Disclosures

Royalties from Browser licenses

Bioinformatics contract, Regeneron, Inc
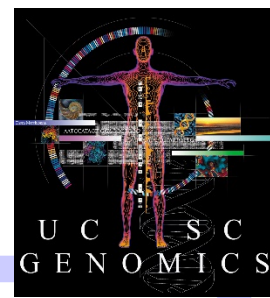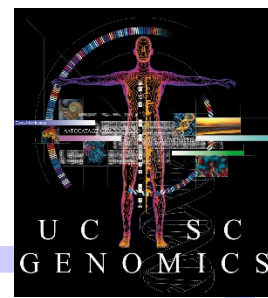
Acknowledgements

Acknowledgements

UCSC Browser team

- **David Haussler – co-PI**

- **Jim Kent – Browser Concept, BLAT, Team Leader, PI**

Engineering	QA, Docs, Support	KiloKluster, Sys-admin
Angie Hinrichs	Brian Lee	Jorge Garcia
Kate Rosenbloom	Matt Speir	Erich Weiler
Hiram Clawson	Jairo Navarro	Haifang Talc
Galt Barber	Chris Villarreal	
Brian Raney	Lou Nassar	
Max Haeussler	Daniel Smelter	**Management**
Jonathan Casper	Conner Powell	Ann Zweig
Christopher Lee		

