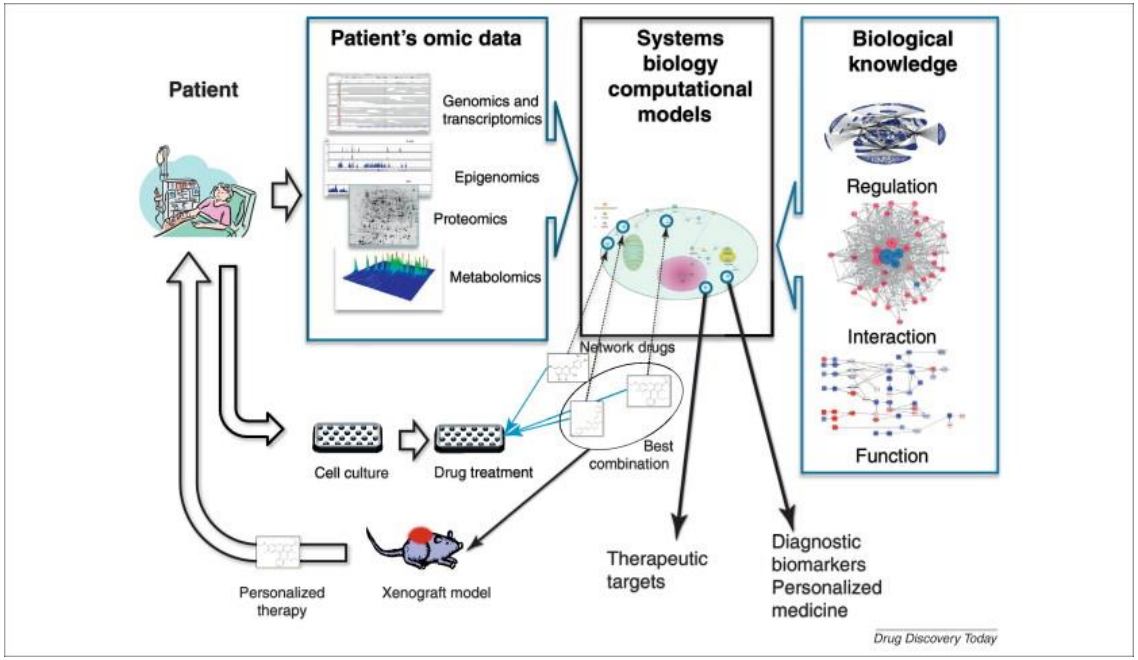
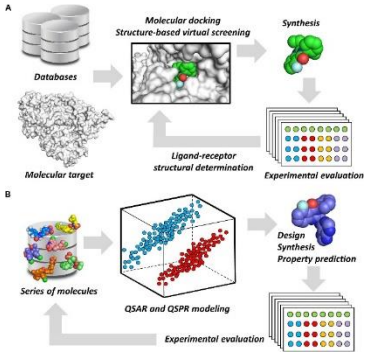
APPLICATION IN MEDICINE

- GENE FUNCTION AND REGULATION
- THERAPEUTIC APPROACHES

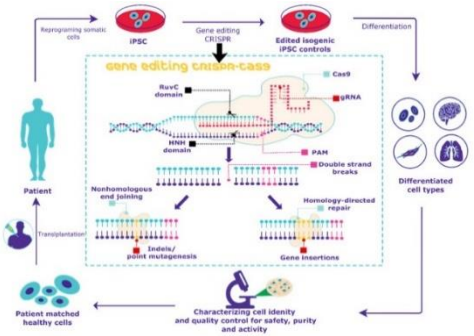


THERAPEUTIC APPROACHES

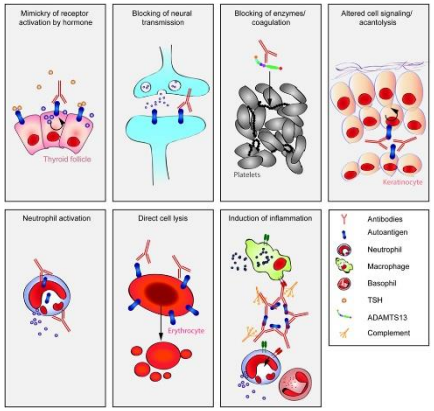
Chemical Drugs



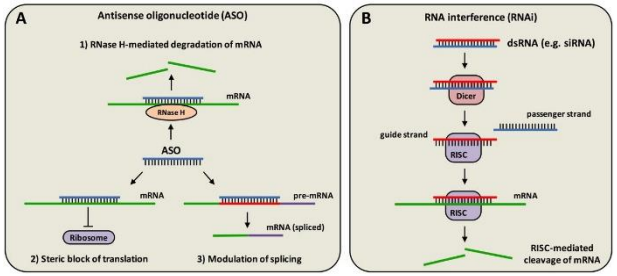
CRISPR-CAS SYSTEM



Antibodies



Oligonucleotides antisense



In this lesson

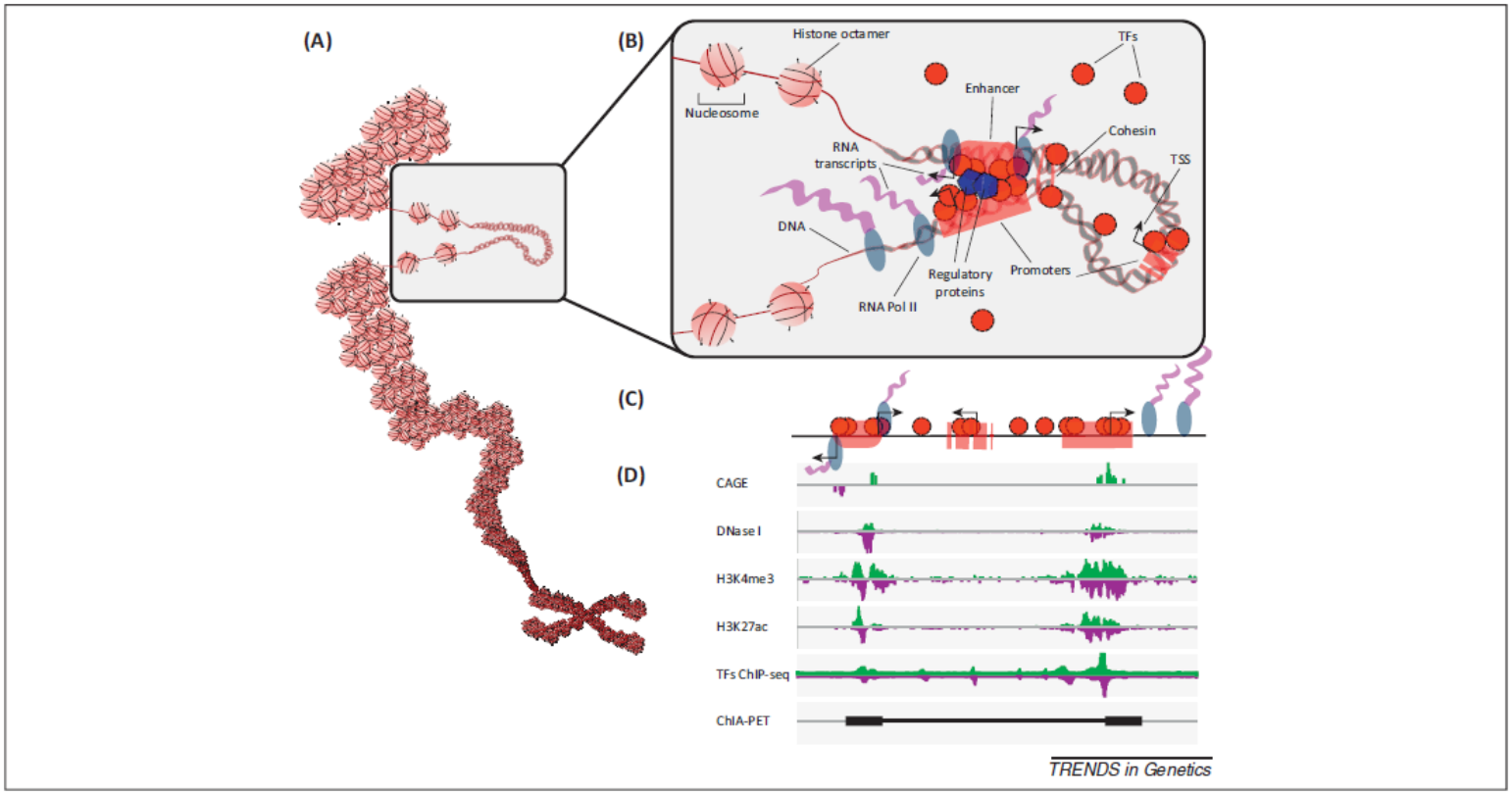
- What is the main focus of the course
- Definition of Functional Genomics
- How Functional Genomics is the basis for understanding diseases
- Application of Functional Genomics and Integration Data
- Role of single nucletotide variants in genomic regulatory regions: an example of functional genomics application

The main focus of this course is
functional genomics

APPLICATIONS ON MEDICINE

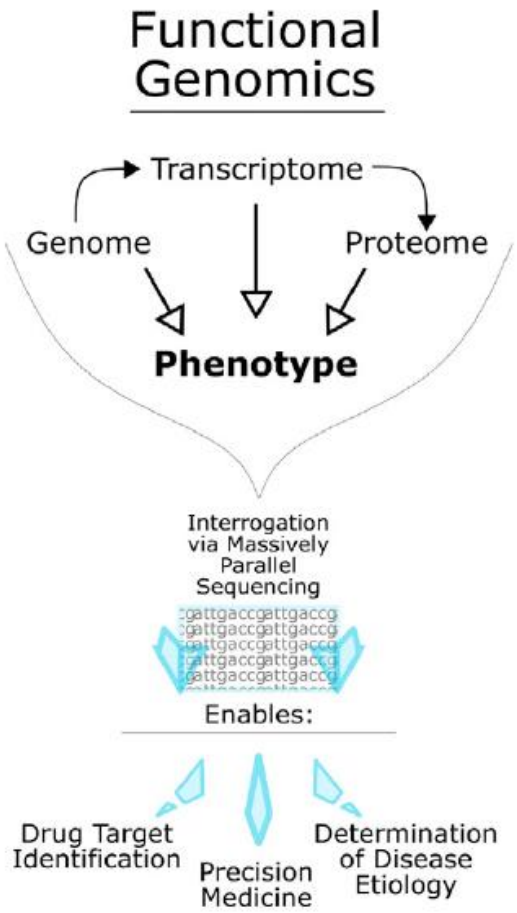
Functional genomics

Functional genomics uses genomic data to study gene expression, regulation and biological functions on a global scale (genome-wide or system-wide), focusing on gene transcription, epigenetic modifications, chromatin remodelling enzymes, transcription factors association involving high-throughput methods.

