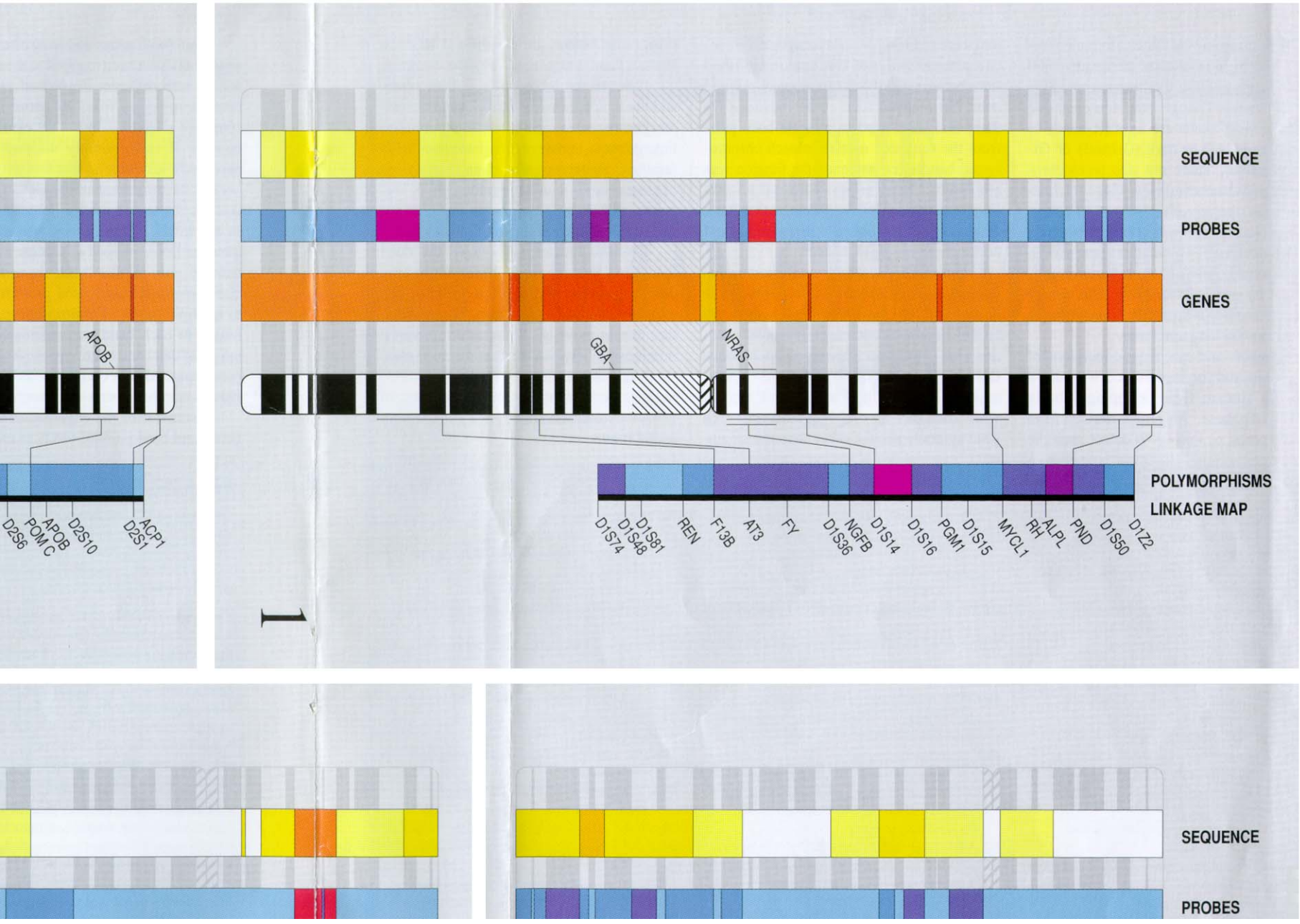

SEQUENCE
PROBES
GENES
APOB
GBA
NRAS
POLYMORPHISMS
LINKAGE MAP
D2S6
POMC
APOB
D2S10
D2S1
ACP1
D1S74
D1S48
D1S81
REN
F13B
AT3
FY
D1S36
NGFB
D1S14
D1S16
PGM1
D1S15
MYCL1
RH
ALPL
PND
D1S50
D1Z2
1
SEQUENCE
PROBES

PROBES
GENES
POLYMORPHISMS
LINKAGE MAP
HEXB
D5S10
D5S48
D5S4
D5S120
HPRTP2
D5S21
D5S76
D5S39
HEXB
DHFR
D5S71
D5S84
D5S70
D5S72
D5S22
D5S2
D5S43
5

