Using ENCODE Data to Interpret Disease-associated Genetic Variation

Dan Gilchrist

National Human Genome Research Institute, NIH

Society of Toxicology Satellite Meeting

March 17, 2016

ENCODE 2016: Research Applications and Users Meeting

June 8-10, 2016 at Stanford University

- Hands-on workshops on how to navigate, analyze, and integrate ENCODE and mouseENCODE data into your research
- Leading-edge research applications from distinguished invited speakers from across the research community
- Tutorials on newly-available informatics pipelines that greatly facilitate working with ENCODE data
- Short talks selected from abstracts
- For details and registration see:

https://www.encode2016.org

Overview

- The ENCODE Resource
- Use Cases of ENCODE to illuminate the role of genetic variation in human disease
- Accessing ENCODE materials

Overview

- The ENCODE Resource
- Use Cases of ENCODE to illuminate the role of genetic variation in human disease
- Accessing ENCODE materials

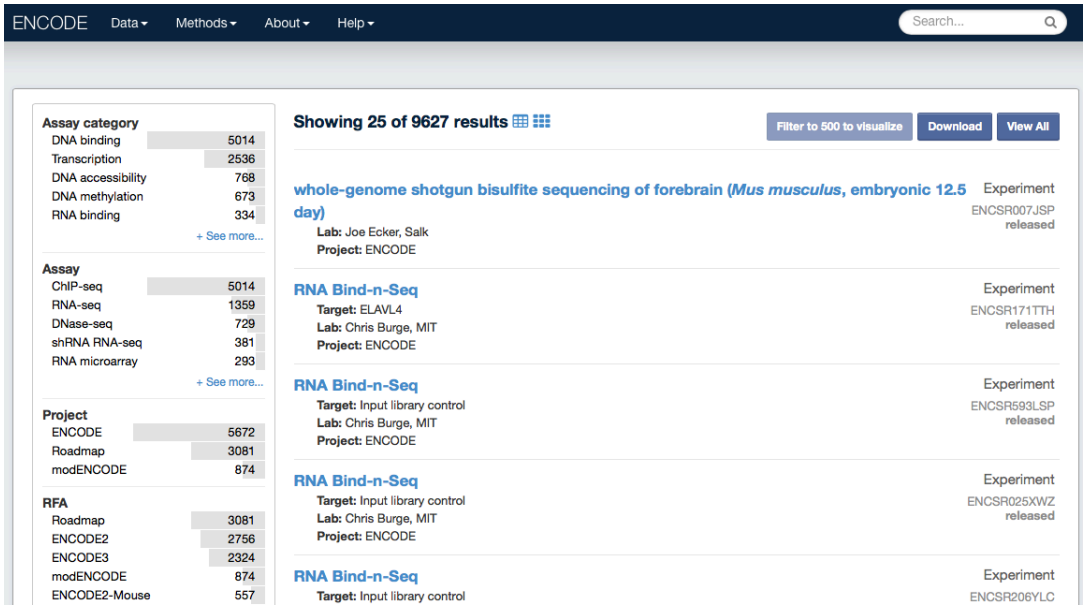
ENCODE: Encyclopedia Of DNA Elements

- Identify all candidate functional elements in the genome
  - Promoters, enhancers, transcribed regions
- Make resource freely available to community for use in studies of:
  - genetic basis of disease
  - gene regulation
  - whatever you want

Research Parasites Welcome!

ENCODE: Encyclopedia Of DNA Elements

- Thousands of data sets
- Hundreds of different bio-samples
- Data sets related to exposure



ENCODE: Encyclopedia Of DNA Elements

ENCODE 'Phase 4' RFAs –

Applications Due March 21st

- Expanding the Encyclopedia of DNA Elements in Human and Mouse
- Characterizing ENCODE Functional Elements
- Computational Analysis of ENCODE Data
- Data Coordination Center
- Data Analysis Center

Understanding Non-coding DNA Is Central To NHGRI Goals

Non-coding DNA is important for disease and gene regulation

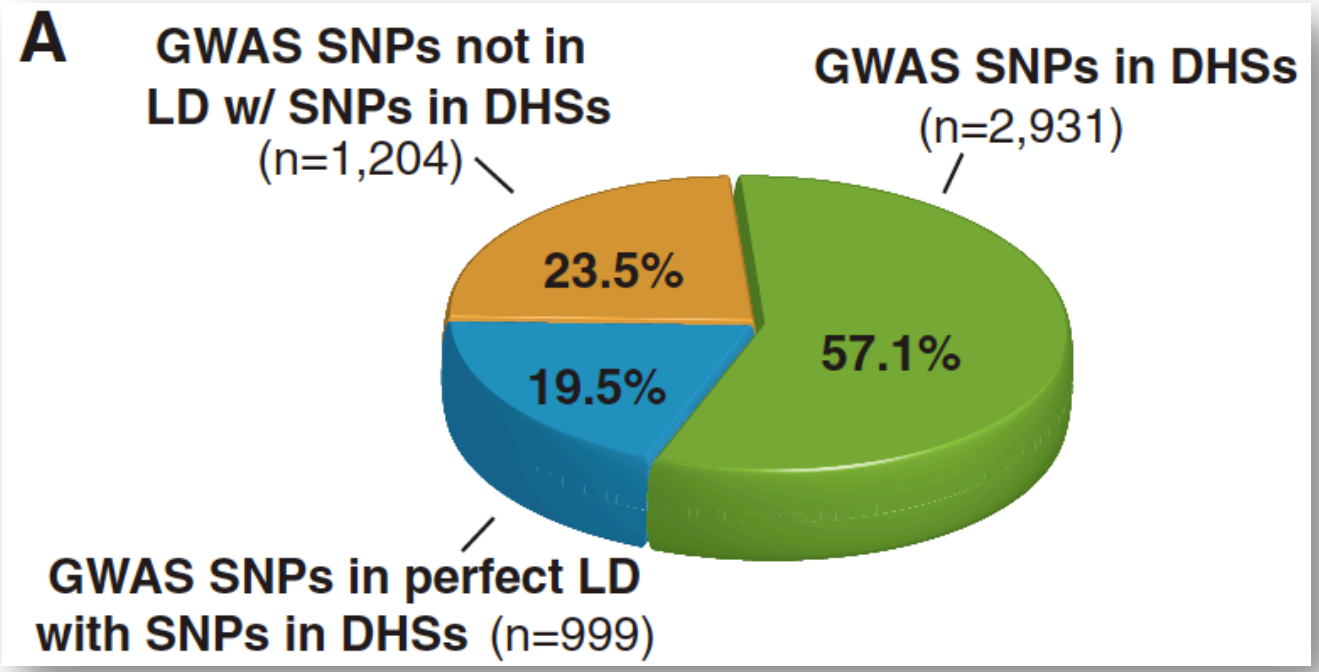
- Vast majority of common disease associations and heritability lie outside of protein-coding regions
- Non-coding DNA variants are known to cause human diseases and alter human traits (FXS, ALS)

Functional information is needed to interpret the role of genetic variation in human disease, and to apply genomics in the clinic.

PMID: 22955828, PMID: 25439723
PMID: 17477822, PMID: 25679767

National Human Genome Research Institute

Many GWAS Associations Lie In Regions Annotated By ENCODE And Epigenomics Data

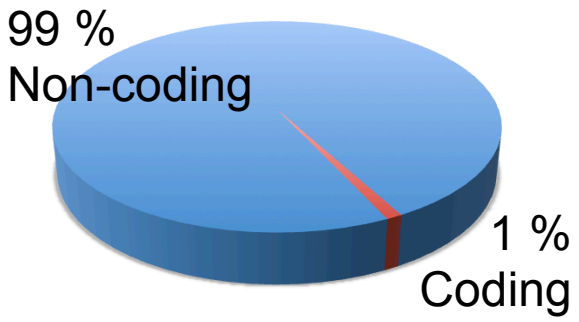


Stamatoyannopoulos, Science 337:1190, 2012

Reading The Human Genome Is Difficult

- Genetic code very powerful for 1% of the human genome
- No correspondingly powerful regulatory code
- Sequence conservation can identify candidate functional elements (but not when or where they act)

➢ Need unbiased experimental investigation

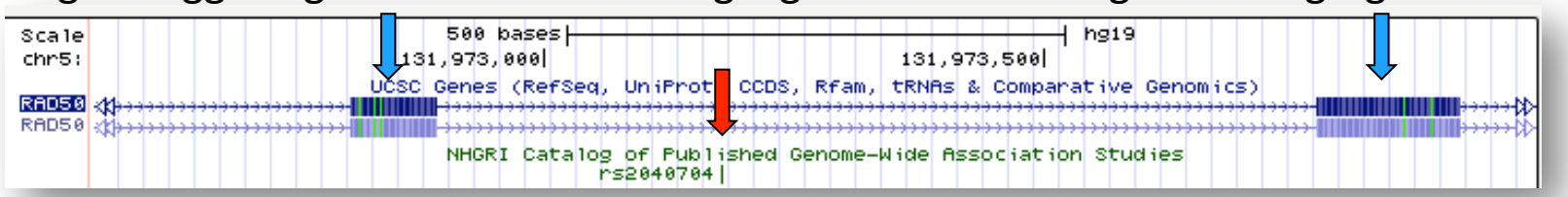


1,500 Letters Of Our 3 Billion Letter Genome

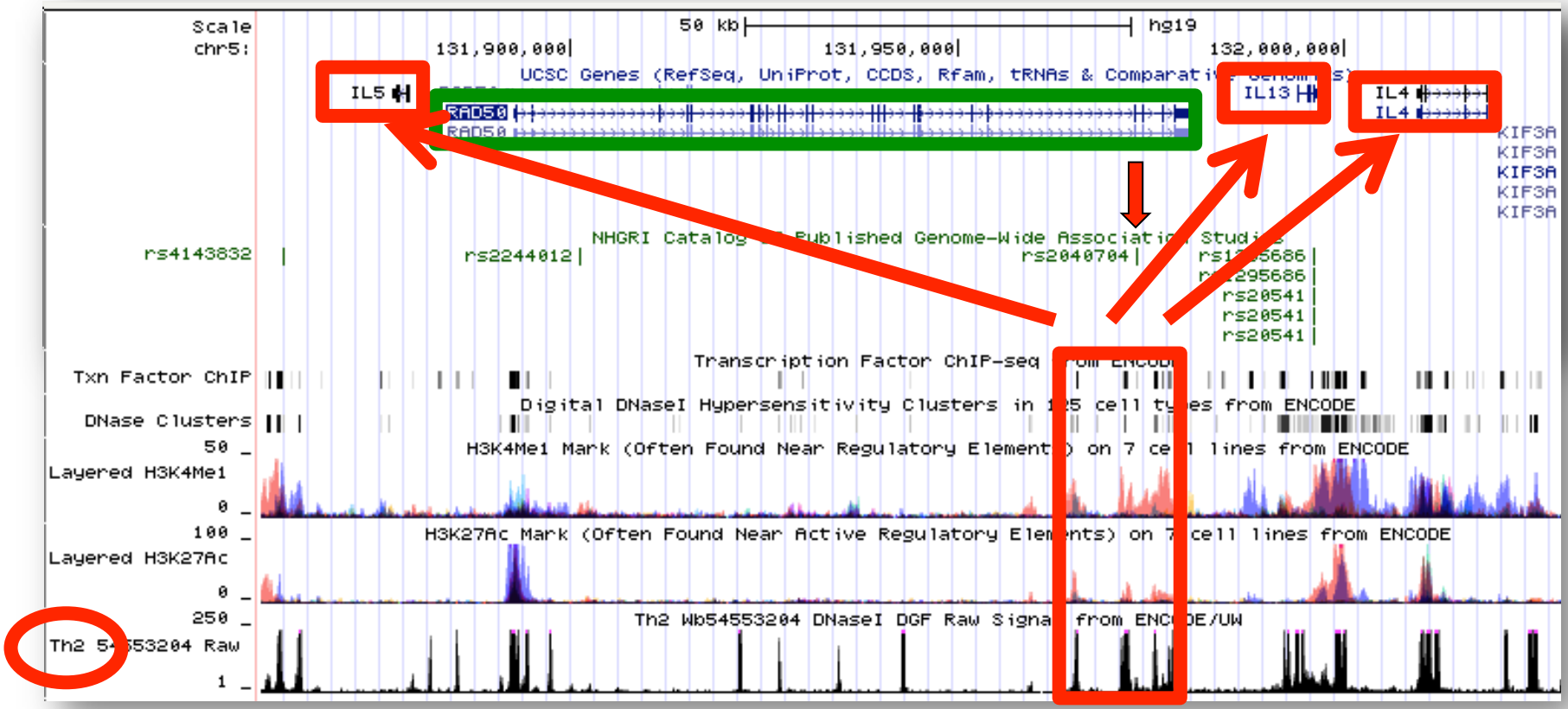
agccaagcagcaaagttttgctgctgtttatttttgtagctcttactatattctacttttaccattgaaaatattgaggaagttatt
tatatttctatttttatatattatatattttatgtattttaatattactattacacataattatttttatatatatgaagtaccaatg
acttccttttccagagcaataatgaaatttcacagtatgaaaatggaagaaatcaataaaattatacgtgacctgtggcgaa
gtacctatcgtggacaaggtgagtaccatggtgtatcacaaatgctctttccaaagccctctccgcagctcttccccttatga
cctctcatcatgccagcattacctccctggacccctttctaagcatgtctttgagattttctaagaattcttatcttggcaacatc
ttgtagcaagaaaatgtaaagttttctgttccagagcctaacaggacttacatatttgactgcagtaggcattatatttagctg
atgacataataggttctgtcatagtgtagatagggataagccaaaatgcaataagaaaaaccatccagaggaaactctttt
ttttttctttttctttttttttttttccagatggagtctcgcacttctctgtcacccgggctggagcgcagtggtgcaatcttggctca
ctgcaacctccacctcctgggttcaggtgattctcccacctcagcctcccgagtagtagctggaattacaggtgcgcgctccc
acacctggctaatttttgtattcttagtagagatggggtttcaccatgttggccaggctggtctcaaactcctgccctcaggtg
atctgcccaccttggcctcccagtgttgggtttacaggcgtgagccaccgcgcctggcctggaggaaactcttaacagggaa
actaagaaagagttgaggctgaggaactggggcatctgggttgcttctggccagaccaccaggctcttgaatcctcccagc
cagagaaagagtttccacaccagccattgttttcctctggtaatgtcagcctcatctgttgttcctaggcttacttgatatgtttg
taaatgacaaaaggctacagagcataggttcctctaaaatattcttcttcctgtgtcagatattgaatacatagaaatacggt
ctgatgccgatgaaaatgtatcagcttctgataaaaggcggaattataactaccgagtggtgatgctgaagggagacacag
ccttggatatgcgaggacgatgcagtgctggacaaaaggcaggtatctcaaaagcctggggagccaactcacccaagtaa
ctgaaagagagaaacaaacatcagtgcagtggaagcacccaaggctacacctgaatggtgggaagctctttgctgctata
taaaatgaatcaggctcagctactattattacactctcctgaagctaaccaacatttcctgcaacattatgtagactt

