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LINKAGE MAPS OF HUMAN CHROMOSOMES

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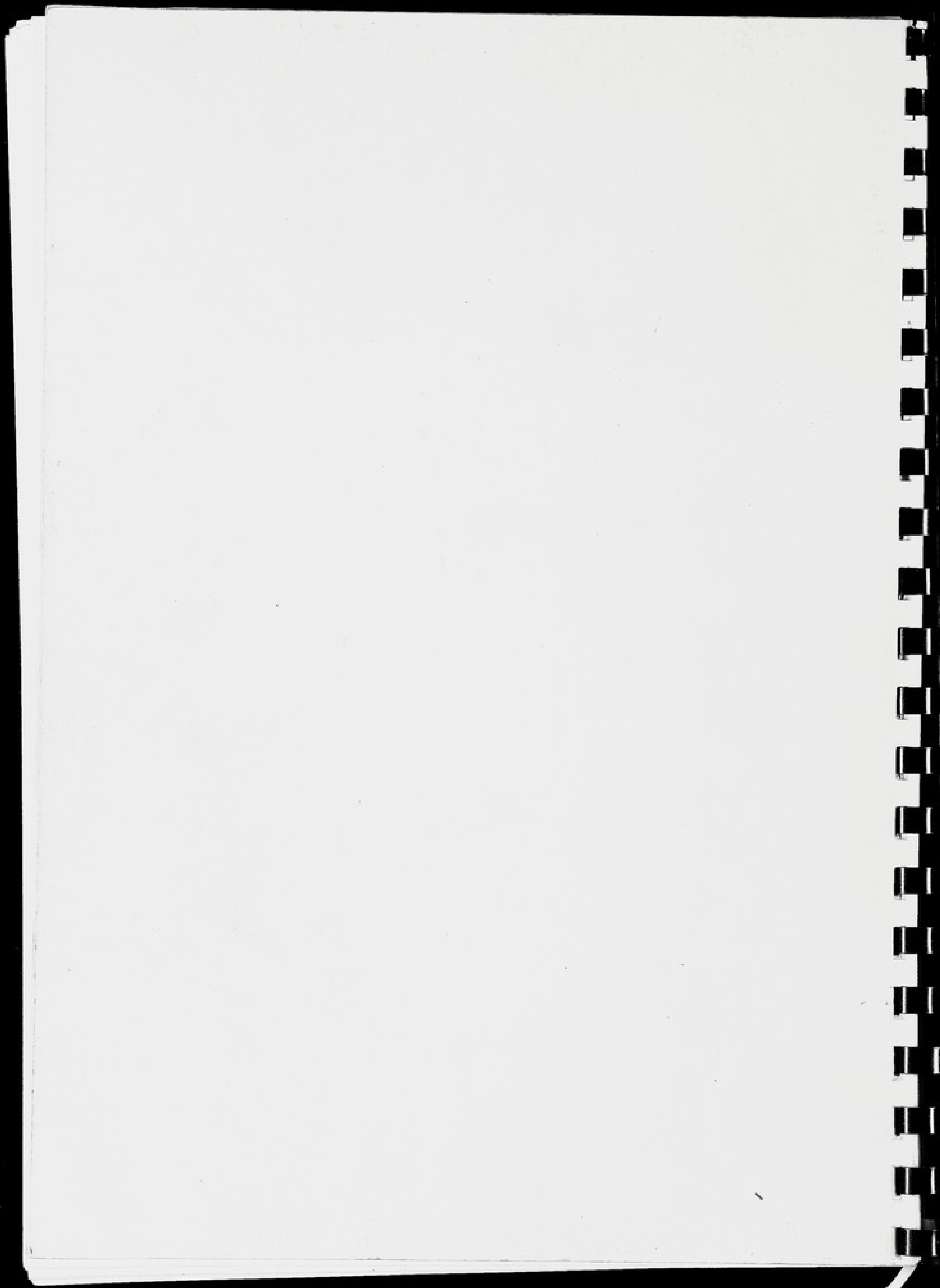

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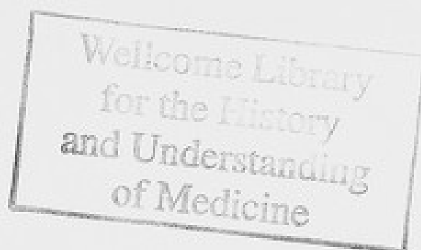

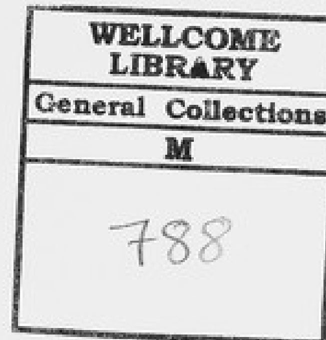

I. Introduction

Over the past seven years, the major focus of the Salt Lake City linkage group has been on the development of tools that would permit, through family studies, the localization of genes that cause human genetic disease. It is well understood now that gene localization can be the first step in the identification and cloning of a gene. Our goal was to develop economical sets of mapped DNA marker loci capable of detecting a disease gene wherever it might lie. Progress toward that goal made by the Salt Lake City group is documented in this collection of abstracts and chromosome maps.

II. Overall Strategy

The overall strategy has been to identify DNA sequence polymorphisms, determine the segregation pattern of the polymorphisms in three generation families with large sibships and build linkage maps based on analysis of the segregation patterns. The polymorphic loci, identified with restriction enzymes and DNA probes, become the primary tools for searching out linkages with genetic disease loci. In addition, however, maps of the marker loci have already proven valuable and will become more so both in defining the set of marker loci that span a large region and in identifying clusters of tightly linked marker loci that map within a region of interest.

A. Probe Development

The probe-enzyme combinations that reveal polymorphism were, in the beginning, detected by random searches, picking arbitrary clones and screening panels of unrelated individuals for variation. Although many site polymorphisms have been detected in this manner, these two-allele systems leave many individuals uninformative

for linkage. A large percentage of uninformative matings in either a disease linkage study or in high resolution studies with closely linked markers in the CEPH families can be devastating, yielding quite inconclusive results.

Fortunately, a paradigm approach developed by Alec Jeffreys using sequences from known, highly polymorphic loci to screen genomic libraries at low stringency has, permitted the ascertainment by our group of a large collection of highly informative, multi-allelic markers based on Variable Number Tandem Repeat (VNTR) loci. We expect these marker loci to become the primary anchor points of the genetic linkage maps, especially useful in the initial localization phase of linkage studies with disease families and in the development of high resolution chromosome maps.

In addition, the screening produces a number of single and multiple restriction site polymorphisms. These become particularly important in genetically defining regions where the VNTR loci are only widely spaced and in fine structure mapping.

B. Reference Families

The choice of family resources for the development of the linkage maps has been critical. Complete, three generation families with large sibships have proven a highly efficient source of segregation data. We have ascertained, sampled and established lymphoblastoid cell lines from all available members of 46 large Utah families. Interestingly, the efficiency has been found not only in the collection of data, but in the analysis as well. The CEPH initiative has made DNAs from a defined set of 40 reference pedigrees, including 27 of the Utah families, widely available to investigators. Use of this archival set of reference families makes it possible for an investigator to take advantage of the

segregation patterns already characterized for a large number of marker loci by other investigators in these families. An investigator need, therefore, only develop the segregation pattern of his marker locus in the CEPH families in order to map his marker locus with respect to many other marker loci.

Ultimately, for high resolution studies with tightly linked markers, even more families than the CEPH collection are required and we routinely type the entire collection of 59 families available to us. As shown in the accompanying abstract, the complete set of 59 reference families does represent an adequate panel for fine structure mapping.

C. Chromosome Assignment of Linkage Groups through Assigned Genes

Family studies develop linkage groups, but do not reveal their chromosomal assignment. However, if even only one member of the linkage group has been assigned to a chromosome, it specifies the chromosomal location of the entire linkage group. We have, therefore, taken care to include in our linkage studies a number of gene loci that have been previously assigned to a chromosome or that were assigned as part of a collaborative effort.

D. Marker Order Determined by Rational Strategy

The linkage groups that form the chromosome maps are often now continuous with over 20 linked marker loci. The number of calculations required to determine the most favored gene order by brute force would be 20!/2. Even with new, high speed algorithms for the calculation of likelihoods, it has proven useful to develop methods that permit the exclusion of broad classes of marker orders that are clearly not favored. Furthermore, keeping track

of the results of the thousands of likelihoods that are calculated in such analyses has proven exceptionally burdensome. For this reason an intelligent database system consisting of the results of the likelihood calculations has been developed and combined with an automated system of analysis.

III. Progress Report

This collection of abstracts and chromosome linkage maps constitutes a preliminary progress report from the Utah linkage group. As such, the data reported herein should be regarded as provisional and likely to be revised in detail, although not in substance. Because significant differences between male and female recombination frequencies have been observed, the analyses include a preliminary look at the question of sex specific map distances. However, the reader should take careful note that the analyses of sex specific map distance are indeed very preliminary and have been carried out only under the assumption of a constant ratio of sex specific map distance for each chromosome. We fully expect that further examination will often reveal regions of intrachromasomal heterogeneity in this ratio, as has been found for both chromosomes 11 and 12.

The great majority of our marker loci lie within chromosomally assigned linkage groups. However, a significant number of markers are as yet unassigned and are likely to fall within the sparsely populated regions of a few chromosomes. In particular, the genotyping of a number of very informative VNTR markers is still in progress and is expected to add a number of strong anchor points to the maps. Even with that, however, most chromosomes are now well described; the probability of linkage of an unknown marker with one of the linkage groups is now well over 90%.

IV. Use of the Maps and Markers

The primary use of the markers and maps will be in the initial localization of genes that cause disease. We expect that it will very soon be possible to derive, for each chromosome, a set of evenly spaced and highly informative markers that will reveal whether or not a disease gene is located on that chromosome. Furthermore, once a disease gene is initially localized, the availability of a secondary collection of markers mapped to the region for the purpose of more precise localization as a prerequisite for physical approaches to the gene will become critically important. As there are literally thousands of human genes that will be handled in this fashion it is well worthwhile to contemplate the development of a higher resolution set of chromosomal maps, with markers spaced at 1 cM intervals.

Finally, the CEPH families and CEPH database should now become a primary tool for localizing new genes as they are cloned. The resolution obtainable at present can be expected to be, on the average, perhaps 10 cM (10 megabases), making linkage an efficient tool for this primary identification. Furthermore, the localization of genes of known identity within the linkage maps may prove an invaluable tool in the future as disease genes are mapped within the same linkage groups. Positional overlap will identify already cloned and characterized genes as important candidates for the disease gene. Of perhaps equal importance, many physiologically suggested candidate genes will be rigorously eliminated by the demontration that they are not linked to the region of the disease locus.

CURRENT STATUS IN MAPPING THE HUMAN GENOME: 470 RFLPs in 59 FAMILIES AND 600 NEW RFLPs

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More than 600 new RFLPs, including 207 VNTR loci, have been isolated from a human cosmid library (Nakamura et al., Science 235:1616-1622, 1987 and accompanying abstract). As these new clones are isolated, the genotypes of the more informative ones are determined in a set of 59 large, three-generation families (White et al., Nature 313:101-105, 1985) that include 822 individuals; 40 of these families constitute the CEPH panel. This sample size is a minimum requirement for determining gene order between closely linked loci with reasonable statistical power.

In addition, 165 RFLPs cloned previously in our laboratory and in others, as well as 24 protein polymorphisms (almost all assigned to specific chromosomes), have been characterized in these families. They serve as reference points for mapping and chromosomal assignment of the new markers by linkage analysis. At present, genotypes at 470 marker loci have been determined in our reference panel of families. Linkage analysis routinely performed using the LINKAGE programs on this expanding data set has allowed us to demonstrate linkage for more than 90% of the markers. Efficient multilocus linkage analysis, coupled with an automated computer system for the construction of genetic maps (see accompanying abstract), has yielded primary genetic maps of most human chromosomes (see accompanying abstracts on chromosomes 1, 2, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, and 19) as well as linkage groups on other chromosomes.

The availability of these markers, genetic maps, genotypic data, and analytical tools is proving of great value for the efficient mapping of new loci, for known genes and for Mendelian disorders.

VARIABLE NUMBER OF TANDEM REPEAT (VNTR) MARKERS FOR HUMAN GENE MAPPING

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A large collection of good genetic markers is needed to map the genes that cause human genetic diseases. Although hundreds of polymorphic DNA markers for human chromosomes have been described, the majority have only two alleles and are thus uninformative for analysis of genetic linkage in many families. However, a small proportion of these markers detect loci that respond to restriction enzyme cleavage by producing a fragment that can have many different lengths, due to variation in the number of tandem repeats of a short DNA sequence. Because most individuals will be heterozygous at such loci, these markers will provide linkage information in almost all families. Ten oligomeric sequences derived from the tandem repeat regions of the myoglobin gene, the zeta-globin pseudogene and the insulin gene, and from the X-gene region of hepatitis B virus, $(GT)_{10}$, were used to screen a human cosmid library, yielding a series of single-copy probes. (Y. Nakamura et al., Science 235:1616-1621, 1987). This abstract updates the previous publication. A total of 500 cosmid clones hybridized with oligonucleotides have been tested for polymorphism. In 128 such DNA markers (26%), polymorphism in allele sizes reflected variation in the number of tandem repeats (only three of 89, 3%, of unselected cosmid clones showed the same type of polymorphism). These VNTR markers revealed 33-97% heterozygosity, with an average of 70%. Fifty-seven of them have been examined for linkage to localized markers; 39 clones showed linkage with marker loci on chromosomes 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, or 19. Thus, VNTR marker loci are well dispersed in the genome and they will become a very powerful tool for mapping human chromosomes. Detailed mapping information is provided in accompanying abstracts.

VNTR DNA Markers

	Enzyme*	Allele size range (kb)	Allele number	Hetero-zygosity	Chromosome
YNZ2	RsaI	1.0 - 3.0	5	65%*	1
YNZ21	MspI	1.0 - 4.0	>10	89%*	
YNZ22	BamHI	1.1 - 2.0	>10	86%*	17
YNZ23	PstI	2.0 / 2.5	2	41%	1
YNZ32	TaqI	2.3 - 2.8	5	57%*	4
YNZ86	MspI	0.6 - 0.8	3	52%*	3
YNZ132	TaqI	1.8 - 2.3	6	69%*	8
YNZ186	BamHI	1.2 - 2.0	6	83%	
YNZ195	TaqI	1.0 - 2.5	6	83%	
JCZ3	TaqI	1.5 - 3.0	7	82%*	19
JCZ19	BglII	1.8 - 3.1	6	83%	
JCZ30	EcoRI	3.0 - 4.8	4	75%*	6
JCZ37	BglII	0.8 - 1.5	5	83%	
JCZ42	TaqI	2.8 - 3.5	5	75%	
JCZ45	PstI	1.4 / 1.9	2	50%	
JCZ67	RsaI	3.5 - 5.0	>10	83%*	
JCZ69	PvuII	0.9 - 1.3	4	67%	
JCZ70	MspI	1.5 / 1.7	2	50%	
YNM3	RsaI	2.5 - 2.8	4	34%*	8
YNM4	TaqI	2.3/3.0/5.0	3	60%*	
MLJ1	HinfI	2.0 - 3.0	5	64%*	
MLJ14	RsaI	4.0 - 15.0	>20	95%*	14
MLJ101	MspI	2.2 - 3.5	6	89%	
MLJ102	BglII	6.0 - 8.0	6	78%	
MLJ103	TaqI	0.6 - 0.8	4	67%	
CMM1	MspI	0.9 / 1.0	2	45%	
CMM3	BamHI	1.9 - 3.3	7	83%	
CMM5	RsaI	2.5 - 3.4	4	67%	
CMM6	TaqI	2.5 - 4.3	>10	90%*	
CMM8	MspI	2.3 / 2.8	3	59%*	1
CMM12	BamHI	3.5 - 6.0	6	78%*	
CMM19	RsaI	1.2 - 2.0	4	67%	
CMM22	MspI	2.0 / 2.8	2	44%	
CMM62	PstI	4.3 - 8.0	4	61%	
CMM64	PvuII	3.7 / 4.3	2	50%	
CMM65	RsaI	2.3 / 3.0	2	39%*	16
CMM66	PstI	5.0 -10.0	>10	83%	
CMM71	BglII	2.0 - 4.5	6	78%	
CMM73	PstI	1.0 - 2.0	5	83%	
CMM77	PstI	2.1/4.2/6.0	3	50%	
CMM86	RsaI	3.0 - 5.0	>10	93%*	
CMM101	MspI	1.0 - 5.0	>10	90%*	1
CMM103	PvuII	4.3 - 5.0	5	75%	
YNI10	TaqI	10.0 - 15.0	>10	85%	1
CMI37	RsaI	2.3 - 3.0	6	68%*	7
CMI40	TaqI	2.5 - 4.5	4	46%	

CMI214	BglII	4.0 - 5.0	3	61%	
CMI296	RsaI	2.3 - 6.0	5	75%	
CMI297	MspI	4.0 - 8.0	5	83%	
CMI327	PvuII	2.5 - 4.0	>10	83%	
THI54	PvuII	5.0 / 6.0	2	46%*	1
THI62	RsaI	1.0 - 2.0	5	80%*	13
THIZ53	BamHI	2.1 / 2.3	2	27%*	12
THH5	PvuII	1.1 - 2.0	4	55%*	8
THH7	RsaI	3.0 - 4.3	4	66%	
THH18	MspI	4.5 / 4.8	2	50%*	
THH33	RsaI	3.5 - 5.0	>10	78%	
THH39	PstI	2.1 - 3.0	4	61%*	14
THH50	TaqI	4.0 / 4.4	2	50%	
THH51	MspI	5.0 - 7.0	3	67%	
THH59	PvuII	0.8 - 1.8	6	75%*	17
HHH104	RsaI	0.8 - 1.8	6	67%	
HHH116	RsaI	2.5 - 2.8	3	67%	
HHH123	MspI	0.8 - 1.2	4	56%	
HHH129	TaqI	3.2 - 5.0	3	64%*	
HHH141	BamHI	4.5 - 6.0	4	67%	
HHH164	HindIII	14.0/16.0	2	30%	
HHH170	HindIII	5.0 / 6.0	2	50%	
HHH212	TaqI	3.4 / 3.8	2	41%*	1
YNH24	MspI	1.0 - 7.0	31	97%*	2
YNH37	TaqI	2.0 - 4.0	5	78%*	17
EKZ101	RsaI	2.0 / 2.2	2	71%*	
EKZ103	MspI	2.0 - 2.4	3	50%	
EKZ107	TaqI	2.5 - 4.4	4	67%	
EKZ109	TaqI	2.0 - 2.5	2	50%	
EKZ127	MspI	3.0 - 4.5	4	61%	
EKZ130	RsaI	1.0 - 2.0	5	78%	
EFD4	PvuII	2.1 / 2.4	2	44%*	19
EFD6	RsaI	2.0/2.4/3.5	3	67%	
EFD7	PvuII	1.0 - 1.8	3	56%	
EFD11	MspI	1.0 - 2.0	3	48%*	
EFD13	TaqI	2.0 - 3.0	3	67%	
EFD19	MspI	3.0 - 4.5	6	83%	
EFD20	MspI	3.2 - 3.7	3	67%	
EFD33	MspI	3.0 - 9.0	4	68%*	12
EFD52	PstI	4.0 -10.0	>10	90%*	17
EFD61	MspI	1.0 - 2.3	6	78%	
EFD63	RsaI	2.0 - 4.0	4	72%	
EFD64	MspI	1.0 - 5.0	>10	85%*	
EFD70	PvuII	1.8 - 2.0	4	55%*	
EFD72	PvuII	0.6 - 0.8	3	61%	
EFD75	RsaI	1.5 - 2.0	6	65%*	
EFD77	MspI	2.0 - 2.7	4	56%	
EFD91	PvuII	2.5 - 2.9	3	61%	
EFD95	MspI	4.0 - 7.0	4	78%	
EFD97	EcoRI	6.0 / 8.0	2	45%	
EFD126	TaqI	1.5 - 2.0	6	71%*	9
EFD127	MspI	2.0 - 2.5	3	61%	
EFD131	TaqI	1.8 - 2.3	3	61%	
EFD134	MspI	1.5 - 2.5	6	75%*	

EFD137	MspI	2.5 - 3.0	4	75%	
EFD139	PstI	5.0 - 8.0	>10	85%*	
MHZ10	MspI	1.4 - 2.0	6	83%*	9
MHZ13	PstI	1.5 - 2.3	5	78%*	9
MHZ15	MspI	3.0 - 3.6	3	67%	
MHZ16	MspI	1.2 / 1.3	2	38%	
MHZ19	MspI	0.8 - 1.2	4	67%	
MHZ30	TaqI	2.7 / 3.9	2	33%	
MHZ32	MspI	3.2 - 4.3	4	67%	
MHZ44	TaqI	2.4 - 3.3	4	78%	
MHZ45	MspI	2.0 - 3.0	5	75%	
MHZ47	MspI	1.5 - 3.2	>10	83%*	
MHZ48	PstI	3.0 - 3.3	3	61%	
MCK2	RsaI	0.9 - 1.5	6	50%*	10
MCT6	BamHI	8.5 -12.0	3	53%*	19
MCT7	PstI	4.0 - 8.0	4	70%	
MCT15	MspI	1.0 - 1.5	4	49%*	
MCT32	TaqI	2.8 - 6.0	4	75%*	3
MCT46	TaqI	1.7 / 2.2	2	45%	
MCT58	PvuII	1.4 - 1.6	6	75%*	
MCT96	MspI	0.9 - 1.5	4	48%*	
MCT106	PvuII	2.3 - 3.5	3	67%	
MCT118	PvuII	1.5 - 1.8	3	67%	
MCT128	PstI	1.0 - 1.6	4	65%*	11
MCT136	PstI	2.0 / 2.2	2	50%*	9
TBAB5.7	PvuII	4.3 - 5.0	5	65%*	2
ATBI20	MspI	1.0 - 1.5	5	75%	
TBZ27	PvuII	5.0 -10.0	8	80%	
EFZ10	PstI	3.4 - 6.0	6	75%*	18
EKMDA2	RsaI	3.0 - 5.3	8	83%*	16
RMU3	PvuII	0.7 - 1.3	>10	85%*	17

* Only the enzymes that gave the best resolution are shown. Probes YNZ and JCZ were isolated by the zetaglobin oligonucleotide; YNM and MLJ, by myoglobin-1; CMM, by myoglobin-2 or 3; THH, by HBV-1; YNH, by HBV-2; YNI and CMI, by insulin; EKZ, by HBV-3; EFD, by HBV-4 and -5; MHZ and TB, by YNZ22; MC, by $(GT)_{10}$.