SEQUENCE
PROBES
GENES
FNRB
CDC2
OAT

INS
HRAS
HBB@
WAGR
CAT
MEN1

PROBES
GENES
HLA@
C2
D6S7
F13A1
D6S8
HLA
GLO1
D6S5
MUT
PGM3
D6S26
D6S33
D6S21
D6S22

POLYMORPHISMS
LINKAGE MAP
D10S31
D10S32
D10S35
D10S28
VIM
D10S49
FNRB
RPB3
D10S22
EGR2
D10S16
D10S29
D10S4
D10S20
OAT
D10S6
10

HRAS1
HBB@
PTH
CAT
SEA
D11S141
D11S137
D11S132
D11S133
D11S129
11

SEQUENCE
PROBES
GENES
POLYMORPHISMS
LINKAGE MAP
HBA1
HBA2
HP
TAT
HBA@
D16S74
D16S70
D16S54
D16S48
D16S65
HP
D16S50
D16S40
APRT
16

TP53
NF1
HOX2@
COL1A1
D17S34
D17S5
POLR2
MYH2
D17S71
D17Z1
NF1
PPY
COL1A1
D17S74
GH
TK1
GAA
D17S75
17

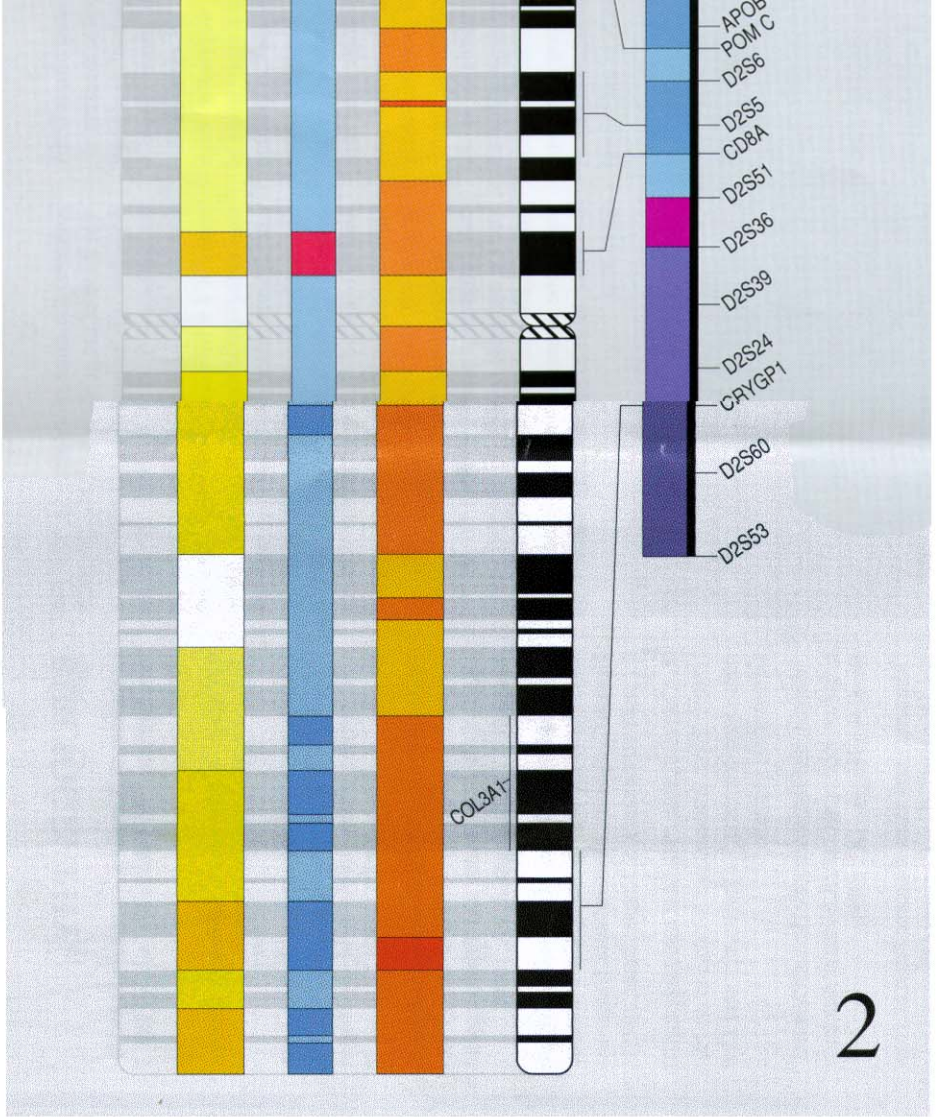
PALB
BCL2
MBP
D18S3
D18S21
D18S12
D18S1
JK
D18S22
D18S14
D18S5
D18S11
18

