Bioinformatics Chapter 6.

Genomic Mapping and Mapping Databases

지 성 욱
서울대 바이오정보기술연구센터
E-mail: swchi@cbit.snu.ac.kr

Sung-Wook Chi
Center for Bioinformation Technology (CBIT)
Seoul National University

장 병 탁
서울대 컴퓨터공학부 바이오지능연구실 &
바이오정보기술연구센터
E-mail: btzhang@cse.snu.ac.kr

Byoung-Tak Zhang
Center for Bioinformation Technology (CBIT) &
Biointelligence Laboratory
School of Computer Science and Engineering
Seoul National University

This material is available at http://bi.snu.ac.kr./ &
http://cbit.snu.ac.kr/

Outline

- Indroduction
- Genomic Mapping
- Types of Maps
- Data Repositories
  - GDB, NCBI, MGI/MGD
- Mapping Projects and Associated Resources
- Practical Uses of Mapping Resources

Introduction

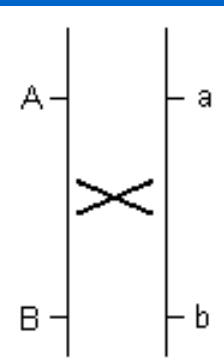
- "Map of Maps"
- The different types of markers and methods used for genomic mapping
- The inherent complexities in the construction and utilization of genome maps
- Several large community databases and method-specific mapping projects
- Practical examples of how these tools and resources can be used to aid in specific types of mapping studies

Genomic Mapping

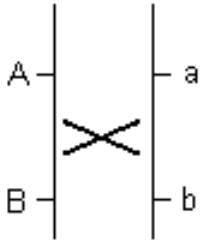
- **Genetic Mapping**
  - Crossbreeding and pedigree
  - Calculation of recombination frequency by linkage analysis
- **Cytogenetic Mapping**
  - FISH(Fluorescent In Situ Hybridization)
- **Physical Mapping**
  - Molecular biology technique (hybridization, PCR)
  - Restriction Mapping
  - STS(Sequence Tagged Site) Mapping

  Radiation-hybrid method, Clone library based method.

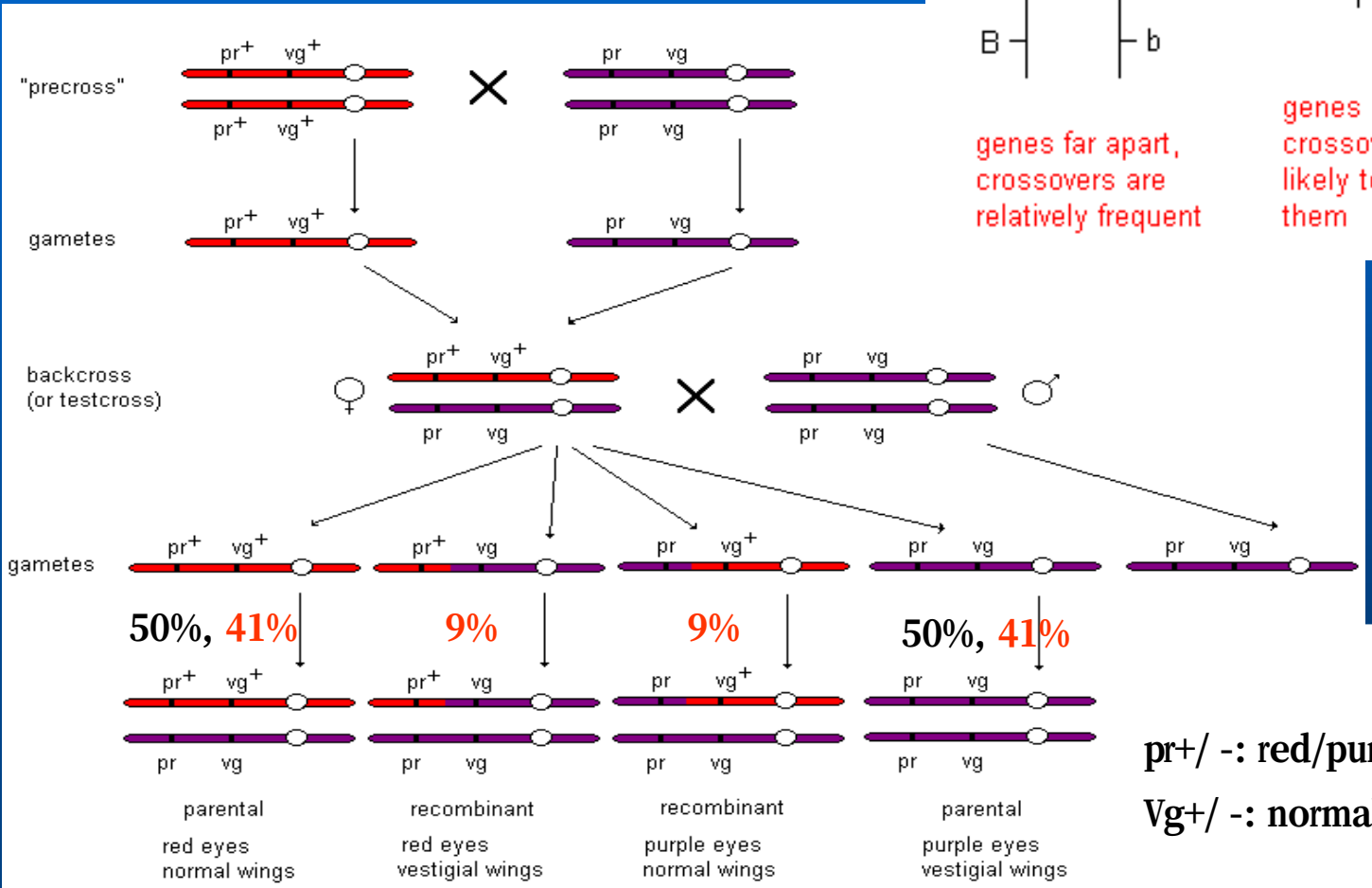
Linkage Analysis



genes far apart, crossovers are relatively frequent



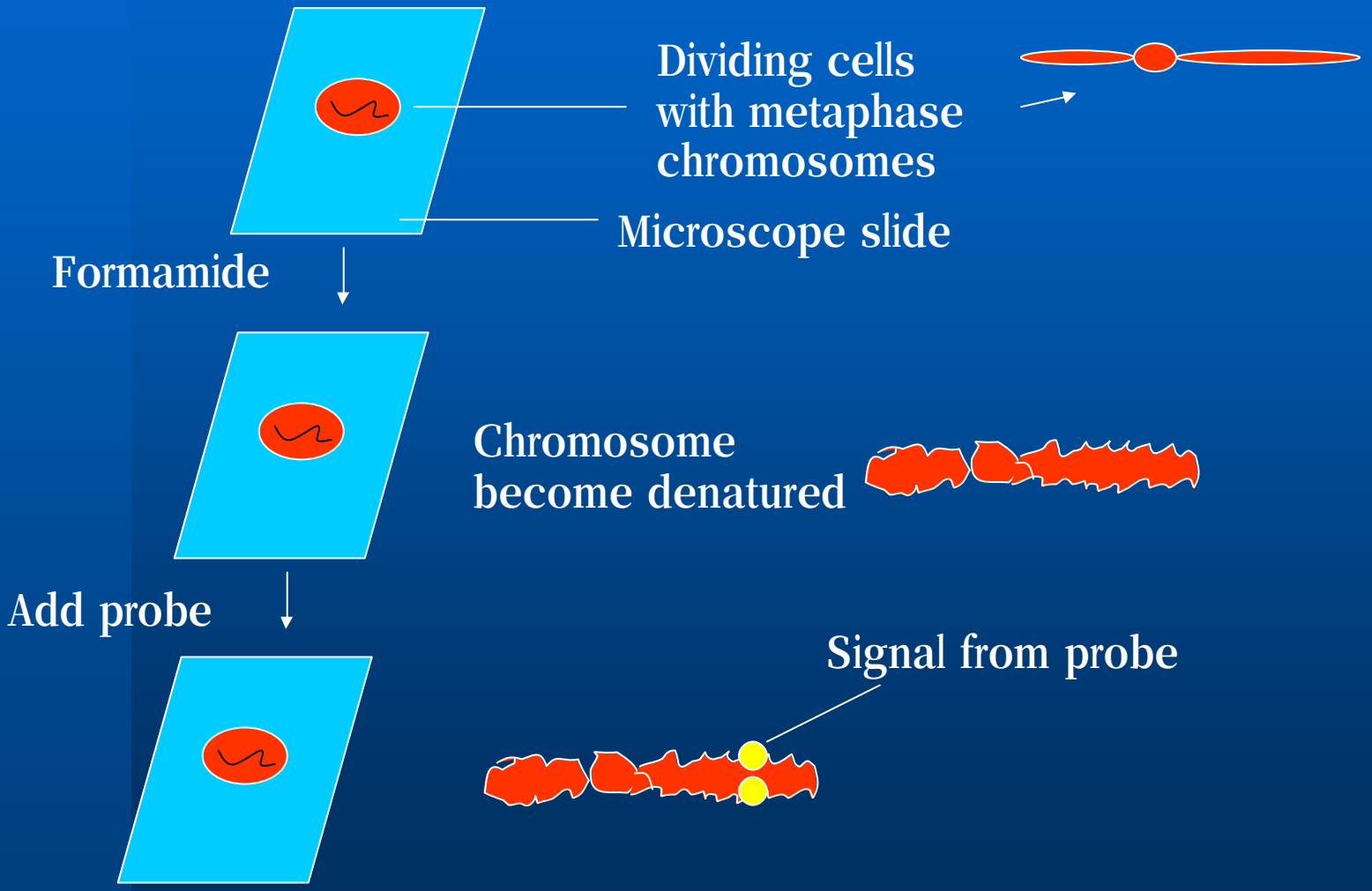
genes close together, crossovers are less likely to occur between them