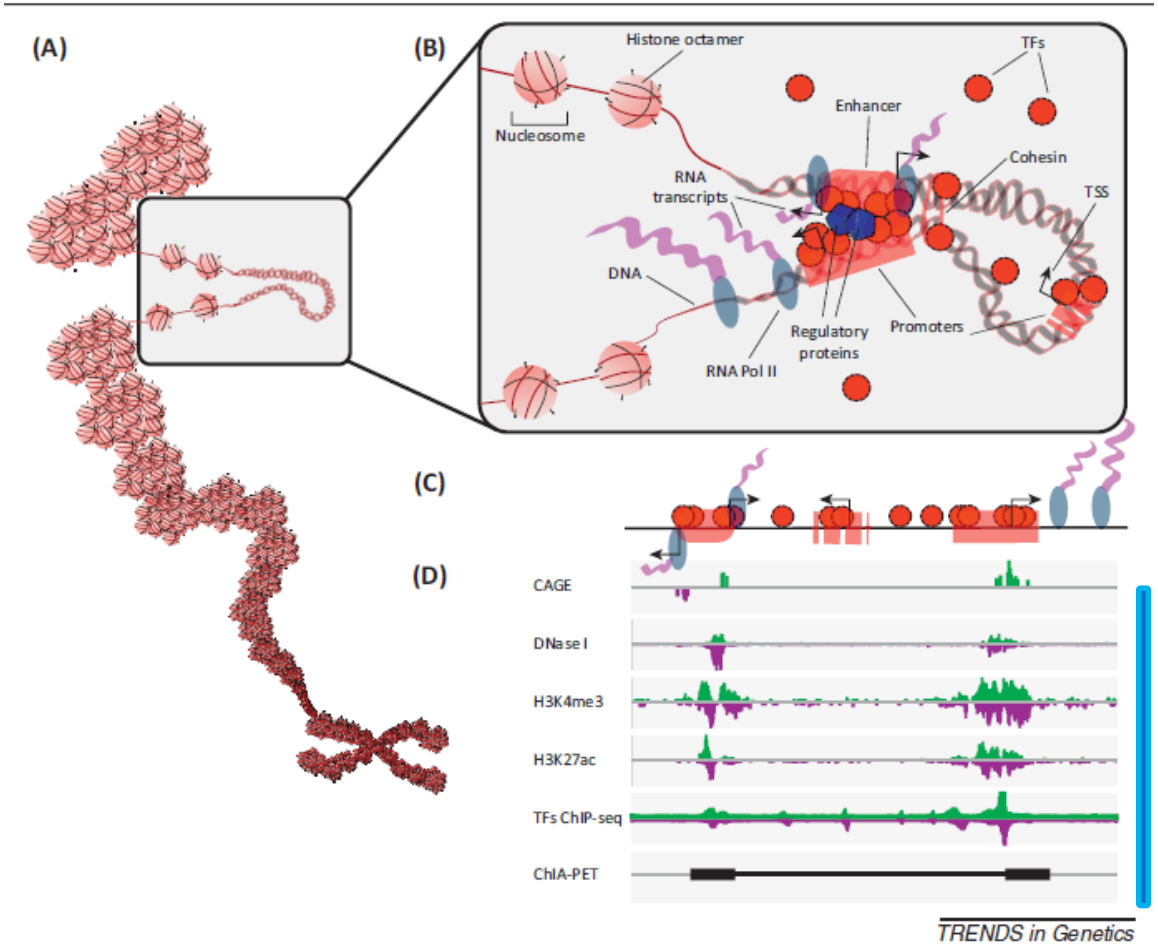


GENE REGULATION
How we can understand gene regulation
Using genome-wide sequencing data

- **FUNCTIONAL GENOMICS**



GENOMIC REGULATORY REGIONS



GENE FEATURES

GENE REGULATION

GENE REGULATION
How we can understand gene regulation
Using genome-wide sequencing data

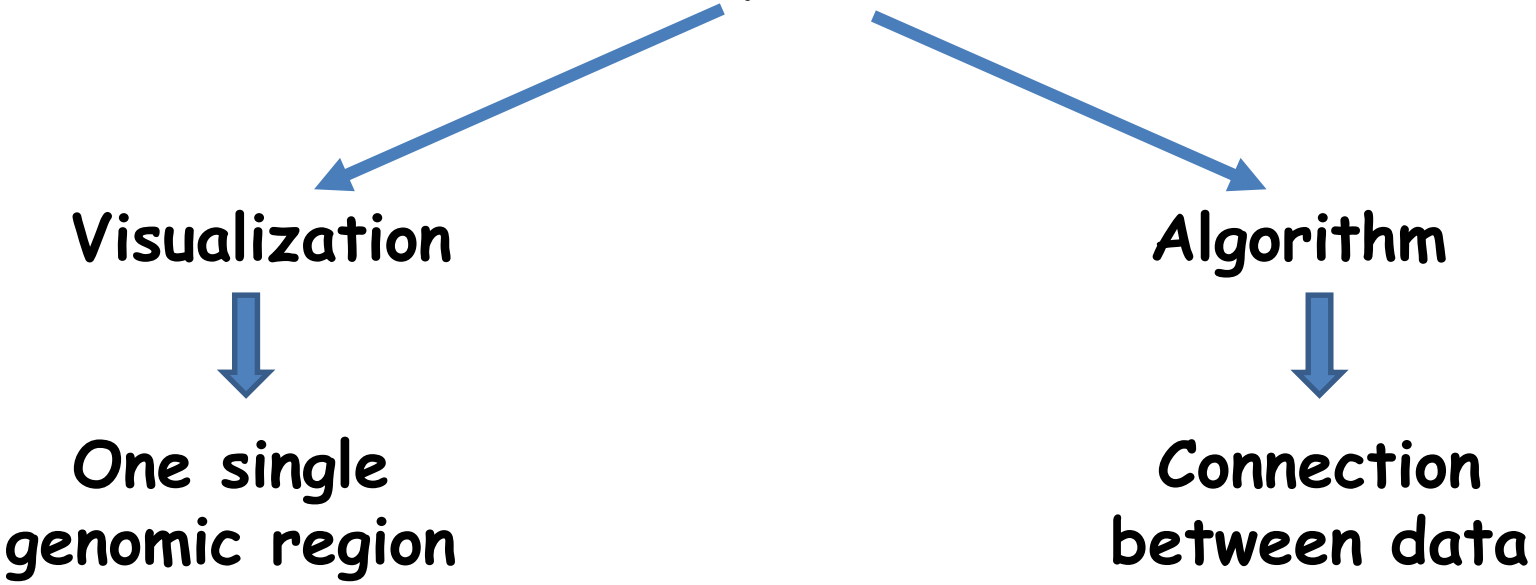
- FUNCTIONAL GENOMICS

- INTEGRATION DATA APPROACH

GENE REGULATION
How we can understand gene regulation Using genome-wide sequencing data

- **INTEGRATION DATA APPROACH**

Is based on the comparison of different data



Framework for interpretation of individual disease-associated variants

- Single nucleotide polymorphisms (SNPs) is the nucleotide variations associated with disease

- Genome-wide association studies (GWAS) have successfully identified thousands of common genetic variants associated with complex diseases (http://www.ebi.ac.uk/gwas/)

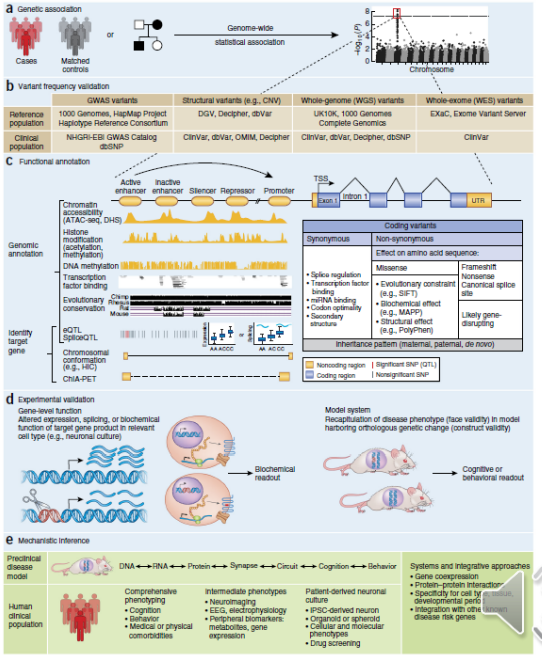
- Functional annotation: to define genomic regulatory regions by genome-wide integration data