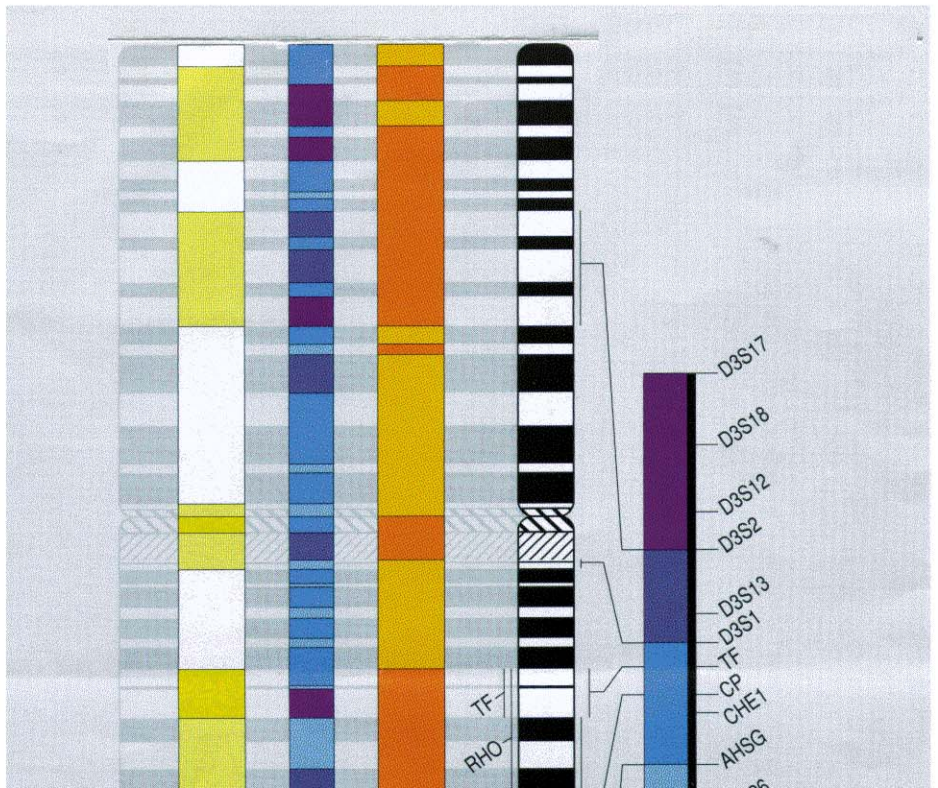
INSR
LDLR
D19S21
D19S26
INSR

6

7

8


APOB
POM C
D2S6
D2S5
CD8A
D2S51
D2S36
D2S39
D2S24
CRYGP1
D2S60
D2S53
COL3A1
2


D3S17
D3S18
D3S12
D3S2
D3S13
D3S1
TF
CP
CHE1
AHSG
TF
RHO

D6S21
D6S22
6

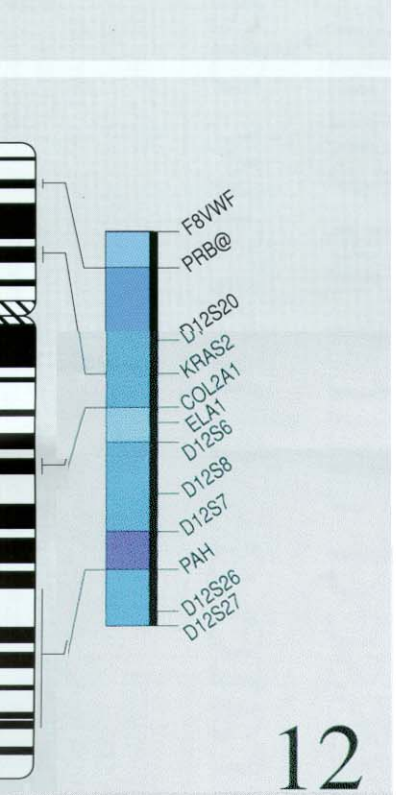
PRB@
