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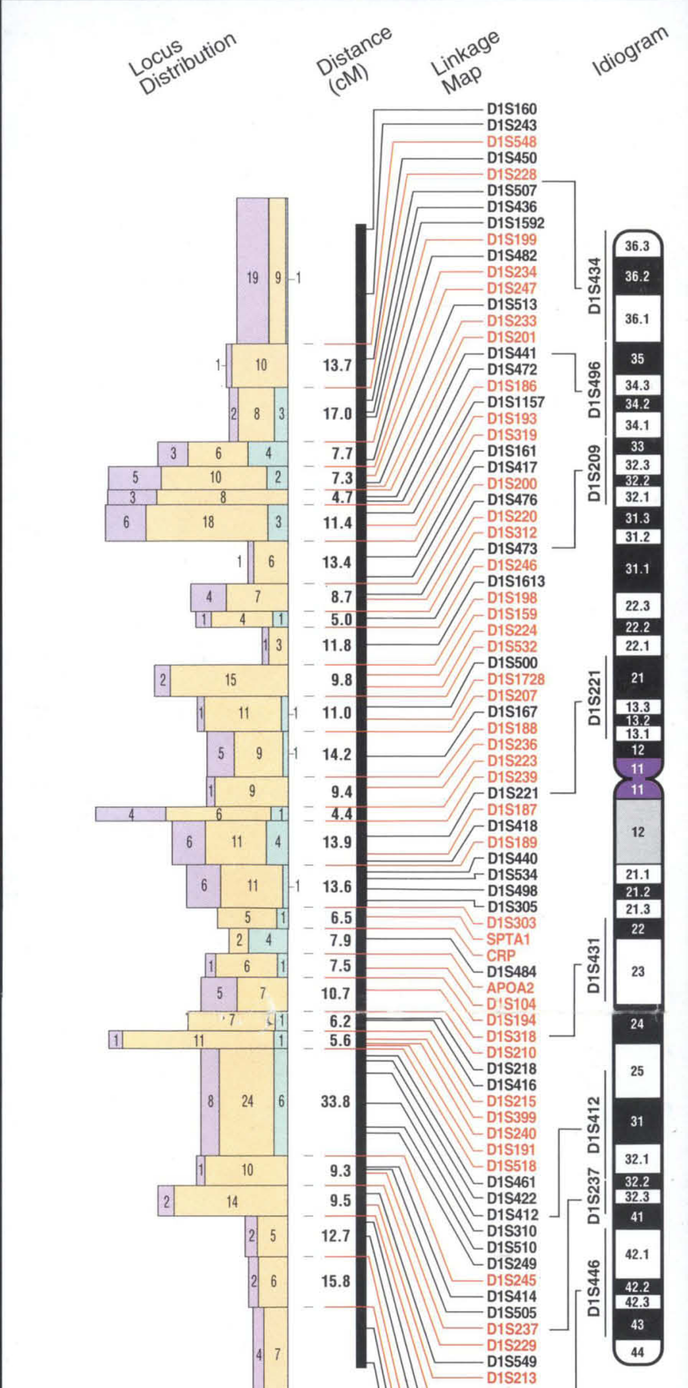
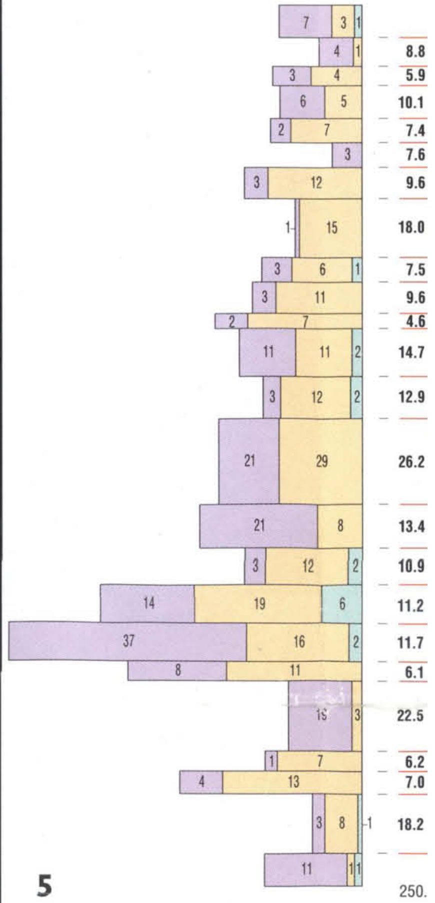




Locus Distribution

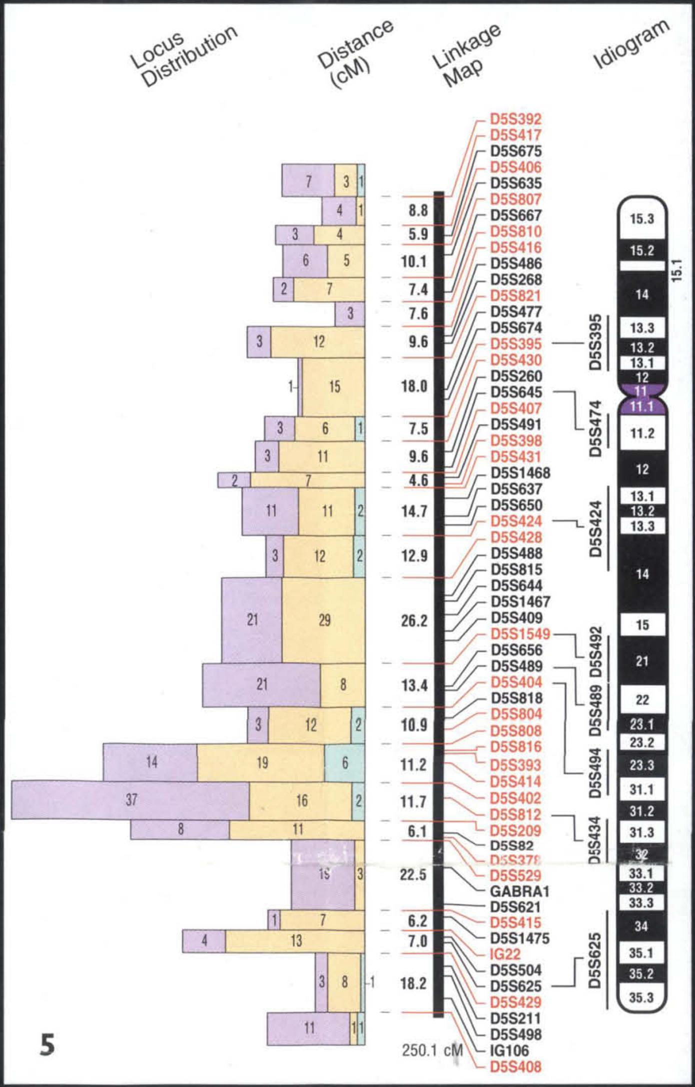
Distance (cM)