- Experimental validation

- Disease Animal models

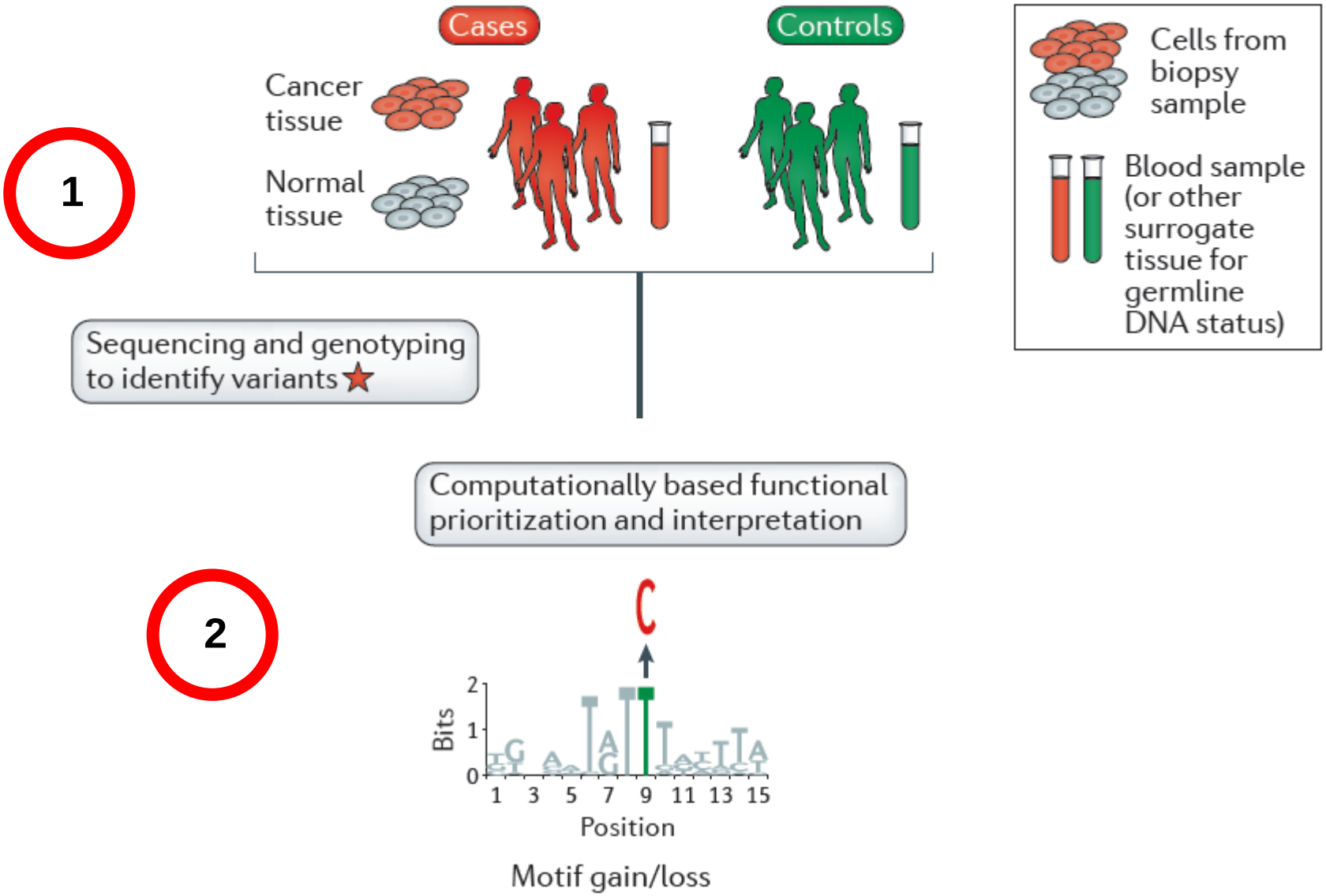
- Correlation between molecular mechanisms and disease symptoms

- Drug Discovery



SNPs with an impact in tumorigenesis

Steps for studying the role of SNP



Genome-wide association studies (GWAS) have capitalized on the millions of common single nucleotide polymorphisms (SNPs) to identify those SNPs that are genome-wide significantly associated with a disease or trait.

Framework for interpretation of individual disease-associated variants

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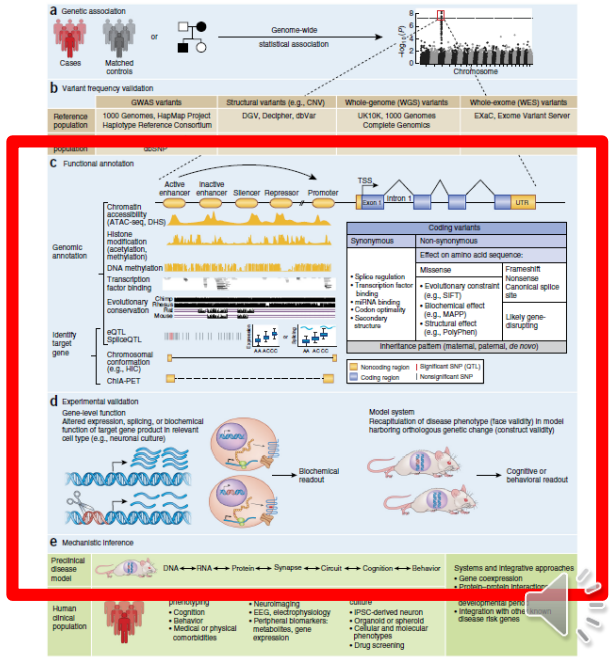
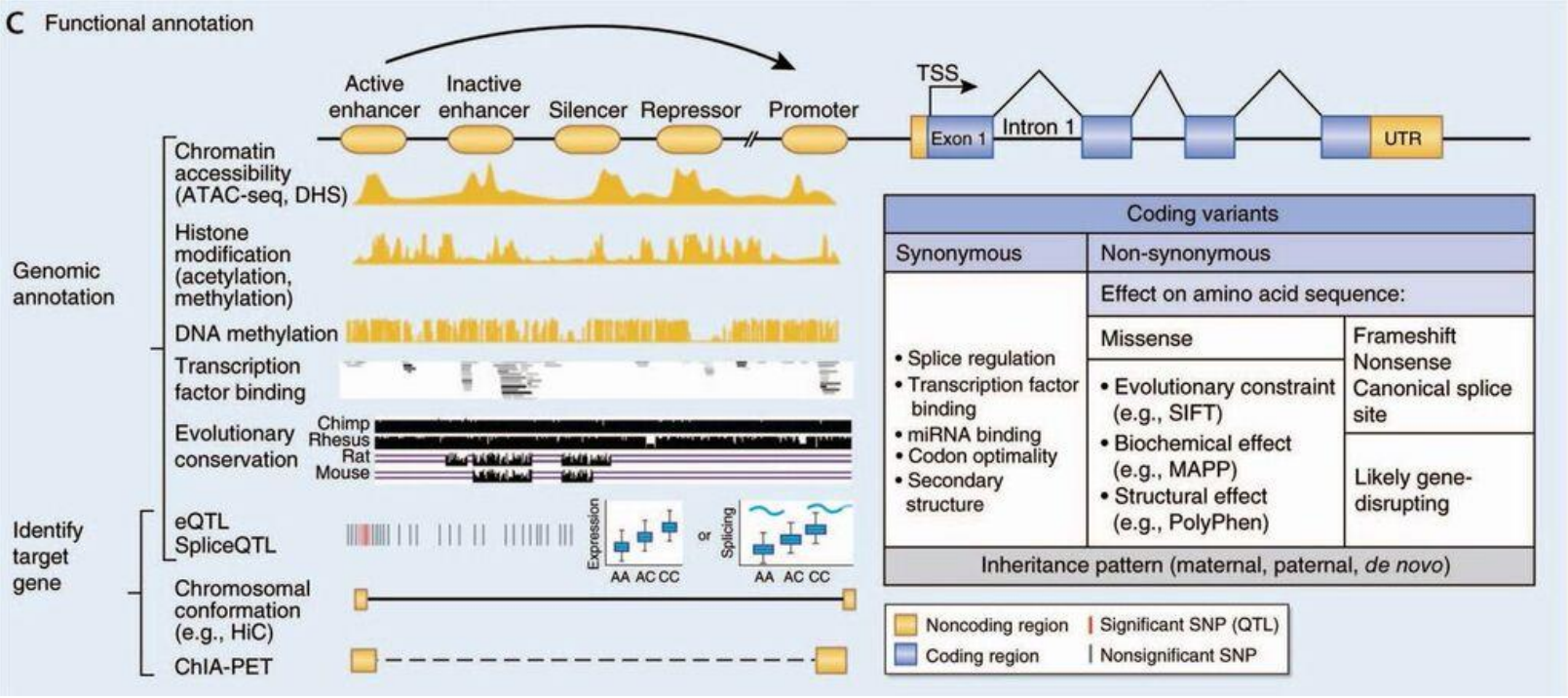


Functional Genomics

Functional genomics is a branch that integrates molecular biology and cell biology studies, and deals with the whole structure, function and regulation of a gene in contrast to the gene-by-gene approach of classical molecular biology technique.