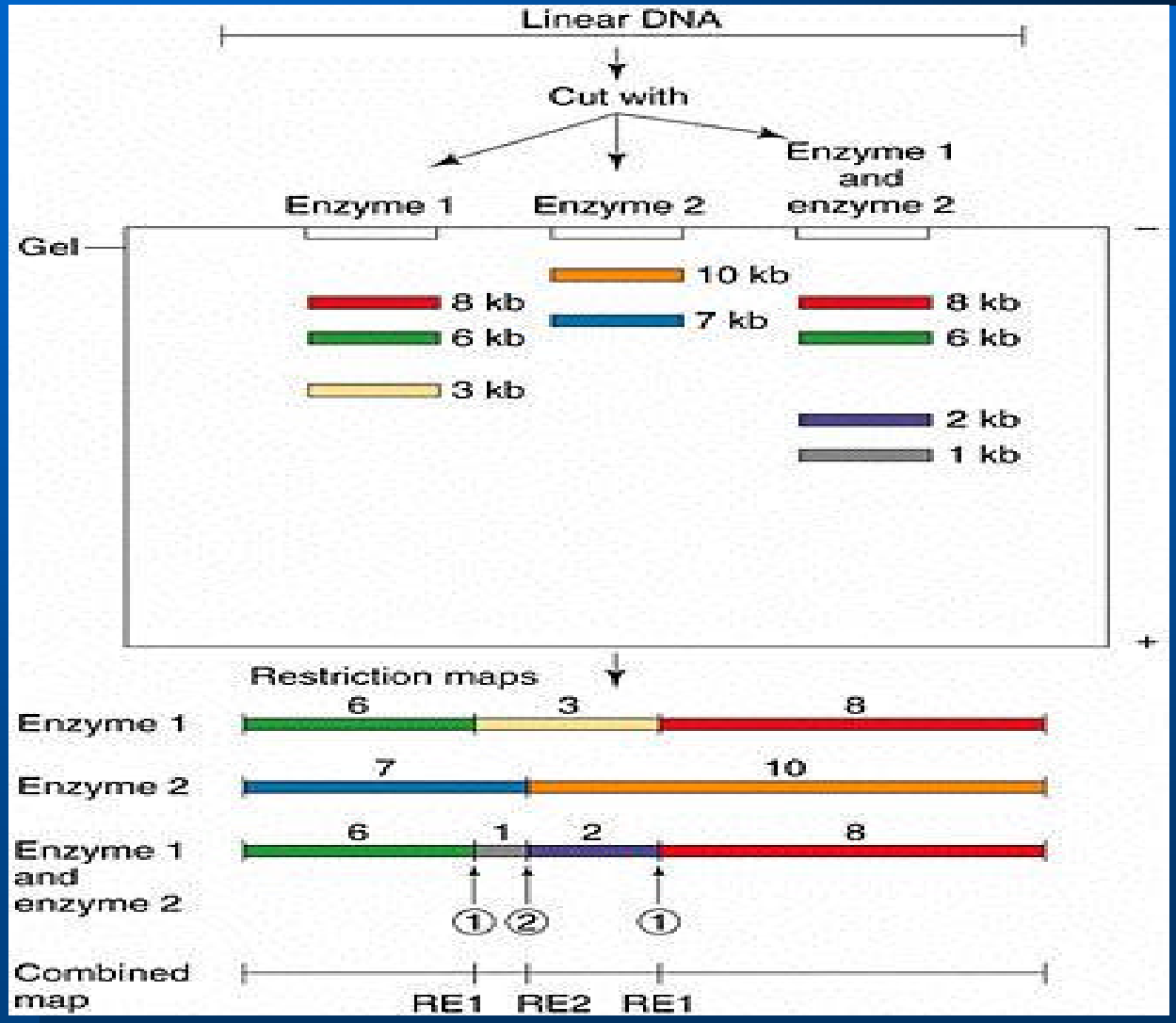
pr+/ -: red/purple eyes

Vg+/ -: normal/vestigial wings

FISH(Fluorescent In Situ Hybridization



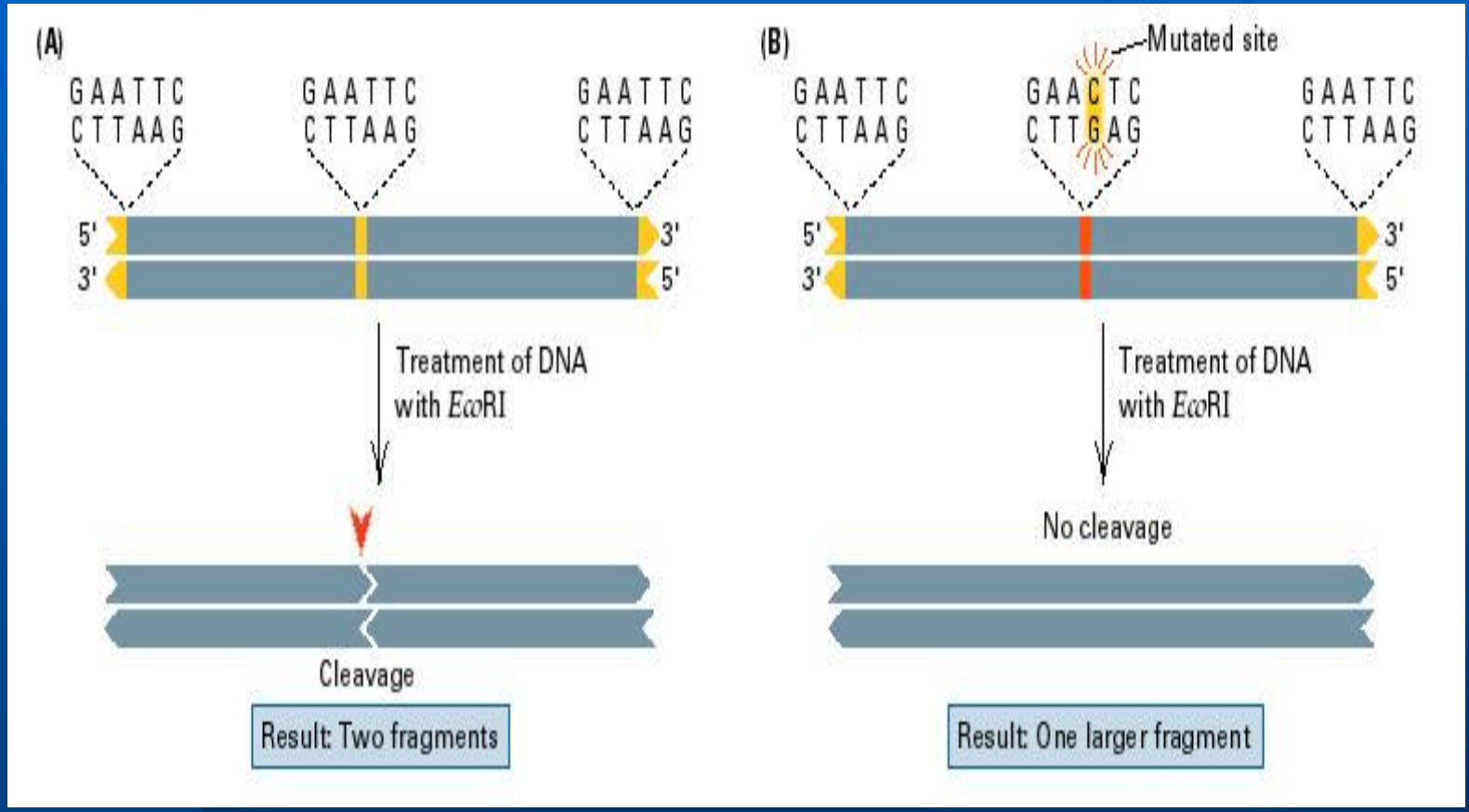
Restriction Mapping



Genomic Map Elements

- DNA Markers
  - A uniquely identifiable segment of DNA
  - Usually ranging in size from one to 300-400 nucleotide bases in size
  - Detection of markers may be either PCR based or hybridization based.
- Polymorphic Markers
  - Show sequence variation among individuals
  - To construct genetic linkage maps
  - RFLP (Restriction fragment length polymorphism)
- DNA Clones
  - Yeast artificial chromosome (YAC)
  - Bacterial artificial chromosome (BACs)
  - P1-artificial chromosome (PACs)

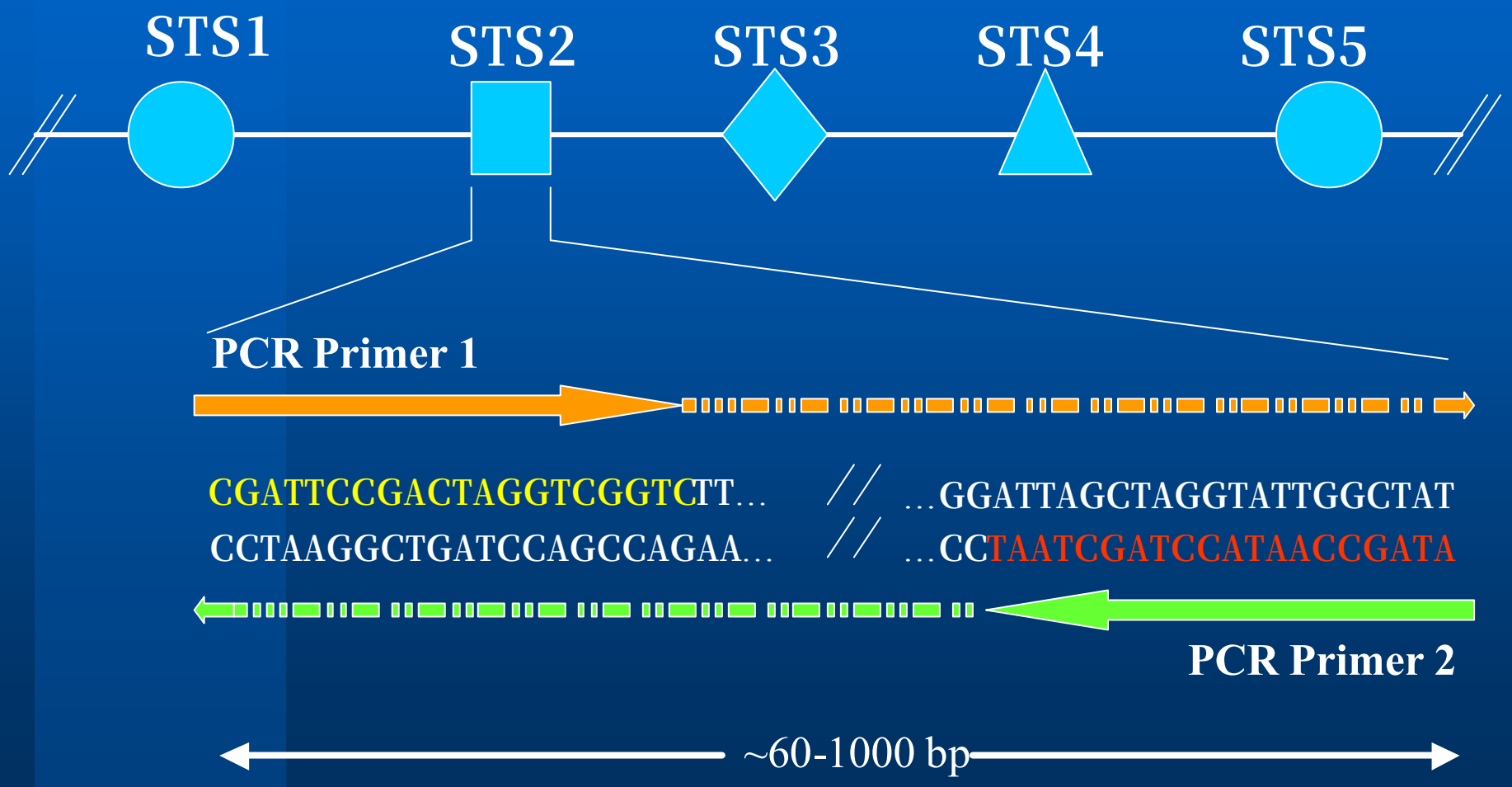
Basis for RFLP mapping



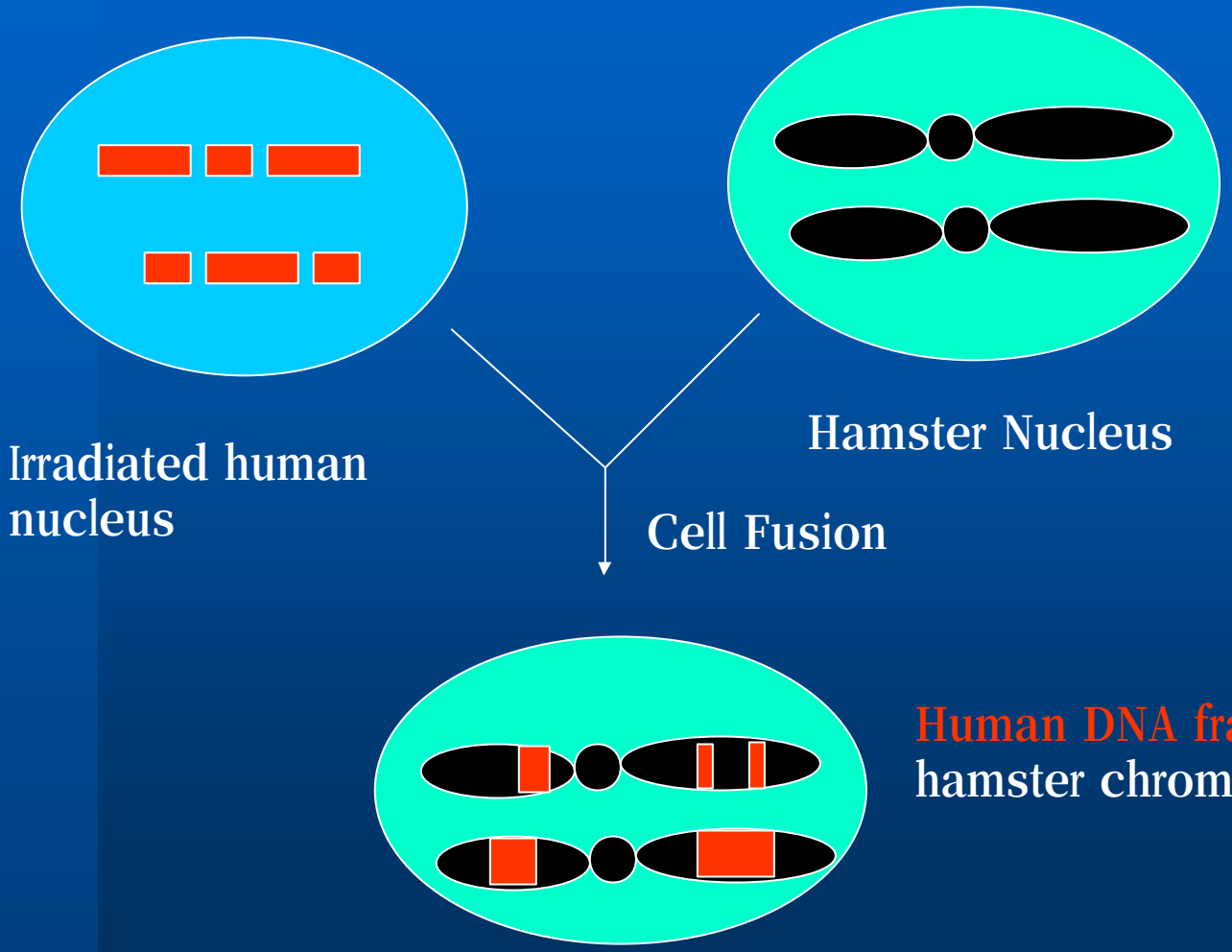
STS(Sequence Tagged Site)

- Simply a short sequence (100 ~ 500bp)
  - sequence must be known (PCR)
  - must have a unique location.
- Expressed sequence tags (ESTs)
  - comes from a unique gene
- SSLP (Simple sequence length polymorphism)
  - Minisatellites, VNTR(Variable number of tandem repeats)
  - Microsatelliyes, STRs(Simple tandem repeats)
- Random genomic sequences
  - obtained by sequence random pieced of cloned genomic DNA or from databases.

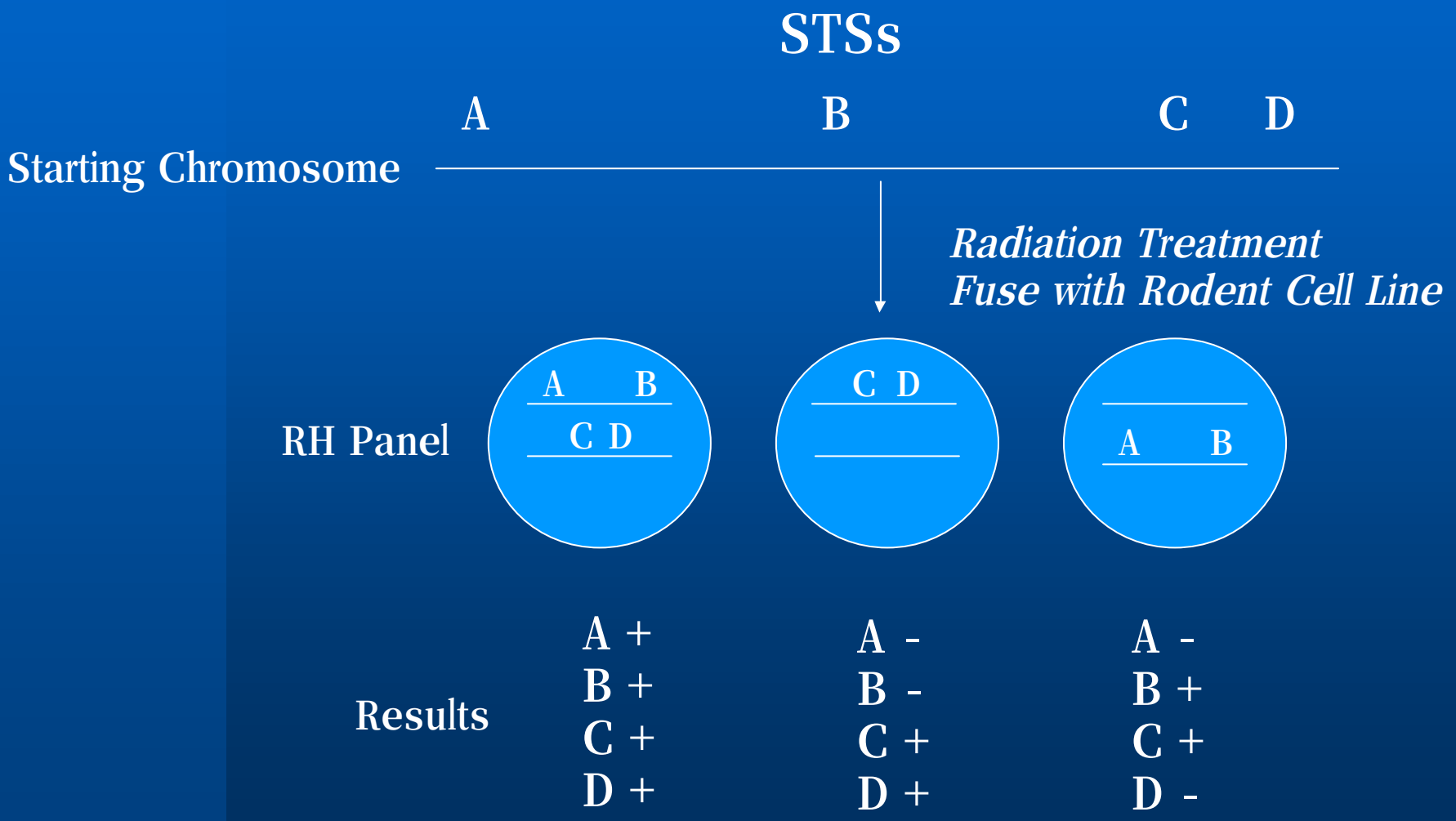
Sequence-Tagged Sites (STS) Mapping



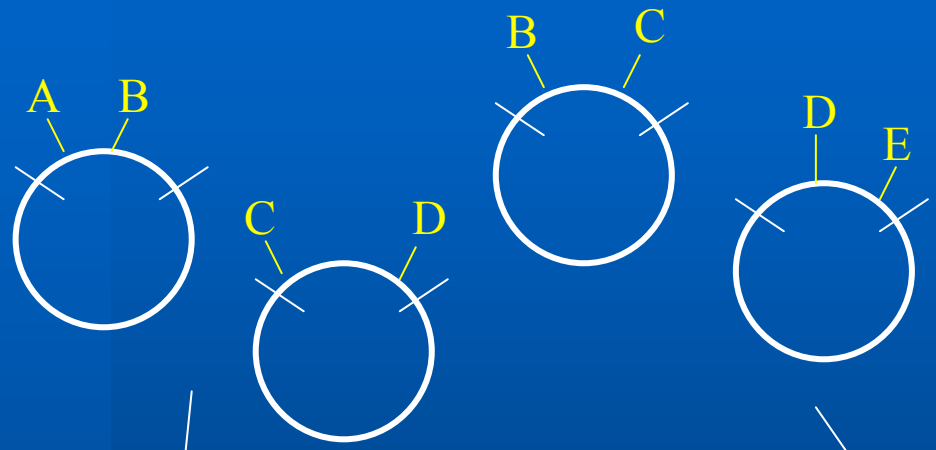
Radiation Hybrid (RH) Method



Radiation Hybrid (RH) Mapping



Clone library based Mapping



Clone library

Use the clone library as mapping reagent.

