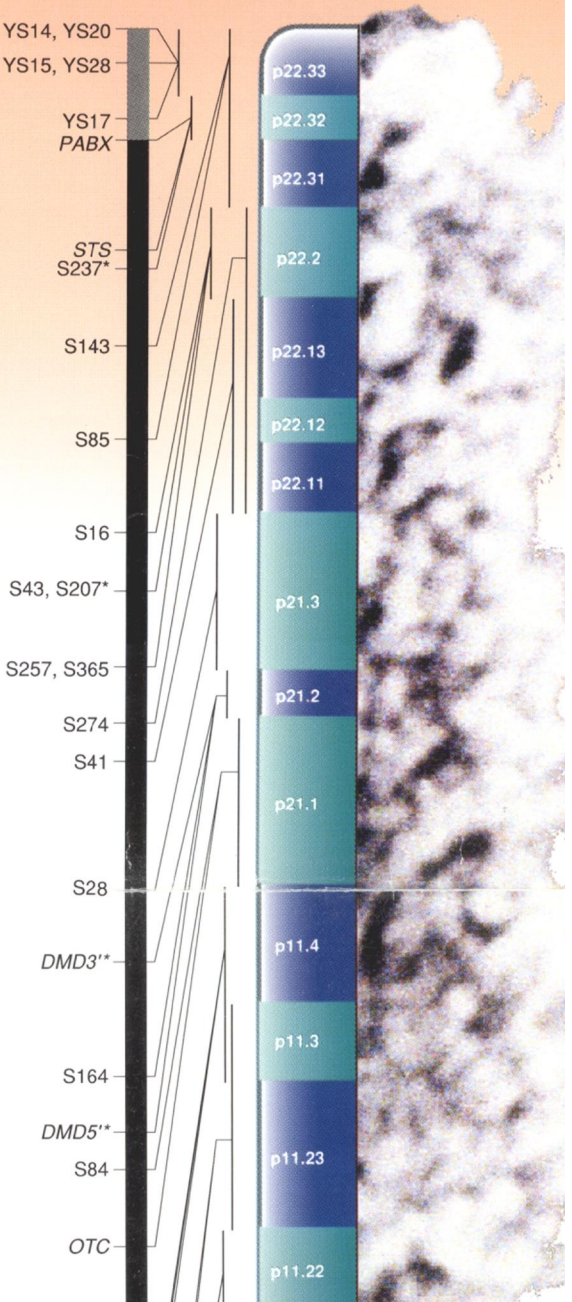
GEN

Linkage Map



The wall chart highlights advances in genetic and physical mapping of the X chromosome, which has been the center of considerable excitement in mapping of disease-related genes. At the far left, the genetic linkage map is a composite of information presented at the Third X Chromosome Workshop (Naples, Italy, April 3-4, 1992) by P. Fain and D. Barker, information from the CEPH database, and published regional maps. The linkage map is estimated to be 200 cM in length. The markers shown here (and on the physical map) were selected to be representative of the information currently available. The pseudoautosomal region is indicated in grey. Genetic distances are approximations and, in some cases, represent averages from different sources. For the anonymous markers, D numbers have been abbreviated as S for X-linked segments, and YS for pseudoautosomal loci. Highly informative markers are indicated (asterisk). Diagonal lines relate the genetic linkage map to the cytogenetic banding pattern. The right half of the chromosome image is a rendering of the X chromosome as viewed by scanning electron microscopy.

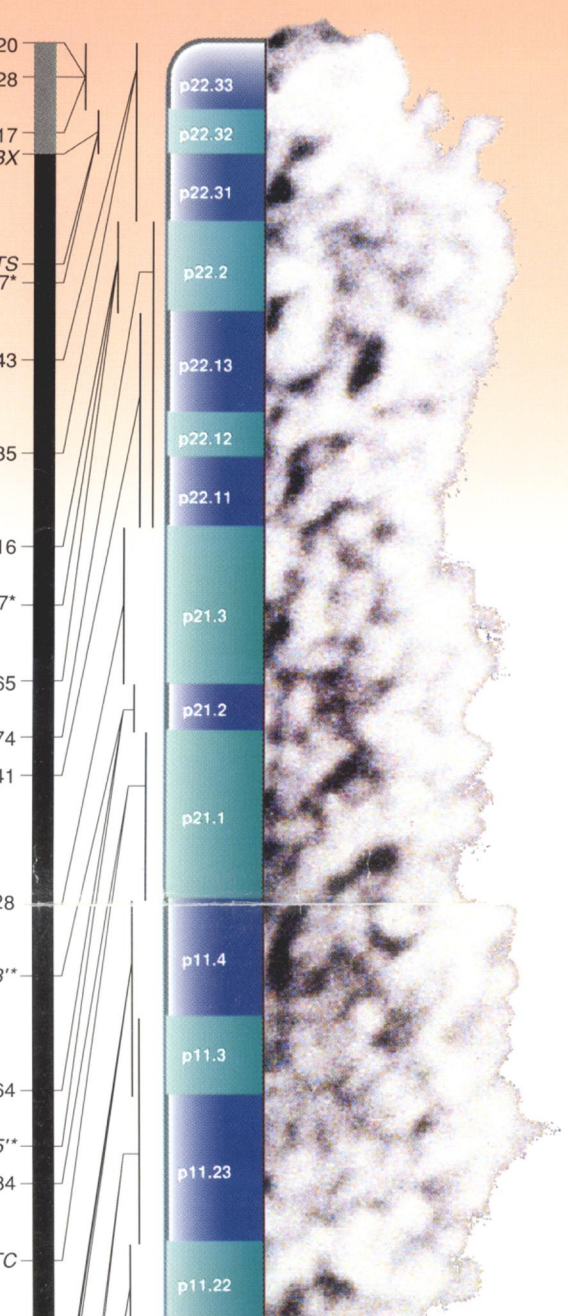
The physical map is a summary of information presented at the Third X Chromosome Workshop and maps that are published or in press. The diagram indicates regions that have been mapped as YAC contigs (thick box), regions where YAC contigs have not been generated but where distances can be estimated by PFGE maps (thin box), and regions where no information is available (line). The only exact distances are represented by the sizes of the YAC contigs. When neither YAC contigs nor PFGE information was available, distances were estimated on the basis of the maximum amount of DNA predicted to be in the particular band. The location and relative order of representative genes [(black) if cloned; (blue) if uncloned] and anonymous markers with respect to the diagram are shown in the columns next to the YAC contigs. Brackets indicate the limits of uncertainty in localizing the adjacent genes or markers or an area in which the relative order is uncertain. Some anonymous markers and genes were categorized as highly informative (asterisk) or as reference markers (red); all genes shown as reference markers on the chart have been