From: Encyclopedia of Bioinformatics and Computational Biology, 2019



GENE REGULATION
How we can understand gene regulation
Using genome-wide sequencing data

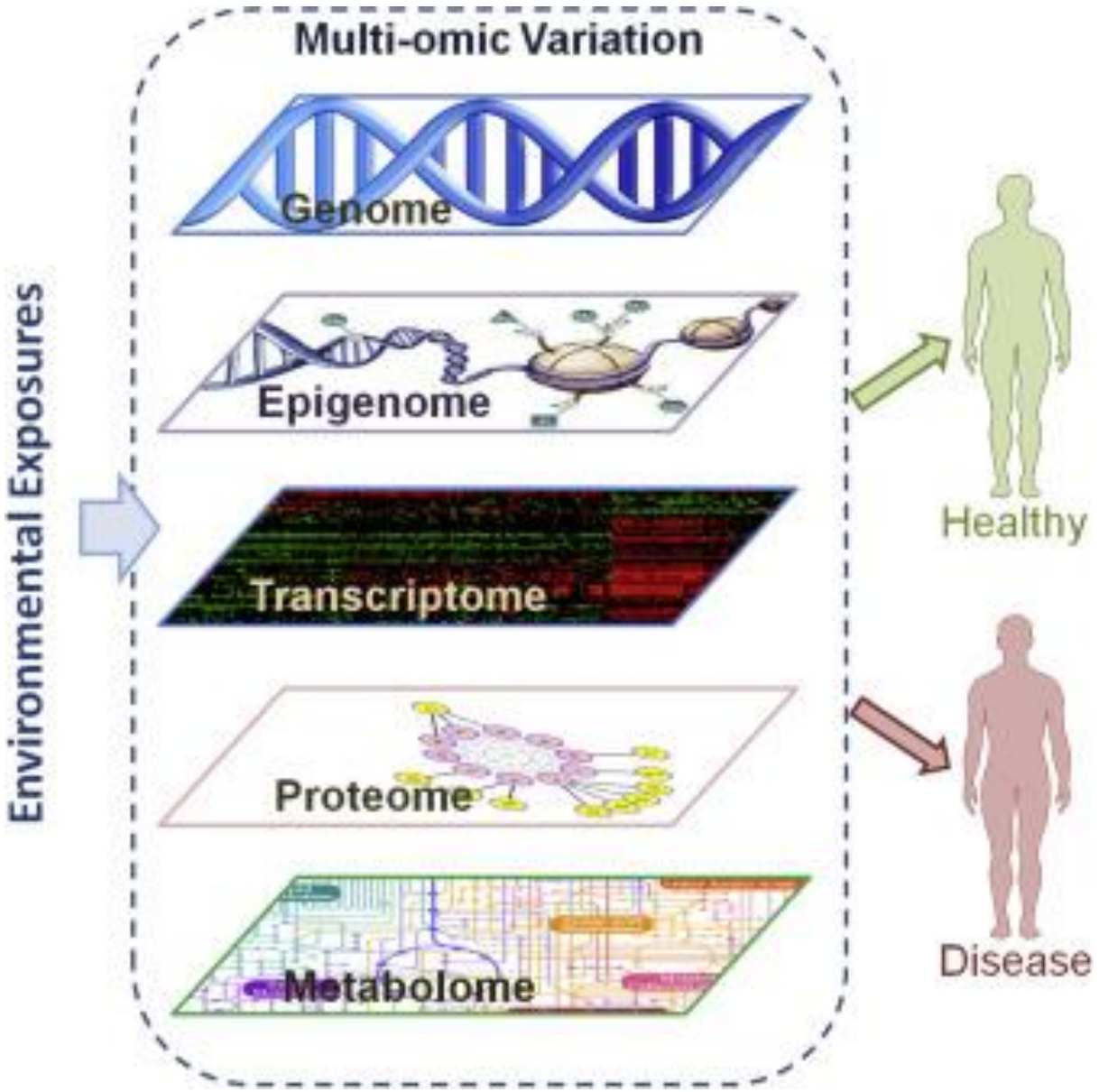
- **INTEGRATION DATA APPROACH**

Integrative omics for health and disease

Konrad J. Karczewski[1,2] and Michael P. Snyder[3]

Abstract | Advances in omics technologies — such as genomics, transcriptomics, proteomics and metabolomics — have begun to enable personalized medicine at an extraordinarily detailed molecular level. Individually, these technologies have contributed medical advances that have begun to enter clinical practice. However, each technology individually cannot capture the entire biological complexity of most human diseases. Integration of multiple technologies has emerged as an approach to provide a more comprehensive view of biology and disease. In this Review, we discuss the potential for combining diverse types of data and the utility of this approach in human health and disease. We provide examples of data integration to understand, diagnose and inform treatment of diseases, including rare and common diseases as well as cancer and transplant biology. Finally, we discuss technical and other challenges to clinical implementation of integrative omics.

Integrative Omics for health and disease



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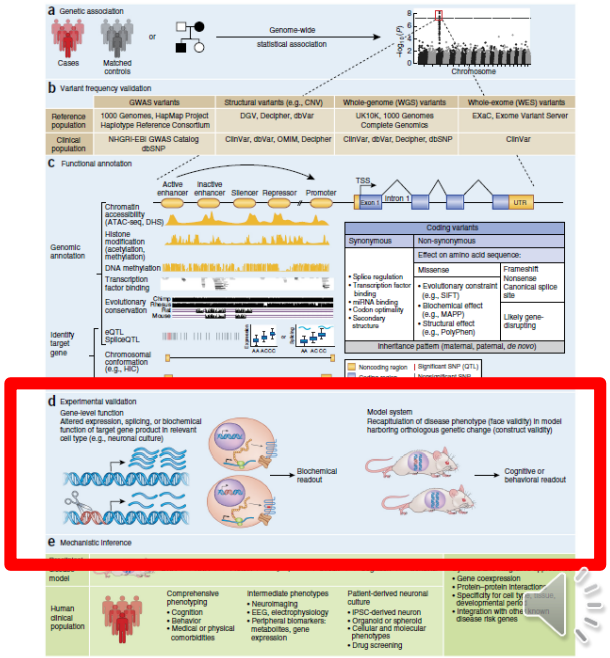
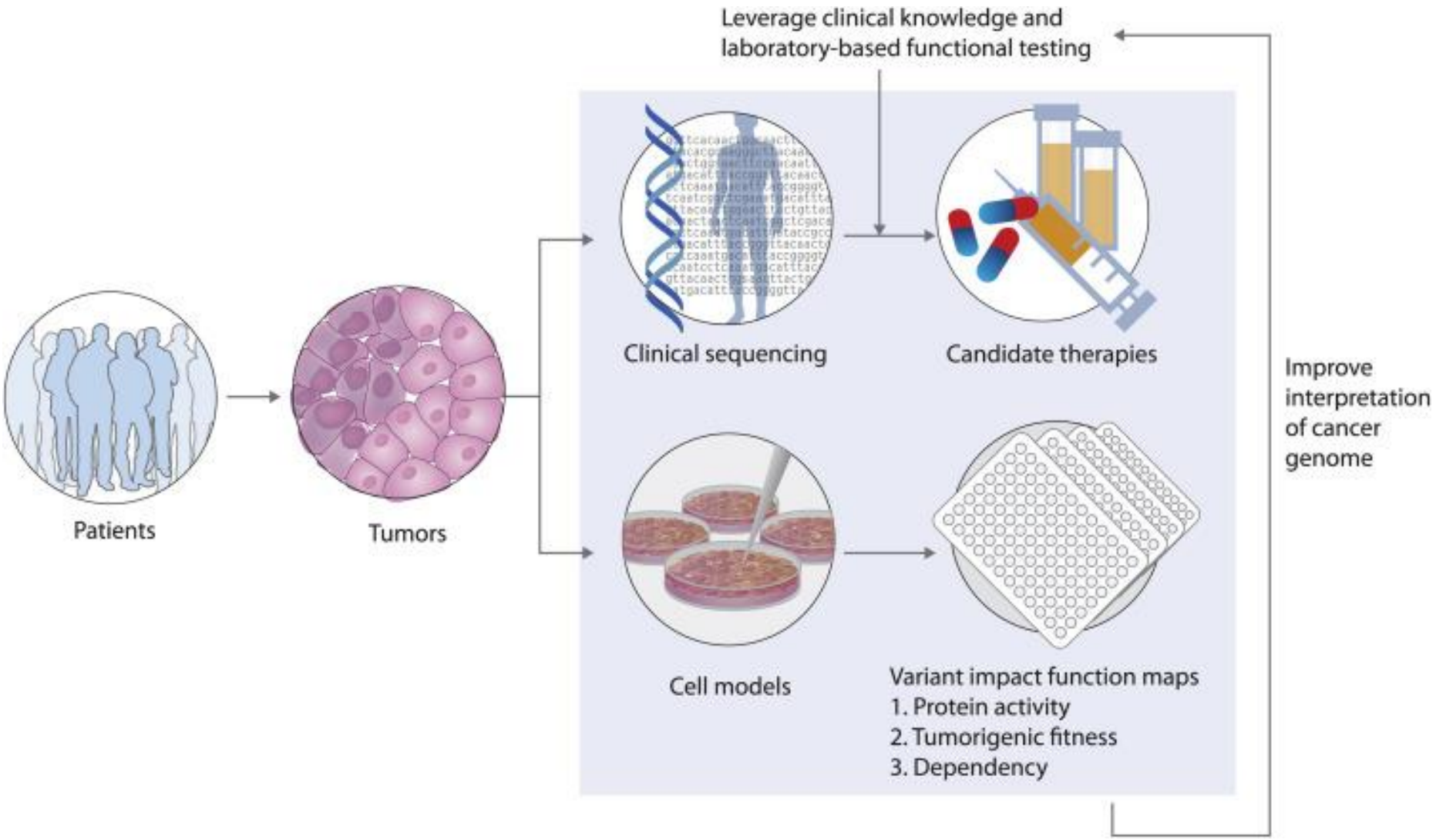
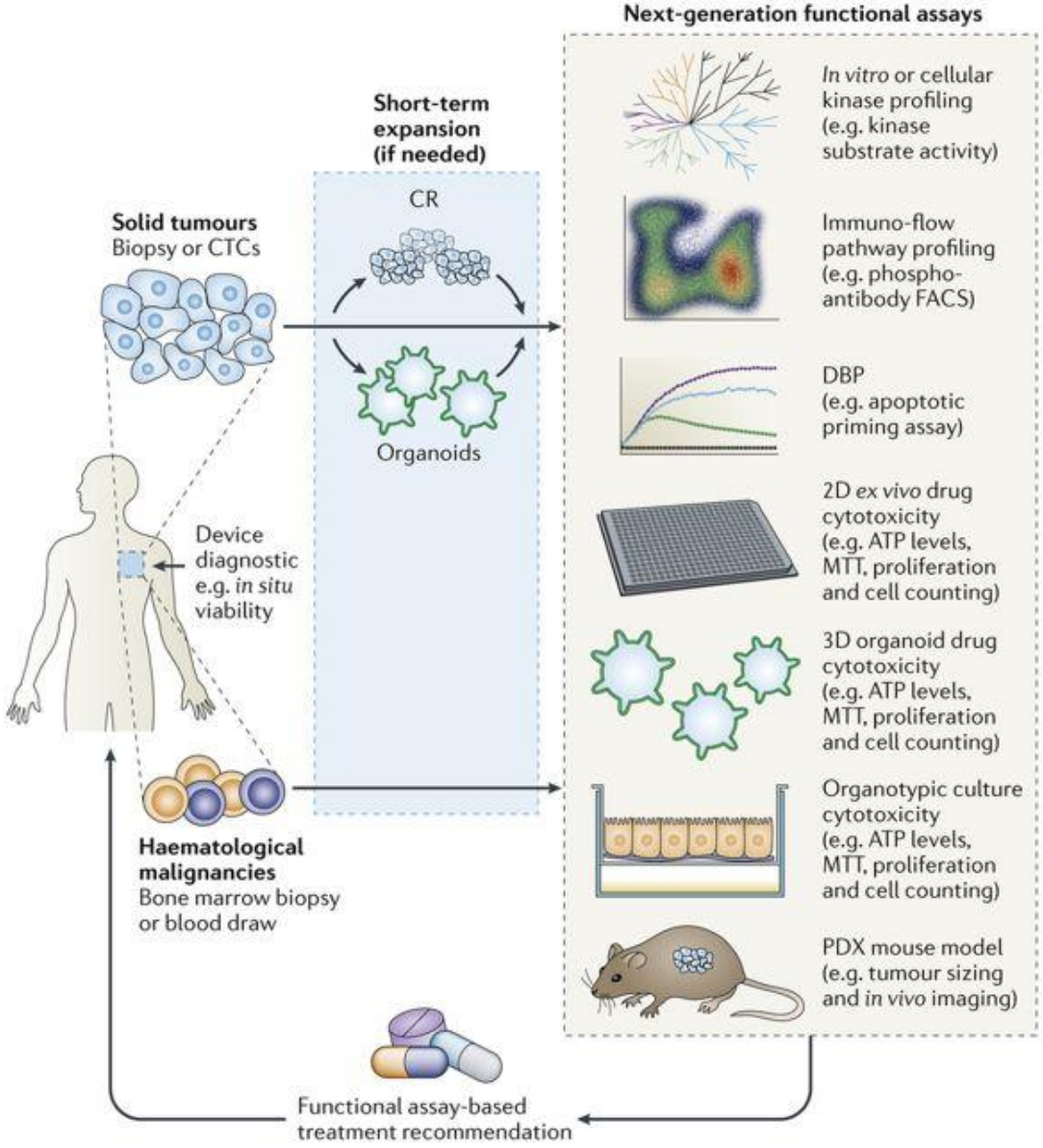