Sequence the overlapping clones

STS map

…TAGGCATCGATCGGG…

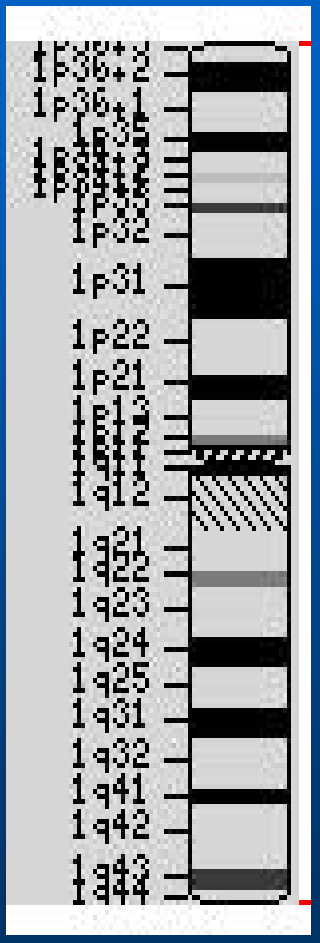
DNA sequence

Type of Maps

- Cytogenetic maps
- Genetic Linkage maps
- Radiation hybrid maps
- Transcript maps
- Physical maps
- Comparative maps
- Integrated maps

Cytogenetic Maps

- Chromosome staining by Giemsa: G-bands
- Using FISH method
- Limited ordering range (<1-2mb)
- Not well-suited for high-throuput mapping.



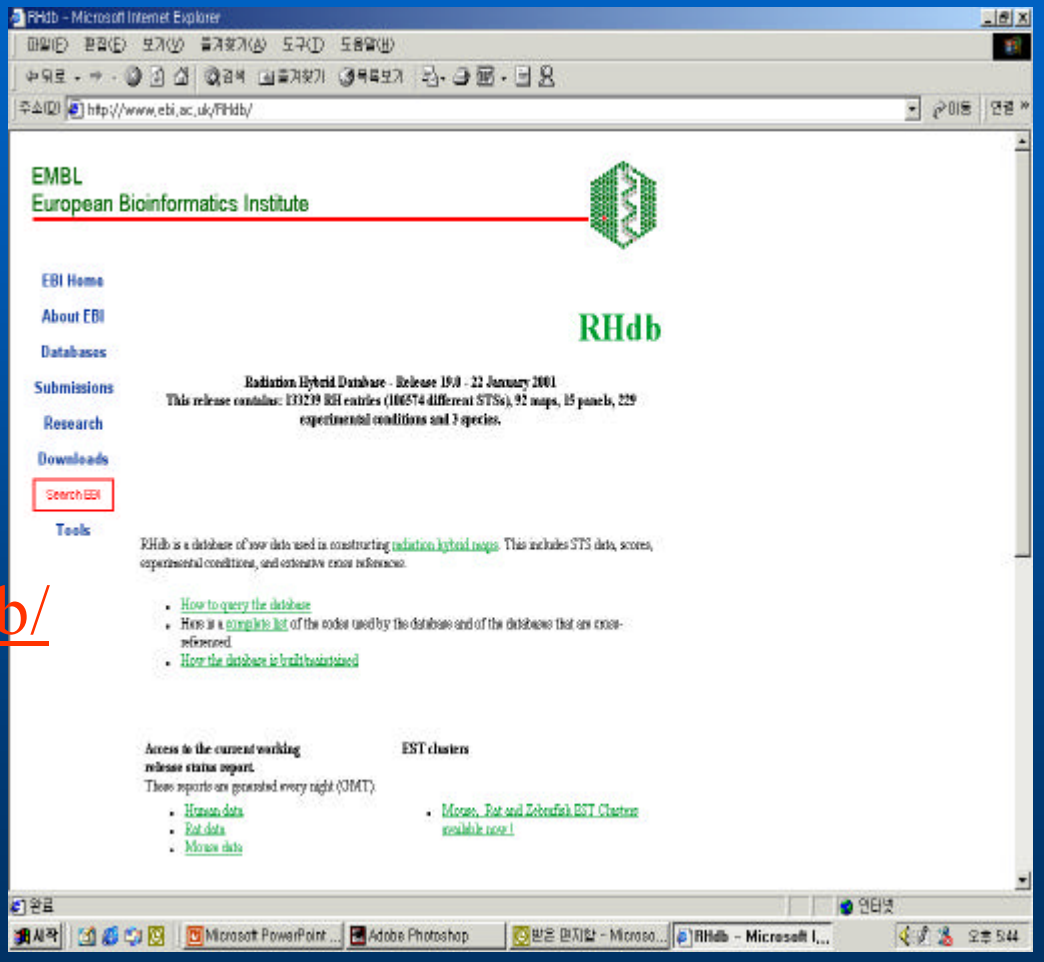
Genetic Linkage Maps

- 1centiMorgans (cM) represents 1% probability of recombination.
- Not directly proportional to physical distance.
- MAP-O-MAT (map distance, statical support for order)
  - http://compgen.rutgers.edu/mapomat
- CEPH(Centre d'Etude du Polymorphism Humain)
  - Human DNAs from a set of reference pedigrees
  - highly polymorphic STR markers , SNP
  - http://www.cephb.fr/cephdb/

Radiation Hybrid Maps

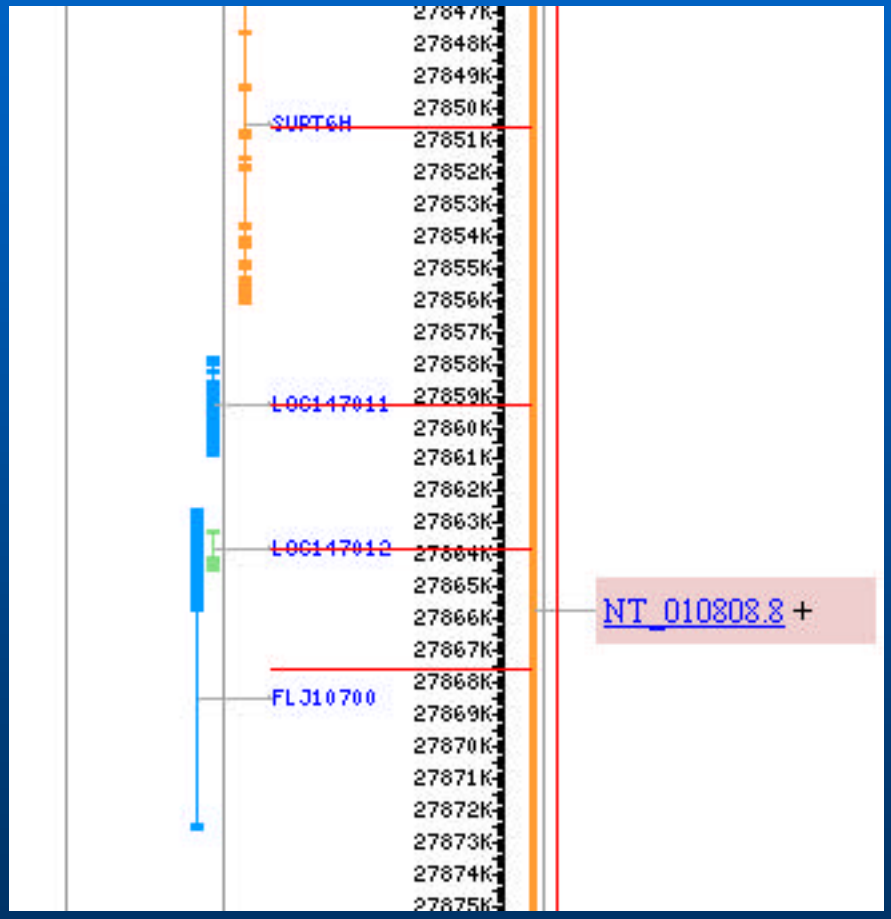
- 1 Centirays (cR) representing a 1% probability of chromosome breakage.
- Radiation Hybrid Database (RHdb)

http://www.ebi.ac.uk/RHdb/



Transcript Maps

- Maps of transcribed sequences.
- Using Expressed Sequence Tag (EST) and known gene

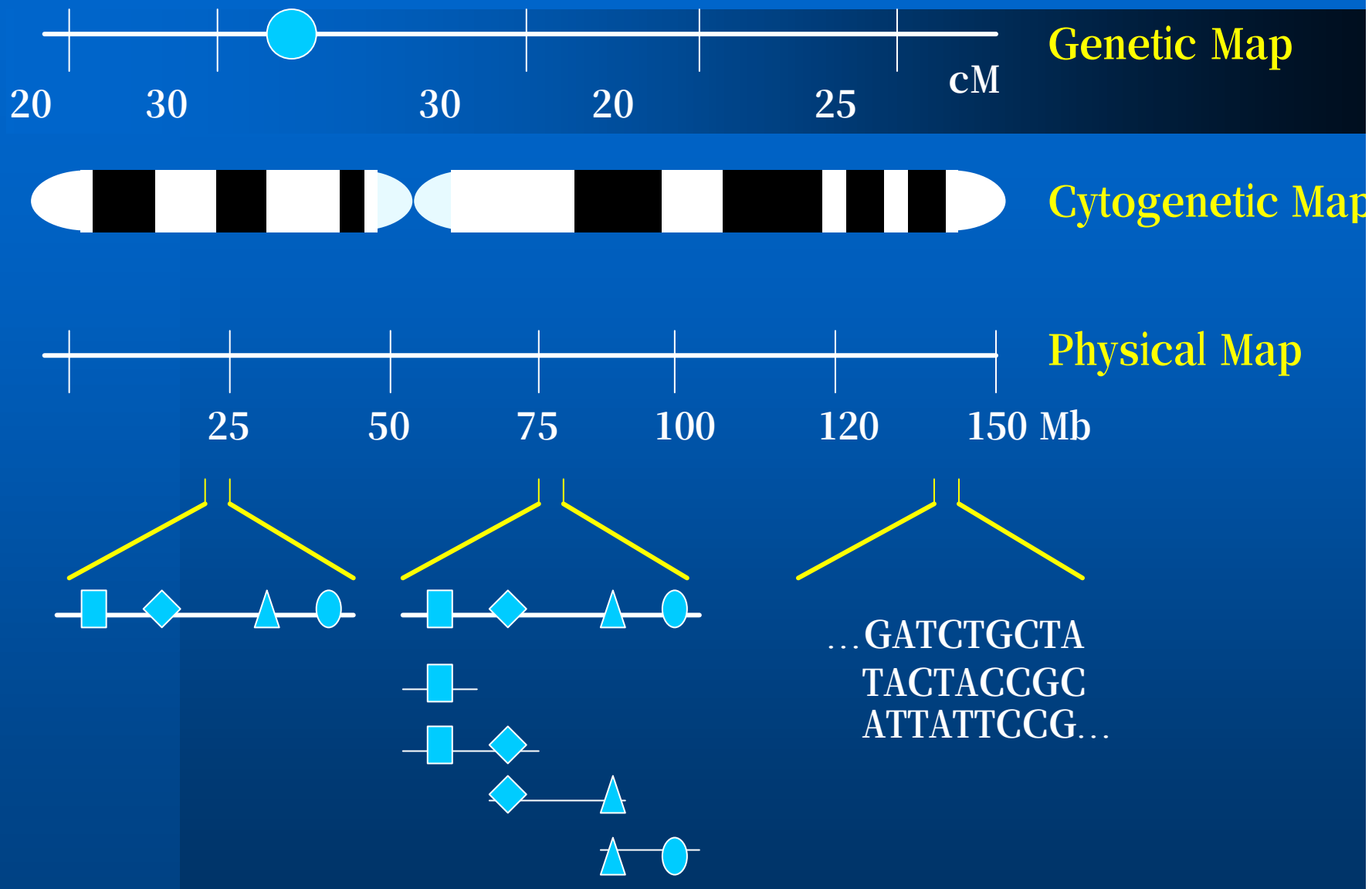


Physical Maps

- STS content mapping (>1Mb)
  - using PCR-based positional markers.
  - Ordering of marker in clone library
  - distance is measured by restriction mapping
- CEPHYAC map
  - used a combination of fingerprinting.
- Optical Mapping

Comparative Maps

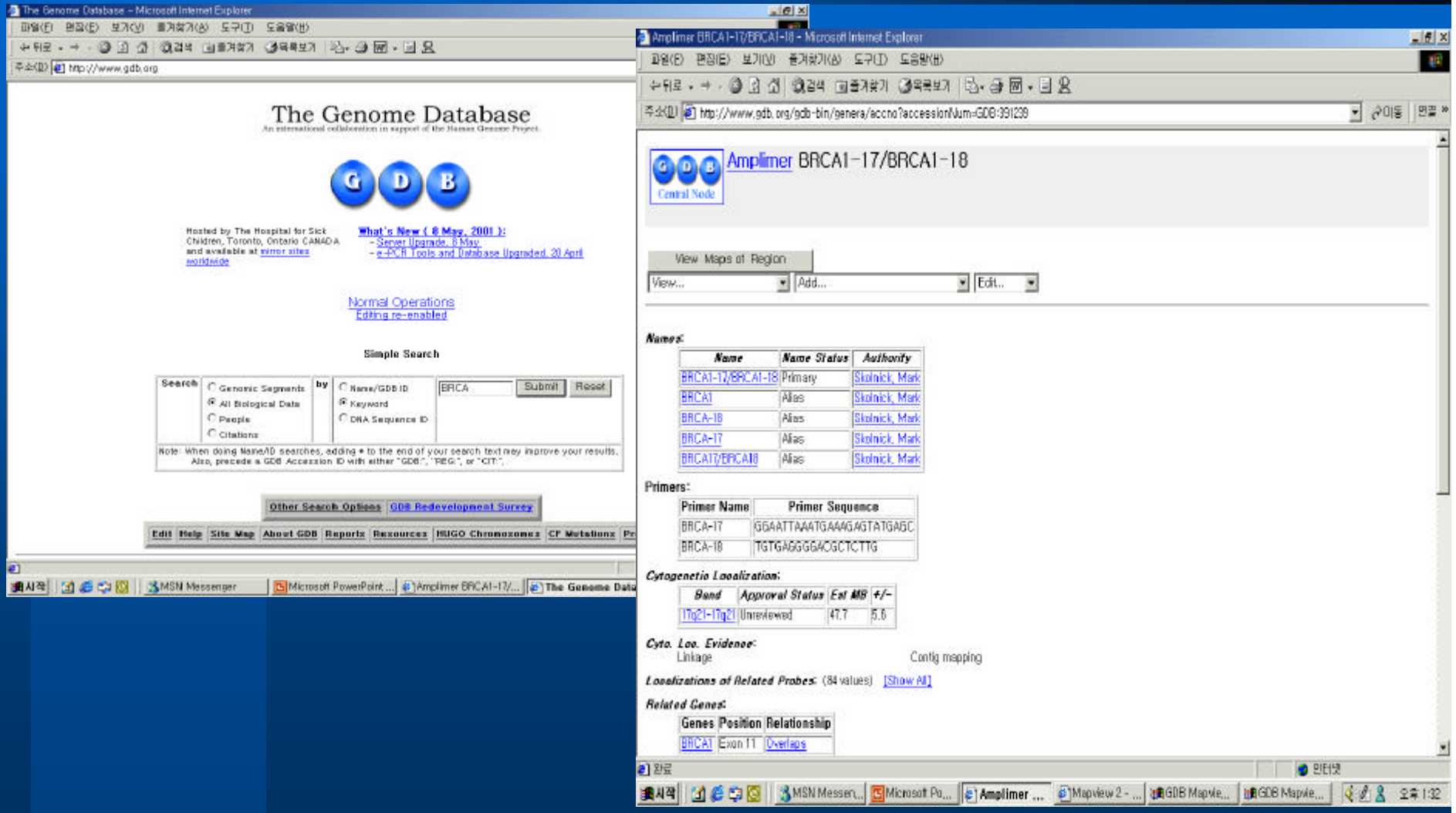
- Process of identifying conserved chromosome segments across different species.
- Orthologous genes sharing an identical linear order within a chromosome region.
- Identify conserved segments and ancient chromosome breakpoints.