Maps And Annotation Help Us To Understand The Sequence

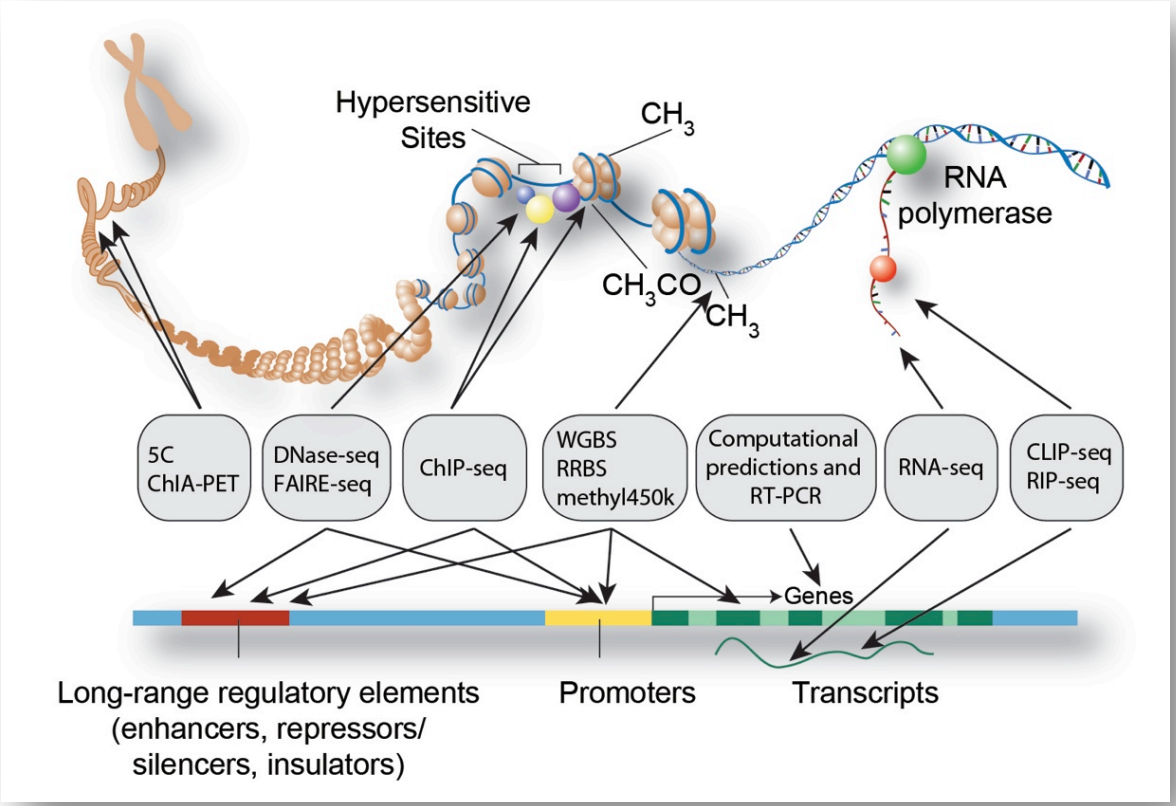
agccaagcagcaaagttttgctgctgtttatttttgtagctcttactatattctacttttaccattgaaaatattgaggaagttatt
tatatttctatttttatatattatatattttatgtattttaatattactattacacataattatttttatatatatgaagtaccaatg
acttccttttccagagcaataatgaaatttcacagtatgaaaatggaagaaatcaataaaattatacgtgacctgtggcgaa
gtacctatcgtggacaaggtgagtaccatggtgtatcacaaatgctctttccaaagccctctccgcagctcttccccttatga
cctctcatcatgccagcattacctccctggacccctttctaagcatgtctttgagattttctaagaattcttatcttggcaacatc
ttgtagcaagaaaatgtaaagttttctgttccagagcctaacaggacttacatatttgactgcagtaggcattatatttagctg
atgacataataggttctgtcatagtgtagatagggataagccaaaatgcaataagaaaaaccatccagaggaaactctttt
ttttttctttttctttttttttttttccagatggagtctcgcacttctctgtcacccgggctggagcgcagtggtgcaatcttggctca
ctgcaacctccacctcctgggttcaggtgattctcccacctcagcctcccgagtagtagctggaattacaggtgcgcgctccc
acacctggctaatttttgtattcttagtagagatggggtttcaccatgttggccaggctggtctcaaactcctgccctcaggtg
atctgcccaccttggcctcccagtgttgggtttacaggcgtgagccaccgcgcctggcctggaggaaactcttaacagggaa
actaagaaagagttgaggctgaggaactggggcatctgggttgcttctggccagaccaccaggctcttgaatcctcccagc
cagagaaagagtttccacaccagccattgttttcctctggtaatgtcagcctcatctgttgttcctaggcttacttgatatgtttg
taaatgacaaaaggctacagagcataggttcctctaaaatattcttcttcctgtgtcagatattgaatacatagaaatacggt
ctgatgccgatgaaaatgtatcagcttctgataaaaggcggaattataactaccgagtggtgatgctgaagggagacacag
ccttggatatgcgaggacgatgcagtgctggacaaaaggcaggtatctcaaaagcctggggagccaactcacccaagtaa
ctgaaagagagaaacaaacatcagtgcagtggaagcacccaaggctacacctgaatggtgggaagctctttgctgctata
taaaatgaatcaggctcagctactattattacactctcctgaagctaaccaacatttcctgcaacattatgtagactt



Richer Maps Provide More Information



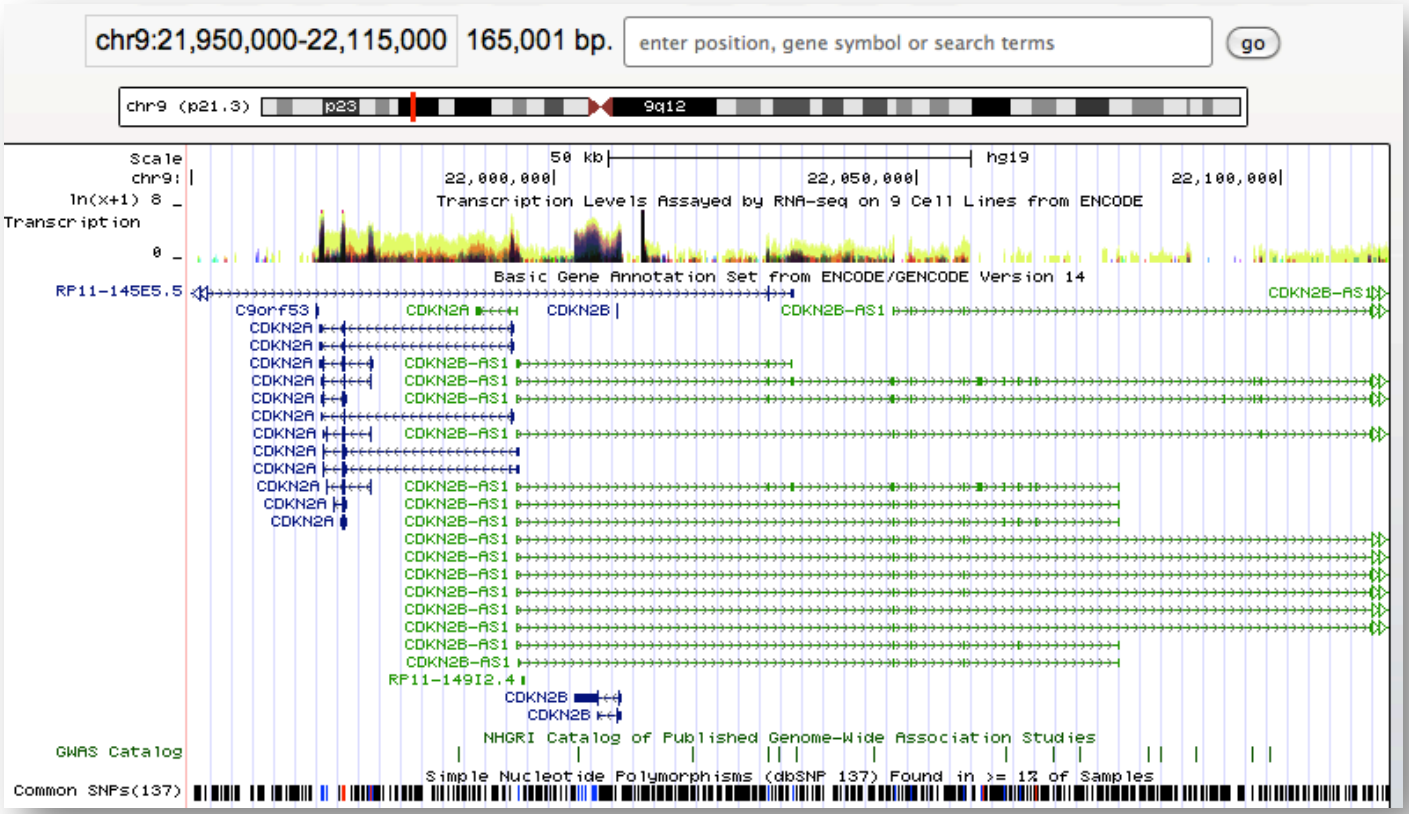
ENCODE Data: Built on Decades of Research Into Gene Regulation



Modified from PLoS Biol 9:e1001046, 2011
Science 306:636, 2004

RNA Data

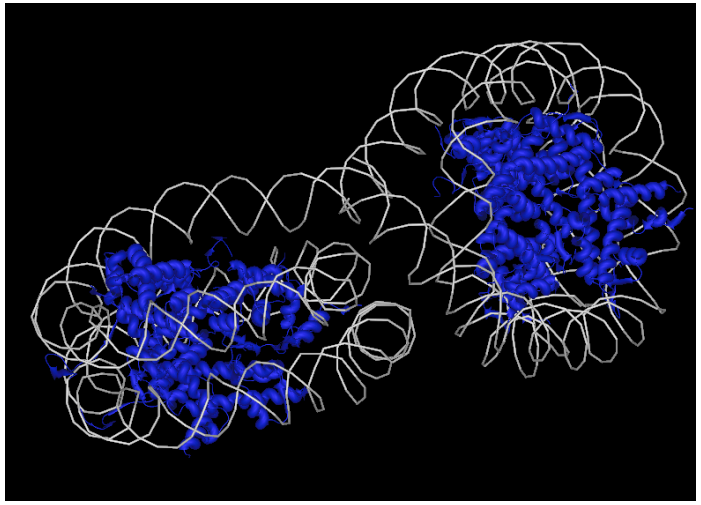
- RNA amount (mRNA and short RNA)
- Cell Specificity
- Transcript modeling (GENCODE)



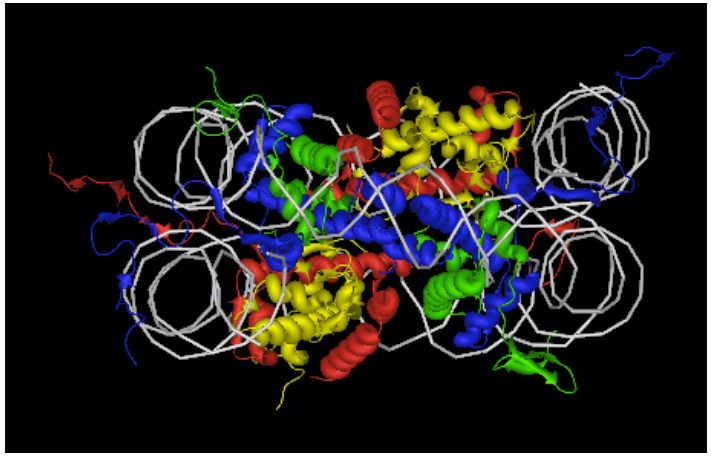
https://encodeproject.org

ENCODE Chromatin Structure Data

- DNase
- Histone modifications
- DNA methylation
  - Enhancers
  - Promoters
  - Transcription factor footprints
  - Transcribed regions
  - Active and repressed regions
  - Cell specificity