UCSC = UC Santa Cruz
!= USC, USCS, UCSF, UCSD....
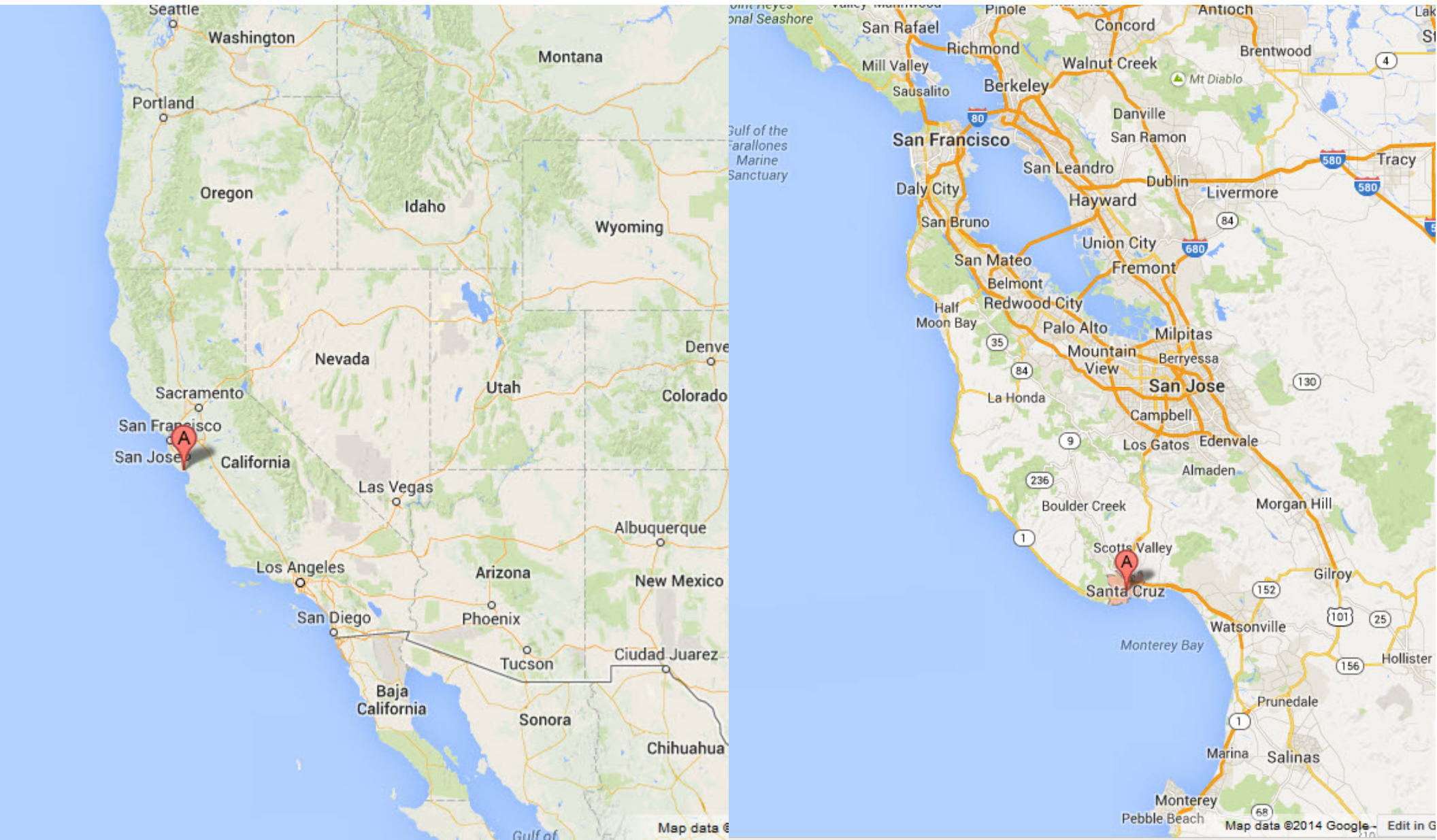
Browser Team
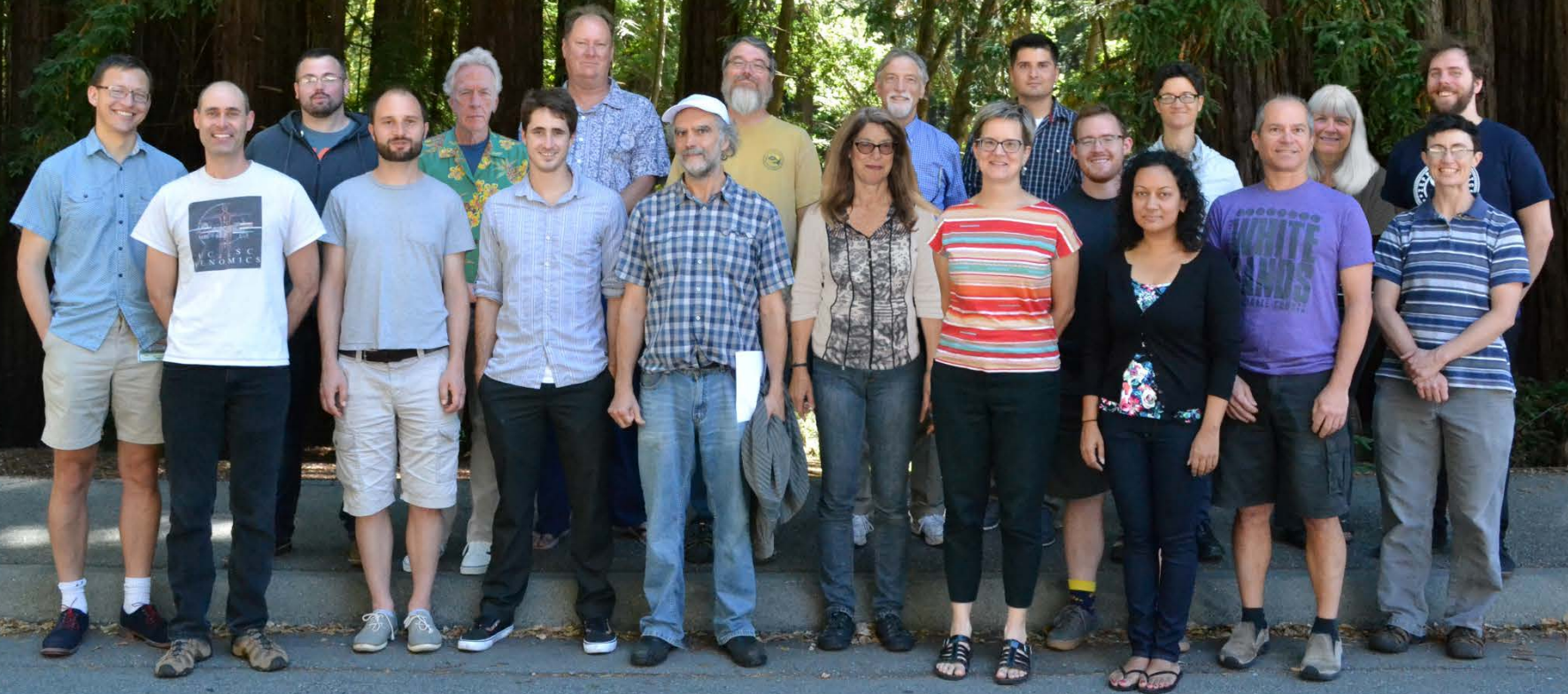
Variants with phenotypic association

All Variants:

= LOVD
+ ClinVar
+ OMIM SNPs
+ HGMD
+ UniProt
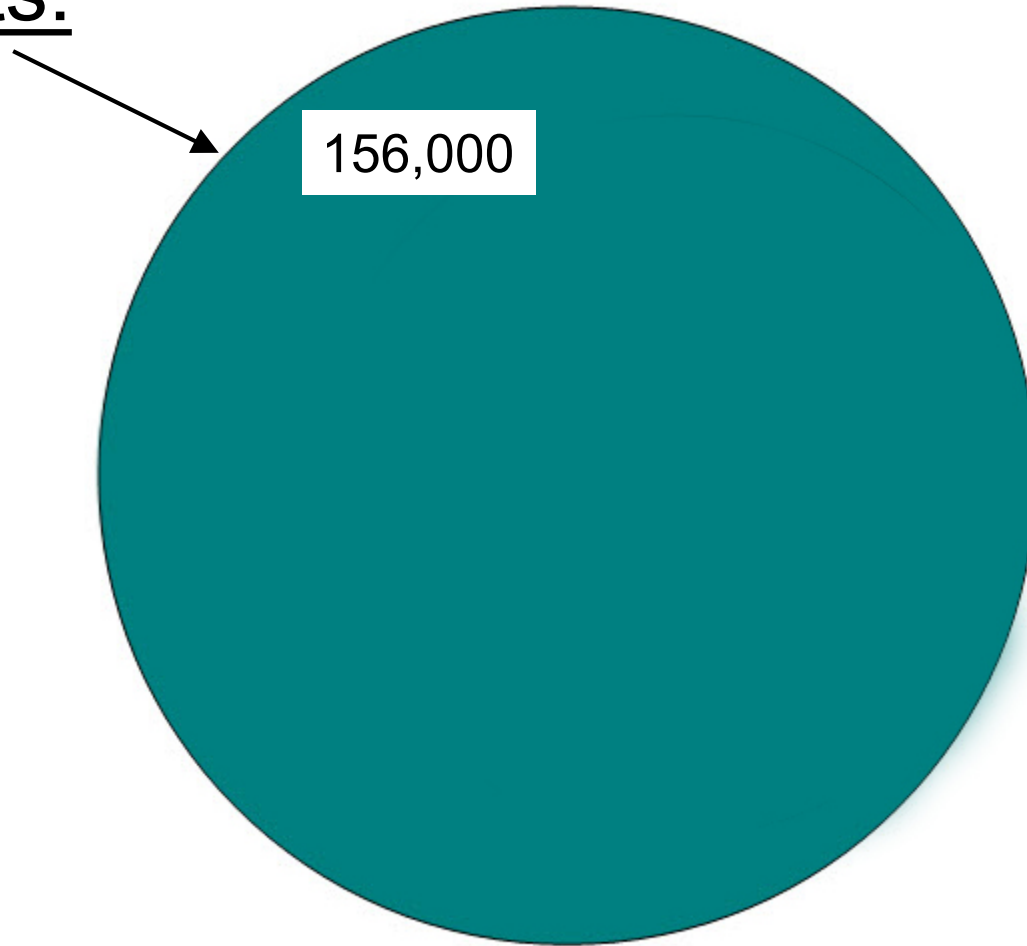
156,000

Variants with phenotypic association

All Variants
156,000

LOVD
92,000
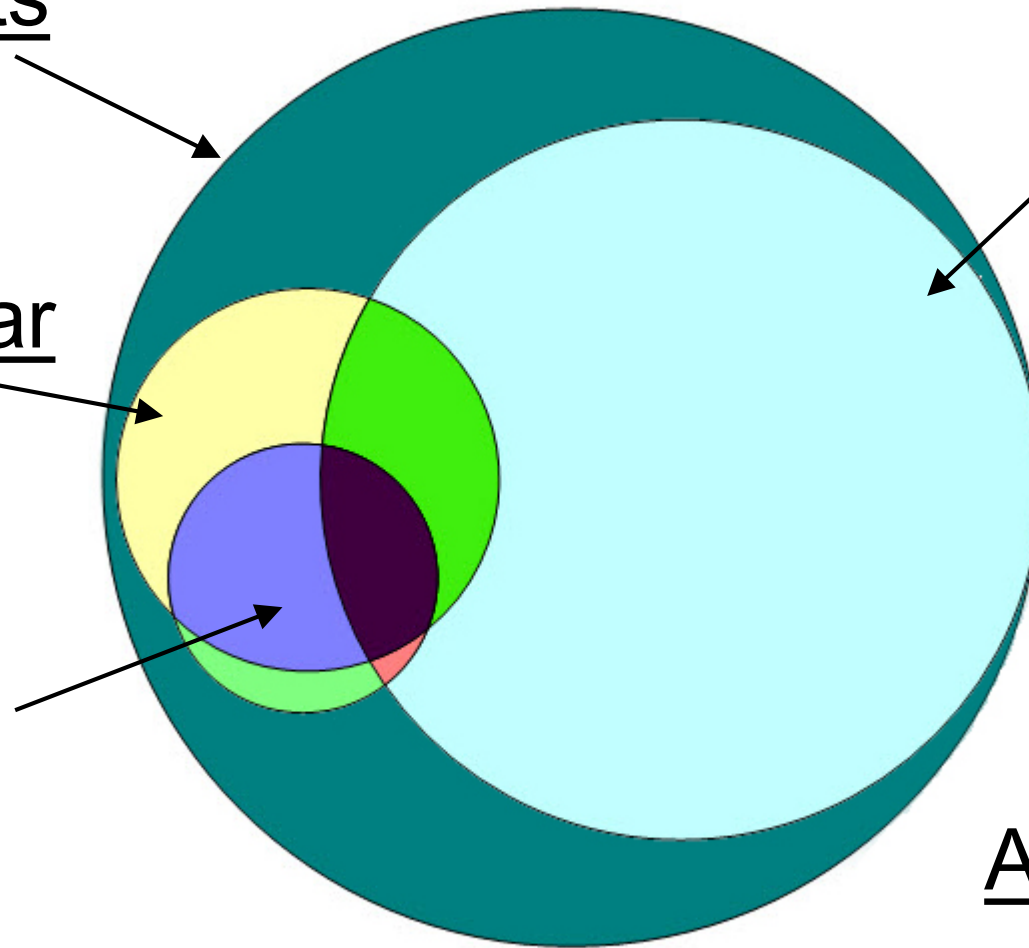
Variants with phenotypic association