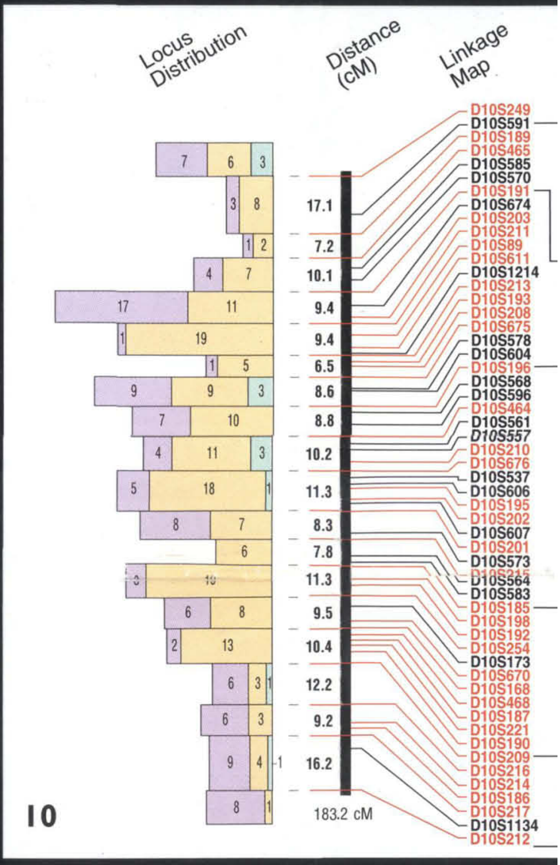
5

SCIENCE

HUMAN GENE

GENOME M

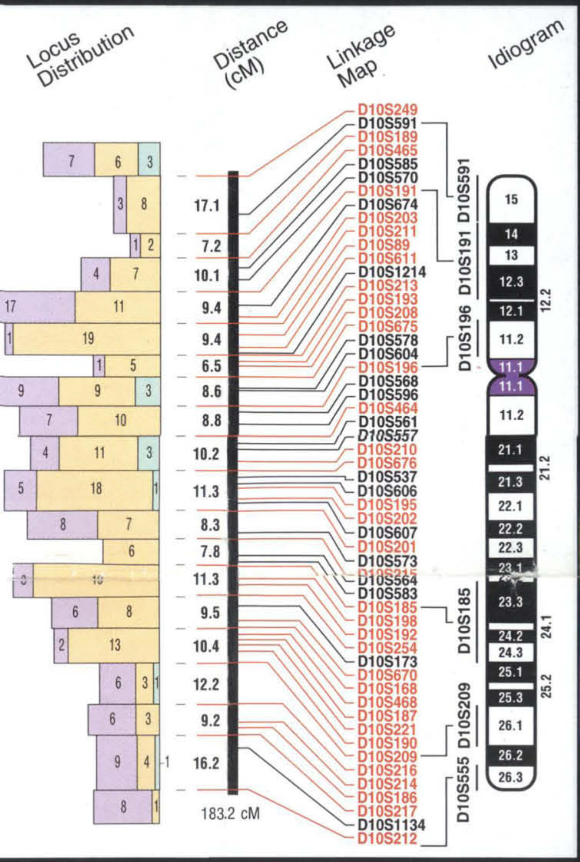


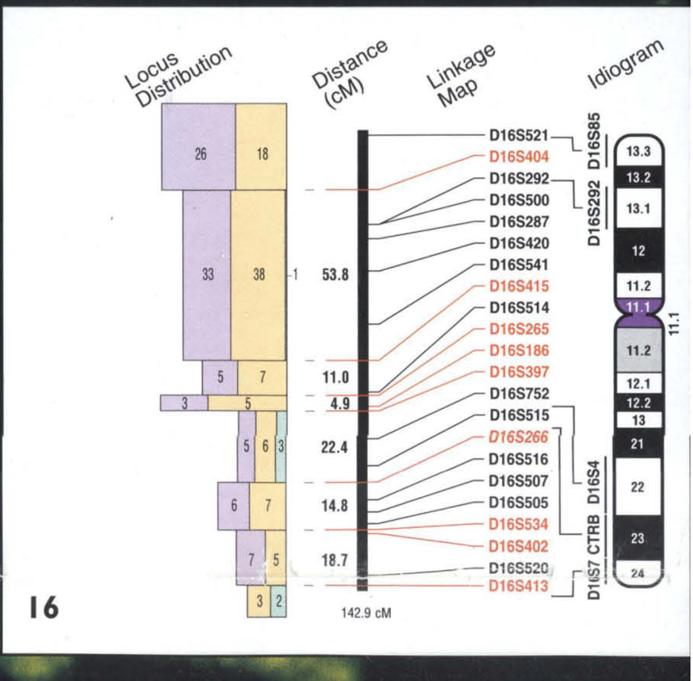


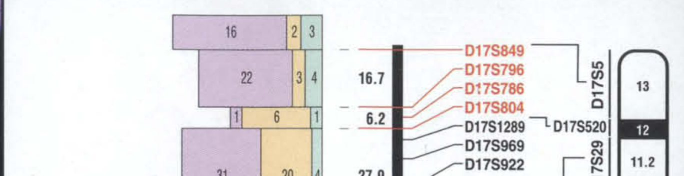
Science

GENETIC MAP

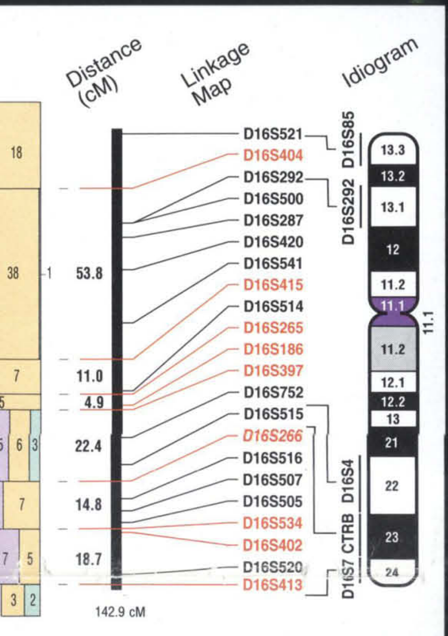
ME MAPS V







MAP


Distance (cM)
Linkage Map
Idiogram
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53.8
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4.9
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22.4
7
14.8
7
5
18.7
3
2
D16S521
D16S404
D16S292
D16S500
D16S287
D16S420
D16S541
D16S415
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D16S265
D16S186
D16S397
D16S752
D16S515
D16S266
D16S516
D16S507
D16S505
D16S534
D16S402
D16S520
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D16S85
D16S292
D16S4
CTRB
D16S7
13.3
13.2
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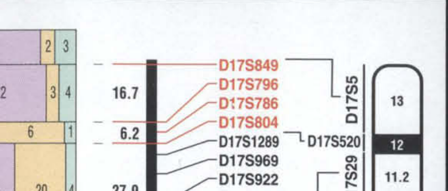
142.9 cM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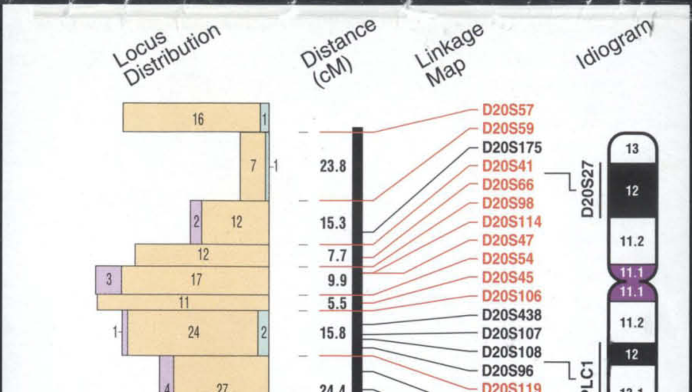
Locus Distribution
Distance (cM)
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15.8
24.4
D20S57
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D20S41
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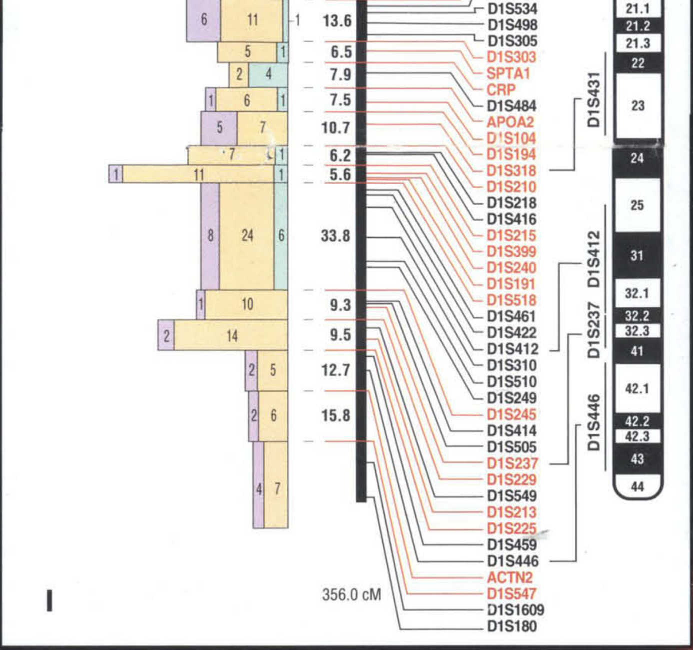
13.1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7 1
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8 24 6
33.8
1 10
9.3
2 14
9.5
2 5
12.7
2 6
15.8
4 7
356.0 cM
D1S534
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CRP
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21.2
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42.1
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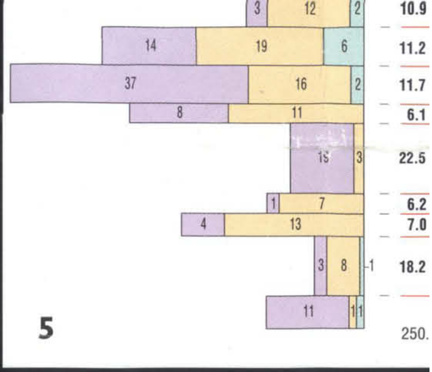
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3 8 1
18.2
11 1 1
250.
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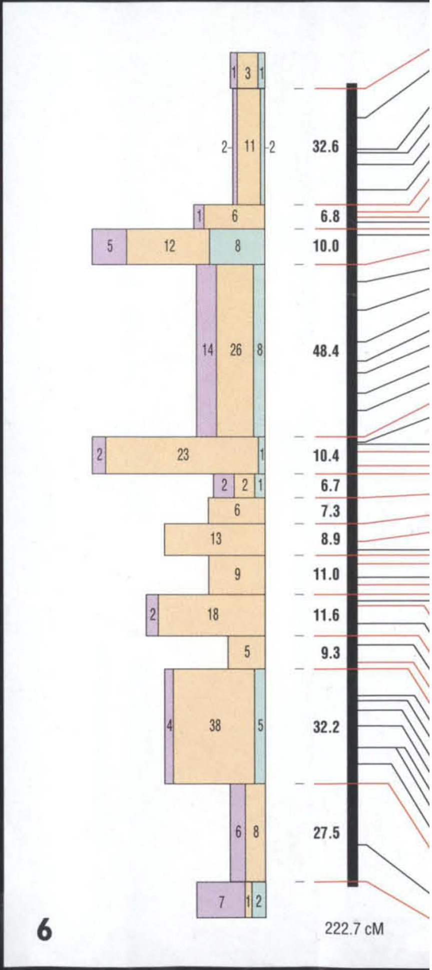
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10.4
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6
7.3
13
8.9
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9.3
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6 8
27.5
7 1 2
222.7 cM
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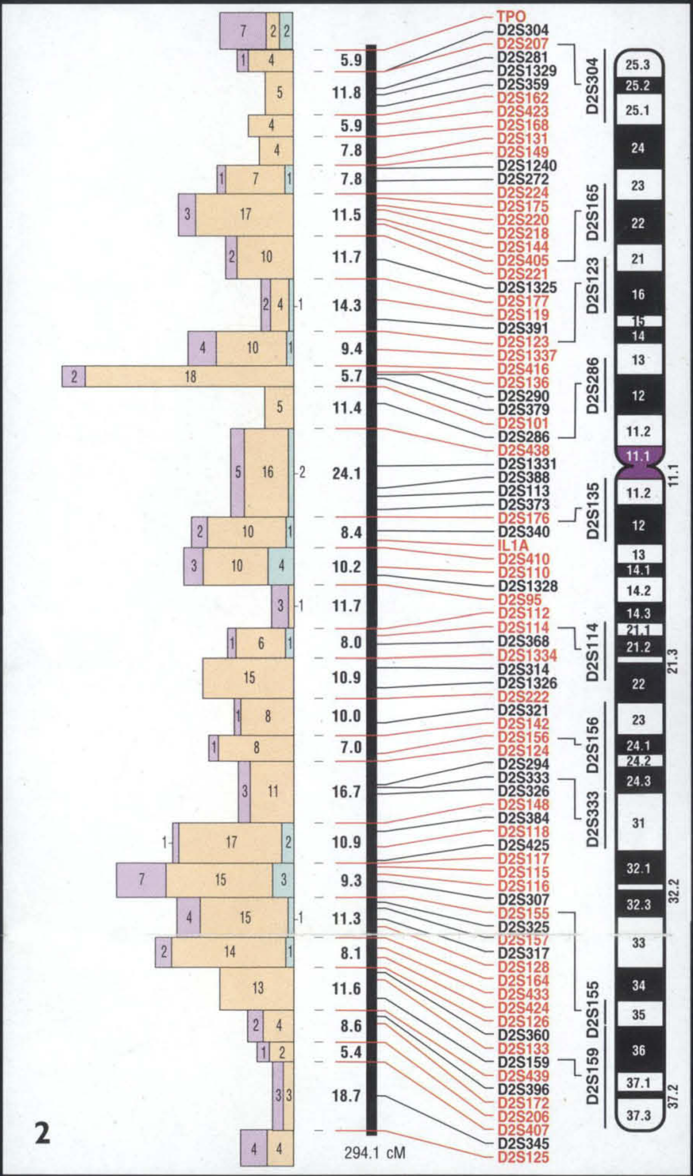
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5
11.4
5 16 2
24.1
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10.2
3 1
11.7
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10.0
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7.0
3 11
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18.7
4 4
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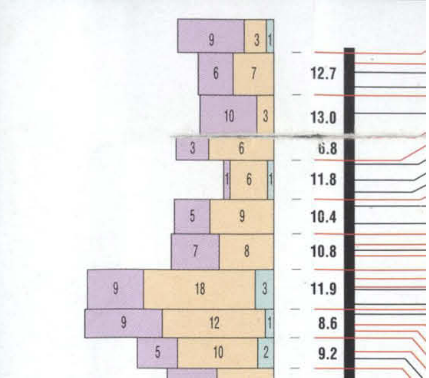
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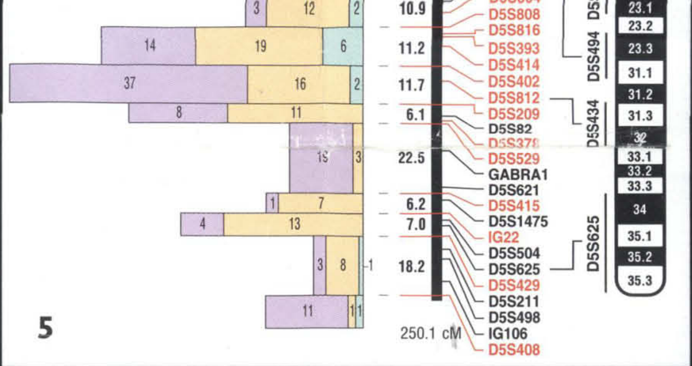
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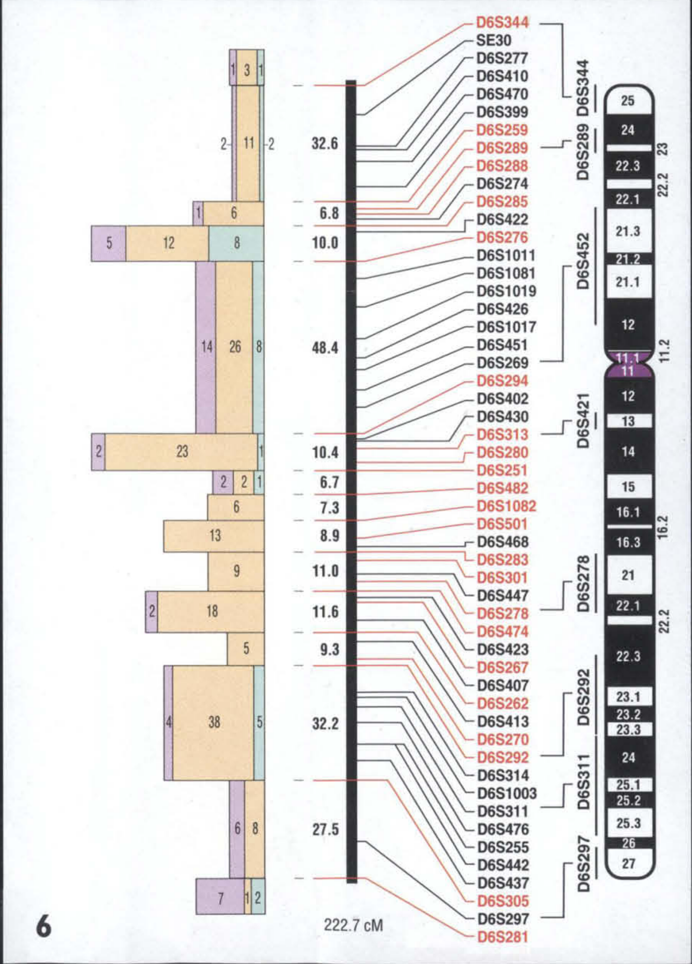
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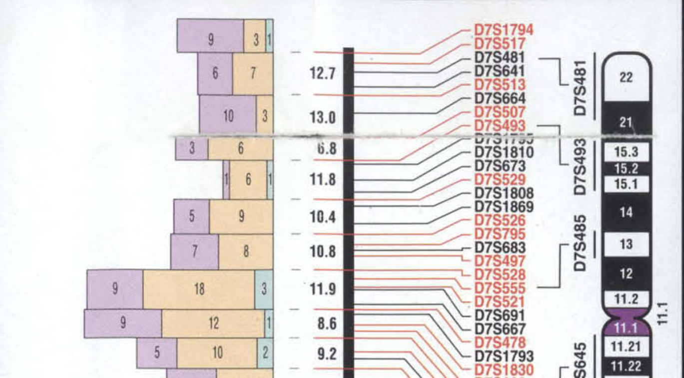
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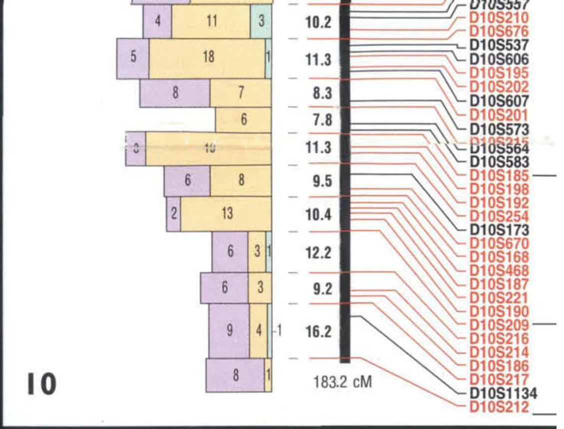