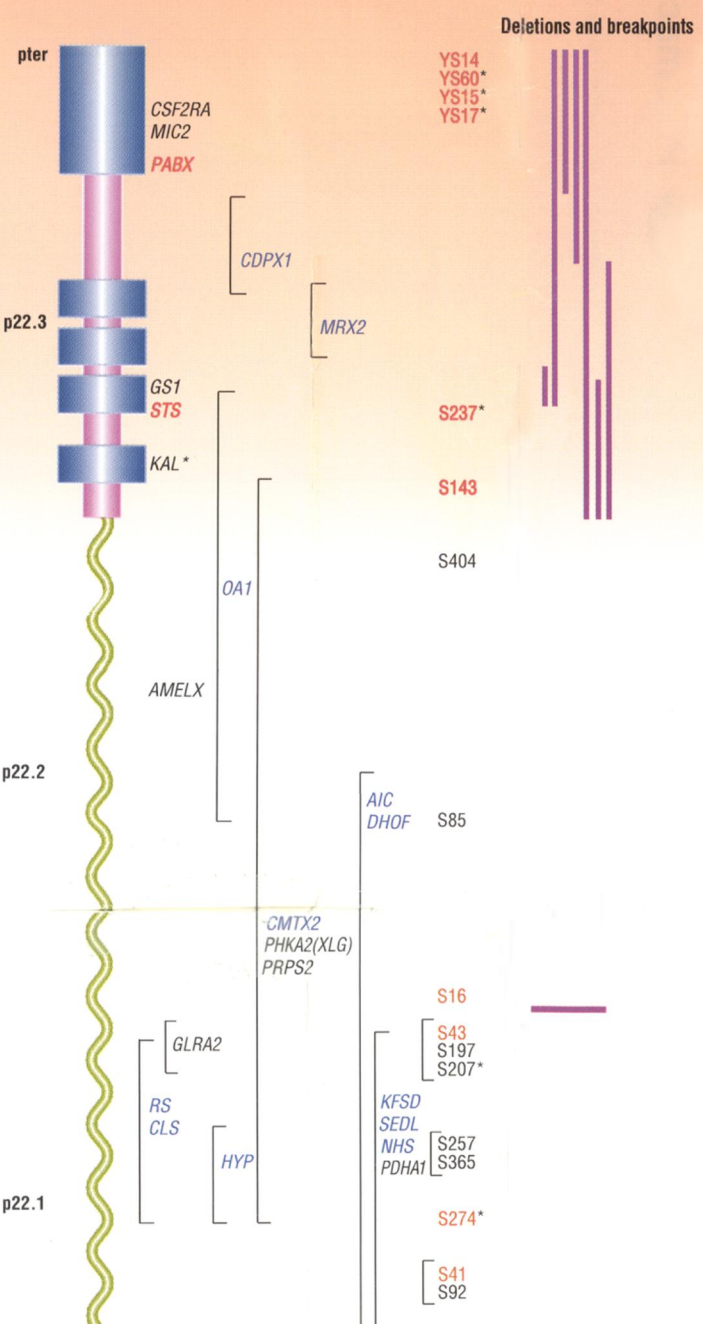
SCIENCE

GENOME M

nkage Map

Physical

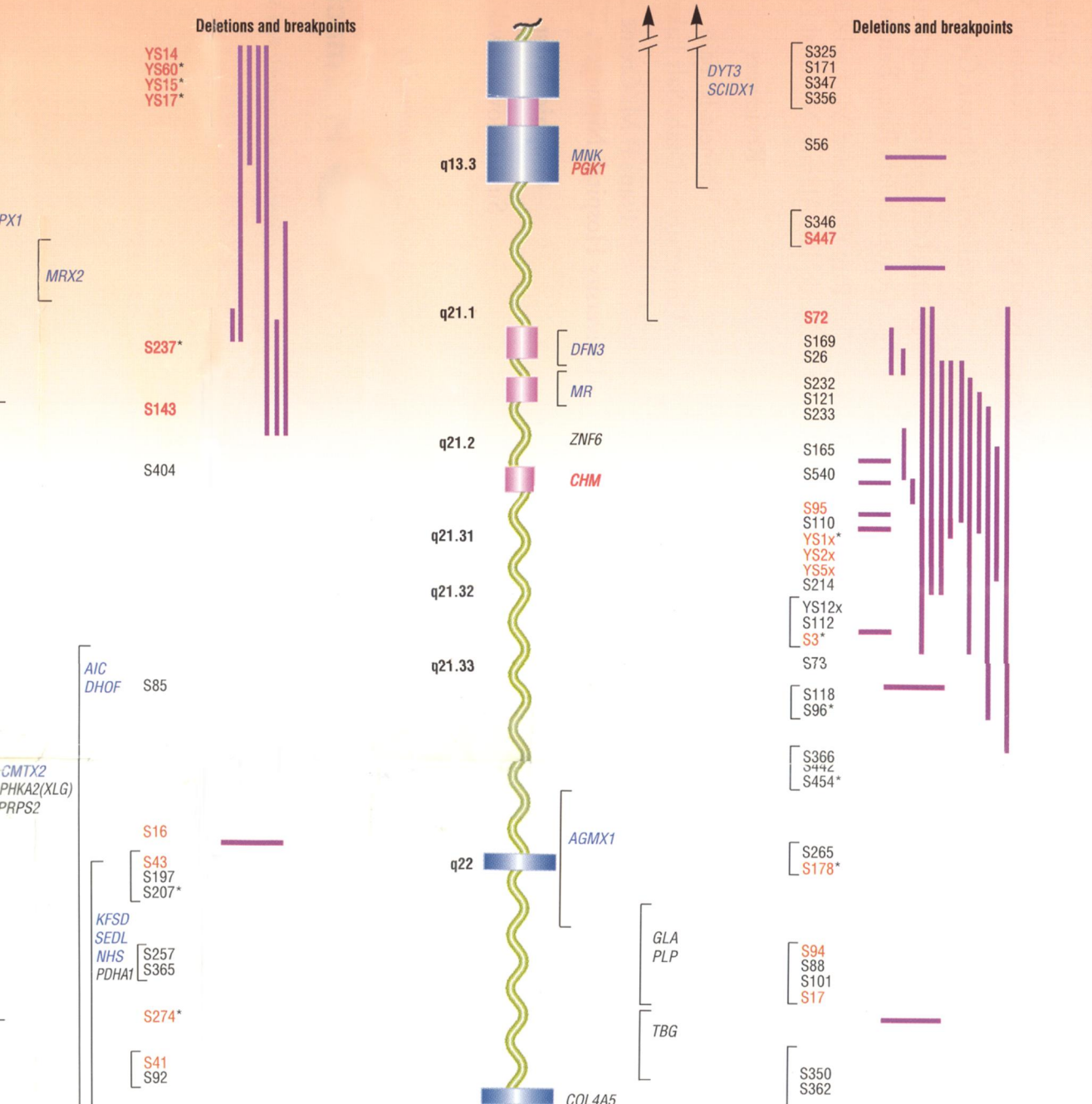




SCIENCE

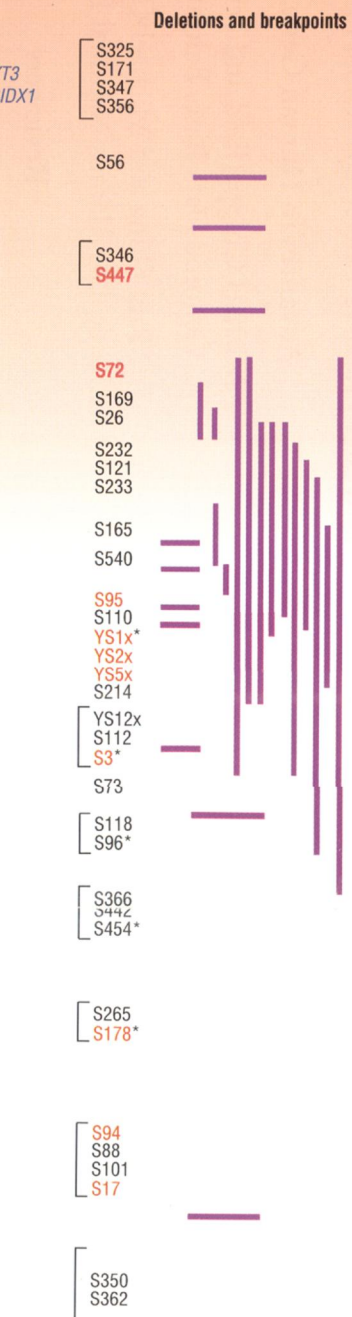
ME MAPS III

Physical Map



S III

Disease-Related Genes on X



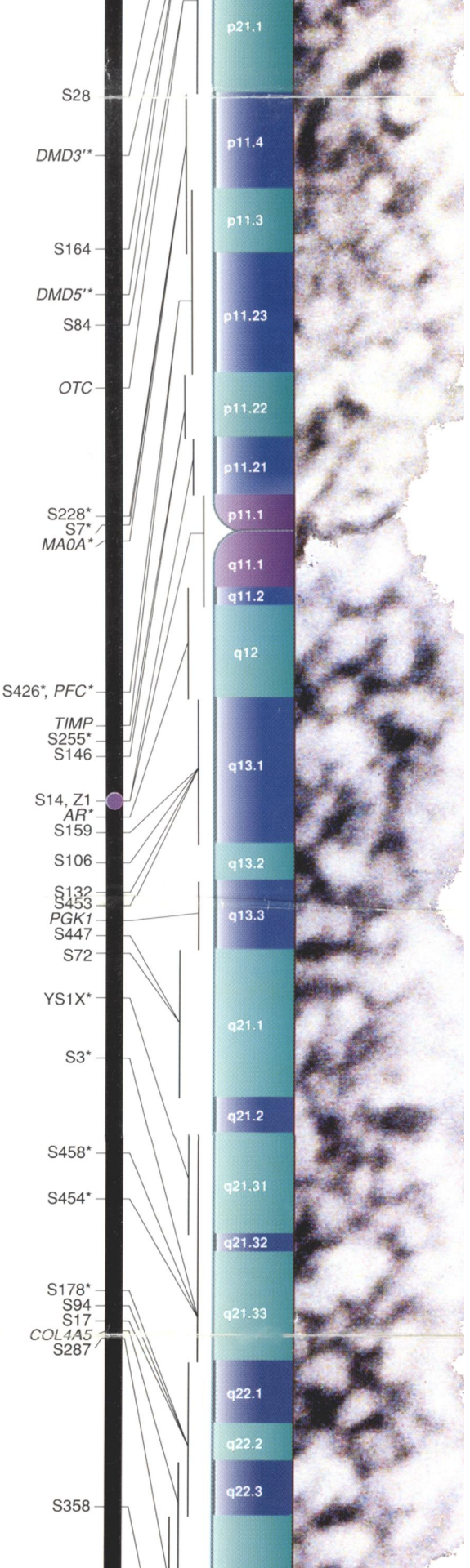
Region	Symbol	Disease	Nearest markers or name and function of protein
EYE			
p22.3-22.2	*OA1*	Ocular albinism, Nettleship-Falls type	S237 - S143, *OAI* - S16 (~10 cM)
p22.2-p22.1	*RS*	Retinoschisis	S207, S43 - *RS* - S274 (6 cM)
p22.1	*NHS*	Nance-Horan cataract-dental syndrome	S43 - *NHS* - S67
p21.1	*RP3*	Retinitis pigmentosa-3	*CYBB* - *RP3* - BB deletion breakpoint (160 kb)
p11.4	*NDP*	Norrie disease (retinal dysplasia and ocular degeneration)	Candidate cDNA cloned
p11.3	*CSNB1*	Congenital stationary night blindness	*MAOA* - *CSNB1* - S255
p11.3	*RP2*	Retinitis pigmentosa-2	S7 - *RP2* - S426
p11-q11	*AIED*	Aland island eye disease (ocular albinism, Forsius-Eriksson type)	Linked to S255
q21.2-q21.31	*CHM*	Choroideremia	Possible G-protein regulator
q21.3-q22	*MGC1*	Megalocornea, X-linked	Linked to S94, S87
q28	*MYP1*	Myopia-1, X-linked; Bornholm eye disease	Linked to *F8C*, S52
q28	*RCP, GCP*	Blue cone monochromacy; deutan or protan color blindness	Red and green cone pigments (opsins)
HEMATOLOGIC AND IMMUNODEFICIENCIES			
p21.1	*XK*	McLeod phenotype (acanthocytosis and absence of K^x red blood cell antigen)	S709 - *XK* - *CYBB* (400 kb)
p21.1	*CYBB*	Chronic granulomatous disease	ß subunit of cytochrome b
p11.3-p11.23	*PFC*	Properdin deficiency, X-linked	Properdin P factor, complement
p11.3-p11.22	*WAS*	Wiskott-Aldrich syndrome (immunodeficiency and thrombocytopenia)	*TIMP* - *WAS*, S255 - S146 (1 cM)
p11.21	*ALAS2*	Anemia, sideroblastic/hypochromic	Erythroid δ aminolevulinate synthase