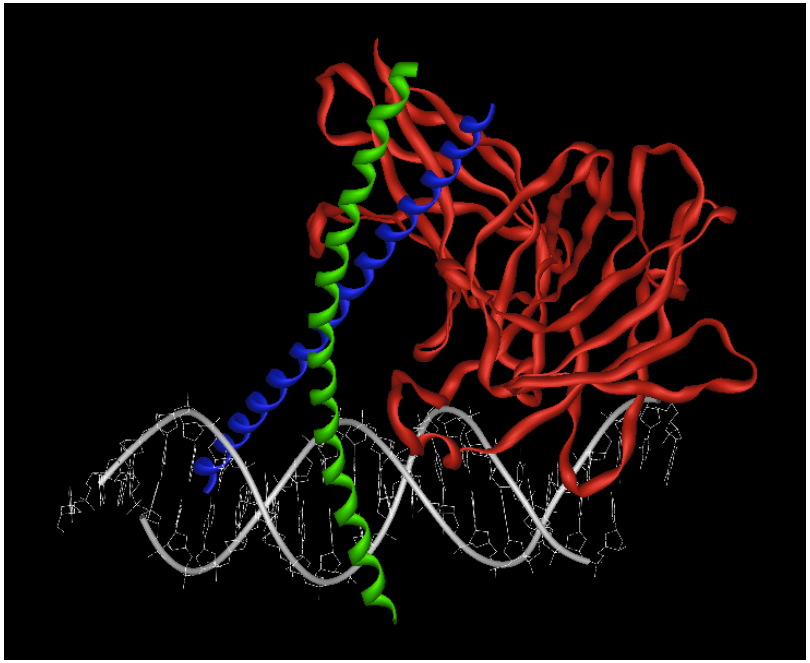
Richmond, PDB 1ZBB



Richmond, PDB 1KX5

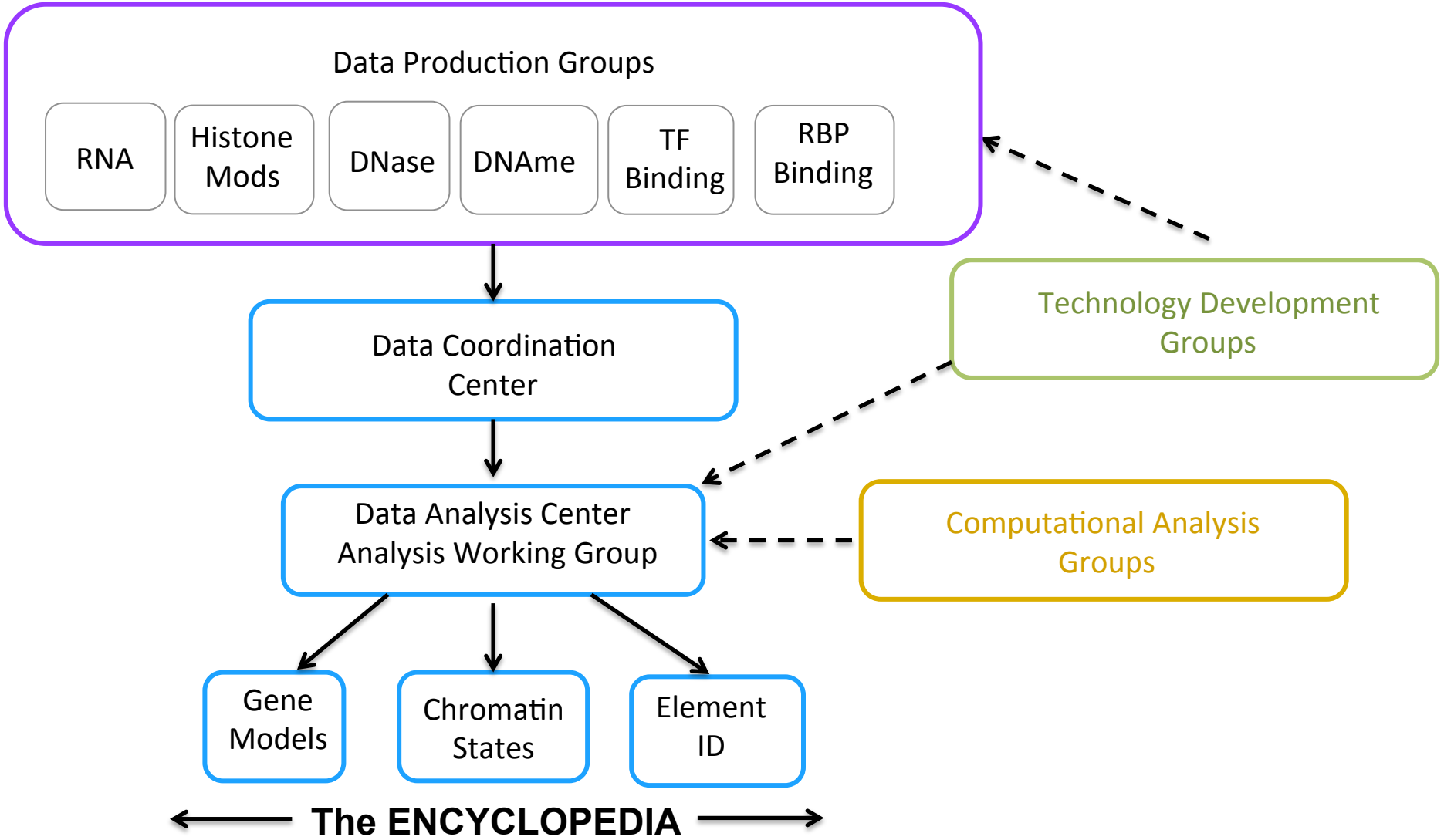
ENCODE Nucleic Acid Binding Data

- DNA binding proteins (Transcription factors)
  - Activators
  - Repressors
  - Remodelers
  - RNA Polymerases
  - Cell specificity
- RNA binding proteins
  - RNA Splicing
  - Translation
  - RNA Stability
  - RNA Localization
  - Cell specificity



Harrison, PDB_1A02

ENCODE Consortium Structure



Summary- ENCODE Resource

- Freely shared catalog of candidate genomic functional elements
- ENCODE is built upon established techniques and interpretations developed for the study of gene regulation
- ENCODE maps can be used to make predictions about genome function

Overview

- The ENCODE Resource
- Use of ENCODE to illuminate the role of genetic variation in human disease
- Accessing ENCODE materials

Using ENCODE Data: Access for Scientists with Varying Expertise

- Many tools for deriving biological insight and hypotheses from ENCODE data
- Many do not require informatics experience
- Many do not require deep functional genomics background
- Encouraging broad use of ENCODE resources

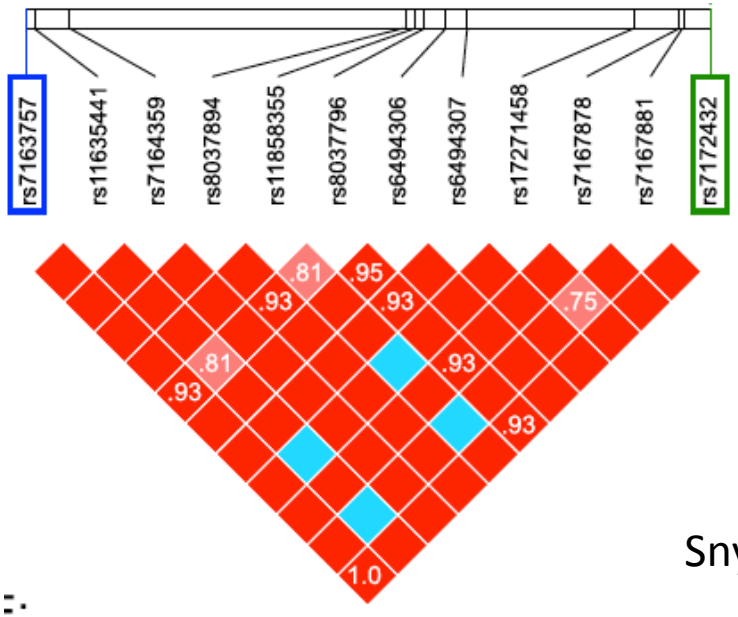
Standard ENCODE Use Cases: Hypothesis Generation

- Prediction of causal variants/regulatory elements
- Prediction of target genes
- Prediction of target cell types

- Applied to germline genetic variation, but many other applications (e.g., differentially methylated regions)

Prediction of Causal Variants

- Multiple variants may be in linkage disequilibrium
- The causal variant may not have been tested during data collection
- Multiple variants may be causal



Snyder, Genome Research 22:1748, 2012

ENCODE/Epigenomics Data From HaploReg

HaploReg v4.1

HaploReg is a tool for exploring annotations of the noncoding genome at variants on haplotype blocks, such as candidate regulatory SNPs at disease-associated loci. Using LD information from the 1000 Genomes Project, linked SNPs and small indels can be visualized along with chromatin state and protein binding annotation from the Roadmap Epigenomics and ENCODE projects, sequence conservation across mammals, the effect of SNPs on regulatory motifs, and the effect of SNPs on expression from eQTL studies. HaploReg is designed for researchers developing mechanistic hypotheses of the impact of non-coding variants on clinical phenotypes and normal variation.

Update 2015.11.05: Version 4.1 GWAS and eQTL have been updated; a simpler pruning strategy is applied when combining GWAS; and links out to other NHGRI/EBI GWAS hits and GRASP QTL hits are provided.

Update 2015.09.15: Version 4.0 now includes many recent eQTL results including the GTEx pilot, four different options for defining enhancers using Roadmap Epigenomics data, and a complete set of source files for download and local analysis. Older versions available: v3, v2, v1.

Build Query | Set Options | Documentation

Use one of the three methods below to enter a set of variants. If an r² threshold is specified (see the Set Options tab), results for each variant will be shown in a separate table along with other variants in LD. If r² is set to NA, only queried variants w be shown, t her in on able.

Query (comma-delimited list of

Query SNP: rs6575353 and variants with $r^2 >= 0.8$

chr	pos (hg38)	LD (r^2)	LD (D')	variant	Ref	Alt	AFR freq	AMR freq	ASN freq	EUR freq	SiPhy cons	Promoter histone marks	Enhancer histone marks	DNAse	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	dbSNP func annot
14	93736606	0.83	-0.96	rs77582682	G	A	0.03	0.06	0.00	0.08				9 tissues	CTCF,RAD21	4 altered motifs				PRIMA1	intronic
14	93738999	1	1	rs6575353	G	A	0.71	0.85	0.51	0.92						Sox,TCF4	1 hit	1 hit		PRIMA1	intronic
14	93739616	0.95	1	rs12896080	G	A	0.61	0.84	0.51	0.91						4 altered motifs				PRIMA1	intronic
14	93739927	0.83	1	rs4905084	A	G	0.60	0.83	0.51	0.90						4 altered motifs				PRIMA1	intronic
14	93742184	0.95	1	rs4900194	A	G	0.61	0.84	0.51	0.91			4 tissues	BRN		Gfi1,KAP1,Smad3		1 hit		PRIMA1	intronic
14	93743570	0.97	1	rs11160137	A	G	0.69	0.85	0.52	0.91			5 tissues	ESC,HRT		4 altered motifs				PRIMA1	intronic
14	93743836	0.85	0.93	rs12587586	T	G	0.59	0.84	0.52	0.91			6 tissues			Roaz				PRIMA1	intronic

www.broadinstitute.org/mammals/haploreg/

Ward and Kellis, Nucleic Acids Research 40-D930, 2011

ENCODE Data From RegulomeDB

RegulomeDB has been updated to Version 1.1. This includes bringing our database up-to-date with current ENCODE releases: Xie et al. (2013) and Boyle et al. (2014). We have also added Chromatin States from the Roadmap Epigenome Consortium (unpublished) as well as updates to DNase footprinting, PWMs, and DNA Methylation.

Enter dbSNP IDs, 0-based coordinates, BED files, VCF files, GFF3 files (hg19).

rs4900194 1

Submit 2

Use RegulomeDB to identify DNA features and regulatory elements in non-cc regions of the human genome by entering ...

dbSNP IDs | Single nucleotides | A chromosomal region

Enter dbSNP ID(s) (example) or upload a list of dbSNP IDs to identify DNA features a regulatory elements that contain the coordinate of the SNP(s).

A project of the Center for Genomics and Personalized Medicine at Stanford Univer

Chromatin structure Filter:

Method	Location	Cell Type	Additional Info	Reference
DNase-seq	chr14:94207796..94208834	Cerebellumoc		ENCODE
DNase-seq	chr14:94208390..94208598	Panislets		ENCODE
DNase-seq	chr14:94208414..94209060	T47d		ENCODE
DNase-seq	chr14:94208516..94209130	Hepatocytes		ENCODE

Histone modifications Filter:

Method	Location	Chromatin State	Tissue Group	Tissue	Reference
ChromHMM	chr14:94201400..94210600	Weak Repressed PolyComb	ESC	ES-UCSF4 Cell Line	REMC
ChromHMM	chr14:94201400..94211200	Quiescent/Low	ESC	H1 Cell Line	REMC
ChromHMM	chr14:94201400..94211400	Quiescent/Low	ESC	HUES6 Cell Line	REMC
ChromHMM	chr14:94201400..94211600	Quiescent/Low	ESC	ES-I3 Cell Line	REMC

Summary of SNP

Show 10 entries

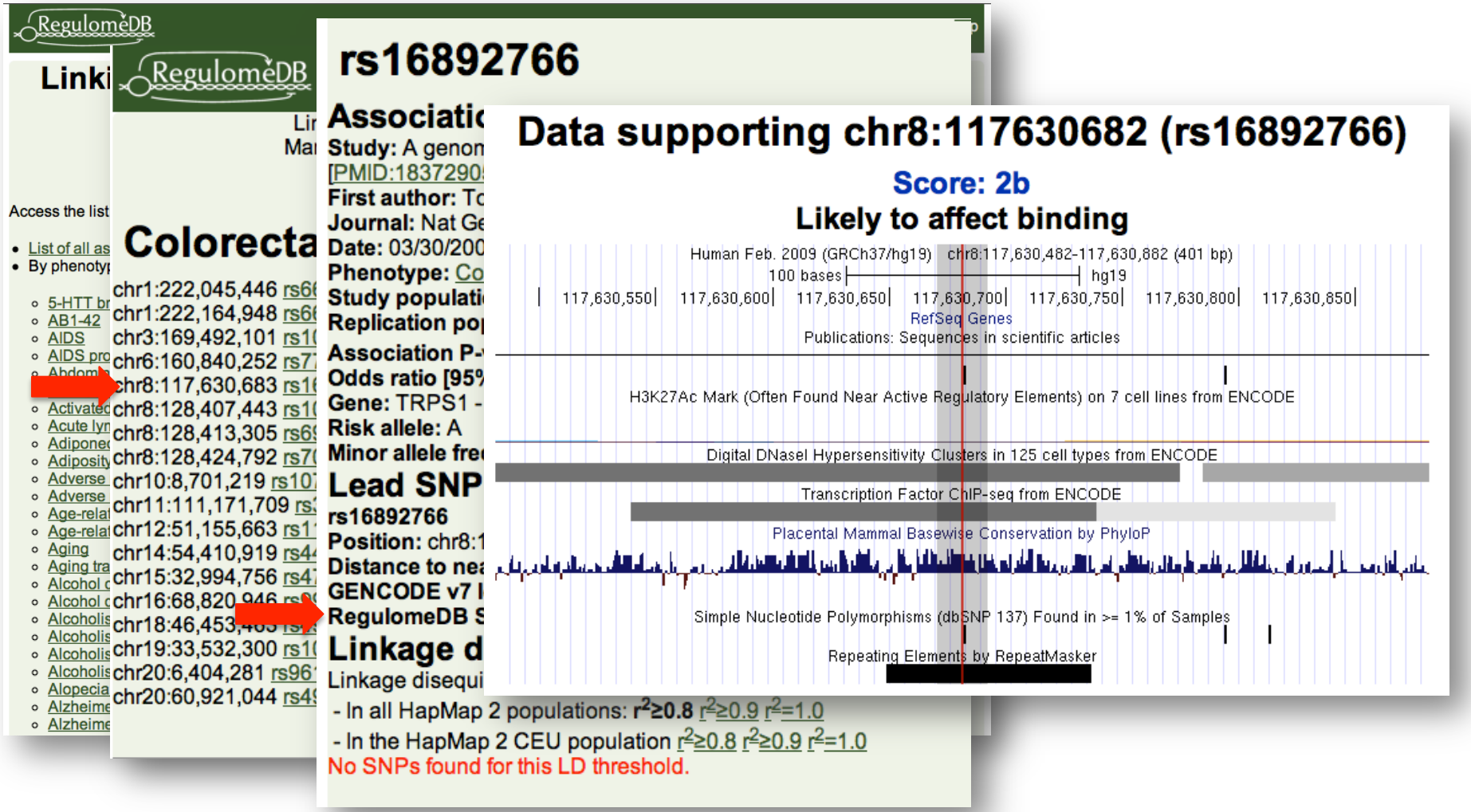
Coordinate (0-based)	dbSNP ID	Regulome DB Score	Other Resources
chr14:94208529	rs4900194	5	UCSC | ENSEMBL | dbSNP