Genetic Map
20
30
30
20
25
cM
Cytogenetic Map
Physical Map
25
50
75
100
120
150 Mb
…GATCTGCTA
TACTACCGC
ATTATTCCG…
RH Map
Clone-Based Map
Sequence Map

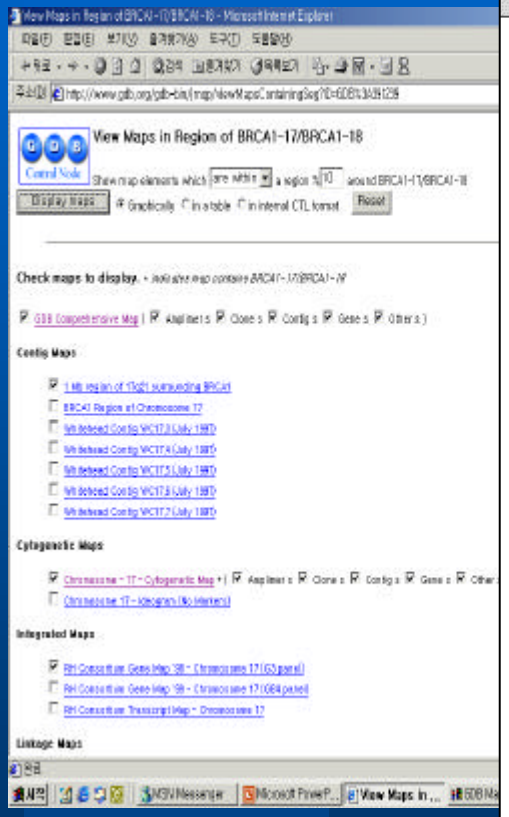
Genome Database (GDB)

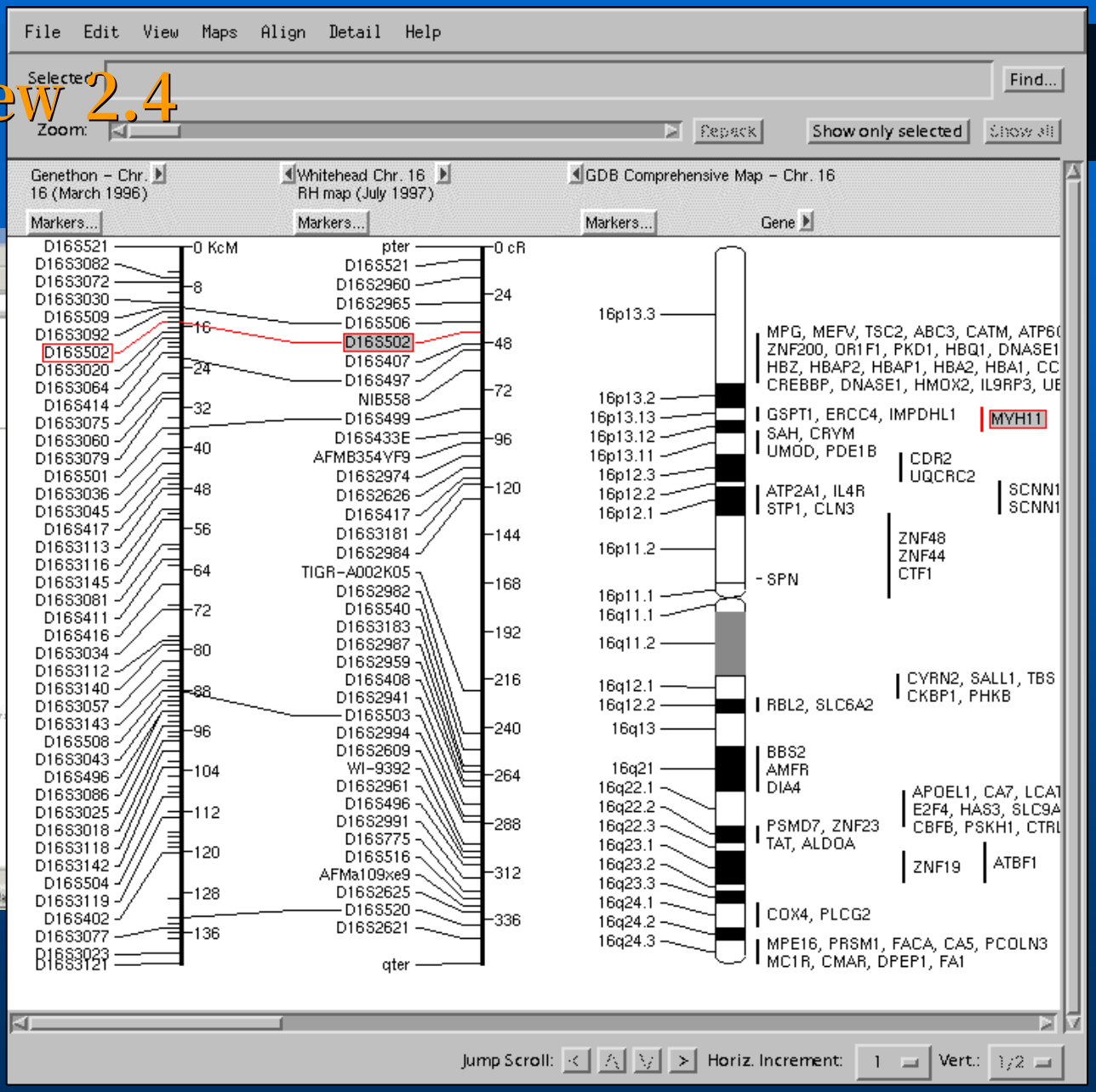
- The official central repository for genomic mapping data created by the Human Genome Project
- Currently, GDB comprises descriptions of three types of objects from humans
  - Genomic Segments (genes, clones, amplimers, breatkpoints, cytogenetic marakers, fragilesites, ESTs, syndromic regions, contigs, and repeats)
  - Maps (including cytogenetic, GL, RH, STS-content, and integrrated)
  - Variations (primarily relating to polymorphisms)

Genome Database (GDB)



GDB Mapview 2.4



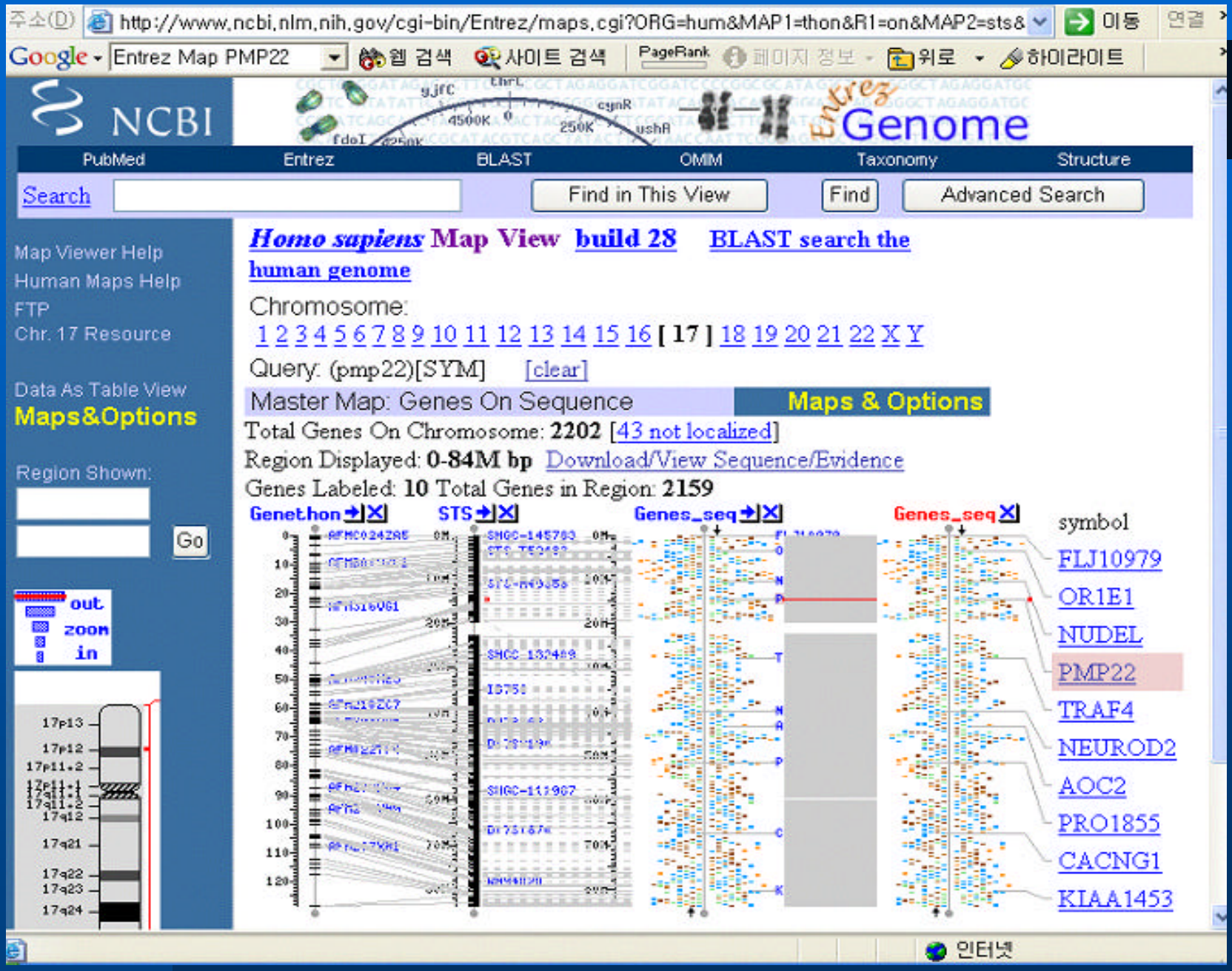


NCBI

- Entrez provides integrated access to several different types of data for over 600 organisms
  - Nucleotide sequences
  - Protein structures and sequences
  - PubMed/MEDLINE
  - Genomic mapping information
- NCBI Human Genome Map Viewer
  - Human genome sequence data as well as cytogenetic, genetic, physical, and radiation hybrid maps