q13.3	*PGK1*	Hemolytic anemia due to PGK deficiency	Phosphoglycerate kinase
q13.1-q13.3	*SCIDX1*	Severe combined immunodeficiency, X-linked	S132 - *SCIDX1, PGK1* - S447 (4 cM)
q21.3-q22	*AGMX1*	X-linked agammaglobulinemia	S366, S442 - *AGMX1*, S178, S265 - S94 (~5 cM)
q24-q27	*HIGM1*	X-linked immunodeficiency with hyper-IgM	Linked to S42
q25	*LYP*	Lymphoproliferative syndrome, X-linked	S37 - *LYP* - S42
q27.1	*F9*	Hemophilia B	Coagulation factor IX

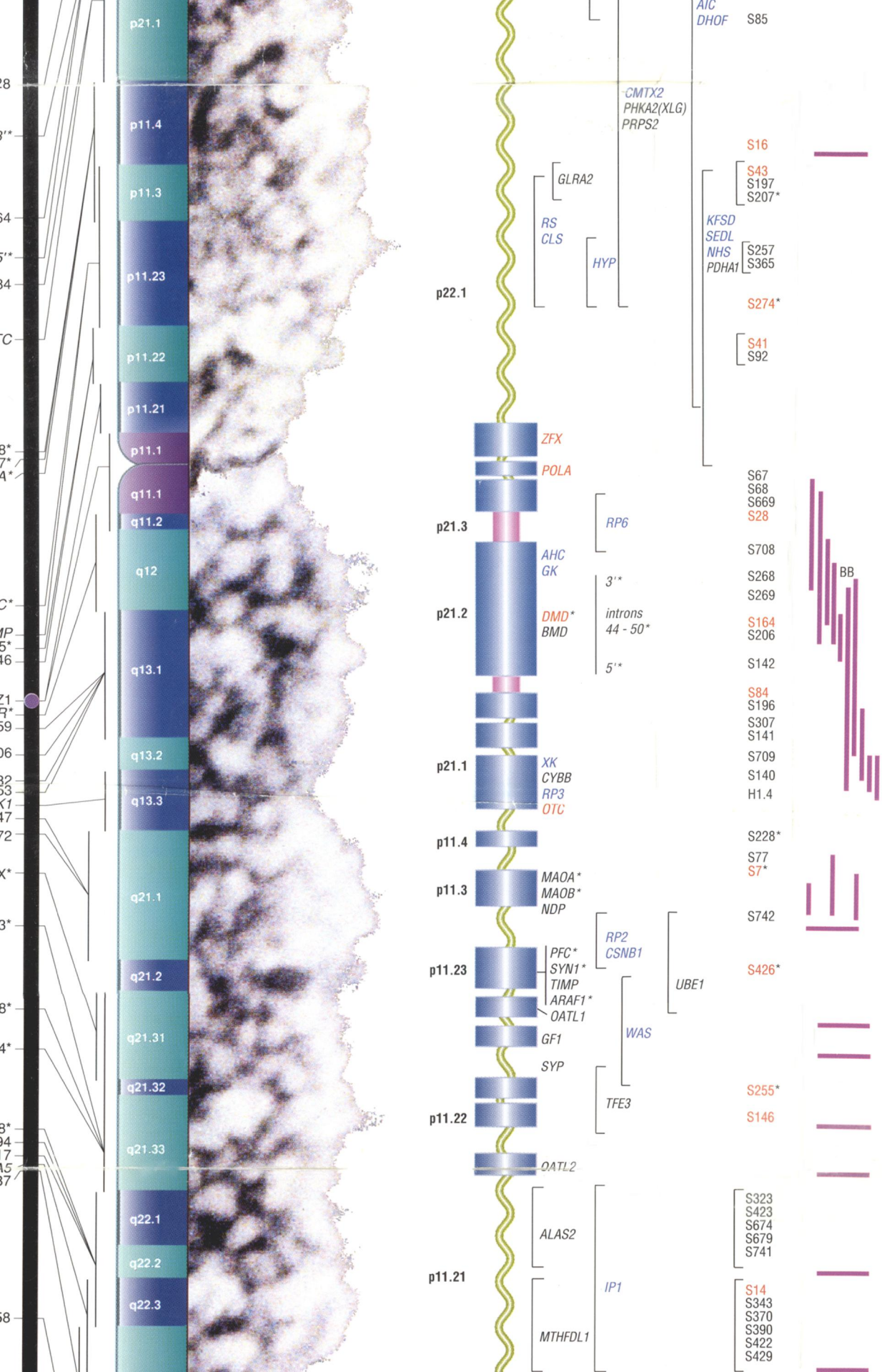
YAC contigs have not been generated but where distances can be estimated by PFGE maps (thin box), and regions where no information is available (line). The only exact distances are represented by the sizes of the YAC contigs. When neither YAC contigs nor PFGE information was available, distances were estimated on the basis of the maximum amount of DNA predicted to be in the particular band. The location and relative order of representative genes [(black) if cloned; (blue) if uncloned] and anonymous markers with respect to the diagram are shown in the columns next to the YAC contigs. Brackets indicate the limits of uncertainty in localizing the adjacent genes or markers or an area in which the relative order is uncertain. Some anonymous markers and genes were categorized as highly informative (asterisk) or as reference markers (red); all genes shown as reference markers on the chart have been cloned. At the far right, vertical and horizontal lines indicate deletion intervals and translocation breakpoints or other breakpoints, respectively, that were important historically in assembling the map and in isolating disease genes. For example, the deletion in patient BB was instrumental in isolating the genes for Duchenne muscular dystrophy and chronic granulomatous disease and is being used to isolate a gene for retinitis pigmentosa-3.