*: the result in 120 unrelated individuals

: the result in 18 unrelated individuals

DNA Sequences and Hybridization Conditions for Oligonucleotide Probes

		Hybridization Temperature	Washing Temperature
Zetaglobin (18mer)	TGGGGCACAGG$^{T}_{C}$TGTGAG	42°C	48°C
Insulin (14mer)	ACAGGGGTGTGGGG	30°C	37°C
Myoglobin-1 (16mer)	GGAGGTGGGCAGGAAG	37°C	44°C
Myoglobin-2 (14mer)	GGAGGCTGGAGGAG	37°C	42°C
HBV-1 (16mer)	GGAGTTGGGGGAGGAG	37°C	44°C
HBV-2 (20mer)	GGACTGGGAGGAGTTGGGGG	50°C	60°C
HBV-3 (15mer)	GGTGAAGCA$^{G}_{C}$AGGTG	37°C	42°C
HBV-4 (15mer)	GAGAGGGGTGTAGAG	37°C	42°C
HBV-5 (15mer)	GGTGTAGAGAGGGGT	37°C	42°C
YNZ22 (15mer)	CTCTGGGTGTCGTGC	37°C	42°C
$(GT)_{10}$ (20mer)	GTGTGTGTGTGTGTGTGTGT	45°C	55°C

Hybridization was carried out in a solution of 5 X SSC (1 X SSC = 0.15M NaCl and 0.015M Na Citrate); 50mM Tris.HCl (pH 7.4); 1 X Denhardt's solution (0.02% Bovine serum albumin, 0.02% Polyvinyl-Pyrrolidone, 0.02% Ficoll); 10 mcg/mL of yeast tRNA; and 1 X 10^5 cpm/ml of ^{32}P 5'-end labeled probe (2 X 10^6 cpm/pmol) for 16 hours. Washing was done three times in 5 X SSC-0.1% SDS for 5 min.

Summary of screening for VNTR polymorphism

	Positive clones per genome	Clones tested for RFLPs	VNTR marker	%*	Site polymorphism
Zetaglobin	180	86	18	21	33 (7)
Insulin	220	48	10	21	19 (1)
Myoglobin-1	150	35	7	20	19 (8)
Myoglobin-2 and 3	38	50	18	36	19 (8)
HBV-1	200	65	16	25	38 (13)
HBV-2	40	9	2	22	6 (3)
HBV DR 1	50	20	6	30	6 (2)
HBV DR 2 and 3	150	86	25	29	40 (25)
YNZ22-1 and 2	68	50	14	28	25 (11)
$(GT)_{10}$	100	48	12	25	19 (6)
Totals		497	128	26	224 (84)
Random		89	3	3	45 (18)

* The proportion of VNTR DNA markers among the tested cosmids.

( ) The number of cosmids which showed site polymorphisms with two or more restriction enzymes.

THE NUMBER OF MEIOSES NEEDED TO RESOLVE GENE ORDER IN A 1% LINKAGE MAP

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Maps of highly polymorphic loci, based on VNTR's (Nakamura et al., Science 235: 1616, 1987), in which adjacent loci span approximately 1cM (3000 to 4000 loci) are technically feasible; they could provide a powerful tool for the localization and the isolation of disease genes. Because of the close linkage between adjacent markers, large samples sizes will be needed to determine the map order.

Ordering of the linkage map will require the observation of at least one recombinant between each pair of adjacent loci A and B. Using VNTR's, informative flanking loci, F1 and F2, would be available to distinguish the true order F1-A-B-F2 from the alternative F1-B-A-F2: one recombination under the true order (F1-A-x-B-F2) requires three recombinations under the alternative order (F1-x-B-x-A-x-F2). The observation of two or more recombinants between A and B would be desirable to exclude typing error. Based on Poisson recombination events and 1% recombination between adjacent loci, we have calculated the probability distribution of the number of unresolved orders in a 4000 locus map in terms of meioses informative for adjacent markers:

	At least one recombinant		At least two recombinants	
Phase-Known Informative Meioses	Prob. to Resolve All Orders	95% Upper[1] Limit on Number NOT Resolved	Prob. to Resolve All Orders	95% Upper[2] Limit on Number NOT Resolved
1200	0.98	0	0.73	1
1000	0.83	1	0.00	5
800	0.26	3	0.00	18
600	0.00	15	0.00	82
400	0.00	87	0.00	397
200	0.00	577	0.00	1675

[1] The number of intervals in which no recombinants will be observed equals or exceeds this bound with 95% probability.

[2] The number of intervals in which 0 or 1 recombinant will be observed equals or exceeds this bound with 95% probability.

The assumption of 1% recombination between adjacent loci throughout the map is an approximation; calculations taking account of unequal recombination will be presented elsewhere. Average heterozygosity of 70% will require sample sizes at least twice those we report to obtain the requisite number of doubly informative matings.

COMPUTATION TIMES FOR LINKAGE ANALYSIS IN GENE MAPPING

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Initial computer implementations of multilocus analysis in the LINKAGE programs were designed primarily to investigate the scientific merits of this approach for the detection of linkage and the construction of linkage maps of human chromosomes. The proven usefulness of multilocus analysis has led to the search for more efficient likelihood calculations.

Optimization of the original LINKAGE algorithms, and the application of statistical techniques as described in Lathrop et al. (Genet Epidem 3: 39-52, 1986) makes extensive multilocus analysis feasible on a wide range of computers. As an example, we provide the following benchmarks of CPU times and the number of likelihood evaluations required to obtain estimates of recombination under a single gene order for various number of codominant marker loci typed in 30 reference families (416 individuals) from the CEPH family panel:

Number of Loci	Seconds of CPU Time for a Single Likelihood Evaluation			Number of Evaluations to Convergence
	VAX 8650[1]	Micro-VAXII[2]	IBM-AT[3,4]	
5	0.05	0.45	7.52	71
10	0.20	1.64	37.40	320
15	0.43	3.48	83.10	1145
20	0.56	4.60	110.51	1162
50	6.34	54.48	not done	7386

[1] VAX 8650 with 80 Mbytes of memory; DEC Pascal Compiler V3.5
[2] Micro-VaxII with 9 Mbytes of memory; DEC Pascal Compiler V3.5
[3] IBM-AT at 6 Mhz with 640 Kbytes of memory; TURBO Pascal without 8087 support.
[4] The 50 locus calculation was not possible because of memory limitations.

Maximum likelihood estimates are obtained by numerical optimization; a large number of likelihood evaluations is required to meet conservative convergence criteria. Calculation times for general pedigrees and disease loci are described in Lathrop and Lalouel (submitted).

AN AUTOMATED SYSTEM OF LINKAGE ANALYSIS (Gene Mapping System or GMS)

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Howard Hughes Medical Institute, University of Utah, Salt Lake City, USA.

We have developed an automated system of linkage analysis, GMS, to aid in the construction of human genetic maps.

The GMS program interfaces with LINKAGE, and uses a database of genotypes on 59 reference families, including 38 families from the CEPH panel. Genetic maps are constructed from markers assigned to each chromosome using a series of algorithms to select appropriate multilocus tests.

The strategy employed in GMS is to use two-point lod scores to construct a preliminary map (trial map). Multilocus analysis of the trial map gene order results in the division of the loci into sub-linkage groups of closely linked markers; gene orders are determined within each group separately, and the order and orientations of the groups are established by multilocus analysis.

A variety of different algorithms have been implemented for the selection of the appropriate tests when the number of sub-linkage groups excludes the possibility of testing all orders and orientations. Validation runs are made using different gene orders within the sub-linkage groups, and different initial divisions of the loci. When the maximum likelihood gene order is not the same as the trial map, the former is used to establish new sub-linkage groups, and the analysis is repeated.

The GMS program has been used to establish primary maps of most chromosomes (see abstracts on chromosomes 1, 6, 7, 9, 11, 12, 13, 14, 15, 16, 17, 18, and 19). Recombination rates and likelihoods from all tests are stored in a results database. This database will permit rapid evaluation of other algorithms for obtaining trial maps and for restricting tests of alternatives when searching for the maximum likelihood gene order.

THE GENE FOR FAMILIAL POLYPOSIS COLI MAPS TO THE LONG ARM OF CHROMOSOME 5

Mark Leppert[1], Mark Dobbs[2], Peter Scambler[3], Peter O'Connell[1], Yusuke Nakamura[1], Dora Stauffer[1], Scott Woodward[1], Randall Burt[4], J.P. Hughes[5], Eldon Gardner[6], Mark Lathrop[1], John Wasmuth[2], Jean-Marc Lalouel[1], and Ray White[1].

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Multiple, or adenomatous, polyposis coli is characterized by the presence of hundreds of adenomatous polyps in the colon and by the inevitable development of adenocarcinoma of the colon at a relatively young age. Persons with inherited colonic adenomatous polyposis are frequently divided into two groups, familial polyposis coli (FPC) and Gardner's syndrome (GS). While both conditions are similar with respect to colonic polyposis and colorectal cancer, individuals with Gardner's syndrome are distinguished by a number of benign extraintestinal growths.

Using five polyposis pedigrees, we found evidence for linkage of the disease gene to three markers on the long arm of chromosome 5. A maximum lod score of 3.37 at a recombination fraction of zero was observed with the marker C11p11 (one-lod-unit confidence upper bound 0.023). Two other markers, J0205E-C and TP5E, yielded positive, yet non-significant lod scores. All four loci were analyzed with the LINKAGE programs in the 5 GS/FPC and 59 normal reference families to determine gene order and to test the significance of linkage. The gene order (FPC, C11p11) - TP5E - p213-205 (where the orientation of (FPC,C11p11) cannot be established), is supported by odds of nine to one over the second most likely order,(FPC,C11p11)-p213-205 - TP5E. Support for linkage between FPC and C11p11 was strengthened by multilocus analysis, with a lod score of 5.0. Moreover, multilocus analysis of both data sets jointly allowed us to establish the significance of linkage between C11p11 and TP5E, which was not achieved in each data set when considered singly, and between TP5E and p213-205.

ETIOLOGICAL HETEROGENEITY IN X-LINKED SPASTIC PARAPLEGIA

M. Leppert, *L. Keppen, P. O'Connell, Y. Nakamura, D. Stauffer, M. Lathrop, J.-M. Lalouel, and R. White

Howard Hughes Medical Institute and Department of Human Genetics, University of Utah Medical Center, Salt Lake City, UT

*Department of Pediatrics, Arkansas Children's Hospital, Little Rock, AR

We describe a large family (K313) having 12 males affected with X-linked recessive hereditary spastic paraplegia. The disease phenotype in K313 is characterized by hyperreflexia and a spastic gait, but intelligence is normal. Carrier females have normal gait and unremarkable reurologic profies. Eight widely spaced X-chromosome linked DBA markers were used to genotype 43 family members. In contrast to a published report of complete linkage of X-linked spastic paraplegia in another family to distal chromosome Xq markers DXS15 and DXS52 (Kenwrick et al., Hum. Genet. 73:264-266, 1986), we observed complete linkage with two DNA markers located on the middle of the long arm of the X chromosome, pYNH3 and DXS17. Lod scores for linkage between the disease locus and the DNA markers were 4.48 for pYNH3 and 4.00 for DXS17. In contrast to the linkage reported by Kenwrick to markers in the X227-28 region, our family (K313) is unlinked to the distal markers DXS15 and DXS52. Location score analysis showed evidence of significant genetic heterogeneity between the two pedigrees (X^2 = 21.08), suggesting that both pure and complicated forms of spastic paraplegia exist on the X chromosome.

LINKAGE OF THE POLYMORPHIC PROTEIN MARKERS F13B, C1S, C1R, AND BLOOD GROUP ANTIGEN KIDD IN CEPH REFERENCE FAMILIES

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*Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA
+LDS Hospital, Salt Lake City, UT

The gene for blood clotting factor 13B (F13B) was localized to chromosome 1 by linkage to two DNA markers, pMLAJ1 and EKH7.4. The maximum lod scores were 6.00 at a theta of 0.217, and 18.69 at theta 0.088, respectively. C1S and C1R (subcomponents of human complement 1) were closely linked to the proline-rich protein (PRP) gene cluster on chromosome 12p13.2. A maximum lod score of 5.99 at theta 0.038 was found between C1S and one of the PRP loci; the maximum lod score between C1R and another PRP locus was 4.21 at theta 0.001. Another subcomponent of human complement, C1Q-- previously assigned to the short arm of chromosome 1 -- is thus unlinked to C1S and C1R. The gene for blood group antigen Kidd was localized to chromosome 18 by linkage to two DNA markers, pL2.7 and pHF12-62 (maximum lod scores 3.61 at theta 0.168 and 4.18 at 0.218, respectively). Protein and blood type marker data were colllected on the Utah subset (29 families) of the CEPH panel. Linkage analysis was carried out as two-factor analysis on the program LINKAGE.

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 1

P. O'Connell, M. Leppert, Y. Nakamura, G.M. Lathrop, P. Cartwright, J.-M. Lalouel, and R. White.
Howard Hughes Medical Institute, U. of Utah, Salt Lake City, USA

A primary genetic linkage map of chromosome 1 was constructed from data on 24 markers typed in 40-60 reference families (including the 38 families of the CEPH reference panel). The following loci were studied:

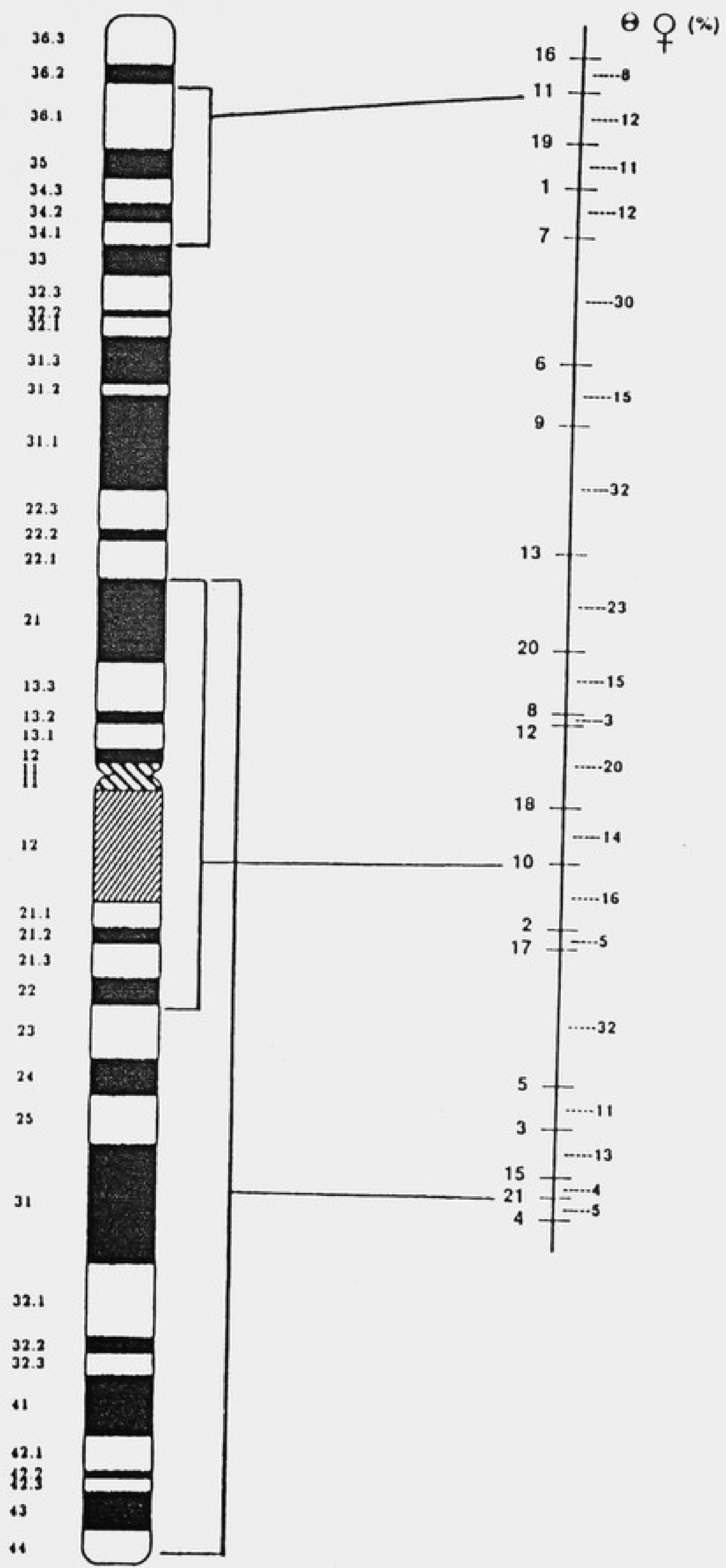
	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pYNZ2	MspI	VNTR >10 ALLELES 0.5-2.5KB		0.65	615
2	pMLAJ1	HinfI	VNTR >6 ALLELES 1.5-3.0KB		0.64	359
3	pEKH7.4	TaqI	5.0 3.8	0.47 0.52	0.53	674
4	pTHH18.1	MspI	5.6 5.0	0.46 0.54	0.40	657
5	FXIIIB	FXIIIB	A1 A2 A3 A4	0.72 0.12 0.16 0.01	0.45	598
6	PGM	PGM	A1 A2 A3 A4	0.64 0.12 0.20 0.05	0.58	584
7	pTHI54	PvuII	6.0 5.0	0.51 0.49	0.46	661
8	N8C6(NGFB)	BglII	6.0 1.4	0.19 0.81	0.36	588
9	pL1.22(D1S2)	BglII	10.0 7.0	0.81 0.19	0.37	675
10	Duffy(FY)	FY	A1 A2	0.44 0.56	0.49	630

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
11	Rhesus(RH)	RH	A1	0.41	0.60	639
			A2	0.44		
			A3	0.12		
			A4	0.01		
			A5	0.01		
			A6	>0.01		
			A7	0.01		
			A8	0.01		
12	pMCR3(NRAS)	EcoRI	6.0	0.74	0.36	707
			4.8	0.26		
13	pAP8(HTF)	MspI	3.2	0.29	0.36	397
			2.6	0.71		
14	AT3(AT3)	AT3	A1	0.88	0.22	580
			A2	0.11		
			A3	0.01		
15	pHHH119	MspI	6.2	0.10	0.15	514
			4.4	0.90		
16	pCMM8.1	MspI	1.6	0.74	0.40	667
			1.0	0.26		
17	pHBI40	MspI	8.0	0.72	0.37	786
			4.4	0.28		
18	pHHH106	MspI	2.3	0.45	0.53	746
			2.0	0.55		
19	pMHZ5	MspI	2.5	0.08	0.17	654
			1.9	0.92		
20	pEFZ13	MspI	5.0	0.66	0.51	640
			3.3	0.34		
21	pHRnES1.9(REN)	HindIII	8.7	0.70	0.40	674
			6.2	0.30		

Twenty loci form a continuous linkage map spanning approximately 198 cM in males and 370 cM in females. Multilocus analysis with the LINKAGE programs, under the assumption of a constant ratio of female/male genetic distances, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
82038:1          10^8:1           10^32:1          10^18:1

|       |        |       |        |       |        |       |
| .03   | .02    | .08   | .06    | .21   | .03    | .09   |  .08
4 ---- 21----- 15 ---- 3 ----   5 ---- 17 ---- 2 ---- 10 ---- 18
  .05   | .04    | .13   | .11    | .32   | .05    | .16   |  .14  |
        |        |       |        |       |        |       |       |
         1.00:1           10^5:1           620:1            10^9:1

 10^20:1          10^11:1          10^13:1          10^27:1

|       |        |       |        |       |        |       |
| .12   | .02    | .09   | .14    | .21   | .09    | .19   |  .07
18 ----12 ----- 8 ---- 20 ---- 13 ----- 9----- 6 ----- 7 ---- 1
  .20   | .03    | .15   | .23    | .32   | .15    | .30   |  .12 |
        |        |       |        |       |        |       |      |
          6:1                              183:1            10^11:1

  10^10:1          2.7:1

|       |        |       |
| .06   |  .07   | .04   |
1 ----- 19 -----11 ---- 16
| .11   |  .12   | .08   |
|       |        |       |
         10^10:1
```

Locus 14 is not linked to others in this map.



1

THREE GENETIC LINKAGE GROUPS ON CHROMOSOME 2

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Three linkage groups have been constructed from data for twenty loci typed in 40-60 reference families (including the forty families of the CEPH panel). The following loci were studied:

	PROBE (LOCUS)		ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	(APOB)	pB23	XbaI	8.6	0.44	0.71	220
				5.0	0.56		
		pB8	EcoRI	13.0	0.16	0.27	646
				11.0	0.84		
2	p5-1-25(D2S3)		PstI	VNTR		0.55	417
				4 ALLELES			
				2.5-3.0KB			
3	pYNZ15		TaqI	1.8	0.53	0.56	672
				1.0	0.47		
4	pYNH24		MspI	VNTR		0.91	632
				>20 ALLELES			
				1.3-6.0KB			
5	KM (IGK)		KM	A1	0.41	0.31	510
				A2	0.59		
7	ACP		ACP	A1	0.33	0.37	614
				A2	0.67		
8	pL2.3(D2S1)		BglII	9.0	0.66	0.57	371
				6.3	0.34		
9	pHHH133		MspI	1.4	0.29	0.37	563
				1.3	0.71		
10	pYNZ9.1		TaqI	1.1	0.55	0.59	602
				1.0	0.45		
11	pXG-18(D2S6)		TaqI	5.5	0.45	0.56	661
				4.6	0.55		

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
12	pTBAB-5-7	PvuII	VNTR >4 ALLELES 3.0-6.0KB		0.55	602
13	pEFD122	MspI	3.2 3.0	0.45 0.55	0.43	760
14	pYNA15.1	MspI	7.0 6.0	0.60 0.40	0.53	312
15	IMR-6(D2S5)	MspI	6.8 6.1,0.7	0.74 0.26	0.37	310
16	cYNA4	MspI	VNTR >7 ALLELES 3.0-6.0KB		0.79	717
17	pCMM63	MspI	7.0 4.5 4.3	0.07 0.02 0.91	0.15	759
18	pEKZ105	RsaI	3.0 2.6	0.52 0.48	0.45	666
19	cMCOE32	TaqI	VNTR >5 ALLELES 1.7-6.0KB		0.74	733
20	p5G1(CRYG)	TaqI	3.5 3.3	0.68 0.32	0.46	656
		TaqI	2.1 1.7	0.33 0.67	0.47	656
		TaqI	2.3 1.2	0.18 0.82	0.32	656
21	pHHH115	MspI	4.8 4.6 4.5	0.17 0.83 0.01	0.31	650
		MspI	2.4 1.7	0.42 0.58	0.49	616

The twenty loci form three linkage groups spanning approximately 226 cM in females and 188 in males for linkage group 1; 22 cM in females and 24 cM in males for linkage group 2; and 99 cM in females and 70 cM in males for linkage group 3. Locus 5, IGK, does not show linkage to the map and may be on chromosome 18 with JK. Locus 15 (D2S5) shows no evidence of linkage to other elements of the map. Multilocus analysis with the LINKAGE programs,

under the assumption of a constant female/male genetic distance ratio, gave the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

Linkage Group 1

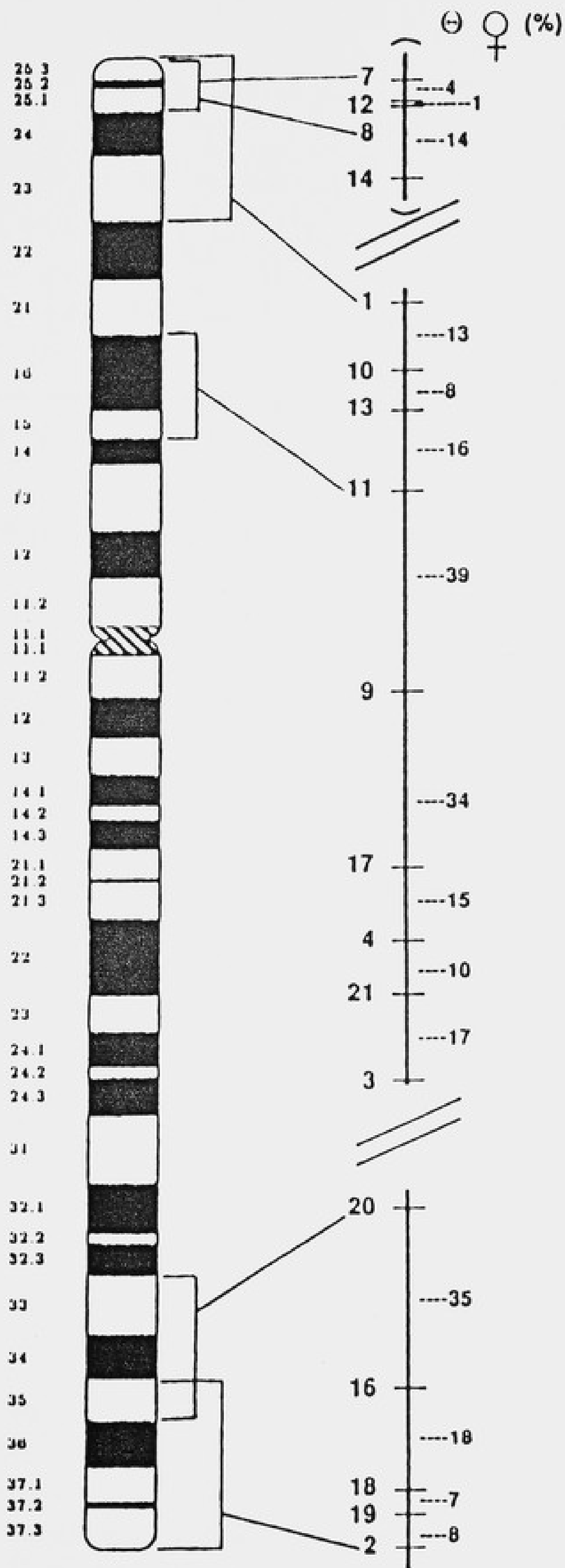
```
           73496:1          10^20:1           10^6:1          10^15:1
|          |         |         |        |         |        |         |
| .07      | .05     | .09     | .27    | .22     | .09    | .06     | .10
1 ---- 10 ---- 13 ---- 11 ---- 9 ---- 17 ---- 4 ---- 21 ---- 3
  .13      | .08     | .16     | .39    | .34     | .15    | .10     | .17    |
           |         |         |        |         |        |         |        |
329311:1           10^10:1          10^11:1              25:1
```

Linkage Group 2

