

# **Mouse Chromosome 3**

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## Introduction

During the past year, more than 80 new loci have been assigned to Chromosome (Chr) 3, including 15 genes and a large number of anonymous DNA markers. This wealth of markers makes it increasingly difficult to represent the genetic maps of mouse chromosomes in traditional formats. In this report, map positions for Chr 3 loci are presented in tabular form. A traditional graphic representation of Chr 3 is available in the first and second committee reports (103, 103a).

This report provides an updated locus list and map, updated strain distribution patterns for recombinant inbred lines, recombination data from seven large multilocus crosses, a new map entirely based on PCRbased microsatellite loci that span Chr 3, and primer sequences for a large number of markers that can be detected by the PCR.

#### Locus list and chromosome map

The main features of Chr 3 loci are presented in Table 1. Map positions were calculated by Seldin using the methods previously described (103, 103a). Entries that have been added or changed since the previous report are marked with an asterisk. The map positions are composites based on a large number of measurements. The 95% confidence intervals for the primary data are in most cases greater than 2 cM, and those for the composite data are greater than 5 cM. As discussed in the previous reports, there may be errors in the indicated gene orders for closely linked loci that have not been mapped in the same cross.

The map positions that are listed alphabetically in Table 1 are also listed in order of increasing distance from the centromere in Table 2, providing a tabular representation of the Chr 3 map.

Data on gene order obtained from seven multilocus crosses are summarized in Fig. 1A. Unambiguous gene order can be determined only for loci that were mapped within the same cross. The data from the seven crosses generate a consistent gene order. The quantitative data from these crosses are presented in Fig. 1B.

#### PCR primers for Chr 3 loci

The development of PCR-based assays that detect genetic variation has greatly reduced the time and effort required for genotyping, as well as the amount of genomic DNA required per assay. PCR primers amplify products of different lengths as a result of variation in simple sequence repeat length. Published gene sequences have been used to derive primers that detect variation at known loci. In addition, a large number of primers that detect (CA)n repeat length variation have been developed from anonymous genomic clones by the Mouse Genome Center at the Massachusetts Institute of Technology (MIT) (37). Primer sequences for 72 Chr 3 loci of both types are presented in Table 3.

#### Microsatellite map of Chr 3

During the past year, microsatellite markers have been widely adopted by many investigators as convenient and reliable genetic markers. The presence of variation among inbred strains, the reproducibility of as-

<sup>\*</sup> Chair of Committee for Mouse Chromosome 3

ew Symbol	Name	A	Map	Т	Method	H. symbol	H. location	Notes	References
								<u></u>	
Acrb-2	acetylcholine receptor beta 2 neural		43.0	D	L		1.01	8	11
Acts	skeletal alpha actin	1	X	ע תם	S,R	ACTA1	1p21-qter	8,12	33
Adn-I	alconol denydrogenase-1	1	08.1	ы,D	L,K	AUNI	4y21-q23	4,3	13,13,20,22,34, 68 150 159
Adh_Inc	alcohol dehydrogenase-1 pseudogene		52.0	D	R				20
Adh-1t	alcohol dehydrogenase-temporal		68.1	ñ	ĩ			13	6,71
Adh-3	alcohol dehydrogenase-3		68.1	В	R,L	ADH3	4q21-q23	12	43,67,68,69,72,
									112,124
Adh-3t	alcohol dehydrogenase-3-temporal		68.1	B	L			12	66,69
Adh-5	alcohol dehydrogenase-5		X	B	S	ADH5	4q21-q25		53
Ahr-1	aldehyde reductase-1		68.1	B	R,L	434001	1-12	12	43
Ampa-1	AMP deaminase-1 (muscle form)		4/.4	ע	L	AMPDI	1015	1	79 111 118
Ampa-2	AMP desiminase-2 (nonindiscre torin)	1	49.6	BD	LR	AMYI	1021	8.10.12	13.15.45.52.
11//·y-1	uniyinso, surring	•		-,-				-,,	59,86,121,
									137,138,156
Amy-2	amylase, pancreatic	1	49.6	B,D	L,R	AMY2	1p21	1,2	13,14,109,121
Ank-2	brain specific ankyrin-2		58.4	D	L			12	122
Ap2	adipocyte protein aP2		9.7	B,D	R,L	4.03.75	1 -410	4	61,150
Arnt	aryl hydocarbon receptor nuclear translator		X 47.2	R	5	AKN1 ATD1A1	ipter-q12	1 1 2	1/
Atpiai	Na, K Al Pasc alpha-1		47.3	D	L	AIPIAI	1915	1,15	//,/9,01,109
Aipa-1 Rolan	bone matrix Gla protein			D	S	BGLAP			76
Bmn	Beta-mannosidase activity (liver. kidnev)		68.1	B	R				97
BRS-3	see Odc-rs3								
Cacy	calcyclin		42.9	D	L	CACY	1q21-q25	1,12	39,79,109,118
Calll	calpactin I light chain		42.9	D	R				131,151
Calla	see Mme					<b>C</b> 1 <b>F</b>	1.10		20 151
Capl	calcium binding protein, placental		42.9	ע	ĸ	CAPL	1q12-q22	13	59,131 44
Car-1	carponic annydrase-1	1	0.5 6 2	ы рр	L I P	CA1 CA2	oy13-922 8a13-a22	17812	15 23 28 44
Car-2	cardonic annydrase-2	T	U.J	U,U	ь,к	CAL	0410-422	1,7,0,13	47.109
									117,121.156.161
Car-3	carbonic anhydrase-3		7.5	D	L	CA3	8q13-a22	13	9
Ccna	Cyclin a		15.0	D	L		• •	1,2	92,129,134
Cdl	cluster designation 1		43.9	D	L	CD1	1q22-23	1	23,110,111,118
Cd2	cluster designation 2		46.4	D	L	CD2	lp13	1	78,79,109,118
Cd10	see Mme			r					168
Cd53	cluster designation 53		47.4	D	L			1	108
cdm CC	cadmium resistance		61.6	V D	K D	E3	1-22 -21		142,140
· CJ-3	coaguiatioon lactor 5		49.0 19 9	n n	R	гэ	1422-651		10
Cnp-2	connexin (see Gia.5)		20.0	D	ĸ				10
C12+0	cocoa		8.3	v	L			13	117,142
Csfm	colony stimulating factor, macrophage		48.4	B,D,V	L	CSF1	1p13-21	2,8	18,54,86,93,169
-	(alternative for op)			_	_				
D3Byul	DNA segment, Brig Young Univ. 1 (RAPD)		6.9	D	ĸ				107
D3Byu2	DNA segment, Brig Young Univ. 2 (KAPD		0.9 P 1	D	K D				167
	DNA segment, Brig Young Univ. 3 (KAPD)		8.1 45 2	ע	R D				167
· D3Byu4	DNA segment Brig Young Univ. 5 (RAPD)		34.4	D	R				167
<ul> <li>D3Byu6</li> </ul>	DNA segment, Brig Young Univ. 6 (RAPD)		42.3	D	R				167
D3Byul	DNA segment, Brig Young Univ. 17 (RAPD)		30.1	D	R				167
D3Dol	P40-4 clone ? high affinity laminin		76.4	D	R				40
D3Huni	DNA segment, Chr 3, Hunter 1		56.1	D	L			1	73
* D3J1	DNA segment, Chr 3, Jackson Lab 1		33.1	D	R				114
D3J2	DNA segment, Chr 3, Jackson Lab 2		65.6	D	K D				114 114
D3J3	DNA segment, Chr 3, Jackson Lab 3		34.7	ע	к р				75
	DNA segment, Chr 3, MJeners-1		47.4 60 A	D D	r R				99
DIAN	DNA segment, Chr 3, Ian Jackson i DNA segment Chr 3, Lebrach 1		176	Ď	L			2	31
Dileni	DNA segment, Chr 3, Lehrach 2		10.2	Ď	ĩ			2	31
D3Ler1	DNA segment, Chr 3, Leroy 1		41.5	D	L			8	91
D3Ler2	DNA segment, Chr 3, Leroy 2		41.5	D	L			8	91
D3Mit1	DNA segment, Chr 3, MIT 1		7.0	D	L			3,4,5	37,150,159
D3Mit3	DNA segment, Chr 3, MIT 3		20.0	D				3	21 27
D3Mit4	DNA segment, Chr 3, MIT 4		20.0	D D	L			34	37 150
D3Mit5	DNA segment, Chr 3, MIT 5	1	24.U 22.0	л Ц	L I			3	37.150
	DNA segment Chr 3 MIT 7		30.0	Ď	Ĺ			3	37
D 2Mi+0	DNA segment, Chr 3, MIT 9		38.6	Ď	ĩ			3	37
D3Mit10	DNA segment, Chr 3, MIT 10		48.6	D	Ĺ			4,5	37,159
D3Mit1	DNA segment, Chr 3, MIT 11		48.6	D	L			3,4	37,150
D3Mit12	2 DNA segment, Chr 3, MIT 12		50.3	D	L			3	37
D3Mit13	B DNA segment, Chr 3, MIT 1		57.7	D	L			3	84
* D3Mit14	DNA segment, Chr 3, MIT 14		61.0	D	L			3	57
D3Mill	5 DNA segment, Chr 3, MIT 15		63.1	D	L			2	ر د 37
D3Mit1	DNA segment, Chr 3, MIT 16		63.1	ע	L I			3	37
D3Mit12	DNA segment, Chr 3, MIT 17		08.7	ע ח	L			1.3	37.134.161
D3Mit12	DNA segment, Chr 3, MIT 18 DNA segment Chr 2, MIT 10	1	73.0 81 A	D D	L			1.3.4	134,150,159
D3Mill D3Mill	see II-2	T	01.0	5	~			- ,- , '	
► D3Mit23	DNA segment. Chr 3. MIT 22	1	35.0	D	L			3,4	84,150
* D3Mit23	DNA segment, Chr 3, MIT 23	-	0.0	D	L			3	84
* D3Mit24	DNA segment, Chr 3, MIT 24		20.0	D	L			3	84

Continued on next page

Table 1. Continued.