All Variants

156,000

All 5 Databases

only 2,200 common

Variants with phenotypic association

All Variants:
= LOVD
+ ClinVar
+ OMIM SNPs
+ HGMD
+ UniProt

156,000
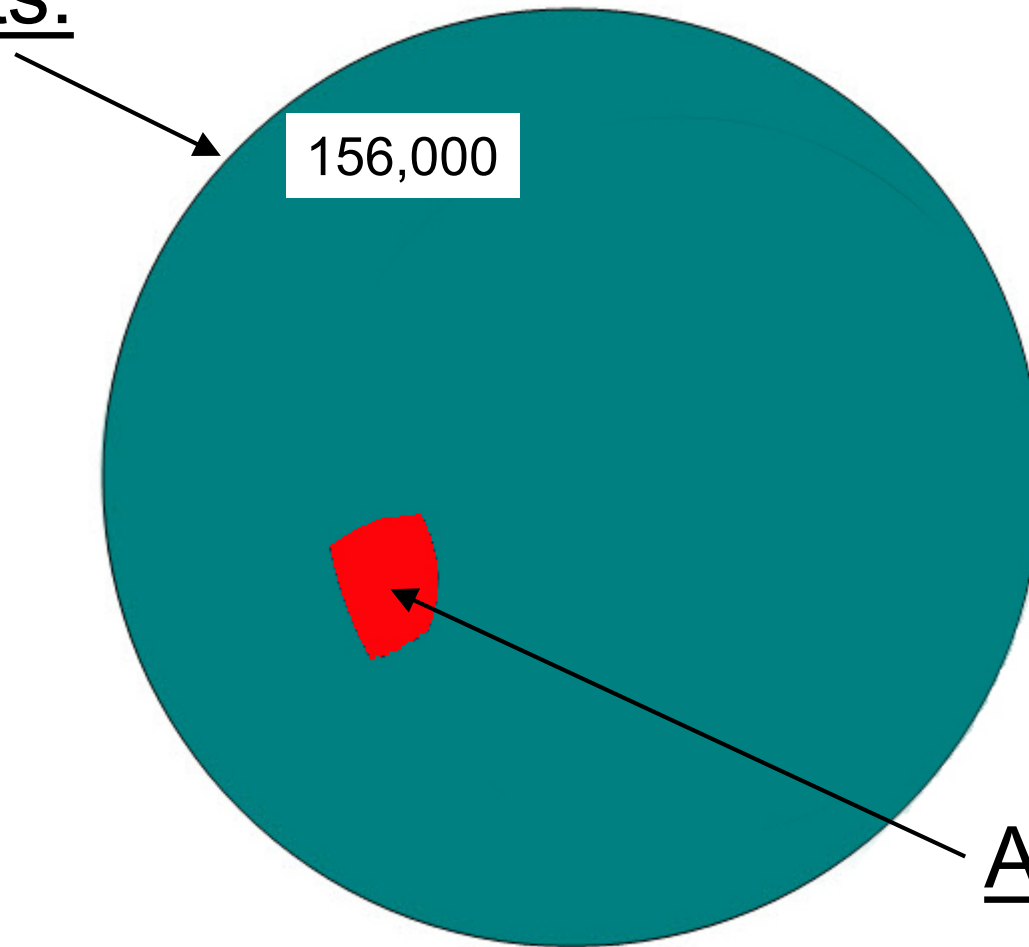
All 5 Databases

only 2,200 common
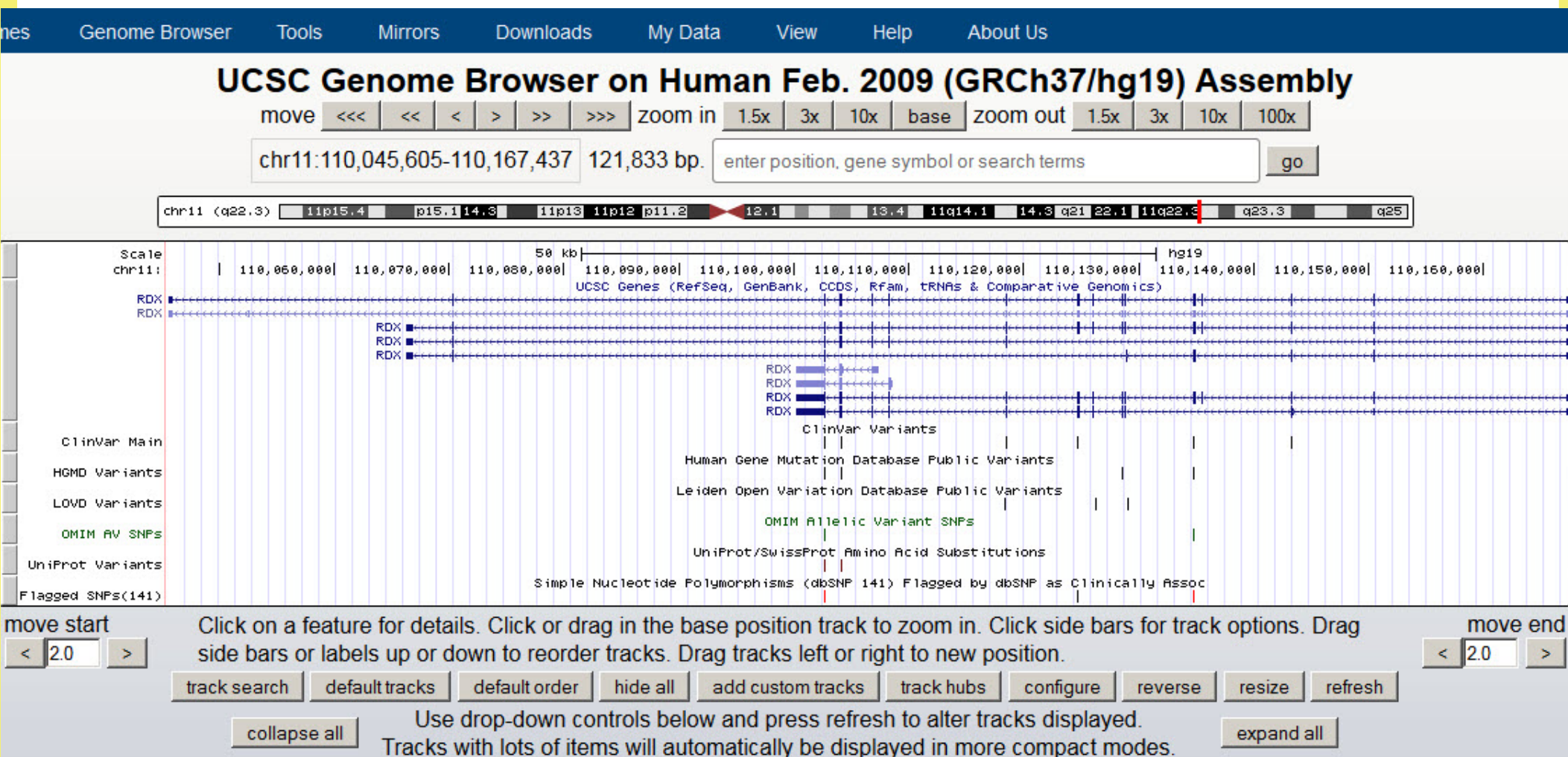
Variants

user: example

session: hg19_variants3   ==   http://bit.ly/ucscVariants

ACMG STANDARDS AND GUIDELINES | Genetics inMedicine

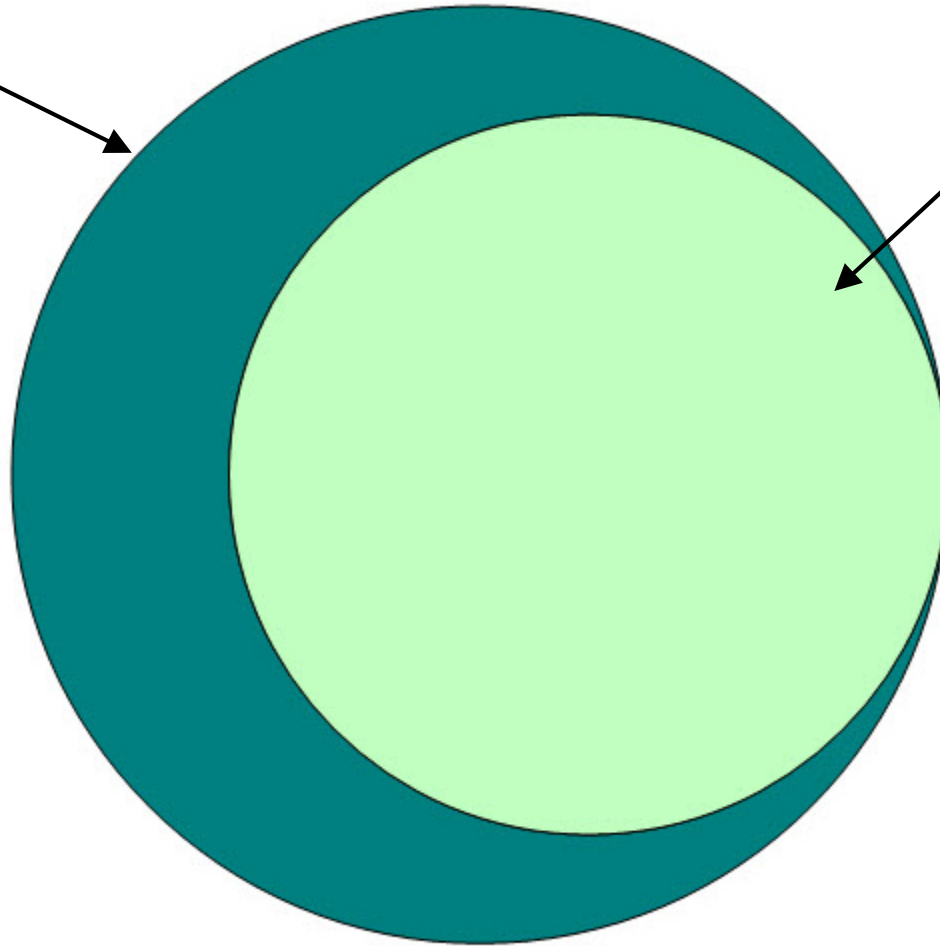# Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology

Sue Richards, PhD[1], Nazneen Aziz, PhD[2,16], Sherri Bale, PhD[3], David Bick, MD[4], Soma Das, PhD[5], Julie Gastier-Foster, PhD[6,7,8], Wayne W. Grody, MD, PhD[9,10,11], Madhuri Hegde, PhD[12], Elaine Lyon, PhD[13], Elaine Spector, PhD[14], Karl Voelkerding, MD[13] and Heidi L. Rehm, PhD[15]; on behalf of the ACMG Laboratory Quality Assurance Committee

available at:

http://   bit.ly/ucscMalaysia2018

Table 1 Population, disease-specific, and sequence databases

Population databases	
Exome Aggregation Consortium http://exac.broadinstitute.org/	Database of variants found during exome sequencing of 61,486 unrelated individuals sequenced as part of various disease-specific and population genetic studies. Pediatric disease subjects as well as related individuals were excluded.