Example: *Homo sampiens* Genome View page

- A genome-wide search for the term CMT* returns 33 hits. representing the loci for forms of Charcot-Marie-Tooth neuropathy on eight different chromosomes.
- Selecting the Genes_seq link for the PMP2 gene (the gene symbol for CMT1A, on chromosome 17) returns the view of the sequence map for the region surrounding this gene.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Entrez Map PMP22
NCBI
Entrez Genome
PubMed
Entrez
BLAST
OMIM
Taxonomy
Structure
Search
Find in This View
Find
Advanced Search
Map Viewer Help
Human Maps Help
FTP
Chr. 17 Resource
Data As Table View
Maps&Options
Region Shown:
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out
zoom
in
Homo sapiens Map View build 28
BLAST search the human genome
Chromosome:
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 [17] 18 19 20 21 22 X Y
Query: (pmp22)[SYM]
[clear]
Master Map: Genes On Sequence
Maps & Options
Total Genes On Chromosome: 2202 [43 not localized]
Region Displayed: 0-84M bp
Download/View Sequence/Evidence
Genes Labeled: 10 Total Genes in Region: 2159
Genethon
STS
Genes_seq
Genes_seq
symbol
FLJ10979
OR1E1
NUDEL
PMP22
TRAF4
NEUROD2
AOC2
PRO1855
CACNG1
KIAA1453
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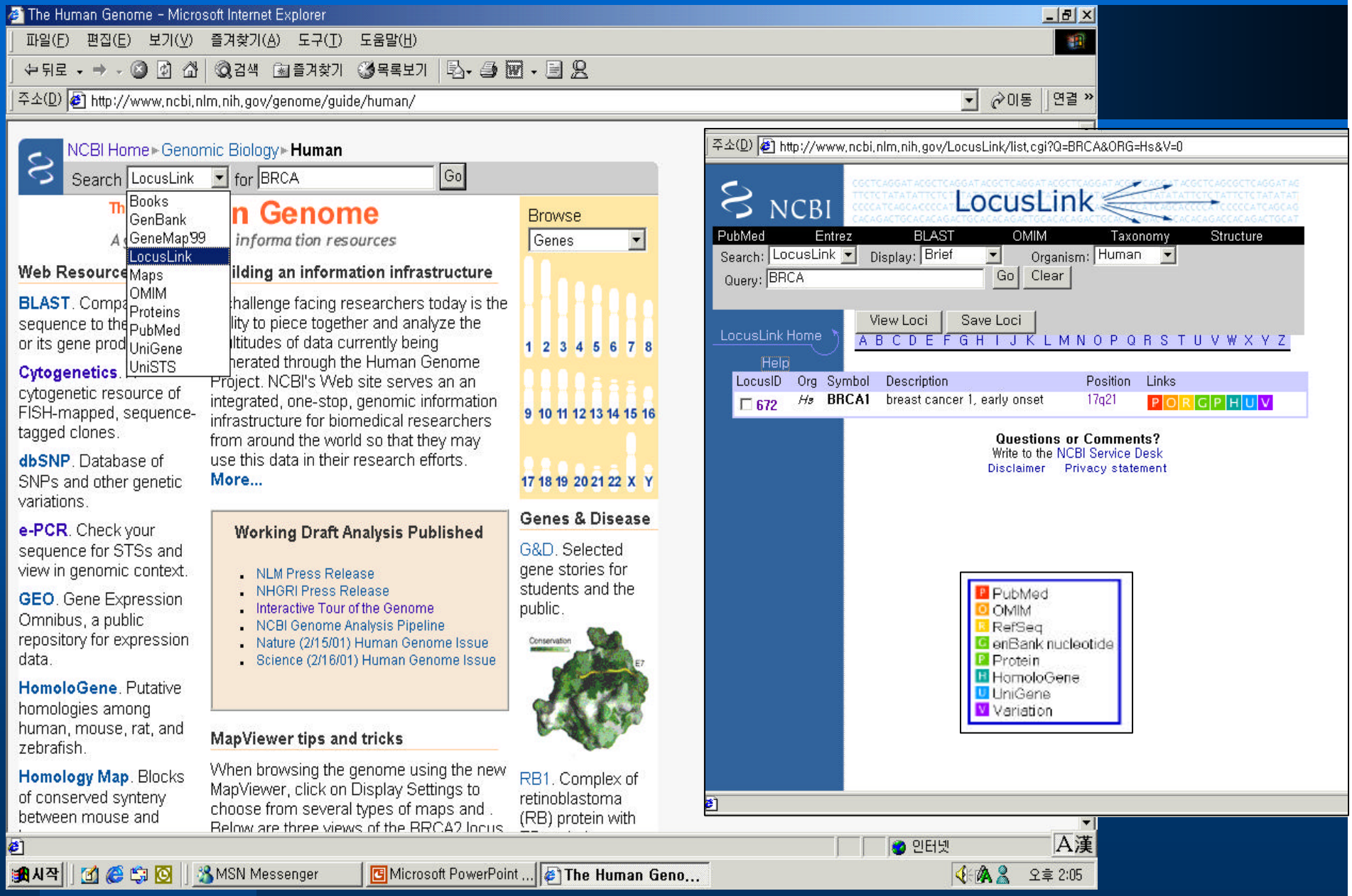
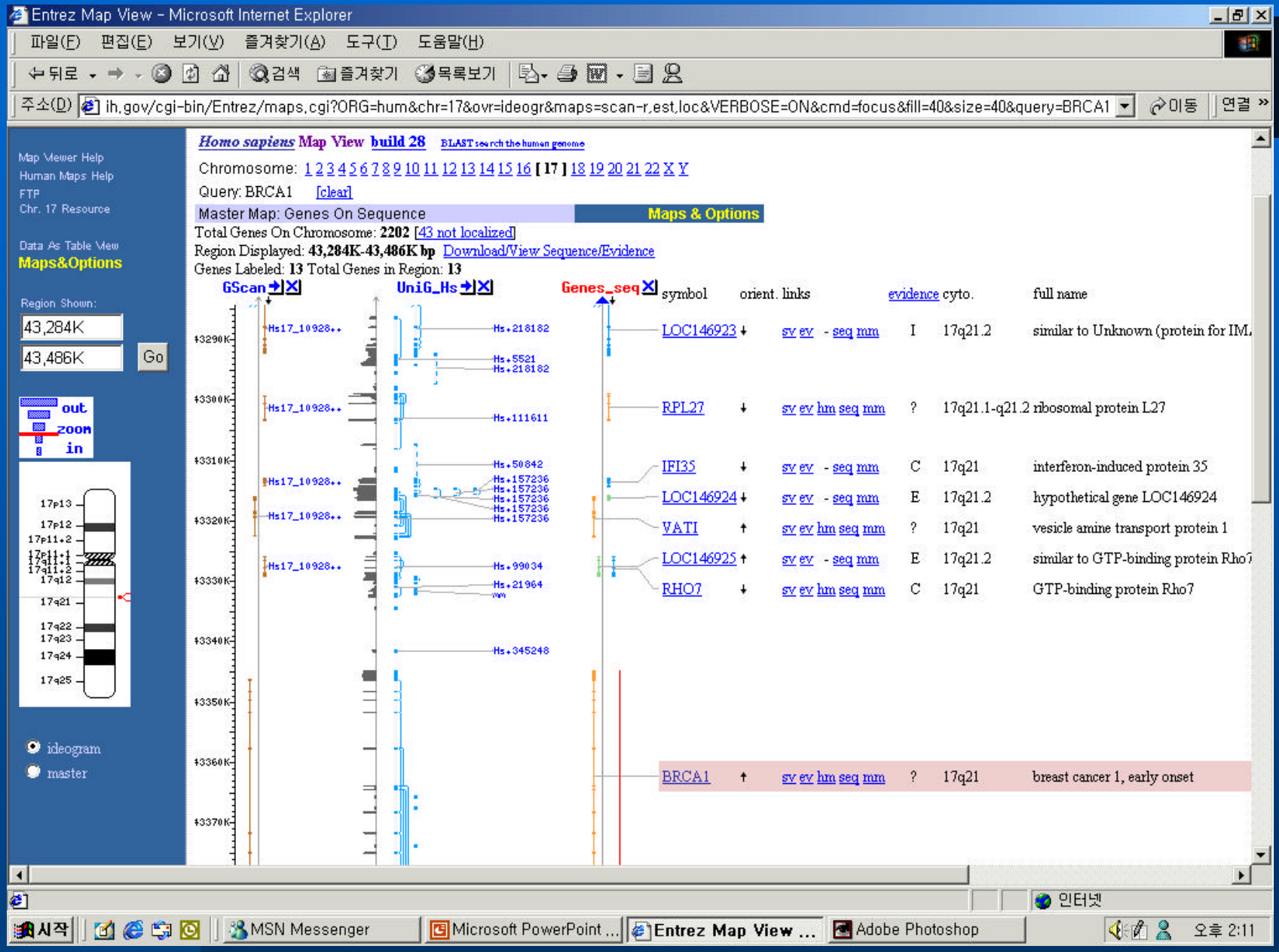
17p12
17p11.2
17q12
17q21
17q22
17q23
17q24
인터넷


The Human Genome - Microsoft Internet Explorer
http://www.ncbi.nlm.nih.gov/genome/guide/human/
NCBI Home ▸ Genomic Biology ▸ Human
Search LocusLink for BRCA Go
Books
GenBank
GeneMap'99
LocusLink
Maps
OMIM
Proteins
PubMed
UniGene
UniSTS
Web Resource
BLAST. Compa
sequence to the
or its gene prod
Cytogenetics.
cytogenetic resource of FISH-mapped, sequence-tagged clones.
dbSNP. Database of SNPs and other genetic variations.
e-PCR. Check your sequence for STSs and view in genomic context.
GEO. Gene Expression Omnibus, a public repository for expression data.
HomoloGene. Putative homologies among human, mouse, rat, and zebrafish.
Homology Map. Blocks of conserved synteny between mouse and
n Genome
informa tion resources
ilding an information infrastructure
challenge facing researchers today is the lity to piece together and analyze the ltitudes of data currently being herated through the Human Genome Project. NCBI's Web site serves an an integrated, one-stop, genomic information infrastructure for biomedical researchers from around the world so that they may use this data in their research efforts.
More...
Working Draft Analysis Published
NLM Press Release
NHGRI Press Release
Interactive Tour of the Genome
NCBI Genome Analysis Pipeline
Nature (2/15/01) Human Genome Issue
Science (2/16/01) Human Genome Issue
MapViewer tips and tricks
When browsing the genome using the new MapViewer, click on Display Settings to choose from several types of maps and . Below are three views of the BRCA2 locus
Browse
Genes
1 2 3 4 5 6 7 8
9 10 11 12 13 14 15 16
17 18 19 20 21 22 X Y
Genes & Disease
G&D. Selected gene stories for students and the public.
RB1. Complex of retinoblastoma (RB) protein with
http://www.ncbi.nlm.nih.gov/LocusLink/list.cgi?Q=BRCA&ORG=Hs&V=0
NCBI
LocusLink
PubMed Entrez BLAST OMIM Taxonomy Structure
Search: LocusLink Display: Brief Organism: Human
Query: BRCA Go Clear
View Loci Save Loci
LocusLink Home
Help
A B C D E F G H I J K L M N O P Q R S T U V W X Y Z
LocusID Org Symbol Description Position Links
672 Hs BRCA1 breast cancer 1, early onset 17q21 P O R G P H U V
Questions or Comments?
Write to the NCBI Service Desk
Disclaimer Privacy statement
P PubMed
O OMIM
R RefSeq
G enBank nucleotide
P Protein
H HomoloGene
U UniGene
V Variation
시작
MSN Messenger
Microsoft PowerPoint ...
The Human Geno...
오후 2:05


Entrez Map View - Microsoft Internet Explorer
파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)
주소(D) ih.gov/cgi-bin/Entrez/maps.cgi?ORG=hum&chr=17&ovr=ideogr&maps=scan-r,est,loc&VERBOSE=ON&cmd=focus&fill=40&size=40&query=BRCA1
Map Viewer Help
Human Maps Help
FTP
Chr. 17 Resource
Data As Table View
Maps&Options
Region Shown:
43,284K
43,486K
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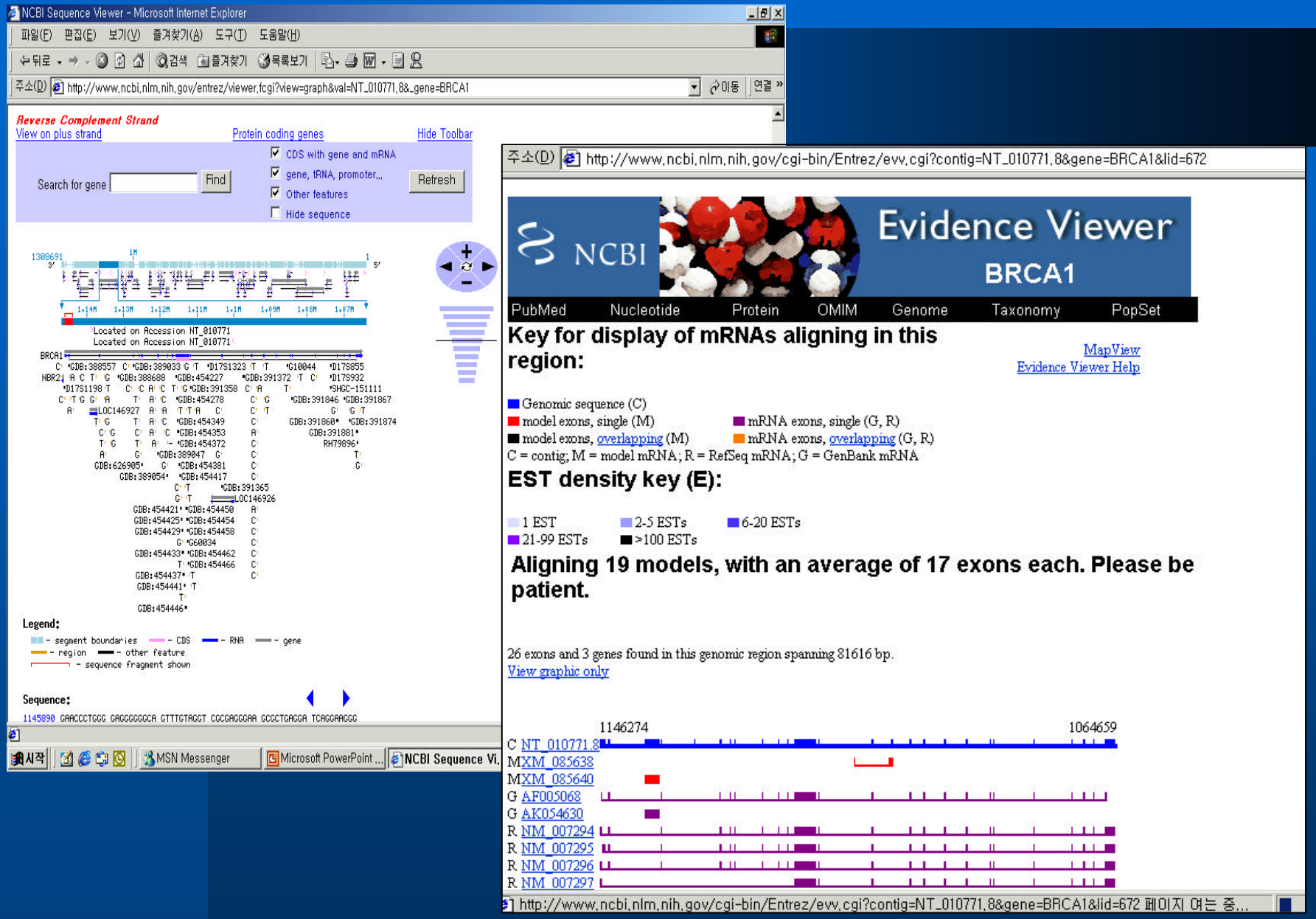
in
ideogram
master
Homo sapiens Map View build 28
BLAST search the human genome
Chromosome: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 [17] 18 19 20 21 22 X Y
Query: BRCA1 [clear]
Master Map: Genes On Sequence
Maps & Options
Total Genes On Chromosome: 2202 [43 not localized]
Region Displayed: 43,284K-43,486K bp Download/View Sequence/Evidence
Genes Labeled: 13 Total Genes in Region: 13
GScan
UniG_Hs
Genes_seq
symbol orient. links evidence cyto. full name
LOC146923 sv ev - seq mm I 17q21.2 similar to Unknown (protein for IM
RPL27 sv ev hm seq mm ? 17q21.1-q21.2 ribosomal protein L27
IFI35 sv ev - seq mm C 17q21 interferon-induced protein 35
LOC146924 sv ev - seq mm E 17q21.2 hypothetical gene LOC146924
VATI sv ev hm seq mm ? 17q21 vesicle amine transport protein 1
LOC146925 sv ev - seq mm E 17q21.2 similar to GTP-binding protein Rho7
RHO7 sv ev hm seq mm C 17q21 GTP-binding protein Rho7
BRCA1 sv ev hm seq mm ? 17q21 breast cancer 1, early onset
시작
MSN Messenger
Microsoft PowerPoint ...
Entrez Map View ...
Adobe Photoshop
오후 2:11