$\begin{array}{cccccccccccccccccccccccccccccccccccc$											
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	*	D3Mit25	DNA segment, Chr 3, MIT 25		30.0	D	L			3	84
b) Bidding DAX segment, Cur, b, MT 28         44,9         D         L         3         8,4           b) Bidding DAX segment, Cur, b, MT 36         73,0         D         L         3         8,4           c) Bidding DAX segment, Cur, b, MT 36         73,0         D         L         3         8,4           c) Bidding DAX segment, Cur, b, MT 36         53,4         D         L         3         8,4           c) Bidding DAX segment, Cur, b, MT 30         50,1         D         L         3         8,4           c) Bidding DAX segment, Cur, b, MT 40         46,1         D         L         3         8,4           c) Bidding DAX segment, Cur, b, MT 40         56,1         D         L         3         8,4           c) Bidding DAX segment, Cur, b, MT 40         50,2         D         L         3         8,4           c) Didding DAX segment, Cur, b, MT 40         50,2         D         L         3         8,4           c) Didding DAX segment, Cur, b, MT 40         50,0         D         L         3         8,4           c) Didding DAX segment, Cur, b, Nettragement         20,0         D         L         3         8,4           c) Didding DAX segment, Cur, b, Nettragement         20,0         D <td< td=""><td>*</td><td>D3Mit26</td><td>DNA segment, Chr 3, MIT 26</td><td></td><td>38.6</td><td>D</td><td>L</td><td></td><td></td><td>3</td><td>84</td></td<>	*	D3Mit26	DNA segment, Chr 3, MIT 26		38.6	D	L			3	84
b) SAA segment, Cr. 3, MAT 31         73.0         D         L         3.4         #4, 150           D) SAA segment, Cr. 3, MAT 36         73.0         D         L         3         #4           D) SAA segment, Cr. 3, MAT 36         73.0         D         L         3         #4           D) SAA segment, Cr. 3, MAT 36         53.4         D         L         3         #4           D) SAA segment, Cr. 3, MAT 36         53.4         D         L         3         #4           D) SAA segment, Cr. 3, MAT 42         53.4         D         L         3         #4           D) SAA segment, Cr. 3, MAT 42         53.4         D         L         3         #4           D) SAA segment, Cr. 3, MAT 42         53.4         D         L         3         #4           D) SAA segment, Cr. 3, Notinghan         32.0         D         L         3         #4           D) SAA segment, Cr. 3, Notinghan         61.0         D         L         3         #4           D) SAA segment, Cr. 3, Notinghan         61.0         D         L         8         133           D) SAA segment, Cr. 3, Notinghan         61.0         D         L         8         133           D) SAA segment, Cr. 3,	*	D3Mit28	DNA segment, Chr 3, MIT 28		44.9	D	L			3	84
• DAKA segment, Cor J, MIT 32 • DAKA segment, Cor J, MIT 32 • DAKA segment, Cor J, MIT 32 • DAKA segment, Cor J, MIT 34 • DAKA segment, Cor J, MIT 43 • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, MIT 43 • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, So J, D L • DAKA segment, Cor J, Mater J, MIT 43 • DAKA segment, Cor J, Mater J, J, J, J, D L • DAKA segment, Cor J, Mater J, J, MIT 43 • DAKA segment, Cor J, Mater J, J, MIT 44 • DAKA segment, Cor J, Mater J,	*	D3Mit31	DNA segment, Chr 3, MIT 31		73.0	D	L			3,4	84,150
DMAHSS         DNA segment, Cur 3, MIT 36         53.4         D         L         3         84           DMAHSS         DNA segment, Cur 3, MIT 36         53.4         D         L         3         84           DMAHSS         DNA segment, Cur 3, MIT 36         53.2         D         L         3         84           DMAHSS         DNA segment, Cur 3, MIT 36         40.1         D         L         3         84           DMAHSS         DNA segment, Cur 3, MIT 36         53.0         D         L         3         84           DMAHSS         DNA segment, Cur 3, MIT 36         55.0         D         L         3         84           DMAHSS         DNA segment, Cur 3, Natingham         55.0         D         L         3         84           DMAHSS         DNA segment, Cur 3, Natingham         27.0         D         L         4.5.9         150.159           DMAHSS         DNA segment, Cur 3, Natingham         20.0         R         81.2         2.2         2.2         Natingham         2.2         2.2         Natingham         2.2         2.2         Natingham         2.2         2.2         1.2         2.2         Natingham         2.2         2.2         Natingham <td< td=""><td>*</td><td>D3Mit32</td><td>DNA segment, Chr 3, MIT 32</td><td></td><td>77.0</td><td>D</td><td>L</td><td></td><td></td><td>3,4</td><td>84,150</td></td<>	*	D3Mit32	DNA segment, Chr 3, MIT 32		77.0	D	L			3,4	84,150
• DMAID         DNA segments, Cur J, MIT 38         67.2         D         L         3         B44           DMAID         DNA segments, Cur J, MIT 43         510, D         L         3         84           DMAID         DNA segments, Cur J, MIT 43         46, I         D         L         3         84           DMAID         DNA segments, Cur J, MIT 43         510, I         D         L         3         84           DMAID         DNA segments, Cur J, MIT 43         46, I         D         L         3         84           DMAID         DNA segments, Cur J, MIT 43         46, I         D         L         3         84           DMAID         DNA segments, Cur J, MIT 43         52, 0         D         L         3         84           DMAID         DNA segments, Cur J, Monigham         510, 0         D         L         45, 9         150, 150           DMAID         DNA segments, Cur J, Monigham         61.0         D         L         84         3         84           DMAID         DNA segments, Cur J, Monigham         61.0         D         L         5         153, 15         153, 15         153, 15         153, 15         153, 15         153, 15, 15, 15         153, 15, 15, 1	*	D3Mit36	DNA segment, Chr 3, MIT 36		53.4	D	L			3	84
b) BAKergener, Cur, S, MIT 99       53,4       D       L       3       84         b) BAKergener, Cur, S, MIT 42       44,1       D       L       3       84         b) BAKergener, Cur, S, MIT 42       54,1       D       L       3       84         b) BAKergener, Cur, S, MIT 43       56,1       D       L       3       84         b) BAKergener, Cur, S, MIT 45       56,0       D       L       3       84         b) BAKergener, Cur, S, MIT 45       36,0       D       L       3       84         b) BAKergener, Cur, S, MIT 35       35,0       D       L       3       84         b) BAKergener, Cur, S, Marger, 2       Cur, S       84       3       84         b) BAKergener, Cur, S, Marger, 2       Cur, S       84       3       84         c) BAKergener, Cur, S, Marger, 2       Cur, S       8       123       3       84         c) BAKergener, Cur, S, Marger, 2       12,2       D       L       8       123         DAMAergener, Cur, S, Marger, 2       12,2       D       L       8       123         DAMAergener, Cur, S, Marger, 2       12,2       D       L       8       123         DAMAergener, Cur, S, Marger, 2 <td>*</td> <td>D3Mit38</td> <td>DNA segment, Chr 3, MIT 38</td> <td></td> <td>67.2</td> <td>D</td> <td>L</td> <td></td> <td></td> <td>3</td> <td>84</td>	*	D3Mit38	DNA segment, Chr 3, MIT 38		67.2	D	L			3	84
b       D34440       DAX segment, Cur 3, MIT 40       40.1       D       L       3       84         D34447       DXA segment, Cur 3, MIT 43       75.3       D       L       3       84         D34447       DXA segment, Cur 3, MIT 43       75.3       D       L       3       84         D34447       DXA segment, Cur 3, MIT 43       75.3       D       L       3       84         D34447       DXA segment, Cur 3, MIT 43       75.3       D       L       3       84         D34447       DXA segment, Cur 3, MIT 43       35.0       D       L       3       84         D34447       DXA segment, Cur 3, MIT 43       35.0       D       L       4.5,9       150,159         D34467       DXA segment, Cur 3, Mattra 40       Cur 3, Mattra 40       A.5,9       30       30         D34467       DXA segment, Cur 3, Nater, An       12.2       D       L       8       123         D34467       DXA segment, Cur 3, Nater, An       12.2       D       L       8       123         D34467       DXA segment, Cur 3, Nater, An       12.2       D       L       8       123         D34467       DXA segment, Cur 3, Nater, An       12.2	*	D3Mit39	DNA segment, Chr 3, MIT 39		53.4	D	L			3	84
• DAMA: J. DNA segment, Cr. 5. MIT 41         45.1         D         L         3         84           • DAMA: DNA segment, Cr. 5. MIT 45         55.3         D         L         3         84           • DAMA: DNA segment, Cr. 5. MIT 46         9.6         D         L         3         84           • DAMA: DNA segment, Cr. 5. MIT 46         9.6         D         L         3         84           • DAMA: DNA segment, Cr. 5. MIT 46         9.6         D         L         3         84           • DAMA: DNA segment, Cr. 5. MIT 43         35.0         D         L         3         84           • DAMA: DNA segment, Cr. 5. Notingham         Dit         3         84         3         84           • DAMA: DNA segment, Cr. 2. Notingham         Dit         K         5         3         84           • DAMA: DNA segment, Cr. 3. Patter Institut-1         20.9         D         L         8         123           • DAMA: Segment, Cr. 3. Patter Institut-1         20.9         D         K         11         162           • DAMA: Segment, Cr. 3. Patter Institut-1         20.9         D         K         3         135           • DAMA: Segment, Cr. 3. Patter Institut-1         20.9         D         K <td< td=""><td>*</td><td>D3Mit40</td><td>DNA segment, Chr 3, MIT 40</td><td></td><td>40.1</td><td>D</td><td>L</td><td></td><td></td><td>3</td><td>84</td></td<>	*	D3Mit40	DNA segment, Chr 3, MIT 40		40.1	D	L			3	84
• D3M42       DNA segment, Cr 5, MIT 42       36, 1       D       L       3       84         • D3M440       DNA segment, Cr 5, MIT 43       36, 0       D       L       3       84         • D3M441       DNA segment, Cr 5, MIT 43       36, 0       D       L       3       84         • D3M415       DNA segment, Cr 5, MIT 43       36, 0       D       L       3       84         • D3M415       DNA segment, Cr 5, MIT 43       36, 0       D       L       3       84         • D3M415       DNA segment, Cr 5, MIT 43       35, 0       D       L       3       84         • D3M415       DNA segment, Cr 2, Notinghum       20, 0       D       L       4, 5, 9       150, 159         • D3M42       DNA segment, Cr 3, Notinghum       61, 0       D       L, R       3       84         • D3M42       DNA segment, Cr 3, Pateur 1a       20, 0       R       8       123         • D3M42       DNA segment, Cr 3, Pateur 1a       20, 0       R       8       123         • D3M42       DNA segment, Cr 3, Pateur 2       13, 2       D       L       8       163         • D3M42       DNA segment, Cr 3, Pateur 2       13, 2       D       L </td <td>*</td> <td>D3Mit41</td> <td>DNA segment, Chr 3, MIT 41</td> <td></td> <td>46.1</td> <td>D</td> <td>L</td> <td></td> <td></td> <td>3</td> <td>84</td>	*	D3Mit41	DNA segment, Chr 3, MIT 41		46.1	D	L			3	84
• D3M45       DNA segment, Cr. 5, MIT 46       7,3       D       L       3       84         • D3M460       DNA segment, Cr. 3, MIT 49       9,0       D       L       3       84         • D3M461       DNA segment, Cr. 3, MIT 49       9,0       D       L       3       84         • D3M4101       DNA segment, Cr. 3, MIT 31       36.2       D       L       3       84         • D3M4101       DNA segment, Cr. 2, Notingham       27.0       D       L       4,5.9       150,159         • D3M42       DNA segment, Cr. 2, Notingham       63.0       D       R       3       84         • D3M42       Dr. A, segment, Cr. 2, Notingham       63.0       D       R       15       3         • D3M42       Dave, Abit       Cr. 2, Notingham       20.0       R       15       15         • D3M42       Dave, Abit       Dr. 3, Paters 20.1       8.2       D       R       15         • D3M42       DvA segment, Cr. 3, Paters 20.1       8.2       D       L       8       16         • D3M42       DvA segment, Cr. 3, Sedin 1       10       L       10       162       15         • D3M42       DvA segment, Cr. 3, Sedin 2       30.1	*	D3Mit42	DNA segment, Chr 3, MIT 42		56.1	D	L			3	84
* D3Mer DNA expans. CP 5, MIT 46 D3Mer DNA expans. CP 5, MIT 51 D3Mer DNA expans. CP 5, MIT 53 D3Mer DNA expans. CP 5, Notingham Day, Suppry 1 D3Mer DNA expans. CP 2, Notingham Day, Suppry 1 D3Mer DNA expans. CP 2, Notingham Day, Suppry 2, Notingham Day, Suppry 2, Notingham Day, Suppry 2, Notingham D3Mer DNA expans. CP 3, Netror Super D3Mer D3Mer DNA expans. CP 3, Netror Super D3Mer D3Mer D3M	*	D3Mit45	DNA segment, Chr 3, MIT 45		75.3	D	L		•	3	84
• D3M499         DNA segmen, Cr. 5. MIT 49         40.1         D         L         3         84           D3M417         DNA segmen, Cr. 3. Notingham         30.0         D         L         3         84           D3M417         DNA segmen, Cr. 3. Notingham         27.0         D         L         3         84           D3M417         DNA segmen, Cr. 2. Notingham         27.0         D         L         4.5.9         15.0           D3M42         DNA segmen, Cr. 2. Notingham         61.0         D         L,R         3         84           D3M42         DNA segmen, Cr. 3. Notingham         63.0         D         R         30         50           D3M42         DNA segmen, Cr. 3. Pateur 2.         13.2         D         L         8         123           D3M42         DNA segmen, Cr. 3. Pateur 2.         13.2         D         L         8         123           D3M42         DNA segmen, Cr. 3. Seldin 1         43.1         D         L         162         162           D3M42         DNA segmen, Cr. 3. Seldin 1         43.1         D         L         162         153           D3M42         DNA segmen, Cr. 3. Seldin 1         43.1         D         L         162 <td>*</td> <td>D3Mit46</td> <td>DNA segment, Chr 3, MIT 46</td> <td></td> <td>9.6</td> <td>D</td> <td>L</td> <td></td> <td></td> <td>3</td> <td>84</td>	*	D3Mit46	DNA segment, Chr 3, MIT 46		9.6	D	L			3	84
* DJAMACS DNA segment, Car 3, Mar 31 DJAMAC segment, Car 3, Natagham Det, Sagery 1 DJAMAC segment, Car 3, Natagham Det, Sagery 2 DJAMAC segment, Car 3, Natagham Det, Sagery 2 DJAMAC segment, Car 3, Natagham Dot, Sagery 2 DJAMAC segment, Car 3, Natagham Dot, Sagery 2 DJAMAC segment, Car 3, Natagham DJAMAC segment, Car 3, Natagham DJAMAC segment, Car 3, Paters Institute.1 DJAMAC segment, Car 3, Datas Institute.1 DJAM	*	D3Mit49	DNA segment, Chr 3, MIT 49		40.1	D	L			3	84
b) DNA agemen, Chr. 2), Notingham         27.0         D         L         3         84           b) DNA agemen, Chr. 2), Notingham         27.0         D         L         4,5,9         150,159           b) DNA agemen, Chr. 2), Notingham         61.0         D         L,R         3         84           b) DNA agemen, Chr. 2), Notingham         63.0         D         R         30         30           DDNA agemen, Chr. 3, Nature 20.1         8.2         D         L         8         135           DDNA agemen, Chr. 3, Nature 20.1         8.2         D         L         8         123           DDNA agemen, Chr. 3, Nature 20.1         8.2         D         L         8         123           DDNA agemen, Chr. 3, Nature 20.1         8.2         D         L         8         123           DDNA agemen, Chr. 3, Saldn 1         43.1         D         L         1         162           DDNA agemen, Chr. 3, Saldn 2         30.1         D         L         1         162           DDNA agemen, Chr. 3, Saldn 2         30.1         D         L         1         162           DDNA agemen, Chr. 3, Saldn 2         30.1         D         L         1         162           DDN	*	D3Mit51	DNA segment, Chr 3, MIT 51		36.2	D	L			3	84
DNAM agament, Chr. 3, Notingham       27.0       D       L       4.5.9       150,159         • DNAM 2004, Suppert 2       61.0       D       L,R       3       84         DNM 2004, Suppert 2       61.0       D       L,R       3       84         DNM 2004, Suppert 2       61.0       D       L,R       3       84         DNM 2004, Suppert 2       61.0       D       L,R       3       84         DNM 2004, Suppert 2       61.0       D       R       30         DNM 2004, Suppert 2       7       13.2       D       L       8       123         DNM 2004, Suppert 2       13.2       D       L       8       123       123         DNM 2004, Suppert 2       13.2       D       L       8       123       132         DNM 2004, Suppert 2       13.2       D       L       8       123       131         DNM 2004, Suppert 2       13.1       45.1       D       L       161       161         DNM 2004, Suppert 2       14.1       D       L       161       161       161         DNM 2004, Suppert 2       14.1       D       L       161       161       161       161	*	D3Mit53	DNA segment, Chr 3, MIT 53		35.0	D	L			3	84
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DMAR Segment, Ltr J, Neingham         61.0         D         L,R         3         84           DMMAS         Diversity DNA regeners, Corport S, Senter Journal, Corport S, Senter Journal, Corport S, Pateur J, Scholl 2, 20 L, Kanger, Corport S, Scholl 2, 20 L, Kanger, Corport Mal, CAZD 2, Corport Mal, CAZD 2, Corport Mal, Mal, Corport 2, Corport Mal, Mal, Corport 2, Corport Mal, Mal, Corport 2, Corport 2		-	Dept. Surgery 1		27.0	D	L			4,5,9	150,159
• DJNd.j       Diff. Super 7.       61.0       D       L,k       3       84         • DJNd.d       res 1.2       63.0       D       R       30         DJMd.d       res 1.2       0.0       R       30         DJMd.d       res 1.2       1.2       1.5       30         DJMd.d       res 1.2       1.2       0.1       8       20         DJMd.d       res 7.1       1.2       2.1       8       2.2         DJMassignen, Chr.3, Paster 30.0       8.2       D       L       8       1.5         DJScill       DNA segnen, Chr.3, Paster 30.0       4.2       D       L       1       162         DJScill       DNA segnen, Chr.3, Soldan 1       4.1       D       L       1       162         DJScill       DNA segnen, Chr.3, Soldan 2       30.1       D       L       1       162         DJT/2       DNA segnen, Chr.3, Soldan 2       30.1       D       L       1       162         DJT/2       DNA segnen, Chr.3, Soldan 1       42.5       D       L,k       3       1.5         DJT/2       DNA segnen, Chr.3, Soldan 1       42.5       D       L,k       1.1       1.6       1.1	*	D3Nds2	DNA segment, Chr 2, Nottingham			-					
• D/Mark gunner, Lur J, Notingham         63.0         D         R         30           D/Mark gunner, Lur J, Notingham         63.0         D         R         33           D/Mark gunner, Lur J, Notingham         63.0         D         R         33           D/Mark gunner, Lur J, Nataur JD,         13.2         D         R         135           D/Mark gunner, Cur J, Pateur JD,         5.2         D         R         8         123           D/Mark gunner, Cur J, Pateur JD,         5.2         D         L         8         123           D/Mark gunner, Cur J, Pateur JD,         5.2         D         L         8         123           D/Mark gunner, Cur J, Nataur JD,         4.1         D         L         1         162           D/Mark gunner, Cur J, Nataur JD,         4.1         D         L         1         162           D/Mark gunner, Cur J, Nataur JD,         4.4         V         L         5         159           D/Mark gunner, Cur J, Nataur JD,         4.4         V         L         13         144           D/Mark gunner, Cur J, Nataur JD,         4.4         V         12         12.13         12.13         12.13         12.13         12.13         12.13         12		D 317 1 3	Dept. Surgery 2		61.0	D	L,R			3	84
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* $D3Pasion 2 DNA segment, Cur 3, Stein 2 DNA segment, Cu$	-	DSFasSUI	DNA segment, Chr 5, Pasteur 501-		8.2	ע	L			8	26
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b 23/37/ D 23/37         DNA segment Crs 3 Wakeland 1 (0 APD) d d copy or Egf         transformer epidemal growth factor         1         5         139 5           b 23/37         DNA segment Crs 3 Wakeland 2 (RAPD)         43.4         V         1         /         1,13         3,268,8,87           c d copy or Egf         epidemal growth factor         1         62.1         D         L,R         KGF         4q25         1,2,7         3,2109,112,137, 161,170           Env-27         endogenous costropic MuLV-27         49.6         D         L         13         148           Ev-6         esteras-26         10.1         B         L         12         17,154,156,158           Ev-1         cectoropic Vini Integration site-1         10.2         D         L,R         FVI         3q24-q28         1,2,6         2,12,6         2,12,6         2,12,6         2,12,6         2,12,6         1,3         1,45,6         2,12,6         2,12,6         2,12,6         2,12,6         1,3         1,45,6         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5         1,5,6         1,5         1,5         1,5         1,5,6         1,5,6         1,5		DITUSI	DNA segment Chr 3 Tubingen-55		120	n	TD			3	133
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Egfepidermal growth factor162.1DL,REGF $4q25$ 1,2,752,100,02,137, 51,100,02,137,100,02,123,10,02,137,100,		de	droopy ear		48 4	v	Ē		1	1212	27 68 86 87
Emw-27 endogenous ecotropic MoLV-27 esterass-1649,6 10,1DL13148 142 $B-16$ esterass-1610,1BL12154,156,158 12171,154,156,158 $B-27$ esterass-27, serum cholinesterase23,3BL12171,154,156,158 $Evi-1$ ecotropic viral integration site-110.2DL,REVI13q24-q281,2,621,23,27,28, 33,154,62,Fabpifaty acid binding protein intestinal54,7DRFABP24q28-q31143Fegrhigh affinity fC gamma ecorptor42.9DLFCGRI14112,112,112,121Fgggamma fibrinogen42.3DL,RFCGR12,23,27,28,13,62,92,109,112,141Fggfarmeoy i provent factor basic15.7DL,RFCG4q282133,159,92,29,93,94Findfarmeoy i provent factor basic15.7DL,RFCG4q282133,159,92,29,93,94Fpdr-r1farmeoy i provent probability a structure42.6VLGBA132144fobbinocion protein - connexin 4042.5VL12124,42fda-5gg juanice no protein - connexin 4044.6B,DL12124,4fda-6gbuardate cocoptoriz10.2DLGLNT232,62,562fda-6gamine mucloide binding protein, alpha minibiting activity-348.4DL2166fda-5<		Egf	epidermal growth factor	1	62.1	Ď	Ĩ.R	EGE	4025	12,13	52,00,00,07
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E-6       cetterss-16       10.1       B       L       12       154, 156, 158         Es-27       cetterss-27, serum cholinestersse       23.3       B       L       12       137, 158         Ev-1       cectoropic viral integration site-1       10.2       D       L,R       EVI1       3q24-q28       12, 62       22, 23, 72, 82         Pabpi       fatty soid binding protein intestinal       54, 7       D       R       FABP2       4q28-q31       43       112, 118, 120         Fgg?       fibroblast growth factor basic       15.7       D       L       FGGRI       112, 118, 120       102, 1241         Fgg?       fibroblast growth factor basic       15.7       D       L,R       FGGG       4q28       2       13, 31, 59, 92, 93, 93, 93, 92, 93, 94, 93, 94         Fgs/ref       fibroblast growth factor basic       10.2       D       L       FSGI       164, 142, 12, 109, 118, 120         f       facty viail       farres/1 prophosphast arynthese - like 1       43, 9       D       L       FSGI       164, 142, 12, 109, 118, 120         Gba-       gag junction protein - concenti 40       42.4       V       L       112, 120, 109, 118       112       144, 64, 55       12       112, 120, 109, 118       112, 120,		Emv-27	endogenous ecotropic MuLV-27		49.6	D	L			13	148
$E_{3-26}$ exterses-26 setterses-27, serum cholinesterase       33.3       B       L       12       117,154,156,158 $E_{3-27}$ ecotropic viral integration site-1       10.2       D       L,R       EVI1 $3q24-q28$ 1,2,6       21,23,27,28,31,54,62,31,54,62,31,54,62,31,54,62,32,109,112,141 $Fapi       high affinity FC gamma receptor       42.9       D       L       FGCRI       14       143         Fgf2       fibroblast growth factor basic       15.7       D       L, R       FGG2       4q25-c71       1,2,18,120         Fgg2       gamma fibrinogen       42.3       D       L, R       FGG       4q25-c71       1,2,18,120         Fgg3       gamma fibrinogen       42.3       D       L, R       FKG       4q25-c71       1,2,18,120         Fim-3       friend MaLV integration site-3       10.2       D       L       FIM3       3q27       2,8       7,27,54,139         Gba       gamine molecide-binding protein-1       42.6       B,D       L       GRA       1q2       1,11,141       134,159,92,         Gba       gamine molecide-binding protein-1       42.6       B,D       L       GRA       1q2       1,21,141         Gba       gamine $		Es-16	esterase-16		10.1	В	L			12	154.156.158
Es-27       exterse-27, serum cholinesterse       23.3       B       L       12       157,158         Evi-1       ecotropic viral integration site-1       10.2       D       L,R       EVI1       3q24-q28       1,2,6       21,23,72,8, 31,54,62, 92,104         Pabpi       fatty acid binding protein intestinal       54.7       D       R       FABP2       4q28-q31       143       112,118,120         Fgg7       fibroblast growth factor basic       15.7       D       L,R       FGGR       143       112,118,120       102,141         Fgg7       fibroblast growth factor basic       15.7       D       L,R       FGGR       42.3       D       L,R       FGG       4q28-q21       13,15,9,92, 93,93,92, 93,91,12,141         Fgg7       fibroblast growth factor basic       10.2       D       L       FNGS       4q22       13,31,59,92, 93,91,12,141         Fgg7       fibroblast growth factor basic       102,11       14       12,24,40,11       134,159,92, 93,92,93,92,93,92,93,92,93,92,93,92,93,93,92,93,92,93,93,92,93,93,92,93,93,92,93,93,92,93,93,92,93,93,92,93,93,93,93,93,93,93,93,93,93,93,93,93,		Es-26	esterase-26		33.3	В	L			12	117,154,156,158
Evi-1       ecotropic viral integration site-1       10.2       D       L,R       EVI1 $3q24-q28$ $1,2,6$ $21,23,27,28,32,09,112,141$ Fabpi       fatty acid binding protein intestinal $54,7$ D       R       FABP2 $4q28-q28$ $1,2,6$ $21,23,27,28,32,09,112,141$ Fegr       high affinity FC gamma receptor $42.9$ D       L       FCGR1 $1q$ $1,2,118,120,29,20,20,20,20,20,20,20,20,20,20,20,20,20,$		Es-27	esterase-27, serum cholinesterase		23.3	в	L			12	157.158
Fabpi Feptfatty scid binding protein intestinal $Fept$ 54.7 high affinity FC gamma receptor fibroblast growth factor basic54.7 to $12, 141$ R to $15.7$ FABP2 to $15.7$ 428-q31 to $15.7$ $143$ to $15.7$ $143$ to $15.7$ $143$ to $15.7$ $143$ to $15.7$ $143$ to $15.7$ $12, 118, 12.0$ Fgggamma fibrinogen42.3 farneyl prophosphate synthetase - like 1 farneyl prophosphate synthetase - like 1 to $15.7$ $10, 2$ to $15.7$ L to $15.7$ FIM3 to $15.7$ $3q27$ to $2, 87$ to $2, 75, 4, 139$ $3q27$ to $2, 87, 72, 75, 4, 139$ to $3q, 94$ Figsgamma modeloide-binding protein-1 farmeyl prophosphate synthetase - like 1 to $43.9$ $10, 2$ to $2, 141$ L to $2, 141$ to $2, 141$ $134$ to $2, 17, 54, 139$ to $3q, 94$ Gib- fibro base glucocerebrosidase fibro protein - connexin 40 alpha inhibiting activity-2 guaniam enceloide -binding protein, - alpha inhibiting activity-2 guaniam enceloide -binding protein, - to ancein 40 $45.5$ to $12$ to $12, 2$ to $13, 2$ to $12, 2$ to $12, 2$ to $13, 2$ to $13, 2$ $10, 12, 118, 120$ t		Evi-1	ecotropic viral integration site-1		10.2	D	L,R	EVI1	3q24-q28	1,2,6	21,23,27,28,