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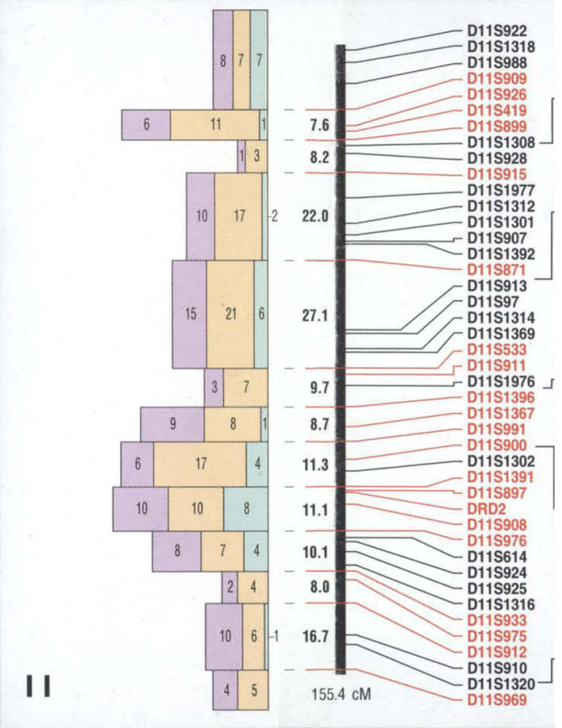
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155.4 cM
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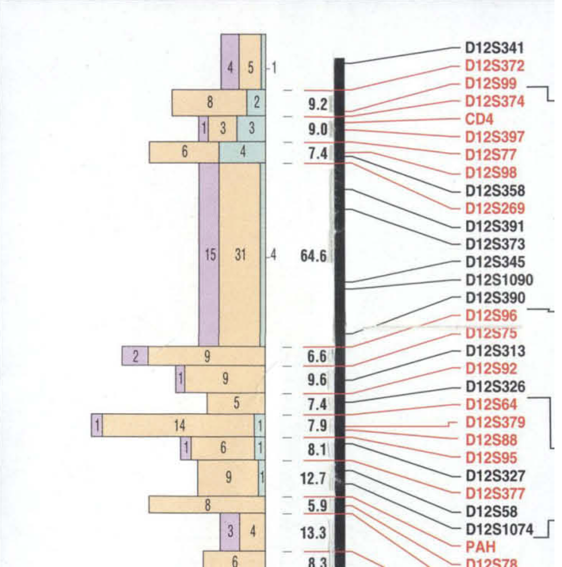
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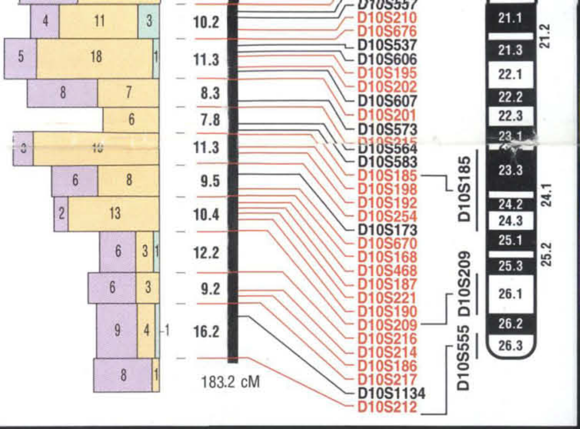
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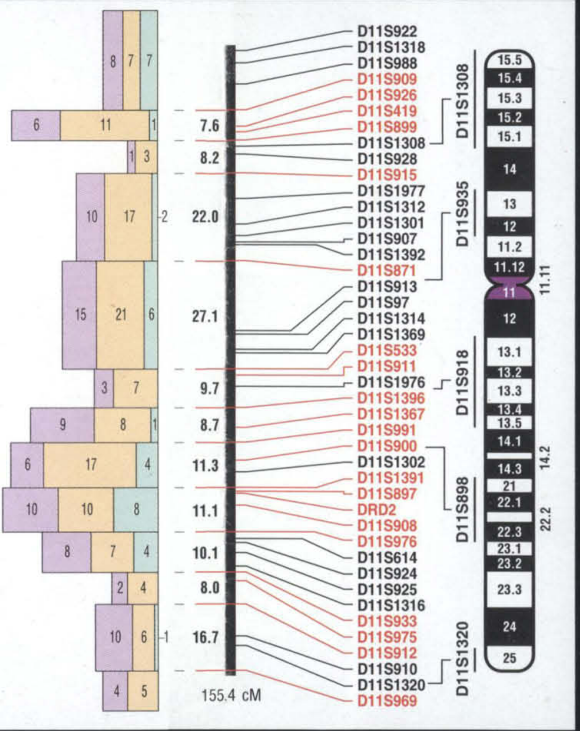
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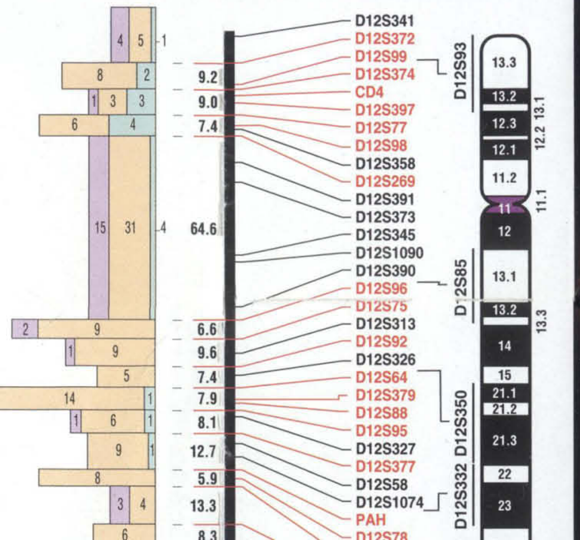
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6.6
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7.4
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8.1
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5.9
13.3
8.3
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D12S99
D12S374
CD4
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D12S77
D12S98
D12S358
D12S269
D12S391
D12S373
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D12S96
D12S75
D12S313
D12S92
D12S326
D12S64
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D12S88
D12S95
D12S327
D12S377
D12S58
D12S1074
PAH
D12S78
D12S93
D12S85
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D12S332
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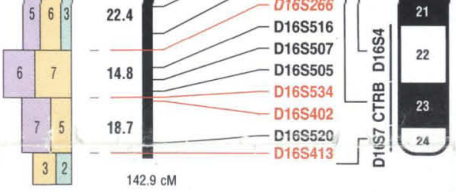
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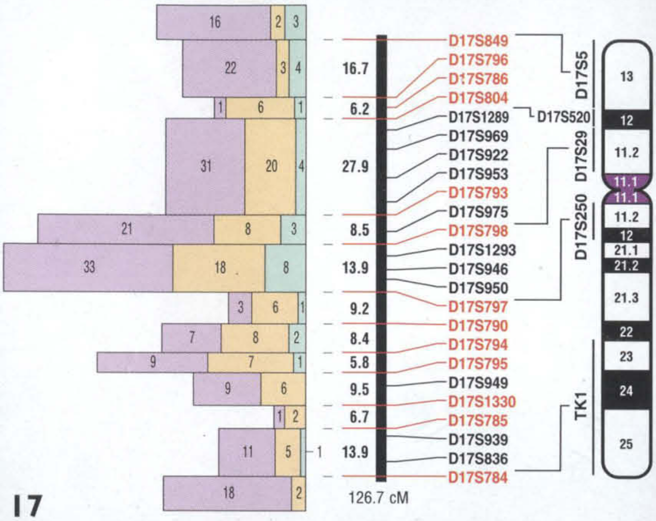
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18 2
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6.2
27.9
8.5
13.9
9.2
8.4
5.8
9.5
6.7
13.9
126.7 cM
D17S849
D17S796
D17S786
D17S804
D17S1289
D17S969
D17S922
D17S953
D17S793
D17S975
D17S798
D17S1293
D17S946
D17S950
D17S797
D17S790
D17S794
D17S795
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D17S785
D17S939
D17S836
D17S784
D17S5
D17S520
D17S29
D17S250
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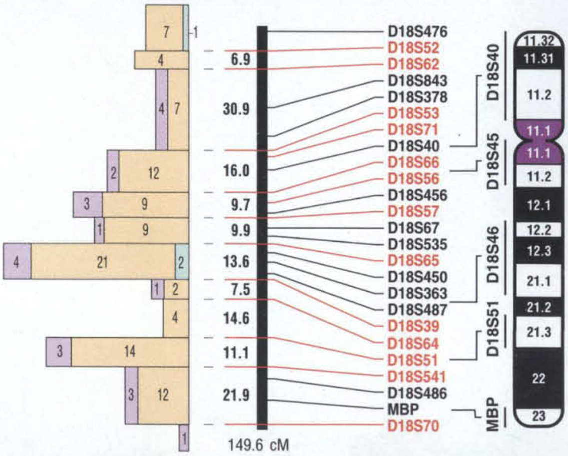
17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7.5
14.6
11.1
21.9
149.6 cM
D18S476
D18S52
D18S62
D18S843
D18S378
D18S53
D18S71
D18S40
D18S66
D18S56
D18S456
D18S57
D18S67
D18S535
D18S65
D18S450
D18S363
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D18S39
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D18S51
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D18S40
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D18S51
MBP
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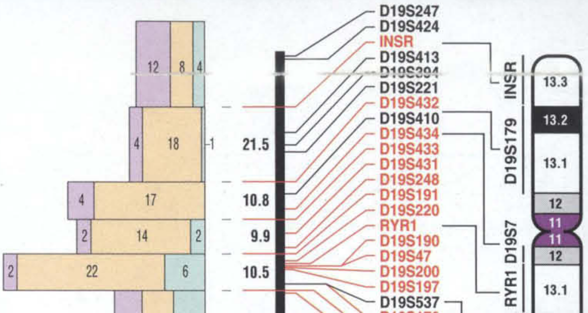
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D19S413
D19S394
D19S221
D19S432
D19S410
D19S434
D19S433
D19S431
D19S248
D19S191
D19S220
RYR1
D19S190
D19S47
D19S200
D19S197
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13.1
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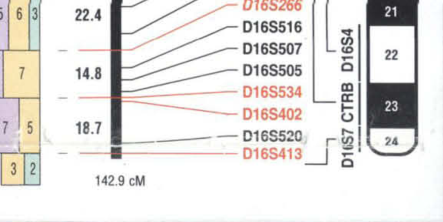
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D16S505
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D16S4
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D16S7
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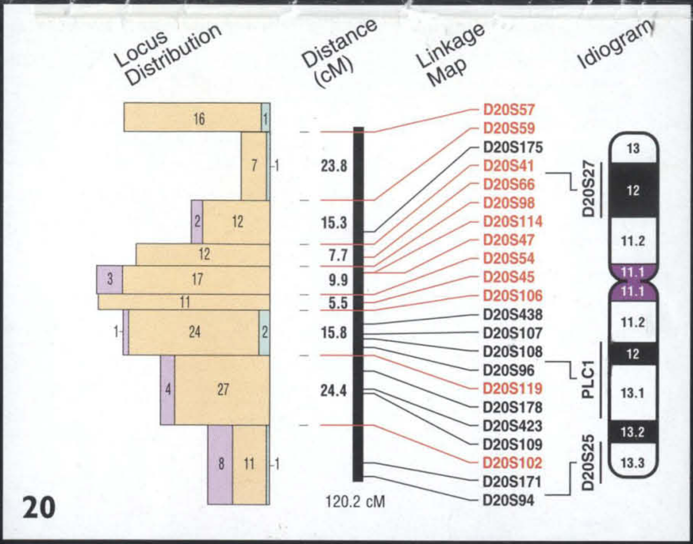
142.9 cM