KRAS2
COL2A1
PAH

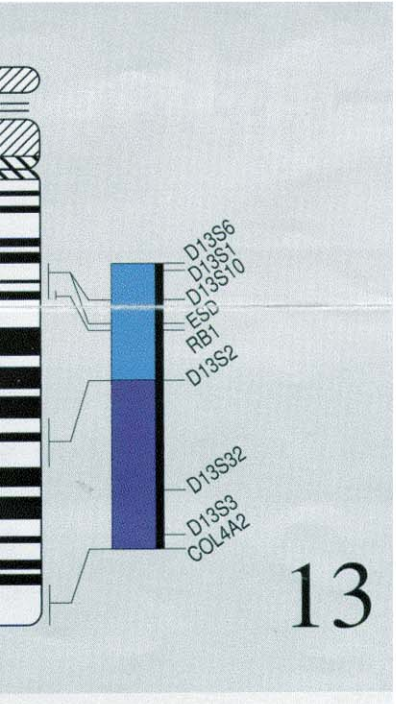
TCRG
EGFR
CF
TCRB
D7S135
D7S150
D7S370
TCRG
EGFR
ERV3
COL1A2
MET
TCRB
D7S372
D7S392
7

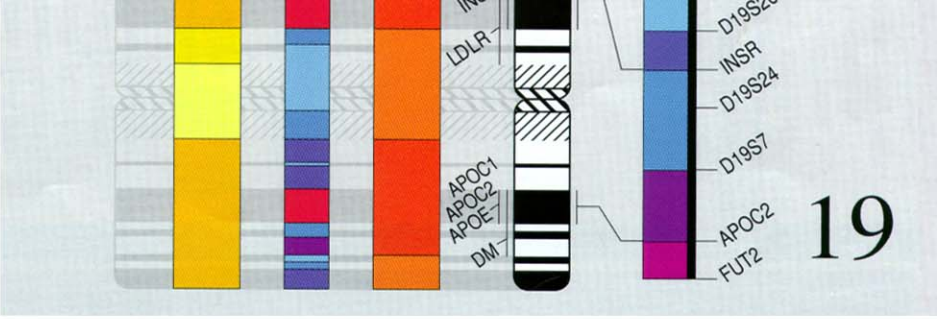
RB1

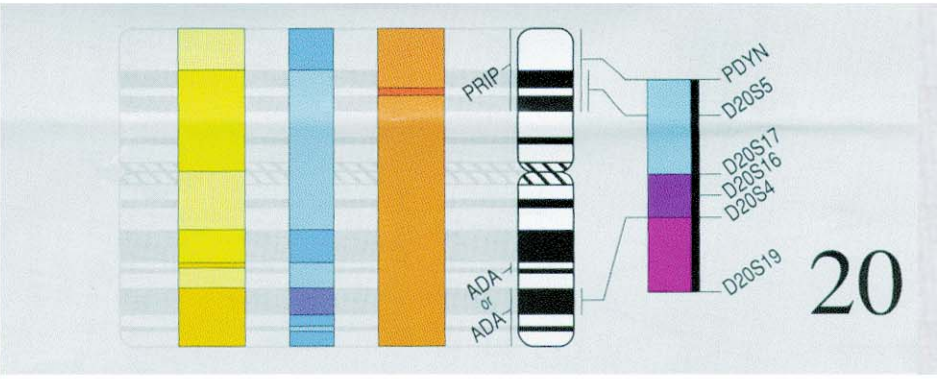
LPL
D8S23
PLAT
D8S33
D8S35
D8S26
D8S31
D8S24
D8S25