Fabpi Fep1fatty acid binding protein intestinal Fep154,7 high affnity FC garmar receptor fibroblast growth factor basic54,7 42.9DRFABP2 FCR1fq2.6q2.6q1143 143Fg2fibroblast growth factor basic15.7DLFGR24q28.52.71,223,316.2.92, 102,141Fgggamma fibrinogen42.3DL,RFGG4q28.213,315.9.92, 93,94Fim-3Friend MuLV integration site-3 f10.2DLFIM33q27 124.42,87,72,54,139Fpal-relfarreeyl pyrophosphate synthetase - like 143.9DLFFSL1q24-q311134Gbabeta glucocerebrosidase142.6B,DLGBA1q211,12109,118Gba-gamina elocitide-binding protein-164.3DL,RCBLR24q25.34158.6Gba-gluanatic receptor 234.9DLGLR23q26.2,5622Gba-gluanatic receptor 234.9DLGLR23q26.2,562Gua-2gluanatic receptor 210.2DLGLR23q26.2,56262Gua-2gluanatic receptor 210.2DLGRA11p1.32,4166Gau-3guanite moleotide binding protein, a lipha inhibiting activity-248.4DLGRA11p1.21,016H-23histocompatibility-23Sp.6VR124,1061											31,54,62,
Fabpi       fatty acid binding protein intestinal       54,7       D       R       FABP2 $4(28-31)$ 143         Fep1       high affinity FC garma receptor       42.9       D       L       FCRI       1q       11.12.118.120         Fg2       fibroblast growth factor basic       15.7       D       LL       FGF2 $4(25-27)$ 1,2       23.31,62.92,102,141         Fgg       gamma fibrinogen       42.3       D       L       FGR4 $4(25-27)$ 1,2       23.31,52.92,131,143         Find       MuLV integration site-3       10.2       D       L       FIM3 $3q27$ 2,8       7,27,34,139         Find-Intro       famesty prophosphate synthetase - like 1       43.9       D       L       FPM3 $3q27$ 2,8       7,27,34,139         Gib-3       gamma fibrinogen       42.4       V       L       FSL $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21}$ $12^{21-21$											92,109,112,141
Fegr/ Fg/2high affinity FC gamma receptor fbroblast growth factor basic42.9 15.7DLFCGR1 FGF21q1,1,118,120Fg2fibrobast growth factor basic15.7DLLFGF24q25-271,2,23,16,292, 102,141Fg8gamma fibrinogen42.3DLFGF24q25-271,2,23,16,292, 102,141Fin-3Friend MuLV integration site-310.2DLFIM3 FP81-rs13q27 framesyl pyrophosphate synthetase - like 1 42.442.3DLFIM3 FP813q27 124-q312,87,27,34,139Gibabeca ghrocorebrosidase142.6BDLGBA 42.61q211,12118 124124Giba-gamma necleotide-binding protein-164.3DL,RCBLR 42.52259,94Giba-2glucoser transporter 210.2DLGLUR2 422.5422.5,562Giba-2glucoser transporter 210.2DLGLUR2 422.5423.512Gaai-3guanne nucleotide binding protein, alpha inhibiting activity.248.4DLGNA131p132,4166Giba-3guanne nucleotide binding protein, alpha inhibiting activity.248.4DLGNA131p132,4166Giba-3guanne nucleotide binding protein, alpha inhibiting activity.279.3BL,R124,106H-33histocompatibility.2879.3BL,R124,106<		Fabpi	fatty acid binding protein intestinal		54.7	D	R	FABP2	4q28-q31		143
Fg2fibroblast growth factor basic15.7DI.LFG2 $4q25-27$ $1,2$ $23,31,62,92,102,14$ $Fgg$ gamma fibrinogen42.3DL,RFGG $4q28$ $2$ $13,31,59,92,93,94$ $Fin-3$ Friend MuLV integration site-310,2DLFIM3 $3q27$ $2,8$ $7,27,54,139$ $Fin-3$ friend MuLV integration site-310,2DLFIM3 $3q27$ $2,8$ $7,27,54,139$ $Fin-3$ guanine mucleotide-binding protein-43.9DLFIM3 $3q27$ $2,8$ $7,27,54,139$ $Gibp-1$ guanine mucleotide-binding protein- $43.4$ VLGBA $122124$ $1344$ $Gibr-2$ guanine mucleotide-binding protein- $42.4$ VLGBA $122124$ $259,94$ $Gibr-2$ guanine mucleotide binding protein, $48.4$ DLGLUT2 $3q26$ $2,5$ $62$ $Giar-2$ guanine mucleotide binding protein, $48.4$ DLGNAI3 $1p13$ $2,4$ $166$ $alpta inhibiting activity-259,6BL,R12<4,1064,106H-23histocompatibility-2359,6BL,R12<4,106H-24histocompatibility-37XDS12<4,106H-24histocompatibility-37XDS12<4,106H-24histocompatibility-37XDS12<4,106H-25histocompatibility-37XFcgrlhigh affinity FC gamma receptor42.9DLFCGR11q1,12,118,120$		Fcgrl	high affinity FC gamma receptor		42.9	D	L	FCGR1	1q		1,12,118,120
Fgggamma fibrinogen42.3DL.RRGG4q282102,141 13,159,92,93,93,94Fin-3Friend MuLV integration site-310.2DLFIM33q272,87,27,54,139Fpel-relfmesyl pyrophosphate synthetase - like 143.9DLFPSL1q24-q311134.6Gibbeta glucocerbroxidase142.6VLFPSL1q24-q311134.6Gib-5gap junction protein - connexin 4045.5DL2259,94.Gia-2glucose transporter 210.2DLGLUR24q25-34158Gia-2glucose transporter 210.2DLGLUR24q25-34158Gia-3guanine nucleotide binding protein, alpha inhibiting activity-248.4DLGLUR24q262.562Gaai-3guanine mucleotide binding protein, alpha inhibiting activity-348.4DLGLUR24q26-22166Gai-4globagivolipid expression-4XVR115124,106H-28histocompatibility-2359.6BL,R124,106H-37histocompatibility-37CXBR4244H-38histocompatibility-37CXBR124,66,65H-34histocompatibility-37CXB124,66,6512H-37histocompatibility-37CXB124,6611		Fgf2	fibroblast growth factor basic		15.7	D	I,L	FGF2	4q25-27	1,2	23,31,62,92,
$Fgg$ gamma hormogen42.3DL.RFGG $4q28$ 2 $13,31,59,92, 93,43$ $Fins.3$ fireind MuLV integration site-310.2DLFIM3 $3q27$ 2.8 $7,27,54,139$ $Fpols.1$ faxes prophosphate synthetase - like 1 $43.9$ DLFPSL $1q24-q31$ 1134 $fi$ faky tail42.4VLFPSL $1q24-q31$ 1124 $Gab$ bets glucoscerbroidase142.6B,DLGBA $1q21$ $1,12$ $109,118$ $Gis-5$ ggp junction protein - connexin 4045.5DL2 $59,94$ $Gia-2$ gluosse transporter 234.9DL $GLR2$ $4q25-34$ 158 $Gia-2$ guanine nucleotide binding protein,48.4DL $GLR2$ $3q26$ 2,562 $Gai-3$ guanine nucleotide binding protein,48.4DL $GLR3$ $1p13$ 2,4 $166$ $alpha inhibiting activity-348.4DLGNAI31p132,4166H-23histocompatibility-2359.6BL,R124_{106}H-24histocompatibility-37XVR124_{106}H-37histocompatibility-37XDS621Ha2histocompatibility-37XDS621Ha2histocompatibility-37XDS621$			<b>.</b>			_					102,141
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<i>inv-3integration</i> site-310.2DL <i>HM3</i> $3q27$ 2,8 $7,27,54,139$ <i>ipt freesters</i> fartesy prophosphate synthetase - like 1 $43.9$ DL <i>HM3</i> $1q24-q31$ 1134 <i>if</i> faky tail42.4VL <i>HM3</i> $1q24-q31$ 1134 <i>Gba</i> beta glucocerebrosidase142.6B,DL <i>GBA</i> 1q211,12109,118 <i>Gba-2</i> gap incino protein - connexin 4045.5DL259,94* <i>Glar-2</i> glucose transporter 210.2DL <i>GLUT2</i> 3q262,562 <i>Glar-2</i> glucose transporter 210.2DL <i>GLUT2</i> 3q262,562 <i>Glar-3</i> guanine nucleotide binding protein, alpha inhibiting activity-248.4DL <i>GNAI3</i> 1p132,4166 <i>Gold</i> glocose transporter79.3BL,R124,106 <i>H-28</i> histocompatibility-2359.6BL,R124,106 <i>H-37</i> histocompatibility-37CXB44 <i>Hao-2</i> hydroxysteroid deixdes-2 (kidney)40.0BL8,1254,64,65 <i>Haith</i> hypothalamic norepinephrine levelS9.6VL8,1256 <i>Haith</i> hypothalamic norepinephrine levelS9.6VL62,12132 <i>Haith</i> histoce gene (2)XDRH3F21q21-21132<		Ei 2	Think M.T.M. internation site 0			-					93,94
<i>PpBr31</i> intresy i pyrophosphate synthese - like 143.9DLPSL $1q24-q31$ 1134 <i>fi</i> faky taile2.4VLBDLGBA $1q21$ $1,12$ $109,118$ <i>Gbp-1</i> guanne nucleotid-binding protein-164.3DL,R12 $124$ $25,9,94$ * <i>Glar-2</i> guanne nucleotid-binding protein,45.5DLGLUR2 $4q25.34$ 158 <i>Glur-2</i> glucante receptor 234.9DLGLUR2 $4q25.34$ 158 <i>Glur-2</i> glucante receptor 210.2DLGLUR2 $4q25.34$ 158 <i>Glur-2</i> glucante nucleotid-binding protein,48.4DLGNA131p132,4166 <i>alpha</i> inhibiting activity-3*fakNLGNA131p132,4166 <i>H-23</i> histocompatibility-2359.6BL,R124,106 <i>H-34</i> histocompatibility-2359.6BL,R124,106 <i>H-34</i> histocompatibility-2359.6NR124,66,65 <i>H-34</i> histocompatibility-2444.9DR8,1254,64,65 <i>H-34</i> histocompatibility-27MNS56 <i>H-34</i> histocompatibility-2359.6VL8,1254,64,65 <i>H-35</i> histocompatibility-24MNNN8,1256 <i>H-34</i> histocompatibility-23 <td></td> <td>rim-3 Fastant</td> <td>Friend MuL V integration site-3</td> <td></td> <td>10.2</td> <td>D</td> <td>L</td> <td>FIM3</td> <td>3q27</td> <td>2,8</td> <td>7,27,54,139</td>		rim-3 Fastant	Friend MuL V integration site-3		10.2	D	L	FIM3	3q27	2,8	7,27,54,139
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$		r psi-rs1	farnesyl pyropnosphate synthetase - like 1		43.9	D	L	FPSL	1q24-q31	1	134
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$Gig-3$ $Gig-3$ $Gig-2$ $Giu-2$ $Giu-2$ $gluame necleotide control of d_0d_{45,5}DGiu-2gluame necleotide binding protein,alpha inhibiting activity-2d_{44,4}Dd_{45,5}DLGlu-2DLGlu-2gluamine nucleotide binding protein,alpha inhibiting activity-2d_{8,4}DLGlu-2Glu-2gluamine nucleotide binding protein,alpha inhibiting activity-2d_{8,4}DLGlu-2L2Glu-3glooglycolipid expression-4XVRVRR115115H-23<$		Ghn.1	oua gracoccicorositizse	I	42.0	ъ		GBA	1q21	1,12	109,118
• Glue-2       glutation protein - contextin 40       43.3       D       L       GLUE 2       2       59,94         • Glue-2       glucose transporter 2       10.2       D       L       GLUE 2       4q25-34       1       58         • Gnai-2       guanine nucleotide binding protein, alpha inhibiting activity-2       10.2       D       L       GLUE 2       3q26       2,5       62         • Gai-3       guanine nucleotide binding protein, alpha inhibiting activity-2       48.4       D       L       GNAI3       1p13       2,4       166         • Gai-4       globoglycolipid expression-4       X       V       R       115       12       4,106         H-23       histocompatibility-23       59.6       B       L,R       12       4,106         H-37       histocompatibility-23       79.3       B       L,R       12       4,106         H-37       histocompatibility-37       (X)       B       R       132       14         Hao-2       hydroxyacid oxidase-2 (kidney)       40.0       B       L       8,12       54,64,65         * Haj2       histone gene (2)       X       D       S       12       46         Hadib       3-btat-hydroxy ster	*	Gia-5	gramme nucleonide-binding protein-1		04.5	D	L,K			12	124
Guide intervente 2       34.7       D       L       GLUR2       4q25-34       1       58         Gai-2       guanine nucleotide binding protein, alpha inhibiting activity-2       10.2       D       L       GLUR2       3q26       2,5       62         Gai-3       guanine nucleotide binding protein, alpha inhibiting activity-3       48.4       D       L       GNAI3       1p13       2,4       166         *       Gsl-4       globoglycolipid expression-4       X       V       R       115         H-23       histocompatibility-23       59.6       B       L,R       12       4,106         H-23       histocompatibility-23       79.3       B       L,R       12       4,106         H-37       histocompatibility-37       (X)       B       R       12       4,106         H-37       histocompatibility-37       (X)       D       S       56       56     <	*	Glur-2	slutamate recentor ?		4J.J 34 A	J L	L	CIII	1-05	2	59,94
• Grad.2guesses inspired 210.2JJ10.2JJ <th< td=""><td></td><td>Glut.2</td><td>shicose transporter 2</td><td></td><td>10.2</td><td>ע</td><td></td><td>GLUK2</td><td>4925-34</td><td>1</td><td>58</td></th<>		Glut.2	shicose transporter 2		10.2	ע		GLUK2	4925-34	1	58
alpha inhibiting activity-240.4DL2166Gnai-3guanine nucleotide binding protein, alpha inhibiting activity-348.4DLGNAI31p132,4166*Gsl-4globoglycolipid expression-4XVR115H-23histocompatibility-2359.6BL,R124,106H-37histocompatibility-37(X)BR124,106H-37histocompatibility-37(X)BR1324*H37histocompatibility-37(X)BR1324*H37histocompatibility-37(X)BR1324*H37histocompatibility-37(X)BR1324*H37histocompatibility-37(X)BR1321224,106H-37histocompatibility-37(X)BR1321324,106H-37histocompatibility-37(X)BR1321324,106Ha0-2hydroxacid oxidase-2 (kidney)40.0BL8,1254,64,656Ha10hypothalamic norepinephrine level59.6VL8,1256107,108Ha333-beta-hydroxy streid dehydrogenase45.0DLHSDB31p11-p135Ha34-2-9Intracistemal A-particle a1-742.3DR95Iapla2-14Intracistemal A-particle a2-9 (near Fgg)	*	Gnai-2	sugnine nucleotide hinding protein		10.2	7	L T	GLU12	3q26	2,3	02
Gnai-3guain nuclead binding protein, alpha inhibiting activity-348.4DLGNAI3 $1p13$ $2,4$ $166$ * Gsl-4globoglycolipid expression-4XVR115H-23histocompatibility-2359.6BL,R12 $4,106$ H-37histocompatibility-2879.3BL,R12 $4,106$ H-37histocompatibility-2879.3BL,R4H-37histocompatibility-2344.9DRH3F2 $1q21-21$ $132$ Hao-2hydroxyacid oxidase-2 (kidney)40.0BL $6$ $21$ Hao-2hydroxyacid oxidase-2 (kidney)40.0BL $6$ $21$ Has2histone gene (2)XDS $6$ $21$ Haithypothalamic norepinephrine level59.6VL $46$ Hs3b3-beta-hydroxy steroid dehydrogenase45.0DLHSDB3 $1p11-p13$ 5Hap86-ps2hart shock protein 86. pseudogene 219.3DS,L107,108 $94$ *Iap1a1-7Intracisternal A-particle a2-9 (near Fgg)XDR $94$ *Iap1a2-14Intracisternal A-particle a3-1328.0DR $149$ I-17interlevin 2115.0DS,L12 $36,106$ I-12interlevin 2115.0DS,L12 $36,106$ I-151-2115.0DS,L			alpha inhibiting activity.7		40.4	U	r			2	100
alpha inhibiting activity-3To YDLGNAIS1p132,4166# Gsl-4globoglycolipid expression-4XVR115124,106H-23histocompatibility-2359.6BL,R124,106H-37histocompatibility-37(X)BR124,006H-37histocompatibility-37(X)BR4Hao-2hydroxyacid oxidase-2 (kidney)40.0BL8,1254,64,65*Hc3heterochromatin, Chr 30.0L621Hait2histone gene (2)XDS5646Had3b3-beta-hydroxy steroid dehydrogenase45.0DLHSDB31p11-p135# Iap1a2-9Intracisternal A-particle al-742.3DR9595107,108* Iap1a2-9Intracisternal A-particle al-742.3DR9594* Iap1a3-13Intracisternal A-particle al-1474.6DR9595Idd-3insulin dependent diabetes 3XVL149159,162,163I/-1interferon inducibility locus84.6VL,R1236,106I/-2interleukin 72.0B,DL2,621,62,137*Kv1.2potassium channel gene48.2DL2,621,62,137*Kv1.2potassium channel gene48.2DL2,621,62,137 <td></td> <td>Gnai-3</td> <td>guanine nucleotide hinding protein</td> <td></td> <td>4 9 A</td> <td>p</td> <td>T</td> <td>CNIATO</td> <td>1-12</td> <td><b>a</b> 4</td> <td>166</td>		Gnai-3	guanine nucleotide hinding protein		4 9 A	p	T	CNIATO	1-12	<b>a</b> 4	166
* $Gsl-4$ globoglycolipid expression-4 X V R H-33 histocompatibility-23 59.6 B L.R 12 4,106 H-36 histocompatibility-28 79.3 B L.R 12 4,106 H-37 histocompatibility-37 $(X)$ B R + H37 histocompatibility-37 $(X)$ B R + H37 histocompatibility-37 $(X)$ B R Hao-2 hydroxyacid oxidase-2 (kidney) 40.0 B L Hao-2 hydroxyacid oxidase-2 (kidney) 40.0 B L Hait hist histone gene (2) X D S Hait hypothalamic norepinephrine level 59.6 V L Had bydroxy steroid dehydrogenase 45.0 D L Haglal-7 Intracisternal A-particle a1-7 42.3 D R + Iapla2-14 Intracisternal A-particle a2-14 74.6 D R + Iapla2-14 Intracisternal A-particle a3-13 28.0 D R + Iapla3-13 Intracisternal A-particle a3-13 28.0 D R + Iapla3-13 insulin dependent diabetes 3 X V L I17 interleukin 7 2.0 B,D L 2.0 B,D L + Kv1.2 potassium channel gene 48.2 D L 2.0 93			alpha inhibiting sctivity.3		70,4	U	L	ONALS	1612	2,4	100
H-23histocompatibility-2359.6BL,R115H-28histocompatibility-2879.3BL,R124,106H-37histocompatibility-37(X)BR124,106H-37histocompatibility-37(X)BR124,106*H37histocompatibility-37(X)BR124,106*Hao-2hydroxyacid oxidase-2 (kidney)40.0BL8,1254,64,65*Hc3heterochromatin, Chr 30.0L8,1254,64,65621Hist2histone gene (2)XDS56564636Halhypothalamic norepinephrine level59.6VL46363-beta-hydroxy steroid dehydrogenase45.0DLHSDB31p11-p135*Iap1a2-7Hazaisternal A-particle a1-742.3DR9595107,108*Iap1a2-14Intracisternal A-particle a2-9 (near Fgg)XDR9494*Iap1a2-13Intracisternal A-particle a3-1328.0DR951236,106Il-2interferon inducibility locus84.6VL,R1236,106159,162,163Il-2interleukin 2115.0DS,LIL24q26-q271,3,4,949,134,149,150,11-7interleukin 211.50DS,LIL22,621,62,137<	*	Gsl-4	globoglycolipid expression-4		x	v	P				115
H-28histocompatibility-2879.3BL,R124,106H-37histocompatibility-37(X)BR124,106H-37histone 3, family 244.9DRH3F21q21-21132Hao-2hydroxyacid oxidase-2 (kidney)40.0BL8,1254,64,65+ Hc3heterochromatin, Chr 30.0L621Hist2histone gene (2)XDS56Ha1hypothalamic norepinephrine level59.6VL46Hs3b33-beta-hydroxy steroid dehydrogenase45.0DLHSDB31p11-p135Hsg86-ps2heat shock protein 86- pseudogene 219.3DS,L107,10895*Iapla2-9Intracisternal A-particle a1-742.3DR94*Iapla2-14Intracisternal A-particle a2-1674.6DR94*Iapla3-13Intracisternal A-particle a3-1328.0DR95Idd-3insulin dependent diabetes 3XVL1236,106II-2interleukin 72.0B,DL2,621,62,137*Kv1.2potassium channel gene48.2DL293		H-23	histocompatibility-23		59.6	R	TP			10	115
H-37histocompatibility-37K.B.DL.K.124,106*H3f2histone 3, family 244.9DRH3F21q21-21132Hao-2hydroxyacid oxidase-2 (kidney)40.0BL8,1254,64,65*Hc3heterochromatin, Chr 30.0L621Hist2histone gene (2)XDS56Halhypothalamic norepinephrine level59,6VL46Hsd33-beta-hydroxy steroid dehydrogenase45.0DLHSDB31p11-p135*Iap1al-7Intracisternal A-particle a1-742.3DR95*Iap1a2-9Intracisternal A-particle a2-1474.6DR94*Iap1a3-13Intracisternal A-particle a3-1328.0DR95Idd-3insulin dependent diabetes 3XVL1236,106II-2interferon inducibility locus84.6VL,R1236,106II-2interleukin 72.0B,DL2,621,62,137*Kv1.2potassium channel gene48.2DL293		H-28	histocompatibility-28		793	ñ	L,R [ P			12	+,100 A 106
*       H3f2       histone 3, family 2       44.9       D       R       H3F2       1q21-21       132         Hao-2       hydroxyacid oxidase-2 (kidney)       40.0       B       L       8,12       54,64,65         *       Hc3       heterochromatin, Chr 3       0.0       L       6       21         Hist2       histone gene (2)       X       D       S       56         Hal       hypothalamic norepinephrine level       59.6       V       L       46         Hsb3b       3-beta-hydroxy steroid dehydrogenase       45.0       D       L       HSDB3       1p11-p13       5         *       Iapla1-7       Intracisternal A-particle a1-7       42.3       D       R       95         *       Iapla2-9       Intracisternal A-particle a2-9 (near Fgg)       X       D       R       94         *       Iapla3-13       Intracisternal A-particle a3-13       28.0       D       R       95         Idd-3       insulin dependent diabetes 3       X       V       L       149         Idd-3       interferon inducibility locus       84.6       V       L,R       12       36,106         II-2       interleukin 2       1       15.0 <td></td> <td>H-37</td> <td>histocompatibility-37</td> <td></td> <td>00</td> <td>ñ</td> <td>R.</td> <td></td> <td></td> <td>14</td> <td>7,100 A</td>		H-37	histocompatibility-37		00	ñ	R.			14	7,100 A
Hao-2hydroxyacid oxidase-2 (kidney) $40.0$ BL $15.2$ $162.2$	*	H3f2	histone 3, family 2		44.9	Ď	R	H3F2	1021-21		132
* Hc3 heterochromatin, Chr 3 $0.0$ L $3.12$ $3.12$ $3.00$		Hao-2	hydroxyacid oxidase-2 (kidney)		40.0	ñ	Ť.	11512	1421-21	8 1 2	54 64 65
Hist2histone gene (2)XDS56Halhypothalamic norepinephrine level $59.6$ VL46Hsd3b3-beta-hydroxy steroid dehydrogenase $45.0$ DLHSDB3lp11-p135Hsp86.ps2heat shock protein 86- pseudogene 219.3DS,L107,108*laplal-7Intracisternal A-particle a1-742.3DR95*lapla2-9Intracisternal A-particle a2-9 (near Fgg)XDR94*lapla3-14Intracisternal A-particle a3-1328.0DR95lad-3insulin dependent diabetes 3XVL149lf-1interferon inducibility locus84.6VL,R12ll-2interleukin 72.0B,DL2,621,62,137*Kv1.2potassium channel gene48.2DL293	*	Нс3	heterochromatin, Chr 3		0.0	_	ĩ			6	27,07,02 21
Halhypothalamic norepinephrine level $59.6$ VL $50.6$ Hsd3b3-beta-hydroxy steroid dehydrogenase $45.0$ DLHSDB3 $1p11-p13$ 5Hsg86-ps2heat shock protein 86- pseudogene 2 $19.3$ DS,L $107,108$ Iapla1-7Intracisternal A-particle a1-7 $42.3$ DR $95$ *Iapla2-9Intracisternal A-particle a2-9 (near Fgg)XDR $94$ *Iapla2-14Intracisternal A-particle a3-13 $28.0$ DR $94$ *Iapla13-13Intracisternal A-particle a3-13 $28.0$ DR $95$ Idd-3insulin dependent diabetes 3XVL $149$ $149$ II-2interferon inducibility locus $84.6$ VL,R $12$ $36,106$ II-2interleukin 21 $15.0$ DS,LIL.2 $4q26-q27$ $1,3,4,9$ $49,134,149,150,$ $19.7$ interleukin 72.0B,DL $2,6$ $21,62,163$ *Kv1.2potassium channel gene $48.2$ DL $2$ $93$		Hist2	histone gene (2)		X	D	s				56
Hsd3b       3-beta-hydroxy steroid dehydrogenase       45.0       D       L       HSDB3       1p11-p13       50         Hsp86-ps2       heat shock protein 86- pseudogene 2       19.3       D       S,L       107,108         *       Iapla1-7       Intracisternal A-particle a1-7       42.3       D       R       95         *       Iapla2-9       Intracisternal A-particle a2-9 (near Fgg)       X       D       R       94         *       Iapla3-13       Intracisternal A-particle a2-14       74.6       D       R       94         *       Iapla3-13       Intracisternal A-particle a3-13       28.0       D       R       95         Idd.3       insulin dependent diabetes 3       X       V       L       149         If-1       interferon inducibility locus       84.6       V       L,R       12       36,106         II-2       interleukin 2       1       15.0       D       S,L       IL2       4q26-q27       1,3,4,9       49,134,149,150,         II-7       interleukin 7       2.0       B,D       L       2,6       21,62,163         *       Kv1.2       potassium channel gene       48.2       D       L       2,93		Hnl	hypothalamic norepinephrine level		59.6	v	Ĺ				46
Hsp86-ps2       heat shock protein 86- pseudogene 2       19.3       D       S,L       107,108         * $laplal-7$ Intracisternal A-particle al-7       42.3       D       R       95         * $lapla2-9$ Intracisternal A-particle al-7       42.3       D       R       95         * $lapla2-9$ Intracisternal A-particle al-17       42.3       D       R       94         * $lapla2-9$ Intracisternal A-particle al-14       74.6       D       R       94         * $lapla3-13$ Intracisternal A-particle al-13       28.0       D       R       95 $ldd.3$ insulin dependent diabetes 3       X       V       L       149 $lf-1$ interferon inducibility locus       84.6       V       L,R       149 $ll-2$ interleukin 2       1       15.0       D       S,L       IL2       4q26-q27       1,3,4,9       49,134,149,150, $ll-7$ interleukin 7       2.0       B,D       L       2,6       21,62,163         *       Kv1.2       potassium channel gene       48.2       D       L       2       93		Hsd3b	3-beta-hydroxy steroid dehydrogenase		45.0	D	Ĺ	HSDB3	1p11-n13		5
*       lap1a1-7       Intracistemal A-particle a1-7       42.3       D       R       95         *       lap1a2-9       Intracistemal A-particle a2-9 (near Fgg)       X       D       R       94         *       lap1a2-9       Intracistemal A-particle a2-14       74.6       D       R       94         *       lap1a2-14       Intracistemal A-particle a2-14       74.6       D       R       94         *       lap1a3-13       Intracistemal A-particle a2-13       28.0       D       R       95         !ada-3       insulin dependent diabetes 3       X       V       L       149         !f-1       interferon inducibility locus       84.6       V       L,R       12       36,106         !l-2       interleukin 2       1       15.0       D       S,L       IL2       4q26-q27       1,3,4,9       49,134,149,150,         !l-7       interleukin 7       2.0       B,D       L       2,6       21,62,137         *       Kv1.2       potassium channel gene       48.2       D       L       2       93		Hsp86-ps2	heat shock protein 86- pseudogene 2		19.3	D	S.L		-r p.p		107.108
*       lap1a2-9       Intracistemal A-particle a2-9 (near Fgg)       X       D       R       94         *       lap1a2-14       Intracistemal A-particle a2-14       74.6       D       R       94         *       lap1a3-13       Intracistemal A-particle a3-13       28.0       D       R       95         Idd-3       insulin dependent diabetes 3       X       V       L       149         If-1       interferon inducibility locus       84.6       V       L,R       12       36,106         II-2       interleukin 2       1       15.0       D       S,L       IL2       4q26-q27       1,3,4,9       49,134,149,150, 159,162,163         II-7       interleukin 7       2.0       B,D       L       2,6       21,62,137         *       KvI.2       potassium channel gene       48.2       D       L       2       93	*	laplal-7	Intracisternal A-particle a1-7		42.3	D	R				95
*       Iapla2-14       Intracisternal A-particle a2-14       74.6       D       R       94         *       Iapla3-13       Intracisternal A-particle a3-13       28.0       D       R       95         Idd-3       insulin dependent diabetes 3       X       V       L       149         If-1       interferon inducibility locus       84.6       V       L,R       12       36,106         II-2       interleukin 2       1       15.0       D       S,L       IL2       4q26-q27       1,3,4,9       49,134,149,150,         II-7       interleukin 7       2.0       B,D       L       2,6       21,62,163         *       Kv1.2       potassium channel gene       48.2       D       L       2       93	*	lap1a2-9	Intracisternal A-particle a2-9 (near Fgg)		х	D	R				94
- Iap1a3-13       Intracisternal A-pariticle a3-13       28.0       D       R       95         Idd.3       insulin dependent diabetes 3       X       V       L       149         If-1       interferon inducibility locus       84.6       V       L,R       149         II-2       interleukin 2       1       15.0       D       S,L       II.2       4q26-q27       1,3,4,9       49,134,149,150,         II-7       interleukin 7       2.0       B,D       L       2,6       21,62,163         *       Kv1.2       potassium channel gene       48.2       D       L       2       93	•	1ap1a2-14	Intracisternal A-particle a2-14		74.6	D	R				94
<i>law-3</i> insuin dependent diabetes 3       X       V       L       149 <i>If-1</i> interferon inducibility locus $84.6$ V       L,R       12 $36,106$ <i>II-2</i> interfeukin 2       1 $15.0$ D       S,L       IL2 $4q26-q27$ $1,3,4,9$ $49,134,149,150,$ <i>II-7</i> interleukin 7       2.0       B,D       L       2,6 $21,62,163$ *       Kv1.2       potassium channel gene $48.2$ D       L       2 $93$	+	1ap1a3-13	Intracisternal A-pariticle a3-13		28.0	D	R				95
IJ-I       interferon inducibility locus       84.6       V       L,R       12       36,106 $II-2$ interleukin 2       1       15.0       D       S,L       II.2       4q26-q27       1,3,4,9       49,134,149,150, 159,162,163 $II-7$ interleukin 7       2.0       B,D       L       2,6       21,62,137         *       Kv1.2       potassium channel gene       48.2       D       L       2       93		100-3 1f 1	insuin dependent diabetes 3		X	V	L				149
II-2       Interleakin 2       I       15.0       D       S,L       II.2       4q26-q27       1,3,4,9       49,134,149,150, 159,162,163 $II-7$ interleakin 7       2.0       B,D       L       2,6       21,62,137         *       Kv1.2       potassium channel gene       48.2       D       L       2       93		1J-1 11-2	interferon inducionity locus		84.6	V	L,R			12	36,106
II-7         interleukin 7         2.0         B,D         L         159,162,163           *         Kv1.2         potassium channel gene         48.2         D         L         2,6         21,62,137		11-6		T	15.0	D	S,L	IL.2	4q26-q27	1,3,4,9	49,134,149,150,
* $Kv1.2$ potassium channel gene $48.2$ D L $2,6$ $21,62,137$ 2 93		11-7	interlenkin 7		3.0	BD	Ŧ				159,162,163
	*	Kv1.2	Dotassium channel gene		487	ц. Д	L			2,6	21,62,137
	<u> </u>				+0.2				<b>.</b>	<u> </u>	73