Locus Distribution
Distance (cM)
Linkage Map
Idiogram
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15.3
7.7
9.9
5.5
15.8
24.4
120.2 cM
D20S57
D20S59
D20S175
D20S41
D20S66
D20S98
D20S114
D20S47
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D20S45
D20S106
D20S438
D20S107
D20S108
D20S96
D20S119
D20S178
D20S423
D20S109
D20S102
D20S171
D20S94
D20S27
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11.2
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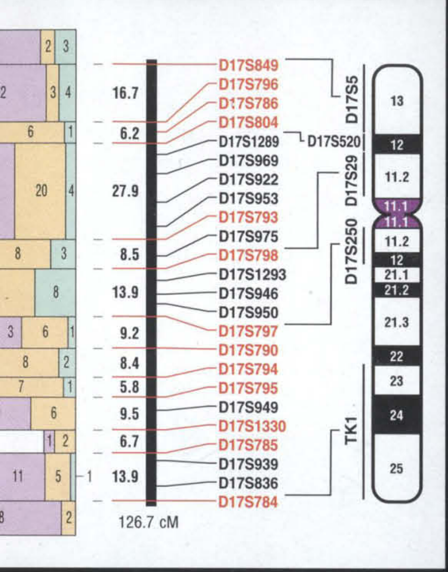
13.1
13.2
13.3

20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8 2
7 1
6
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11 5 1
8 2
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6.2
27.9
8.5
13.9
9.2
8.4
5.8
9.5
6.7
13.9
126.7 cM
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D17S796
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D17S804
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D17S250
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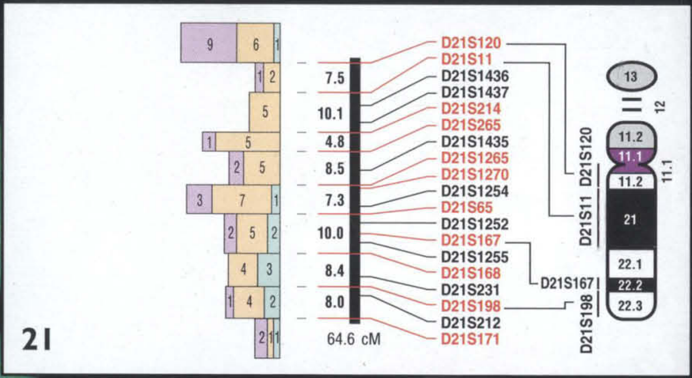
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7.3
10.0
8.4
8.0
64.6 cM
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D21S11
D21S1436
D21S1437
D21S214
D21S265
D21S1435
D21S1265
D21S1270
D21S1254
D21S65
D21S1252
D21S167
D21S1255
D21S168
D21S231
D21S198
D21S212
D21S171
D21S120
D21S11
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22.2
22.3