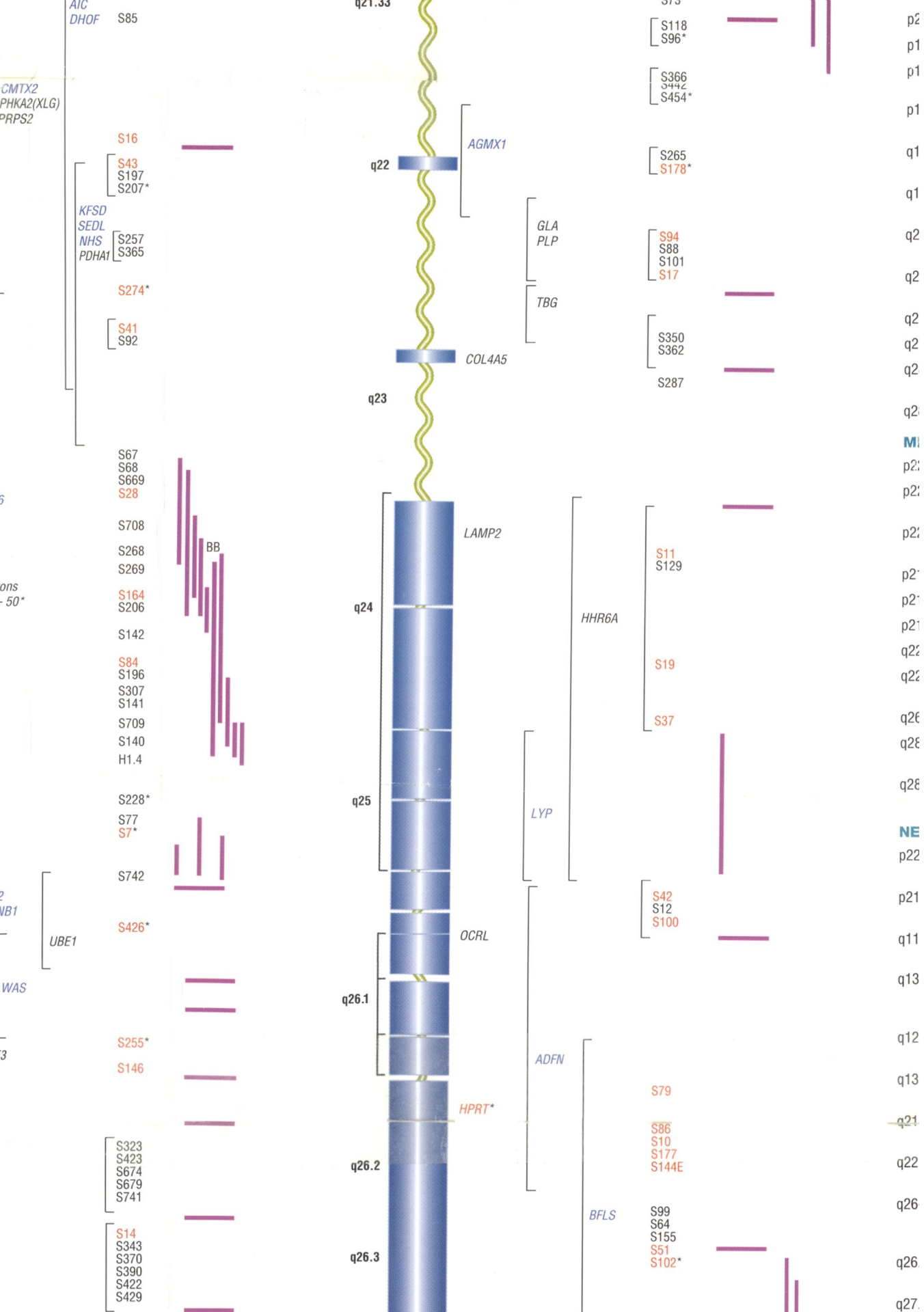
The table of disease-related genes on the X is based on the report of the Eleventh International Workshop on Human Gene Mapping and information presented at the Third X Chromosome Workshop. For characterized genes, which have been cloned and sequenced, the name or function of the encoded protein is listed. For the remaining genes, flanking markers (in order pter - disease locus - qter) are shown and the size of the segment in which the gene has been mapped. Commas indicate closely linked markers within the interval delineated by the flanking markers; the orientation of these markers with respect to the disease gene is arbitrary. The categorization of diseases into groups was arbitrary for the diseases that are associated with multiple abnormalities. Furthermore, because of space constraints, some rare diseases have been omitted for which mapping information was derived from a single family or was imprecise. This is especially true for X-linked mental retardation syndromes.

The X chromosome is expected to contain about 160,000 kb (160 Mb) of DNA and sequencing of those nucleotides has barely begun. Nonredundant sequences covering about 400 kb have been determined and deposited in databases (GenBank and EMBL). The longest continuous stretch of 56.7 kb corresponds to the hypoxanthine phosphoribosyl transferase gene (*HPRT*). Other long sequences include the coaguiation factor IX gene (*F9*; 38.1 kb), a region including the glucose-6-phosphate dehydrogenase gene (*G6PD*; 20.1 kb), and two sequences from the enormous dystrophin gene (*DMD*; 14.0 kb of complementary DNA sequence and 14.9 kb of genomic sequence around exon 44).

Further information can be found in the accompanying article (J.-L. Mandel *et al.*) in the 2 October, 1992 issue of *Science*.




p21.1
p11.4
p11.3
p11.23
p11.22
p11.21
p11.1
q11.1
q11.2
q12
q13.1
q13.2
q13.3
q21.1
q21.2
q21.31
q21.32
q21.33
q22.1
q22.2
q22.3
p22.1
p21.3
p21.2
p21.1
p11.4
p11.3
p11.23
p11.22
p11.21
AIC
DHOF
S85
CMTX2
PHKA2(XLG)
PRPS2
S16
GLRA2
S43
S197
S207*
RS
CLS
HYP
KFSD
SEDL
NHS
PDHA1
S257
S365
S274*
S41
S92
ZFX
POLA
S67
S68
S669
S28
RP6
S708
AHC
GK
S268
S269
3'*
DMD*
BMD
introns
44 - 50*
5'*
S164
S206
S142
S84
S196
S307
S141
S709
S140
H1.4
XK
CYBB
RP3
OTC
S228*
S77
S7*
MAOA*
MAOB*
NDP
S742
RP2
CSNB1
PFC*
SYN1*
TIMP
ARAF1*
OATL1
GF1
SYP
UBE1
WAS
S426*
S255*
TFE3
S146
OATL2
ALAS2
S323
S423
S674
S679
S741
IP1
MTHFDL1
S14
S343
S370
S390
S422
S429
BB


AIC
DHOF
S85
CMTX2
PHKA2(XLG)
PRPS2
S16
S43
S197
S207*
KFSD
SEDL
NHS
PDHA1
S257
S365
S274*
S41
S92
S67
S68
S669
S28
S708
S268
S269
S164
S206
S142
S84
S196
S307
S141
S709
S140
H1.4
BB
S228*
S77
S7*
S742
S426*
UBE1
WAS
S255*
S146
S323
S423
S674
S679
S741
S14
S343
S370
S390
S422
S429
q21.33
AGMX1
q22
GLA
PLP
TBG
COL4A5
q23
LAMP2
q24
HHR6A
LYP
q25
OCRL
q26.1
ADFN
HPRT*
q26.2
BFLS
q26.3
S118
S96*
S366
S454*
S265
S178*
S94
S88
S101
S17
S350
S362
S287
S11
S129
S19
S37
S42
S12
S100
S79
S86
S10
S177
S144E
S99
S64
S155
S51
S102*

p21.1	*CYBB*	Chronic granulomatous disease	ß subunit of cytochrome b
p11.3-p11.23	*PFC*	Properdin deficiency, X-linked	Properdin P factor, complement
p11.3-p11.22	*WAS*	Wiskott-Aldrich syndrome (immunodeficiency and thrombocytopenia)	*TIMP* - *WAS*, S255 - S146 (1 cM)
p11.21	*ALAS2*	Anemia, sideroblastic/hypochromic	Erythroid δ aminolevulinate synthase
q13.3	*PGK1*	Hemolytic anemia due to PGK deficiency	Phosphoglycerate kinase
q13.1-q13.3	*SCIDX1*	Severe combined immunodeficiency, X-linked	S132 - *SCIDX1, PGK1* - S447 (4 cM)
q21.3-q22	*AGMX1*	X-linked agammaglobulinemia	S366, S442 - *AGMX1*, S178, S265 - S94 (~5 cM)
q24-q27	*HIGM1*	X-linked immunodeficiency with hyper-IgM	Linked to S42
q25	*LYP*	Lymphoproliferative syndrome, X-linked	S37 - *LYP* - S42
q27.1	*F9*	Hemophilia B	Coagulation factor IX
q28	*G6PD*	G6PD deficiency; favism	Glucose-6-phosphate dehydrogenase
q28	*F8C*	Hemophilia A	Coagulation factor VIII