```
 6186:1          107:1
|         |         |         |
| .04     | .02     | .15     |
7 ---- 12 ---- 8 ---- 14
  .04     | .01     | .14
          |         |
            1:1
```

Linkage Group 3

```
  50:1            10^16:1
|         |         |         |
| .06     | .05     | .14     | .29
2 ---- 19 ---- 18 ---- 16 ---- 20
  .08     | .07     | .18     | .35    |
          |         |         |        |
           4664:1            10^28:1
```



2

TWO LINKAGE GROUPS ON CHROMOSOME 3

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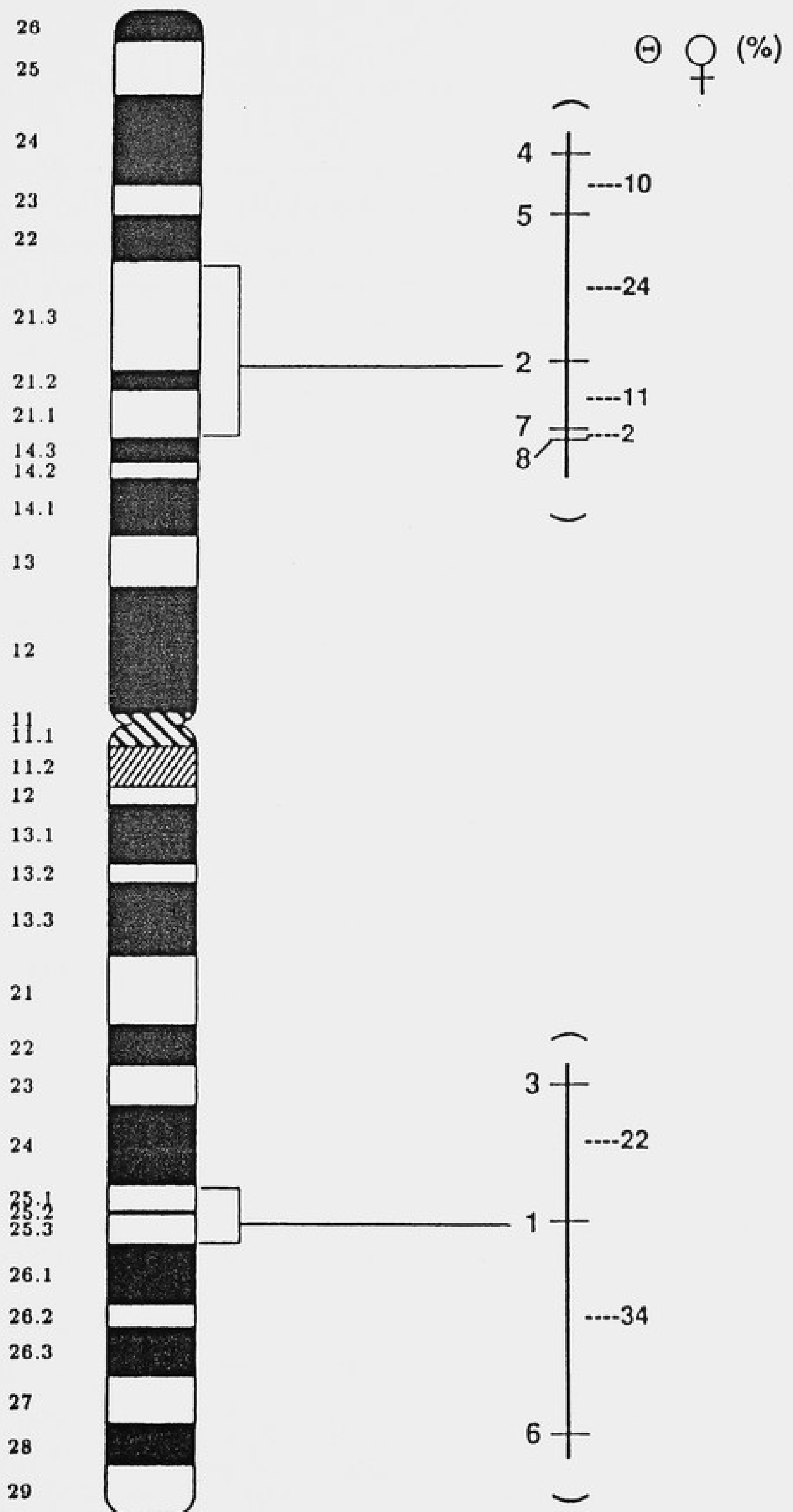
Linkage was found for eight loci on chromosome 3. They were typed in 40-60 families (including 38 from CEPH). The loci are:

PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER OF INDIVIDUALS TYPED
1 pHCP-1 (CP)	PstI	14.0 11.5	0.39 0.61	0.48	456
2 H3H2 (DNF15S2)	HindIII	2.3 2.0	0.46 0.54	0.50	378
3 ABL11-3	TaqI	8.5 1.5	0.54 0.46	0.58	656
ABL11-3	PvuII	4.1 0.9	0.48 0.52	0.61	169
4 pB67 (D3S4)	TaqI	13.0 12.0	0.14 0.86	0.27	599
5 pYNZ86.1	MspI	2.6 2.1	0.51 0.49	0.52	564
6 pMCT32.1	PvuII	15.0 14.0 12.0	0.11 0.37 0.52	0.75	346
7 pEFD145.1	RsaI	2.4 1.3	0.46 0.54	0.46	568
8 pHF12-32 (D3S2)	MspI	2.9 1.3	0.83 0.17	0.23	448

Multilocus analysis with the LINKAGE program under the assumption of a constant effect of sex on crossing overfrequency yielded two separate linkage groups, of 44 and 56 cM in males and 86 and 58 cM in females. The gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of the adjacent loci are:

```
      9:1
 |         |         |
 | .13     | .22     |
 3 ----- 1 ----- 6
 | .22     | .34     |
 |         |         |
            7708:1

      23:1                 343:1
 |         |         |         |         |
 | .11     | .27     | .13     | .02     |
 4 ----- 5 ----- 2 ----- 7 ----- 8
 | .10     | .24     | .11     | .02     |
 |         |         |         |         |
            10^7:1              3:1
```



26
25
24
23
22
21.3
21.2
21.1
14.3
14.2
14.1
13
12
11
11.1
11.2
12
13.1
13.2
13.3
21
22
23
24
25.1
25.2
25.3
26.1
26.2
26.3
27
28
29
Θ ♀ (%)
4
----10
5
----24
2
----11
7
----2
8
3
----22
1
----34
6

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 5

M. Leppert, *J. Wasmuth, *J. Overhauser, *M Dobbs, Y. Nakamura, M. Lathrop, P. O'Connell, P. Cartwright, J.-M. Lalouel, and R. White
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*Dept. of Biol. Chemistry, California College of Medicine, Irvine, USA

Sixteen loci were characterized in 40 to 60 families (including 38 from CEPH):

PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER OF INDIVIDUALS TYPED
1 L1.4 (D5S4)	EcoRI	0.7 0.6	0.80 0.20	0.31	346
2 pC11p11	TaqI	4.2 2.7	0.17 0.83	0.32	681
3 pL500 (HPRTP2)	MspI	3.6 1.3	0.23 0.77	0.42	460
4 p105-153Ra	MspI	8.0 5.0	0.40 0.60	0.53	771
5 p213-205Ed	MspI	6.0 3.9 3.8	0.43 0.35 0.22	0.60	721
6 LM4 (D5S6)	BamHI	11.0 9.6 7.6	0.36 0.54 0.11	0.68	264
7 TP5E	TaqI	13.0 5.0	0.77 0.23	0.40	597
8 pJO110HC	MspI	8.7 7.2 6.9	0.69 0.30 0.00	0.38	751
9 p105-798Rb	MspI	14.0 2.3	0.57 0.43	0.58	471
10 L565RI-b	MspI	6.2 4.6	0.44 0.56	0.44	192
11 L599H-a	TaqI	17.0 14.0 10.0	0.32 0.16 0.52	0.67	748

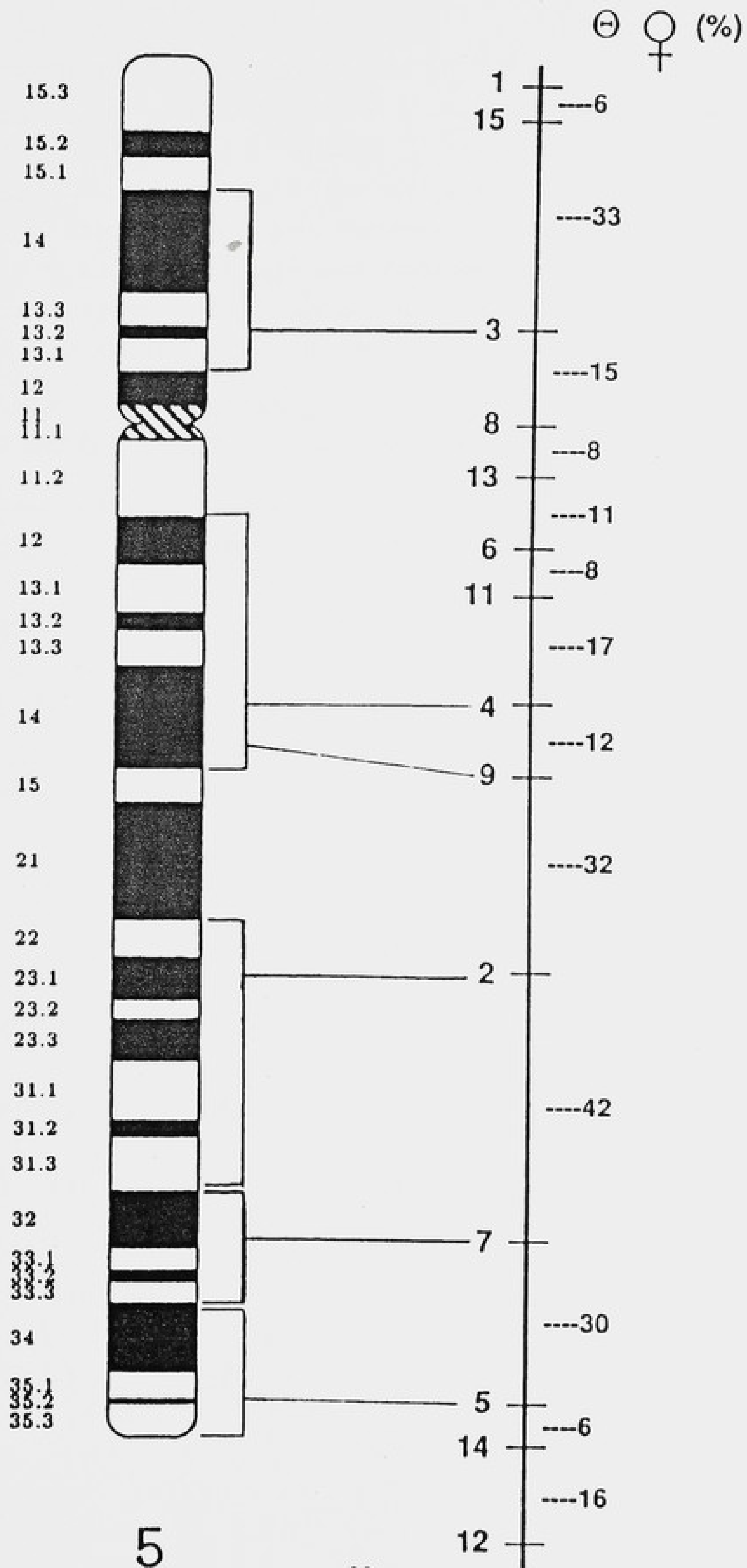
12	pHF12-65 (D5S2)	MspI	4.1 3.7	0.87 0.13	0.23	621
13	PP8C	TaqI	5.0 4.8	0.31 0.69	0.42	539
14	J0157E-A	MspI	4.0 3.5	0.38 0.63	0.52	754
15	L647H-C	MspI	9.0 7.0 5.5 4.4	0.07 0.29 0.33 0.31	0.74	273
16	Kell	Kel		0.02 0.98	0.04	630

Multilocus analysis was performed with the LINKAGE program. Fourteen of these loci form a continuous map of the chromosome spanning 207 cM in males and 357 cM in females. The gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of the adjacent loci are :

```
   <2:1          5514:1         103777:1        327747:1       10^12:1
|       |       |       |       |       |       |       |       |       |
| .04   | .23   | .09   | .05   | .07   | .05   | .11   | .08   | .22   |
1 -----15 ----- 3 ----- 8 -----13 ----- 6 -----11 ----- 4 ----- 9 ----- 2
| .06   | .33   | .15   | .08   | .11   | .08   | .17   | .12   | .32   |
|       |       |       |       |       |       |       |       |       |
        10^12:1          469:1           2:1            128669:1
```

```
        10^27:1         10^9:1
|       |       |       |       |
| .33   | .20   | .03   | .10   |
2 ----- 7 ----- 5 -----14 -----12
| .42   | .30   | .06   | .16   |
|       |       |       |       |
 10^9:1          291:1
```

Kell (locus 16) has a maximum lod score of 3.92 with L565RI-b (locus 10) at a recombination rate of 0.0. The latter was isolated from a chromosome specific library. Because no linkage was observed with our other markers, the assignment of the these two loci to chromosome 5 remains unproven.


Θ ♀ (%)
15.3
15.2
15.1
14
13.3
13.2
13.1
12
11
11.1
11.2
12
13.1
13.2
13.3
14
15
21
22
23.1
23.2
23.3
31.1
31.2
31.3
32
33.1
33.2
33.3
34
35.1
35.2
35.3
5
1
----6
15
----33
3
----15
8
----8
13
----11
6
----8
11
----17
4
----12
9
----32
2
----42
7
----30
5
----6
14
----16
12

EXTENSION TO A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 6p

M. Leppert, P. O'Connell, Y. Nakamura, R. Leach, G.M. Lathrop, P. Cartwright, J.-M. Lalouel, and R. White.
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A primary genetic linkage map of chromosome 6 was constructed from data on 12 markers typed in 30-60 reference families (including 38 families of the CEPH reference panel). This map revises and extends that of Leach et al. (PNAS USA 83:3909-3913, 1986). The following loci were studied:

	PROBE (LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pYNB3.6	MspI	7.5	0.45	0.55	623
			4.5	0.55		
2	pHHH157	BamHI	13.0	0.50	0.50	719
			6.0	0.50		
3	pAGB6	MspI	6.0	0.14	0.25	400
			4.0	0.86		
4	p7H4 (D6S7)	EcoRI	11.0	0.82	0.30	403
			10.5	0.04		
			9.2	0.05		
			9.1	0.08		
5	pCH6 (D6S10)	TaqI	5.8	0.43	0.43	396
			5.0	0.51		
			3.7	0.06		
6	p2C5 (D6S8)	MspI	5.9	0.19	0.38	395
			0.6	0.81		
7	pHM26 (MYB)	EcoRI	2.6	0.56	0.58	604
			1.5	0.44		
8	p4c11 (D6S4)	BglII	6.5	0.59	0.60	483
			5.7	0.41		
9	OL43 (DNF14)	EcoRI	5.0	0.88	0.25	718
			4.7	0.13		
10	p2-2 (D6S2)	PvuII	2.9	0.57	0.60	351
			2.8	0.24		
			2.6	0.19		
			2.2	0.00		

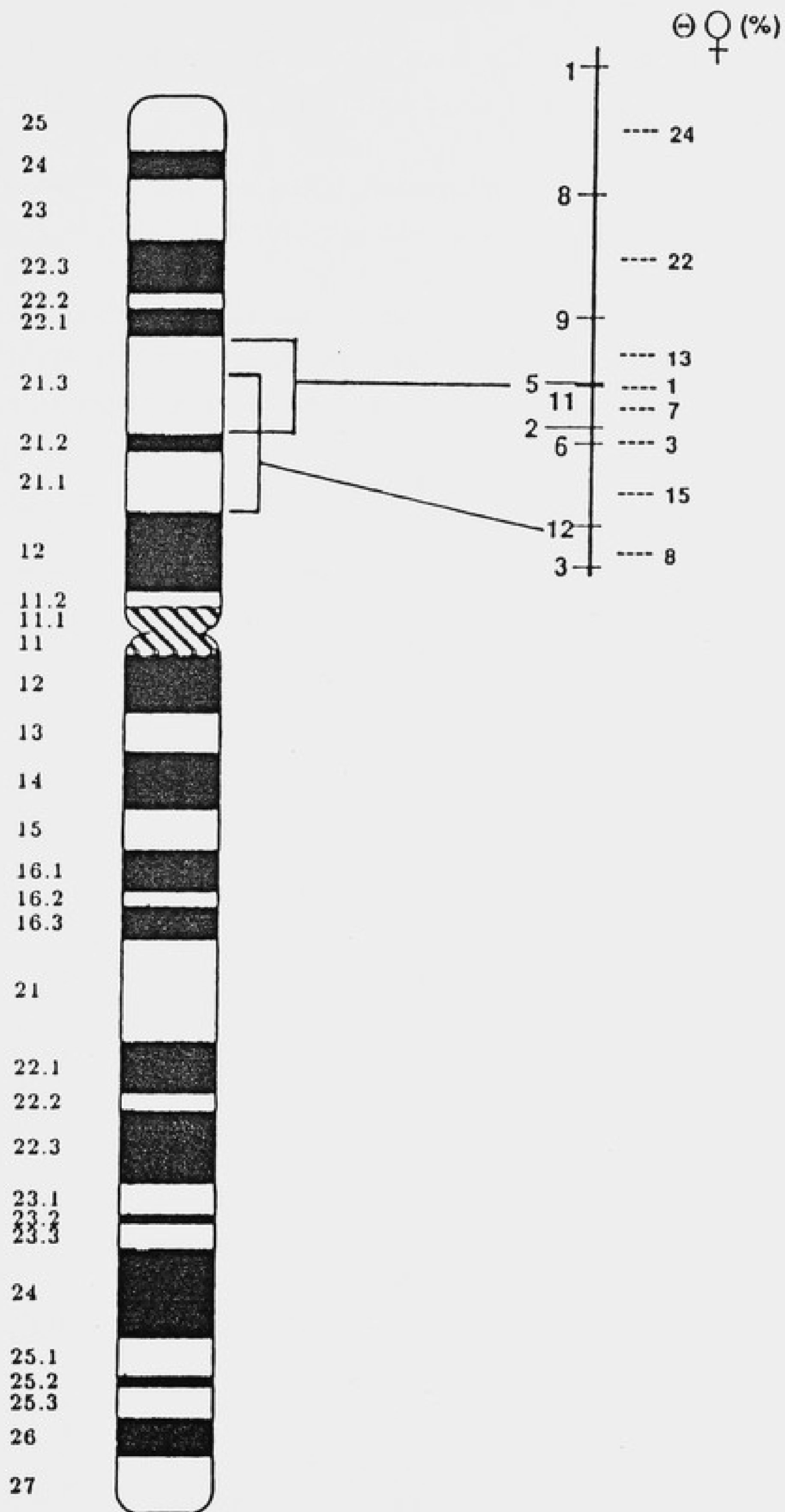
11	DRH7(HLA-D)	EcoRV	13.1	0.76	0.38	399
			9.1	0.24		
		BglII	4.3	0.74	0.38	397
			4.1	0.07		
			3.8	0.19		
	pDP001(HLA-D)	EcoRV	8.6	0.13	0.25	388
			---	0.87		
	pDCH1(HLA-D)	HindIII	7.7	0.03	0.62	394
			7.3	0.28		
			5.6	0.25		
			4.6	0.43		
12	Glyoxalase(GLO)	GLO	A1	0.44	0.55	389
			A2	0.56		

Nine loci form a continuous linkage map spanning approximately 39 cM in males and 113 cM in females. Multilocus analysis with the LINKAGE programs, under the assumption of a constant ratio of female/male genetic distance, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
 1.4:1          20:1          3:1          10^8:1

|      |       |      |       |      |      |      |      |
| .03  | .06   | .01  | .03   | .00  | .05  | .09  | .10  |
3 ---- 12 ---- 6 ---- 2 ---- 11 ---- 5 ---- 9 ---- 8 ---- 1
  .08  | .15   | .03  | .07   | .01  | .13  | .22  | .24  |
       |       |      |       |      |      |      |      |
         10^11:1        1.1:1        10^10:1       65153:1
```

The other three loci are unlinked to the markers in this map, and to each other.