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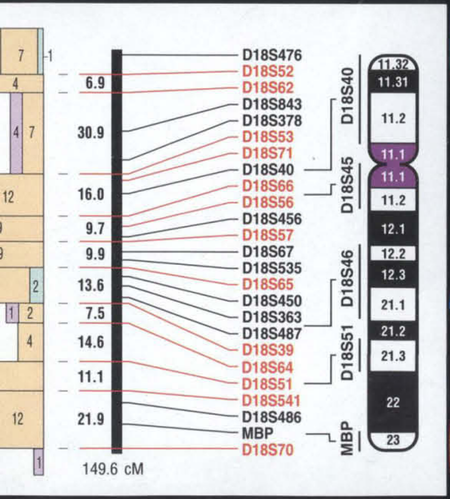
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11.1
21.9
149.6 cM
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D18S843
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MBP
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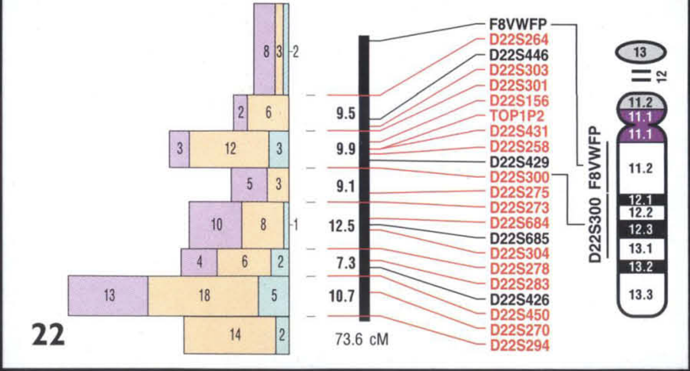
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10.7
73.6 cM
F8VWFP
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D22S156
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D22S300
D22S275
D22S273
D22S684
D22S685
D22S304
D22S278
D22S283
D22S426
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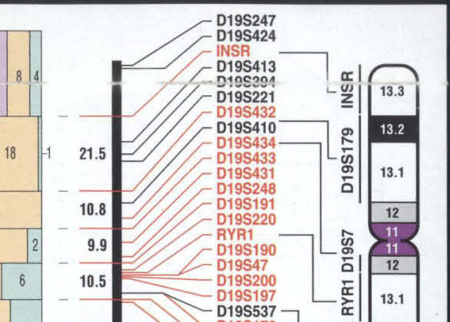
8 4
18 1
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6
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D19S247
D19S424
INSR
D19S413
D19S394
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D19S434
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D19S248
D19S191
D19S220
RYR1
D19S190
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D19S200
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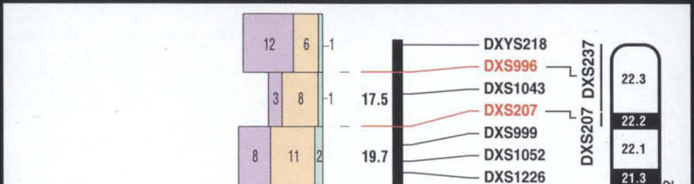
13.1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19.7
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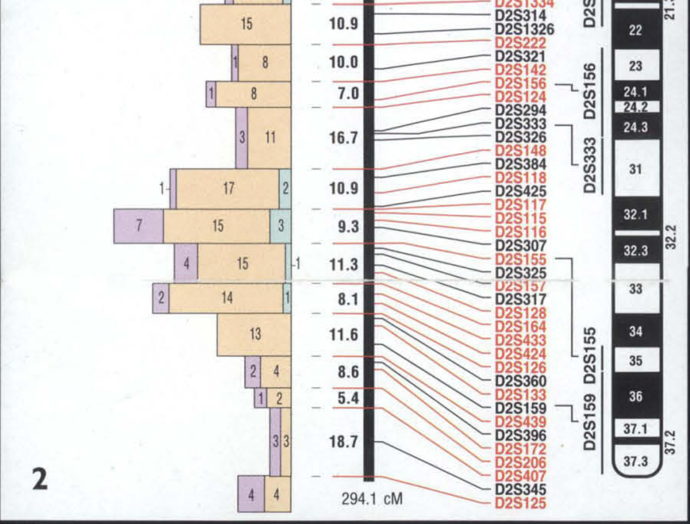
21.3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D2S148
D2S384
D2S118
D2S425
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D2S307
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D2S157
D2S317
D2S128
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11.6
8.6
5.4
18.7
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D2S156
D2S333
D2S155
D2S159
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24.2
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37.2
37.3