METABOLIC AND ENDOCRINE

p22.2-p22.1	*HYP*	Hereditary hypophosphatemia	S43, S207 - *HYP* - S274
p22.2-p22.1	*XLG (PHKA2)*	X-linked liver glycogenosis	Liver isoform of phosphorylase kinase α subunit
p22.2-p22.1	*PDHA1*	Pyruvate dehydrogenase deficiency	Pyruvate dehydrogenase, E1α subunit
p21.3-p21.2	*AHC*	Primary adrenal hypoplasia	S28 - *AHC* - S708
p21.3-p21.2	*GK*	Glycerol kinase deficiency	S708 - *GK* - 3' DMD (420 kb)
p21.1	*OTC*	Ornithine transcarbamylase deficiency	Ornithine transcarbamylase
q22	*GLA*	Fabry disease	α galactosidase
q22-q24	*PRPS1*	Phosphoribosylpyrophosphate synthetase-related gout	Phosphoribosylpyrophosphate synthetase I
q26-q27	*HPT*	Hypoparathyroidism, X-linked	S105 - *HPT* - S98
q28	*IDS*	Hunter syndrome, Mucopolysaccharidosis II	Iduronate 2-sulfatase
q28	*DIR*	Nephrogenic diabetes insipidus, vasopressin V2 receptor deficiency	S52 - *DIR* - *G6PD* (1.5 Mb)

NEUROLOGIC AND NEUROMUSCULAR

p22.2-p22.1	*CMTX2*	Charcot-Marie-Tooth neuropathy, X-linked recessive	Linked to S143, S16 and S43 (a second locus may be in Xq26)
p21.2	*DMD, BMD*	Muscular dystrophy, Duchenne and Becker types	Dystrophin
q11.2-q12	*SBMA (AR)*	Spino-bulbal muscular atrophy	Androgen receptor
q13.3	*MNK*	Menkes disease (cerebral degeneration, kinky hair, and abnormal copper transport)	S56 - *MNK* - *PGK1* (800 kb)
q12-q21.1	*CMTX1*	Charcot-Marie-Tooth neuropathy, X-linked dominant	*AR* - *CMTX1* - YS1X
q13.1-q13.3	*DYT3*	Torsion dystonia-parkinsonism, filipino type	S159 - *DYT3*, S106 - S56
q21-q22	*SPG2*	Spastic paraplegia, X-linked, uncomplicated	Linked to S17, S287 (may be heterogeneous)
q22	*PLP*	Pelizaeus-Merzbacher syndrome (demyelinating disease)	Myelin proteolipid
q26-q27	*BFLS*	Borjeson-Forssman-Lehmann syndrome (mental retardation with gynecomastia and facial features)	Linked to S51
q26.1-q26.2	*HPRT*	Lesch-Nyhan syndrome; HPRT-related gout	Hypoxanthine phosphoribosyl transferase
q27.3	*FRAXA*	Fragile X mental retardation	FMR1 protein of unknown function

The X chromosome is expected to contain about 160,000 kb (160 Mb) of DNA and sequencing of those nucleotides has barely begun. Nonredundant sequences covering about 400 kb have been determined and deposited in databases (GenBank and EMBL). The longest continuous stretch of 56.7 kb corresponds to the hypoxanthine phosphoribosyl transferase gene (*HPRT*). Other long sequences include the coaguiation factor IX gene (*F9*; 38.1 kb), a region including the glucose-6-phosphate dehydrogenase gene (*G6PD*; 20.1 kb), and two sequences from the enormous dystrophin gene (*DMD*; 14.0 kb of complementary DNA sequence and 14.9 kb of genomic sequence around exon 44).

Further information can be found in the accompanying article (J.-L. Mandel *et al.*) in the 2 October, 1992 issue of *Science*.

Glossary

Anonymous marker: a locus of unknown gene content.

Complementary DNA (cDNA): DNA that has been made by reverse transcription from RNA.

Contig: a set of overlapping pieces of DNA that span an uninterrupted stretch of the genome.

D number: a number assigned by the DNA Committee of a Human Gene Mapping Workshop to identify a piece of DNA that has been localized to a chromosome but that has not been characterized with respect to gene content.

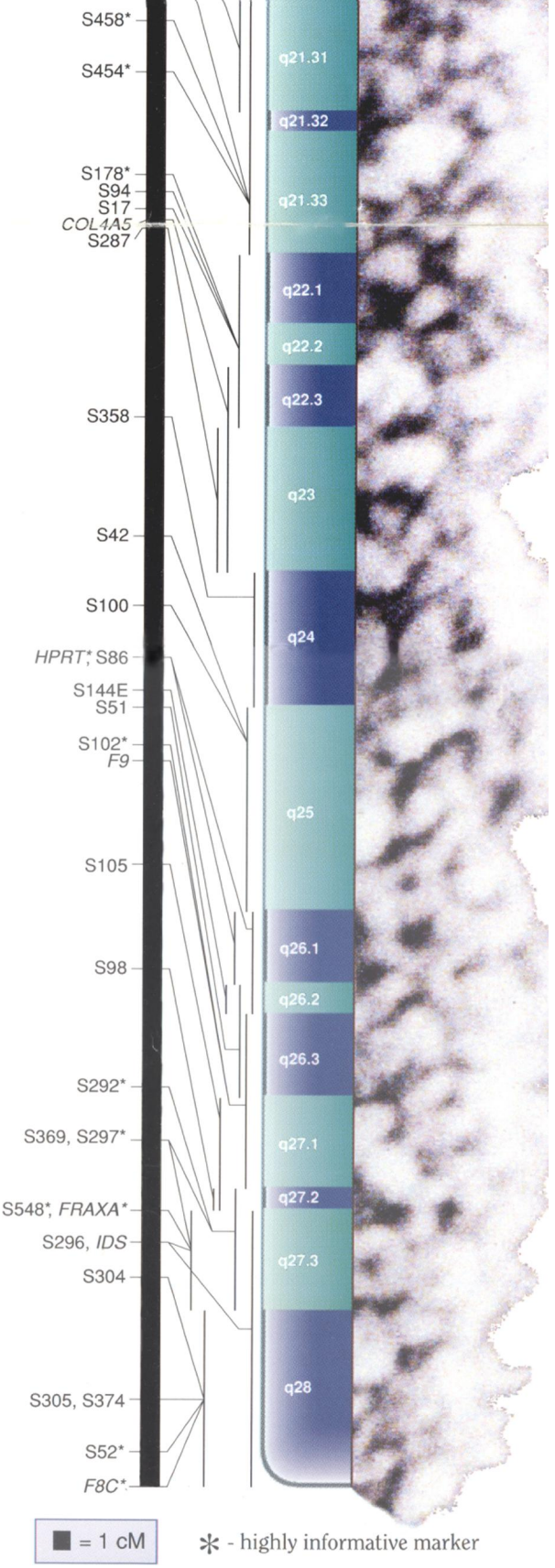
Genetic linkage map: a map that shows the relative position of loci on the basis of the frequency of recombination events. Units are in centimorgans (cM) where, over small distances, 1 cM is equivalent to a 1% chance of recombination.