Exome Variant Server http://evs.gs.washington.edu/EVS	Database of variants found during exome sequencing of several large cohorts of individuals of European and African American ancestry. Includes coverage data to inform the absence of variation.
1000 Genomes Project http://browser.1000genomes.org	Database of variants found during low-coverage and high-coverage genomic and targeted sequencing from 26 populations. Provides more diversity compared to the Exome Variant Server but also contains lower-quality data, and some cohorts contain related individuals.
dbSNP http://www.ncbi.nlm.nih.gov/snp	Database of short genetic variations (typically ≤50 bp) submitted from many sources. May lack details of the originating study and may contain pathogenic variants.
dbVar http://www.ncbi.nlm.nih.gov/dbvar	Database of structural variation (typically >50 bp) submitted from many sources.
Disease databases	
ClinVar http://www.ncbi.nlm.nih.gov/clinvar	Database of assertions about the clinical significance and phenotype relationship of human variations.
OMIM http://www.omim.org	Database of human genes and genetic conditions that also contains a representative sampling of disease-associated genetic variants.
Human Gene Mutation Database http://www.hgmd.org	Database of variant annotations published in the literature. Requires fee-based subscription to access much of the content.
Locus/disease/ethnic/other-specific databases	
Human Genome Variation Society http://www.hgvs.org/dblist/dblist.html	The Human Genome Variation Society site developed a list of thousands of databases that provide variant annotations on specific subsets of human variation. A large percentage of databases are built in the Leiden Open Variation Database system.
Leiden Open Variation Database http://www.lovd.nl	
DECIPHER http://decipher.sanger.ac.uk	A molecular cytogenetic database for clinicians and researchers linking genomic microarray data with phenotype using the Ensembl genome browser.
Sequence databases	
NCBI Genome http://www.ncbi.nlm.nih.gov/genome	Source of full human genome reference sequences.
RefSeqGene http://www.ncbi.nlm.nih.gov/refseq/rsg	Medically relevant gene reference sequence resource.
Locus Reference Genomic (LRG) http://www.lrg-sequence.org	
MitoMap http://www.mitomap.org/MITOMAP/HumanMitoSeq	Revised Cambridge reference sequence for human mitochondrial DNA.