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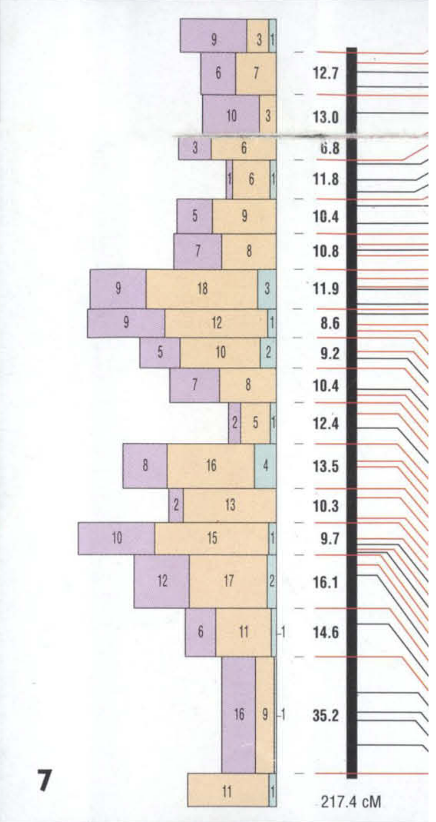
222.7 cM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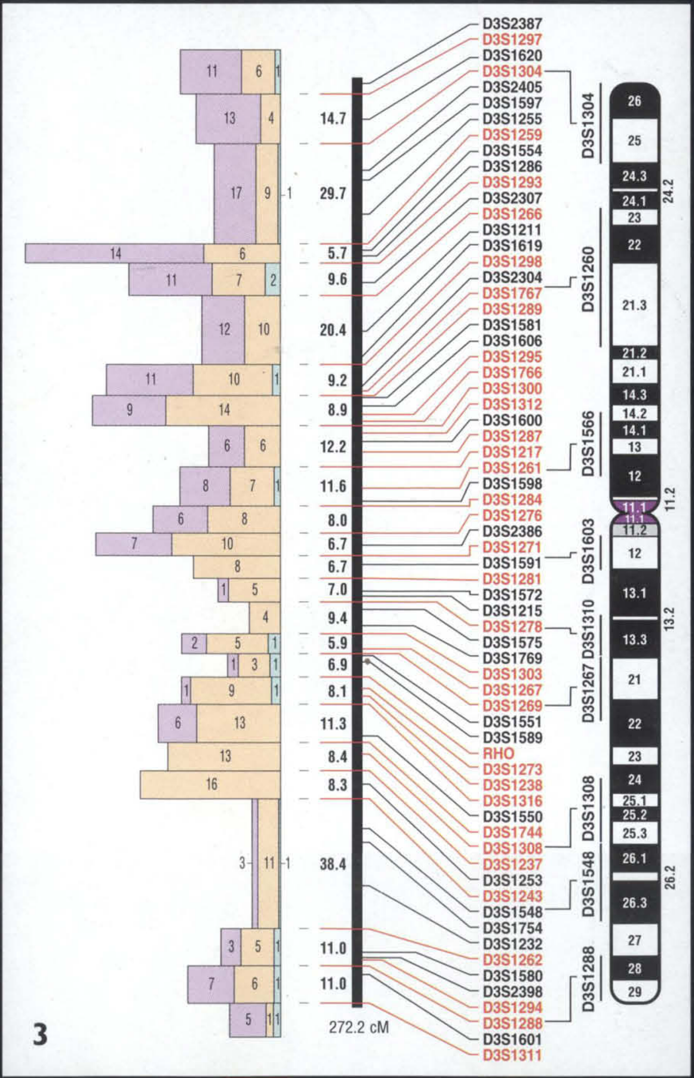
35.2
217.4 cM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272.2 cM
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D3S1288
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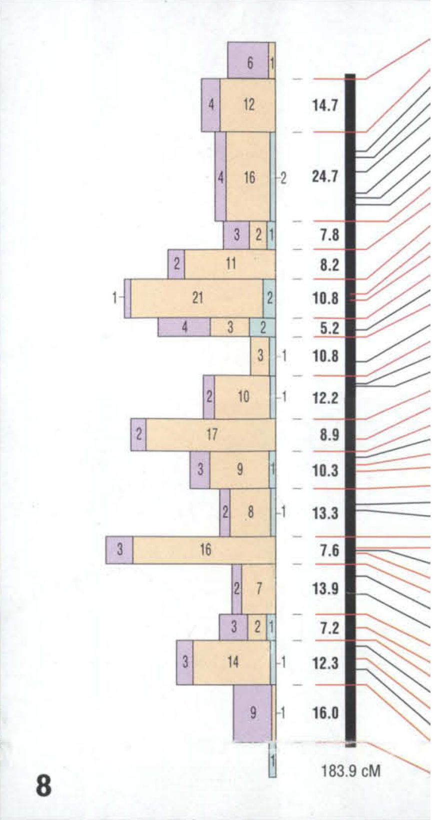
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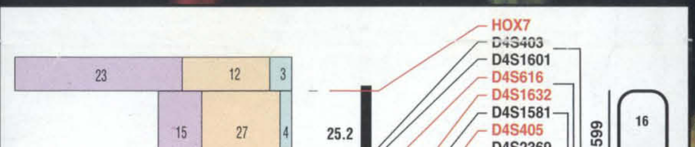
13.9
7.2
12.3
16.0
183.9 cM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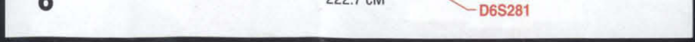
6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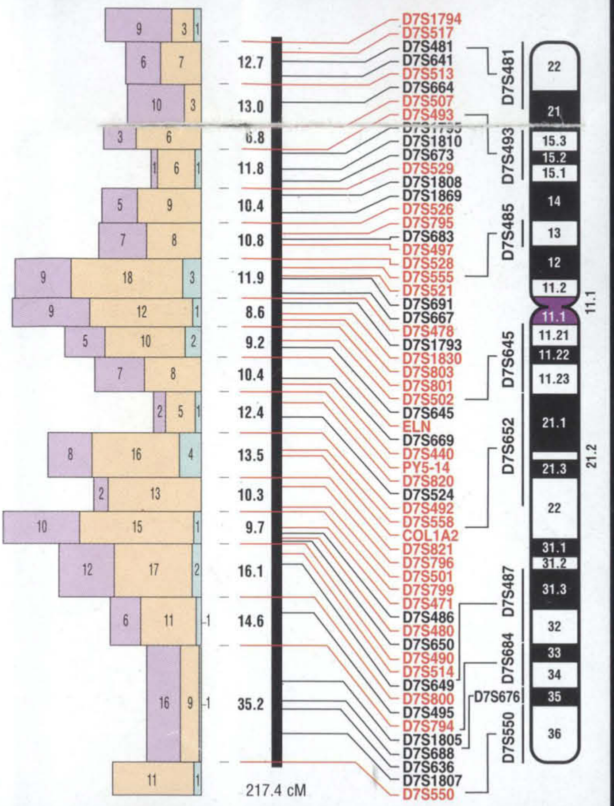
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12 17 2
6 11 1
16 9 1
11 1
12.7
13.0
6.8
11.8
10.4
10.8
11.9
8.6
9.2
10.4
12.4
13.5
10.3
9.7
16.1
14.6
35.2
217.4 cM
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D7S481
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D7S664
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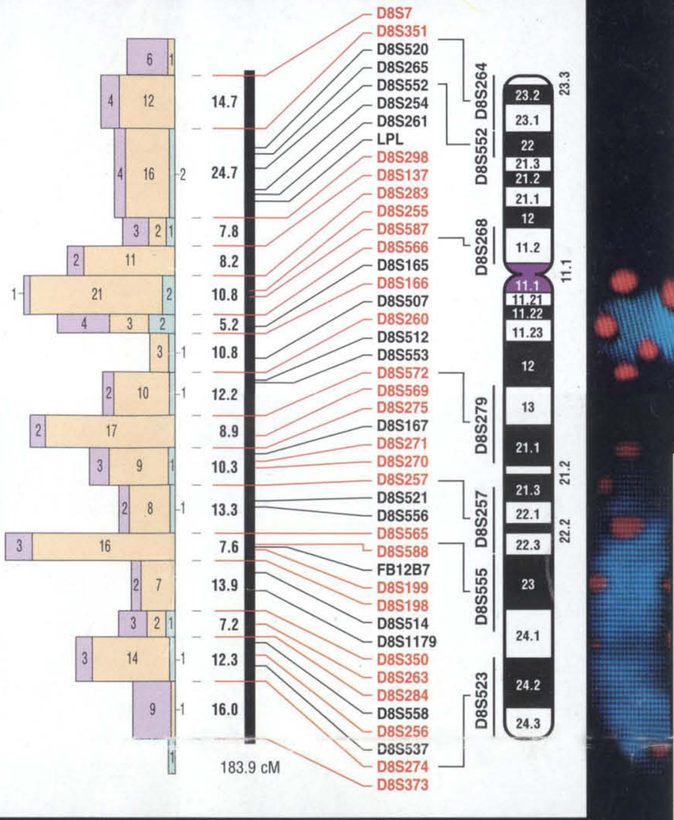
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D8S284
D8S558
D8S256
D8S537
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D8S268
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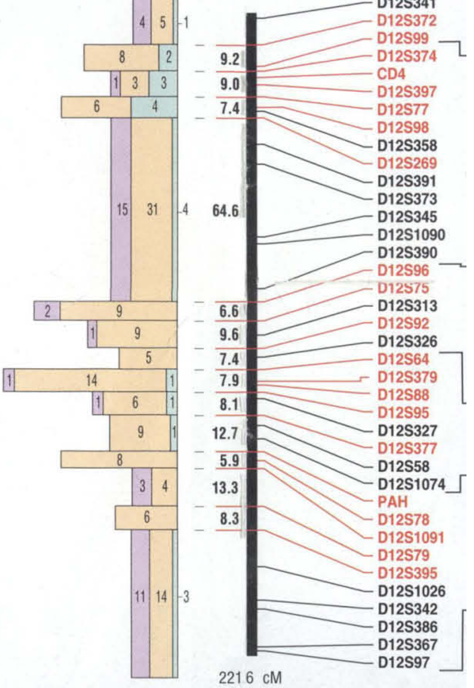
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221.6 cM
D12S341
D12S372
D12S99
D12S374
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D12S358
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D12S391
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D12S88
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D12S327
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D12S58
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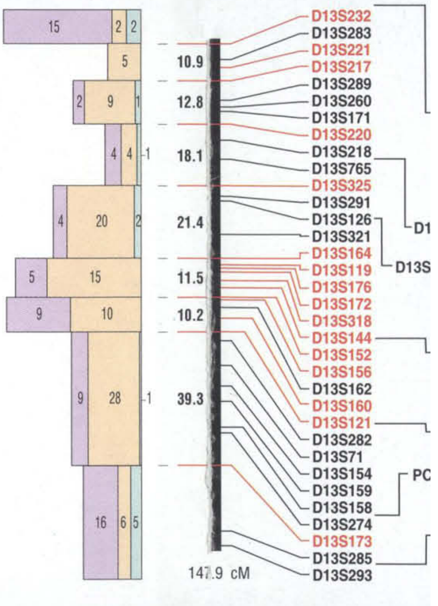
12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147.9 cM
D13S232
D13S283
D13S221
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D13S289
D13S260
D13S171
D13S220
D13S218
D13S765
D13S325
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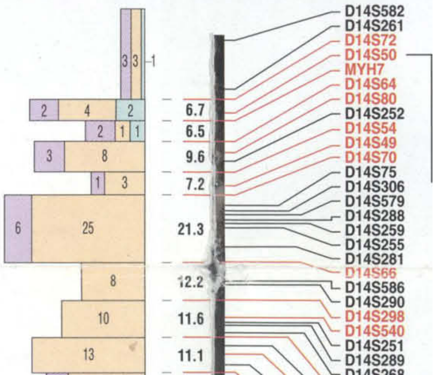
13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1 3
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11.1
D14S582
D14S261
D14S72
D14S50
MYH7
D14S64
D14S80
D14S252
D14S54
D14S49
D14S70
D14S75
D14S306
D14S579
D14S288
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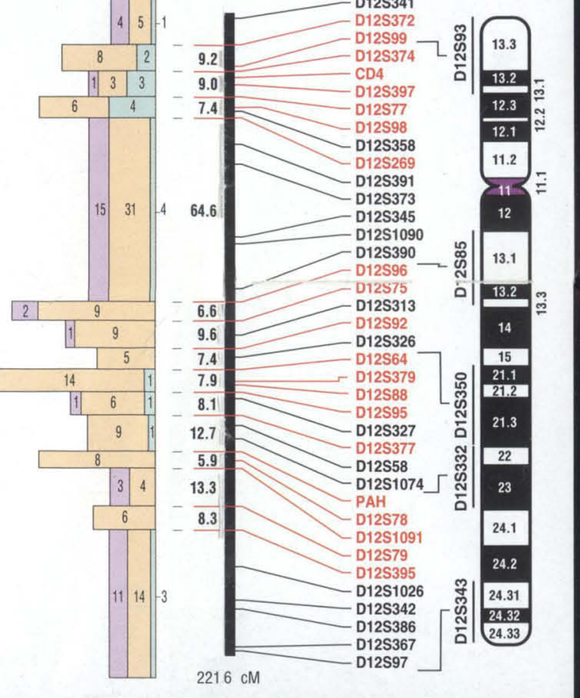

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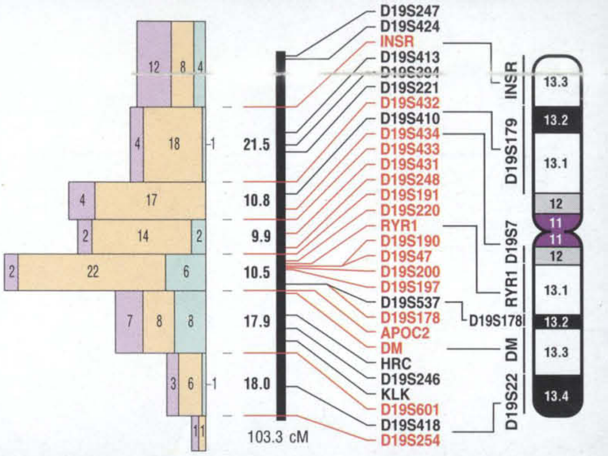

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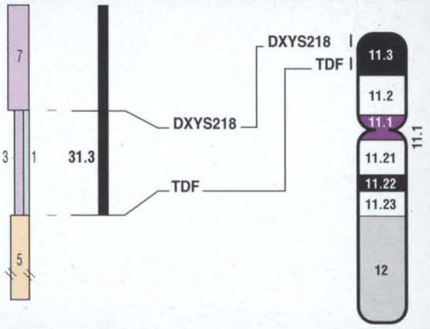
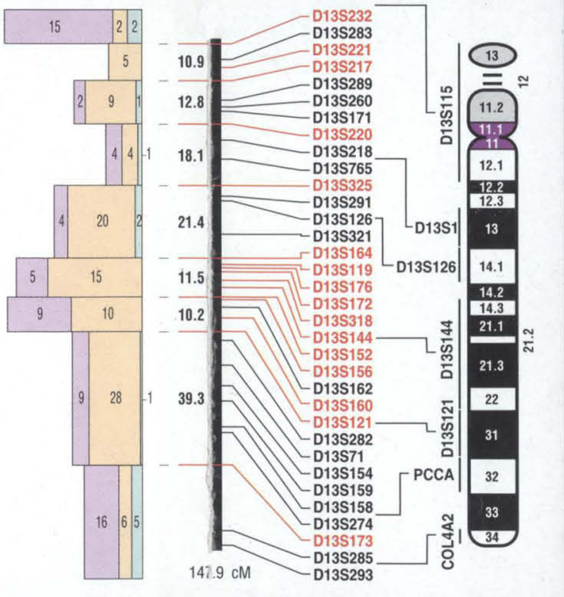
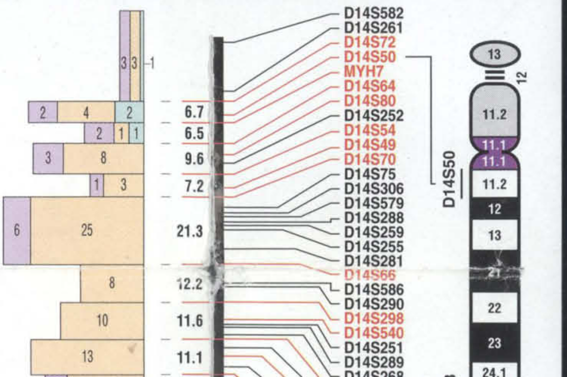