Functional genomics uses genome-wide data with functional tests



Functional genomics uses genome-wide data with functional tests

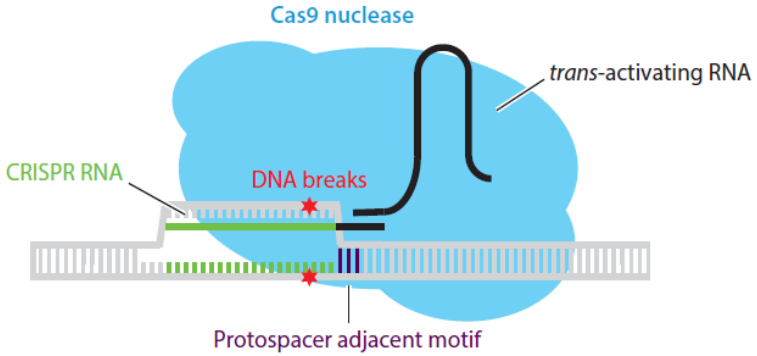


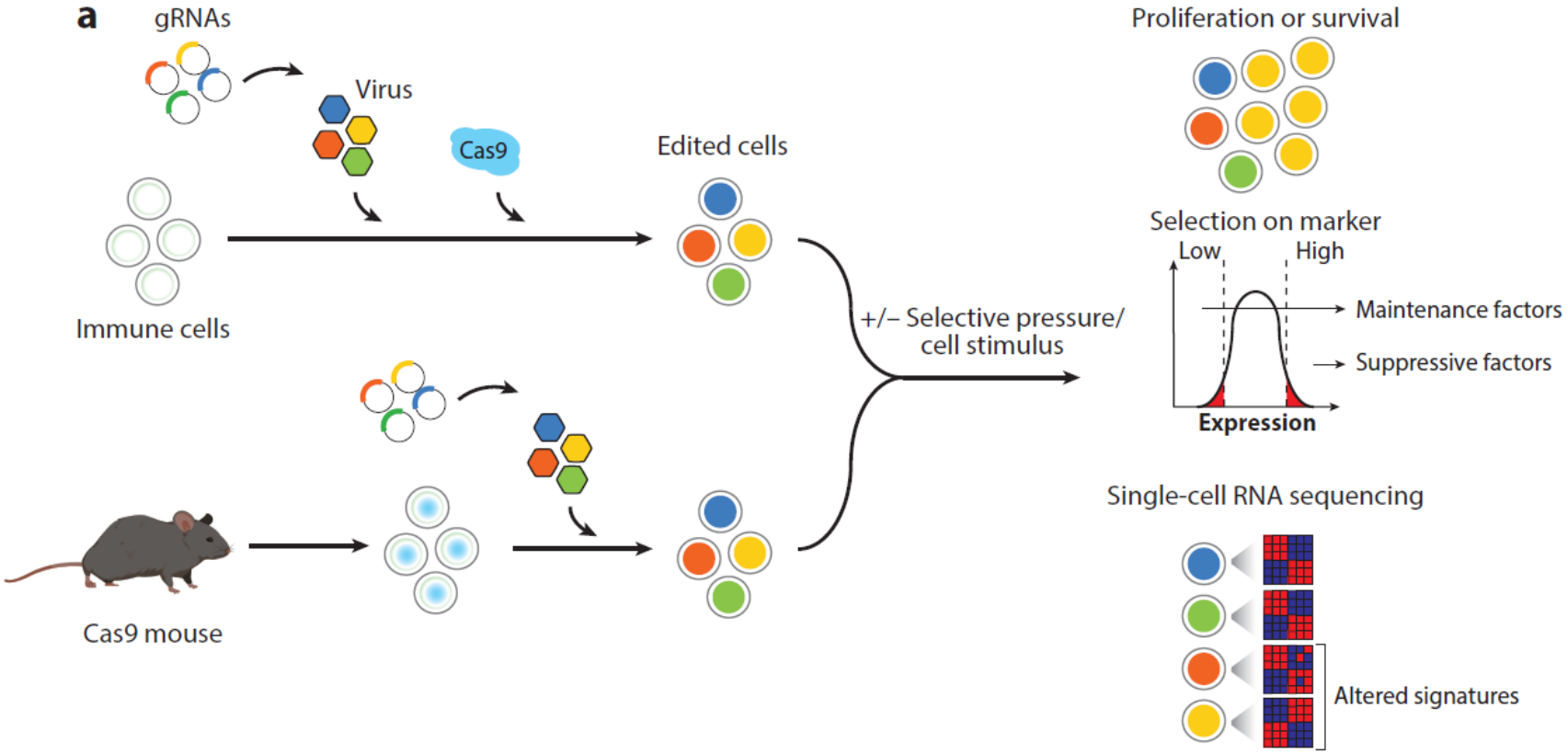
Nature Reviews | Cancer

Annual Review of Immunology

CRISPR-Based Tools in Immunity

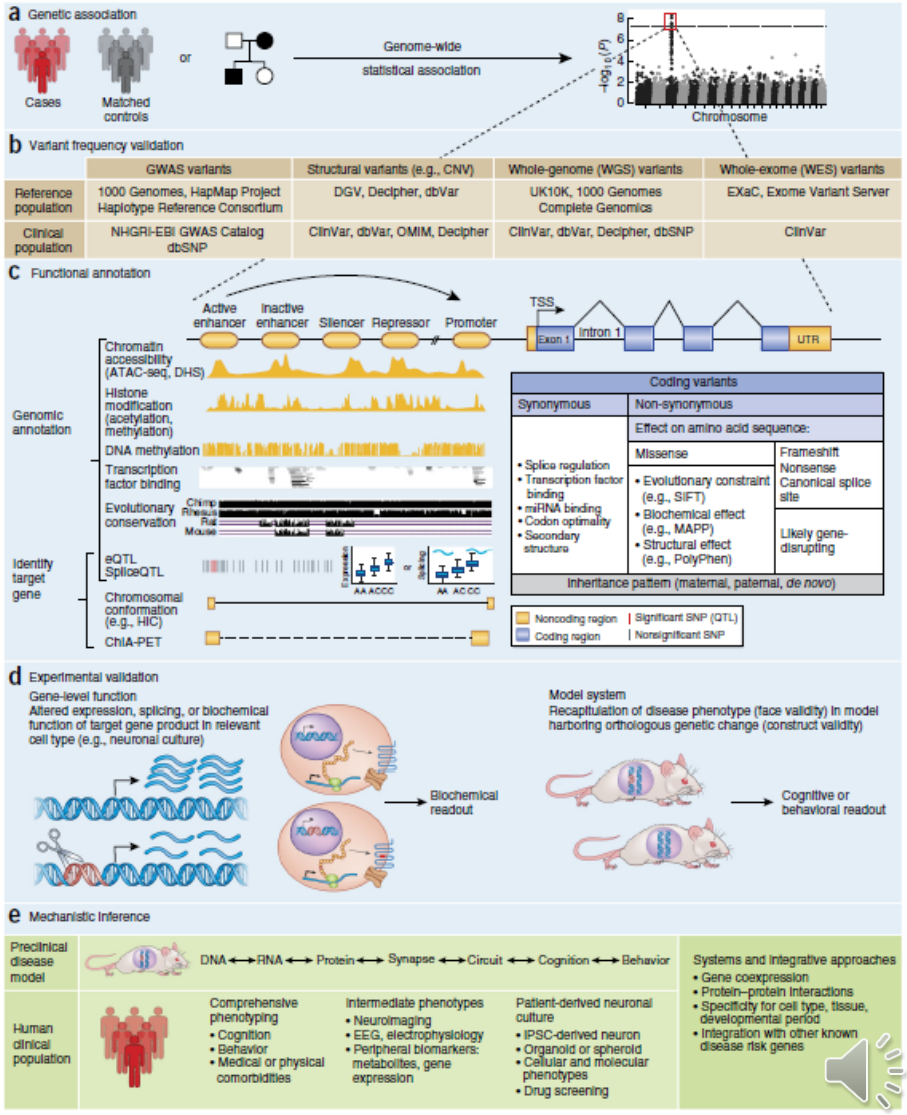
Dimitre R. Simeonov[1,2,3] and Alexander Marson[2,3,4,5,6,7]





Which are the steps to understand the SNPs meaning?