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		· · · · ·		_					
*	Kv1.3	potassium channel gene	48.2	D	L			2	93
*	Kv1.3rs3	potassium channel gene 1.3 related sequence	48.4	D	L			2	93
	Lef-1	lymphoid enhancer-binding factor 1	X	D	R,S	LEF1	4q23-q25		105
Ŧ	M6pr-ps	cation-dependent mannose 6-	45.5	D	L			2	94
		phosphate receptor pseudo gene							
	ma	matted	40.4	V	L			10,12	85,86,87,106
	Mme	membrane metallo-endo peptidase	30.1	D	L	MME	3q21-27	1,7	23,161
		(neutral endopeptidase)							
	Mmv-2	MCF endogenous virus-2	х	D	S				63
	Mmv-12	MCF endogenous virus-12	Х	D	S				63
	Mov-10	Moloney leukemia virus-10	Х	D	S				74,113
	Mpmv-9	modified polytropic murine leukemia virus-9	88.2	D	L,R			11	51
	Mpmv-20	modified polytropic murine leukemia virus-20	9.6	D	R				51
	my	blebs	30.4	V	L			10	19,35,45
	Ngfb	nerve growth factor beta	47.4	D	L	NGFB	1p13	1,2	18,42,52,59,79,94,
									109,118,166,171
	Nras	Nras oncogene	47.4	D	L	NRAS	1p13	1,2	18,93,118,128
*	Nscl-2	see Tau-1		-					
	Oat-rs2	ornithine aminotransferase related sequence 2	52.4	D	L				125
	Odc-rs3	ornithine decarboxylase-3	Х	D	R				126
	op	osteopetrosis (Csfm mutation see Csfm)							
	Otf-3rs3	octamer transcription factor -3 related sequence 3	0.0	D	L	_		2,7	137,161
	Otf-3rs4	octamer transcription factor-3 related sequence 4		62.1	D	L			1,2,7,137,161
*	Otf-3rs9	octamer transcription factor-3 related sequence 9		16.4	D	L			7,161
	Oua-1	ouabain resistance-1	х	V	S				83
	Pgk-1ps3	phosphoglycerate kinase-1 pseudogene 3	8.7	D	S,R				1
	Pk-1	pyruvate kinase (may be the same as Pklr)	33.6	В	L			8	54,139
	Pkir	pyruvate kinase liver, red blood cells (see Pk-1)		42.6	D	L	PKLR	1q21	1,118
*	Pmp-1	peroxisomal membrane protein (70k)	54.6	D	L	PMP1	1p21-22	2	52
	Pmv-26	polytropic murine virus-26	71.8	D	R				50
	Pmv-28	polytropic murine virus-28	42.9	D	R				50
	Pmv-38	polytropic murine virus-38	43.1	D	R				50
	Pmv-39	polytropic murine virus-39	53.8	D	R				50
	Rapia	member of RAS oncogene family	47.4	D	L	RAPIA	1p12-p13	1	41
	rcm	rostral cerebellar malformation	65.4	v	L			12	89,90
*	Rn7s-3	7s RNA related sequence -3	63.0	D	R				147
	Rnu1b-1	U1b1 small nuclear RNA	42.7	D	R	RNU1			96
	Rnu1b-3	U1b3 small nuclear RNA	42.9	D	R				13,96
	SOC	soft coat	43.4	V	L			10	45,140
	spa	spastic	37.4	V	L			10	85,86
	suc-1	see Suc-1r			_				
	Suc-Ir	sucrase-isomaltase, regulatory	33.3	B	L				12
	Suc-Is	sucrase-isomaltase, structural	33.3	D	ĸ	SI	3q25-26		12
	sut	subtle gray	12.2	V	L			12	88
	Tau-I	basic domain helix-loop-helix (bHLH)	50.6	D	L			12	33
*	Thbs3	thrombospondin 3	43.9	D	Ļ			1	38
*		tyrosine kinase receptor (NgI is ligand)	43.9	ע	L			1	80
	Tmevd-2	TMEV induced demyelinating			D				104
		disease susceptibility	8.4	v	ĸ				104
*	Tpi-2	triosephosphate isomerase		<b>D</b>	-				120
	<i>m</i> 11	related sequence-2	30.4	ע	L			2	120
	ISAD	inyrotropin stimulating	47.4	D		100110	1-12	1	12 42 70 82 100
		hormone beta subunit	4/.4	D	L	ISHB	1013	1	13,42,79,82,109,
	12 -	sussisting and disc	71 6	v	т			10.12	27 42 45 67 68
	va	variunt-waddier	0.1/	v	L			10,12	26,43,43,07,08, 86 87 106
	V	and the MCE last and the second	42.2	D	р				12
	AMMV-22	xenoropic-MCF leukernia Virus - 22	44.3	U U	л D				164
	AMMV-4/	xenotropic-MCF leukemia virus - 4/	12 3	D	K T D			12	164
*	AMMV-03	VD 1 DNA binding protein related converse d	44.5	D D	L,R T			2	141
•	1010	I D-1 DIVA officing protein related sequence a	14.0	U	L.			~	171