NCBI Sequence Viewer - Microsoft Internet Explorer
http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?view=graph&val=NT_010771.8&_gene=BRCA1
Reverse Complement Strand
View on plus strand
Protein coding genes
Hide Toolbar
CDS with gene and mRNA
gene, tRNA, promoter...
Other features
Hide sequence
Search for gene
Find
Refresh
Legend:
Sequence:
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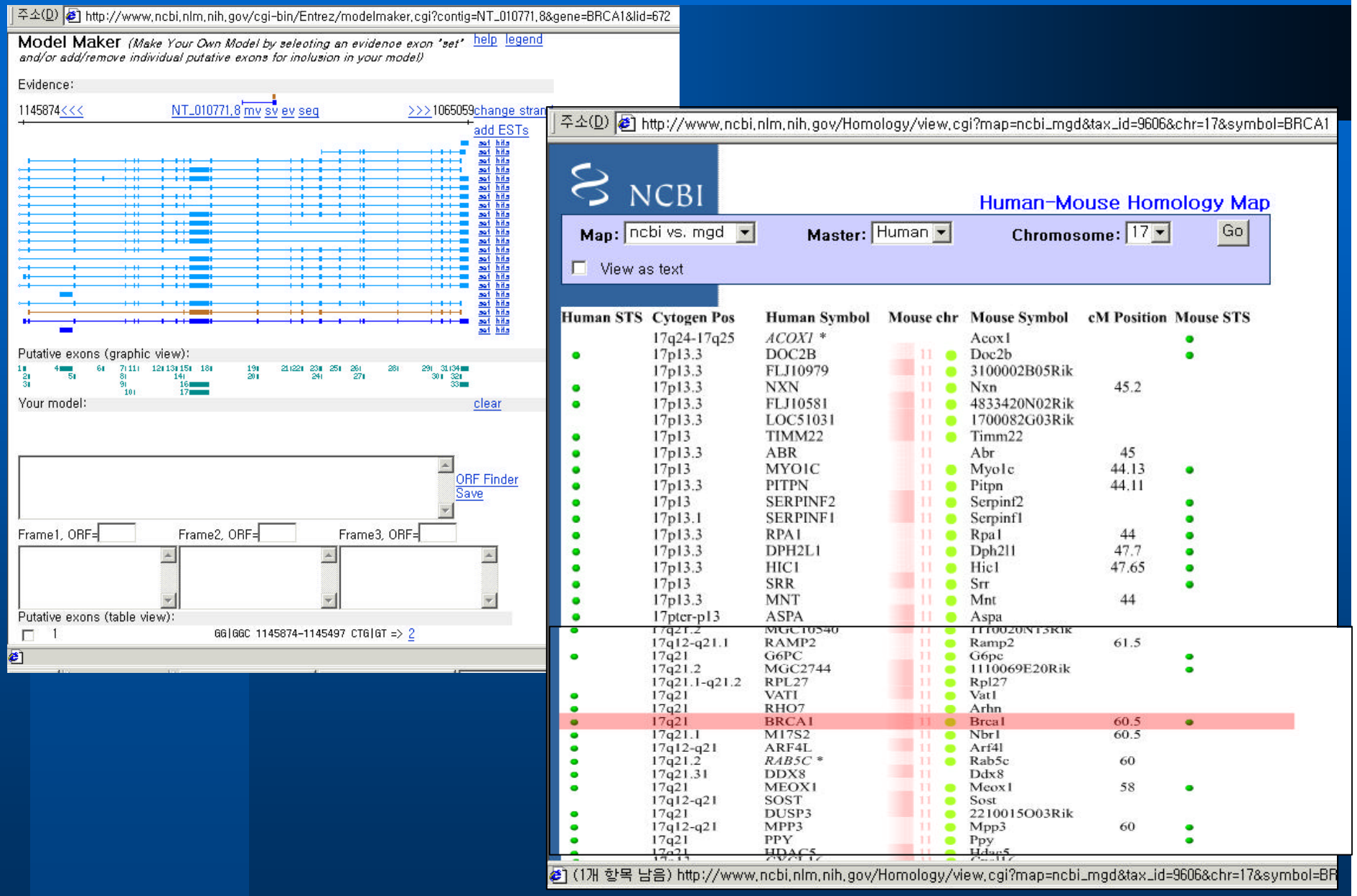
NCBI
Evidence Viewer
BRCA1
PubMed
Nucleotide
Protein
OMIM
Genome
Taxonomy
PopSet
Key for display of mRNAs aligning in this region:
MapView
Evidence Viewer Help
Genomic sequence (C)
model exons, single (M)
mRNA exons, single (G, R)
model exons, overlapping (M)
mRNA exons, overlapping (G, R)
C = contig; M = model mRNA; R = RefSeq mRNA; G = GenBank mRNA
EST density key (E):
1 EST
2-5 ESTs
6-20 ESTs
21-99 ESTs
>100 ESTs
Aligning 19 models, with an average of 17 exons each. Please be patient.
26 exons and 3 genes found in this genomic region spanning 81616 bp.
View graphic only
1146274
1064659
C NT_010771.8
M XM_085638
M XM_085640
G AF005068
G AK054630
R NM_007294
R NM_007295
R NM_007296
R NM_007297
http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/evv.cgi?contig=NT_010771.8&gene=BRCA1&lid=672 페이지 여는 중...


주소(D) http://www.ncbi.nlm.nih.gov/cgi-bin/Entrez/modelmaker.cgi?contig=NT_010771.8&gene=BRCA1&lid=672
Model Maker (Make Your Own Model by selecting an evidence exon 'set' and/or add/remove individual putative exons for inclusion in your model)
help legend
Evidence:
1145874<<< NT_010771.8 mv sv ev seq >>>1065059change strand
add ESTs
Putative exons (graphic view):
Your model:
clear
ORF Finder
Save
Frame1, ORF=
Frame2, ORF=
Frame3, ORF=
Putative exons (table view):
1 GG|GGC 1145874-1145497 CTG|GT => 2
주소(D) http://www.ncbi.nlm.nih.gov/Homology/view.cgi?map=ncbi_mgd&tax_id=9606&chr=17&symbol=BRCA1
NCBI
Human-Mouse Homology Map
Map: ncbi vs. mgd
Master: Human
Chromosome: 17
Go
View as text
Human STS | Cytogen Pos | Human Symbol | Mouse chr | Mouse Symbol | cM Position | Mouse STS
17q24-17q25 | ACOX1 * | Acox1
17p13.3 | DOC2B | Doc2b
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17p13.3 | ABR | Abr | 45
17p13 | MYO1C | Myo1c | 44.13
17p13.3 | PITPN | Pitpn | 44.11
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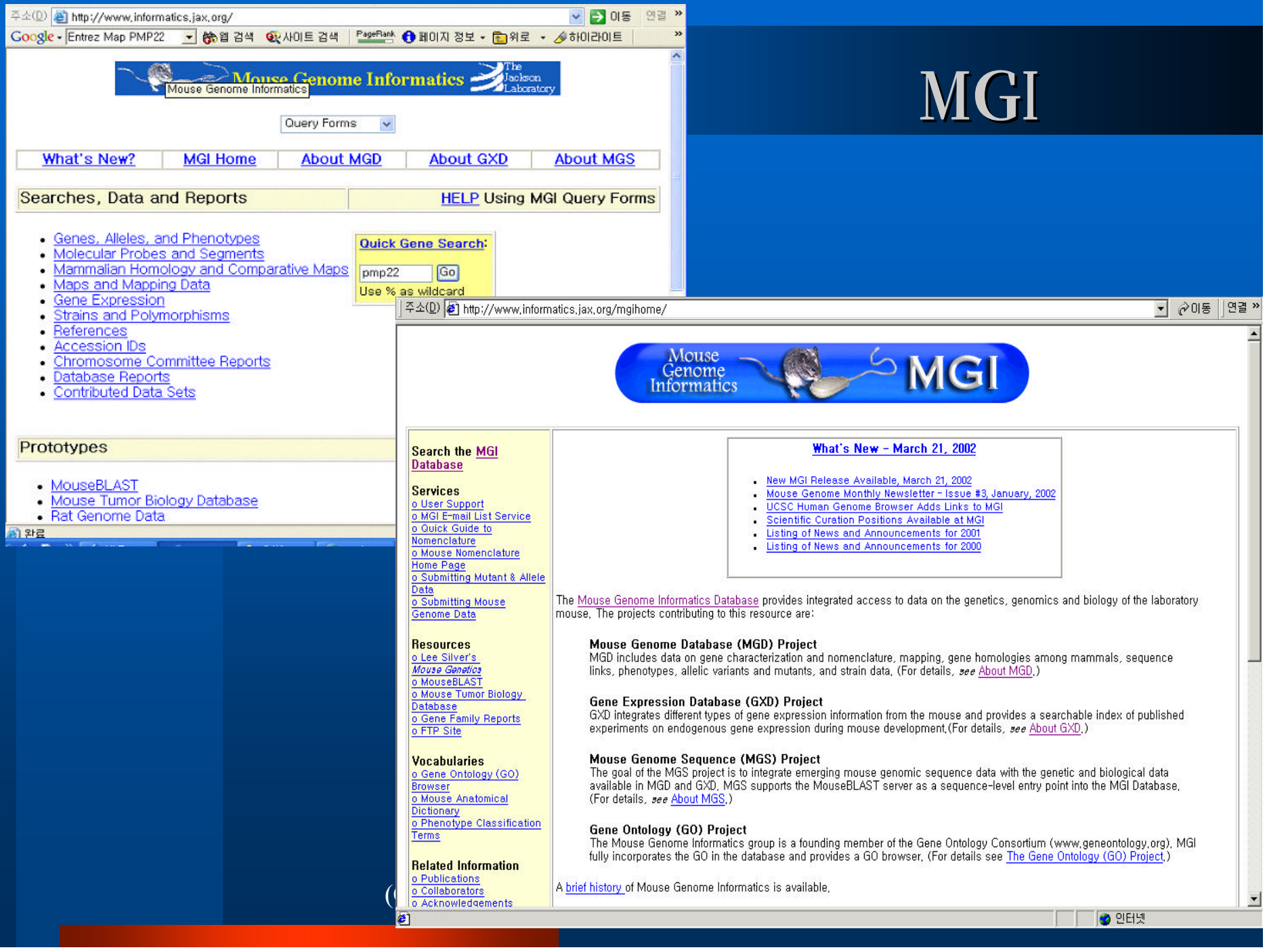
17p13.1 | SERPINF1 | Serpinf1
17p13.3 | RPA1 | Rpa1 | 44
17p13.3 | DPH2L1 | Dph2l1 | 47.7
17p13.3 | HIC1 | Hic1 | 47.65
17p13 | SRR | Srr
17p13.3 | MNT | Mnt | 44
17pter-p13 | ASPA | Aspa
17q12-q21.1 | RAMP2 | Ramp2 | 61.5
17q21 | G6PC | G6pc
17q21.2 | MGC2744 | 1110069E20Rik
17q21.1-q21.2 | RPL27 | Rpl27
17q21 | VAT1 | Vat1
17q21 | RHO7 | Arhn
17q21 | BRCA1 | Brca1 | 60.5
17q21.1 | M17S2 | Nbr1 | 60.5
17q12-q21 | ARF4L | Arf4l
17q21.2 | RAB5C * | Rab5c | 60
17q21.31 | DDX8 | Ddx8
17q21 | MEOX1 | Meox1 | 58
17q12-q21 | SOST | Sost
17q21 | DUSP3 | 2210015O03Rik
17q12-q21 | MPP3 | Mpp3 | 60
17q21 | PPY | Ppy
(1개 항목 남음) http://www.ncbi.nlm.nih.gov/Homology/view.cgi?map=ncbi_mgd&tax_id=9606&chr=17&symbol=BR

MGI/MGD

- The Mouse Genome Initiative Database (MGI): the primary public mouse genomic catalogue resource.
- Located at The Jackson Laboratory, the MGI currently encompasses three cross-linked topic-specific database
  - The Mouse Genome Database (MGD)
  - The mouse Gene Expression Database (GXD)
  - The Mouse Genome Sequence project (MGS)

MGI


http://www.informatics.jax.org/
Mouse Genome Informatics
The Jackson Laboratory
Query Forms
What's New?
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Quick Gene Search:
pmp22
Go
Use % as wildcard
Prototypes
MouseBLAST
Mouse Tumor Biology Database
Rat Genome Data
http://www.informatics.jax.org/mgihome/
Mouse Genome Informatics
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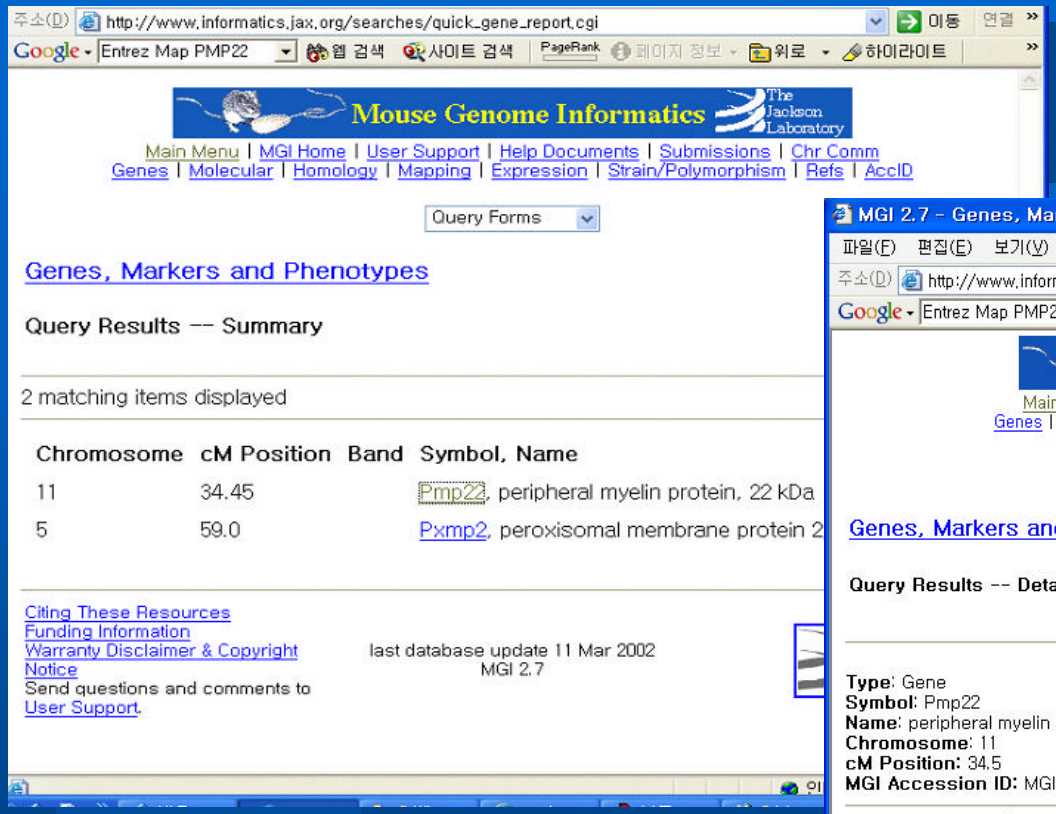
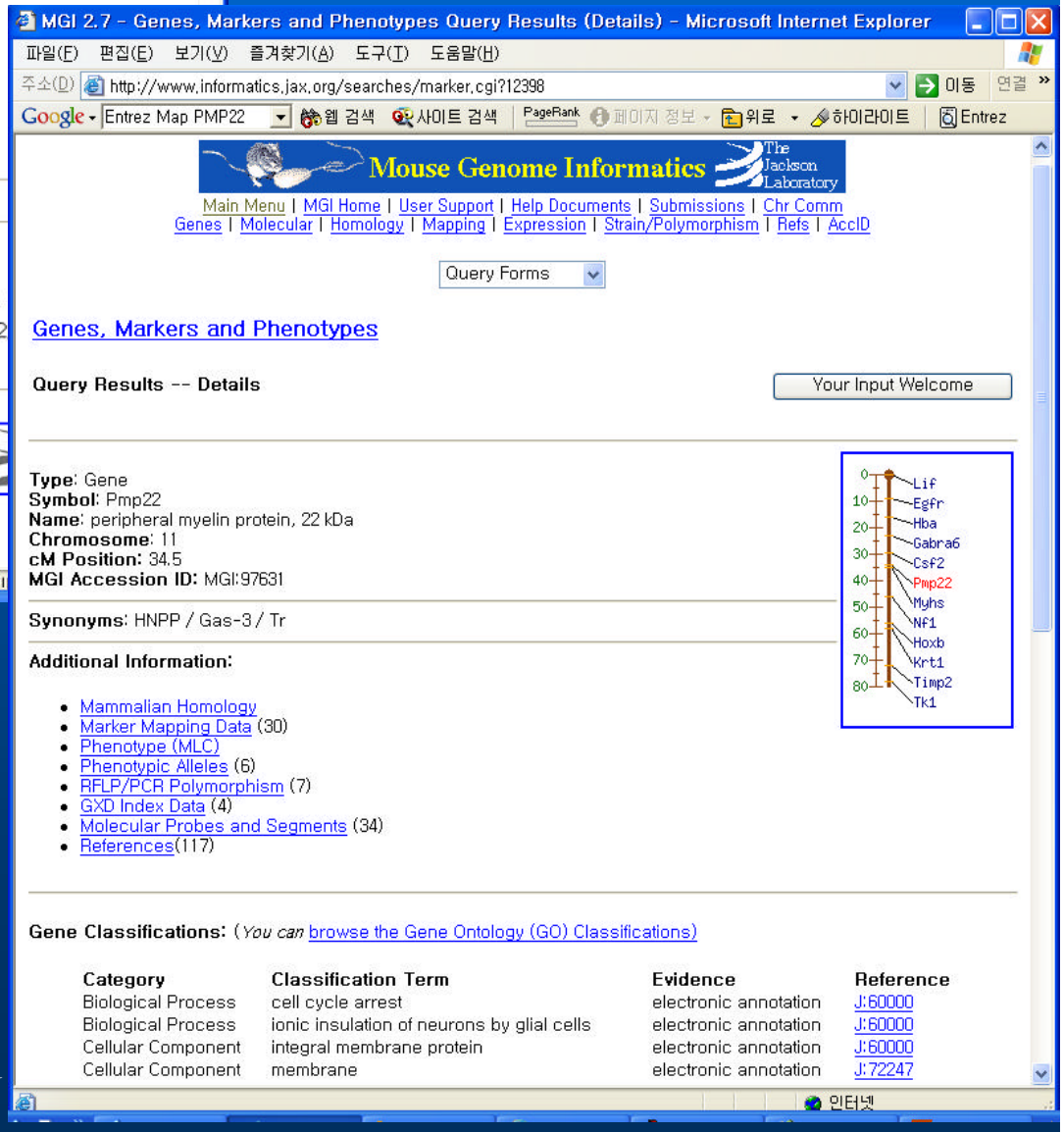
What's New - March 21, 2002
New MGI Release Available, March 21, 2002
Mouse Genome Monthly Newsletter - Issue #3, January, 2002
UCSC Human Genome Browser Adds Links to MGI
Scientific Curation Positions Available at MGI
Listing of News and Announcements for 2001
Listing of News and Announcements for 2000
The Mouse Genome Informatics Database provides integrated access to data on the genetics, genomics and biology of the laboratory mouse. The projects contributing to this resource are:
Mouse Genome Database (MGD) Project
MGD includes data on gene characterization and nomenclature, mapping, gene homologies among mammals, sequence links, phenotypes, allelic variants and mutants, and strain data. (For details, see About MGD.)
Gene Expression Database (GXD) Project
GXD integrates different types of gene expression information from the mouse and provides a searchable index of published experiments on endogenous gene expression during mouse development.(For details, see About GXD.)
Mouse Genome Sequence (MGS) Project
The goal of the MGS project is to integrate emerging mouse genomic sequence data with the genetic and biological data available in MGD and GXD. MGS supports the MouseBLAST server as a sequence-level entry point into the MGI Database. (For details, see About MGS.)
Gene Ontology (GO) Project
The Mouse Genome Informatics group is a founding member of the Gene Ontology Consortium (www.geneontology.org). MGI fully incorporates the GO in the database and provides a GO browser. (For details see The Gene Ontology (GO) Project.)
A brief history of Mouse Genome Informatics is available.