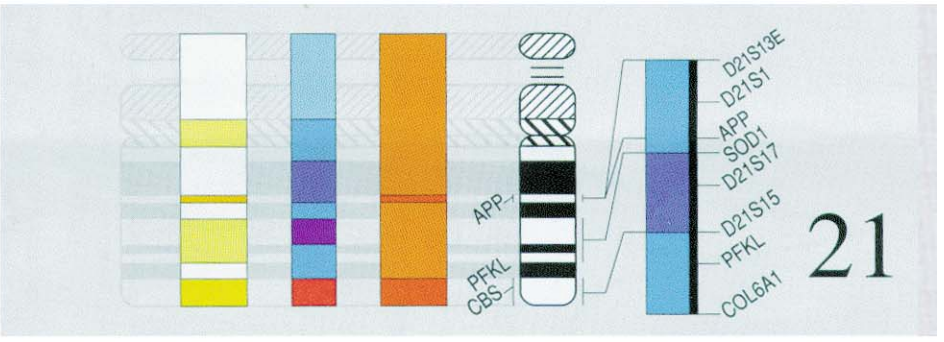
TCRA
TCRD

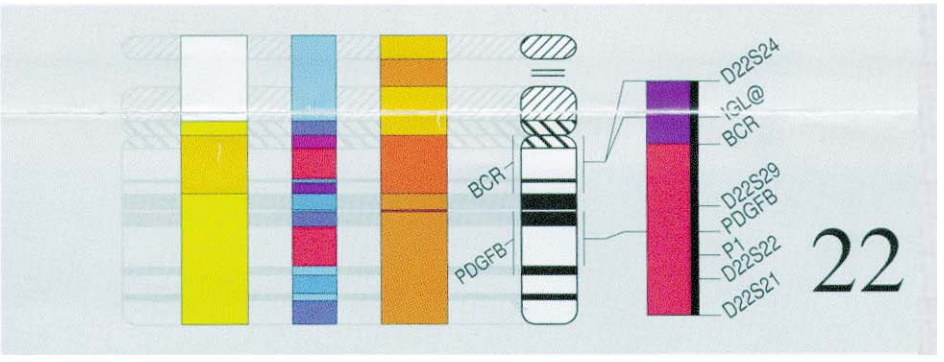

F8VWF
PRB@
D12S20
KRAS2
COL2A1
ELA1
D12S6
D12S8
D12S7
PAH
D12S26
D12S27
12

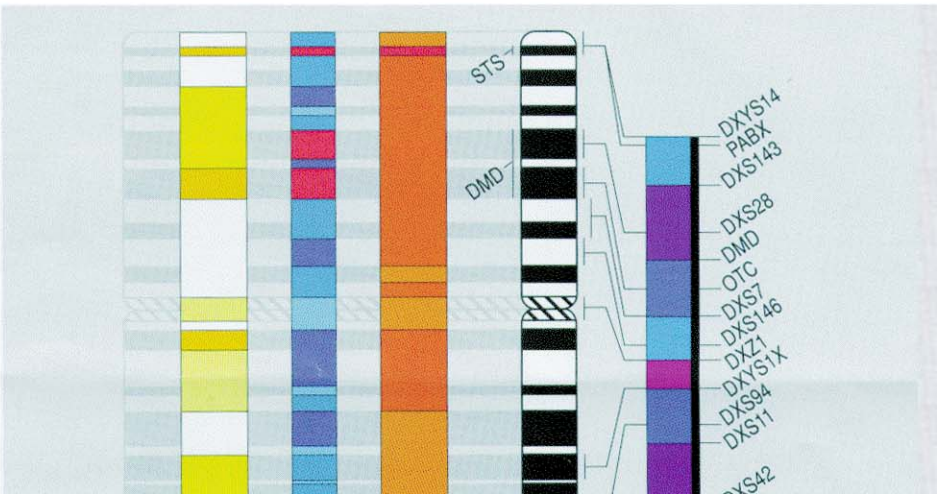

D13S6
D13S1
D13S10
ESD
RB1
D13S2
D13S32
D13S3
COL4A2
13


LDLR
APOC1
APOC2
APOE
DM
INSR
D19S24
D19S7
APOC2
FUT2
19


PRIP
ADA
or
ADA
PDYN
D20S5
D20S17
D20S16
D20S4
D20S19
20


APP
PFKL
CBS
D21S13E
D21S1
APP
SOD1
D21S17
D21S15
PFKL
COL6A1
21


BCR
PDGFB
D22S24
IGL@
BCR
D22S29
PDGFB
P1
D22S22
D22S21
22

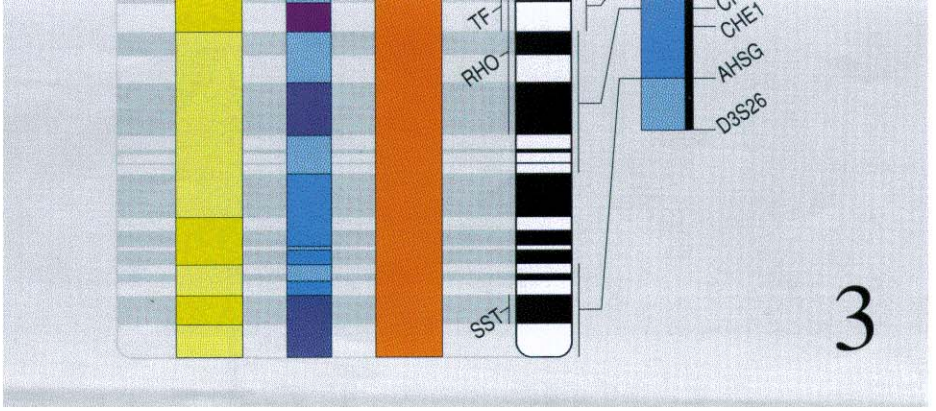

STS
DMD
DXYS14
PABX
DXS143
DXS28
DMD
OTC
DXS7