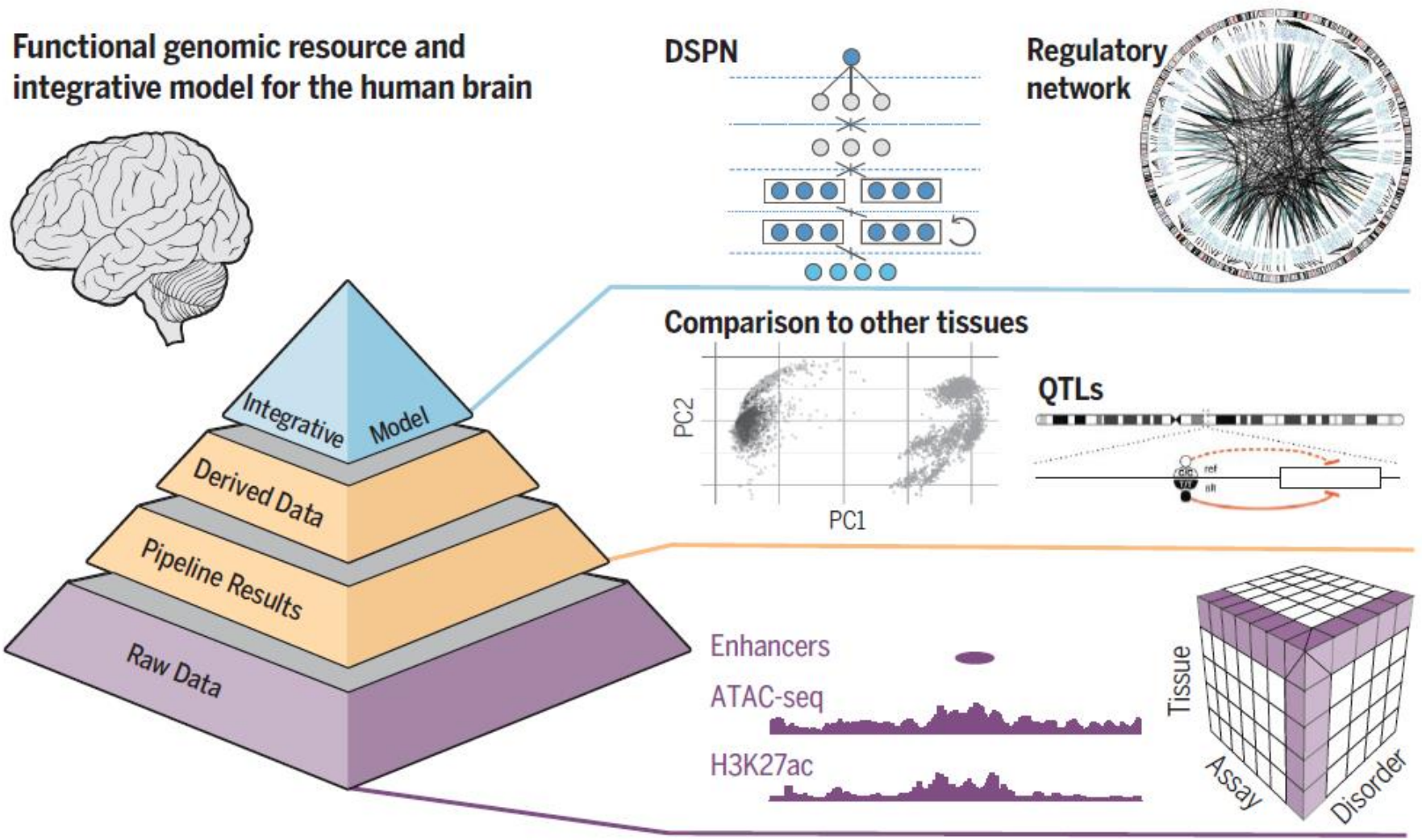
- **Experimental validation**
- **Disease Animal models**
- **Correlation between molecular mechanisms and disease symptoms**
- **Drug Discovery**



PSYCHIATRIC GENOMICS

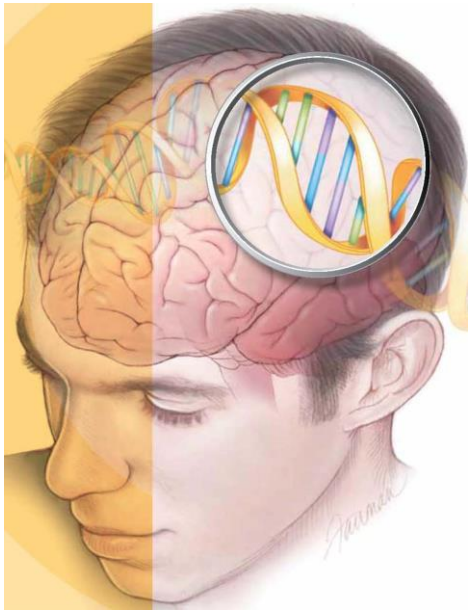
Comprehensive functional genomic resource and integrative model for the human brain

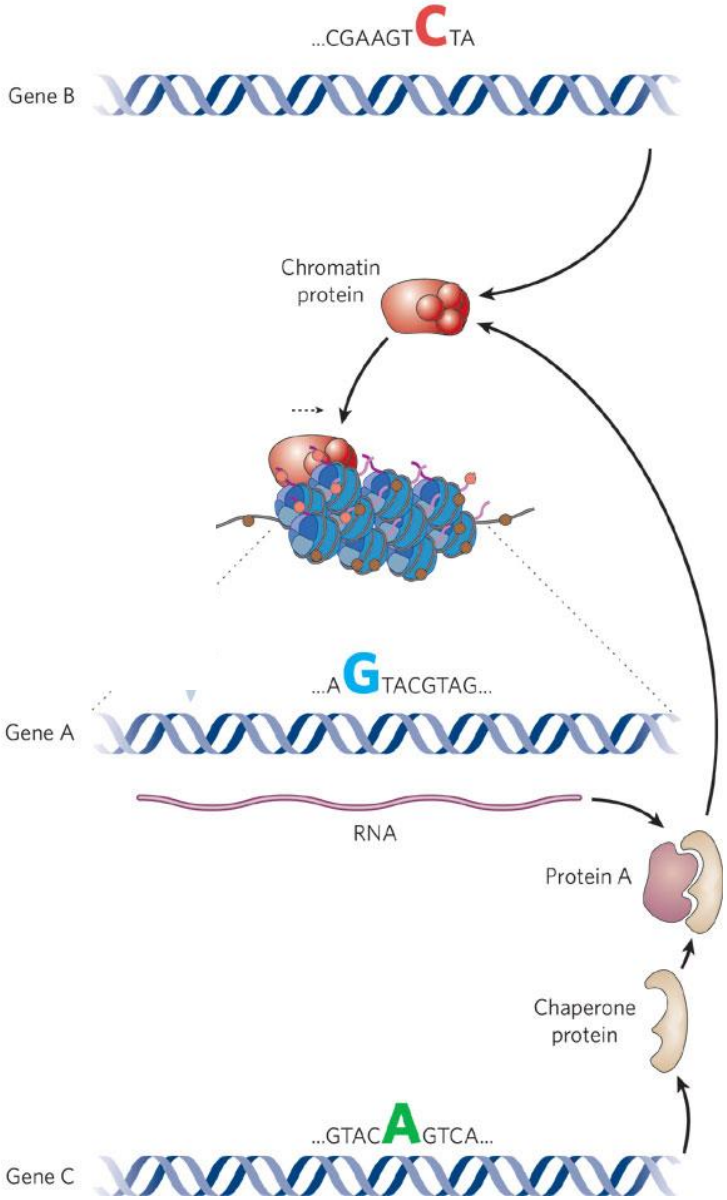
Daifeng Wang*, Shuang Liu*, Jonathan Warrell*, Hyejung Won*, Xu Shi*, Fabio C. P. Navarro*, Declan Clarke*, Mengting Gu*, Prashant Emani*, Yucheng T. Yang, Min Xu, Michael J. Gandal, Shaoke Lou, Jing Zhang, Jonathan J. Park, Chengfei Yan, Suhn Kyong Rhie, Kasidet Manakongtreecheep, Holly Zhou, Aparna Nathan, Mette Peters, Eugenio Mattei, Dominic Fitzgerald, Tonya Brunetti, Jill Moore, Yan Jiang, Kiran Girdhar, Gabriel E. Hoffman, Selim Kalayci, Zeynep H. Gümüş, Gregory E. Crawford, PsychENCODE Consortium†, Panos Roussos, Schahram Akbarian, Andrew E. Jaffe, Kevin P. White, Zhiping Weng, Nenad Sestan, Daniel H. Geschwind‡, James A. Knowles‡, Mark B. Gerstein‡


Functional genomic resource and integrative model for the human brain
Integrative Model
Derived Data
Pipeline Results
Raw Data
DSPN
Regulatory network
Comparison to other tissues
PC2
PC1
QTLs
Enhancers
ATAC-seq
H3K27ac
Tissue
Assay
Disorder

INTRODUCTION: Strong genetic associations have been found for a number of psychiatric disorders. However, understanding the underlying molecular mechanisms remains challenging.