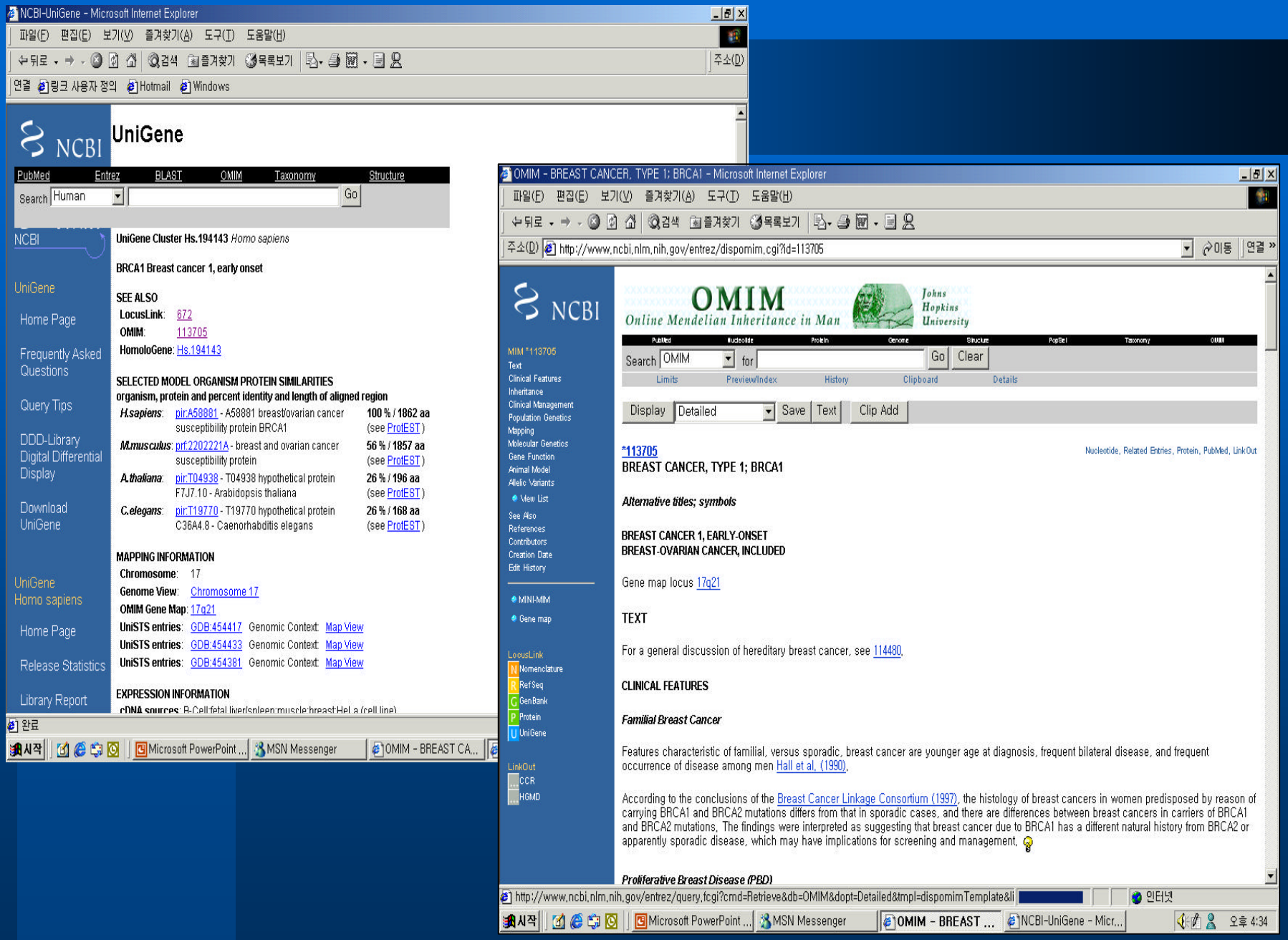
Result of an MGD Quick Gene Search for pmp22.

Mapping Projects and Associated Resources

- Cytogenetic resources
- Genetic linkage map resources
- Radiation hybrid map resources
- STS content maps and resources
- DNA sequence
- Integrated maps and genomic cataloguing
- Comparative resources
- Single-chromosome and regional map resources

Cytogenetic Resources

- The central repository for human cytogenetic information is GDB
  - Query for marker map and map information using cytogenetic coordinates
  - Cross-referencing cytogenetic positions with genes or regions of interest
- NCBI's LocusLink, UniGene, OMIM catalogues
  - Valuable repositories of cytogenetic positions
- NCI's Cancer Chromosome Aberratio Project
- Southeastern Regional Genetic Group
- Coriell Cell Repositories

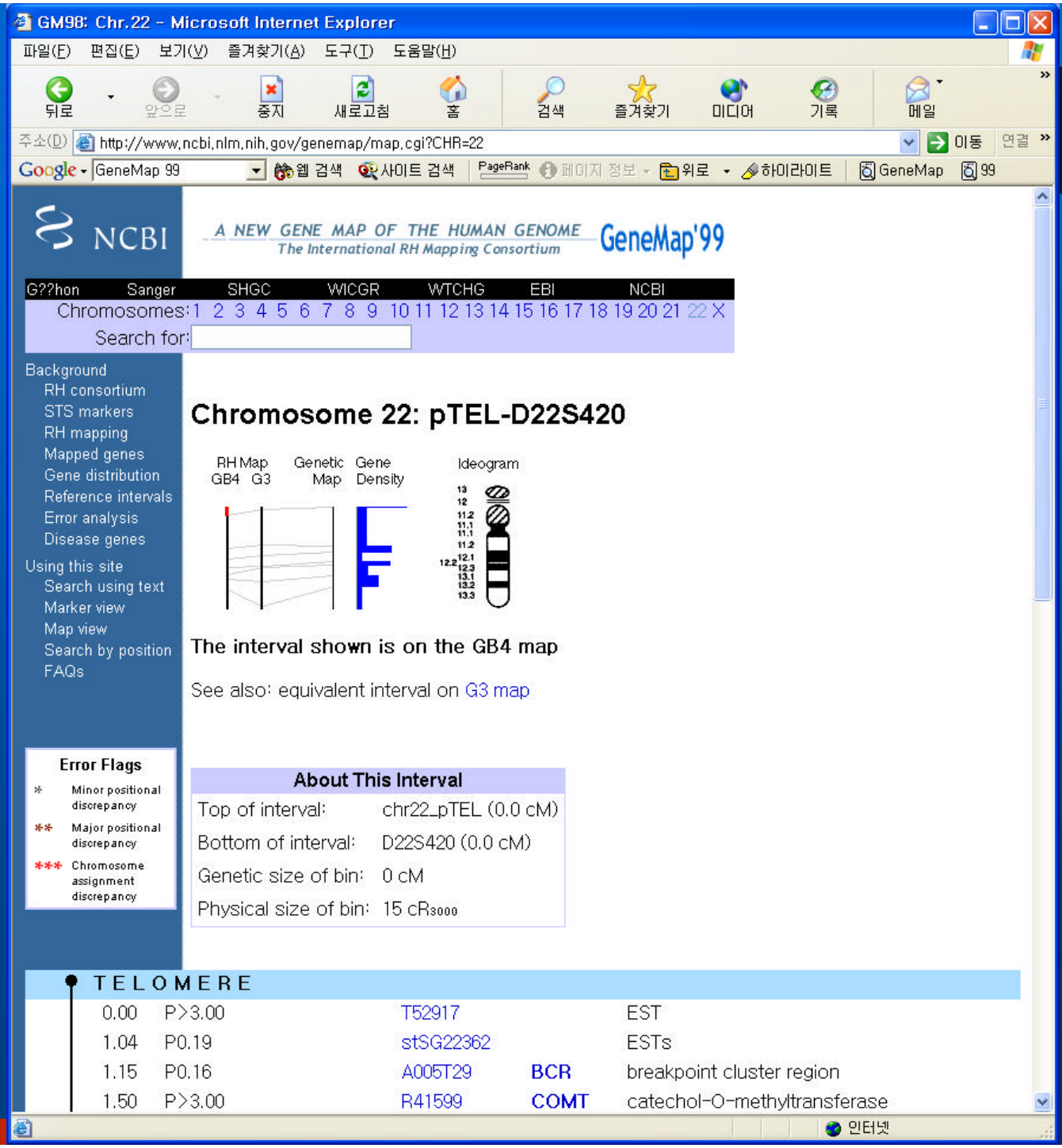

NCBI-UniGene - Microsoft Internet Explorer
NCBI
UniGene
PubMed Entrez BLAST OMIM Taxonomy Structure
Search Human Go
UniGene Cluster Hs.194143 Homo sapiens
BRCA1 Breast cancer 1, early onset
SEE ALSO
LocusLink: 672
OMIM: 113705
HomoloGene: Hs.194143
SELECTED MODEL ORGANISM PROTEIN SIMILARITIES
organism, protein and percent identity and length of aligned region
H.sapiens: pir:A58881 - A58881 breast/ovarian cancer susceptibility protein BRCA1 100 % / 1862 aa (see ProtEST)
M.musculus: prf:2202221A - breast and ovarian cancer susceptibility protein 56 % / 1857 aa (see ProtEST)
A.thaliana: pir:T04938 - T04938 hypothetical protein F7J7.10 - Arabidopsis thaliana 26 % / 196 aa (see ProtEST)
C.elegans: pir:T19770 - T19770 hypothetical protein C36A4.8 - Caenorhabditis elegans 26 % / 168 aa (see ProtEST)
MAPPING INFORMATION
Chromosome: 17
Genome View: Chromosome 17
OMIM Gene Map: 17q21
UniSTS entries: GDB:454417 Genomic Context: Map View
UniSTS entries: GDB:454433 Genomic Context: Map View
UniSTS entries: GDB:454381 Genomic Context: Map View
EXPRESSION INFORMATION
UniGene
Home Page
Frequently Asked Questions
Query Tips
DDD-Library Digital Differential Display
Download UniGene
UniGene Homo sapiens
Home Page
Release Statistics
Library Report
OMIM - BREAST CANCER, TYPE 1; BRCA1 - Microsoft Internet Explorer
http://www.ncbi.nlm.nih.gov/entrez/dispomim.cgi?id=113705
OMIM
Online Mendelian Inheritance in Man
Johns Hopkins University
Search OMIM for Go Clear
Limits Preview/Index History Clipboard Details
Display Detailed Save Text Clip Add
*113705
Nucleotide, Related Entries, Protein, PubMed, LinkOut
BREAST CANCER, TYPE 1; BRCA1
Alternative titles; symbols
BREAST CANCER 1, EARLY-ONSET
BREAST-OVARIAN CANCER, INCLUDED
Gene map locus 17q21
TEXT
For a general discussion of hereditary breast cancer, see 114480.
CLINICAL FEATURES
Familial Breast Cancer
Features characteristic of familial, versus sporadic, breast cancer are younger age at diagnosis, frequent bilateral disease, and frequent occurrence of disease among men Hall et al. (1990).
According to the conclusions of the Breast Cancer Linkage Consortium (1997), the histology of breast cancers in women predisposed by reason of carrying BRCA1 and BRCA2 mutations differs from that in sporadic cases, and there are differences between breast cancers in carriers of BRCA1 and BRCA2 mutations. The findings were interpreted as suggesting that breast cancer due to BRCA1 has a different natural history from BRCA2 or apparently sporadic disease, which may have implications for screening and management.
Proliferative Breast Disease (PBD)
MIM *113705
Text
Clinical Features
Inheritance
Clinical Management
Population Genetics
Mapping
Molecular Genetics
Gene Function
Animal Model
Allelic Variants
View List
See Also
References
Contributors
Creation Date
Edit History
MINI-MIM
Gene map
LocusLink
Nomenclature
RefSeq
GenBank
Protein
UniGene
LinkOut
CCR
HGMD