Θ ♀ (%)
25
24
23
22.3
22.2
22.1
21.3
21.2
21.1
12
11.2
11.1
11
12
13
14
15
16.1
16.2
16.3
21
22.1
22.2
22.3
23.1
23.2
23.3
24
25.1
25.2
25.3
26
27
1
24
8
22
9
13
5
1
11
7
2
6
3
15
12
8
3
6

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 7

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+Research Institute, Hospital for Sick Children, Toronto, Ontario

A primary genetic linkage map of chromosome 7p was constructed from data on 20 loci typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1 phage-6(D7S11)	HindIII	9.8	0.23	0.36	387
		7.8	0.77		
2 Pst/Bam(TCRG)	PvuII	14.7	0.20	0.57	665
		12.6	0.59		
		10.5	0.21		
3 pADJ641	TaqI	2.0	0.20	0.34	672
		1.0	0.80		
4 pTHH28	MspI	3.4	0.29	0.43	453
		2.3	0.71		
5 pM60	TaqI	5.3	0.37	0.47	648
		5.0	0.63		
6 pS194	TaqI	1.8	0.79	0.42	654
		1.5	0.21		
7 pM102L	TaqI	12.0	0.37	0.49	668
		8.5	0.63		
8 pRM7-4	MspI	5.5	0.38	0.49	545
		2.3	0.62		
9 pHP1.7(ERV3)	MspI	3.3	0.55	0.37	713
		2.8	0.45		
10 pS93	PstI	4.4	0.28	0.38	579
		4.2	0.72		
11 pCMI37	RsaI	VNTR >4 ALLELES 2.0-5.0KB		0.50	675

12 pNJ-3(COLIA2)		EcoRI	13.0	0.66	0.45	624
			9.5	0.34		
13 pJ-2(TCRB)		BglII	10.0	0.55	0.56	583
			9.5	0.45		
14 pJ3.11(D7S8)		MspI	4.0	0.38	0.55	639
			1.6	0.62		
		TaqI	6.0	0.96	0.08	587
			3.1	0.04		
15 pB79a(D7S13)		HindIII	8.1	0.16	0.24	628
			4.3	0.84		
		MspI	11.6	0.31	0.41	654
			8.4	0.69		
16 MET	pmetD	TaqI	5.0	0.80	0.31	659
			4.3	0.20		
	pmetH	MspI	4.8	0.05	0.62	185
			2.3	0.54		
			1.7	0.42		
		TaqI	7.0	0.51	0.64	432
			4.2	0.49		
			3.0	0.00		
	pHOS6	TaqI	2.9	0.34	0.47	663
			1.3	0.66		
17 p7C22(D7S16)		EcoRI	7.0	0.80	0.35	507
			5.0	0.20		
18 C33		HindIII	4.3	0.20	0.51	543
			4.0	0.14		
			3.6	0.66		
19 A37		PstI	7.0	0.45	0.38	716
			5.0	0.55		
20 pYNB3.1R		RsaI	3.9	0.29	0.46	672
			2.4	0.71		

The loci form a continuous linkage group spanning approximately 148 cM in males and 338 cM in females. Multilocus analysis with the LINKAGE programs, under the assumption of a constant ratio of female/male genetic distance, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

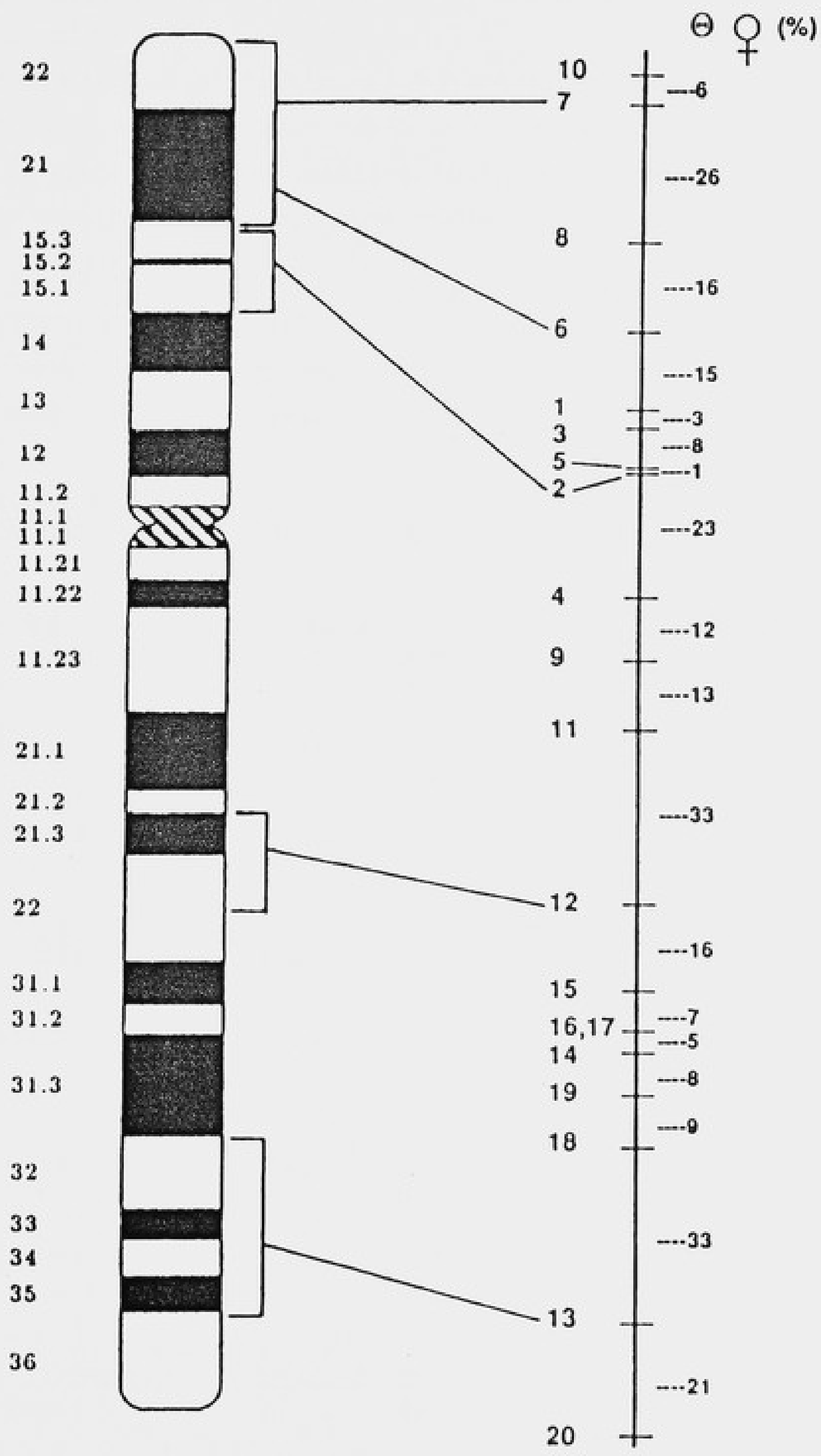
```
  5:1           2:1           82:1        10^28:1

|     |     |     |     |     |     |     |
| .03 | .13 | .08 | .07 | .02 | .04 | .00 | .12
10 --- 7 ---- 8 --- 6 --- 1 --- 3 --- 5 --- 2 --- 4
  .06 | .26 | .16 | .15 | .03 | .08 | .01 | .23 |
      |     |     |     |     |     |     |     |
        10^16:1     10^12:1     10^16:1     10^22:1


 125:1     10^27:1      10^8:1            10^9:1   10^24:1

|     |     |     |     |         |       |     |     |     |
| .06 | .06 | .18 | .08 | .03     |   .02 | .04 | .04 | .19 | .11
4 --- 9 --- 11----12----15----(16----17)----14----19----18----13----20
  .12 | .13 | .33 | .16 | .07     |   .05 | .08 | .09 | .33 | .21 |
      |     |     |     |         |       |     |     |     |     |
     614:1      10^7:1            23:1         939:1      1018:1
```

Brackets indicate that the loci were haplotyped for the analysis.


Θ ♀ (%)
22
21
15.3
15.2
15.1
14
13
12
11.2
11.1
11.1
11.21
11.22
11.23
21.1
21.2
21.3
22
31.1
31.2
31.3
32
33
34
35
36
10
7
8
6
1
3
5
2
4
9
11
12
15
16,17
14
19
18
13
20
----6
----26
----16
----15
----3
----8
----1
----23
----12
----13
----33
----16
----7
----5
----8
----9
----33
----21
7

THREE GENETIC LINKAGE GROUPS ON CHROMOSOME 8

P. O'Connell, Y. Nakamura, G.M. Lathrop, M. Leppert, P. Cartwright, J.-M. Lalouel and R. White.

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Three linkage groups have been constructed from data for eleven loci typed in 40-60 reference families (including the forty families of the CEPH panel). The following loci were studied:

	PROBE (LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pYNM3	PstI	VNTR 3 ALLELES 3.2-3.6KB		0.33	685
2	GPT(GPT)	GPT	A1 A2	0.53 0.47	0.45	596
3	pTHH5	HindIII	4.0 2.5 2.3	0.56 0.43 0.01	0.55	696
4	pABL4-2	RsaI	2.3 1.8	0.32 0.68	0.42	593
5	pYNZ132	TaqI	VNTR 4 ALLELES 1.7-2.3		0.69	666
6	pHHH171	MspI	2.3 1.9	0.74 0.26	0.39	642
7	LIIA-2	PstI	VNTR 5 ALLELES 4.0-6.5KB		0.46	636
8	pCHT16-8.0(TG)	TaqI	5.8 5.2	0.20 0.80	0.35	712
9	p380-8A	TaqI	3.3 2.5 2.3	0.47 0.44 0.09	0.54	708
10	LTL11(D8S5)	HindIII	11.8 10.6	0.76 0.24	0.35	457
11	pMCT128.2	PstI	VNTR 3 ALLELES 1.4-1.8KB		0.54	166

The eleven loci form three linkage groups spanning approximately 65 cM in females and 79 cM in males for linkage group 1; 5 cM in females and 6 cM in males for linkage group 2; and 55 cM in females and 44 cM in males for linkage group 3. The assignment of linkage group 2 to chromosome 8 is provisional. Multilocus analysis with the LINKAGE programs, under the assumption of a constant female/male genetic distance ratio, gave the following gene orders, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

Linkage Group 1

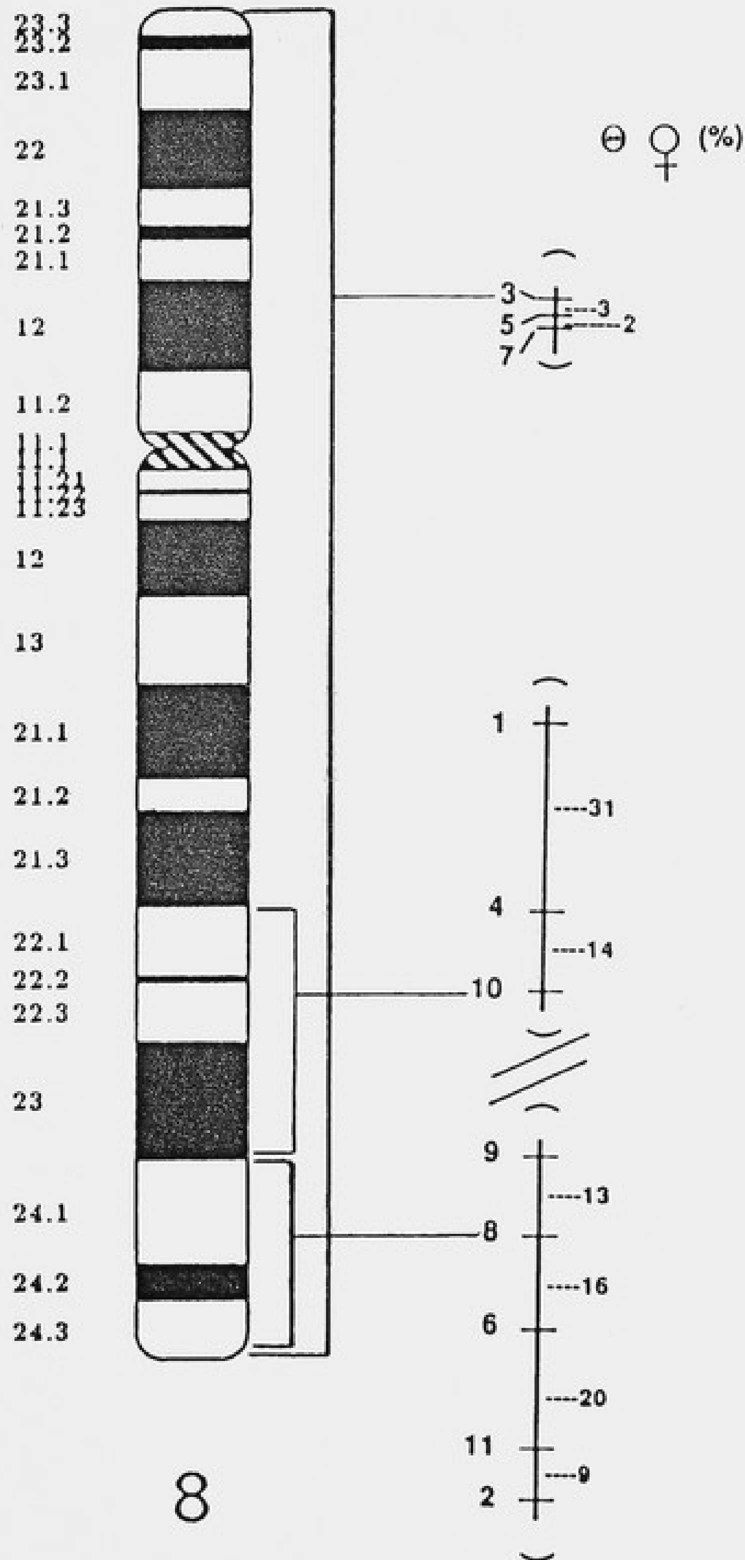
```
  456:1
|      |
| .35  | .16
1 ---- 4 ---- 10
  .31  | .14  |
       |      |
        20:1
```

Linkage Group 2

```
  10^6:1
|      |
| .04  | .02
3 ---- 5 ---- 7
  .04  | .01  |
       |      |
       4915:1
```

Linkage Group 3

```
  5:1               10^7:1
|      |       |       |
| .06  |   .14 | .11   | .09
2 ---- 11 ---- 6 ---- 8 ---- 9
  .09  |   .20 | .16   | .13  |
       |       |       |      |
       9701:1          6:1
```


23.3
23.2
23.1
22
21.3
21.2
21.1
12
11.2
11.1
11.1
11.21
11.22
11.23
12
13
21.1
21.2
21.3
22.1
22.2
22.3
23
24.1
24.2
24.3
8
Θ ♀ (%)
3
5
7
3
2
1
31
4
14
10
9
13
8
16
6
20
11
9
2

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 9

G.M. Lathrop, M. Leppert, P. O'Connell, Y. Nakamura, P. Cartwright, J.-M. Lalouel and R. White.
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A primary genetic linkage map of chromosome 9 was constructed from data on 16 markers typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pYNM17	TaqI	7.5	0.62	0.47	581
			5.0	0.38		
2	pAblK2(ABL)	TaqI	7.6	0.09	0.17	657
			6.7	0.91		
			5.0	0.01		
3	pAS-1(ASSP3)	HindIII	10.1	0.74	0.43	662
			5.3	0.26		
4	pHF12-8(D9S1)	TaqI	3.6	0.40	0.36	665
			3.2	0.60		
5	Adenylate(AK1) kinase 1	AK1	A1	0.95	0.10	626
			A2	0.05		
6	pTHH22	TaqI	12.0	0.09	0.16	711
			8.0	0.91		
7	Orosomucoid(ORM)	ORM	A1	0.58	0.58	619
			A2	0.42		
8	ABO	ABO	A1	0.69	0.44	553
			A2	0.17		
			A3	0.07		
			A4	>0.01		
			A5	0.07		
9	pHHH220	TaqI	4.3	0.78	0.32	614
			3.0	0.21		
			2.3	0.01		

PROBE(LOCUS)		ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
10	Galactose(GALT) 1-P-uridyltransferase	GALT	A1	0.93	0.14	637
			A2	0.06		
			A3	0.01		
11	pEK130	MspI	6.2	0.72	0.41	609
			4.5	0.28		
12	pMCT136	Pstl	2.2	0.46	0.50	767
			2.0	0.54		
14	pEFD126.3	BamHI	VNTR >5 ALLELES 1.0-3.0KB		0.66	747
15	pEFD40.3	MspI	5.3	0.70	0.38	763
			4.4	0.30		
16	pMCT96.1	RsaI	4.7	0.76	0.36	608
			3.7	0.24		
		RsaI	1.0	0.99	0.02	602
			0.9	0.01		
17	pMCT112	MspI	6.0	0.71	0.37	783
			4.9	0.29		

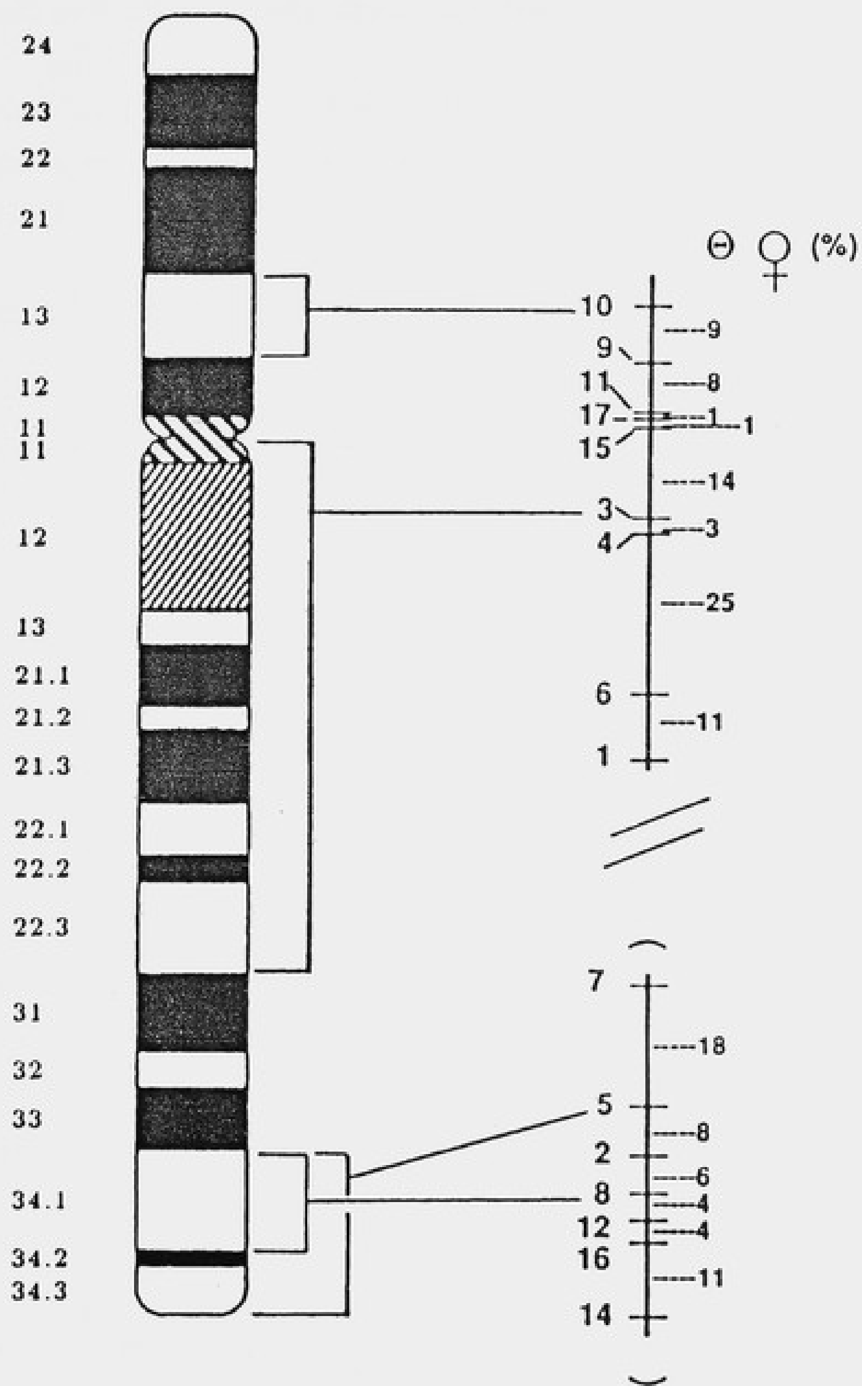
The loci form two linkage groups spanning approximately 178 cM in males and 207 cM in females. Multilocus analysis with the LINKAGE programs, under the assumption of constant female/male ratio of genetic distance, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

Linkage group 1

```
          10^10:1          10^23:1          3056:1          4:1
|        |        |       |        |       |        |        |       |
|  .07   |  .17   | .02   | .09    | .01   |  .01   |  .05   | .06   |
1 ------ 6 ------ 4 ----- 3 ------ 15 ---- 17 ----- 11 ----- 9 ----- 10
   .11   |  .25   | .03   | .14    | .01   |  .01   |  .08   | .09   |
         |        |       |        |       |        |        |       |
   75:1              88:1             5289:1           152:1
```

Linkage group 2

```
           10^6:1          4:1            5511:1
|        |         |       |        |       |       |
|  .13   |  .05    | .05   | .08    | .10   | .21   |
14 ----- 16 ------ 12 ---- 8 ------ 2 ----- 5 ----- 7
|  .11   |  .04    | .04   | .06    | .08   | .18   |
|        |         |       |        |       |       |
  10^12:1            161:1           16:1
```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23
22
21
13
12
11
11
12
13
21.1
21.2
21.3
22.1
22.2
22.3
31
32
33
34.1
34.2
34.3
9
Θ ♀ (%)
10
9
9
8
11
17
1
1
15
14
3
3
4
25
6
11
1
7
18
5
8
2
6
8
4
12
4
16
11
14

A PRIMARY LINKAGE MAP OF CHROMOSOME 10

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Howard Hughes Medical Institute, Salt Lake City, Utah USA

