A D A D D A D D D D A <u>D</u> A A A A D D A A D D D 19 D A D A D D D D D A <u>D</u> A A A A D D A A D D D 166
Mpmv-15 BYD B and	
Locus	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
Pmv-22 D11Byui D11Mit2 Glas-psi D11Byu3 Hba D11Byu4 P40-rs5 Sparc I1-5 D11H4S10 Hist2b-rs1 Rcvrn D11HMit4 Glut-4 Asgr-1 Asgr-2 Acrb Atp1b-2 Zlp-3 D11Nds1 Mpmv-2 Brp-8 Tca-3 Xmmv-3 Mpmv-4 D11Birl Xmv-42 Mpo Mip1a Mpip AntP91a HozB Krt-1 D11Nds2 Glap Empb3 Myla Mpmv-8 Es-3 D11Nds1 Mpmv-8 Es-3 D11Nds1 Mpmv-8 Es-3 D11Jkn1e Tk-1 Gaa	B B D B D D B D D B D
AKXL. A an Locus	ad L represent alleles derived from AKR/J and C57L/J, respectively.
Pmv-22	<u>1 2 4 5 6 7 8 9 1 2 3 4 6 7 8 9 1 3 4 5 8 9 6 7 8</u>
Pmv-22 Pmv-2 Erbb Mpmv-18 Hba Emv-18 Env-14 Evi-2 Mpmv-2 Mpmv-2 Mpmv-4 Mip1a Xmv-42 Xmv-20 HoxB Cnp-1 Mpmv-8 Es-3 Gaa Gik Mpmv-15	$ \begin{array}{c} A \ L \ A \ L \ A \ L \ A \ A \ A \ A \$

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

Locus	U	0	U	U	U.	U	U	v	1	1	1	1	1	1	1	4	Kalarances
	2	3	4	5	6	7	8	9	0	1	2	4	5	8	9	0	
Pmv-22	Н	Н	н		Н	B	В	В	B	H	B	Н			Н		88
Pmv-2	Н	Н	H		н	В	В	В	В	Н	В	Н			н		88
Hba	B	Н	B	н	Н	B	B	В	В	B	В	Н		В	н	В	49
Sparc	В	Н	В		н	H	Ĥ	В	В	В	В	B					167
D11H4S10	В	н	В		н	н	н	В	B	В	B	B			Н		49
Momv-2	Ĥ	н	B		н	Н	н	В	В	В	Ħ	Ĥ			B		89
Mpmy-4	Н	н	Ĥ		н	Н	н	B	В	В	Н	н			В		89
Xmv-42	H	H	H		H	н	H	В	в	B	B	н			В		87
Krt-1	B	H	H		н	н	н	В	в	Ħ	В	Н			B		194
Gfap	В	н	Н		н	н	н	B	В	н	В	н			В		19
Myla			н		B	н	н	B	В	Н	В	н			в		217
Momv-8	В	Н	н		В	н	н	В	В	Н	В	Н			В		89
Es-3	B	B	Н	Н	В	н	н	В	в	Н	B	B	В	В	В	В	185
Tk-1	В	В	Н		В	Н	н	В	В	Н	B	B			В		166
Gaa	Ĥ	B	H		B	Н	Н	В	в	Н	в	Ħ			В		166
Glk	B	В	н	Н	В	н	Н	B	В	Н	В	Н		В	в		185

UXA. U and A represent alleles derived from U20/A and AAR/FURDA.
--

respectr	vely.					_									
Locus	1	1	1	1	1	2	2	2	2	2	2	2	2	2	References
	5	6	7	8	9	0	1	2	3	4	5	6	7	8	-
11-5	0	0	Α	A	Α	Α	σ	0	Α	0	Α	Α	A	0	270
II-4	0	0	Α	Α	Α	А	0	0	Α	0	Α	Α	Α	0	251
11-3	0	0	Α	А	Α	Α	0	0	Α	0	Α	Α	Α	Q	251
Tca-3	Ā	Ā	ō	Α	Α	Α	0	0	Α	0	Α	Α	Α	A	270

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

Locus	0	0	0	0	0	0	0	0	1	1	1	1	References
	1	2	3	4	5	6	7_	9	0	1	2	3	
Pmv-22	C	C	В	B	В	B	С						88
Pmv-2	С	С	В	B	в	В	С						88
Erbb	С	B	В	Ĉ	В	В	С						237
Mpmv-18	С	В	В	С	В	В	С						89
Hba	С	В	в	С	В	В	С						221
Ck-rs5	Č	в	B	С	В	В	С	С	В	С	С	В	50
Mpmy-2	Č	В	Ē	С	В	Ē	С			_			89
Xmy-42	B	B	B	B	B	Ĉ	Ċ						87
Mnmv-8	ñ	B	č	Ĉ	B	č	Ř						89
Gaa	B	B	Ď	č	Ĉ	č	B	С	С	B	С	С	166