Genetic Linkage Map Resources

- The starting point for many disease-gene mapping projects
- The backbone of many physical mapping efforts
- Genome-wide maps
  - The Cooperative Human Linkage Center
    - The CHLC has identified, genotyped, and/or mapped over 3,300 microsatellite repeat markers
  - The group at Généthon
    - Identified and genotyped over 7,800 dinucleotide repeat markers
  - The Center for Medical Genetics
    - Identified over 300 dinucleotide repeats
    - Constructed high-desity maps using over 8,000 markers
- The ABI PRISM linkage mapping
  - Dinucleotide repeat markers derived from the Généthon linkage map
- The Map-O-MAT Web site
  - A marker-based linkage map server that provides several map-specific queries

Radiation Hybrid Map Resources

- Intermediate level of resolution between linkage and physical maps
- They are helpful for sequence alignment and will aid in completion of the human genome sequencing project
- The Radiation Hybrid Database (RHdb)
- The lowest-resolution human RH panel: the Genebridge4 (GB4)
- An intermediate level panel: The Stanford Generation 3 (G3)
- The height resolution panel (“The Nest Generation”, or TNG): Stanford


GM98: Chr. 22 - Microsoft Internet Explorer
파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)
뒤로 앞으로 중지 새로고침 홈 검색 즐겨찾기 미디어 기록 메일
주소(D) http://www.ncbi.nlm.nih.gov/genemap/map.cgi?CHR=22
이동 연결
Google GeneMap 99 웹 검색 사이트 검색 PageRank 페이지 정보 위로 하이라이트 GeneMap 99
NCBI
A NEW GENE MAP OF THE HUMAN GENOME
The International RH Mapping Consortium
GeneMap'99
G??hon Sanger SHGC WICGR WTCHG EBI NCBI
Chromosomes: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X
Search for:
Background
RH consortium
STS markers
RH mapping
Mapped genes
Gene distribution
Reference intervals
Error analysis
Disease genes
Using this site
Search using text
Marker view
Map view
Search by position
FAQs
Chromosome 22: pTEL-D22S420
RH Map GB4 G3
Genetic Map
Gene Density
Ideogram
The interval shown is on the GB4 map
See also: equivalent interval on G3 map
Error Flags
* Minor positional discrepancy
** Major positional discrepancy
*** Chromosome assignment discrepancy
About This Interval
Top of interval: chr22_pTEL (0.0 cM)
Bottom of interval: D22S420 (0.0 cM)
Genetic size of bin: 0 cM
Physical size of bin: 15 cR3000
TELOMERE
0.00 P>3.00 T52917 EST
1.04 P0.19 stSG22362 ESTs
1.15 P0.16 A005T29 BCR breakpoint cluster region
1.50 P>3.00 R41599 COMT catechol-O-methyltransferase
인터넷

STS Content Maps and Resources

- The WICGR physical map
  - STS content based and contains more than 10,000 markers for witch YAC clones have benne identified.
  - Integrated with the Généthon GL and the WICGR RH maps
- CEPH/Généthon YAC project
  - Centered around screening of the CEPH MegaYAC library with a large set of STSs

DNA Sequence

- The existing human and forthcoming mouse draft genomic sequences are excellent sources for confirming mapping information, positioning and orienting localized markers, and bottom-up mapping of interesting genomic regions
- NCBI tools like BLAST can be very powerful in finding marker/sequence links.
- As the mammalian sequencing projects progress, a “sequence first” approach to mapping becomes more feasible

Integrated Maps and Genomic Cataloguing

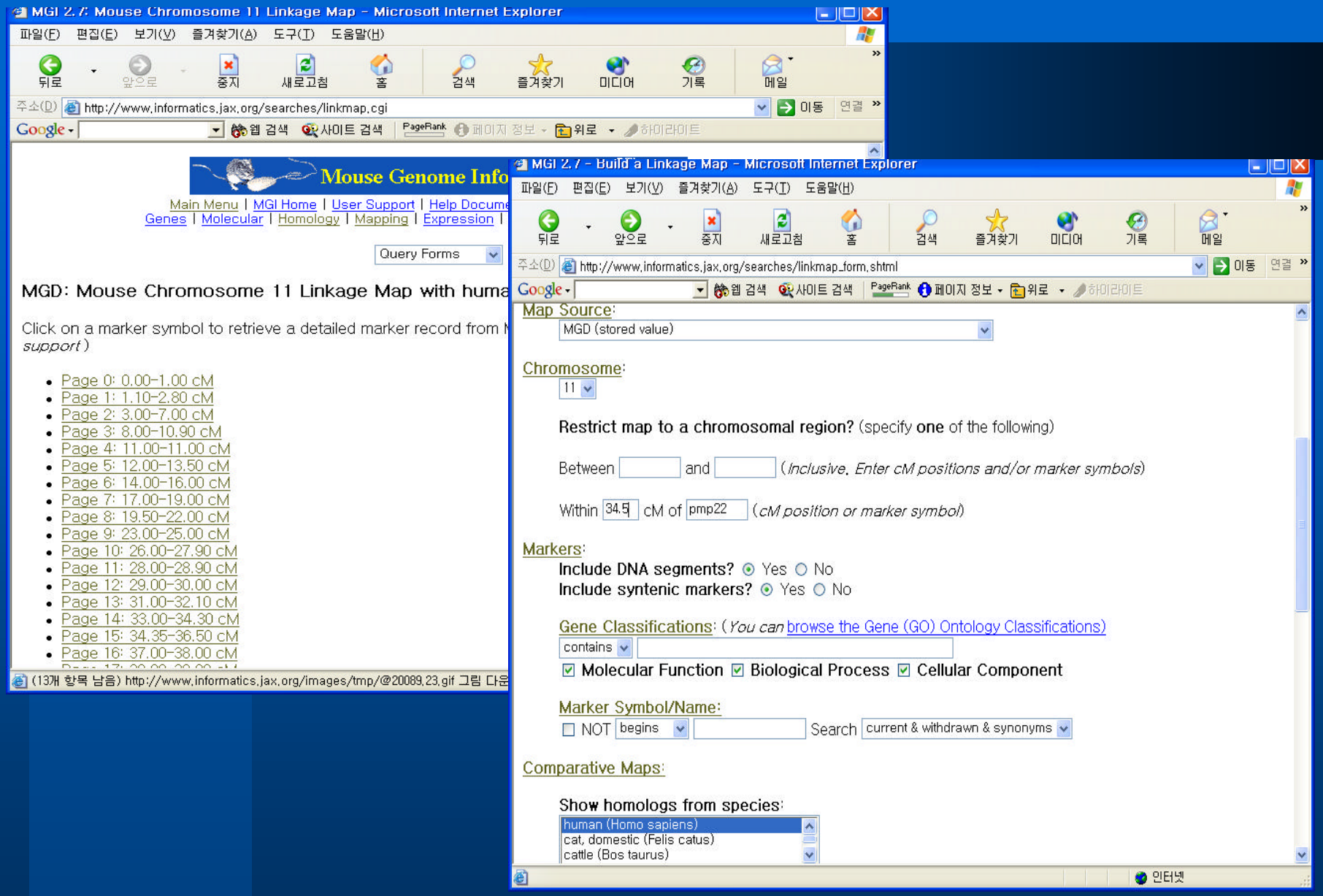
- GDB's Comprehensive Maps provide an estimated position of all genes, markers, and clones in GDB on a megabase scale.
- The estimated Mb position of the marker on each map:

Element	Chromosome	Map	Coordinate	Units	EST MB-	+/ -
D1S228	1	CeneMap '99	782.0000	cR	32.2	0.0

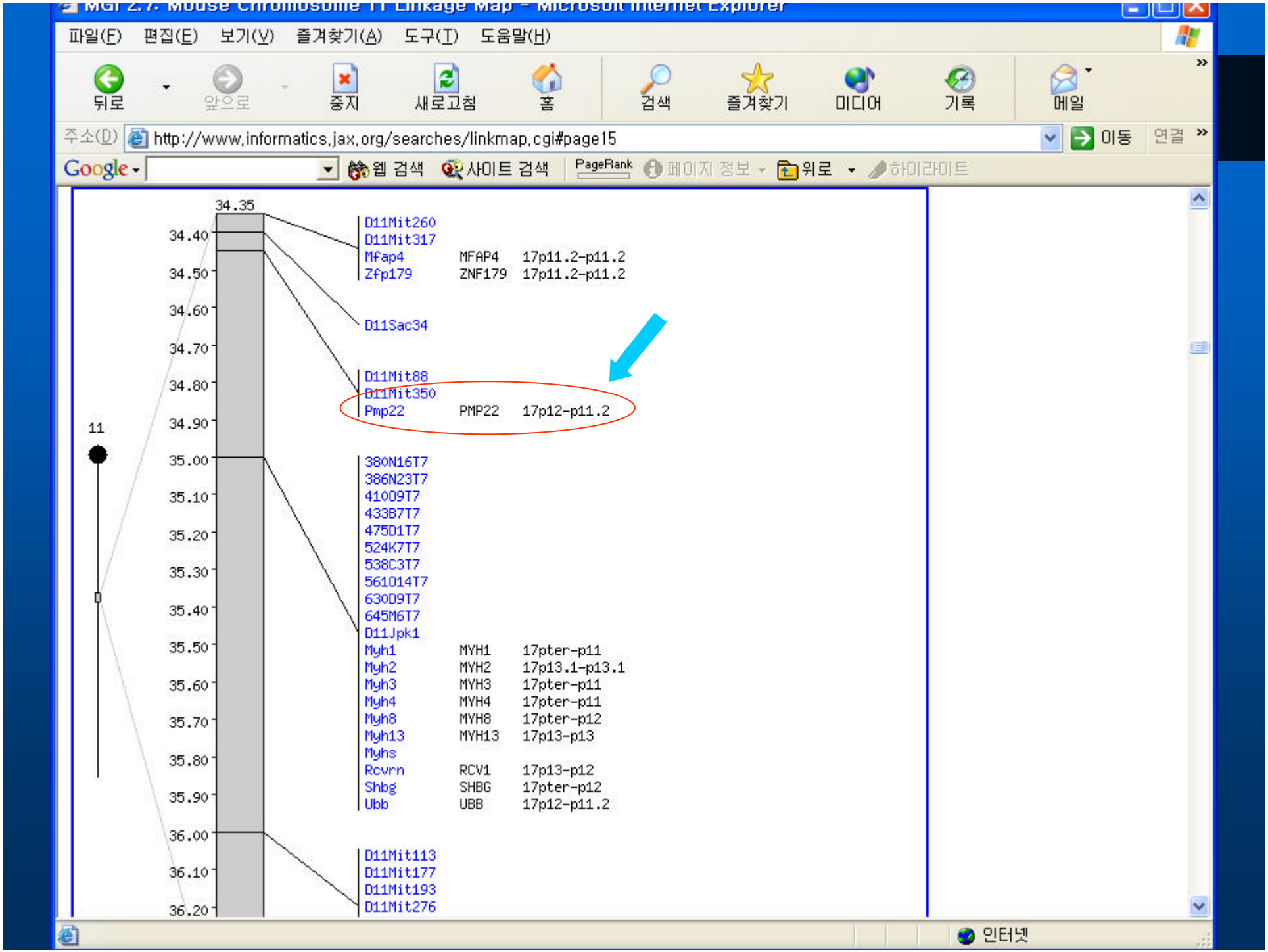
- LDB and UDB are two additional sites that infer physical position of a large, heterogeneous set of markers from existing maps using algorithm analogous to GDB's
- The eGenome project uses a slightly different approach for creating integrated maps of the human genome.
- Genomic catalogues help both to provide a single initial source containing most of the publicly available genomic information for a region and to make the task of monitoring new information easier.

Comparative Resources

- Studying the evolution and relatedness of genes between species and finding disease genes through position based orthology.
- NCBI's LocusLink database: Links to HomoloGene, a resource of curated and computed cross-species gene homologies
- The GDB does provide homology maps that simplify the reported literature for mouse, human, rat, and 17 other species.
- The Comparative Mapping by Annotation and Sequence Similarity (COMPASS) approach has been by researchers studying the cattle genome to construct cattle-human comparative maps with 638 identified human orthologs



URL: http://www.informatics.jax.org/searches/linkmap_form.shtml


MGI 2.7: Mouse Chromosome 11 Linkage Map - Microsoft Internet Explorer
파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)
뒤로 앞으로 중지 새로고침 홈 검색 즐겨찾기 미디어 기록 메일
주소(D) http://www.informatics.jax.org/searches/linkmap.cgi#page15
이동 연결
Google 웹 검색 사이트 검색 PageRank 페이지 정보 위로 하이라이트
11
34.35
34.40
34.50
34.60
34.70
34.80
34.90
35.00
35.10
35.20
35.30
35.40
35.50
35.60
35.70
35.80
35.90
36.00
36.10
36.20
D11Mit260
D11Mit317
Mfap4 MFAP4 17p11.2-p11.2
Zfp179 ZNF179 17p11.2-p11.2
D11Sac34
D11Mit88
D11Mit350
Pmp22 PMP22 17p12-p11.2
380N16T7
386N23T7
410O9T7
433B7T7
475D1T7
524K7T7
538C3T7
561O14T7
630D9T7
645M6T7
D11Jpk1
Myh1 MYH1 17pter-p11
Myh2 MYH2 17p13.1-p13.1
Myh3 MYH3 17pter-p11
Myh4 MYH4 17pter-p11
Myh8 MYH8 17pter-p12
Myh13 MYH13 17p13-p13
Myhs
Rcvrn RCV1 17p13-p12
Shbg SHBG 17pter-p12
Ubb UBB 17p12-p11.2
D11Mit113
D11Mit177
D11Mit193
D11Mit276
인터넷

Single-Chromosome and Regional Map Resources

- Data generated for only a single chromosome or a subchromosomal region are often important for fine mapping
- Most published human chromosome maps are listed and be viewed at GDB's Web site.
- Human Genome Organization (HUGO) has developed individual human chromosome Web pages.
- The Sanger Centre and the WUGSC have two of the most advanced collections of chromosome-specific genomic data, informatics tools, and resources.

Practical USES of Mapping Resources

- Defining a genomic region
- Determining and ordering the contents of a defined region
- Defining a map position from a clone or DNA sequence

Defining a Genomic Region

- A genomic region of interest is best defined by two flanking markers that are commonly used mapping purposes
  - Ploymorphic Généthon markers in humans
  - MIT microsatellites in mice
- Commonly used markers are often present on multiple, independently derived maps, so their "position" on the chromosome provides greater confidence for anchoring a regional endpoint
- In contrast, the exact location of less commonly used markers is often locally ambiguous.

Determining and Ordering the Contents of a Defined Region

- A good way to start is to identify a map that contains both flanking markers, either from a chromosome-wide or genome-wide map from the sources
- The map or maps containing the flanking markers can be used to create a consensus integrated map of the region.
- The most reliable tool for marker ordering is a DNA sequence or sequence contig.

Defining a Map Position from a Clone or DNA Sequence

- To determine whether the element of interest has already been localized
- If gene-specific or closely linked markers have been used previously for mapping, a position can usually be described in terms specific to the mapping method that was employed.
- If no previously localization exists for a genomic element, some experimental work must be undertaken.