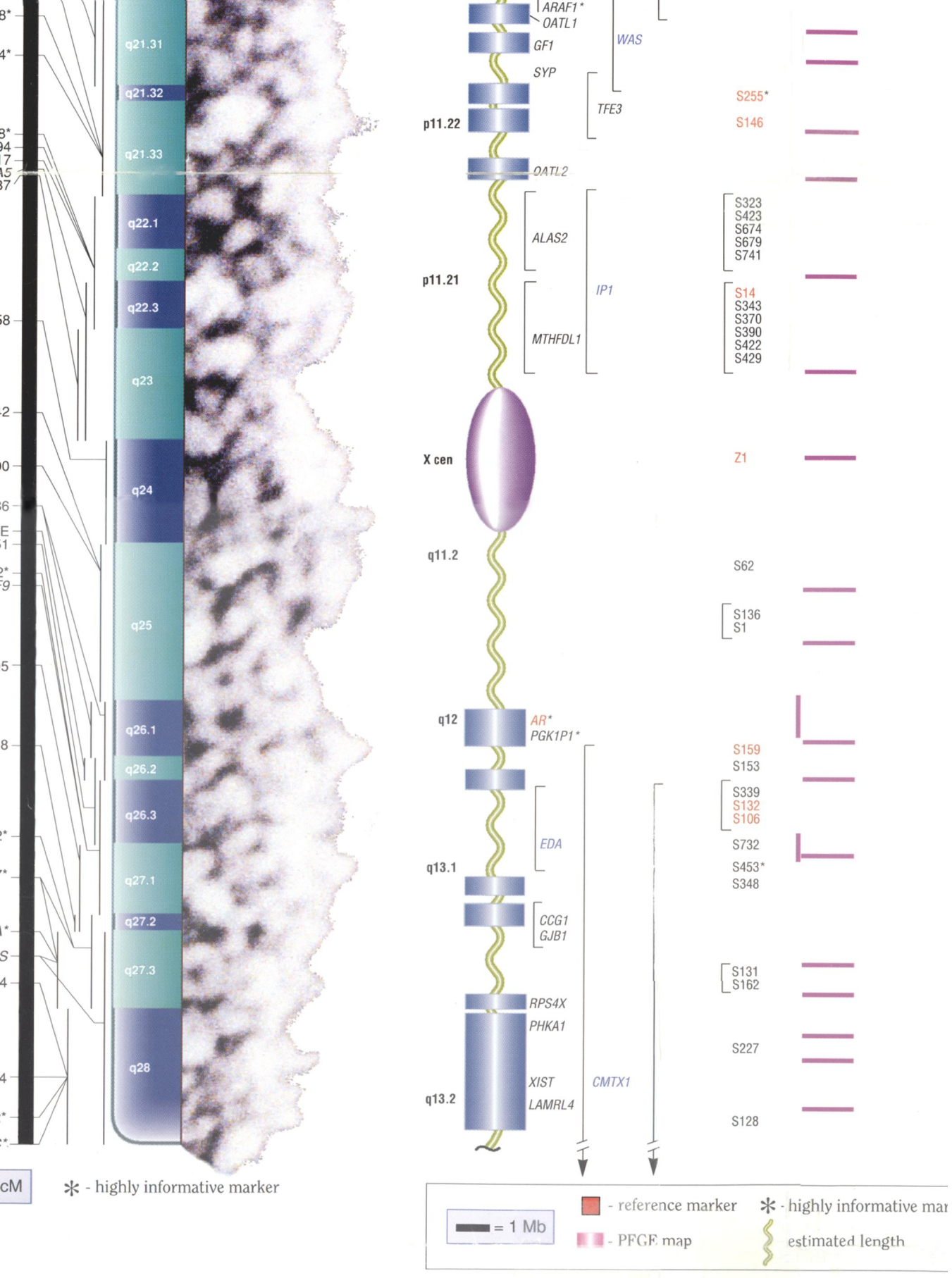
Informative marker: a polymorphic marker that shows sufficient variation in the population that it can be used to detect differences between individuals at a high frequency. The frequency can be expressed as the heterozygosity index or HET. Highly informative markers shown on the chart are very polymorphic, multi-allelic markers (HET frequently ≥ 0.7) with sequence variations that can usually be detected by PCR.

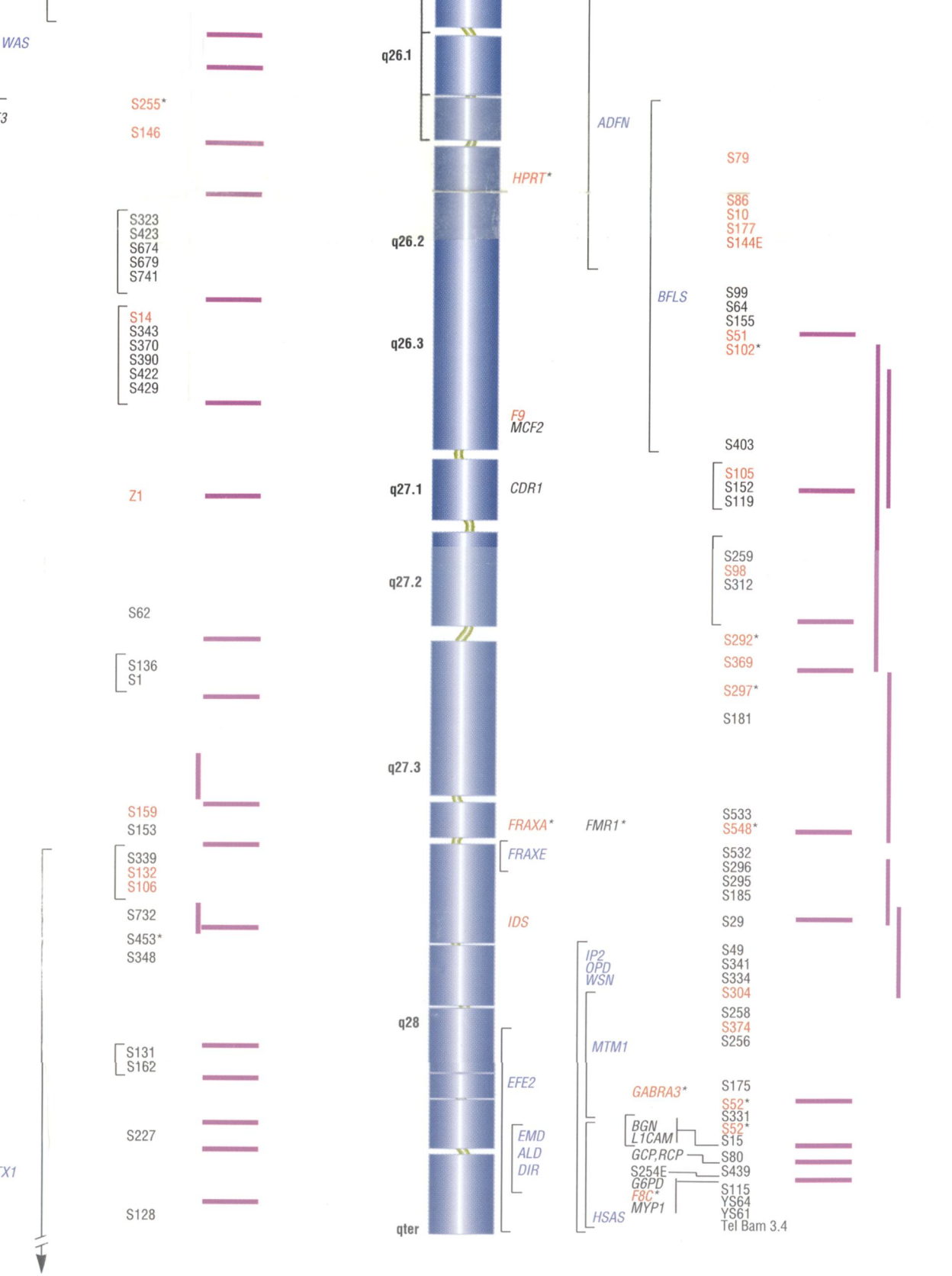
Physical map: a map in which distances between landmarks such as clones, restriction endonuclease sites, or specific loci are expressed in bases of DNA.

Polymerase chain reaction (PCR): a technique that involves repeated cycles of DNA denaturation, renaturation with short lengths of DNA (primers) separated by up to 4 kb, and polymerase-mediated replication. This results in an exponential increase in the number of copies of the sequence between the primers.

Polymorphic marker: a locus at which there is




q21.31
q21.32
q21.33
q22.1
q22.2
q22.3
q23
q24
q25
q26.1
q26.2
q26.3
q27.1
q27.2
q27.3
q28
ARAF1*
OATL1
GF1
SYP
WAS
TFE3
p11.22
OATL2
ALAS2
IP1
p11.21
MTHFDL1
X cen
q11.2
q12
AR*
PGK1P1*
EDA
q13.1
CCG1
GJB1
RPS4X
PHKA1
XIST
CMTX1
q13.2
LAMRL4
S255*
S146
S323
S423
S674
S679
S741
S14
S343
S370
S390
S422
S429
Z1
S62
S136
S1
S159
S153
S339
S132
S106
S732
S453*
S348
S131
S162
S227
S128
cM
* - highly informative marker
= 1 Mb
- reference marker
- PFGE map
* - highly informative mar
estimated length