Showing 1 to 1 of 1 entries

http://regulomedb.org/

Cherry, Snyder, Genome Research 22-1790,2012

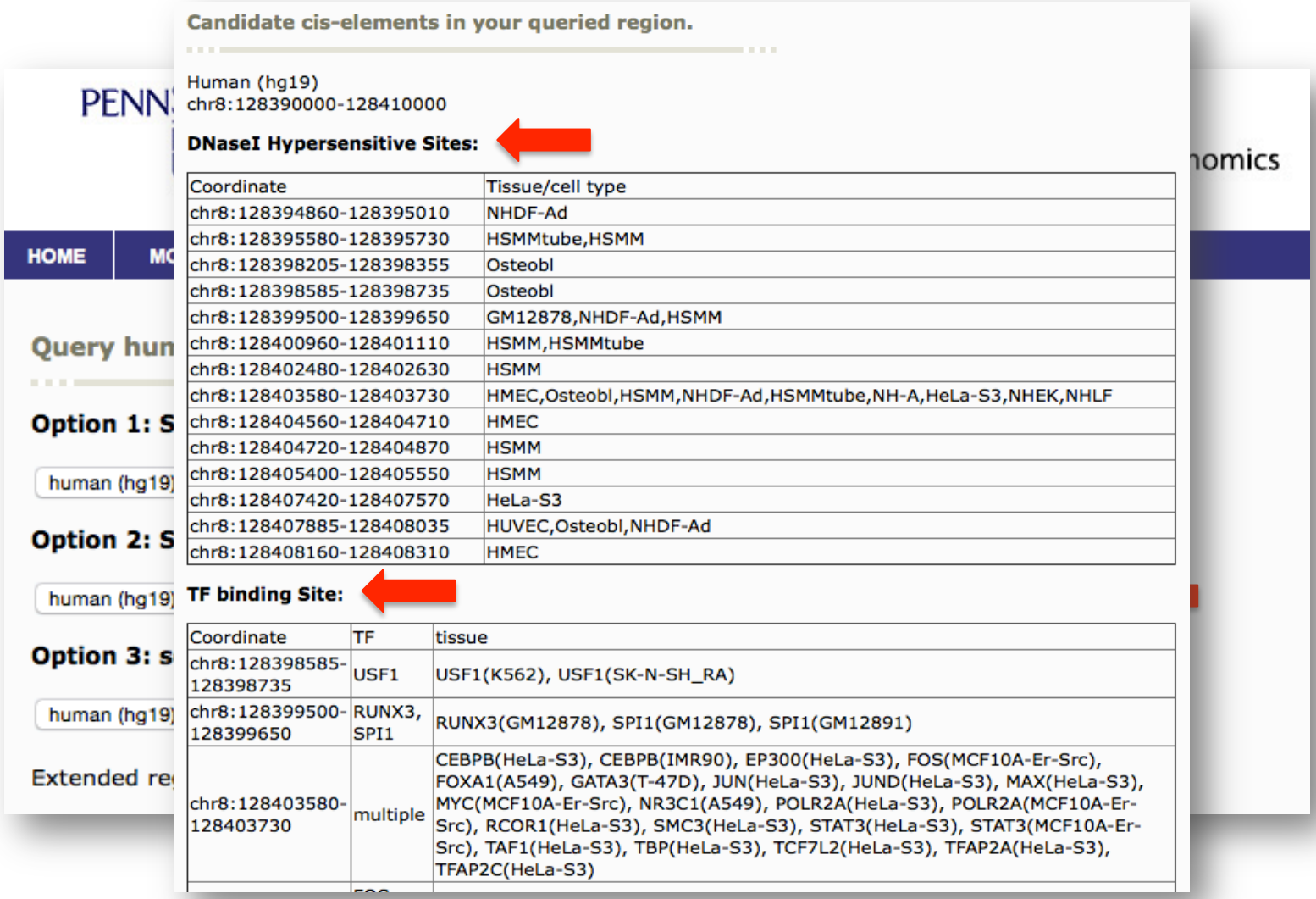
RegulomeDB GWAS Database



http://www.regulomedb.org/GWAS/

Cherry, Snyder, Genome Research 22-1790,2012

ENCODE cis-element Browser



Candidate cis-elements in your queried region.

Human (hg19)
chr8:128390000-128410000

DNaseI Hypersensitive Sites:

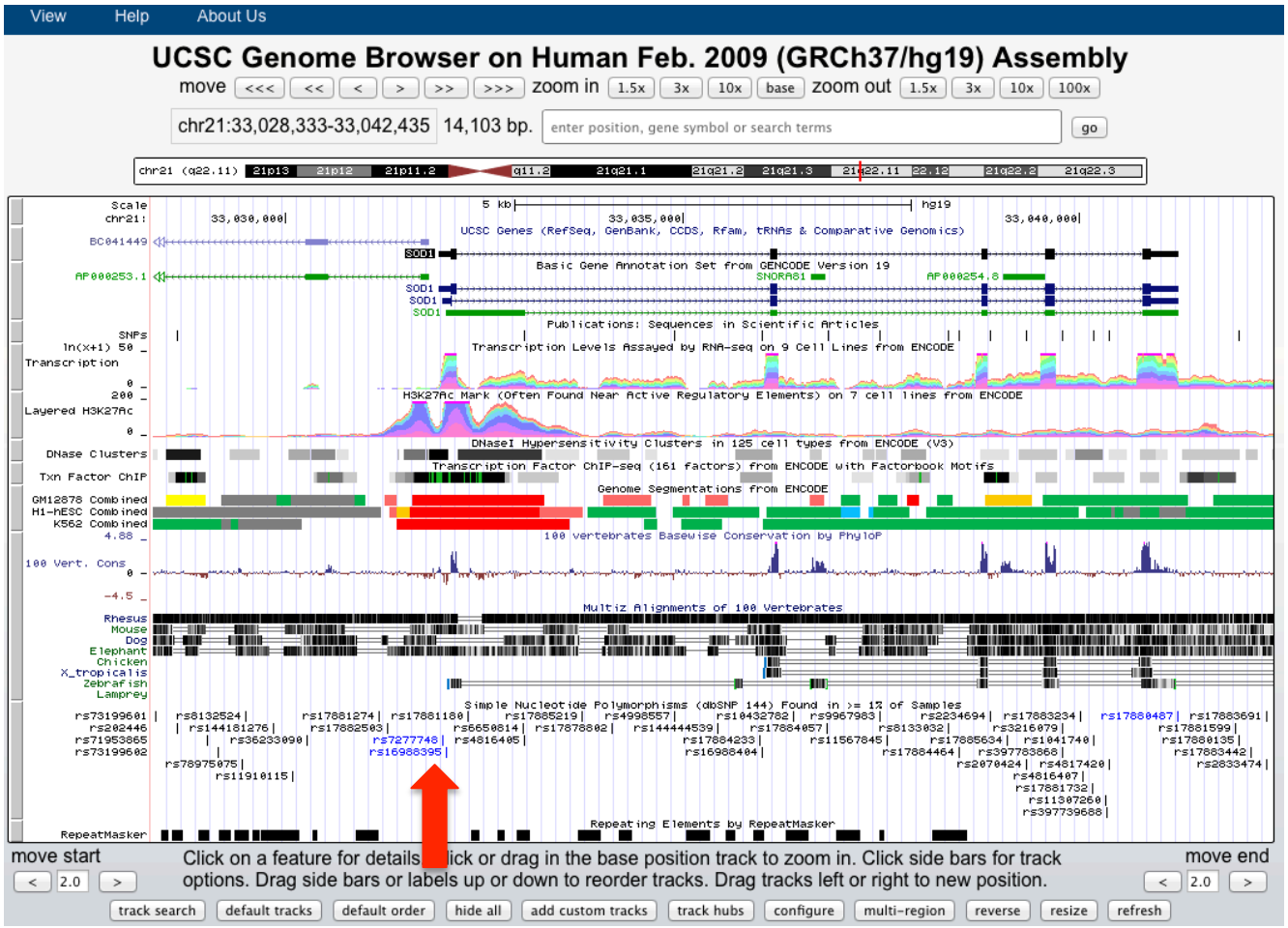
Coordinate	Tissue/cell type
chr8:128394860-128395010	NHDF-Ad
chr8:128395580-128395730	HSMMtube,HSMM
chr8:128398205-128398355	Osteobl
chr8:128398585-128398735	Osteobl
chr8:128399500-128399650	GM12878,NHDF-Ad,HSMM
chr8:128400960-128401110	HSMM,HSMMtube
chr8:128402480-128402630	HSMM
chr8:128403580-128403730	HMEC,Osteobl,HSMM,NHDF-Ad,HSMMtube,NH-A,HeLa-S3,NHEK,NHLF
chr8:128404560-128404710	HMEC
chr8:128404720-128404870	HSMM
chr8:128405400-128405550	HSMM
chr8:128407420-128407570	HeLa-S3
chr8:128407885-128408035	HUVEC,Osteobl,NHDF-Ad
chr8:128408160-128408310	HMEC

TF binding Site:

Coordinate	TF	tissue
chr8:128398585-128398735	USF1	USF1(K562), USF1(SK-N-SH_RA)
chr8:128399500-128399650	RUNX3, SPI1	RUNX3(GM12878), SPI1(GM12878), SPI1(GM12891)
chr8:128403580-128403730	multiple	CEBPB(HeLa-S3), CEBPB(IMR90), EP300(HeLa-S3), FOS(MCF10A-Er-Src), FOXA1(A549), GATA3(T-47D), JUN(HeLa-S3), JUND(HeLa-S3), MAX(HeLa-S3), MYC(MCF10A-Er-Src), NR3C1(A549), POLR2A(HeLa-S3), POLR2A(MCF10A-Er-Src), RCOR1(HeLa-S3), SMC3(HeLa-S3), STAT3(HeLa-S3), STAT3(MCF10A-Er-Src), TAF1(HeLa-S3), TBP(HeLa-S3), TCF7L2(HeLa-S3), TFAP2A(HeLa-S3), TFAP2C(HeLa-S3)

https://www.encodeproject.org/data/annotations/

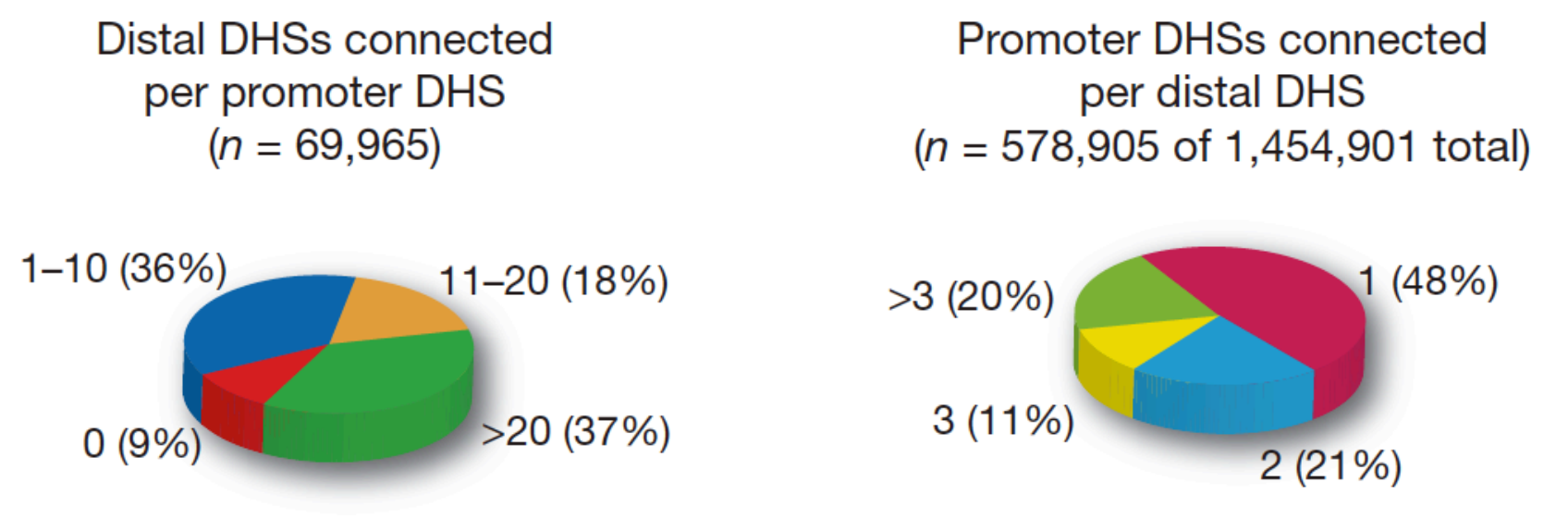
ENCODE Browser
Viewing Locus Of Interest



https://genome.ucsc.edu/encode/

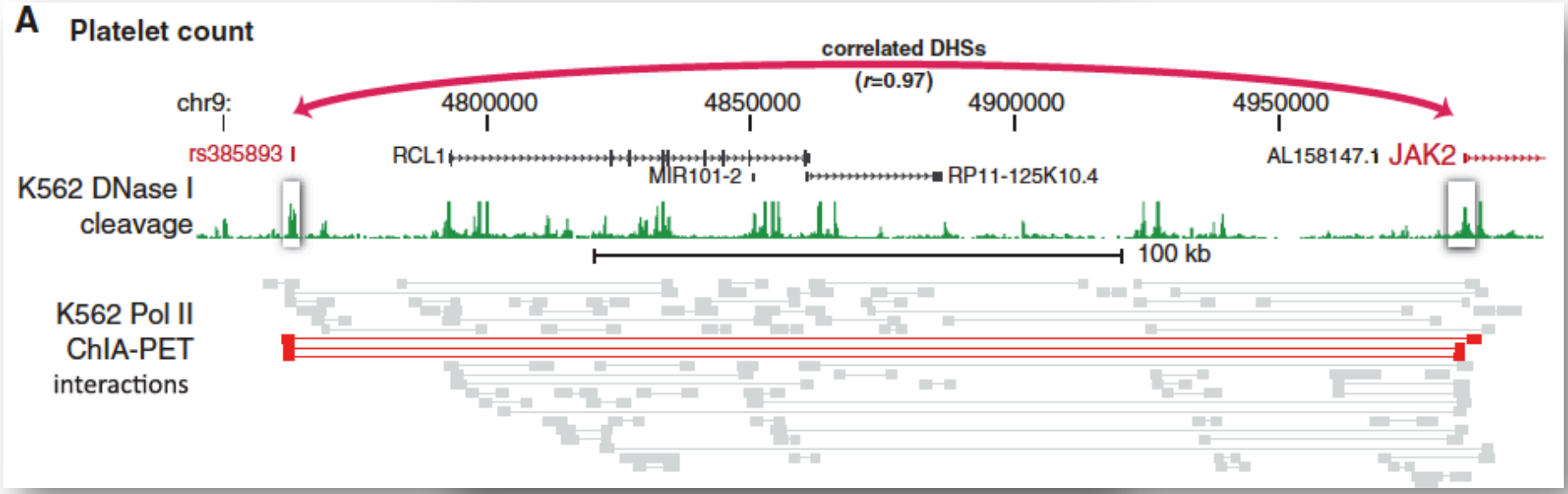
Prediction of Target Genes

- Regulatory regions can operate on multiple, distal genes
- The target gene could be a non-coding RNA