AXB. A and	Br	epre	sen	t all	eles	der	ivec	i fro	m /	√J a	ınd (C57	BL∕	6J,	resp	ecti	vely	<i>.</i>							
Locus	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	References
	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	7	8	9	0	1	2	3	4	5_	
Pmv-2	A	B	A	A	A	A	A	A	A	A	A	Α	Α	Ā			Α		Α	A	В	В	A	A	88
Pmv-22	Α	В	Α	Α	Α	Α	Α	Α	Α	Α	Α						Α		Α	А	В	в		Α	88
Erbb	Α	В	A	Α		Α	Α	Α		Α	Δ	Α		Α	в		Α			Α					195a
Pmv-46	Α	В	Α	Α	Α	Α	Α	Α	Α	Δ	B	Α	Α	В			Α		А	Α	в	Α		в	195a
Hba	В	В	Α	Δ	Α	Α	Α	Α	А	В	Α	Α	в	в	В	В	А	Α				Α			158
11-3	В	В	Α	B	Δ	Α	B	Α	Α	в	A		в	В	В		Α	Α	Α			А	А		158
Mpmv-2	В	В	Α	B	B	B	Ä	Α	Α	в	B	B	В	B			А		А	B	В	Α	Α	Α	89
Myhs	В	B	Α	B	Ä	Ä		Α		В	B	Α	₿	В	Α	А	B	Α	Α	A	<u>B</u>	A	Α		158
Xmv-42	В	В	Α	B	Α	Α	Α	Α	В	в	Α	Α	Α	В			Α		Α	В	Α	Α	А	в	87
Momv-4	В	В	Α	Ä	Α	Α	Α	Α	В	В	Α	Δ	Α	В			Δ		Δ	в	Α	Α	Α	В	89
Hox-2.1	В	в	Α	B	Α	Α	Α	Α	В	В	Α	В	Α	В	в	в	в	В	в	В	Α	Α	Α		158
Hox 2.6	В	в	Α	В	А	Α	Α	Α	В	в	Α	в	Α	В	в	В	В	В	в	В	A	Α	Α		158
Mpmv-8	В	В	В	B	Α	Α	Α	B	В	В	Α	В	Α	В			В		В	В	В	Α	Α	в	89
Pmv-56	В	В	В	B	Α	Α	Α	В	B	В	Α	B	Α	В			в		в	в	в	Α	Α	B	88
Fe.7	R	R	Ā	Ā	Α	R	Α	в	Ā	R	A	Ã	Α	R	B	B	B	B	в	В		Α	Α		158

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

Locus	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	References
	1	2	3	4	5	6	7	8	9	0	1_	2	3	4	6_	7	8	9_	0	1	2	3	4	5	
Pmy-2	A	В		A		В	Α	В	Â	A	В	В	B	A		В	A	A	A		Α	A	A	Α	88
Pmy-22	A	B		Α		В	Α	В	Α	Α	В	В	В	Α		Α	Α	Ē	Α		Α	Α	Α	Α	88
Erbb		-	В	A	Α		Ä	Ā			B	~	-					_							195a
Pmy-46	Α	В	-	Α		Α	Α	Α	Α	Α	В	Α	А	Α		Α	Α	Α	Δ	Α	Α	Α	Α	Α	88
Hha	Ä	-		Α				Α			В	Α	Α	Α	Α	Α	Α	Α	B				Α		158
11-3	Ā	В	в	B		Α	Α	-	B		В		Α	Α			Α	B			Α		Α		158
Momy-2	A	B	-	В		B	Α	В	В	Α	Ā	Α	B	Α		В	Α		B		Α	Α	Α	В	89
Myhs	Α	В		В		В	Α	B	В	Α	B	B	В	Α	Α	B	Α	В			Α		Α		158
Xmv-42	B	B		В		В	Α	Ā	В	Α	Ā	В	В	B		Ā	Α	B	Α		Α	В	Α	₿	87
Momy-4	В	B		В		В	Α	Α	B	Α	Α	В	В	в		Α	Α	-	Α		Α	В	Δ	А	89
Hox-2.1	B	B	Α	В		В	Α	Α	В	Α		В	В	В	Α		Α	Α	Α				в		158
Hox-2.6	B	B		В		В	Α	Α	В	Α	Α	В	В	В	Α	Α	Α	Α	A		Α		в		158
Hox-2.3	В	B	В	В		B	Α	Α	в		Α	В	В	В	Α	Α	Α	Α	Α		Α		в		158
Momv-8	В	В		В		Ā	Α	Α	в	Α	Α	В	В	В		A	Α	Α	Α		Α	Α	в	Α	89
Pmv-56	В	В		В		Α	Α	Α	В	Α	Α	В	В	В		B	Α	Α	Α		A	Α	В	Α	88
Es-3	В	Ā	В	В		B	Α	Α	В		Α		В	Α	Α	Ā	Α	Α	Α		В		В		158