LEGEND

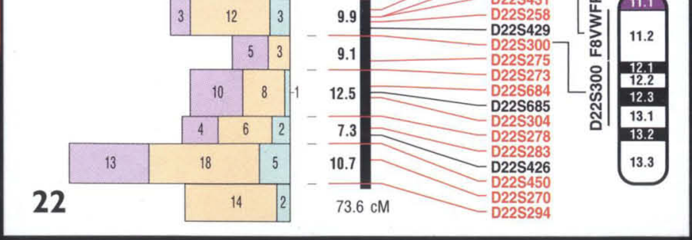
The chart presents a gen
integrates published data
distances, indicated in c
events observed between defined points (loci) on the map that occu

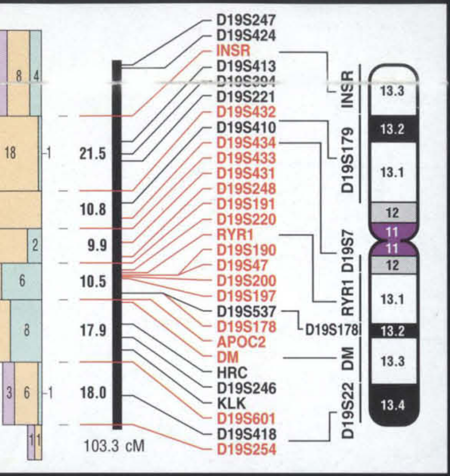
The map is composed solely of loci that contain short tande
within the map. Data contained in the map were obtained from fou
d'Etude du Polymorphisme Humain (CEPH) and the National Institu
the University of Utah Genome Center (UTAH). The data from Géné
CHLC data consist of markers with tri-, tetra-, and pentanucleotide
STRPs. All data used were generated from the CEPH reference pan

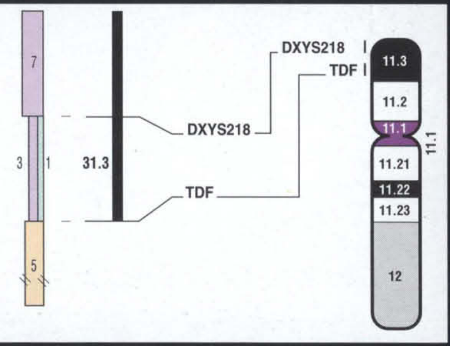
The map presented on the chart was constructed by first bui
map exceeded all others by odds of 1000:1. The map was constrai
the families used and did not inflate the map with their addition by
cy of errors in the primary data. The loci that are contained in this

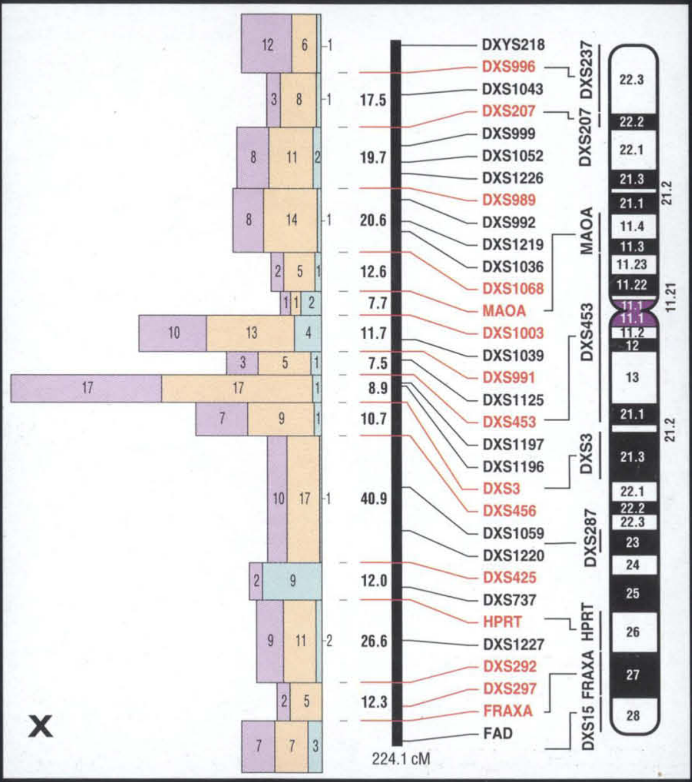
This map was used to define reference intervals for the cons
ence intervals if they could be excluded from all other intervals by
the minimum number of recombination events is shown. A single r
averaged and sex-specific recombination rates for these maps are

The banding patterns for each chromosome shown on the idi
tion. The correspondences between the cytogenetic and the geneti









END

The chart presents a genetic linkage map of the human genome (current as of 1 July, 1994) that
integrates published data sets with those provided by recent genome-wide mapping efforts. Genetic
distances, indicated in centimorgans (cM), are an additive measure of the proportion of cross-over
een defined points (loci) on the map that occurred during meiosis.

mposed solely of loci that contain short tandem repeat polymorphisms (STRPs). A total of 971 loci are uniquely ordered
contained in the map were obtained from four primary sources: Généthon, the mapping consortium of the Centre
nisme Humain (CEPH) and the National Institutes of Health (NIH), the Cooperative Human Linkage Center (CHLC), and
Genome Center (UTAH). The data from Généthon are based on markers containing CA repeat polymorphisms. The
markers with tri-, tetra-, and pentanucleotide repeat polymorphisms. The UTAH markers are primarily tetranucleotide
were generated from the CEPH reference panel of families.

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ers by odds of 1000:1. The map was constrained to contain only loci that showed homogeneity of recombination among
did not inflate the map with their addition by more than 2 cM. The degree of map inflation is an estimate of the frequen-
mary data. The loci that are contained in this map are shown in red.

sed to define reference intervals for the construction of a more detailed map. Additional loci were assigned to the refer-
could be excluded from all other intervals by odds of 1000:1. The relative order of loci within an interval that resulted in
of recombination events is shown. A single recombination event was sufficient to establish order between loci. Sex-
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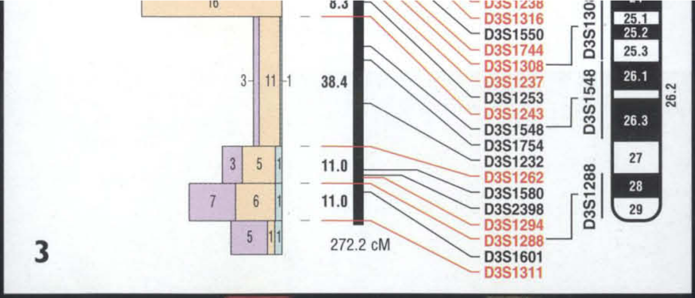