WAS
S255*
S146
S323
S423
S674
S679
S741
S14
S343
S370
S390
S422
S429
Z1
S62
S136
S1
S159
S153
S339
S132
S106
S732
S453*
S348
S131
S162
S227
S128
TX1
q26.1
HPRT*
q26.2
q26.3
F9
MCF2
q27.1
CDR1
q27.2
q27.3
FRAXA*
FRAXE
IDS
q28
EFE2
EMD
ALD
DIR
qter
ADFN
BFLS
FMR1*
IP2
OPD
WSN
MTM1
HSAS
GABRA3*
BGN
L1CAM
GCP,RCP
S254E
G6PD
F8C*
MYP1
S79
S86
S10
S177
S144E
S99
S64
S155
S51
S102*
S403
S105
S152
S119
S259
S98
S312
S292*
S369
S297*
S181
S533
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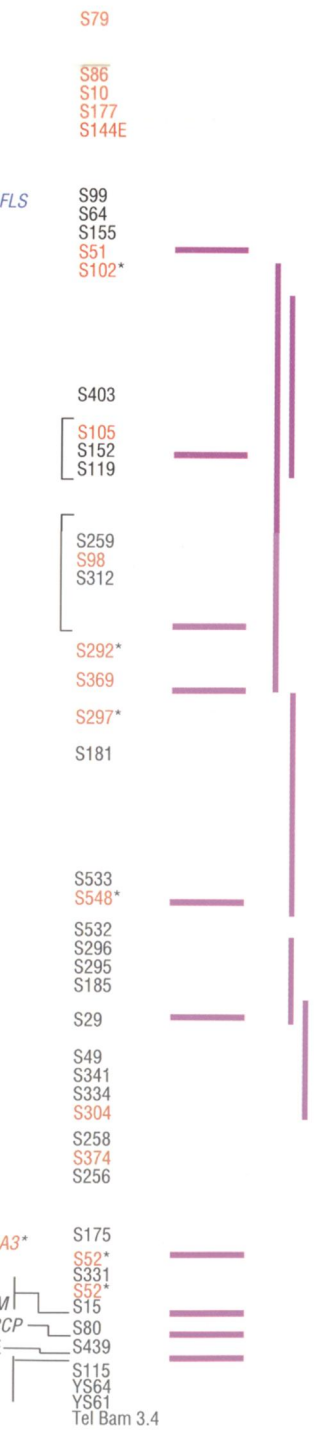
S374
S256
S175
S52*
S331
S52*
S15
S80
S439
S115
YS64
YS61
Tel Bam 3.4
q13
q12
q13
q21
q22
q26
q26
q27
q28
q28
q28
q28
q28
q28
q28
MIS
p22.
p22.
p22.
p22.
p22.
p22.
p11.
q11.
q12-
q21.
q21.
q22
q25-
q25-
q28
reference marker
* - highly informative marker
- cloned gene
- uncloned gene
- YAC contig
PFGE map
estimated length
cen - centromere
- Deletions and breakpoints



	(AR)		
q13.3	*MNK*	Menkes disease (cerebral degeneration, kinky hair, and abnormal copper transport)	S56 - *MNK* - *PGK1* (800 kb)
q12-q21.1	*CMTX1*	Charcot-Marie-Tooth neuropathy, X-linked dominant	*AR* - *CMTX1* - YS1X
q13.1-q13.3	*DYT3*	Torsion dystonia-parkinsonism, filipino type	S159 - *DYT3*, S106 - S56
q21-q22	*SPG2*	Spastic paraplegia, X-linked, uncomplicated	Linked to S17, S287 (may be heterogeneous)
q22	*PLP*	Pelizaeus-Merzbacher syndrome (demyelinating disease)	Myelin proteolipid
q26-q27	*BFLS*	Borjeson-Forssman-Lehmann syndrome (mental retardation with gynecomastia and facial features)	Linked to S51
q26.1-q26.2	*HPRT*	Lesch-Nyhan syndrome; HPRT-related gout	Hypoxanthine phosphoribosyl transferase
q27.3	*FRAXA*	Fragile X mental retardation	FMR1 protein of unknown function
q28	*ALD*	Adrenoleukodystrophy, Adrenomyeloneuropathy	S52 - *ALD* - telomere
q28	*EMD*	Emery-Dreifuss muscular dystrophy	S52 - EMD - F8C (3 cM)
q28	*HSAS*	Hydrocephalus, X-linked	S52 - HSAS - telomere
q28	*MASA*	MASA syndrome (complicated spastic paraplegia, may be allelic to HSAS)	Linked to S52, F8C
q28	*MTM1*	Myotubular myopathy, X-linked	S304 - *MTM1* - S52
q28	*BTHS (EFE2)*	Barth syndrome (cardioskeletal myopathy and neutropenia)	S305, S374 - EFE2 - telomere
MISCELLANEOUS			
p22.3	*CDPX1*	Chondrodysplasia punctata, X-linked recessive	*PABX* - *CDPX1* - DX30F1/4 (3 Mb)
p22.3	*STS*	X-linked ichthyosis	Steroid sulfatase (microsomal)
p22.3	*KAL*	Kallmann syndrome	Possible adhesion molecule involved in neuronal migration
p22.3-p22.2	*AMELX*	Amelogenesis imperfecta	Amelogenin
p22.2-p21.3	*KFSD*	Keratosis follicularis spinulosa decalvans	S16 - S41, *KFSD* - S28 (~20 cM)
p22.2-p22.1	*CLS*	Coffin-Lowry syndrome (mental retardation and skeletal malformations)	S207, S43 - *CLS* - S274 (6 cM)
p22.2-p21.3	*SEDL*	Spondyloepiphyseal dysplasia tarda	Linked to S41, S92
p11.21	*IP1*	Incontinentia pigmenti-1, sporadic type	S323 - *IP1* - S14 - *IP1* - Z1
q11.2-q12	*AR*	Testicular feminization	Androgen receptor
q12-13.1	*EDA*	Hypohidrotic ectodermal dysplasia	S339 - *EDA*, S732 - S453 (1 cM)
q21.1	*DFN3*	Conductive deafness with stapes fixation	S26 - *DFN3* - S232
q21.3-q22	*CPX*	Cleft palate, X-linked	PGK1 - *CPX* - S17
q22	*COL4A5*	Alport syndrome (nephritis and deafness)	α5 chain of collagen IV
q25-q26.1	*OCRL*	Lowe oculocerebrorenal syndrome	Candidate cDNA cloned
q25-q26	*ADFN*	Albinism-deafness syndrome	S37 - *ADFN* - *F9*
q28	*IP2*	Incontinentia pigmenti-2, familial, male-lethal type	Linked to S52, *F8C*; may be heterogeneous

the heterozygosity index or HET. Highly informative markers shown on the chart are very polymorphic, multi-allelic markers (HET frequently ≥ 0.7) with sequence variations that can usually be detected by PCR.

Physical map: a map in which distances between landmarks such as clones, restriction endonuclease sites, or specific loci are expressed in bases of DNA.

Polymerase chain reaction (PCR): a technique that involves repeated cycles of DNA denaturation, renaturation with short lengths of DNA (primers) separated by up to 4 kb, and polymerase-mediated replication. This results in an exponential increase in the number of copies of the sequence between the primers.

Polymorphic marker: a locus at which there is normal sequence variation within the population that is inherited and occurs with a frequency of >1%.

Pseudoautosomal region: a region of homology between the X and Y chromosomes where meiotic pairing and reciprocal exchanges occur.

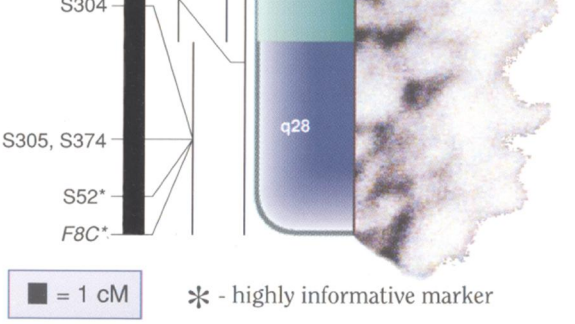
Pulsed field gel electrophoresis (PFGE): a method of separating large fragments of DNA that relies on application of pulses of electrical current at different angles to a mixture of DNAs in a gel.

Reference marker: an informative marker whose position relative to other markers has been unambiguously determined by genetic or physical mapping techniques.

Sequence tagged site (STS): a short DNA sequence, readily located and amplified by PCR techniques, that uniquely identifies a physical genomic location.

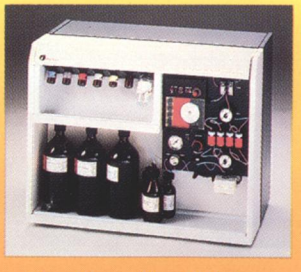
Translocation: the transfer of a chromosomal region to another chromosome by abnormal breakage and rejoining.

YAC (Yeast artificial chromosome): a cloning vector in which sections of yeast chromosomes needed for initiation of DNA synthesis and stability are used to replicate large (>100 kb) pieces of DNA.