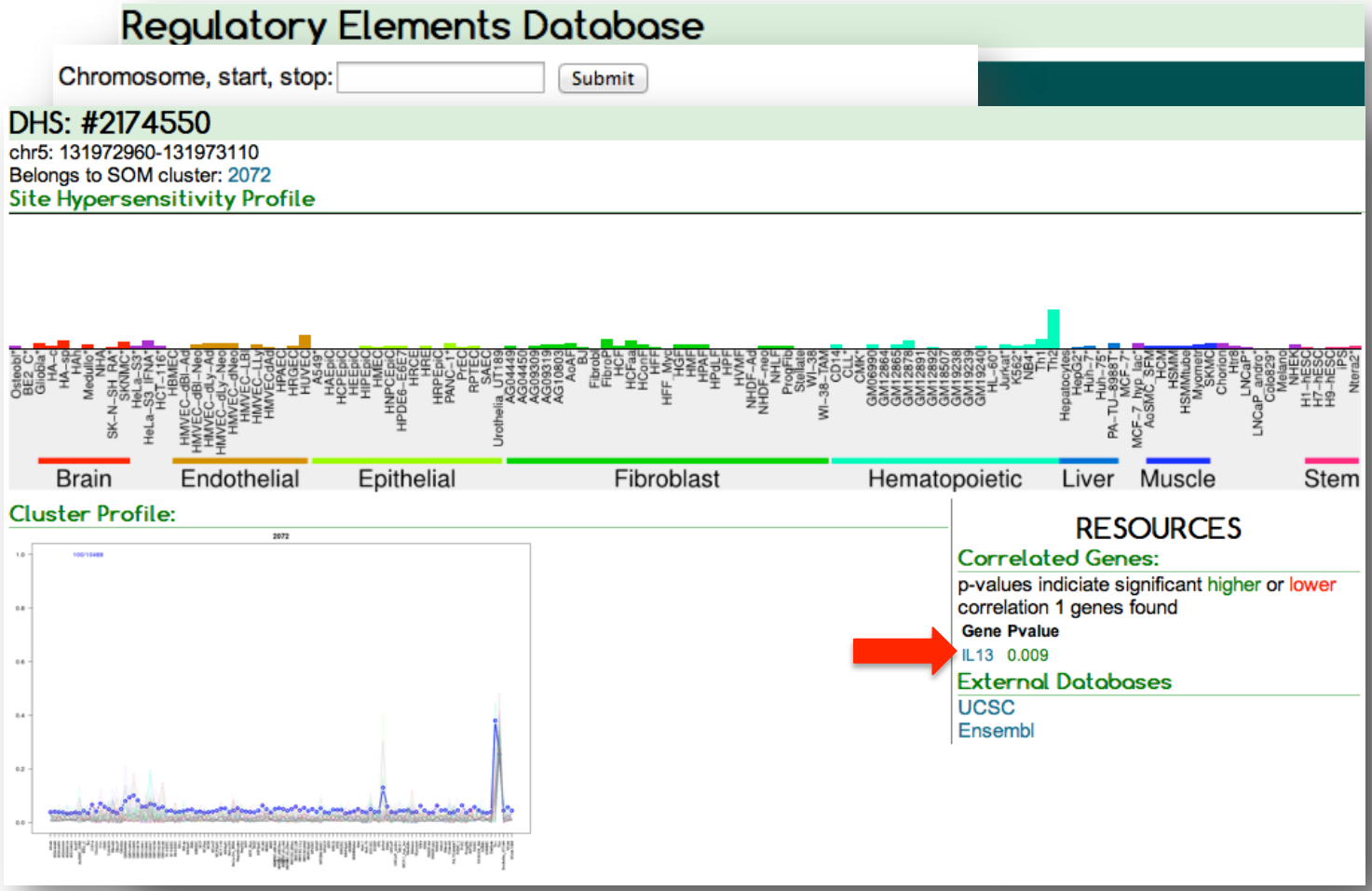
Stamatoyannopoulos, Crawford, Nature 489:75, 2012

Many GWAS Associations Lie In Regions Linked To Distal Genes



Stamatoyannopoulos, Science 337:1190, 2012

Prediction of Linkage Between Regulatory Elements and Genes



http://dnase.genome.duke.edu

Furey, Crawford, Stamatoyannopoulos, Genome Res. 23:777, 2013

ENCODE cis-element Browser

Cis-elements linked to your queried gene.

Human (hg19)
Gene **IL13** [NM_002188, ENSG00000169194, ENST00000304506]

Cis-element lined by DNaseI Hypersensitive Sites Linkage:

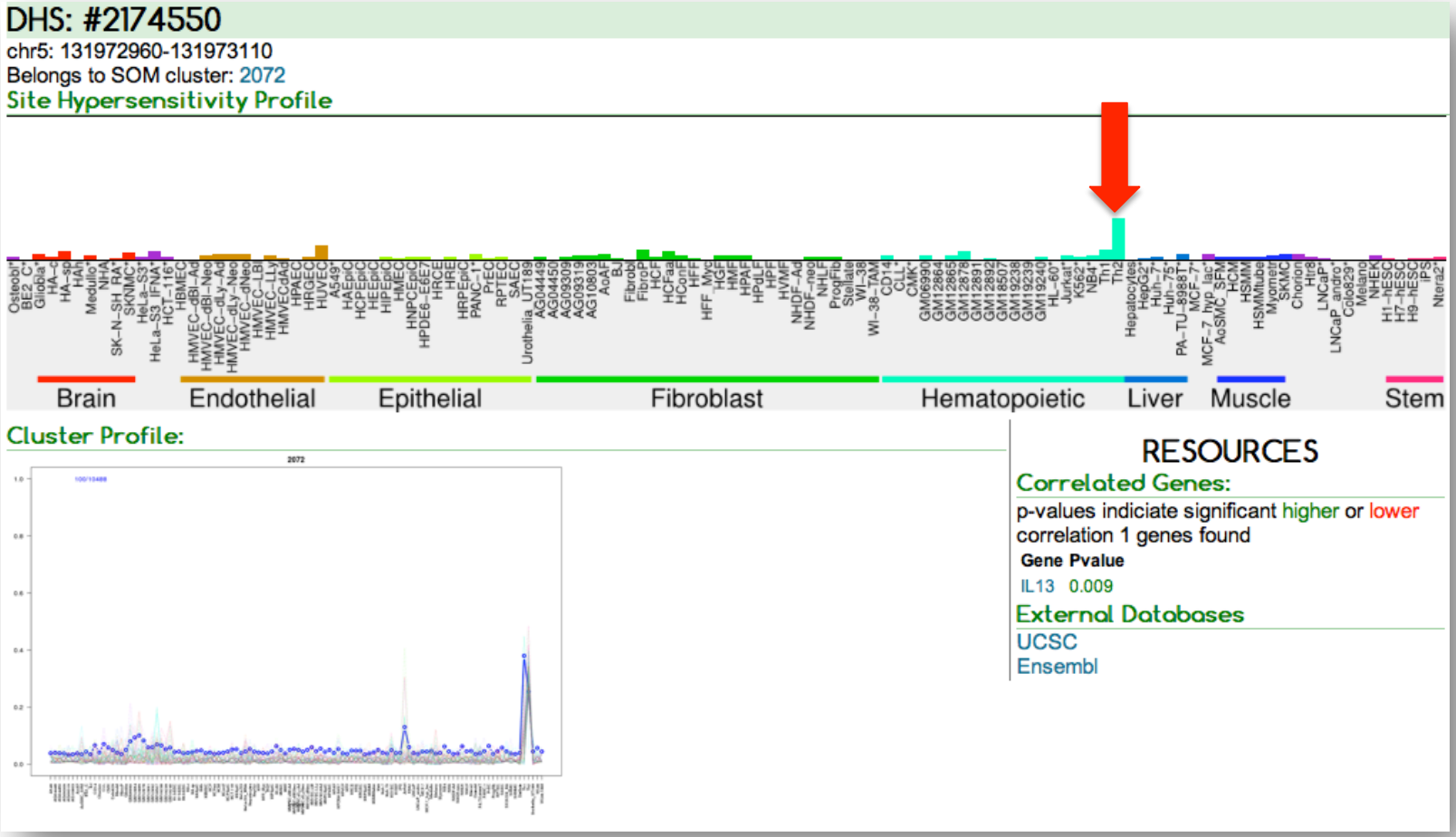
Proximal DHS (TSS)	start	end	Gene	Distal DHS	start	end	correlation
chr5	131992140	131992290	IL13	chr5	131512800	131512950	0.743283
chr5	131992140	131992290	IL13	chr5	131558440	131558590	0.761866
chr5	131992140	131992290	IL13	chr5	131571820	131571970	0.782866
chr5	131992140	131992290	IL13	chr5	131720440	131720590	0.766176
chr5	131992140	131992290	IL13	chr5	131732540	131732690	0.739405
chr5	131992140	131992290	IL13	chr5	131745200	131745350	0.765629
chr5	131992140	131992290	IL13	chr5	131747860	131748010	0.749684
chr5	131993580	131993730	IL13	chr5	131917860	131918010	0.797702
chr5	131993580	131993730	IL13	chr5	131921920	131922070	0.800141
chr5	131993580	131993730	IL13	chr5	131970980	131971130	0.772113
chr5	131993580	131993730	IL13	chr5	131971640	131971790	0.763557
chr5	131993580	131993730	IL13	chr5	131972960	131973110	0.797839
chr5	131993580	131993730	IL13	chr5	131977060	131977210	0.848905
chr5	131993580	131993730	IL13	chr5	131990420	131990570	0.855445
chr5	131993580	131993730	IL13	chr5	131993880	131994030	0.769354
chr5	131993580	131993730	IL13	chr5	132011780	132011930	0.756074
chr5	131993580	131993730	IL13	chr5	132077740	132077890	0.820222
chr5	131993580	131993730	IL13	chr5	132083520	132083670	0.770558
chr5	131993580	131993730	IL13	chr5	132164240	132164390	0.837496

https://www.encodeproject.org/data/annotations/

Prediction of Target Cell Types

- Some diseases are known to affect multiple cell types
- The defect may not be intrinsic to the cell type with obvious pathology
- The disease etiology may not be completely known

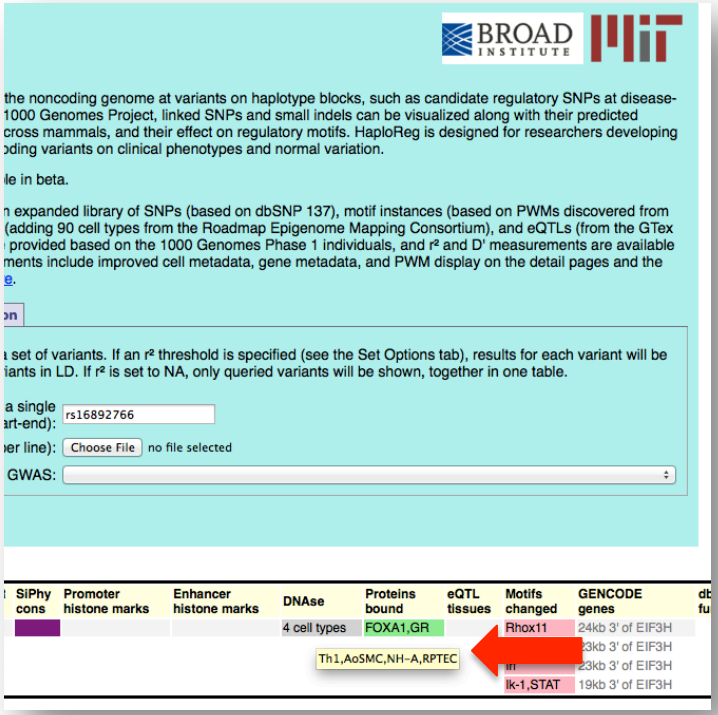
Prediction of Linkage Between Regulatory Elements and Cell Type