RATIONALE: To address this challenge, the PsychENCODE Consortium has developed a comprehensive online resource and integrative models for the functional genomics of the human brain.





RESULTS: The base of the pyramidal resource is the datasets generated by PsychENCODE, including bulk transcriptome, chromatin, genotype, and Hi-C datasets and single-cell transcriptomic data from ~32,000 cells for major brain regions. We have merged these with data from Genotype-Tissue Expression (GTEx), ENCODE, Roadmap Epigenomics, and single-cell analyses. Via uniform processing, we created a harmonized resource, allowing us to survey functional genomics data on the brain over a sample size of 1866 individuals.

1. New genome-wide data

2. Comparison of New genome-wide data with data derived from several databases

From this uniformly processed dataset, we created derived data products. These include lists of brain-expressed genes, coexpression modules, and single-cell expression profiles for many brain cell types; ~79,000 brain-active enhancers with associated Hi-C loops and topologically associating domains; and ~2.5 million expression quantitative-trait loci (QTLs) comprising ~238,000 linkage-disequilibrium–independent single-nucleotide polymorphisms and of other types of QTLs associated with splice isoforms, cell fractions, and chromatin activity. By using these, we found that >88% of the cross-population variation in brain gene expression can be accounted for by cell fraction changes. Furthermore, a number of disorders and aging are associated with changes in cell-type proportions. The derived data also enable comparison between the brain and other tissues. In particular, by using spectral analyses, we found that the brain has distinct expression and epigenetic patterns, including a greater extent of noncoding transcription than other tissues.

ON OUR WEBSITE

Read the full article at http://dx.doi.org/10.1126/science.aat8464

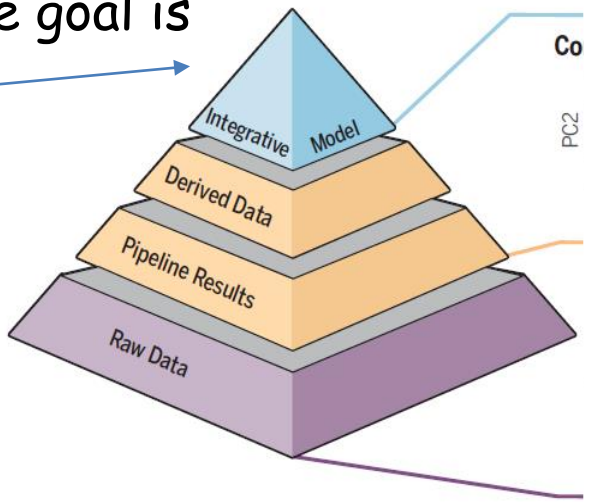
3. Interpretation of data

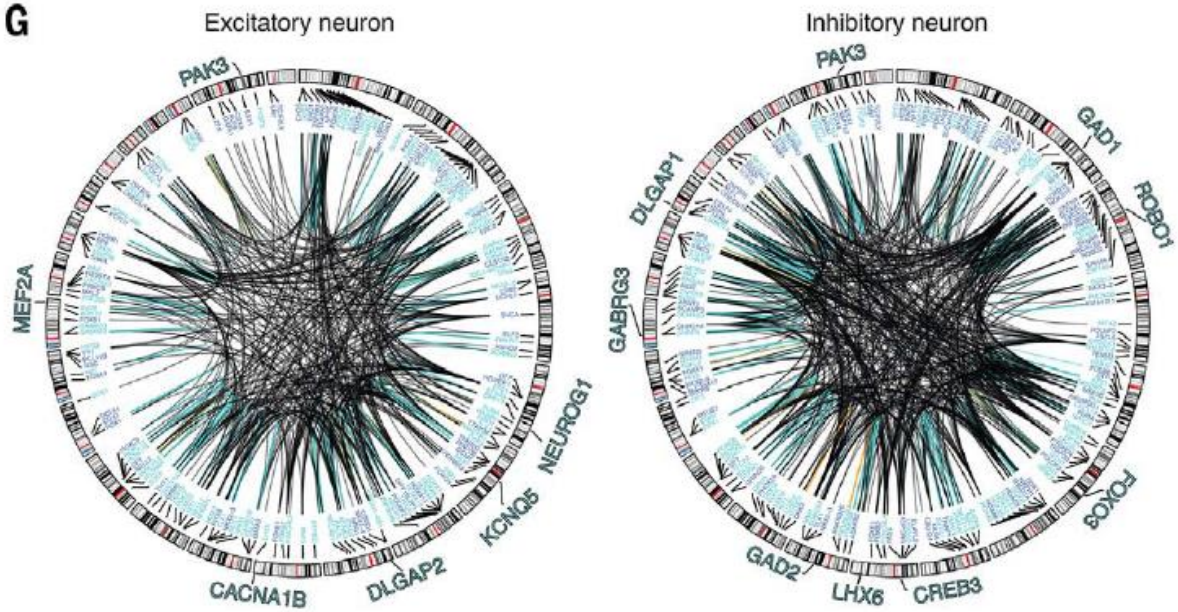
4. Gene expression profile is specific for a group of cells as shown by Single Cell-RNA-Seq

5. Identification of SNPs with specific functions

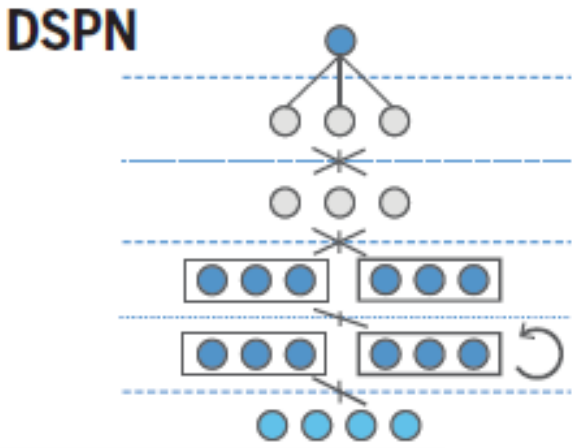
The top level of the resource consists of integrative networks for regulation and machine-learning models for disease prediction. The networks include a full gene regulatory network (GRN) for the brain, linking transcription factors, enhancers, and target genes from merging of the QTLs, generalized element-activity correlations, and Hi-C data. By using this network, we link disease genes to genome-wide association study (GWAS) variants for psychiatric disorders. For schizophrenia, we linked 321 genes to the 142 reported GWAS loci. We

The goal is



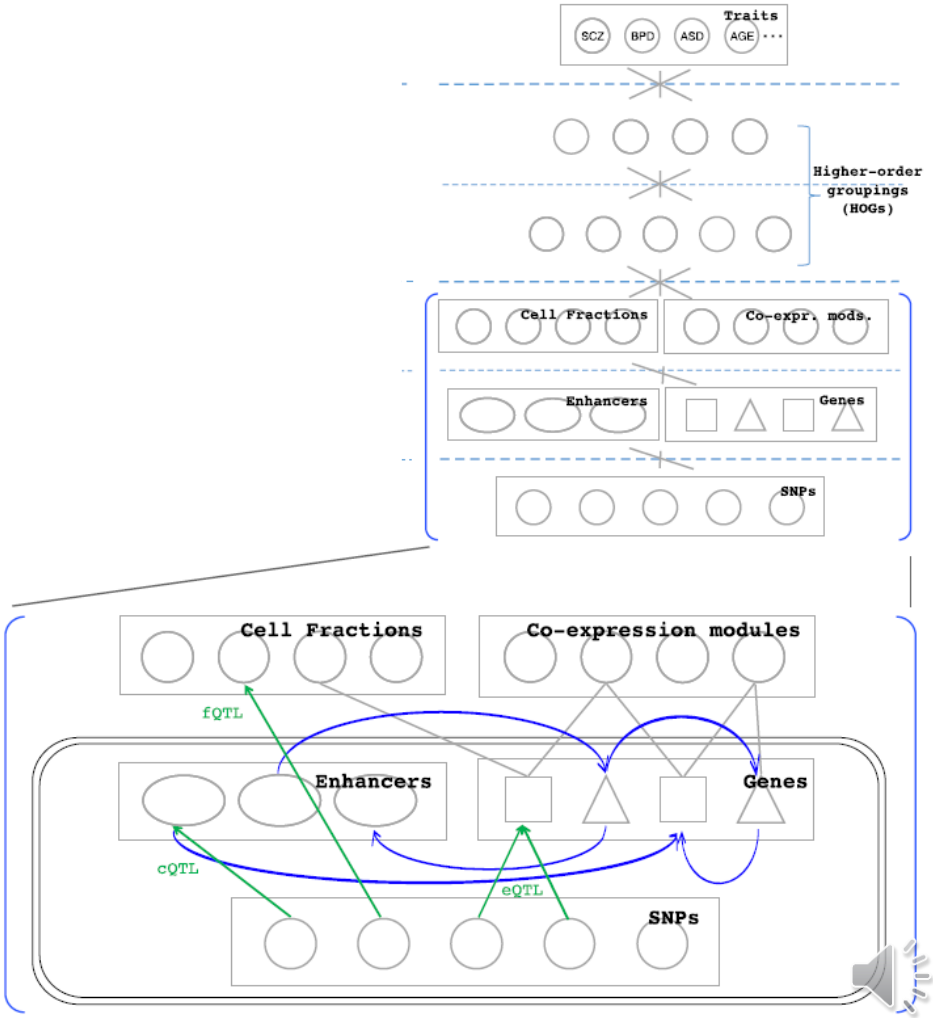


321 genes to the 142 reported GWAS loci. We then embedded the regulatory network into a deep-learning model to predict psychiatric phenotypes from genotype and expression. Our model gives a ~6-fold improvement in prediction over additive polygenic risk scores. Moreover, it achieves a ~3-fold improvement over additive models, even when the gene expression data are imputed, highlighting the value of having just a small amount of transcriptome data for disease prediction. Lastly, it highlights key genes and pathways associated with disorder prediction, including immunological, synaptic, and metabolic pathways, recapitulating de novo results from more targeted analyses.