DXS146
DXZ1
DXYS1X
DXS94
DXS11

9

0

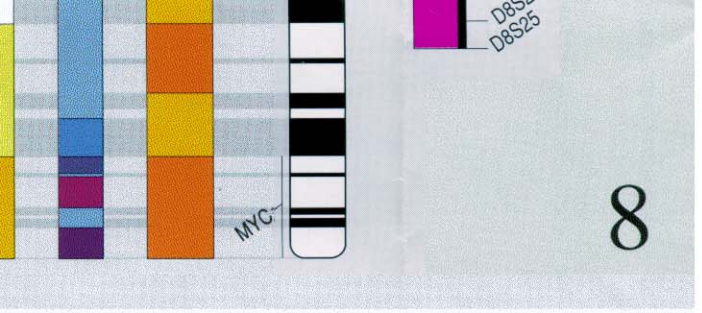
1

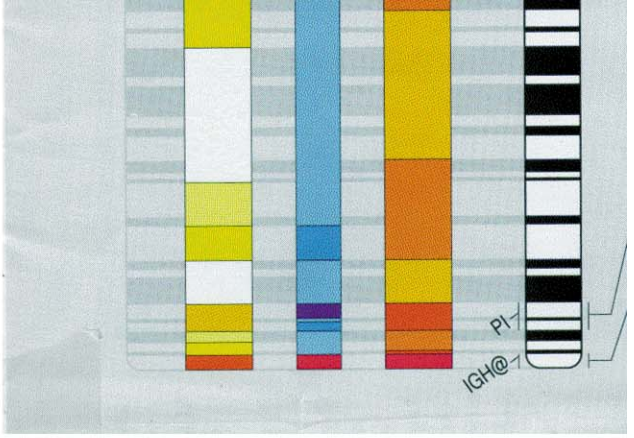
2

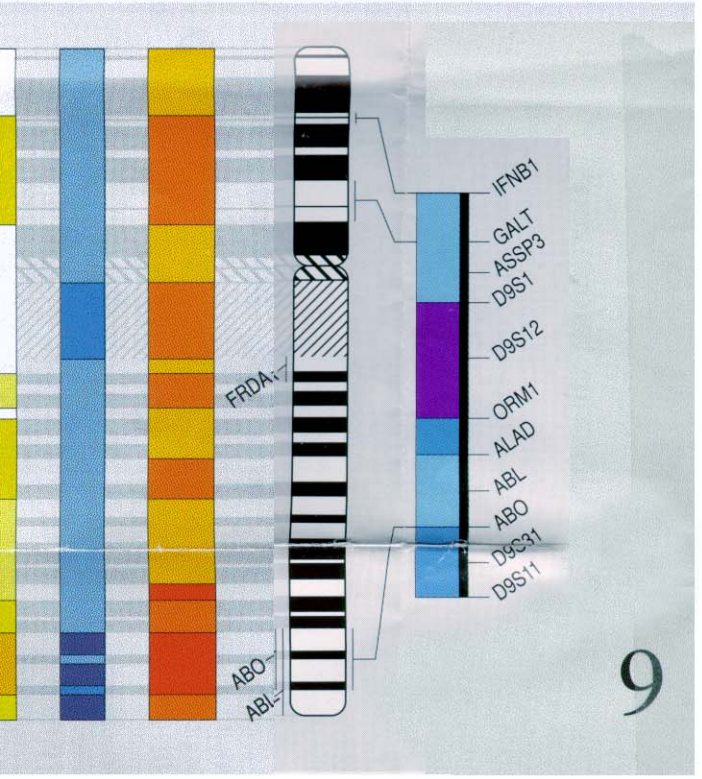


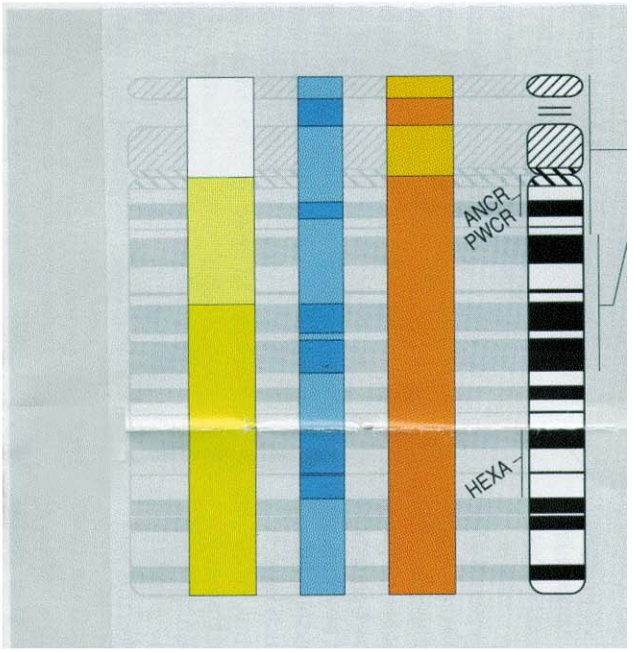
HUM

Results of efforts to map and sequence the human genome, either published or in press by July 31, 1990, are depicted in the bars surrounding the ideogram of each of the 24 chromosomes. Each type of bar is labeled at the top of the wall chart. The data are illustrated as colored intervals according to logarithmic or linear scales, as shown in the legend. Further information, including a