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The Chr 3 map positions are an estimate of distances, in cM, from the centromere. The position of the centromere is determined by heterochromatin mapping data (21, 101). Since recombination frequencies may vary depending on the specific cross, composite map positions may distort gene order when loci have not been mapped in an individual backcross. In deriving the composite map, RI strain data was used to determine gene position only as a supplement to backcross data. For a fuller discussion of the generation of map positions, see text and (133). In addition to the references cited for each locus, data used to derive map positions are described in the following "Notes:" (1) Duke University cross: complete haplotypes in 114 and incomplete haplotypes in 338 interspecific [(C3H/HeJ-gld  $\times$  M. spretus)F<sub>1</sub>  $\times$  C3H/HeJ-gld] backcross mice (134); (1a) same cross as above, but fewer than 40 meiotic events examined; (2) Frederick cross: complete haplotypes in 83-198 interspecific [(C57BL/6J  $\times$  M. spretus)F<sub>1</sub>  $\times$  C57BL/6J] backcross mice; (2a) same cross as 2, but fewer than 50 meiotic events examined; (3) Rockefeller University cross and MIT microsatellite mapping panel: complete haplotype data in 40–48 (C57BL/6J-ob ×CAST/Ei)F<sub>2</sub> intersubspecific intercross mice; (4) European Collaborative Interspecific Backcross [(C57BL/6 × SPR)F<sub>1</sub> × SPR] produced by the UK's Human Genome Mapping Project, with the support of the Medical Research Council (15); (5) data from the cross [(NOD/Uf × C57BL/6)F<sub>1</sub> × NOD/Uf] from the laboratory of E.K. Wakeland. The RAPD polymorphism D3Uf1 was detected with the primer GTGCCTAACC, and D3Uf2 with the primer TGCTCACTGA; (6) RPMI cross: complete haplotypes in 130–140 [(C57BL/6 × M. spretus)F<sub>1</sub> × M. spretus]; (7) Duke University cross #2: complete haplotype data in 100–182 [(MRL/MpJ-lpr × CAST/Ei)F<sub>1</sub> × MRL/MpJ-lpr] intersubspecific backcross mice (161); (8) Pasteur cross: incomplete haplotypes in 38–74 interspecific backcross mice (J.-L. Guénet, unpublished data); (9) same as 4 with complete haplotype data in 92–299 mice; (10) included in nine overlapping three- or four-point crosses that derive from analysis of 125–500 meiotic events in each of multiple individual crosses; (11) haplotype data; (13) two-point mapping data.