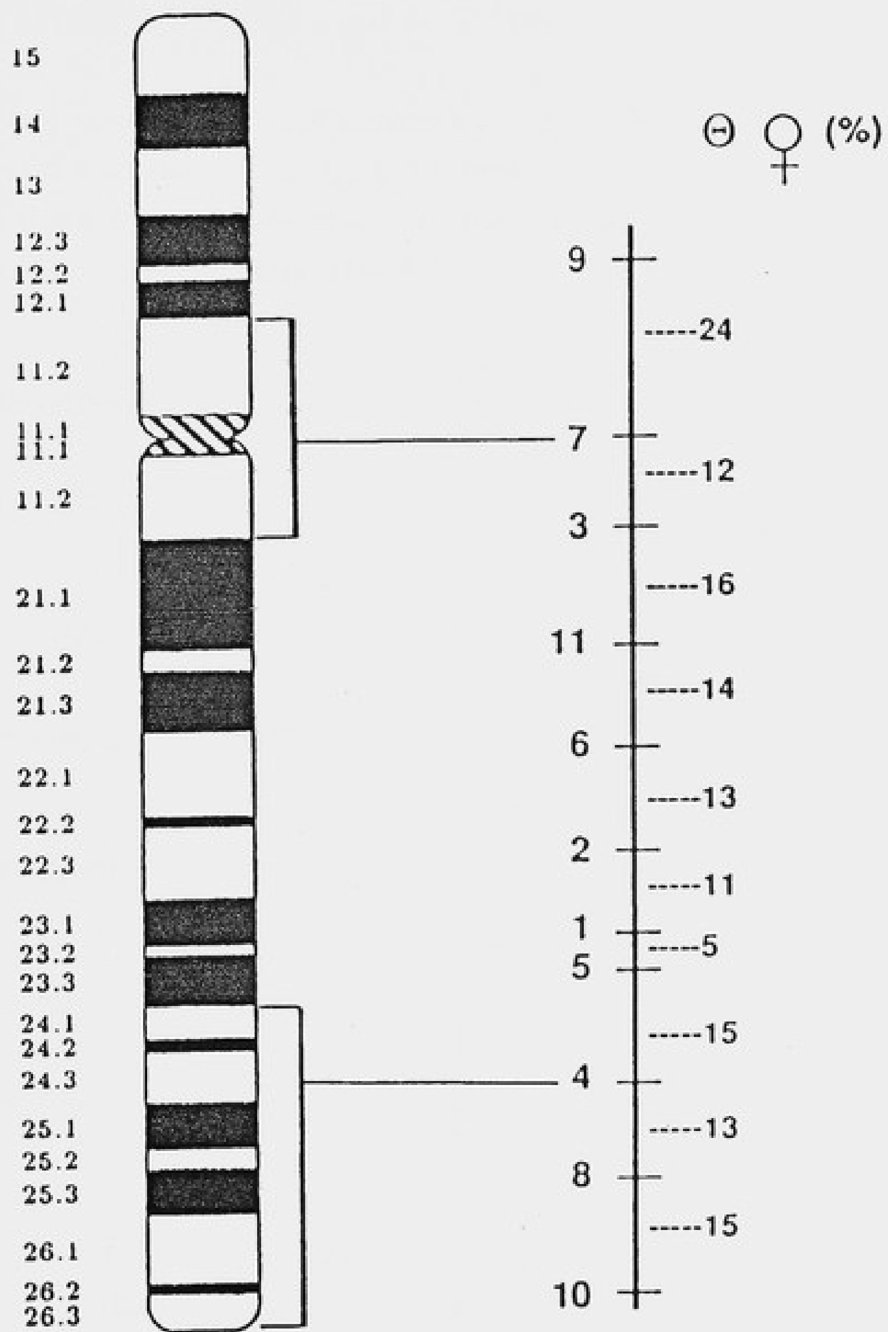
Eleven loci typed in 40-60 families (including 40 from the CEPH panel) constitute a continuous genetic map of chromosome 10. The following loci were studied :

PROBE (LOCUS)		ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER OF INDIVIDUALS TYPED
1	pTHH105.1	BglII	8.5	0.24	0.33	544
			8.3	0.76		
2	pTHH54	MspI	3.7	0.52	0.62	574
			2.9	0.40		
			1.9	0.08		
3	pMCK2	PvuII	VNTR		0.26	646
			>6 alleles			
			2.0 -2.5			
4	pl-101	TaqI	8.5	0.02	0.55	625
			7.0	0.60		
			5.0	0.38		
5	dry5-1 (D10S1)	TaqI	6.3	0.83	0.34	316
			3.6	0.17		
6	pCMM17.1	MspI	2.3	0.35	0.43	658
			1.5	0.65		
7	IRBPH.4	BglII	6.0	0.91	0.14	396
			4.2	0.09		
	IRBPH.4	MspI	3.0	0.76	0.31	654
			2.5	0.24		
8	OS-2	HindIII	10.0	0.38	0.64	602
			5.2	0.52		
			3.2	0.10		
9	pMHZ15	MspI	3.6	0.61	0.54	549
			2.1	0.39		
10	pYNZ156	MspI	11.5	0.79	0.26	525
			9.6	0.21		

10	pYNZ156	MspI	11.5 9.6	0.79 0.21	0.26	525
11	pTB10.171	PvuII	8.0 6.5	0.65 0.35	0.48	731

The genetic map constructed under the assumption of a constant ratio of female/male genetic distance span approximately 106 cM in males and 268 cM in females. The gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of the adjacent loci are :

```
 42404:1          272:1          31257:1       10^8:1          824:1
 |       |       |       |       |       |       |       |       |       |       |
 | .10   | .09   | .10   | .03   | .07   | .09   | .10   | .11   | .08   | .17   |
10 ----- 8 ----- 4 ----- 5 ----- 1 ----- 2 ----- 6 -----11 ----- 3 ----- 7 ----- 9
 | .15   | .13   | .15   | .05   | .10   | .13   | .14   | .16   | .12   | .23   |
 |       |       |       |       |       |       |       |       |       |       |
           180:1          3:1          10^9:1        10^8:1         112420:1
```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11.2
21.1
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21.3
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22.2
22.3
23.1
23.2
23.3
24.1
24.2
24.3
25.1
25.2
25.3
26.1
26.2
26.3
Θ ♀ (%)
9
-----24
7
-----12
3
-----16
11
-----14
6
-----13
2
-----11
1
-----5
5
-----15
4
-----13
8
-----15
10
10

A PARTIAL PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 11

M. Leppert, P. O'Connell, Y. Nakamura, G.M. Lathrop, S. Maslen, M. Litt, P. Cartwright, J.-M. Lalouel and R. White.

A primary genetic map was constructed from data on 21 markers typed in 30-60 reference families (including 38 families of the CEPH reference panel). This map revises and extends that of White et al. (Nature 313:101-105, 1985).The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	(HBB) JW102	SinI	2.2	0.12	0.18	404
			1.8	0.88		
	JW151	HindIII	7.8	0.40	0.48	691
			7.1	0.60		
	JW151	HindIII	3.2	0.79	0.37	616
			2.9	0.21		
2	pINS-310(INS)	PvuII	VNTR >14 ALLELES 0.6-4.0KB		0.80	387
3	pTBB-2(HRAS1)	TaqI	VNTR >10 ALLELES 2.3-4.3KB		0.84	689
4	pPTH-LF(PTH)	PstI	2.7	0.64	0.52	515
			2.2	0.36		
5	pTT42(CALC1)	TaqI	8.5	0.33	0.31	505
			7.5	0.67		
6	pTHH26	PvuII	5.2	0.14	0.26	674
			3.2	0.86		
7	pSV2A1(APOA1)	TaqI	8.5	0.06	0.09	671
			4.6	0.94		
8	p3C7	MspI	5.7	0.70	0.50	395
			3.1	0.30		
9	LamL7(D11S29)	TaqI	13.9	0.23	0.35	657
			10.9	0.77		
10	pHBI18P2	PstI	5.0	0.25	0.33	703
			4.0	0.75		

11 Apolipo-(APOA4) protein AIV	APOA4	A1	0.89	0.22	616
		A2	0.10		
		A3	0.01		
		A4	0.01		
12 pMCMP1	MspI	2.4	0.48	0.36	629
		2.3	0.45		
		2.2	0.07		
13 pMCT128.1	MspI	2.9	0.52	0.60	636
		2.6	0.48		
14 pMCT117	MspI	3.5	0.15	0.27	419
		2.4	0.58		
		2.2	0.27		
15 pPGA(PGA)	BglII	7.0	0.32	0.39	773
		4.0	0.68		
16 p2-7-1D6	TaqI	6.4	0.23	0.40	675
		4.3	0.77		
17 pHBI59	MspI	4.3	0.37	0.47	481
		3.8	0.63		
18 pYNB3.12	MspI	2.8	0.55	0.63	474
		2.4	0.45		
		0.2	0.60		
19 pADJ762	MspI	2.1	0.15	0.25	669
		1.7	0.85		
	MspI	1.5	0.11	0.22	696
		1.3	0.89		
	TaqI	3.2	0.15	0.25	406
		3.9	0.85		
	BclI	7.0	0.57	0.38	399
		7.3	0.43		
20 Phage6-3	MspI	9.5	0.53	0.50	694
		3.9	0.47		
	MspI	2.8	0.35	0.71	634
		2.5	0.65		

The loci form two continuous linkage groups, one of 6 loci (37 cM in males and 24 cM in females) and the other of 14 loci (102 cM in males and 287 cM in females). Multilocus analysis with the LINKAGE programs, assuming a constant ratio of female/male genetic distance within each group, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

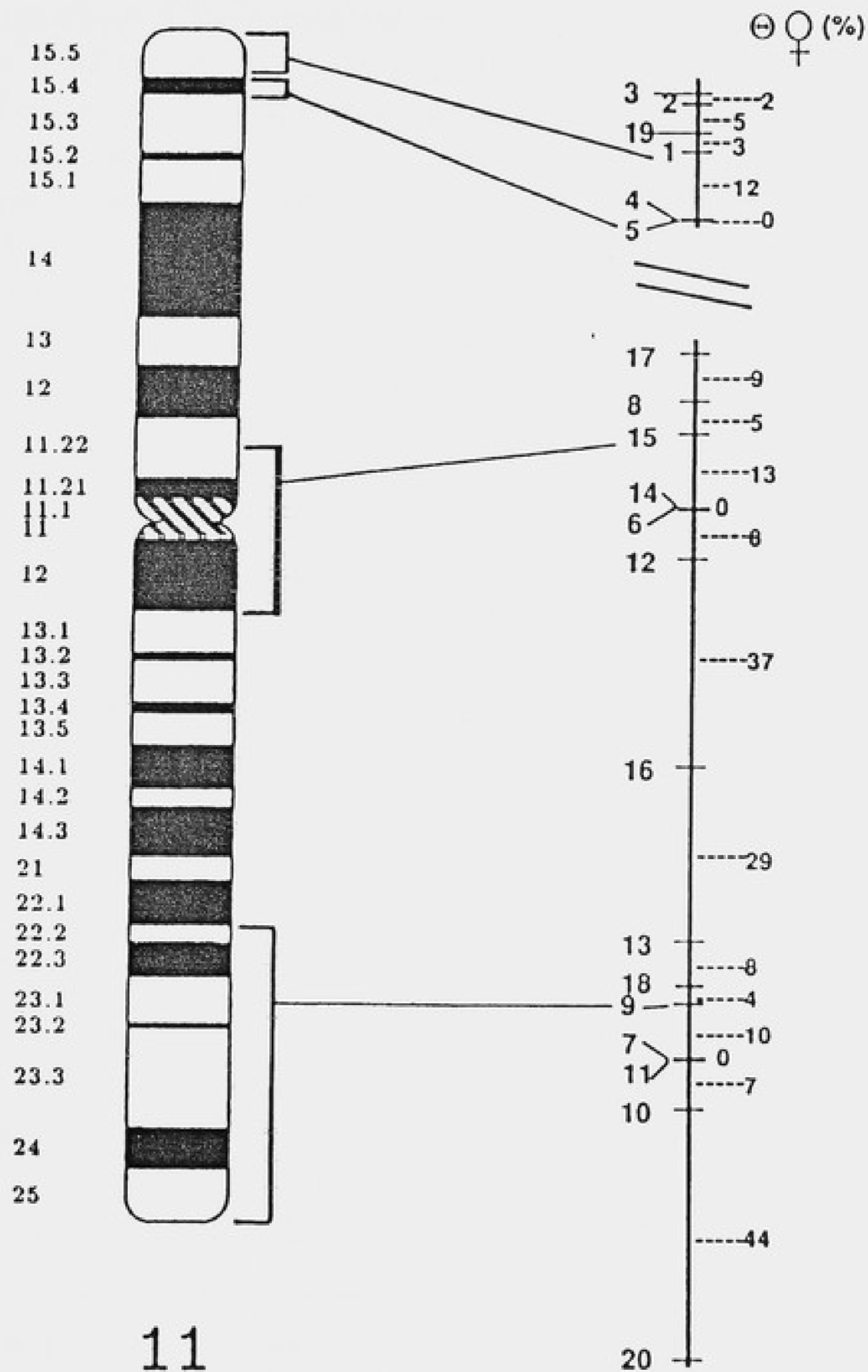
First group:

```
  1:1            10^11:1            483:1
|      |       |       |       |       |
| .00  | .17   | .04   | .07   | .04   |
4 ---- 5 ----- 1 ----- 19 ---- 2 ----- 3
  .00  | .12   | .03   | .05   | .02   |
       |       |       |       |       |
        10^38:1         10^28:1
```

Second group (brackets indicate loci have been haplotyped):

```
10^17:1              101877:1           436:1
|      |          |            |       |       |
| .27  | .03      .00     .04  | .02   | .01   | .13
20---- 10 ----(7 ----- 11)---- 9 ----- 18----- 13 ---- 16
  .44  | .07      .00     .10  | .04   | .08   | .29   |
       |          |            |       |       |       |
        40:1                    81:1            10^34:1
```

```
10^12:1           1:1             16:1
|       |       |       |       |       |       |
| .19   | .03   | .00   | .05   | .02   | .04   |
16 ---- 12 ---- 14 ---- 6 ----- 15----- 8 ----- 17
  .37   | .08   | .00   | .13   | .05   | .09   |
        |       |       |       |       |       |
         105:1           487:1           647:1
```


Θ ♀ (%)
15.5
15.4
15.3
15.2
15.1
14
13
12
11.22
11.21
11.1
11
12
13.1
13.2
13.3
13.4
13.5
14.1
14.2
14.3
21
22.1
22.2
22.3
23.1
23.2
23.3
24
25
11
3
2
19
1
4
5
2
5
3
12
0
17
8
15
14
6
12
16
13
18
9
7
11
10
20
9
5
13
0
8
37
29
8
4
10
0
7
44

SEX-SPECIFIC VARIATION IN HUMAN RECOMBINATION FREQUENCIES

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Investigation of linkage relationships among DNA markers from the short arm of human chromosome 11 has indicated differences in recombination frequencies between males and females in the interval from HBBC to HRAS1. A second, independent set of family data has been developed in order to establish the significance of the initial finding. Examination of the recombination frequencies in the interval from HBBC to PTH/CALC1 indicated a slight excess of recombination in female meioses that was significantly different from the male excess in the HBBC-HRAS1 interval. These ratios also differ strikingly from the female/male ration of map distances previously obtained for intervals on chromosome 13 (Leppert et al., Am. J. Hum. Genet. 39:425-437, 1986). These findings were obtained in the course of adding the genes for two major calcium-regulating hormones, parathyroid hormone (PTH) and calcitonin-1 (CALC1), to an existing genetic linkage map of a region of human chromosome 11p. A new five-locus linkage map, incorporating sex-specific recombination frequencies and providing strong support for gene order, has thus been developed, using the LINKAGE programs, for the loci PTH-CALC1, HBBC, D11S12, INS and HRAS1.

First Sample: 25 families

	HBBC	—	D11S12	—	HRAS1	K, f/m	X^2
Female		0.011		0.035		0.254	6.96
Male		0.040		0.125			

Second Sample: 34 families

	HBBC	—	D11S12	—	HRAS1	K, f/m	X^2
Female		0.028		0.069		0.209	9.90
Male		0.021		0.253			

Combined Samples: 59 families

	HBBC	—	D11S12	—	HRAS1	K, f/m	X^2
Female		0.016		0.055		0.289	13.26
Male		0.053		0.167			

AN EXTENDED MAP FOR HUMAN CHROMOSOME 12 HAS A DOMAIN OF INCREASED MALE RECOMBINATION

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We have prepared a primary genetic map for human chromosome 12, gathering data for 23 RFLP systems from 30-50 normal families with large sibships. The following loci were studied:

PROBE (LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1 p640 (KRAS2)	TaqI	5.7	0.76	0.32	400
		3.3	0.24		
2 p12-16 (D12S2)	EcoRI	9.7	0.89	0.22	396
		8.5	0.11		
3 pXP13 (EIA1)	TaqI	4.3	0.82	0.26	394
		3.7	0.18		
4 p9F11 (D12S4)	TaqI	8.0	0.64	0.59	391
		3.0	0.36		
5 pPRP (PRB1)	EcoRI-1	6.5	0.35	0.66	473
		6.3	0.48		
		6.1	0.07		
		6.3-6.3	0.01		
		6.5-6.1	0.04		
		6.3-6.1	0.01		
		----	0.06		
6 pPRP (PRB2)	EcoRI-2	4.6	0.11	0.33	494
		4.3	0.74		
		4.2	0.10		
		4.0	0.04		
		3.8	0.01		
7 pPRP (PRB3)	EcoRI-3	4.6	0.02	0.14	526
		4.3	0.03		
		4.1	0.93		
		4.0	0.02		

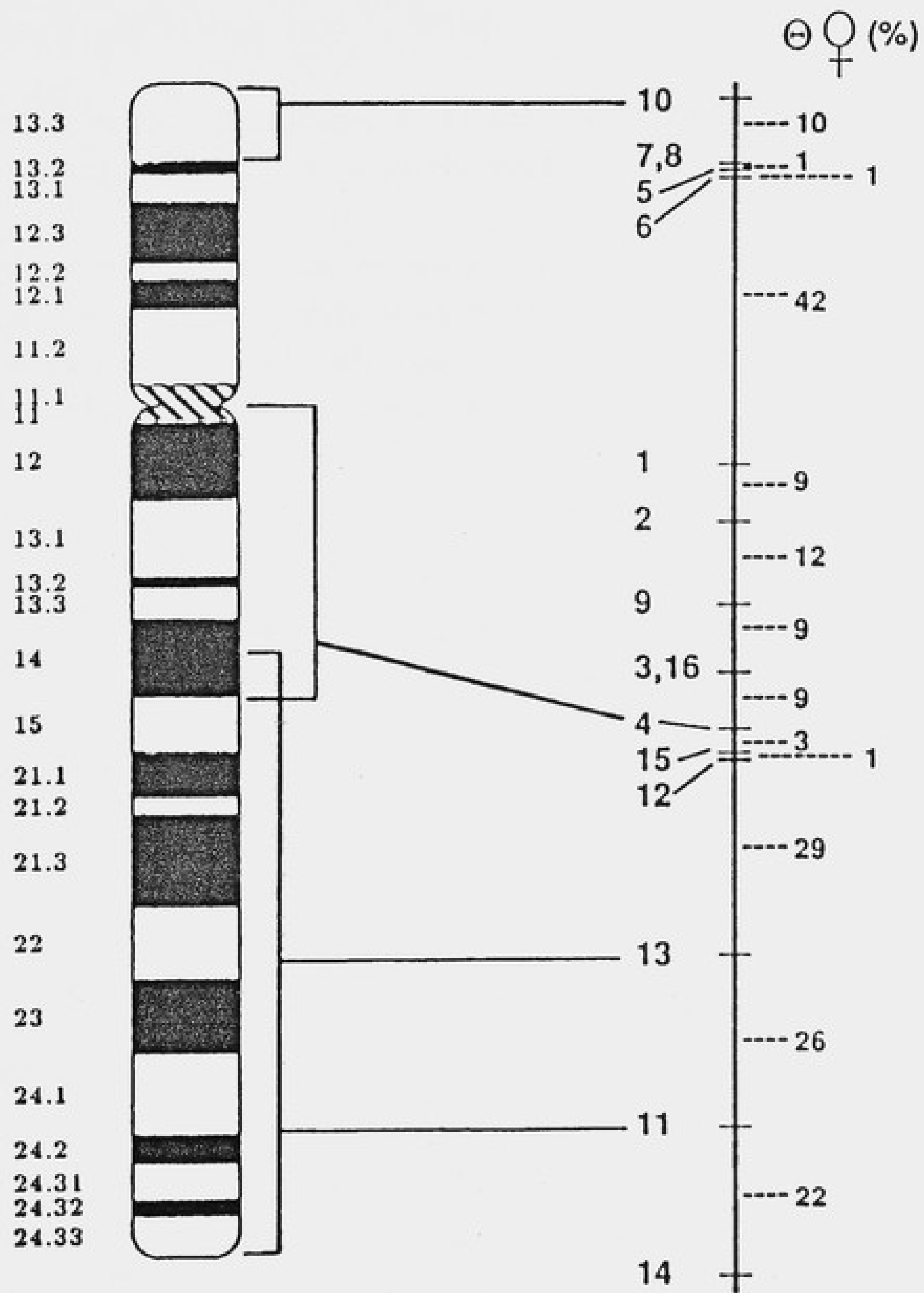
PROBE (LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
8 pPRP (PRB4)	EcoRI-4	3.6	0.25	0.37	517
		3.5	0.63		
		3.3	0.13		
9 cosHcol2A (COL2A1)	HindIII	14.0	0.56	0.70	285
		7.0	0.44		
10 p\SV2 (VWF)	BglII	9.7	0.64	0.40	374
		7.1	0.36		
11 pDL32B (D12S7)	TaqI	6.5	0.08	0.66	496
		5.1	0.29		
		4.1-2.7	0.55		
		2.7-2.4	0.07		
12 pl-7 (D12S6)	MspI	4.4	0.33	0.63	429
		3.6	0.67		
pl-11 (D12S6)	EcoRI	4.9	0.89		
		3.7	0.11		
13 p7G11 (D12S8)	MspI	6.0	0.81	0.62	447
		4.3	0.19		
	TaqI-1	8.0	0.96		
		5.0	0.04		
	TaqI-2	4.0	0.60		
		3.0	0.40		
14 pPH72 (PAH)	MspI	18.0	0.38	0.65	386
		16.0	0.63		
	HindIII	3.3	0.17		
		3.2	0.63		
		3.1	0.20		
15 pYNH15	MspI	4.0	0.17	0.52	598
		3.2	0.63		
		2.6	0.20		
16 pCMM1.2	TaqI	3.0	0.15	0.28	669
		2.8	0.85		

Multipoint linkage analysis with the LINKAGE programs, allowing female recombination estimates to vary from those of males by a constant ratio, has ordered these markers into a continuous genetic map of 92 cM in males and 180 cM in females (male recombination estimates are above the map, female below):

$$14 \ \frac{.09}{.22}\ 11 \ \frac{.12}{.26}\ 13 \ \frac{.14}{.29}\ 12 \ \frac{.00}{.01}\ 15 \ \frac{.02}{.03}\ 4 \ \frac{.02}{.09}\ (3,\ 16) \ \frac{.04}{.09}\ 9 \ \frac{.05}{.12}\ 2 \ \frac{.04}{.09}\ 1$$

$$1 \ \overset{.20}{\underset{.42}{—\ X\ —}}\ 6 \ \frac{.03}{.01}\ 5 \ \frac{.02}{.01}\ (7,\ 8) \ \frac{.23}{.10}\ 10$$

The order for those markers in parentheses is provisional. The chromosome 12 genetic map shows a female/male recombination ratio of 3.17 for the long arm and proximal short arm, 2.9 between KRAS2 and PRB2, but on the distal portion of the short arm (at the X on the above order), this ratio falls to 0.39, indicating that in males recombination rates are higher in this domain of chromosome 12.