Chromosome	1	2	3
Genes			
Mapped	247	138	85
Disease-related	55	24	24
Markers			
Total	466	266	1351
Polymorphic	197	121	442
HET >0.7	24	14	14
STS markers			
Total	63	66	93
Polymorphic	44	36	45
Number of sequenced loci	144	92	52
Number of sequences	734	515	263
Kilobases of sequence	760	867	204

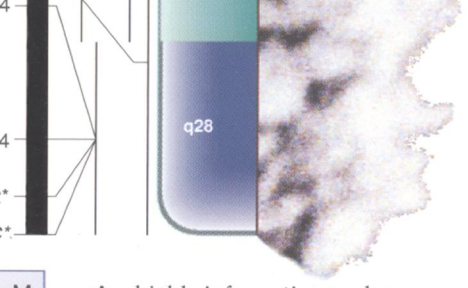
The table describes the state of progess of human genome
1991 Science wall chart, 214 new genes and 806 new pol
sequence known to be mapped is now more than 10.3
overlapping sequences).
The number of disease-related genes was provided by D
Polymorphic markers that have a heterozygosity index (HE



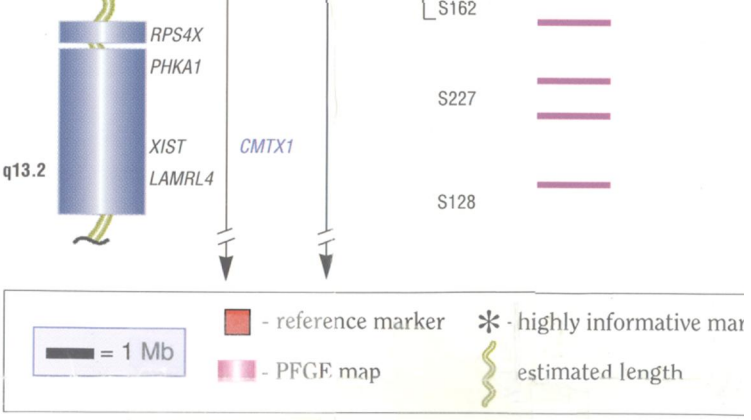
Gene Assembler® 4 Primers
- **Application Note 910:** FluorePrime™
- **Application Note 911:** Primer walking

ALF™ DNA Sequencer
- **Application Note 909:** Bidirectional solid phase sequencing
- **Application Note 913:** Dynamic point mutations

- **Application**
SSCP: a simp
applied to ex
- **Application**
SSCP: a rapi
technique as



cM ✻ - highly informative marker



= 1 Mb - reference marker ✻ - highly informative mar
- PFGE map estimated length

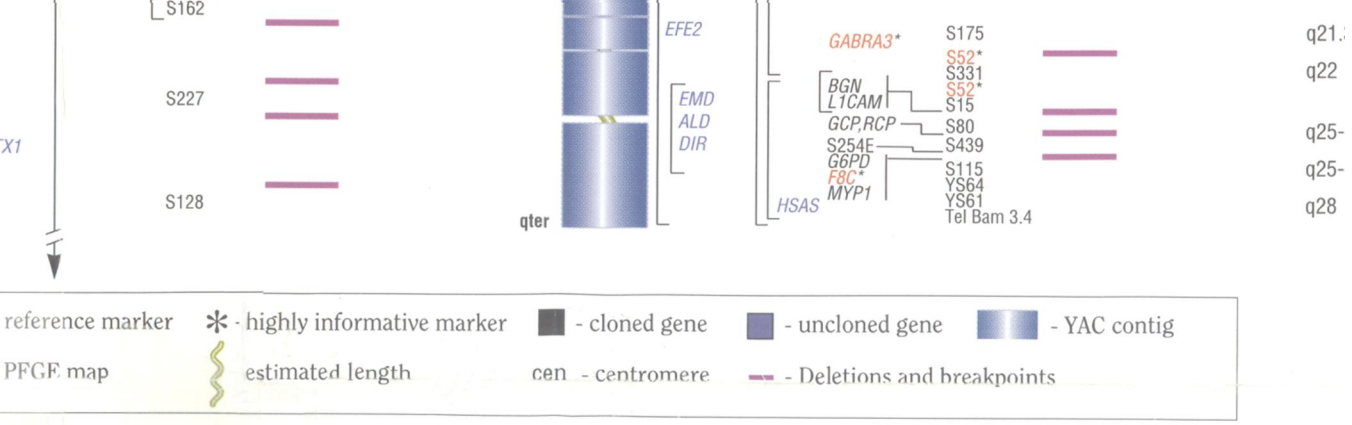
Advances in Human Gene

romosome	1	2	3	4	5	6	7	8	9	10	11	12
Genes												
Mapped	247	138	85	99	92	131	132	64	77	79	154	136
se-related	55	24	24	25	23	27	25	22	26	15	46	23
Markers												
Total	466	266	1351	495	491	396	608	308	242	263	1059	218
lymorphic	197	121	442	179	242	185	226	178	105	116	320	82
HET >0.7	24	14	14	19	28	17	12	12	34	11	23	7
'S markers												
Total	63	66	93	81	51	41	34	34	65	29	67	27
lymorphic	44	36	45	39	46	26	23	26	57	21	48	19
enced loci	144	92	52	148	53	87	83	41	50	43	84	93
sequences	734	515	263	342	211	750	697	170	219	262	432	360
sequence	760	867	204	379	302	778	598	229	277	303	815	648

cribes the state of progess of human genome mapping as of July 15, 1992. Since the publication of the e wall chart, 214 new genes and 806 new polymorphic markers have been added. The total amount of nown to be mapped is now more than 10.3 Mb. (As with last year's sequence data, this includes sequences).

r of disease-related genes was provided by Dr. V. McKusick, Johns Hopkins Hospital, Baltimore, MD. c markers that have a heterozygosity index (HET) of >70% are particularly useful for linkage studies and

the mapping of di sites (STSs) have number of polym during the past y addition to the to which sequence is



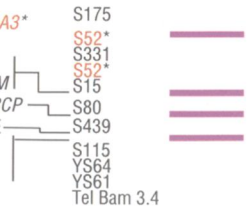
ces in Human Gene Mapping

8	9	10	11	12	13	14	15	16	17	18	19	20	21
64	77	79	154	136	31	66	65	83	135	28	132	45	39
22	26	15	46	23	13	19	17	17	26	9	24	14	8
308	242	263	1059	218	200	133	173	516	932	79	364	143	322
178	105	116	320	82	87	63	76	163	268	51	97	66	110
12	34	11	23	7	11	11	8	19	23	14	11	21	19
34	65	29	67	27	28	20	33	59	269	25	42	42	62
26	57	21	48	19	25	13	29	37	46	19	31	38	44
41	50	43	84	93	12	49	31	53	98	17	86	24	23
170	219	262	432	360	114	881	109	151	288	90	412	129	141
229	277	303	815	648	113	686	183	429	860	137	487	175	95

e publication of the
he total amount of
data, this includes

al, Baltimore, MD.
linkage studies and

the mapping of disease genes. Most of these polymorphisms are simple tandem repeats that can be de
sites (STSs) have proven to be valuable in physical mapping, especially in the construction of large
number of polymorphic STS markers (this is the same as the PCR-based polymorphic markers in the 19
during the past year. These markers are helpful in genetic mapping, in that they are easy to use and
addition to the total amount of sequence per chromosome, the number of sequences per chromosome
which sequence is contained in GenBank have also been included to give some indication of the amoun



		...fixation	S26 - DFN3 - S232
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q28	*IP2*	Incontinentia pigmenti-2, familial, male-lethal type	Linked to S52, *F8C*; may be heterogeneous

ed gene - YAC contig

ns and breakpoints

17	18	19	20	21	22	X	Y
35	28	132	45	39	71	225	18
26	9	24	14	8	17	111	1
932	79	364	143	322	360	1382	406
268	51	97	66	110	140	290	32
23	14	11	21	19	6	21	2
269	25	42	42	62	16	136	180
46	19	31	38	44	11	52	0
98	17	86	24	23	41	72	10
88	90	412	129	141	196	435	17
60	137	487	175	95	402	553	24

isms are simple tandem repeats that can be detected by PCR. Sequence tagged pping, especially in the construction of large contigs from YAC libraries. The the PCR-based polymorphic markers in the 1991 table) has more than doubled tic mapping, in that they are easy to use and often are highly informative. In ne, the number of sequences per chromosome and the number of markers for included to give some indication of the amount of sequence per marker.

GENOME MAPS III

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Gene
mapping of

d separation of

FPLC® System

- **Application Note:** Large scale purification of plasmid DNA by Mono Q® HR5/5 on FPLC® System
- **Technical Note:** FPLC® Automation

SMART™ System

- **Technical Note:** Micropurification by RPC for protein/peptide sequence analysis
- **Application Note:** Micropreparative purification and analysis of DNA