Mon

68.1

68.1

Adh-3

Adh-3t

**Table 2.** Tabular map of Chr 3. Loci described in Table 1 are arranged in order of increasing distance from the centromere. The 95% confidence intervals for these composite data are greater than 5 cM. Unambiguous gene order can only be determined for loci which were mapped within the same cross (Fig. 1B).

Iviap	Locus		
0.0	D3Mit23	28.0 Japla3-13	42.9 Capl
0.0	Hc3	30.0 D3Mit25	42.9 D3Pas502
0.0	Otf-3rs3	30.0 D3Mit7	42.9 D3Tu51
2.0	II-7 Car-1	30.1 D3Byul/ 30.1 D3Sal2	42.9 Fcgri
6.3	Car-2	30.1 D33ei2 30.1 Mme	42.9 <i>Pmv-20</i> 42.9 <i>Rnulb-3</i>
6.9	D3Byu1	30.4 my	43.0 Acrb-2
6.9	D3Byu2	31.0 Xmmv-47	43.1 Pmv-38
7.0	D3Mit1	33.1 <i>D3J1</i>	43.4 soc
7.5	Car-3	33.3 Es-20	43.5 <i>D3Ufl</i>
8.2	D3Pas501	33.3 Suc-18	43.9 Cai 43.9 Ensl.rel
8.3	c0a	33.6 Pk-1	43.9 Thbs3
8.4	Tmevd-2	34.4 D3Byu5	43.9 Tkr
8.7	Pgk-1ps3	34.9 Glur-2	44.9 D3Mit28
9.6	D3Mit46	35.0 D3Mit22	44.9 H3f2
9.0	Mpmv-20	35.0 D3M1133 36.2 D3M1153	45.0 Hsdb3b 45.2 D2PmuA
10.1	Es-16	36.4 Tni-2	45.5 Gia-5
10.2	D3Leh2	37.4 spa	45.5 M6pr-ps
10.2	Evi-1	38.6 D3Mit26	46.1 D3Mit41
10.2	Fim-3	38.6 D3Mit9	46.4 Cd2
10.2	Glut-2	38.8 Cnp-2	47.3 Atplal
13.2	SUL D?Pas?	40.0 Hao-2 40.1 D3Min40	47.4 Ampa-1 AT A C453
14.6	Ybld	40.1 D3Mit49	47.4 D3Jfr1
15.0	Cena	40.4 ma	47.4 Ngfb
15.0	11-2	41.5 D3Lerl	47.4 Nras
15.7	Fgf2	41.5 D3Ler2	47.4 Rapla
17.6	DRI261	42.3 D3Byuo 42.3 Faa	47.4 ISRD 48.1 D3Sall
19.3	Hsp86-ps2	42.3 laplal-7	48.2 Kvl.2
20.0	D3Mit24	42.3 Xmmv-22	48.2 Kv1.3
20.0	D3Mit3	42.3 Xmmv-65	48.4 Csfm
20.0	D3Mit4	42.4 ft	48.4 de
22.0	D3F asr D3Mit6	42.6 Goa 42.6 Phir	48.4 Ghai-2 48.4 Ghai-2
23.3	Es-27	42.7 Rnulb-1	48.4 Kyl.3rs3
24.0	D3Mit5	42.9 Cacy	48.6 D3Mit10
27.0	D3Nds1	42.9 Calll	48.6 D3Mit11
			<u> </u>
49.6	Amy-1	68.1 Ahr-1	
49.6	Amy-2	68.1 Bmn	
49.0	Cj-5 Emv.77	68./ D3Mill/	
50.2	Ampd-2	71.6 Va	
50.3	D3Mit12	71.8 Pmv-26	
50.6	Nscl-2	73.0 D3Mit18	
52.0	Adh-1ps	73.0 D3Mit31	
52.5 52.4	DSUJ2 Oct-rs?	74.0 Iapia2-14 75.2 D2M:45	
53.4	D3Mit36	76.4 D3Dal	
53.4	D3Mit39	77.0 D3Mit32	
53.8	Pmv-39	79.3 H-28	
54.6	Pmp-1	81.0 D3Mit19	
34.7 54 7	DSJS Fahri	84.6 <i>If-1</i>	
56.1	D3Hun1	оо.2 мрту-у Х Ілл.3	
56.1	D3Mit42	(X) <i>H-37</i>	
57.7	D3Mit13	X Acts	
57.9	D3Tu33	X Adh-5	
38.4 50 4	Ank-2 H-23	X Arnt	
59.6	Hnl	л вдіар Х Gel-4	
61.0	D3Mit14	X Hist2	
61.0	D3Nds2	X lapla2-9	
61.6	cdm F	X Lef-1	
02.1 62 1	Egj Otf-3A	X Mmv-12	
63.0	D3Nds3	$\Lambda$ Mmv-2 X Mov-10	
63.0	Rn7s-3	X Odc-rs3	
63.1	D3Mit15	X Oua-l	
63.1	D3Mit16		
0,4.3 65.4	cop-l		
65.6	D3J2		
67.2	D3Mit38		
68.1	Adh-1		
VO.1	Man-11		

says, and the availability of the MIT primers from Research Genetics (Birmington, Ala.) make these markers extremely useful. Additional microsatellite markers have been developed by J. A. Todd and coworkers at the Nuffield Department of Surgery, Oxford, U.K. (Nds). Table 4 presents recombination data for 21 microsatellite markers spanning Chr 3, obtained from the European Interspecific Backcross [(C57BL/ 6J × Spretus].

#### **Recombinant inbred lines**

Like multilocus backcrosses, RI lines provide a cumulative mapping resource. New loci can be mapped by typing the existing RI lines and comparing strain distribution patterns with the corresponding data for previously typed markers. Strain distribution patterns for Chr 3 loci that have been typed on RI lines are presented in Fig. 2.

#### Anchor loci

In the last report we recommended use of six anchor loci to facilitate integration of new genetic data with the current map. It is too early to judge the effectiveness of this recommendation, that is, the degree to which investigators will type these loci in new crosses. To fill in the gaps in the previous anchor map, we recommend two additional microsatellite markers. Either D3Mit5 or D3Mit27 will divide the 28-cM interval between II-2 and Gba approximately in half. D3Mit19 provides a marker for the distal end of Chr 3; it is located approximately 20 cM distal to Adh-1. A subset of these well-mapped anchor markers can be selected to divide Chr 3 into convenient intervals: centromere -D3Mit22 - 8 - Gba - 5 - Tshb - 2 - Amy - 1 - 12 - Egf - 6 - 6Adh-1-13-D3Mit19.

### **Conserved** linkage relationships

Mapping of genes has identified syntenic relationships between mouse Chr 3 and four human chromosomes: 1, 3, 4, and 8. The position of these mouse Chr 3 genes and their relationships to the chromosomal positions of the human homologs are shown in Table 5. These data suggest that rearrangements of chromosomal segments during mouse evolution have resulted in three separate homology groups with human Chr 4 and two separate homology groups with human Chr 3. In addition, the conserved linkage relationship with human Chr 1 spans the centromere of this chromosome. Long-range restriction site analysis has also indicated very strong conservation of some of these relation-



В CROSS 1: (C3H/HeJ-gid x M. spretus)F1 x C3H/HeJ-gid (n = 117 to 338) Car-2 - 3.5 - Evi-1 - 2.6 - II-2 - 0 - Cyca - 0.9 - Fgf2 - 13.5 - Mme - 4.4 - Glur-2 - 7.10 -Gba - 0.9 - Thbs3 - 0 - Pkir - 0 - Fspl-rs1 - 0 - Cd1 - 0 - Trk - 0.6 - D3Tu51 - 0 - Cacy -0.9 - Fcgr1 - 2.6 - Cd2 - 0.9 - Atp1a1 - 0.3 - Nras - 0 - Cd53 - 0 - Ngfb - 0 - Tshb - 0 - Ampd-1 - 1.8 - Amy-2 - 0.6 - Ampd-2 - 13.4 - Egf - 11.7 - D3Mit18 - 9.3 - D3Mit19 CROSS 2: (C57BL/6J x M. spretus)F1 x C57BL/6J (n = 83 to 198) Ott-3rs3 - 2.0 - 11-7 - 7.3 - Evi-1 - 0 - Fim-3 - 0 - Glut2 - 7.6 - Ybld - 0 - Cona - 0 - Fgf2 - 21.8 - Tpi-2 - 6.0 - Fgg - 6.8 - Gja-5 - 0 - M6pr-ps - 5.2 - Ngfb - 0 - Nras - 2.2 -Kv1.2 - 0 - Kv1.3 - 0.6 - Cstm - 0 - Kv1.3-rs3 - 0 - Gnai-2 - 0 - Gnai-3 - 1.5 - Amy-2 -4.9 - Pmp-1 - 5.5 - Egf - 0 - Otf-3rs4 CROSS 3: (C57BL/6J-ob x CAST/Ei)F2 (n = 40 to 48) D3Mit23 - 6.8 - D3Mit1 - 1.4 - D3Mit46 - 2.4 - II-2 - 2.2 - D3Mit4 - 0 - D3Mit3 - 0 -D3Mit24 - 1.1 - D3Mit5 - 0 - D3Mit6 - 4.7 - D3Mit7 - 0 - D3Mit25 - 3.4 - D3Mit22 - 0 -D3Mit53 - 1.1 - D3Mit51 - 2.3 - D3Mit26 - 0 - D3Mit9 - 1.4 - D3Mit40 - 0 - D3Mit49 -4.6 - D3Mit28 - 1.1 - D3Mit41 - 2.3 - D3Mit10 - 0 - D3Mit11 - 1.1 - D3Mit12 - 1.8 -D3Mit39 - 0.5 - D3Mit36 - 1.8 - D3Mit42 - 1.1 - D3Mit13 - 2.2 - D3Nds2 - 0 - D2Mit14 - 1.1 - D3Mit16 - 0 - D3Mit15 - 3.5 - D3Mit38 - 1.2 - D3Mit17 - 4.3 - D3Mit31 - 0 -

D3Mit18 - 3.1 - D3Mit45 - 2.4 - D3Mit32 - 7.3 -D3Mit19

CROSS 4: C57BL/6J x SPR)F1 x SPR: D3Mit1 - 7.6 - Ap2 - 10.8 - II-2 - 7.6 -D3Mit6 - 2.0 - D3Mit5 - 3.0 - D3Nds1 - 8.6 - D3Mit22 - 8.6 - Tshb - 1.0 - D3Mit11 - 1.9

- Adh-1 - 10.8 - D3Mit31 - 4.3 - D3Mit32 - 3.0 - D3Mit19

CROSS 5: (NOD/Uf x C57BL/6J)F1 x NOD/Uf

D3Mit1 - 19.0 - Glut-2 - 4.0 - II-2 - 6.1 - D3Nds1 - 18.8 - D3Uf1 - 7.3 - Tshb - 4.3 -D3Mit10 - 3.2 - D3Uf2 - 14.1 - Adh-1 - 20.5 - D3Mit19

**CROSS 6:** (C57BL/6J x M. spretus) $F_1$  x M. spretus (n = 130 to 140) Hc3 - 0.7 - II-7 - 6.9 - Evi-1

CROSS 7: (MRL/MpJ-*lpr* x CAST/EI)F1 x MRL/MpJ-*lpr*: Otf-3rs3 - 6.3 - Car-2 - 10.6 - Otf-3rs9 - 14.4 - Mme - 24.3 - Otf-3rs4 - 0 - Egf - 26.8 - D3Mit18

Fig. 1. (A) Gene order in seven multilocus crosses. Loci are listed from proximal to distal on the chromosome. The filled boxes represent the loci that were typed in each cross. The shaded boxes represent loci that did not recombine with the locus listed directly above. The observed recombination frequencies from each of these crosses are presented in Fig. 1B. See Table 1 and Fig. 1B for additional information about the crosses.