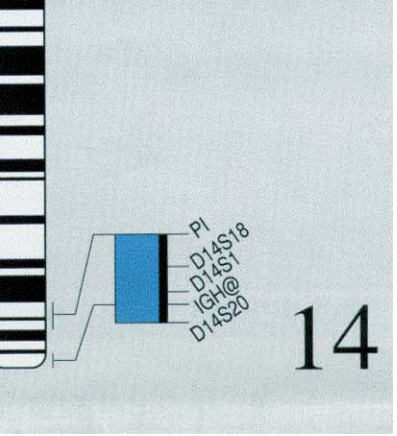


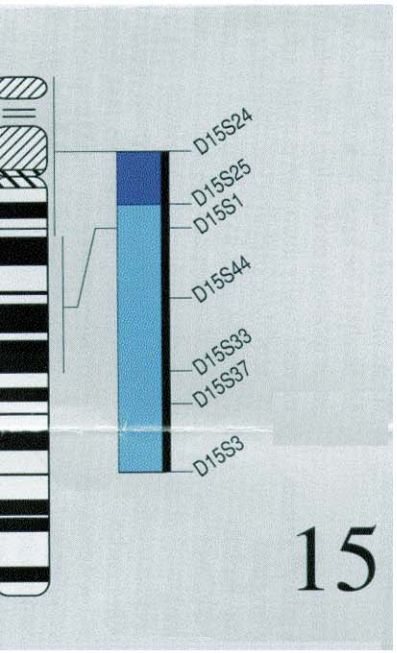


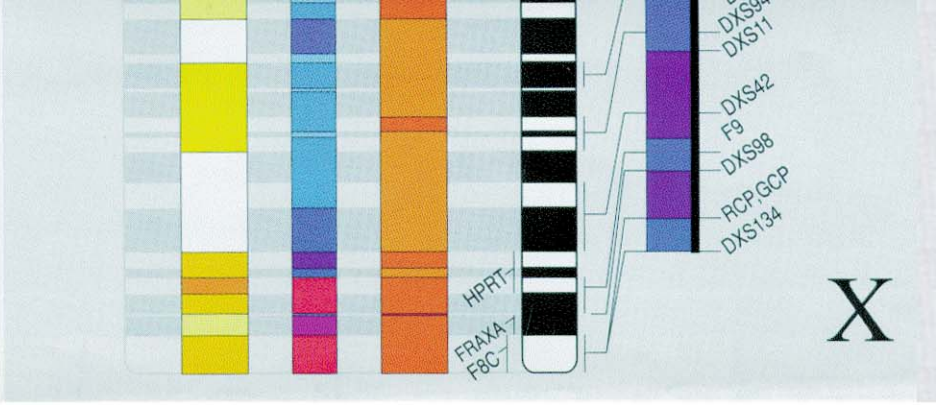


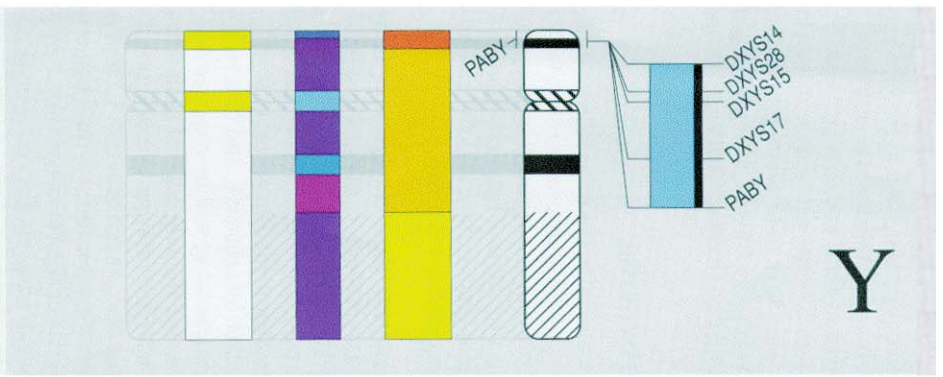


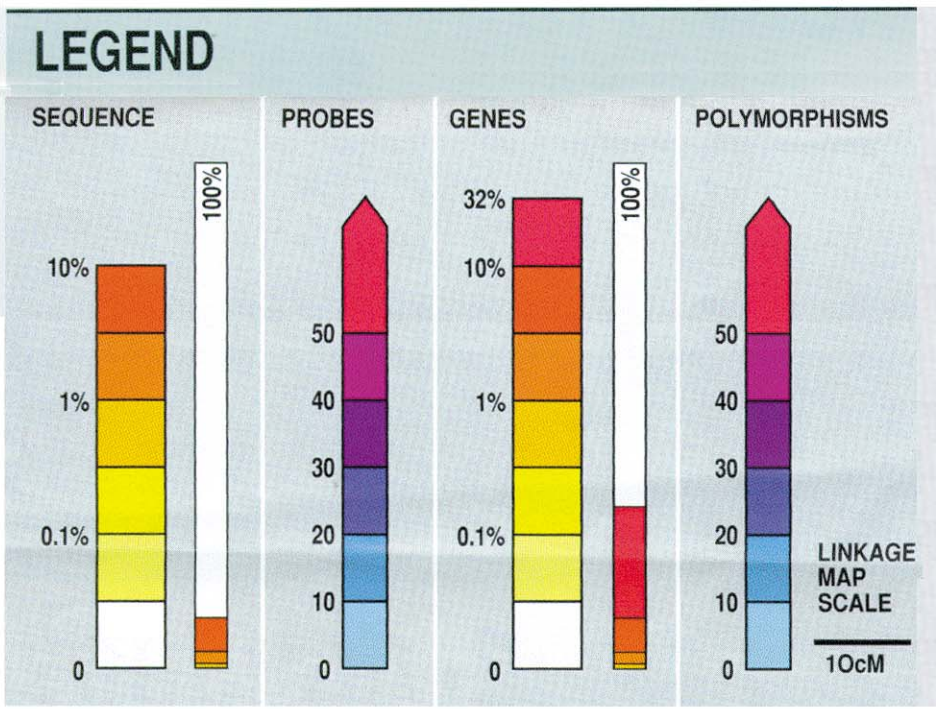
THE
UMAN GENOME M
1990











MAP

in centimorgans for loci selected from published maps to give an illustrative map with a resolution averaging 10 to 20 cM. The POLYMORPHISMS bar indicates the number of known polymorphic loci allocated to the cytogenetic intervals formed by the linkage map. Lines connect the bar to the ideogram for those loci with a precise cytogenetic map localization.

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e bar
netic

of the wall chart. The data are illustrated as colored intervals according to logarithmic or linear scales, as shown in the legend. Further information, including a description of the allocation and estimation procedures, appears on the back and in the accompanying article (J. C. Stephens *et al.*) in the October 12, 1990 issue of *Science*.

The SEQUENCE density bar indicates progress towards determining the complete DNA sequence of each chromosome band. An estimate of progress for each band was obtained by dividing the length of known DNA sequence currently allocated to the band by the length

that was estimated to ex

The PROBES distribu
scientific research activi
number of probes (def
clones and PCR primers

The GENES density b

ted to exist in that band.

s distribution bar reflects the extent of rch activity for each band by showing the bes (defined pieces of DNA including R primers) allocated to the band.

density bar shows progress towards identifying all genes in each band. As wi estimate of progress was calculated by d ber of known genes allocated to the band total number of genes in the band.

The LINKAGE MAP, shown as the hea the polymorphism bar, depicts relative o

As with sequence, an
ed by dividing the num-
ne band by the estimated
d.
he heavy right border of
ative order and distance

to the ideogram for those loci with a precise cytogene
map localization.

Representative genes are identified by their alp
numeric symbols to the left of the ideogram. Vertical b
show the band (or bands if less precisely mapped) kno
to contain each gene. Names and disease associations
in the table on the back. These genes were incluc
because of their location in bands of high informat
content or because of their interest to the broad scienti
community or the general public.

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