12

EXTENSION OF A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 13

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+Ludwig Institute for Cancer Research, McGill Univ., Montreal, Canada

A primary genetic linkage map of chromosome 13 was constructed from data on 16 markers typed in 30-60 reference families (including 38 families of the CEPH reference panel). This map revises and extends that of Leppert et al. (Am J Hum Genet 39:425, 1986).The following loci were studied:

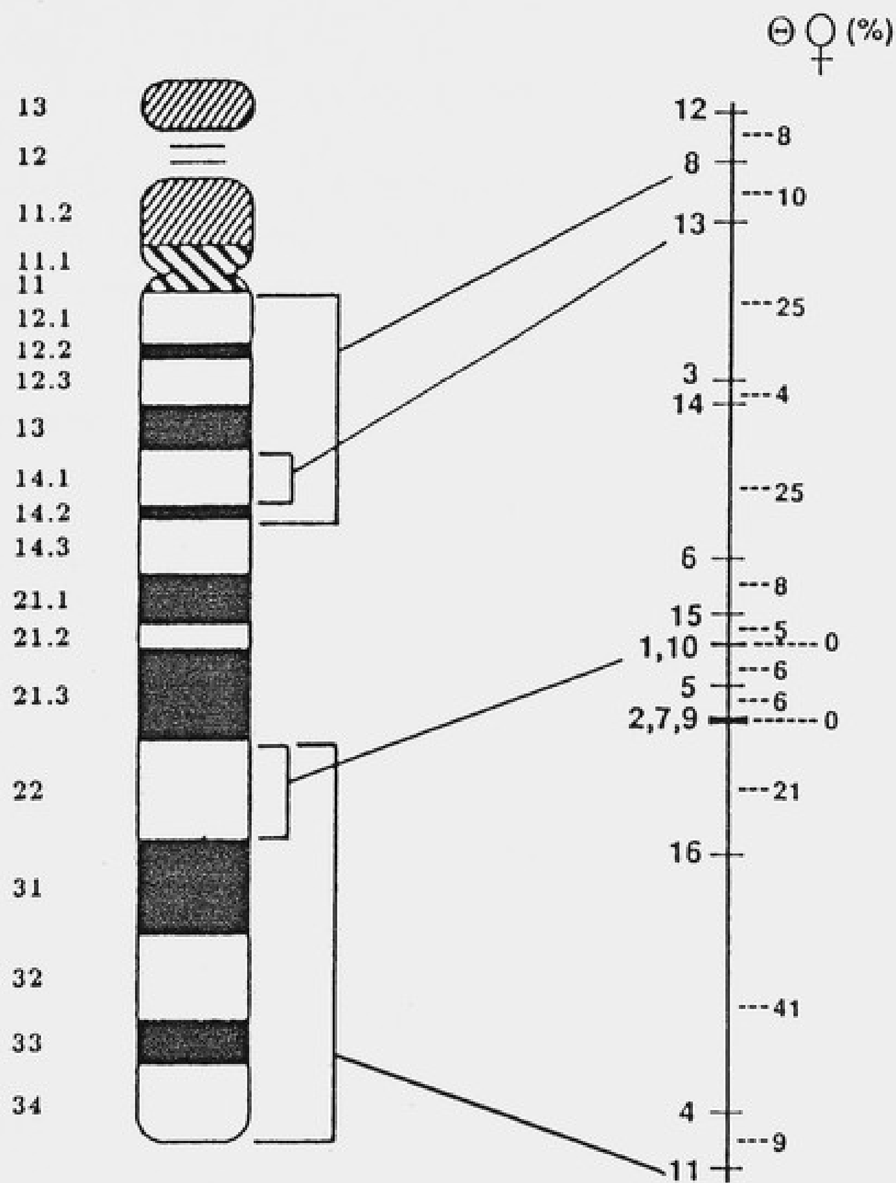
	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pHU26(D13S7)	BglII	7.8	0.82	0.30	398
			9.6	0.18		
2	p1E8(D13S4)	MspI	7.4	0.51	0.43	404
			10.1	0.49		
3	pTHI62	BglII	VNTR		0.69	604
			>4 ALLELES			
			6.0-10.0KB			
4	S54(COL4A1)	TaqI	2.4	0.18	0.25	439
			1.9	0.82		
5	WC64	BglII	5.6	0.38	0.49	729
			5.4	0.62		
6	WC25	MspI	4.2	0.23	0.46	721
			2.4	0.72		
			2.2	0.05		
7	WC47	EcoRI	8.0	0.17	0.27	700
			7.0	0.83		
8	p7F12(D13S1)	MspI	4.3	0.52	0.55	400
			3.4,0.9	0.48		
		TaqI	6.9	0.27	0.35	404
			5.9,1.0	0.73		
		BclI	1.4	0.29	0.37	229
			1.2,0.2	0.71		

9	pHUB8(D13S5)	EcoRI	13.3	0.77	0.34	395
			4.7	0.33		
		HindIII	10.8	0.16	0.23	400
			8.5	0.84		
10	p9D11(D13S2)	MspI	15.0	0.61	0.47	397
			11.0	0.02		
			10.5	0.36		
		TaqI	5.6	0.18	0.28	406
			3.7	0.82		
11	p9A7(D13S3)	MspI	1.5	0.36	0.38	403
			1.0	0.64		
		HindIII	3.2	0.62	0.42	392
			0.9	0.38		
12	pHU10(D13S6)	XmnI	8.6	0.69	0.45	393
			7.0	0.31		
		EcoRI	12.0	0.83	0.33	226
			9.0	0.17		
13	EsteraseD(ESD)	ESD	A1	0.92	0.16	621
			A2	0.08		
14	p7D2(D13S10)	TaqI	12.0	0.21	0.38	406
			11.0	0.79		
15	WC83	TaqI	8.5	0.59	0.52	703
			2.4	0.41		
16	WC95	EcoRI	2.4	0.76	0.32	515
			1.8	0.24		

The 16 loci formed a continuous linkage map spanning approximately 80 cM in males and 243 cM in females. Multilocus analysis with the LINKAGE programs gave the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci (brackets indicate the loci were haplotyped) :

```
  28:1           10^12:1             10^23:1           306:1
|       |      |       |      |       |      |           |
| .03   | .03  | .10   | .02  | .10   | .03  | .02      .00      .02
12 ---- 8 ---- 13 ---- 3 ---- 14 ---- 6 ---- 15 ---- (1 ---- 10) ---- 5
  .08   | .10  | .25   | .04  | .25   | .08  | .05      .00      .06  |
        |      |       |      |       |      |           |            |
         20:1           3:1            1724:1                   10^7:1

   4663:1                       10^6:1
|             |                |       |
| .02     .00 | .00      .08   | .22   |  .03
5 ---- (2 ---- 7 ---- 9) ----- 16 ---- 4 ---- 11
  .06     .00 | .00      .21   | .41   |  .09 |
              |                |       |      |
                  10^19:1                1:1
```



13
12
11.2
11.1
11
12.1
12.2
12.3
13
14.1
14.2
14.3
21.1
21.2
21.3
22
31
32
33
34
Θ ♀ (%)
12
8
13
3
14
6
15
1,10
5
2,7,9
16
4
11
8
10
25
4
25
8
5
0
6
6
0
21
41
9
13

A PRIMARY GENETIC LINKAGE MAP OF DISTAL CHROMOSOME 14q

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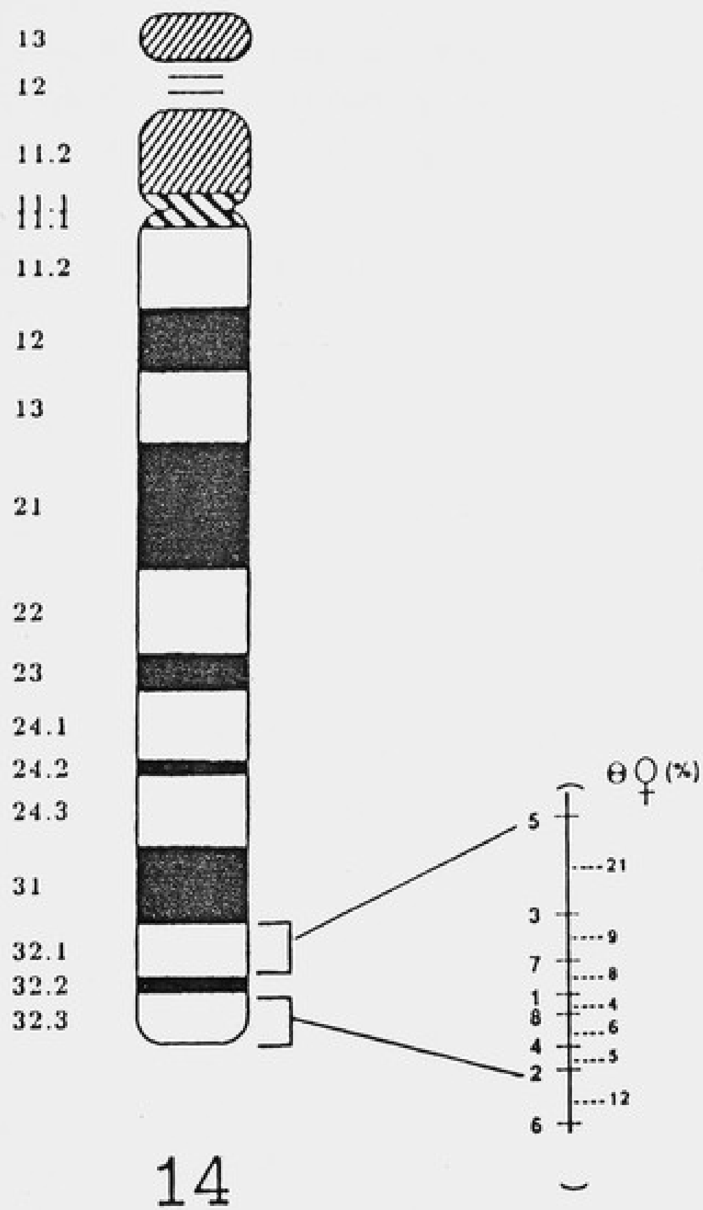
A primary genetic linkage map of chromosome 14 was constructed from data on 8 markers typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pAW101(D14S1)	EcoRI	VNTR >10 ALLELES 15.0-25.0KB		0.64	365
2	p3.4(GM)	BglII	VNTR >5 ALLELES 2.9-3.7KB		0.83	530
3	cMLJ14	RsaI	VNTR >20 ALLELES 4.0-8.0KB		0.83	704
4	pTHH37	TaqI	3.0 2.3 2.1	0.59 0.02 0.39	0.48	635
5	Alpha-1 antitrysin	PI	A1 A2 A3 A4 A5	0.67 0.14 0.11 0.08 >0.01	0.59	605
6	pHHH208	BamHI	6.5 5.8 4.0	0.45 0.47 0.08	0.61	623
7	pMHZ9	EcoRI	4.0 2.7	0.91 0.09	0.16	789
8	pEFZ18.2	TaqI	4.5 3.5	0.32 0.68	0.51	755

The eight loci form a continuous linkage map spanning approximately 58 cM in males and 75 cM in females. Multilocus analysis with the LINKAGE programs, under the assumption of a constant ratio of female/male genetic distance, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
10^12:1         10^13:1           10^10:1          10^30:1
|      |       |       |       |       |       |       |
| .10  | .04   | .05   | .03   | .06   | .07   | .17   |
6 ---- 2------ 4 ---- 8 ---- 1 ----- 7 ---- 3 ---- 5
  .12  | .05   | .06   | .04   | .08   | .09   | .21
       |       |       |       |       |       |
       1523:1          124:1           5:1
```


13
12
11.2
11.1
11.1
11.2
12
13
21
22
23
24.1
24.2
24.3
31
32.1
32.2
32.3
14
Θ ♀ (%)
5
21
3
9
7
8
1
4
8
6
4
5
2
12
6

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 15

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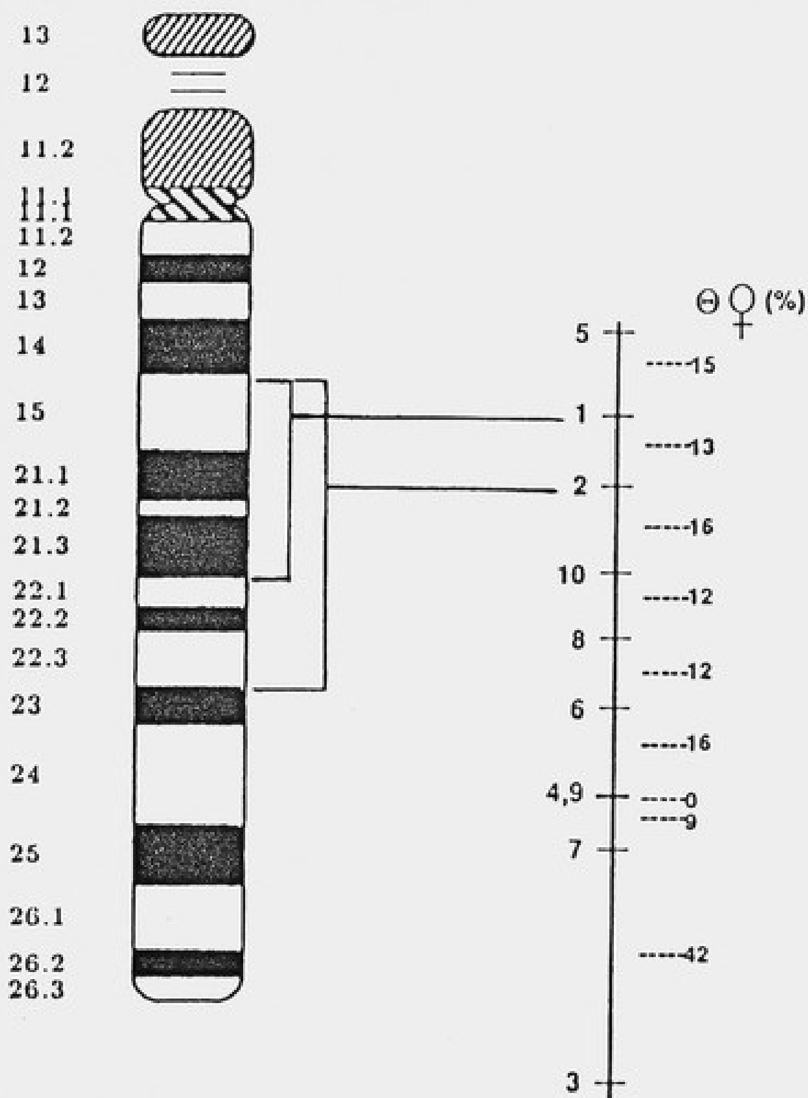
A primary genetic linkage map of chromosome 15 was constructed from data on 10 markers typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pMS1-14(D15S1)	MspI	12.0	0.43	0.65	584
			4.5	0.57		
2	pDP151(D15S2)	EcoRI	11.0	0.22	0.33	269
			9.0	0.78		
3	pJU201(D15S3)	EcoRI	1.9	0.43	0.47	580
			1.8	0.57		
4	pMCA1-1	PvuII	5.7	0.77	0.47	321
			5.2	0.23		
5	pTHH114	RsaI	2.6	0.62	0.44	642
			2.3	0.38		
6	pYNZ90.1	BamHI	6.0	0.76	0.33	721
			5.8	0.24		
7	pTHH55	MspI	4.6	0.33	0.45	586
			3.3	0.67		
8	pEKZ104	MspI	4.0	0.47	0.50	569
			3.7	0.53		
9	pMCT46.2	PvuII	5.9	0.87	0.26	665
			5.3	0.13		
10	pEFD49.3	MspI	3.0	0.39	0.38	740
			2.1	0.60		
			2.0	0.01		

The 10 loci formed a continuous linkage map spanning approximately 75 cM in males and 200 cM in females. Multilocus analysis with the LINKAGE programs, under the assumption of a constant ratio of female/male genetic distance, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
 10^5:1          67:1           32:1          1.0:1         10^18:1
|      |      |      |       |      |      |      |      |      |
| .06  | .05  | .07  | .05   | .05  | .07  | .00  | .03  | .25  |
5 ---- 1 ---- 2 ---- 10 ---- 8 ---- 6 ---- 9 ---- 4 ---- 7 ---- 3
  .15  | .13  | .16  | .12   | .12  | .16  | .00  | .09  | .42
       |      |      |       |      |      |      |      |
          4:1           10^5:1         10^22:1        10^12:1
```


13
12
11.2
11.1
11.1
11.2
12
13
14
15
21.1
21.2
21.3
22.1
22.2
22.3
23
24
25
26.1
26.2
26.3
15
Θ ♀ (%)
5
-----15
1
-----13
2
-----16
10
-----12
8
-----12
6
-----16
4,9
-----0
-----9
7
-----42
3

TWO GENETIC LINKAGE GROUPS ON CHROMOSOME 16

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[+]Oregon Health Sciences University, Portland, USA

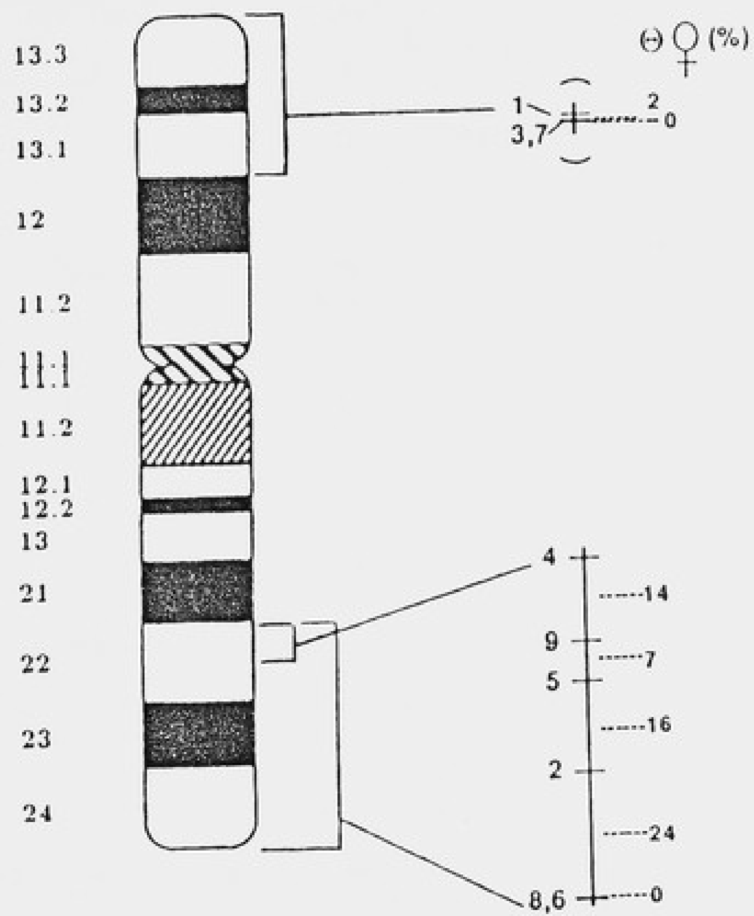
A primary genetic linkage map of chromosome 16 was constructed from data on 9 markers typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	Hag1(HBZP1)	HinfI	VNTR 4 ALLELES 1.6-2.6		0.41	508
2	pLC9	MspI	3.0 2.7	0.72 0.28	0.42	493
3	cEKDA2	RsaI	VNTR 4 ALLELES 2.5-3.5KB		0.23	778
4	Haptoglobin(HP)	HP	A1 A2	0.41 0.59	0.54	597
5	Phage8-9(D16S20)	BglII	10.0 6.0,4.0	0.65 0.35	0.48	703
6	p79-2-23(D16S7)	RsaI	VNTR >10 ALLELES 3.0-8.0KB		0.83	677
7	pCMM65	EcoRI	3.3 2.6	0.37 0.63	0.39	770
8	pHuAPRT(APRT)	TaqI	3.0 2.5	0.28 0.72	0.45	360
		BglII	15.0 13.0	0.05 0.95	0.10	55
9	pEKXp3B(CTRB)	PvuII	4.4 3.5	0.20 0.80	0.32	657
		PvuII	3.0 2.3 2.1	0.74 0.20 0.06	0.38	655

The loci fall into two linkage groups, one 56 cM in males and 76 cM in females, and the other 24 cM in males and 2 cM in females. Multilocus analysis with the LINKAGE programs, under the generalized sex difference model, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
 19:1            93:1              19:1
|       |       |       |         |       |
| .04   | .21   | .00   | .18     | .03   |
8 ---- 6----- 2 ---- 5 ---- 9 ---- 4
  .00   | .24   | .16   | .07     | .14
        |       |       |         |
         10^38           10^10:1
```

```
 2280:1
|       |
| .12   | .09
1 ---- 7----- 3
  .02   | .00   |
        |       |
         2:1
```



13.3
13.2
13.1
12
11.2
11.1
11.1
11.2
12.1
12.2
13
21
22
23
24
Θ ♀ (%)
1
3,7
2
0
4
14
9
7
5
16
2
24
8,6
0
16

A PRIMARY GENETIC MAP OF CHROMOSOME 17

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Howard Hughes Medical Insitute, Salt Lake City, Utah USA

Twenty-one markers were characterized in 40-60 families (including 38 from CEPH), yielding a continuous genetic map of chromosome 17. The following markers were studied:

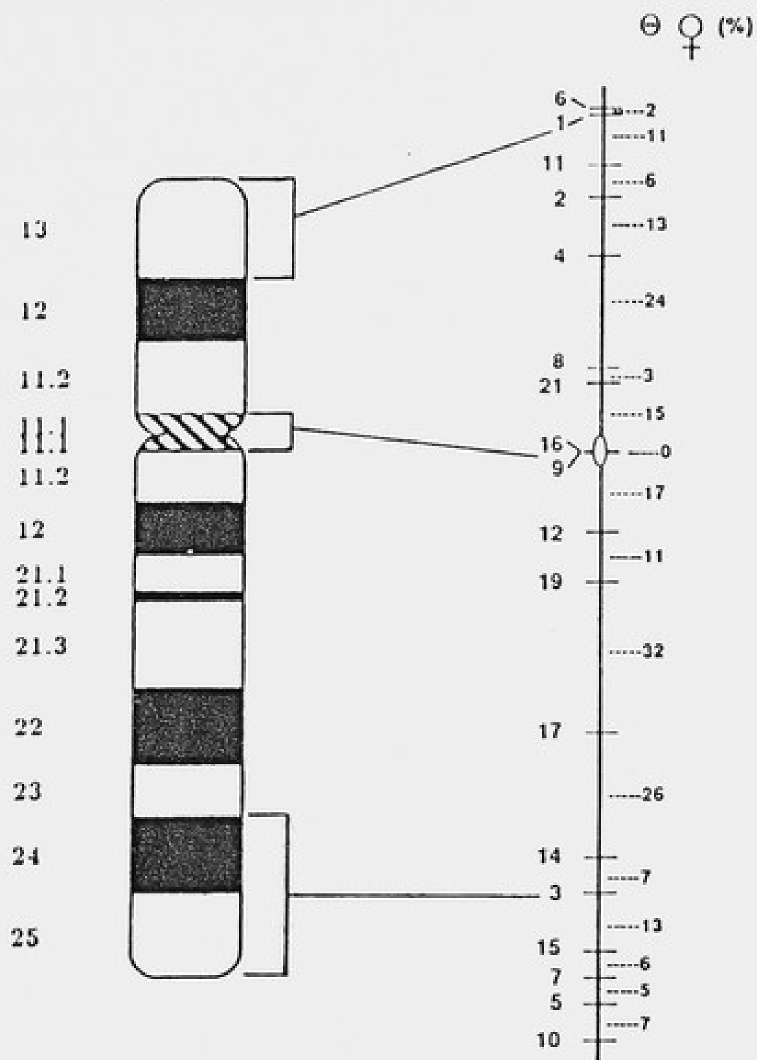
PROBE (LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER OF INDIVIDUALS TYPED
1 pYNZ22	RsaI	VNTR >6 alleles 1.3-2.3 KB		0.83	703
2 pHF12-1 (D17S1)	MspI	2.9 2.1	0.78 0.22	0.40	343
3 pTHH59	TaqI	VNTR >6 alleles 3.0-4.0 KB		0.71	669
4 p10.5 (MYH2)	HindIII	5.3 4.9	0.26 0.74	0.38	626
5 pRMU-3	TaqI	VNTR >4 alleles 3.2-3.8 KB		0.65	651
6 pYNH37-3	TaqI	VNTR >5 alleles 2.0-4.0 KB		0.65	654
7 pAC256	PvuII	VNTR >6 alleles 3 - 7 KB		0.73	646
8 pABL10-41	PvuII	2.7 2.6	0.17 0.83	0.29	658
9 pHHH202	RsaI	2.5 1.9	0.55 0.45	0.49	688
10 pRMU1	PstI	2.0 1.0	0.75 0.25	0.32	540

11	pMCT35.1	MspI	2.4 1.8	0.75 0.25	0.43	735
12	pHHH152	BamHI	10.5 9.6	0.39 0.61	0.45	572
14	pHtK9 (TK1)	TaqI	4.3 1.3	0.54 0.46	0.60	588
15	cEFD52	PvuII	VNTR >10 alleles 3-10 KB		0.83	594
16	p3.6 (D17Z1)	EcoRI	2.0 1.4	0.81 0.19	0.28	465
17	LEW101	MspI	15.0 7.0	0.63 0.37	0.47	541
19	LEW102	TaqI	8.0 5.5	0.34 0.66	0.47	627
21	pYNM67	TaqI	3.8 3.2	0.69 0.31	0.41	593
	1pYNM67	RsaI	3.0 1.3	0.09 0.91	0.18	544
	2pYNM67	RsaI	1.8 0.8	0.18 0.82	0.31	490

The genetic map generated with these loci spans 294 cM in males and 251 cM in females. Multilocus analysis with the LINKAGE program under the assumption of constant ratio of female/male genetic distance, yields the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
 365:1          3463:1          10^14:1          10^7:1
|       |       |       |       |       |       |       |       |
| .02   | .11   | .06   | .14   | .24   | .03   | .15   | .00   |
6 ----- 1 -----11 ----- 2 ----- 4 ----- 8 -----21 -----16 ----- 9
| .02   | .11   | .06   | .13   | .24   | .03   | .15   | .00   |
|       |       |       |       |       |       |       |       |
        10^38:1         2893:1          72:1
```

```
        23:1            102:1           10^38:1         597195:1
|       |       |       |       |       |       |       |       |       |
| .18   | .12   | .33   | .27   | .07   | .13   | .06   | .05   | .07   |
9 -----12 -----19 -----17 -----14 ----- 3 -----15 ----- 7 ----- 5 -----10
| .17   | .11   | .32   | .26   | .07   | .13   | .06   | .05   | .07   |
|       |       |       |       |       |       |       |       |       |
 10^6:1         10^10:1         47:1            10^23:1         282095:1
```