Fig. 1. (B) Recombination frequencies in multilocus crosses. Crosses 1–7 are described in Table 1 and Fig. 1A. The approximate lengths, in cM, of the intervals observed in each cross are presented here. We included only crosses with at least six markers analyzed in at least 80 meiotic events, with the exception of cross 6, which provides data for anchoring the composite maps with respect to the centromere. (Note: Cross 4, n = 92)

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Locus	Sequence	Primer forward (5'-3')	Primer reverse (5'-3')	Product size	Conditions	Size variation
D3Nds1		66ATCT66CACCTCCA666	TATIGTTGCCTTGGCAAATAGATG	06	1mM/55	NOD=NON>>AKR/J>B10/W=B6.PL=B6/J=DBA/2J; SPE:-
D3Nds2		ACACATTGGAGATGCACAGCO	TICTOCATOCCAGOGTTGTGAT	128	3mM/55	SPE>>DBA/2J>>NOD=NON=B10/W=B6.PL=B6/J=AKR/J
D3Nds3		CTGTGAAATTTGCCATCAACT	CATAATATTCATATATAATGC	165	3mM/55	NOD=NON=B10/W=B6.PL=B6/J=AKR/J>>DBA/JJ>>SPE
D3Nds4		ATTTFAAATATTCAFTCATTCATTTGGG	CTCACAAATACCTTCAGAGGA	110	1mM/55	NON>B6/J=B10/W=B67L>DBA/2J>NOD
D3NdeS		AGCATTATTTTAAACATCTGAATAG	TGGAGTCACCTTCTTGAGTTC	148		NOD>>DBA/2I=AKK/J=NON>B10/W=B6.FL_B6/J (SPE doublet)
D3Nda6	11-2	GTGGGAGTGTGTGCAAAAGAC	AAGTATGGGTCAGATTGTGTGGG	170	2mM/58	\$PE>B&PL=B10/W=B6/I>NON>AKR/I>DBA/2I>NOD
D3Nds7	Cacy/Capl	CACAGTGAGACCAAACTC	CTIGGCIGTIATAGIGITIG	117	1.5mM/55	\$PE>>C57L/I>>SWR/I=C57BR=S1L/I=B10/W=NON>C3H/HeJ= A/I=A/RVI/>>CBA=BALB/cByj=NOD>>DBA=PL/I
D3N4s8	Tskb	TCTGAAGAGTTTTGTCCTCATC	TGAATAAAGGACTCCTGAGCT	145	2mM/55	NOD=AKR/i>>NON=B10/W=B10/j=B6/j=DB4/2J>>SPE
03Nde9	I-VPV	CITACTGGGTGACATAGACG	<b>CCTTTCATCCATGTACATATAC</b>	330	2mM/55	B10/J=B10.BR>NOD>A=C58=MEV; SPE=B10/W>NOD>B6.PL>NON
D3Nds11	Fcgrl	GTCCCCAGTCATCAGCTCCTG	<b>CBCTTCTAACTTGCTGAAAGGAA</b>	184-188	1.5mM/63	C3H=DBA=A=B6=AKR=BALB=B10=CAST=SPE=NON>>NOD
D3Nds12	Ghd-2	GGGCGCTGGAAAGCTAATACC	CATAAGAGGGGGGGGGGGGGGGAGATC	120	1mM/55	B6=B6.FL=DBA=B10=AKR=SPE>NON=NOD
D3Nds13	Ghu-2	GTCTCCTTTCTAGTTTCTGA66C	CITCACAGATOGTATTTGAAACAG	113	1mM/55	B6=B6.PL.=DBA=B10=AKR=SPE=NON=NOD
D3Nds14	Ap2	TCCATAGCATTCATGCGTGCA	GTCTGTTGCTTACTATGTGC	146	2mM/55	NON>CBA>B10/W=B6.FL=NOD=SPE=B60>DBA/2J
D3Nds15	Ap2	TATAAGATTCCAGAACACATT	GATAAGAGCATGGATTTAACT	133	2mM/55	NOD=B10/W=B&PL_B&I/2]=NON>SPE
D3Nds16	11-2	TGTACCTCCTGCTTACAACAC	TACCTACACATGATATTTAAC	224	2mM/55	NOD=B10/W=B6J=NON=DB4/2J=SPE
D3Nds17	11-2	ACTAGCAAGAGTTGGTCTCTG	ATTITATATGTCTCTAGTTGCAC	232	2mM/55	NOD=B10/W=B6.PL=B6/J=NON=SPE=DBA/2J
D3Nds18	Ngfb	AGGTTCATCCGGATAGACACA	TTCGGTATACAGGATGCTTTG	232	1.5mM/55	NOD=B10/W=NON=SPE=B4/J=DB4/2J
D3Nds19	Amy-I	ATGAACATATGTGTAAGTAAAATG	AAATAAAAGGCCACTATTTGAAG	153	2mM/45	CBA=MOLD=YBR=C3H=NOD>Brcd>AKR>SPE
D3Nds20	Gba	GAAGGAAAGGACTTAGTCTACC	GGCCTTGGCTCTGTTATTICTGT	190	1.5mM/55	SPE (doublet)>>NOD <b>-</b> B10, W=B6,PL=B6/J=DBA/ZJ
D3Nds21	Ly-38	<b>GTGTAAAATCAACACCAACAGTAT</b>	GGCAGGTTTGATTCTAAGGTAG	166	1mM/55	NOD=B10/W=B6.PL~B6/J=NON=DB4/2J=AKK/J=SPE
D3Nds22	Ly-38	000011111GTTTGCTGGTTAGT	GGACAGCCAGGACTATACAGA	164	1mM/61	NOD=B10/W=B6.PL=B6/J=NON=DB4/2J=AKR/J>>SPE
D3Nds23*	Hsp86-ps2	AGTOCCCAATCACATTCTGC	GATCCTGTAATCTGTCCATAG	1100	2mM/55	RFLP; Hintí NOD∞+; B10, B6, NON=-
D3Nds24**	Cd-10	GTCCT0GAGGTTCATAATG	GGGAGAGAAACGCAACAT	1200	1mM/55	RFLP; Mspl SPE=+; B6=-
D3Nds25***	Gba	GATGCAGTACAGTCACAGCAT	CCATCCAGTTACGTGGTAAAG		1.5mM/58	SPE>>B6
D3Nds26****	Gpi-irs	GTCCCCGTGTCTGGTTTGTCTCTAACATT	TGACCACAGCGAATAGCGGCAACCTACCC	280	2mM/60	NOD=+; B10=-
D3Nds27	11-2	GTGCTTGTCAACAGCGCA	CTCCTGTAGGTCCATCAACAGC	129	1mM/55	NOD=B10/W=B6/J=B6.P1zNON=DBA/2J=AKR>>SPE
D3Mid	M28	TGTGCACAGGGGTACATACA	TCATTITICTTCCTCCCCCTC	118-145	3mM/55	OB-LP>>BALB=NOD>>A=B6=C3H=DBA=AKR=NON>CAST; SPE:-
D3Mil3	M250	CUTTTIGAGGCAAAGCTCC	CTAAGTCCTGCACCTGCCTC	88-200	1mM/55	CAST>>A*BALB=L2>OB=B6=DBA=AKR=NOD>>C3H=NON>>SPE
D3MiM	740	TGTGCCTGCAAGTTGTTCTT	CTACAGTGGGGGCAGAAGGT	140-150	1.5mM/55	CAST>>SFE>>OB=A=B6=C3H=DBA=BALB=AKR=NON=NOD=LP
D3Mid	M123	AGCCCTTCCAAGTGTCTCT	GGTTTCGGAATGAGATGAGC	178-188	1mM/55	OB=A=C3H=DBA=BALB=AKR=NON=NOD>>CAST=B6=LP>>SFE
D3Min6	M149	AACTTCAACATGTGAGGGGC	CCTGAAACAAGCAACAGCA	125-145	1.5mM/55	B6eLP>0B>>A=C3H=DBA=BALB=AKR=NON=NOD>>CAST>>SPE
					E.	Continued on next page

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Continued.	
Table 3.	

Continued on next page		2 + 204		CITICIAAAAAAA	1067	DJMIMY
ייזער אין אין איזיין איזען איזערעייעער אין אראר אראר אראר אראר איז איזער איזער איזער אראר אראר אראר איז איז א	1mM/55	247	GTTGACACAAAACTAGCCAGTACA	TCTGTACCCCTTTCCCCC	D535	D3MiM8
SPE>>CAST>>C3H=A>>B6=0B>BALB>LP=NOD>DBA>NON>>AKR	1mM/55	152-194	TTCCCCAGGGAAATCTCTCT	ATCCCCCACCCAACTCTAAC	D534	D3MiM6
NOD=DBA>B6=OB>NON>>AKR>>LP=BALB=C3H=A>>CAST>>SPE	1 mM/55	124-148	CCCTATCACATAGGGCAACC	CCTGACTCATTTATTTAACTCCCC	B430	D3MiM4
CAST>>BALB=C3H=A>>LP=NOD=NON=AKR=B6=0B>>DBA>SPE	1mM/55	114-146	CTGTGCATGAGACCACTACCA	TGACCTCCAGAGAGTCTTCCA	16EB	D3MiM3
CAST>>NOD>>SPE>>LP=NON=AKR=BALB=DBA=C3H=B6=A=OB	1mM/55	210-236	CATGAGAGCTCCTTCCATCC	AATITCTTCCTGTTACACTGAGCC	B235	D3MiM1
B6=0B>>CAST>>SFE>>LP=NOD=NON=AKR=BALB=DBA=C3H=A	1mM/55	110-140	CCTTATTAAGTGCATGACCTTGC	CAGCTGGTCTAACTATCCCCC	01110	D3Mim0
SPE=CAST>>LP=NOD=NON=AKR=DBA=C3H=B6=A=OB>>BALB	1mM/55	226-242	AATGGAGCITIGCITICGATG	CTGCCACAGAGCTATAGCCC	A869	D3Mi39
CAST>>LP=BALB=C3H=A=SPE>>NOD=NON=AKR=DBA>B6=OB	1mM/55	122-142	ACCATGGCCAGCTTCTAATG	CTGAACCAGAAAGTTGTTTTTCTG	¥294	D3Mil38
NOD>>CAST>>SPE; LP, NON, AKR, BALB, DBA, C3H, B6, A, OB:-	1mM/55	138-226	GAACATATGTGTAAGTAAAATGTAC	GATHTTAATTCATTAAATTAAGGGTTAG	105C	D3MiD6
LF=NOD=NON=AKR=BALB=DBA=C3H=A=SFE>>B6=OB>>CAST	1mM/55	164-178	GCACITIGTGTTTCATGTCACTG	CACCTGGTTAACTCAGAAAGG	B128	D3Mi32
CAST>SFE>>LP=NOD=NON=AKR=BALB=DBA=C3H=A>B6=OB	1mM/55	222-242	GTGCTGCCAGTTAAGCCTG	ACAACCCGAGTTCAGTCCC	A629	D3MiB1
BALB>>CAST>>DBA>>SPE>>B6=A=OB>LP=AKR=C3H>NON>NOD	1mM/55	144-200	CCAGCCTCAGTATCTCAAAACC	GATGAGAGATTCTGATGTOGAGG	D566	D3Mi29
BALB>>CAST>>DBA>>SFE>>OB>NON=AKR=C3H=B6=A; LP, NOD:-	1mM/55	150-202	CCAGCCTCAGTATCTCAAAACC	GATGAGAGATTCTGATGTGGAGG	D627	D3Mi28
CAST>>B6=OB>>LP=NON>>NOD=AKR=BALB=DBA=SPE; C3H, A:-	1mM/55	130-156	CTGGAATCAAGTGGTTTAGTCAA	TTGGATTCATATCAGGACTGTACA	B332	D3Mi26
B6=0B>LP=NOD=AKR=BALB=C3H=A>>129>NON>DBA>>SPE	1@M/55	114-134	TGGAGGCTACCATCTCCCAAG	GTCTGGGTCCTCAGTGGC	A726	D3Mi25
CAST>>SPE>>NON>>LP=NOD=AKR=BALB=DBA=B6=OB>>C3H=A	1 mM/55	130-168	<b>GTCATTGTTTATCATACCCACAGG</b>	AGTITICTAGCCTCAGTGTTCTTCA	A636	D3MiQ4
CAST>>LP=NOD=NON=AKR=BALB=DBA=C3H=B6=A=OB>>SPE	1mM/55	138-162	TCAATCAGAGAGAGATAAGAGCATGG	GATTCCAGAACACATTGTGGG	D102	D3MiQ3
CAST>>A>>NOD>>OB=B6=C3H=NON>DBA=AKR>>BALB=LP>>SPE	1mM/55	207-265	AATCAGCGATTTCAGCACG	AAGGATTGAAGAATGGTTGGG	D122	D3MiQ2
NON=BALB=B6=OB>>LP=NOD=AKR=DBA=C3H=A>CAST>>SPE	1 mM/55	208-236	CIGGGGAGTITICAGGTITCCT	AAGCTCTACAGCCGGAAGCAC	1£0	D3MiQI
5 CAST=A=C3H=DBA=BALB=AKR=N0D>>OB=B6=N0N>LP>>SPE	1.5mM/5	210-238	GAACATTGGGGTGTTTGCTT	CAGCCAGAGAGGAGGCIGTCT	M141	D3Mid9
NOD=B6=OB>>CAST>>LP>>NON=AKR=BALB=DBA=C3H=A; SPE:-	1mM/55	180-208	CCACGGAGAACAACTGAAGA	CATGGCTCCATGGTTCTTG	M235	D3Mid7
SPE>>CAST>>B6=OB=LP=NOD=NON=BALB=C3H=A; AKR, DBA:-	1mM/55	186-220	TGAGAATGGAGGTGAACAGC	TGCTTGTCCTGTGTTAATGA	W159	D3Mid 6
DBA>>CAST>>SPE>>NOD=NON=AKR=BALB=C3H=B6=A=OB; LP:-	1mM/55	145-212	AGGAAGTGACGTTGGGTTTG	AATTTGCATTCCAGGACCAC	A55	D3Mid5
NOD=NON=AKR=BALB=DBA=C3H=A>>LP=B6=OB>>SPE>>CAST	1mM/55	127-198	TCCTGCAAATTGTCCTCGA	ATTGCGGTTAAAGTTTGCTT	M206	D3Mid4
LP>SPE>NOD>>CAST>>OB=B6#DBA=C3H=BALB=AKR=NON	1mM/55	220-237	AACCACAGATGACAATTGAA	TITCIGCATTATUTOGOCIT	137	D3Mid3
SPE=LP>CAST=NOD>>OB=B6=C3H=DBA=BALB=AKR=NON; A:-	1mM/55	228-240	CCACTGAAGGATAACCACAG	<b>CCITITICIDAITTATIGTOGGCT</b>	81	D3Mid3
LP=AKR=A>BALB=C3H=B6=OB>>NOD=NON=DBA>>CAST; SPE:-	1mM/55	120-157	<b>GGAAAAGCATAAGAAACAACCG</b>	TAGACCAATCITGGGAGTGTCC	A60	D3Miu2
CAST>>A=C3H=BALB=AKR>NON>>SPE>>OB=B6=DBA=NOD=LP	1mM/55	146-204	TOGAGACCAATGCGAACAAC	CCAACCACAGTAACACATGT	138	D3Mid1
CA\$T>>B6=OB>>DBA>LP>NON>BALB=A>AKR=SPE>>NOD; C3H:-	1mM/55	121-158	CCTAAGCCAGCTACCACCAC	CIGGCITGGTGGAAGTCCT	<b>A34</b>	D3Min10
CAST>>>OB=B&>>DBA>LP>NOD>A=BALB>SFE#AKR>>NOD, C3H:-	1mM/55	214-238	TGTTTTATATTGCCCTGTATGTGC	AACITCATTICCTF0GAAACTACC	A85	D3MiD
OB=SFE=B6=DBA>>CAST=A=C3H=BALB=AKR=NON=NOD=LP	1mM/55	142-147	TACAATTATCCGGGAGCTA	ATGCAACTAACTITATIGAAAATC	₽ <i>L</i> W	D3MiG