CXS. C and S represent alleles derived from BALB/cHeA and STS/A,	NXSM. N and S represent alleles derived from NZB/BINRe and SM/J, respectively.
respectively.	Locus A C D E F I L N P Q T T U V W X Z References
Locus 0 0 0 0 0 0 0 0 0 1 1 1 1 1 References	1 2
1 2 3 4 5 6 7 8 9 0 1 2 3 4	Tcn-2 SSNSSSNNSNSSSNSSN 77
Tcn-2 CSSCSCSCSCCCS91	Pmv-2 SSNSSSNNSNSSSNSSN86
Hha CSCCCSSCCSCCS91	Erbb SS <u>S</u> SSSNNSSSS <u>S</u> SSN77
11-5 CCCCSSCSSCSSCCS270	Pmv-58 S <u>S</u> ÑSSSNNSSSSSSSSS886
ILA CCCCSSCSSCCS58	Xmv-47 SNNSSSNNSSSSSNSSN 86
11-3 CCCCSSCSSCSCS58	Hba <u>ÑNNŃS</u> SNN <u>S</u> S <u>S</u> S <u>N</u> SSN77
	Evi-2 SNNSNSNNNSNNSSNN77
HaxB C C S S S S S C S S S S C S 270	Mpmy-4 SNNSNSNNNSNNSSSNN86
Tra-3 CCSSSSSCSCSCS270	Mmv-16 SNNSNSNNNSNNSSSNN86
Rmula-1 C C S S S S S C S C S S C S 182	Xmmv-77 SNNSNS S NNS <u>N</u> SSSNN86
Sinia CCSCSSSCSCSCSSS270	Xmv-49 SNNSNSSNNS S SSSNN86
	Mmv-17 SNNSNSÑNN <u>S</u> SSSSNN 86
	Momy-8 SNNSNSNNNNSSS <u>S</u> SNN86
	GA SNNSNSNNNNSSSNSNN77
	Momy-15 SNNSNSNNNSSSSNSN86
	Mtv-3 SNNSNSNNNSSSSNSNN77

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

Band	Reference
location	
A5-B1	198
D	192
A2	31
Chr11	72
A1-A4	191
A5-B1	92
D	190
A5-B1	262
A5-B1	262
D	54
A1-A2	144
B5	192
C-E	218
B2-C	191
A1-A5	173
11	189a
D	189a
D	171
C-D	175
B1-C	214
B1	167
Α	27
Е	27
B3-E2	116
B2-C	191
	Band location A5-B1 D A2 Chr11 A1-A4 A5-B1 D A5-B1 D A5-B1 D A5-B1 D A5-B1 D A5-B1 D C-E B2-C A1-A2 B5 C-E B2-C A1-A5 D D C-D C-D C-D C-D C-D B1-C B1 A E B3-E2 B2-C

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

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)4Bm	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						
<u>Rb(11.16)2H</u>	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						
<u>T(11;19)42H</u>	<u>11D, 19B</u>	230, 79, 17, 142						
Chromosomal inversions								
In(11)2Dn	11A4, 11B1	62						
In(11)20Rk	11A2, 11D	66, 65						

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.

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 wellspaced 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.

Acknowledgments. The online genetic databases GBASE, OMIM, and GDB were invaluable in the preparation of this report. We encourage readers to refer to these databases and to primary references for more complete information than could be included in this report. In particular, we would like to thank Tom Snell for distributing the chromosome data, Linda Siracusa for many helpful discussions, and Kim Chianese for help in preparing this report. Suggestions and comments concerning the consensus linkage map presented here are welcome (buchberg@calvin.jci.tju.edu) and will be incorporated into the next update. We regret any errors or omissions, and we thank those authors who sent reprints of new papers reporting the mapping of genes to mouse Chr 11. We also thank the many researchers who contributed unpublished results and compiled mapping information useful for generating this report. This work was supported in part by National Institutes of Health grant CA58586.