Datasets

Microarray   **CNVs**

    Benign: DGV

    Pathogenic: OMIM, ClinVar, DECIPHER
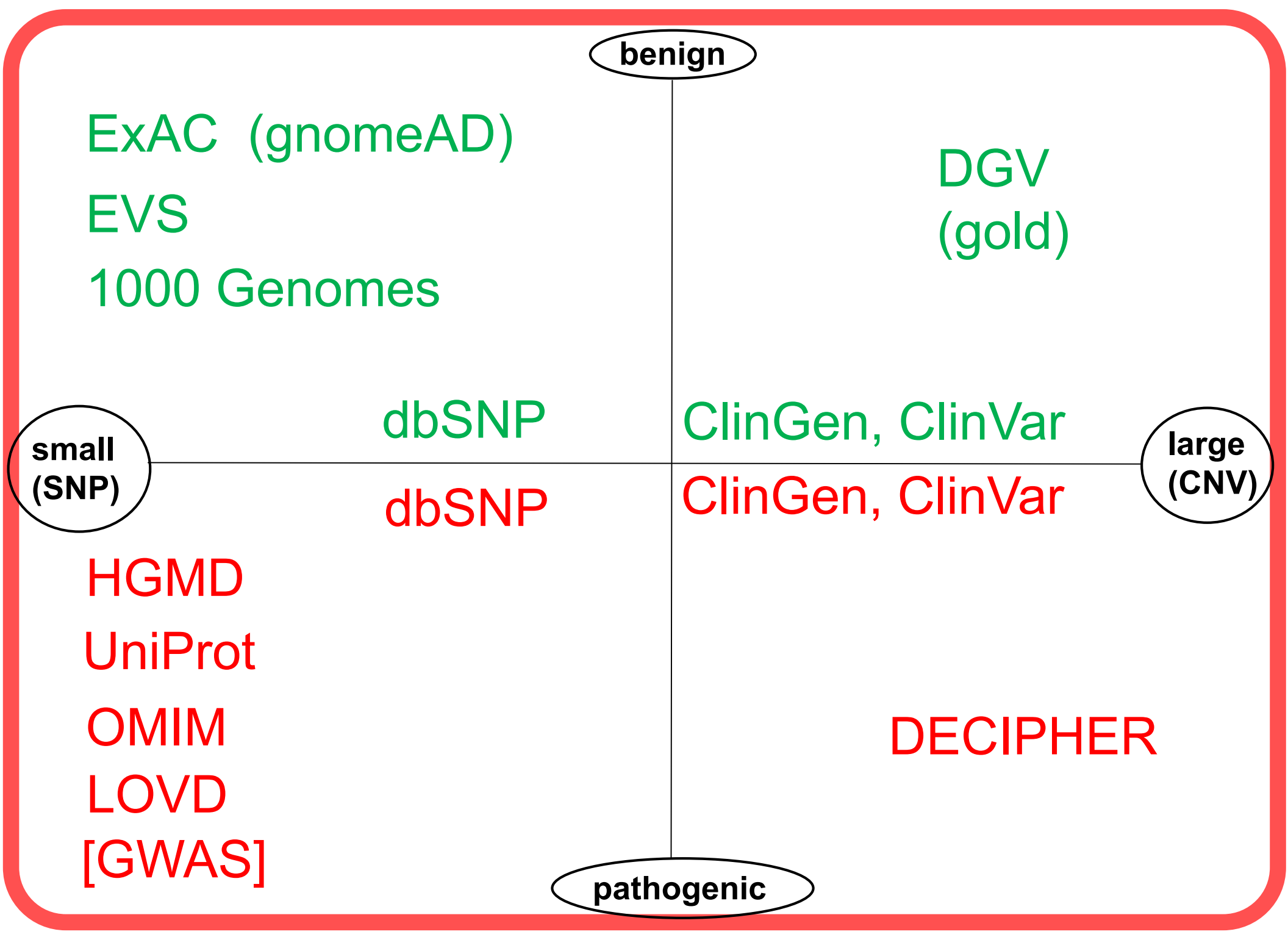
Whole-exome sequencing   **CDS SNPs**