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Locus	Sequence	Primer forward (5'-3')	Primer reverse (5'-3')	Product size	Conditions	Site variation
D3Mir50	F107			168-198	1mM/55	CAST>>LP=AKR=BALB=DBA>C3H=A>NOD=NON=B6+OB; SPE:-
D3MicJ	38	GGCACTGATAGCAGGCCTAG	TCTCTTCTGGTATTTCCTTCCG	230-258	1mM/55	AKR=BALB=DBA>NOD=NON>>LP>>C3H=B6=A=OB>>CAST; SPE;-
D3Mid2	A1081	AGCCAGGATATGGAATATGCC	TGACCAGATTGCATGCATTT	196-204	1 mM/55	A=SPE>OB>NOD=NON=AKR=DBA=C3H>LP>BALB=B& CAST:
D3Mit54	B572	TIGGTTCCACAGCAACTACG	CAGGGAATGTATGTCAATGAGG	122-148	1 mM/55	NOD=BALB=C3H=B6=A=OB>CAST>NON>>LP=AKR=DBA>>SPE
D3Mid55	B536	CTGGGACCACCAGTAGTACCA	TCAGGACTGCAACTGAGGC	116-144	1mM/55	(3)H=A>>LP=NOD=B&>AKR=BALB=DBA=CAST>>NON>>SPG; OB:-
D3Mid6	B713	TCTAGCTATGTGATGAGTGTGTCCG	CAGGATTTTCCAAAAACATCCA	138-148	1mM/55	A>LP=NOD=NON=AKR=DBA=C3H=B6=OB>BALB>>CAST; SPE-
D3Mii67	B493	TCCAGTTACTTGGTGAACTCCA	ATATGTGTACATGTTCATGGT0T0	148-176	1mM/55	CAST>>SPE>>LP>B6>NON=AKR=BALB=C3H=A=OB>>NOD; DBA:-
D3MiD8	B527	ACATCAGAAGAGACATTCATTTCA	GCTCTTCAGTCACAGCTCTGC	140-152	1mM/55	CAST>>NOD=NON=BALB=DBA=C3H=B6=A=OB>>LP=AKR; SPE:-
D3Mic59	B543	GTTGATGCCCAAGGAATGAT	CTACTGCATCCTGGCACAGA	204-212	1mM/55	0B>CAST>LP+AKR=B6=NON=BALB=DBA=C3H=A=SP2>NOD

Recommended magnesium concentrations and annealing temperatures are indicated for most loci. \*D3Nds23: Hsp86-ps2, unpublished sequence was kindly provided by S. Moore, Food and Drug Administration, Division of Metabolism and Endocrine Drug Products, Rockville, Md.; the STS and polymorphism are from N. Rodrigues. \*\*D3Nds24: CD10, clone obtained from M. Shipp, Dana-Farber Cancer Institute, Boston, Mass.; the STS and polymorphism are from N. Rodrigues. \*\*D3Nds25: Gba, (ref. 119). \*\*\*D3Nds26: Gpi-irs, unpublished STS from J. Jones, MRC Radiobiology Unit, UK.

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Table 4. Microsatellite	e map of Chr 3	
Loci	RF	Distance
D3Mitl-D3Nds15	7/92	7.65 cM
D3Nds15-D3Nds27	10/92	11 cM
D3Nds27-D3Mit6	7/92	7.65 cM
D3Mit6-D3Mit5	2/92	2.1 cM
D3Mit5-D3Mit7	3/92	3.2 cM
D3Mit7-D3Nds1	0/92	0
D3Nds1-D3Nds24	3/92	3.2 cM
D3Nds24-D3Mit22	5/92	5.4 cM
D3Mit22-D3Mit51	3/92	3.2 cM
D3Mit51-D3Mit9	1/85	1.1 cM
D3Mit9-D3N4s25	0/85	0
D3Nds25-D3Nds22	0/92	0
D3Nds22-D3Nds8	4/92	4.3 cM
D3N4s8-D3Mit11	1/91	1 cM
D3Mit11-D3Mit42	1 <i>6/L</i>	7.7 сМ
D3Mit42-D3Nds9	12/92	13.3 cM
D3Nds9-D3Mit38	3/92	3.2 cM
D3Mit38-D3Mit31	06/L	7.8 cM
D3Mit31-D3Mit32	4/90	4.4 cM
D3Mit32-D3Mit19	3/92	3.2 cM
Data from the laborat terspecific Backcross Human Genome Map Council, Distances we recombinant fraction	ory of J.A. To [(C57BL/6 × ping Project, v sre calculated (recombinants	dd from the European Collaborative In- SPR) $F_1 \times SPR_1$ produced by the UK's vith the support of the Medical Research with the Kosambi mapping function. RF, fotal analyzed).

Table 5. Relationships between mouse Chr 3 genes and homologous human genes.

Human position	8q13-q22	8q13-q22	8q13-q22	3q24-q28	3q27	2 3q26	4q26-q27	4q25-27	3q21-27	3q25-26	2 4q25-34	4q28	1q21	1921	1q21-q25	1q12-q22	lq	1q22-23	1q24-q31	1q12-21	3 1p11-13	1p13	d 1 1 p 1 3	1 1p13	1p13	1p13	A 1p12-p13	1p13	1p13-21	1p13		1p21	1p21	1p22-p21	1p21-22	e 4q28-31	4q25	4q21-q23	4q21-q23	1 1p21-qter	4q21-q25	1nter.a17
Human	CA1	CA2	CA3	EvII	FIM3	GLUT	11.2	FGF2	MME	SI	GLUR	FGG	PKLR	GBA	CACY	CAPL	FCGR	ē	FPSL	H3F2	HSDB	CD2	ATP1/	AMPD	NGFB	NRAS	RAP1/	TSHB	<b>CSF1</b>	GNAI		AMYI	AMY2	£	PMP1	FABP2	EGF	ADH1	ADH3	ACTA	ADH5	ARNT
Name	carbonic anhydrase-1	carbonic anhydrase-2	carbonic anhydrase-3	ecotropic viral integration site-1	Friend MuLV integration site-3	glucose transporter 2	interleukin 2	fibroblast growth factor basic	membrane metallo-endo peptidase	sucrase-isomaltase, structural	glutamate receptor 2	gamma fibrinogen	pyruvate kinase liver, red blood cells	beta glucocerebrosidase	calcyclin	calcium binding protein, placental	high affinity FC gamma receptor	cluster designation 1	farnesyl pyrophosphate synthetase-like 1	histone 3, family 2	3-beta-hydroxy steroid dehydrogenase	cluster designation 2	Na, K ATPase alpha-1	AMP deaminase-1 (muscle form)	nerve growth factor beta	Nras oncogene	member of RAS oncogene family	thyrotropin stimulating hormone beta subunit	colony stimulating factor, macrophage	guanine nucleotide binding protein,	alpha inhibiting activity-3	amylase, salivary	amylase, pancreatic	coagulation factor 3	peroxisomal membrane protein (70k)	fatty acid binding protein intestinal	epidermal growth factor	alcohol dehydrogenase-1	alcohol dehydrogenase-3	skeletal alpha actin	alcohol dehydrogenase-5	anyl hydocarbon receptor nuclear translator
Locus	Car-I	Car-2	Car-3	Evi-1	Fim-3	Glut-2	11-2	F gf2	Mme	Suc-1s	Glur-2	FRR	Pkir	Gba	Cacy	Capl	Fcgrl	CdI	Fpsl-rs1	H3f2	Hsd3b	CaD	Atplal	Ampd-1	Ngh	Nras	Rapla	Tshb	Csfm	Gnai-3		Amy-I	Amy-2	Cf-3	Pmp-1	Fabpi	Egf	Adh-I	Adh-3	Acts	Adh-5	Arnt
Map	6.3	6.3	7.5	10.2	10.2	10.2	15.0	15.7	30.1	33.3	34.9	42.3	42.6	42.6	42.9	42.9	42.9	43.9	43.9	44.9	45.0	46.4	47.3	47.4	47.4	47.4	47.4	47.4	48.4	48.4		49.6	49.6	49.6	54.6	54.7	62.1	68.1	68.1	×	×	×

Locus	AXL Lines	Ref.	•
	1111112222233		•
	567892346791458978		
(ar-2		121	
APZ Menny - 20		51	
Fvi-1		112	
Xmmv-47	LLLLLAAALLALAALLLL	164	
Xmmv-65	ALALLAAALLLLALLLAA	164	
Pmv-28	ALALLAAALLLLALLLAA	50	
Cal1l	ALALLAAA-LLLALLLAA	131	
D3Tu51	LLALLAAALLLLA-LLAA	153	
Amy	ALALLAAALLLLAAALLA	121	
D31033	AAL-AAAALLLLA-ALLA	123	
PmV-20		96	
Locus	BXD Lines		Ref.
	111111122222222	2333	
	1256891234568901234578	9012	
Car-Z	DDDBDBDDDDDBBDDBBBBBBBBB	DDBB	121
AD2	DDDBDBDDDDBBDDBBBBBBBBBBB		61 167
DSByuz		00000	167
D3RVu3	DDBRDRBDDDBBDDBBDBBBBBBBBBBBBBBBBBBBBBB	DDDB	167
Evi-1	DDRBDBBDBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB	ODDO	112
11-2	DDBBDBDDDDDBDDBDBBBBBBDD	BDDB	37
D3Mit5	- DBBDDDDBDBBBDDBDBBBBDD	B	37
D08yu17	BBDBDDDDBBDBBBBDDB	DDBB	167
Cnp-2	BBDBBDDDB8DBBBBDDBBDDD	BDBB	10
D3J1	880888088808888-088080	BDBB	114
D3Byu£	8506600056065660056060	606B	167
D3Mit22	- 6066600660686660066060	8	37
Xmmv-65	BBDBBBDBBBBDBBBBBDDBBDBB	BOBB	164
USM119		8	37
rgg D3Duré		0000	167
D50900 Pmv-38	RERERENERENERERENEREN	RUBB	10/
D3Mi+10	-BRBDBDBDBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB	8	37
Capl	BBBBBBDB-BDBBBD-BDBD	BDBB	39
Calll	88888808880888	BDBB	131
D3Tu51	B88888-B080688-0088-80	6D	153
D3Byu4	BBDBBBDBBBDBBDBBDBBDBBDBBDBBDBBD	BDBB	167
Amy	BOBBOBOOBOBBBBBOBD	6D66	121
Amy CB	BDBBDBDDDBDBBBBDDBBDBBDB	BD68	13
Fabpi	BDBBDBDDDBDBB-DDDBB-BD	BBBD	143
03.13	BDBBDBDDDBDBBBBDBBDBD	BBBD	114
Adn-1ps	RORROROOROROROOROOROORO	BBBD	20
Cam Day 20	505505000005505000055050	8888	145
Cat-re7	50500000000000000000000000000000000000		125
Eaf	ROBRORDODODODODODODODODODODODODODODODODO	RRAN	112
D3Wit15	-D660600006860000806060	8	37
Adh-3	B0880800-8880000808080	6680	112
Adh-3 RH	80680600-58800-0606060	BBBD	72
Adh-1	SDEEDEDDOBBEDDDDEDEDED	BBBD	20
D3Nds3	BDBBDBDDDDBBBDDDDBDBDBD	BBBD	30
D3Nds2	-088060008880000808080	6	37
Bmn	BDBBDBDD-BBBDD-DB-BDBD	B-BD	97
USJkni	BDBBDBDDDBBBDDDDBDBDBDBD	6668	99
HMV-26	BUBBUDDDDBBBDDDDBBBDBD	BBBD	50
740-4		6660	40
D3Mit17	- B80000808880000888080	6	37
		-	

Locus	AXB Lines	Ref.
	11111111222222	
	123456789012345789012345	
Car-2	BBAAABABABABABAAAABBB-BBBA	73,112
Evi-1	BA-BABABABAA-A-AAAABABAA	112
D3Mit6	BA-ABB-A-BA-BAA-AAABB-	73
D3Mit7	BB-ABA-B-BA-AAA-AAA-BB-	73
Fgg	BBAABABBBBAB-AAABBBB-BBA	13
Inds3	BB-ABA-B-BA-AAA-BBBBB-	73
KNUID-1	ARAABABBBBAB-AABBBBBB-BBA	13
KNULD-3	AAAABABBBBBABAAABBBBBB-BB~	13
Amer. 1 2		73
HUNY-1,C		113
Adh-3		12
Man-J		15
DRMi+18	AA-RAA-A-RA-AAR-A-A-AAR-	72
D3Mi+19	44-444-4-64-446-4-4-46-	73
Locus	BXA Lines	Ref.
	111111111222222	
	1234567890123456789012345	
Car-Z	AABB-ABAA-BAABBBAAAABA	73,112
Evi-1	AA-B-B-AABBAABBBAABB	112
D3Mit6	AB-BBBB-BAAB-BBBA	73
DJMit/	AB-BBBB-BAAB-BBBA	73
-99	A-ABBB-BBABA-BAB	13
isp3	AB-AABB-BAAB-BBBA	73
	A-AABB-BB-BA-BAAA-B	13
NDULD-3	ADAADDADD-DADD-DD	13
/3m1C19	AA-A	73
any-1,c		112
Adh-7		12
Warmy-9	AB-A-AA-RAARBA-AAAAA-ABAB	13 51 100a
D3Mit18	44-4	73
3Mit19	AB-BAAB-ABBB-AAAA	73
ocus	AXD Lines	 Daf
	111111111222222222	
hamv-20		E 1
1-2		51
Cnp-2		100
3Nds1		30
mv-28	DDAAADDAADAADADAAAADADDAA	50
mv-38	DDAAADDAADAADAADAAAADDDDAA	50
shb	DDAAADAAADADDA-AAAADDDDAA	2
₩v-39	DDDDDDAADDADDADADDADDDDAD	50
at-rs2	DDDAADAADDADDADADDADD-DAD	125
)3Nds2	DDDDADAADDADDA-ADDAADDDAD	30
gf	DDDADDADADDDADDADDDAADDDAD	112

2345678901249 Car-2 HBH-SH6666888 121 Pgkps3 HBH-BHBBBBHBB 1 112 HEHBEHBERHHBE Evi-1 Rnu1b3 888-BHBBHHHBB Calll **BBB-BHBBHHHBB** 131 D3Tu51 **ВВВ-ВНВВНННВ** 153 121 126 Amy Odc-rs3 888-BHBHHHBBB НВН-ВНВНВВВ Oat-rs2 BBB-BHBHHHBBB 125 Egf вванвнынные 112 Adh-3 BBB-BHBBHHBBB 124 BBB-BHBBHHBBB 124 Gbp-1 IBF2 132 51 888-BHSBHHHBB 688-86688H6H6 Mpmv-9 Locus CXB Lines Ref. 1234567 Car-2 Car-2 RE Xmmv-65 CCBBCCB 47 CCBBBCB 121 BCBBCBC 164 H-37 BCCBCBC 4 Amy CCCBCCB 121 H-23 Adh-3 CCCCCCB 4 43 43 Ahr-1 CCCBCCB Gbp-1 CCCBCCB 124 H-28 CCBBCCB 4 CCBBCCB BCBBCCB If-1 36 51 Monv-9 Locus NXO Lines Ref. 11 125702 NONODO Xmmv-65 164 124 Gbp-1 NNOONO Locus SXL Lines Ref. 11111 4724567

Locus

BXH Lines

11111

Fig. 2. Strain distribution patterns for recombinant inbred strains. Data from Benjamin Taylor and Beverly Paigen (The Jackson Laboratory).

Calll

Amy

SLLLSSL LLLLSSL 131 121

ships in both gene order and approximate physical length (79).

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Ref.

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