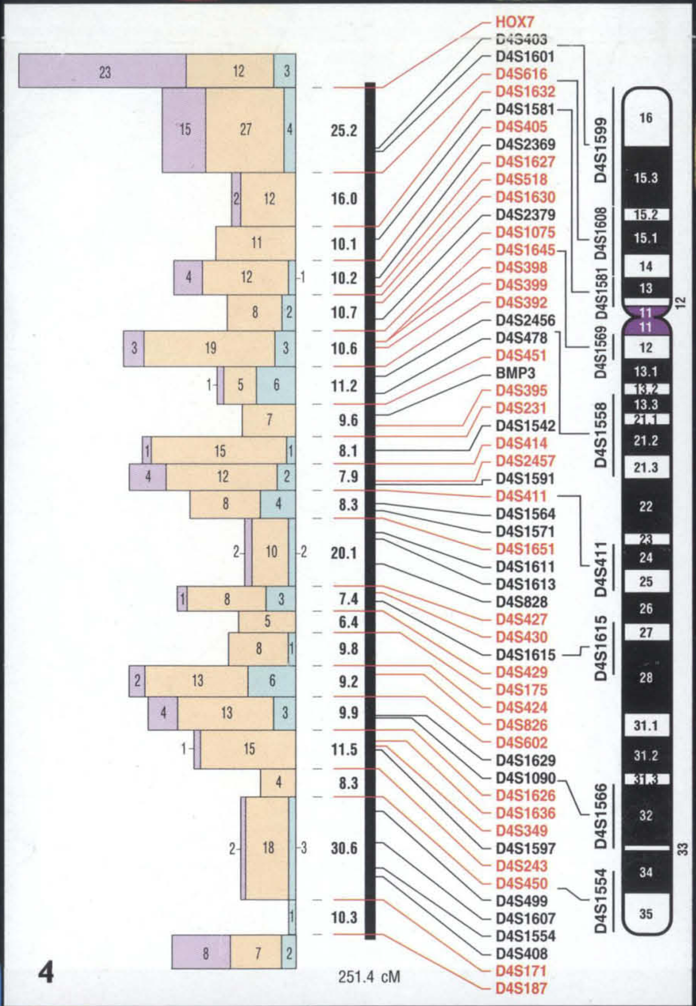

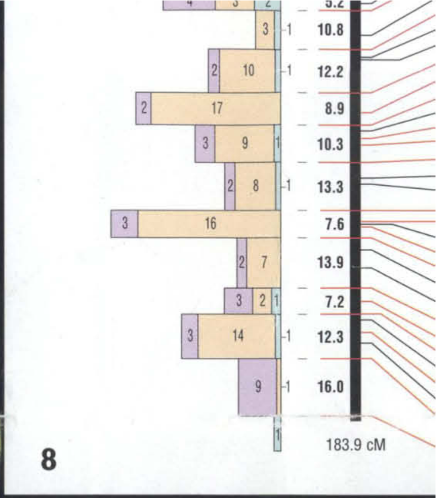

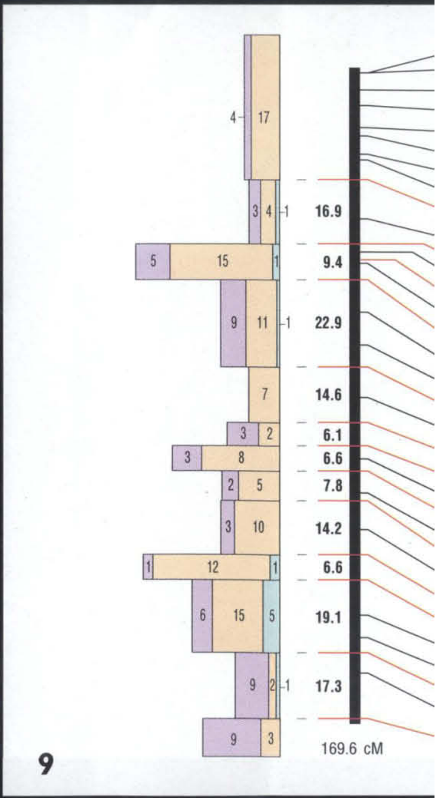

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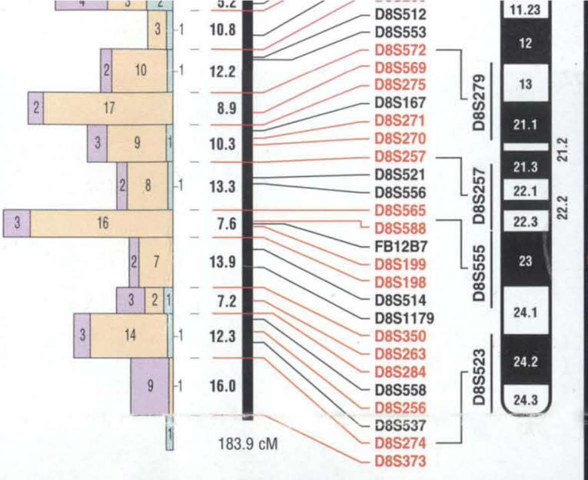

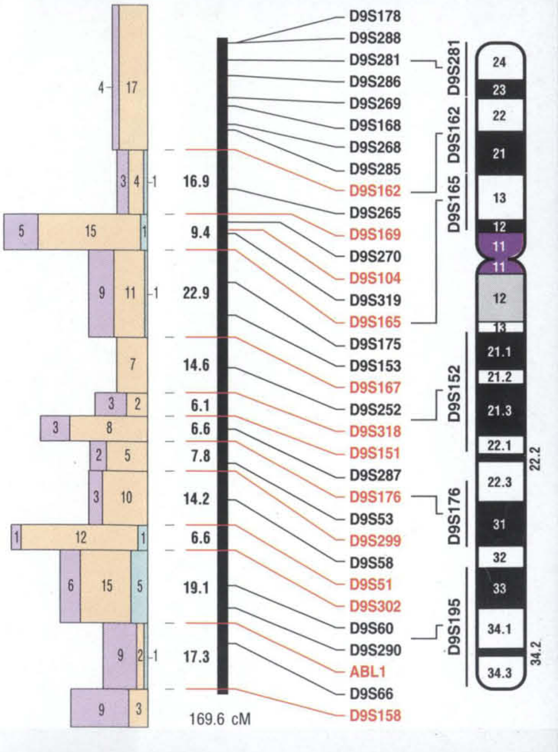

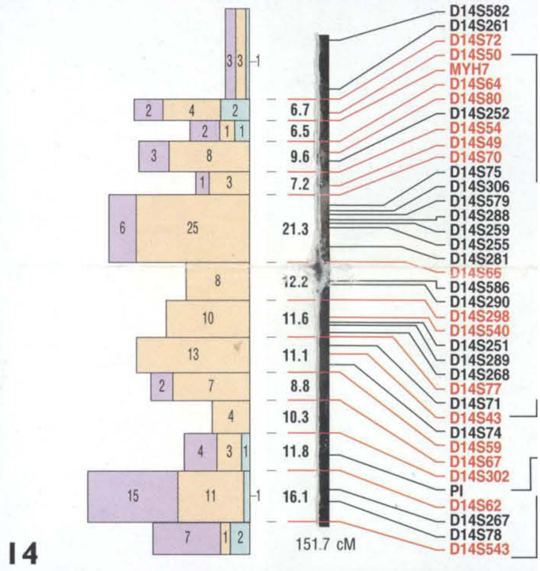

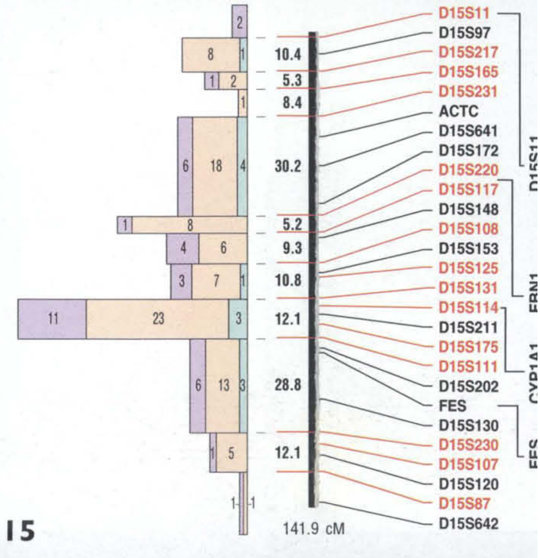

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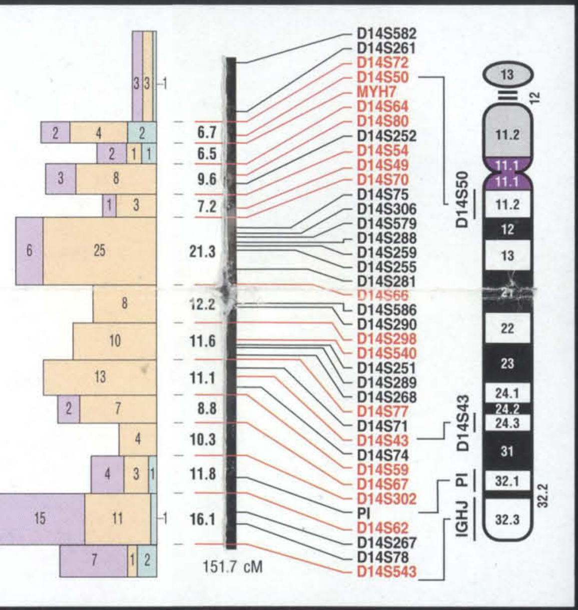

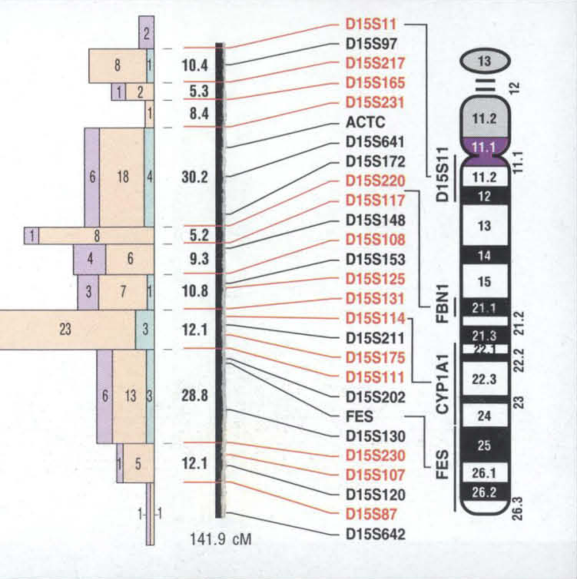

within the map. Data contained in the map were obtained from fou
d'Etude du Polymorphisme Humain (CEPH) and the National Institu
the University of Utah Genome Center (UTAH). The data from Géne
CHLC data consist of markers with tri-, tetra-, and pentanucleotide
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The map presented on the chart was constructed by first bui
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the families used and did not inflate the map with their addition by
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This map was used to define reference intervals for the cons
ence intervals if they could be excluded from all other intervals by
the minimum number of recombination events is shown. A single r
averaged and sex-specific recombination rates for these maps are

The banding patterns for each chromosome shown on the idi
tion. The correspondences between the cytogenetic and the geneti
yeast artificial chromosomes (YACs) and data from the Genome Da
chromosome so that marker density could be evaluated.

Accompanying the map is a histogram that includes the com
ment of additional markers available through the public version of
intervals for the histogram. The map distances between these poin
the exception of the X and Y chromosomes). Each of the loci withi
presented for a total of 5840 polymorphic loci. The histogram is s
each interval. As each interval varies in size, the width of the bar
tance. Therefore, the bar width indicates the density of markers (

Further information on the construction of the chart and the
article (CHLC *et al.*) in the 30 September, 1994 issue of *Science.*
which they were constructed can be obtained electronically throug

▬ Reference marker ▢ Genes ▢ STRPs

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• **Fluorescent chromosomes:** Paul Meltzer, Jeffrey M. Trent, National C
Lieman, David Ward, Yale University. • We would like to acknowledge the
staff at CEPH, whose work was essential to the construction of the huma

contained in the map were obtained from four primary sources: Généthon, the mapping consortium of the Centre
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marker density could be evaluated.

the map is a histogram that includes the complete set of loci from the data sets described above, as well as the place-
rkers available through the public version of the CEPH database. A subset of reference loci was used to define larger
gram. The map distances between these points are shown on the left side of the genetic map and are sex-averaged (with
and Y chromosomes). Each of the loci within the data set was assigned to its most likely interval. Genetic locations are
of 5840 polymorphic loci. The histogram is subdivided to indicate genes, STRPs, and other polymorphisms assigned to
h interval varies in size, the width of the bar was scaled by dividing the number of markers by the interval's map dis-
bar width indicates the density of markers (per centimorgan) in that interval.

ation on the construction of the chart and the state of human genetic linkage mapping can be found in the accompanying
n the 30 September, 1994 issue of *Science*. Access to more detailed presentations of the maps and the data sets from
tructed can be obtained electronically through ftp.chlc.org, gopher.chlc.org, or http://www.chlc.org/.

arker ▢ Genes ▢ STRPs ▢ Other polymorphisms ⟍⟍ Distance uncertain

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