    B: All SNPs, Common SNPs, 1000G, ExAC/gnomeAD

    P: OMIM Alleles, HGMD, UniProt

Whole-genome sequencing   **SNPs everywhere**

    unk: Transcription factors, DNAse hypersensitivity, histone modification

Beacons

Beacon of Beacons

does anyone else have my variant?

http://   beacon-network.org

Input variant and search everywhere

Beacons

Beacon Network   Search Beacons

What's a Beacon?

Beacon is a genetic mutation sharing platform developed by the Global Alliance for Genomics and Health. A beacon is web service that any institution can implement to share genetic data. A beacon answers questions of the form "Do you have information about the following mutation?" and responds with one of "Yes" or "No", among potentially more information.

A site offering this service is called a "beacon". This open web service is designed both to be technically simple while providing data generators options for distributing data through proportional safeguards.

The Beacon Network

The Beacon Network is a search engine across the world's public beacons. It enables global discovery of genetic mutations, federated across a large and growing network of shared genetic datasets.

Search all beacons for allele

| GRCh37 ⌄ | 5:55,250,686 T>D | Search |

Response   **All None**

☑ Found   0
☑ Not Found   38
☐ Not Applicable   25

Organization   **All None**

☑ AMPLab, UC Berkeley
☑ Australian Genomics He...
☑ Belgian Medical Genomi...
☑ BGI
☑ BioReference Laboratori...
☑ Brazilian Initiative on Pre...
☑ BRCA Exchange
☑ Broad Institute
☑ Centre for Genomic Reg...
☑ Centro Nacional de Anali...
☑ Children's Mercy Hospital

Altruist
Hosted by Sequencing.com
Not Found

AMPLab - 1000 Genomes Project
Hosted by AMPLab, UC Berkeley
Not Found

Australian Genomics Health Alliance⊹
Hosted by Australian Genomics Health Alliance
Not Found

Australian Genomics Health Alliance - Germline
Hosted by Australian Genomics Health Alliance
Not Found

Australian Genomics Health Alliance - Somatic
Hosted by Australian Genomics Health Alliance
Not Found

Search all beacons for allele

| GRCh37 ▾ | 17 : 41244802 A > T | Search |

Response All None
☑ Found   1
☐ Not Found   44
☐ Not Applicable 21

Organization All None
☑ AMPLab, UC Berkeley
☑ Australian Genomics …
☑ Belgian Medical Gen…
☑ BGI
☑ Bioinformatics Area, …
☑ BioReference Labora…
☑ Brazilian Initiative on …
☑ BRCA Exchange
☑ Broad Institute
☑ Centre for Genomic …
☑ Centro Nacional de A…

Kaviar   **Found**
Hosted by Institute for Systems Biology

Response   All None

☑ Found   1
☑ Not Found   44
☐ Not Applicable   21

Organization   All None

☑ AMPLab, UC Berkeley
☑ Australian Genomics ...
☑ Belgian Medical Geno...
☑ BGI
☑ Bioinformatics Area, ...
☑ BioReference Labora...
☑ Brazilian Initiative on ...
☑ BRCA Exchange
☑ Broad Institute
☑ Centre for Genomic ...
☑ Centro Nacional de A...
☑ Children's Mercy Hos...
☑ Curoverse
☑ DNAstack
☑ ELIXIR
☑ EMBL European Bioi...
☑ Garvan Institute of Me...
☑ Global Alliance for Ge...
☑ Global Gene Corp
☑ Google
☑ Institute for Systems ...
☑ Instituto Nacional de ...
☑ Japan Science and T...

HGMD Public   Not Found
Hosted by University of California, Santa Cruz

IBD, Native American, Egyptian, U…   Not Found
Hosted by Wellcome Trust Sanger Institute

ICGC - Cancer Projects   Not Found
Hosted by Ontario Institute for Cancer Research

Kaviar   Found
Hosted by Institute for Systems Biology

Leiden Open Variation   Not Found
Hosted by University of California, Santa Cruz

Medical Genome Reference Bank   Not Found
Hosted by Garvan Institute of Medical Research

MyGene2   Not Found
Hosted by MyGene2.org

MyVariant.info   Not Found
Hosted by The Scripps Research Institute

live demo:

http://   bit.ly/ucscMalaysia2018

file: databaseLinks.html