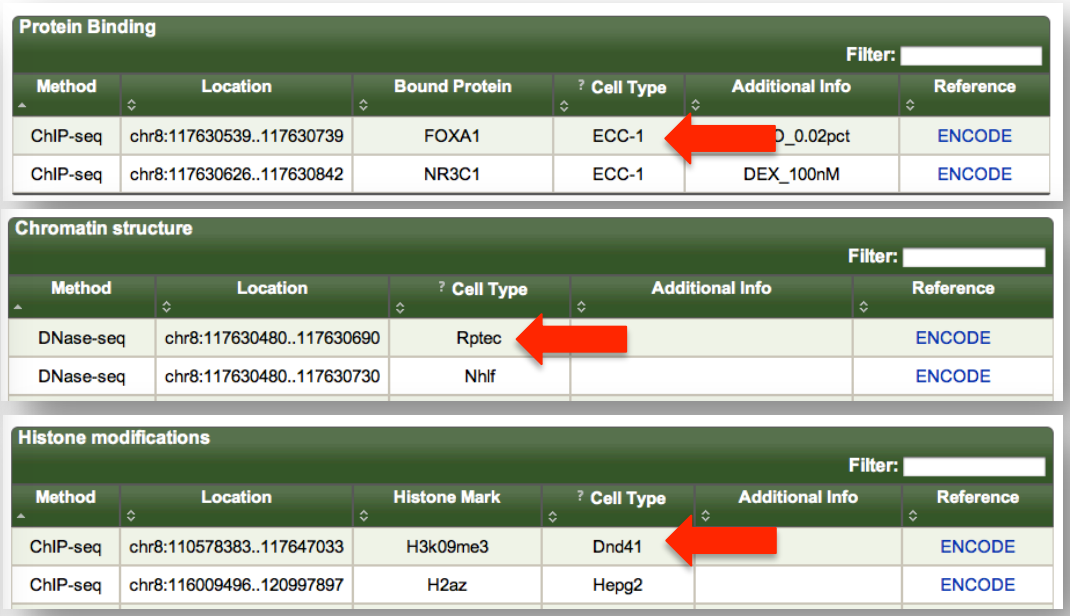


http://dnase.genome.duke.edu

Furey, Crawford, Stamatoyannopoulos, Genome Res. 23:777, 2013

Prediction of Linkage Between Regulatory Elements and Cell Type





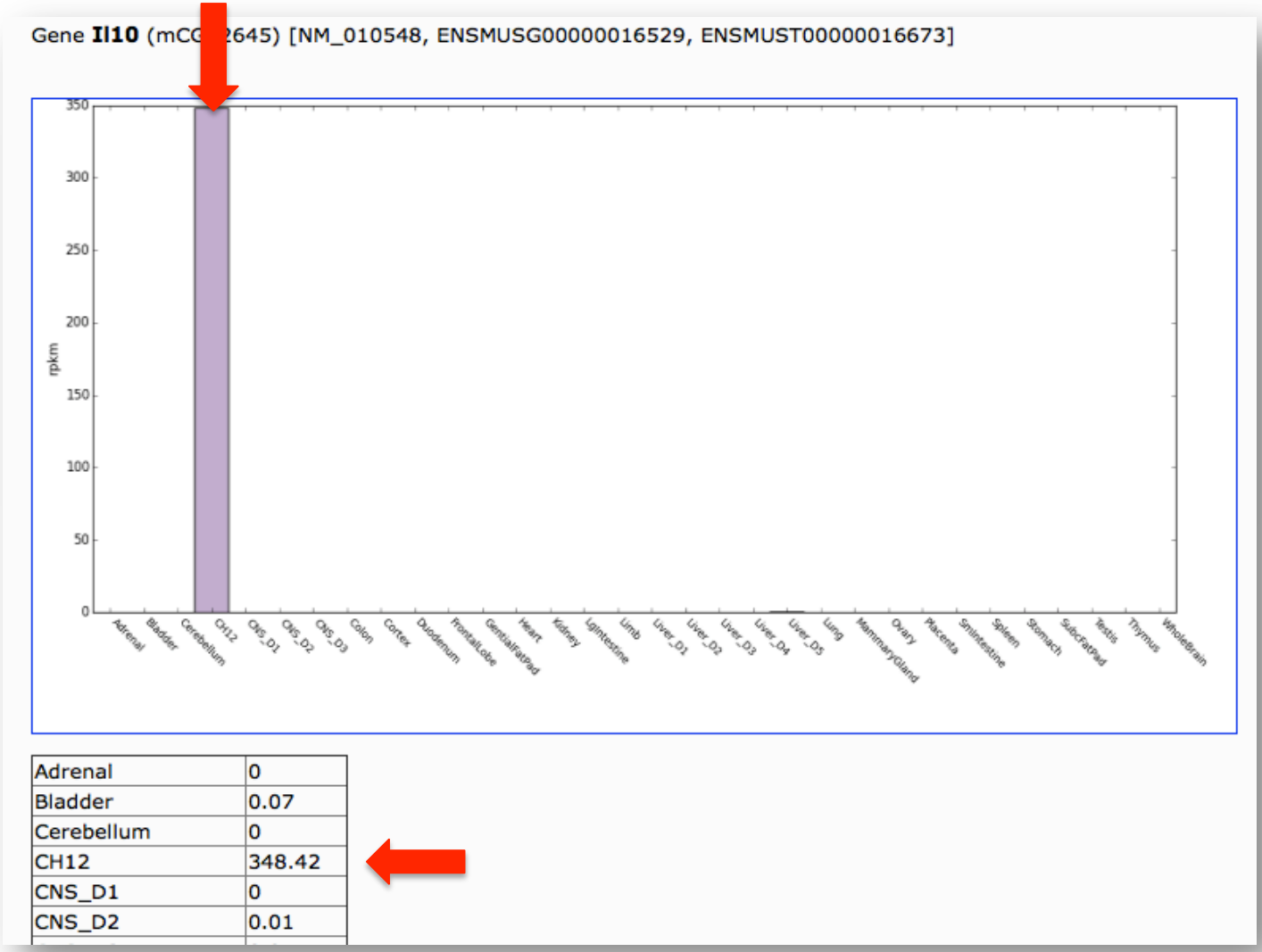
www.broadinstitute.org/mammals/haploreg/

Ward and Kellis, Nucleic Acids Research 40-D930, 2011

http://regulomedb.org/

Cherry, Snyder, Genome Research 22-1790 2012

ENCODE cis-element Browser



Adrenal	0
Bladder	0.07
Cerebellum	0
CH12	348.42
CNS_D1	0
CNS_D2	0.01

https://www.encodeproject.org/data/annotations/

Summary- ENCODE Use Cases

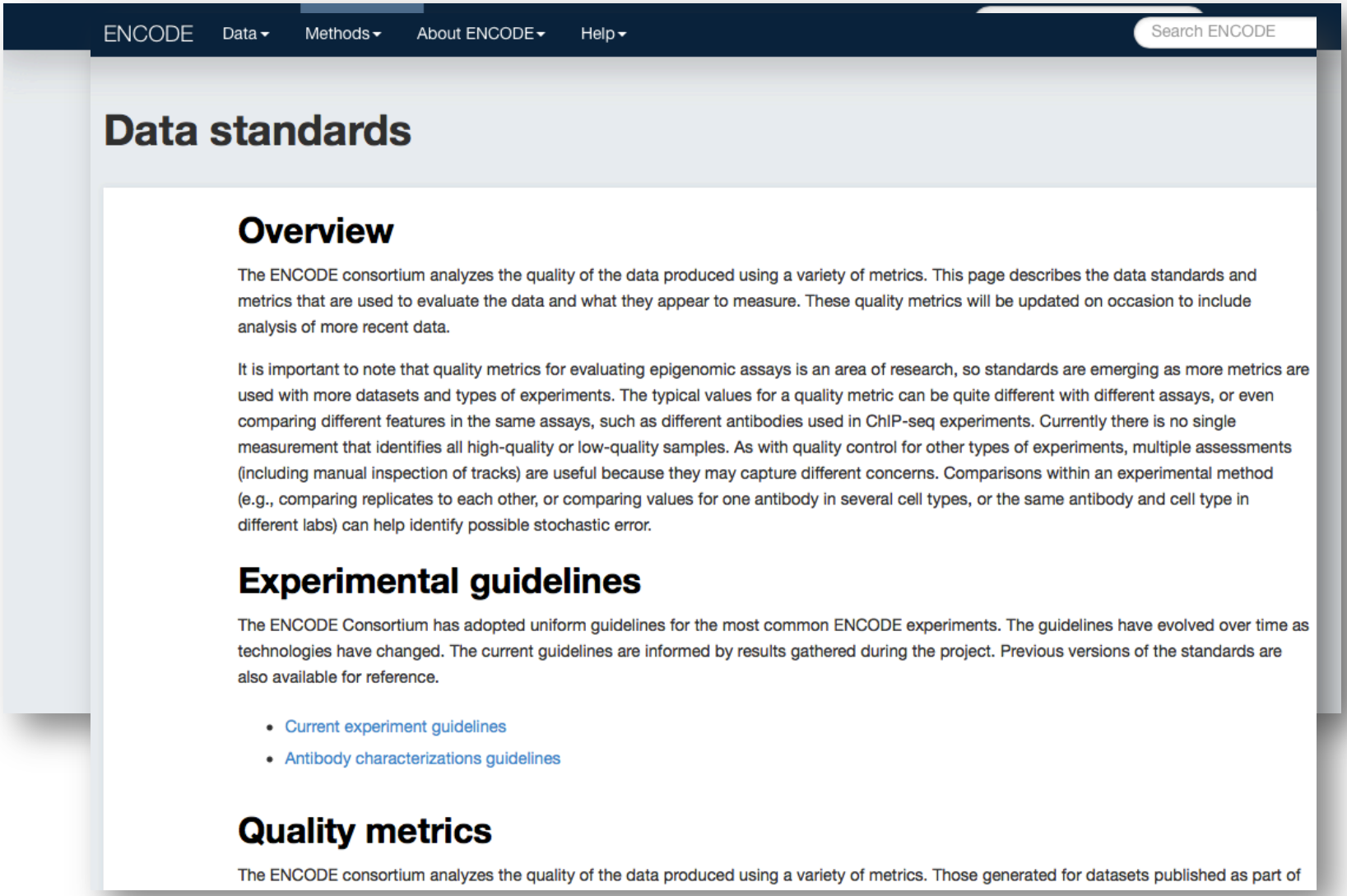
Major use: Hypothesis generation and refinement

- Prediction of causal variants/regulatory elements
- Prediction of target genes
- Prediction of target cell types

Overview

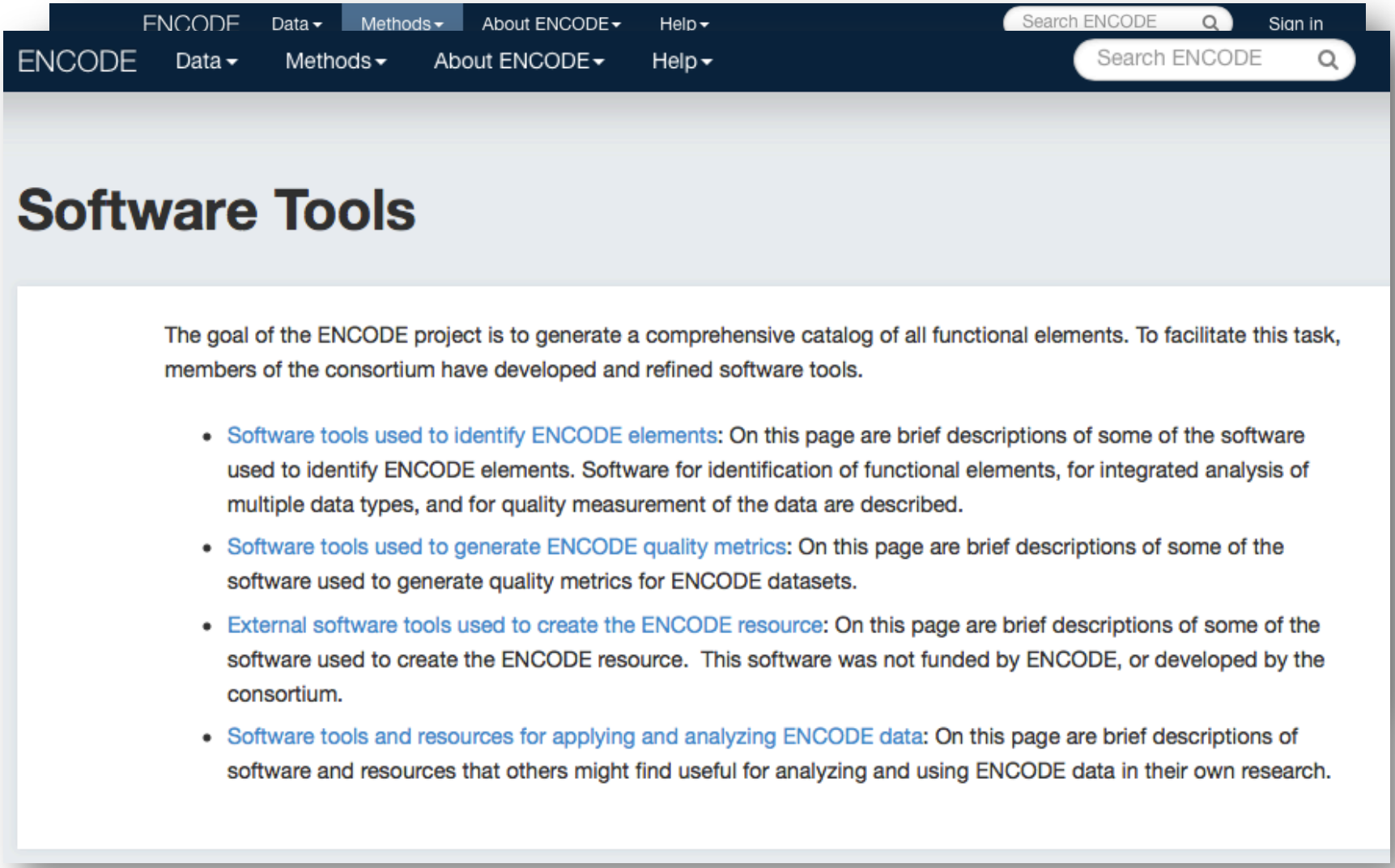
- The ENCODE Resource
- Use of ENCODE by the research community
- Accessing ENCODE materials