13
12
11.2
11.1
11.1
11.2
12
21.1
21.2
21.3
22
23
24
25
17
Θ ♀ (%)
6
1
11
2
4
8
21
16
9
12
19
17
14
3
15
7
5
10
2
11
6
13
24
3
15
0
17
11
32
26
7
13
6
5
7

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 18

P. O'Connell, G.M. Lathrop, M. Leppert, Y. Nakamura, P. Cartwright, J.-M. Lalouel, and R. White

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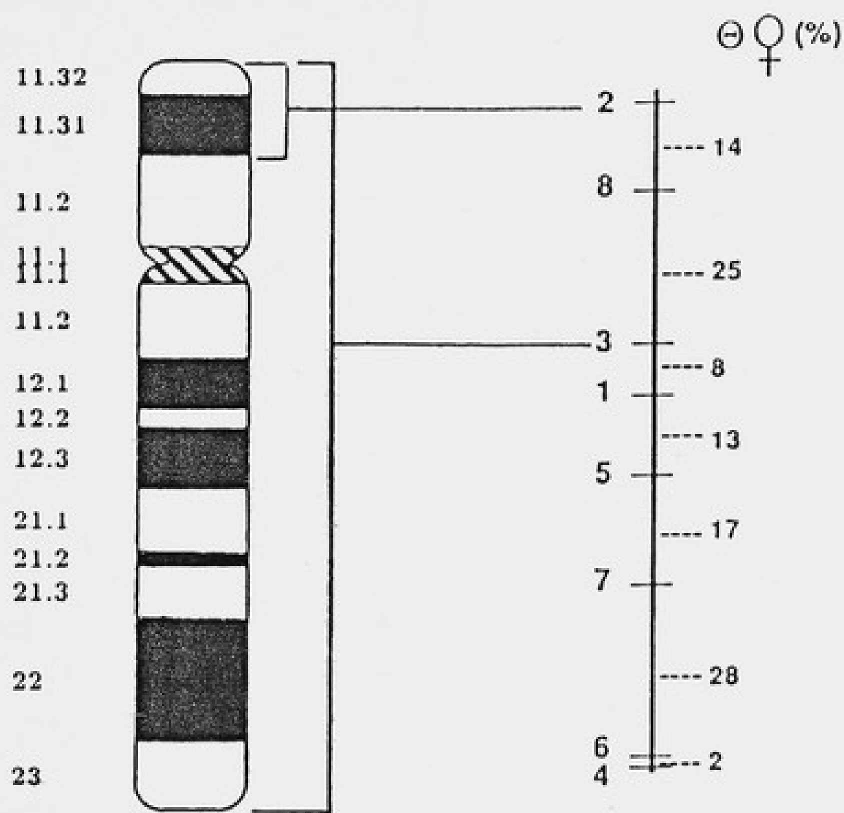
A primary genetic linkage map of chromosome 18 was constructed from data on 8 markers typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	pL2.7(D17S3)	PstI	10.0 7.7	0.23 0.77	0.41	448
2	B74(D18S3)	MspI	4.8 1.7	0.50 0.50	0.41	641
3	pHF12-62(D18S1)	TaqI	6.0 2.0	0.47 0.53	0.58	586
4	pMS1-3	PstI	4.4 3.4	0.55 0.45	0.49	610
5	Kidd(JK)	JK	A1 A2	0.51 0.49	0.50	632
6	OS-4	TaqI	7.6 6.0	0.81 0.19	0.33	648
7	EFZ10	PvuII	VNTR 4 ALLELES 3.5-5.0KB		0.70	586
8	pHHH163	PvuII	4.7 2.8	0.45 0.55	0.38	649

The eight loci form a continuous linkage map spanning approximately 91 cM in males and 139 cM in females. PL2.7 shows tight linkage to the chromosome 18 linkage group despite its designation as D17S3 (HGM 8). Multilocus analysis with the LINKAGE programs, assuming a constant ratio of female/male genetic distance, gives the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
6932:1          2753:1          54:1           1.02:1
|       |       |       |       |       |       |       |
| .10   | .18   | .05   | .09   | .12   | .21   | .01   |
2 ----- 8 ----- 3 ----- 1 ----- 5 ----- 7 ----- 6 ----- 4
  .14   | .25   | .08   | .13   | .17   | .28   | .02
        |       |       |       |       |       |
        10^5:1          28:1            10^29:1
```



18

A PRIMARY GENETIC LINKAGE MAP OF CHROMOSOME 19

Y. Nakamura, M. Leppert, G.M. Lathrop, P. O'Connell, P. Cartwright, J.-M. Lalouel and R. White.

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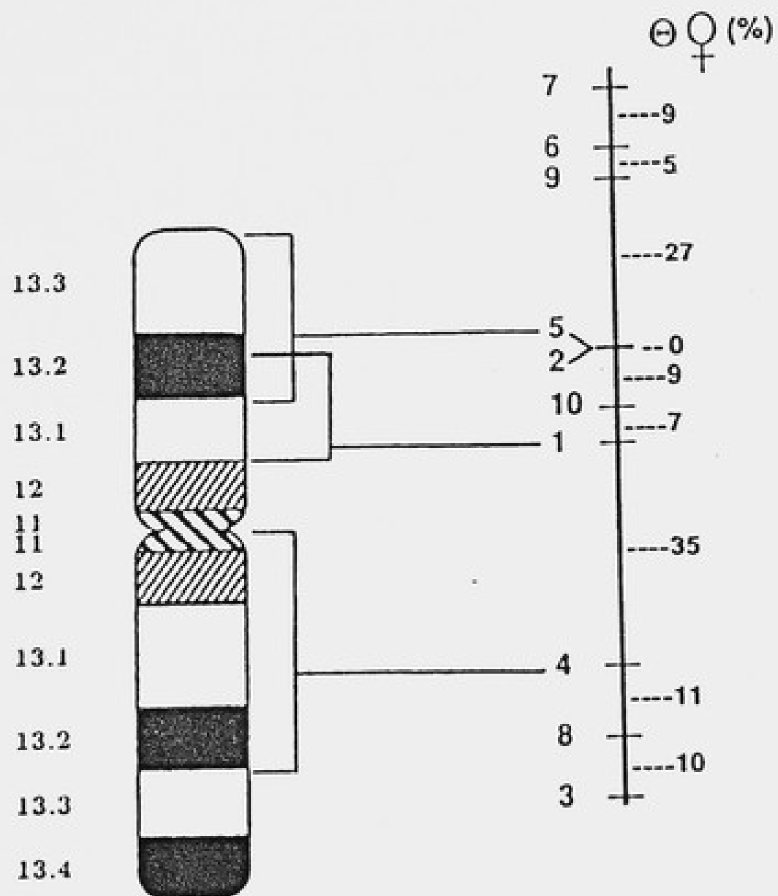
A primary genetic linkage map of chromosome 19 was constructed from data on 10 markers typed in 40-60 reference families (including 38 families of the CEPH reference panel). The following loci were studied:

	PROBE(LOCUS)	ENZYME	ALLELE SIZE (KB)	ALLELE FREQUENCIES	OBSERVED HETERO-ZYGOSITY	NUMBER INDIV. TYPED
1	HHI(LDLR)	PvuII	18.6 16.0,2.6	0.72 0.28	0.40	674
2	Lewis(LE)	LE	A1 A2	0.38 0.62	0.68	108
3	ABH secretion(SE)	SE	A1 A2	0.29 0.71	0.58	276
4	pCII-711(APOC2)	TaqI	3.9 3.5	0.47 0.53	0.51	670
5	12.1p1.6(INSR)	BglII	12.0 10.0	0.77 0.23	0.32	618
6	pJCZ3.1	HinfI	VNTR >10 ALLELES 1.5-4.0KB		0.80	706
7	cMCOB5	PstI	VNTR 5 ALLELES 5.0-10.0KB		0.64	710
8	pEFD4.2	PvuII	2.4 2.2	0.62 0.38	0.44	645

9	cMCOB19	BglII	VNTR 5 ALLELES 5.0-8.0KB		0.70	604
10	pMCT6	BamHI	VNTR 5 ALLELES 8.5-15.0KB		0.53	336
		BamHI	5.5 5.3	0.90 0.10	0.19	507
		BamHI	2.3 2.5	0.36 0.64	0.23	301

The 10 loci form a continuous linkage map spanning approximately 152 cM in males and females. Multilocus analysis with the LINKAGE programs, under the assumption of a constant female/male genetic distance ratio, gave the following gene order, male (above map) and female (below map) recombination fractions, and odds for the inversion of adjacent loci:

```
119:1          10^35:1         10^5:1          10^20:1         10^22:1
|      |      |      |       |      |      |      |      |      |
| .10  | .11  | .35  | .07   | .09  | .00  | .26  | .05  | .08  |
3 ---- 8 ---- 4 ---- 1 ---- 10 ---- 5 ---- 2 ---- 9 ---- 6 ---- 7
  .10  | .11  | .35  | .07   | .09  | .00  | .27  | .05  | .09
       |      |      |       |      |      |      |      |
       99:1          58:1           1:1         10^12:1
```


Θ ♀ (%)
7
----9
6
9
----5
----27
5
2
--0
----9
10
----7
1
----35
4
----11
8
----10
3
13.3
13.2
13.1
12
11
11
12
13.1
13.2
13.3
13.4
19

DISTRIBUTION OF SYSTEMS BY CHROMOSOME

DATE : 28-AUG-1987 ... TIME : 17:17:17.15

sys	probe	enzyme	ch	region	#al	het.
313	1pEKZ101.2	TaqI	0b	100.0100.0	2	0.54
378	cMCOC37	BglII	0b	100.0100.0	6	0.70
327	pEFD70.2	PvuII	0b	100.0100.0	4	0.52
385	pTH-58	MspI	0b	100.0100.0	2	0.47
379	pHHH232	PvuII	0b	100.0100.0	2	0.52
264	pCMM12.1	TaqI	0b	100.0100.0	4	0.58
16	p7A9	TaqI	0b	100.0100.0	2	0.00
23	p9F4	EcoRV	0b	100.0100.0	2	0.36
15	p7A9	MspI	0b	100.0100.0	3	0.00
314	pEFD139.1	PstI	0b	100.0100.0	8	0.78
78	730	TaqI	0b	100.0100.0	2	0.12
140	KM	KM	0p	100.0100.0	2	0.31
371	cEW7.20	MspI	0b	100.0100.0	5	0.54
292	pMCT46.1	BglII	0b	100.0100.0	2	0.33
392	pL1.31	BamHI	0b	100.0100.0	5	0.48
459	pCMM86	HinfI	0b	100.0100.0	8	0.80
447	pMHZ17	TaqI	0b	100.0100.0	2	0.25
417	pEFD19.2	MspI	0b	100.0100.0	2	0.04
384	pYNA2.2	MspI	0b	100.0100.0	3	0.53
377	pMCT96.2	HinfI	0b	100.0100.0	4	0.48
451	cYNA13	MspI	0b	100.0100.0	8	0.96
276	MLZ7.5	EcoRI	0b	100.0100.0	2	0.44
359	pEFD11.2	MspI	0b	100.0100.0	3	0.48
475	cMC5.2	TaqI	0b	100.0100.0	2	0.83
469	cMHZ47	MspI	0b	100.0100.0	7	0.78
453	pKKA40	PvuII	0b	100.0100.0	3	0.45
280	pTHH58	HindIII	0b	100.0100.0	2	0.53
181	pHHH129	TaqI	0b	100.0100.0	3	0.63
458	cYNA12	MspI	0b	100.0100.0	5	0.63
446	pRMR6	TaqI	0b	100.0100.0	2	0.52
465	pMCT129	PvuII	0b	100.0100.0	2	0.49
409	pJCZ29	BglII	0b	100.0100.0	2	0.45
433	pJCZ67	MspI	0b	100.0100.0	6	0.71
456	1cMCOD13	PvuII	0b	100.0100.0	6	0.80
316	2pEKZ101.2	TaqI	0b	100.0100.0	2	0.71
381	pEFD52.1	TaqI	0b	100.0100.0	2	0.32
342	pYNA23.1	HinfI	0b	100.0100.0	4	0.28
455	WC66	BamHI	0b	100.0100.0	2	0.69
461	pMCOB29	MspI	0b	100.0100.0	2	0.31
380	pYNH20	HindIII	0b	100.0100.0	2	0.49
288	EFD64.2	RsaI	0b	100.0100.0	6	0.80
297	MLJ102.1	BglII	0b	100.0100.0	2	0.36
445	pMHZ7	TaqI	0b	100.0100.0	2	0.26
463	2pHHH172	MspI	0b	100.0100.0	2	0.19
364	pHHH160	TaqI	0b	100.0100.0	3	0.48
452	pRMR53	BamHI	0b	100.0100.0	2	0.24
442	pMCOC12	MspI	0b	100.0100.0	6	0.39
398	pCMI40	PvuII	0b	100.0100.0	4	0.46
286	pEFD75	TaqI	0b	100.0100.0	6	0.60
466	pCMM62	HindIII	0b	100.0100.0	2	0.38
284	pMHZ15	MspI	0b	100.0100.0	2	0.54
470	pCMM6	PstI	0b	100.0100.0	8	0.87
405	pJCZ67	RsaI	0b	100.0100.0	6	0.78
328	pEFD134.7	MspI	0b	100.0100.0	4	0.71
464	p2.1	HindIII	0b	100.0100.0	2	0.39
303	pMCT58	PvuII	0b	100.0100.0	6	0.67
304	pMCT15	MspI	0b	100.0100.0	4	0.49
413	1pEFD64.1	PvuII	0b	100.0100.0	8	0.81
471	pCMM17.4	PvuII	0b	100.0100.0	2	0.30
282	pMCT122.2	TaqI	0b	100.0100.0	2	0.27
317	pMCT106	HinfI	0b	100.0100.0	3	0.11
155	pTHI54	PvuII	1b	100.0100.0	2	0.46
194	Duffy	Duf	1b	21.0 23.0	2	0.49
322	pHBI40	MspI	1b	100.0100.0	2	0.37
163	pL1.22	BglII	1b	100.0100.0	2	0.37
82	pYNZ2	TaqI	1b	100.0100.0	3	0.60
325	pHHH106	MspI	1b	100.0100.0	2	0.53
209	pTHH18.1	MspI	1b	100.0100.0	2	0.40
262	pHHH119	MspI	1b	100.0100.0	2	0.15
144	FXIIIB	FXIIIB	1b	100.0100.0	4	0.45
234	pHHH212	PvuII	1b	100.0100.0	2	0.41
241	AP8	MspI	1b	100.0100.0	2	0.35
110	EKH7.4	TaqI	1b	100.0100.0	2	0.53
125	pYNZ23	MspI	1b	100.0100.0	2	0.38
87	pMLAJ1	HinfI	1b	100.0100.0	5	0.65
270	pCMM8.1	MspI	1b	100.0100.0	2	0.40
346	pMHZ5	MspI	1b	100.0100.0	2	0.17
430	pCMM8	EcoRI	1p	100.0100.0	3	0.59
162	NBC6	BglII	1p	22.1 22.1	2	0.35
200	Rh	Rh	1p	36.2 34.0	8	0.60
382	pEFD53.2	TaqI	1p	100.0100.0	2	0.42
146	PGM	PGM	1p	22.1 22.1	4	0.58
347	pEFZ13	MspI	1p	100.0100.0	2	0.52
235	pMCR3	EcoRI	1p	100.0100.0	2	0.36
343	pMHZ14	BamHI	1p	100.0100.0	2	0.47
260	AT3	AT3	1q	23.0 25.0	3	0.22
467	pHRnX3.6	TaqI	1q	0.0 25.0	2	0.43
421	pJCZ29	TaqI	1q	100.0100.0	2	0.41
406	pCMM101	MspI	1q	100.0100.0	8	0.86
422	pTBZ36	TaqI	1q	100.0100.0	2	0.40
389	pHRnES1.9	HindIII	1q	0.0 25.0	2	0.41
372	IMR-6	MspI	2p	16.0 15.0	3	0.37
365	pYNA15.1	MspI	2p	100.0100.0	2	0.53
121	pB8	EcoRI	2p	100.0 23.0	2	0.27
296	pTBAB-5-7.	PvuII	2p	100.0100.0	4	0.55
164	pL2.30	BglII	2p	25.0 25.0	2	0.57
358	pEFD122	MspI	2p	100.0100.0	3	0.43
89	pB23	XbaI	2p	100.0 23.0	2	0.71
229	pYNZ9.1	TaqI	2p	100.0100.0	2	0.59
142	ACP	ACP	2p	23.0 23.0	3	0.37
418	pEKZ105	RsaI	2q	100.0100.0	2	0.45
412	pCMM63	MspI	2q	100.0100.0	3	0.15
98	p5-1-25	PstI	2q	35.0100.0	4	0.55
396	cYNA4	MspI	2q	100.0100.0	7	0.79
211	2pHHH115	MspI	2q	100.0100.0	2	0.49
135	pYNH24	MspI	2q	100.0100.0	8	0.91
120	3p5G1	TaqI	2q	33.0 35.0	2	0.32
205	1pHHH115	MspI	2q	100.0100.0	3	0.31
186	pHHH133	MspI	2q	100.0100.0	2	0.37
119	2p5G1	TaqI	2q	33.0 35.0	2	0.47
118	1p5G1	TaqI	2q	33.0 35.0	2	0.46
294	pIG-18	TaqI	2q	32.0 36.0	2	0.56
429	cMCOE32	TaqI	2q	100.0100.0	5	0.74
108	pYNZ15	TaqI	2q	100.0100.0	2	0.56
423	pHF12-32	MspI	3b	100.0100.0	2	0.23
180	pYNZ86.1	MspI	3b	100.0 21.0	2	0.52
232	pABL11-3	PvuII	3b	100.0100.0	2	0.61

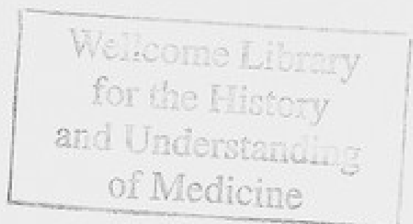
159	pB67	TaqI	3b	100.0	21.0	2	0.27
104	H3H2	HindIII	3p	21.0	21.0	2	0.50
81	c-raf-1	TaqI	3p	25.0	24.0	2	0.29
319	pEFD145.1	RsaI	3p	100.0	100.0	2	0.46
86	pHCP-1	PstI	3q	100.0	100.0	2	0.48
136	ABL11-3	TaqI	3q	100.0	100.0	2	0.58
305	pMCT32.1	PvuII	3q	100.0	100.0	3	0.75
424	LE24	TaqI	4b	100.0	100.0	3	0.45
454	pHM6	EcoRI	4b	11.0	21.0	2	0.46
116	2pK082	HindIII	4p	16.1	16.1	2	0.29
411	pMCOC14	PstI	4p	100.0	100.0	3	0.46
240	pYNZ32	TaqI	4p	100.0	100.0	5	0.48
114	1pK082	HindIII	4p	16.1	16.1	2	0.34
236	p3.6p6	PstI	4q	100.0	100.0	2	0.55
143	GC	GC	4q	12.0	13.0	5	0.60
197	MNSs	MNS	4q	28.0	31.0	8	0.67
460	ADH73	MspI	4q	21.0	25.0	2	0.45
335	pc11p11	TaqI	5b	100.0	100.0	2	0.32
295	L1.4	EcoRI	5b	100.0	100.0	2	0.31
408	L565RI-b	MspI	5b	100.0	100.0	2	0.44
428	L599H-a	TaqI	5b	100.0	100.0	3	0.67
441	PPBC	TaqI	5b	100.0	100.0	2	0.42
438	pHP12-65	MspI	5b	100.0	100.0	2	0.23
474	L647H-C	MspI	5b	100.0	100.0	4	0.78
196	Kell	Kel	5b	100.0	100.0	2	0.04
374	pJO110HC	MspI	5p	100.0	100.0	3	0.38
348	pL500	MspI	5p	13.0	11.0	2	0.42
472	J0157E-A	MspI	5q	100.0	100.0	2	0.52
369	TP5E	TaqI	5q	100.0	100.0	2	0.40
354	p105-153Ra	MspI	5q	12.0	13.0	2	0.53
368	LM4	BamHI	5q	22.0	31.0	3	0.68
386	p105-798Rb	MspI	5q	100.0	100.0	2	0.58
366	p213-205Ed	MspI	5q	11.0	12.0	3	0.60
220	GLO	SER	6p	21.3	21.1	2	0.55
227	DRH7	BglII	6p	21.3	21.3	3	0.38
400	p2-2	PvuII	6p	21.0	0.0	4	0.60
339	OL43	EcoRI	6p	100.0	100.0	2	0.25
224	pDP001	EcoRV	6p	21.3	21.3	2	0.25
410	pEFD6	BglII	6p	100.0	100.0	2	0.06
320	D6S4	BglII	6p	11.0	0.0	2	0.60
221	p7H4	EcoRI	6p	100.0	100.0	4	0.30
223	pCH6	TaqI	6p	100.0	100.0	3	0.43
226	DRH7	EcoRV	6p	21.3	21.3	2	0.38
219	AGB6	MspI	6p	100.0	100.0	2	0.25
370	pEFD84	RsaI	6p	100.0	100.0	2	0.08
217	pHHH157	BamHI	6p	100.0	100.0	2	0.50
190	GLO1	protein	6p	21.3	21.1	2	0.58
228	p2C5	MspI	6p	100.0	100.0	2	0.38
225	DCH1	HindIII	6p	21.3	21.3	5	0.62
99	B3.6	MspI	6p	100.0	100.0	2	0.55
311	pHM26	EcoRI	6q	22.0	24.0	2	0.58
427	pMCOB12	TaqI	6q	100.0	100.0	4	0.76
102	p3B10	MspI	6q	100.0	100.0	3	0.65
439	pJCZ30	HindIII	6q	100.0	100.0	4	0.73
214	pCMI37	RsaI	7b	100.0	100.0	4	0.50
293	A37	PstI	7b	100.0	100.0	2	0.39
291	C33	HindIII	7b	100.0	100.0	3	0.45
61	Phage-6	HindIII	7b	100.0	22.0	2	0.36
253	3pCMI37	RsaI	7b	100.0	100.0	3	0.21
252	2pCMI37	RsaI	7b	100.0	100.0	4	0.57
251	1pCMI37	RsaI	7b	100.0	100.0	3	0.46
187	pS194	TaqI	7b	100.0	100.0	2	0.42
204	pHP1.7	MspI	7p	15.0	15.0	2	0.37
113	TCRG	PvuII	7p	15.0	15.0	3	0.56
210	S93	PstI	7p	100.0	15.1	2	0.38
373	erbB	PstI	7p	13.0	13.0	2	0.27
184	M60	TaqI	7p	100.0	15.1	2	0.48
156	pTHH28	MspI	7p	15.0	15.0	2	0.43
202	M102L	TaqI	7p	100.0	15.1	2	0.49
123	pADJ641	TaqI	7p	15.0	15.0	2	0.34
157	B79a	MspI	7p	32.0	22.0	2	0.41
59	METH	MspI	7q	22.0	32.0	3	0.62
62	COLIA2	EcoRI	7q	21.2	21.3	2	0.45
203	pRM7-4	MspI	7q	100.0	100.0	2	0.49
93	pYNB3.1R	RsaI	7q	32.0	100.0	2	0.45
79	p7C22	EcoRI	7q	22.0	32.0	2	0.35
56	METD	TaqI	7q	22.0	32.0	2	0.31
75	TCRB	BglII	7q	100.0	100.0	2	0.56
58	3.11	TaqI	7q	22.0	32.0	2	0.08
149	pH056	TaqI	7q	22.0	32.0	2	0.47
57	3.11	MspI	7q	22.0	32.0	2	0.55
60	METH	TaqI	7q	22.0	32.0	3	0.64
148	B79a	HindIII	7q	22.0	32.0	2	0.24
183	pABL4-2	RsaI	8b	100.0	100.0	2	0.42
126	pYNM3	PstI	8b	100.0	100.0	4	0.33
151	pTHH5	HindIII	8b	100.0	100.0	3	0.55
255	LILA-2	PstI	8b	100.0	100.0	5	0.46
213	pYNZ132	TaqI	8b	100.0	100.0	4	0.69
399	p380-8A	TaqI	8q	100.0	100.0	3	0.54
403	LTL11	HindIII	8q	22.0	33.0	2	0.35
388	pCHT16-8.0	TaqI	8q	24.0	24.0	2	0.35
138	GPT	GPT	8q	100.0	100.0	3	0.45
239	pHHH171	MspI	8q	100.0	100.0	2	0.39
414	pMCT128.2	PstI	8q	100.0	100.0	3	0.54
330	2pMCT96.1	RsaI	9b	100.0	100.0	2	0.31
367	pMHZ10	PstI	9b	100.0	100.0	3	0.26
331	3pMCT96.1	RsaI	9b	100.0	100.0	2	0.02
275	pEKZ130.3	MspI	9b	100.0	100.0	2	0.38
344	pMCT112	MspI	9b	100.0	100.0	2	0.37
329	1pMCT96.1	RsaI	9b	100.0	100.0	2	0.35
416	pMHZ13	PvuII	9b	100.0	100.0	2	0.55
425	pMCOA12	MspI	9b	100.0	100.0	2	0.43
117	pHP12-8	TaqI	9b	100.0	11.0	2	0.36
259	GALT	GALT	9p	13.0	13.0	3	0.14
281	pMCT136	Pst102	9q	100.0	100.0	2	0.50
112	pAblK2	TaqI	9q	100.0	100.0	3	0.17
96	pYNM17	TaqI	9q	100.0	100.0	2	0.47
402	pEKZ19.3	TaqI	9q	100.0	100.0	2	0.40
145	AK	AK	9q	12.0	100.0	2	0.10
115	pAS-1	HindIII	9q	11.0	22.0	2	0.43
189	ORM	ORM	9q	100.0	100.0	2	0.58
306	pEFD40.3	MspI	9q	100.0	100.0	2	0.38
193	ABO	ABO	9q	34.0	34.0	5	0.44
299	pEFD126.3	BamHI	9q	100.0	100.0	5	0.66
152	pTHH22	TaqI	9q	100.0	100.0	2	0.16
254	pHHH220	TaqI	9q	100.0	100.0	3	0.32
283	pEKZ19	TaqI	9q	100.0	100.0	2	0.36
473	pHHH105	BglII	10b	100.0	100.0	2	0.35
443	IRBPH.4	MspI	10b	11.2	11.2	2	0.31
449	pTB10.171	PvuII	10b	100.0	100.0	2	0.48
426	IRBPH.4	BglII	10b	11.2	11.2	2	0.14
310	dry5-1	TaqI	10b	100.0	100.0	2	0.34
290	p1-101	TaqI	10b	100.0	100.0	3	0.55
334	pCMM17.1	MspI	10b	100.0	100.0	2	0.43
207	pTHH105.1	BglII	10b	100.0	100.0	2	0.33
269	pTHH54	MspI	10b	100.0	100.0	3	0.62

462	pTB10.191	MspI	10b	100.0	100.0	2	0.62
395	OS-2	HindIII	10q	100.0	100.0	3	0.64
272	pMCK2	PvuII	10q	100.0	100.0	6	0.26
238	pYNZ156	MspI	10q	100.0	100.0	2	0.26
222	p3C7	MspI	11b	100.0	100.0	2	0.50
394	pYNB3.12	MspI	11b	100.0	100.0	2	0.63
312	pMCT117	MspI	11b	100.0	100.0	3	0.27
29	pTBB-2	TaqI	11p	15.5	15.5	8	0.00
30	1pADJ762	MspI	11p	15.5	15.5	2	0.00
31	pADJ762	TaqI	11p	15.5	15.5	2	0.25
32	pADJ762	BclI	11p	15.5	15.5	2	0.38
444	pINT-800	TaqI	11p	13.0	13.0	2	0.37
26	1JW151	HindIII	11p	15.5	15.5	2	0.00
287	pMCMP1	MspI	11p	100.0	100.0	3	0.36
28	pINS-310	PvuII	11p	15.5	15.5	10	0.80
212	2pADJ762	MspI	11p	15.3	15.3	2	0.22
35	pCAL	TaqI	11p	15.4	15.1	2	0.31
34	pPTH-LF	PstI	11p	15.4	15.1	2	0.52
25	2JW151	HindIII	11p	15.5	15.5	2	0.37
27	JW102	SinI	11p	15.5	15.5	2	0.18
351	pHBI59	MspI	11q	100.0	100.0	2	0.49
457	P2-25	MspI	11q	100.0	100.0	2	0.59
324	PGA	BglII	11q	100.0	100.0	2	0.39
289	MCT128.1	MspI	11q	100.0	100.0	2	0.60
261	APOA4	APOA4	11q	13.0	100.0	4	0.22
243	D11S29	TaqI	11q	22.0	100.0	2	0.35
250	pHBI18P2	PstI	11q	100.0	100.0	2	0.33
341	p2-7-1D6	TaqI	11q	22.0	22.0	2	0.40
340	2Phage6-3	MspI	11q	22.0	22.0	2	0.71
161	pTHH26	PvuII	11q	100.0	100.0	2	0.26
332	1Phage6-3	MspI	11q	22.0	22.0	2	0.50
165	pApoAI	TaqI	11q	100.0	100.0	2	0.09
353	WC4	TaqI	12b	100.0	100.0	2	0.24
360	WC29	EcoRI	12b	100.0	100.0	2	0.48
437	WC93	EcoRI	12b	100.0	100.0	2	0.54
279	pTHH14	TaqI	12b	100.0	100.0	3	0.40
46	pPRP	EcoRI-3	12p	13.2	13.2	4	0.14
141	C1R	C1R	12p	13.0	13.0	2	0.14
24	pXP13	TaqI	12p	100.0	12.0	2	0.26
48	pPRP	EcoRI-1	12p	13.2	13.2	8	0.67
53	VWF	BglII	12p	100.0	12.2	2	0.40
45	pPRP	EcoRI-2	12p	13.2	13.2	5	0.33
19	p12-16	EcoRI	12p	100.0	12.0	2	0.22
345	pTHIZ53	RsaI	12p	100.0	100.0	3	0.27
18	p640	TaqI	12p	12.1	12.1	2	0.32
192	C1S	C1S	12p	13.0	13.0	3	0.83
47	pPRP	EcoRI-4	12p	13.2	13.2	3	0.38
52	COL2A	HindIII	12q	13.0	14.0	2	0.39
101	pCMM1.2	TaqI	12q	0.0	14.0	2	0.28
21	pPH72	HindIII	12q	22.0	24.2	3	0.43
50	p7G11	TaqI-1	12q	14.0	100.0	2	0.09
55	pDLJ2B	TaqI	12q	14.3	100.0	4	0.66
22	p9F11	TaqI	12q	0.0	14.3	2	0.59
49	p1-7	MspI	12q	14.0	14.0	2	0.53
54	p1-11	EcoRI	12q	14.0	14.0	2	0.19
333	pEFD33.2	MspI	12q	100.0	100.0	4	0.68
20	pPH72	MspI	12q	22.0	24.2	2	0.48
51	p7G11	TaqI-2	12q	14.0	100.0	2	0.53
129	pYNH15	MspI	12q	100.0	100.0	3	0.52
17	p7G11	MspI	12q	21.0	22.0	2	0.35
375	WC95	EcoRI	13b	100.0	100.0	2	0.32
309	WC64	BglII	13q	0.0	100.0	2	0.49
7	pHU26	BglII	13q	12.0	22.0	2	0.30

302	7D2	TaqI	13q	15.0	15.0	2	0.25
8	p9D11	MspI	13q	22.0	22.0	3	0.47
323	WC47	EcoRI	13q	100.0	100.0	2	0.27
355	WC83	TaqI	13q	14.0	22.0	2	0.52
271	S54	TaqI	13q	34.0	34.0	2	0.25
11	p9A7	MspI	13q	22.0	100.0	2	0.38
1	p7F12	MspI	13q	12.0	14.0	2	0.55
12	p9A7	HindIII	13q	22.0	100.0	2	0.42
3	p7F12	BclI	13q	12.0	14.0	2	0.37
33	pHU10	EcoRI	13q	12.0	22.0	2	0.33
14	Esterase-D	serol	13q	14.1	14.1	2	0.22
13	p7D2	TaqI	13q	12.0	22.0	2	0.38
2	p7F12	TaqI	13q	12.0	14.0	2	0.35
4	pHUB8	EcoRI	13q	12.0	22.0	2	0.34
6	pHU10	XmnI	13q	12.0	22.0	2	0.45
5	pHUB8	HindIII	13q	12.0	22.0	2	0.23
10	p1E8	MspI	13q	22.0	100.0	2	0.43
160	pTHI62	BglII	13q	12.0	22.0	4	0.69
397	D13S12	MspI	13q	0.0	21.0	4	0.38
9	p9D11	TaqI	13q	22.0	22.0	2	0.28
318	WC25	MspI	13q	14.0	22.0	3	0.46
188	ESD	ESD	13q	14.1	14.1	2	0.16
468	D13S11	MspI	13q	12.0	13.0	2	0.26
338	pMHZ9	EcoRI	14b	100.0	100.0	2	0.16
298	pHHH208	BamHI	14q	100.0	100.0	3	0.61
352	pEFZ18.2	TaqI	14q	100.0	100.0	2	0.51
185	pTHH37	TaqI	14q	100.0	100.0	3	0.48
137	GM	GM	14q	32.3	32.3	3	0.56
83	pAW101	EcoRI	14q	32.1	32.2	6	0.64
111	p3.4	BglII	14q	32.3	32.3	5	0.83
390	cKKA39	RsaI	14q	100.0	100.0	7	0.83
134	MLJ14	RsaI	14q	100.0	100.0	7	0.83
257	PI	PI	14q	32.1	32.1	5	0.59
307	pEFD49.3	MspI	15b	100.0	100.0	3	0.38
246	pYNZ90.1	BamHI	15b	100.0	100.0	2	0.33
267	EKZ104	MspI	15b	100.0	100.0	2	0.50
249	pTHH55	MspI	15b	100.0	100.0	2	0.45
158	pJU201	EcoRI	15b	100.0	100.0	2	0.47
273	pMCT46.2	PvuII	15b	100.0	100.0	2	0.26
383	pYNA15.2	TaqI	15q	100.0	100.0	2	0.31
92	pMS1-14	MspI	15q	14.0	21.0	2	0.65
387	pYNM18.1	TaqI	15q	100.0	100.0	3	0.36
420	pEFD49.2	TaqI	15q	100.0	100.0	2	0.57
361	pEFD65.7	EcoRI	15q	100.0	100.0	2	0.47
301	pMCT149.2	MspI	15q	100.0	100.0	2	0.24
218	pTHH114	RsaI	15q	100.0	100.0	2	0.44
127	pDP151	EcoRI	15q	15.0	22.0	2	0.33
216	pMCA1-1	PvuII	15q	100.0	100.0	2	0.47
154	2pEKXp3B	PvuII	16b	100.0	100.0	3	0.38
106	LC9	MspI	16b	100.0	100.0	2	0.42
153	1pEKXp3B	PvuII	16b	100.0	100.0	2	0.32
124	cosEKDA2	RsaI	16b	100.0	100.0	4	0.23
321	pCMM65	EcoRI	16b	100.0	100.0	2	0.39
419	pMCOC36	TaqI	16p	100.0	100.0	2	0.37
105	Hag1	HinfI	16p	100.0	12.0	5	0.41
285	Phage8-9	BglII	16q	22.0	24.0	3	0:48
139	HP	HP	16q	22.1	22.1	2	0.54
315	p79-2-23	RsaI	16q	22.0	24.0	7	0.83
85	Aprt	BglII	16q	22.0	22.0	2	0.50
84	Aprt	TaqI	16q	22.0	22.0	2	0.45
407	1CETP.11	TaqI	16q	100.0	100.0	2	0.13
440	2CETP.11	TaqI	16q	100.0	100.0	2	0.73
277	pHHH152	BamHI	17b	100.0	100.0	2	0.45

357	D17Z1	EcoRI	17b	100.0	100.0	2	0.28
362	1pYNM67	RsaI	17b	100.0	100.0	2	0.18
263	D17Z1	HindIII	17b	0.0	0.0	4	0.38
242	pHHH202	RsaI	17b	100.0	100.0	2	0.49
100	pYNM67	TaqI	17b	100.0	100.0	2	0.41
363	2pYNM67	RsaI	17b	100.0	100.0	2	0.31
91	pHF12-1	MspI	17p	13.0	13.0	2	0.40
233	pABL10-41	PvuII	17p	100.0	100.0	2	0.29
256	pMCT35.1	MspI	17p	13.0	13.0	2	0.43
133	p10.5	HindIII	17p	13.0	13.0	2	0.38
215	pYNH37-3	TaqI	17p	100.0	100.0	5	0.65
88	pYNZ22	RsaI	17p	13.0	13.0	6	0.83
391	LEW102	TaqI	17q	100.0	100.0	2	0.47
230	pAC256	PvuII	17q	100.0	100.0	6	0.73
166	pRMU-3	TaqI	17q	100.0	100.0	4	0.65
435	pKKA35	MspI	17q	100.0	100.0	3	0.37
349	pHtK9	TaqI	17q	21.0	22.0	2	0.60
356	cEFD52	PvuII	17q	100.0	100.0	8	0.83
247	pRMU1	PstI	17q	100.0	100.0	2	0.32
376	LEW101	MspI	17q	100.0	100.0	2	0.47
107	pTHH59	TaqI	17q	100.0	100.0	6	0.71
245	EFZ10	PvuII	18b	100.0	100.0	4	0.70
128	pHF12-62	TaqI	18b	100.0	100.0	2	0.58
195	Kidd	Kid	18b	100.0	100.0	2	0.50
97	pL2.7	PstI	18b	100.0	100.0	2	0.41
300	pHHH163	PvuII	18p	100.0	100.0	2	0.38
103	B74	MspI	18p	11.3	11.3	2	0.41
182	pMS1-3	PstI	18q	100.0	100.0	2	0.49
401	pEFD70.3	PstI	18q	100.0	100.0	2	0.35
244	OS-4	TaqI	18q	21.0	100.0	2	0.33
432	pMCT108.2	TaqI	18q	100.0	100.0	2	0.21
336	pEFD4.2	PvuII	19b	100.0	100.0	2	0.44
266	2MCT6	BamHI	19b	100.0	100.0	2	0.19
198	Lewis	Lew	19b	100.0	100.0	2	0.68
337	cMCOB19	BglII	19b	100.0	100.0	5	0.70
431	p4.1	MspI	19b	12.0	13.2	2	0.51
350	OL5	EcoRI	19b	100.0	100.0	3	0.49
404	pIJ2	EcoRI	19b	100.0	100.0	2	0.19
326	cMCOB5	PstI	19b	100.0	100.0	5	0.64
265	1MCT6	BamHI	19b	100.0	100.0	3	0.53
308	pJCZ3.1	HinfI	19b	100.0	100.0	7	0.80
268	3MCT6	BamHI	19b	100.0	100.0	2	0.23
109	HHI	PvuII	19p	13.2	13.1	2	0.40
248	12.1p1.6	BglII	19p	13.3	13.2	2	0.32
206	pCII-711	TaqI	19q	0.0	13.0	4	0.51
199	Secretor	Sec	19q	0.0	13.0	2	0.58
434	pR12.21	MspI	20p	12.0	12.0	2	0.46
448	pD3H12	TaqI	20p	100.0	100.0	2	0.45
258	ADA	ADA	20q	13.2	100.0	2	0.03
130	pMS1-27	MspI	20q	13.4	13.4	3	0.53
415	G21RK	TaqI	21b	100.0	21.0	2	0.46
450	p26C	BglII	21b	100.0	21.1	2	0.59
237	D21S72-1	TaqI	21b	100.0	100.0	2	0.48
147	SODI	SODI	21q	22.1	22.1	2	0.02
274	EFZ31	MspI	22b	100.0	100.0	2	0.54
208	pMS3-18	BglII	22q	11.2	100.0	2	0.48
90	pSIS-R12	HindIII	22q	12.3	13.1	2	0.50
150	pERT87-8	TaqI	23p	21.0	21.0	2	0.23
43	pL1.28	TaqI	23p	11.3	11.3	2	0.00
36	Xga	serol	23p	100.0	22.3	2	0.00
44	p58-1	MspI	23p	11.0	11.0	2	0.00
38	pD2	PvuII	23p	22.2	22.1	2	0.00
40	p99-6	PstI	23p	22.2	22.1	2	0.50
39	1RC8	TaqI	23p	100.0	22.0	3	0.00
41	p754	PstI	23p	21.0	21.0	2	0.00
42	pHO731	MspI	23p	21.0	21.0	4	0.00
37	dic56	BclI	23p	100.0	22.0	2	0.00
173	p43-15	BglII	23q	24.0	100.0	2	1.00
131	pYNH3	RsaI	23q	21.0	21.0	2	0.43
177	X13	BglII	23q	27.0	27.0	2	1.00
170	S21	TaqI	23q	21.3	22.0	2	0.33
167	p8	TaqI	23q	0.0	13.0	2	1.00
174	52A	TaqI	23q	27.0	100.0	2	1.00
172	pDSK1	BamHI	23q	26.0	27.0	3	1.00
169	p19-2	MspI	23q	21.3	22.0	2	0.31
176	F8C	BclI	23q	28.0	28.0	2	1.00
179	St14-1	MspI	23q	28.0	28.0	2	1.00
171	22-33	TaqI	23q	24.0	26.0	2	0.10
201	p19-2	TaqI	23q	21.3	22.3	2	0.44
175	F9	TaqI	23q	26.0	27.0	2	1.00
178	St14-1	TaqI	23q	28.0	28.0	7	1.00
191	6PGD	PGD	23q	28.0	28.0	2	0.03
132	pERT87-1	MspI	23p	21.0	21.0	2	0.14
63	pDP230	TaqI	25p	100.0	100.0	4	0.00
77	601	TaqI	25p	100.0	100.0	4	0.00
64	pDP230	HindIII	25p	100.0	100.0	4	0.00
76	113D	TaqI	25p	100.0	100.0	4	0.00
69	29C1	TaqI	25p	100.0	100.0	4	0.00
68	pDP411a	TaqI	25p	100.0	100.0	4	0.00
66	SEX	XY	25p	100.0	100.0	2	0.00
67	pDP411a	EcoRI	25p	100.0	100.0	3	0.00
65	pDP230	MspI	25p	100.0	100.0	4	0.00
168	pDP34	TaqI	25q	13.0	21.0	2	1.00
74	p1	TaqI	26q	13.0	21.0	3	0.00
73	p31	TaqI	26q	13.0	21.0	2	0.00
71	pDP132	BamHI	26q	13.0	21.0	3	0.00
72	47b	PstI	26q	13.0	21.0	3	0.00
70	pDP7a	PstI	26q	13.0	21.0	3	0.58

Notes : 23 is ch X, 25 is the pseudoautosomal region of X, 26 are DXYS1-like probes. Heterozygosity is 0.0 when it has not been computed. For very early ch X probes, an heterozygosity of 1.0 indicates that only families with an heterozygous mother were tested. The number of alleles of most VNTRs is arbitrary, as they are interpreted within families. The heterozygosity of most VNTRs is highly dependent of the conditions of migration; significantly greater heterozygosity can be achieved at higher resolution or with other enzymes than used in our standard screen. This is a working document; some of the information reported is provisional.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