ENCODE Data Standards



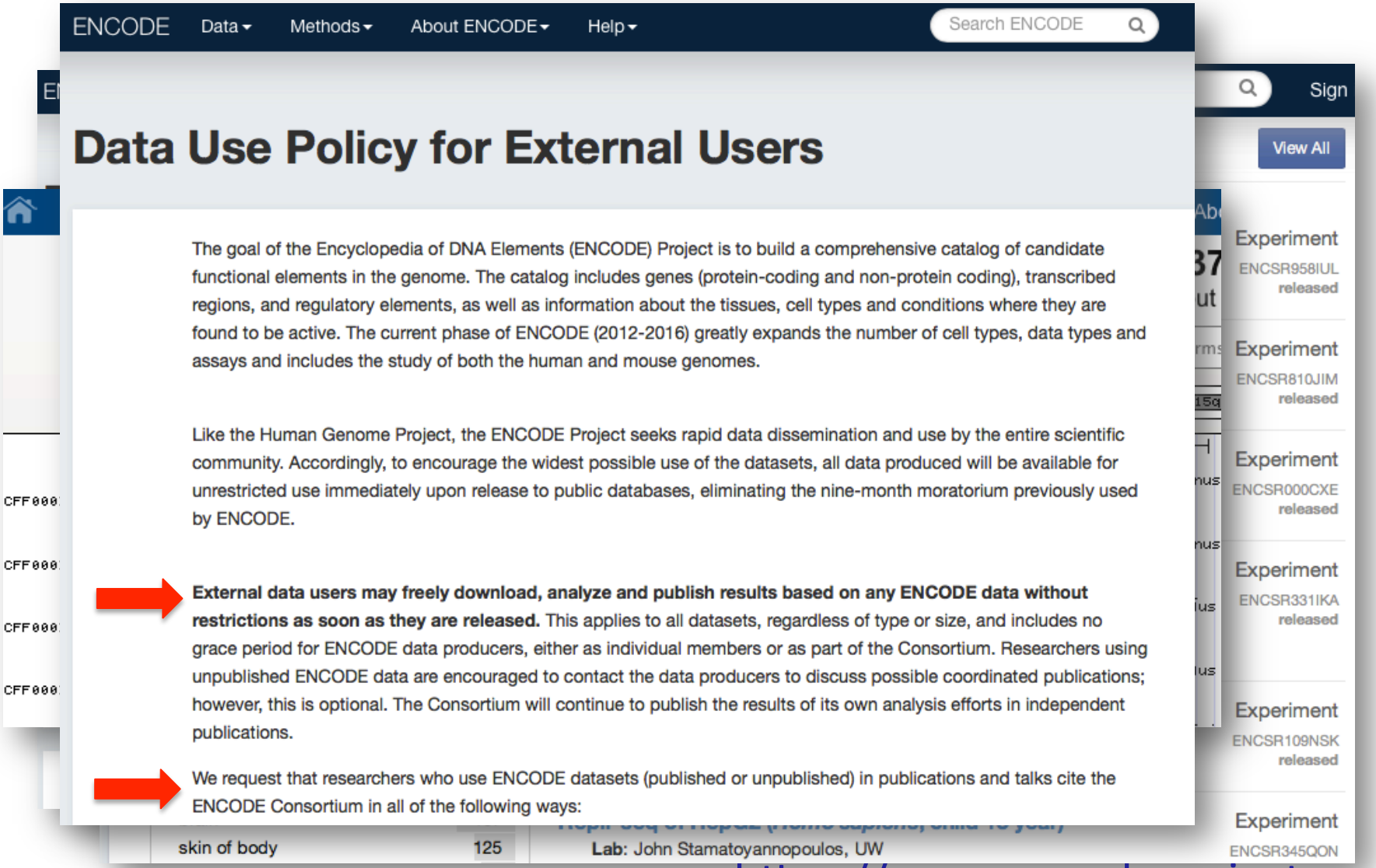
https://www.encodeproject.org

ENCODE Software Tools



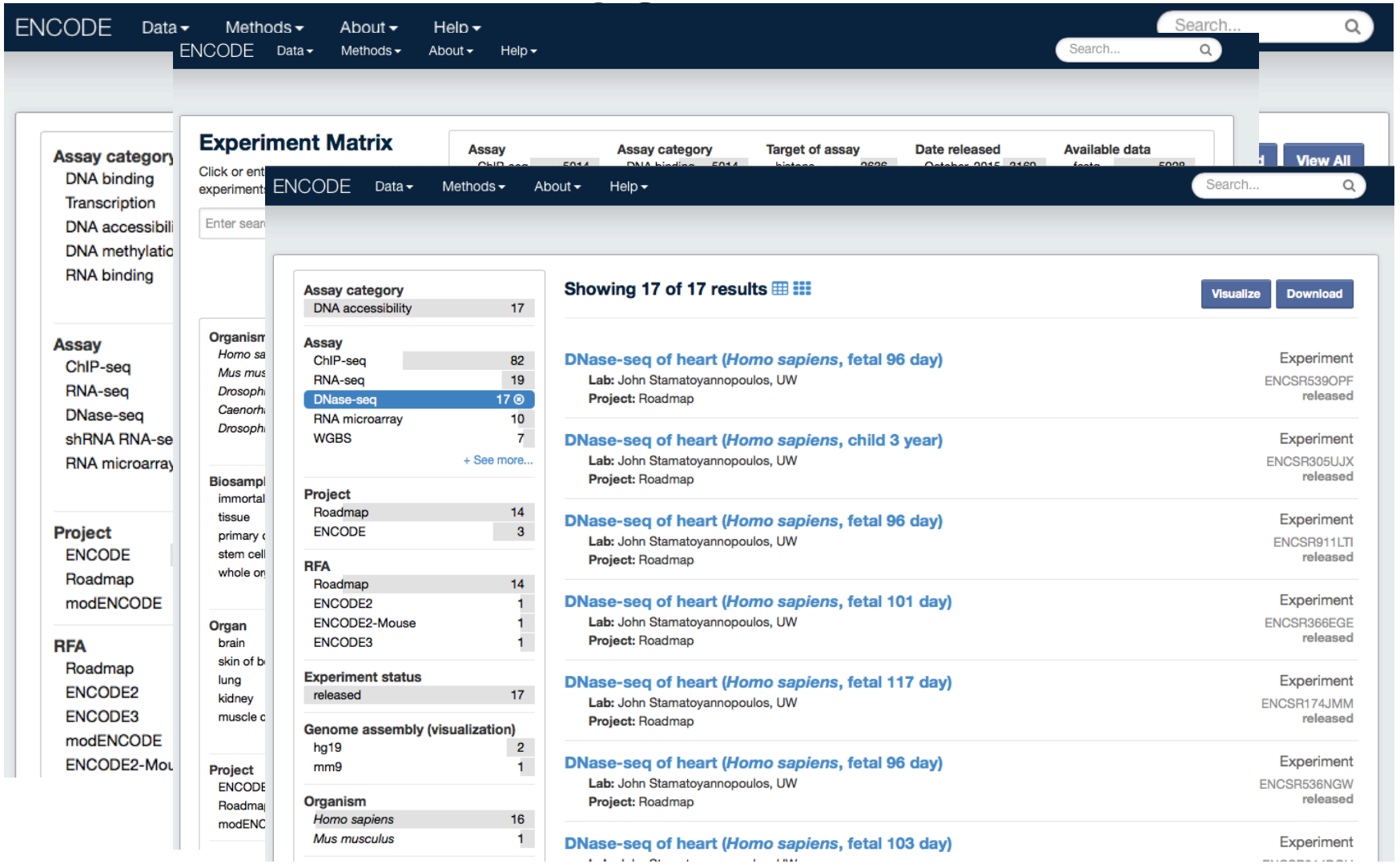
https://www.encodeproject.org

Downloading and Visualizing



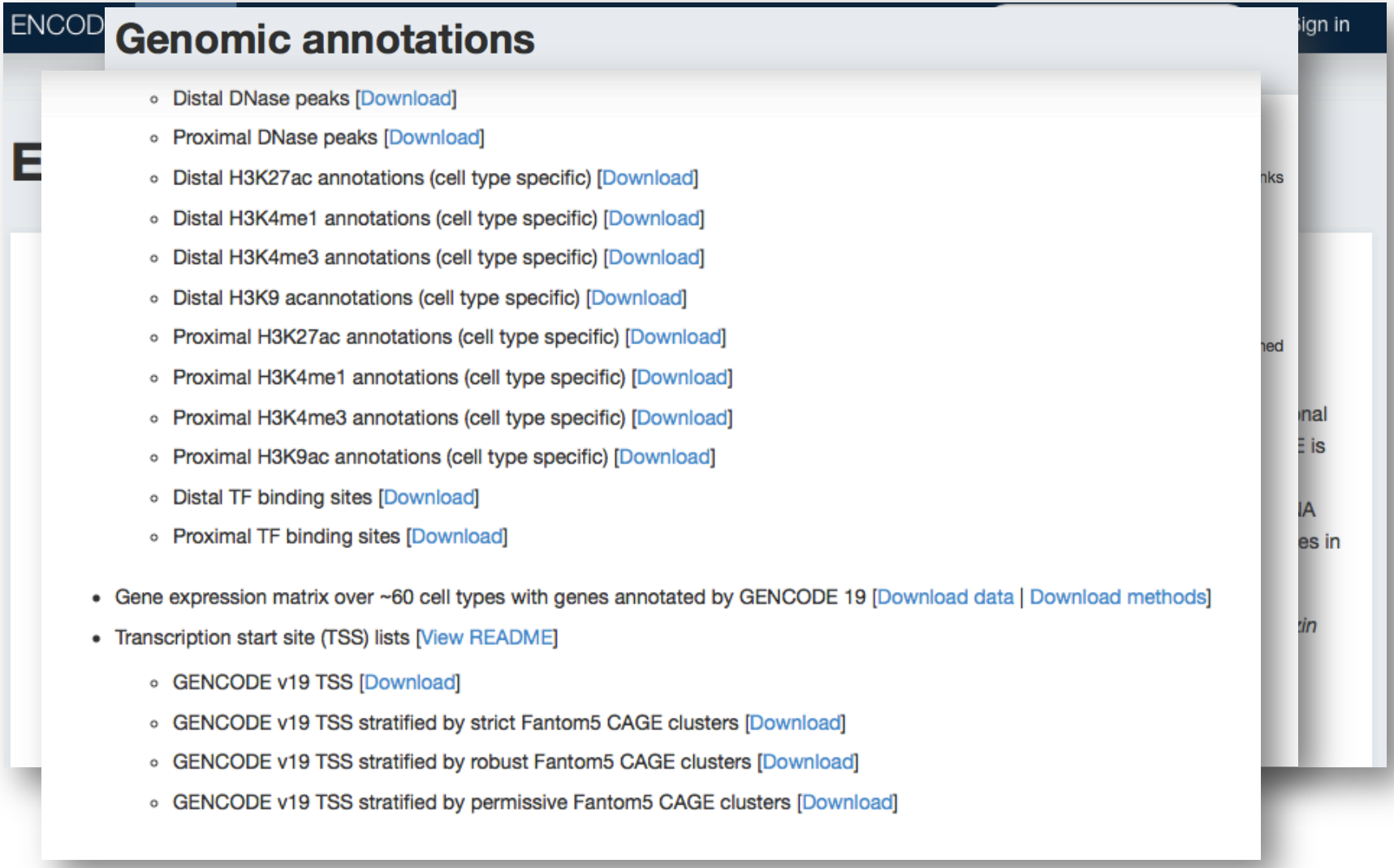
https://www.encodeproject.org

Downloading and Visualizing



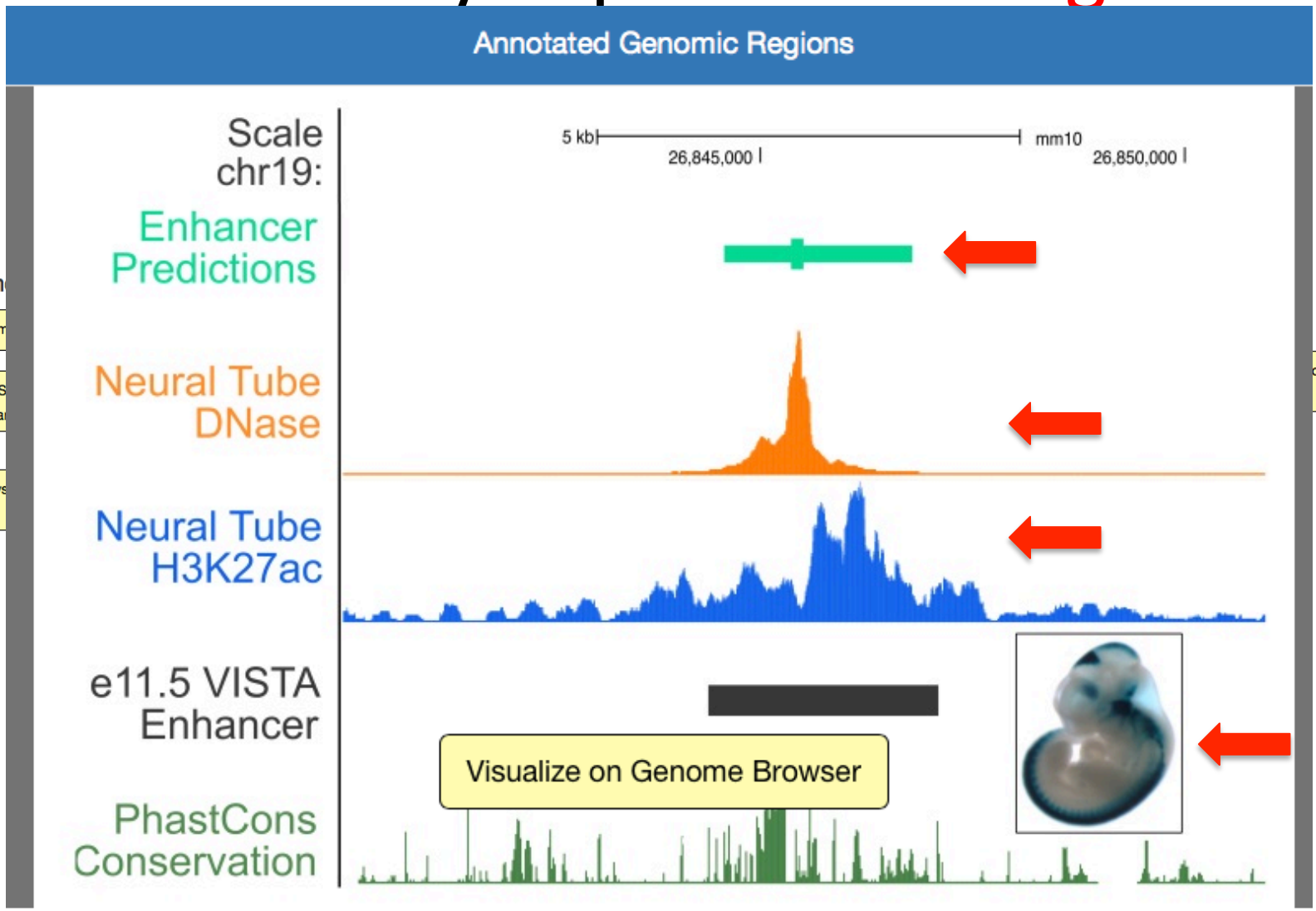
https://www.encodeproject.org

ENCODE Encyclopedia Prototype

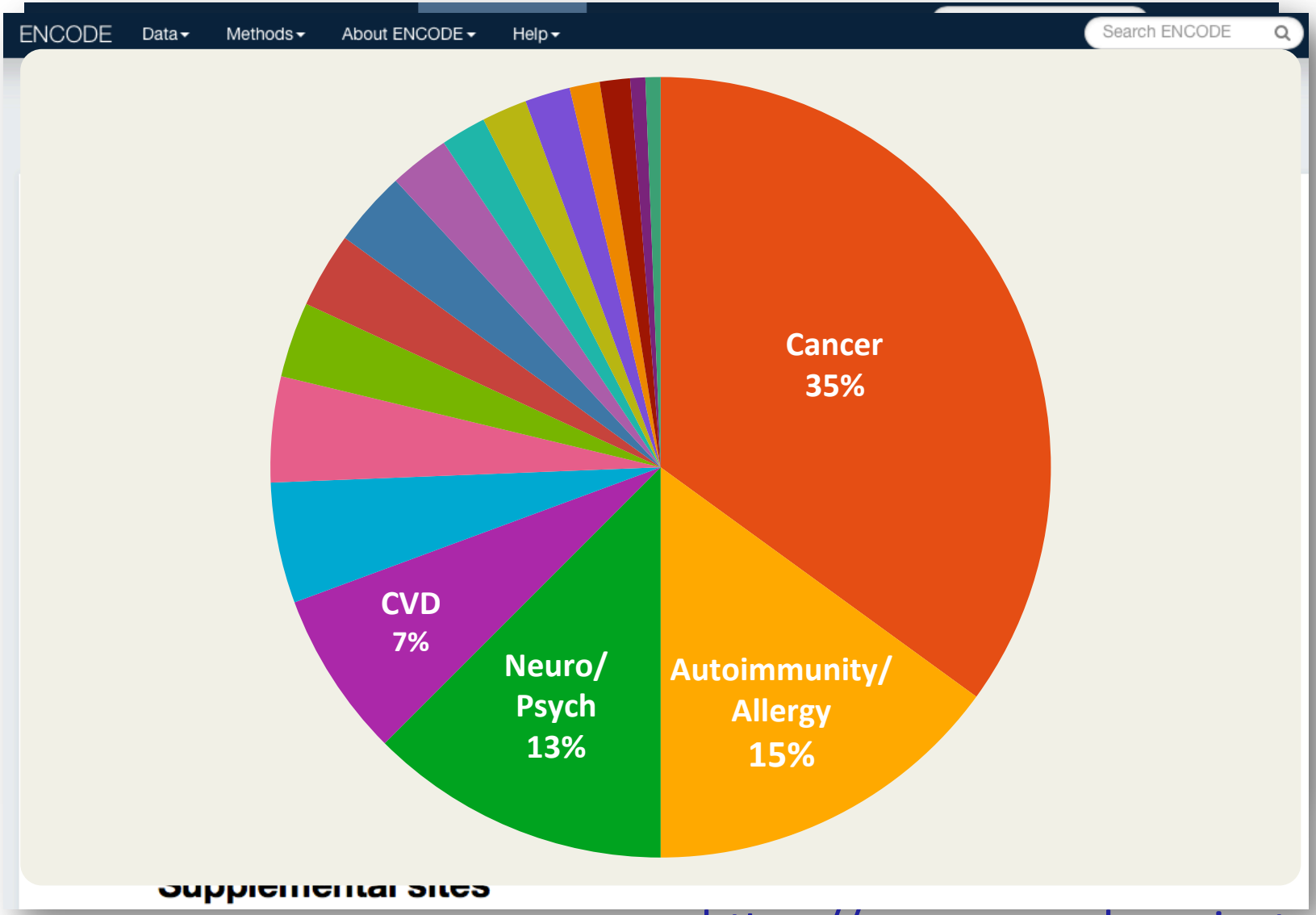


https://www.encodeproject.org

ENCODE Encyclopedia: Coming Soon!



Publications



https://www.encodeproject.org

Goals Of ENCODE

- Catalog all functional elements in the genome
- Develop freely available resource for research community

ENCODE data are being used in the study of human disease and basic biology

ENCODE Accomplishments

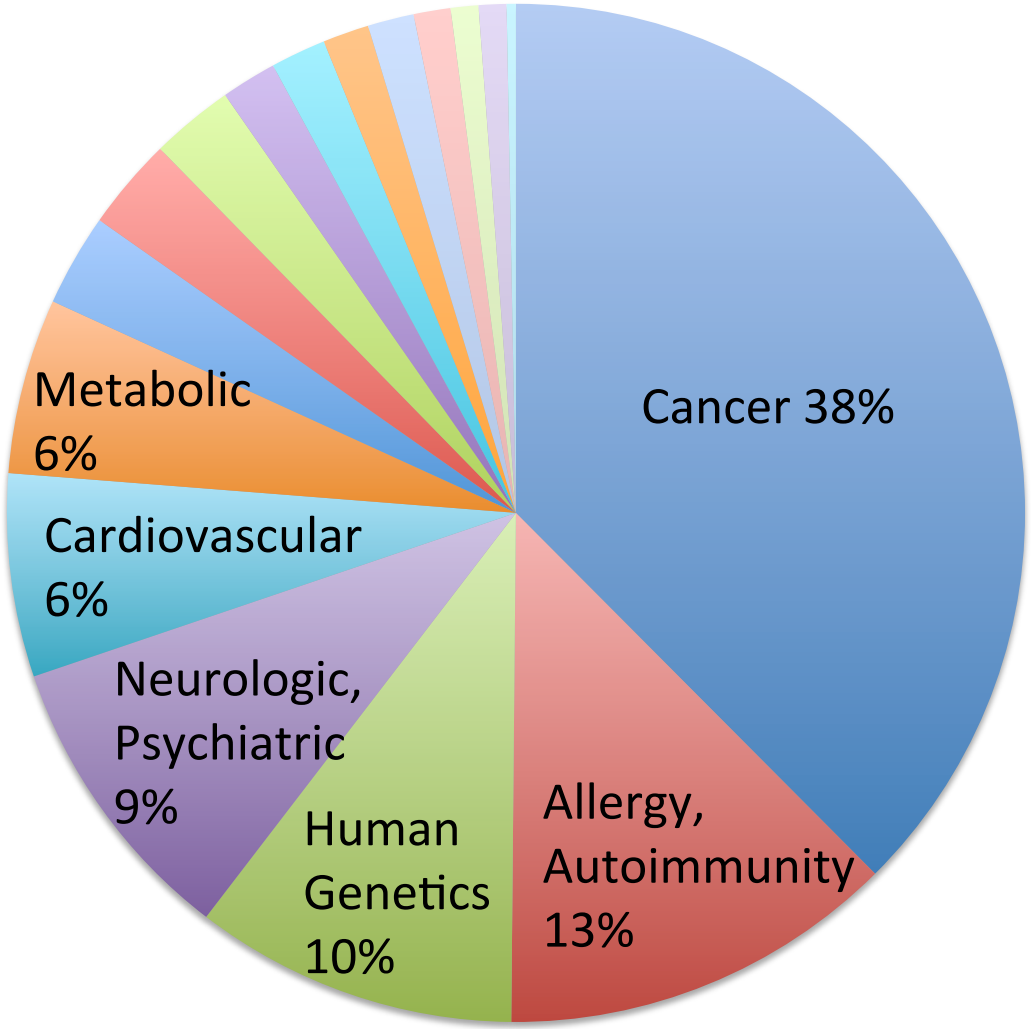
- Sharing 1000s of datasets
  - No embargo
  - High quality
  - Uniformly processed
- Data interoperability
- Sharing software

Publications Using ENCODE Data

Hundreds of Consortium publications

~1500 community publications using ENCODE data:

- ~340 Human Disease
- ~500 Basic Biology
- ~170 Methods/Software Development



ENCODE Consortium

Elise Feingold

Peter Good

Mike Pazin

Summary- Accessing ENCODE Resources

- ENCODE portal https://www.encodeproject.org
  - Display/download ENCODE and Roadmap Epigenomics data
  - Data Standards
  - Software tools
  - Publications
  - Encyclopedia prototype
- ENCODE Analysis Tools
  - RegulomeDB http://regulomedb.org/
  - HaploReg http://www.broadinstitute.org/mammals/haploreg/
  - Regulatory Elements Database http://dnase.genome.duke.edu
  - RegulomeDB GWAS Database http://www.regulomedb.org/GWAS/
- ENCODE Tutorials
  - http://www.genome.gov/27553900
  - https://www.encodeproject.org/tutorials/ http://www.ncbi.nlm.nih.gov/pubmed/25762420
- ENCODE mailing list :
  - https://mailman.stanford.edu/mailman/listinfo/encode-announce
- IHEC resources
  - IHEC Home Page http://ihec-epigenomes.org
  - IHEC Data Portal http://epigenomesportal.ca/ihec/

International Human Epigenome Consortium (IHEC)

- Data Portal: http://epigenomesportal.ca/ihec/
- Goal: Coordinate production of 1000 human epigenome maps for cellular states relevant to health and disease http://ihec-epigenomes.org
- Can view by consortium, by assay, by cell type
- Data from 7 consortia

IHEC
International Human Epigenome Consortium

ROADMAP epigenomics PROJECT

ENCODE

BLUEPRINT epigenome

CEEHRC

CREST IHEC
International Human Epigenome Consortium, Team Japan

DEEP

A Toxicology User's Guide to the Roadmap Epigenomics and ENCODE Data Resources

Thursday, March 17, 1:00 PM–6:00 PM

Room 205

Hosted by: *Ivan Rusyn, Texas A&M University, College Station, TX; and Lisa Chadwick, NIEHS, Research Triangle Park, NC.*

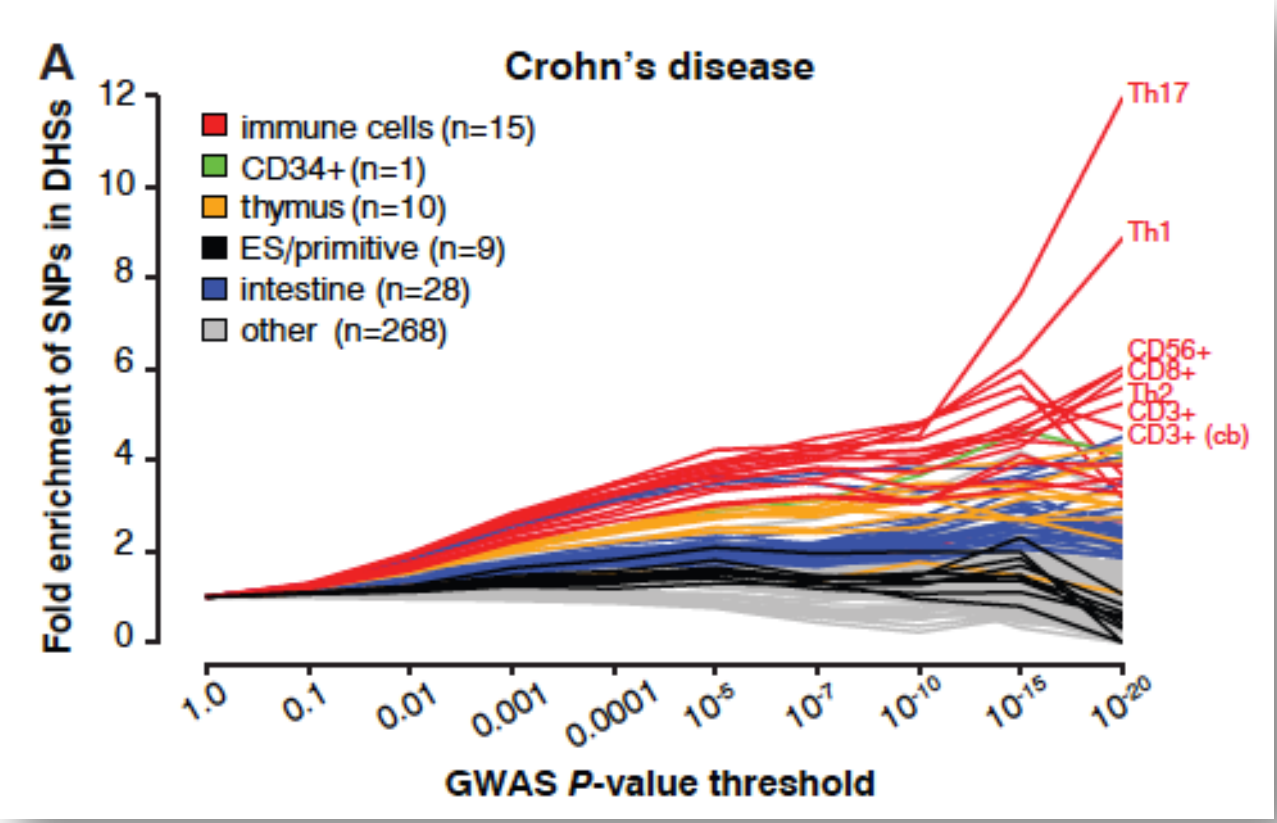
Purpose of the Meeting: Improvements in DNA sequencing technologies have resulted in an exponential increase in the amount of genomic and epigenomic data available. Some of these data have been generated as part of large-scale, focused mapping efforts aimed at understanding how genes are regulated, such as the NIH Roadmap Epigenomics Program, and ENCODE (Encyclopedia of DNA Elements). Efforts such as these can be extremely valuable for hypothesis generation and data mining, but can only be useful if one knows what is available and how to use it. This SOT satellite meeting will provide toxicology researchers with an overview of these two NIH-funded programs, introduce attendees to the informatics tools that have been developed to help navigate these large datasets, and walk through several use cases. The meeting will be of broad interest to researchers interested in learning more about how environmental exposure might impact gene regulation.

Registration: Open registration. No fee to register and attend.

Lectures followed by Q&A and a poster session.

For more information on this Satellite Meeting, contact Lisa Chadwick.

ENCODE And Epigenomics Data Can Be Used To Predict Cell Types



Stamatoyannopoulos, Science 337:1190, 2012

Prediction of Linkage Between Regulatory Elements and Genes

Data from Table S7, Stamatoyannopoulos, Crawford, Nature 489:75, 2012