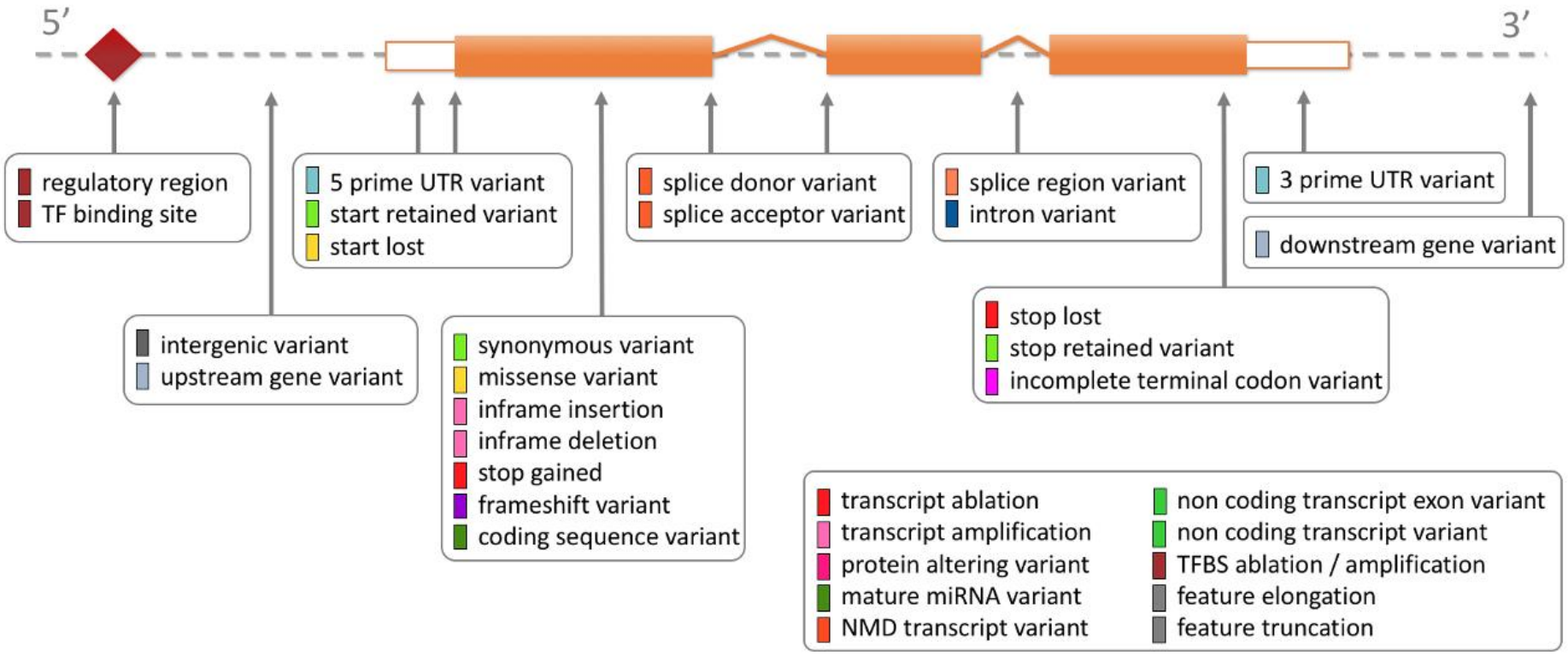
How integrative analysis is done?

- Gene regulatory network
- **Deep-learning model**



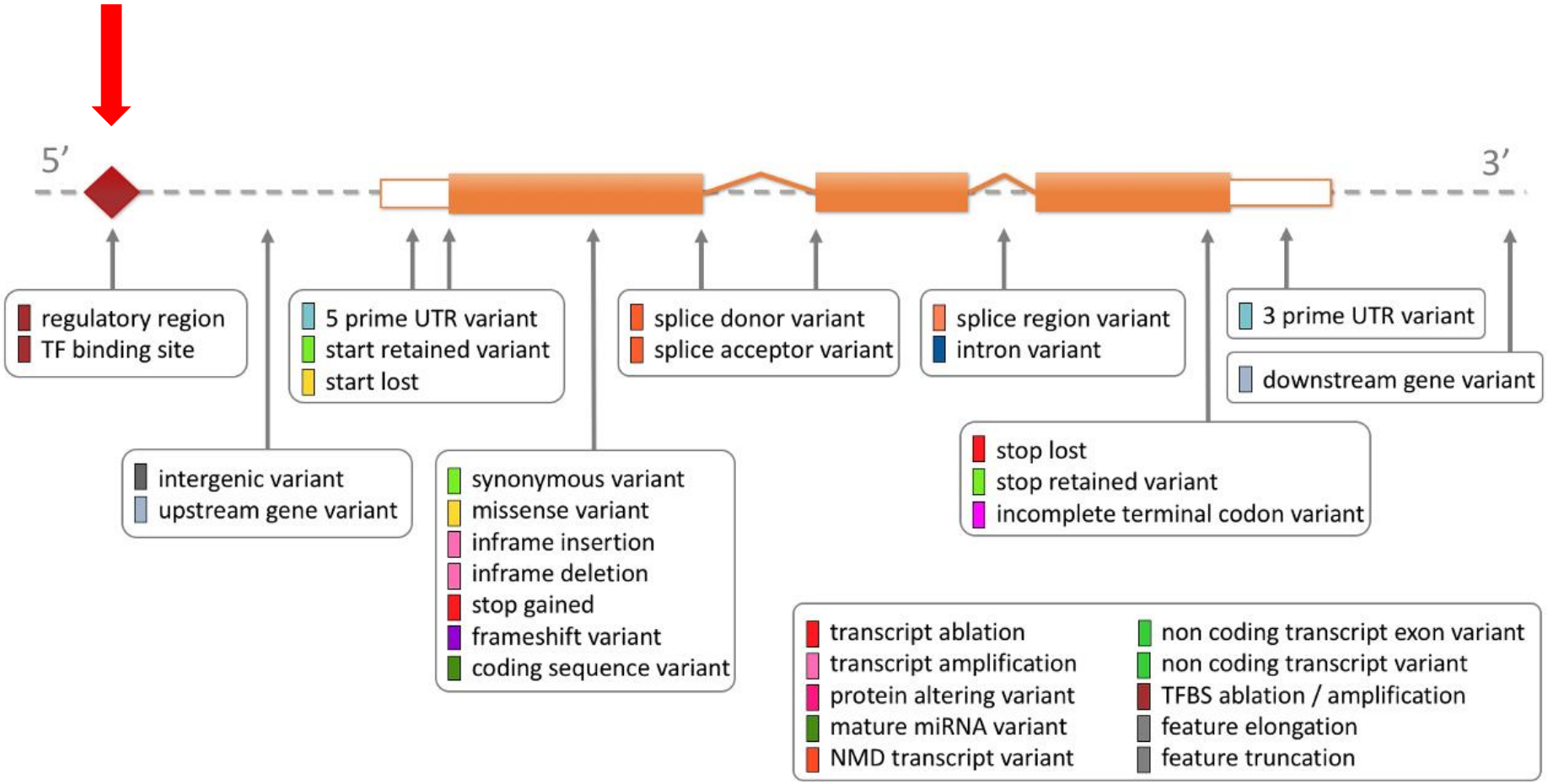
Task 2- What is the impact of single nucleotide variants

CLASSIFICATION OF SINGLE NUCLEOTIDE VARIANTS



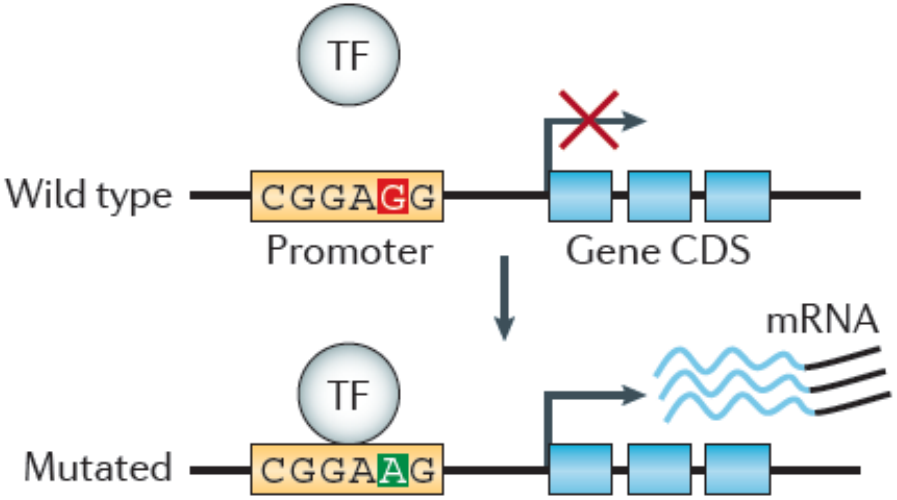
https://m.ensembl.org/info/genome/variation/prediction/predicted_data.html

Role of single nucleotide variants in the genomic regulatory regions

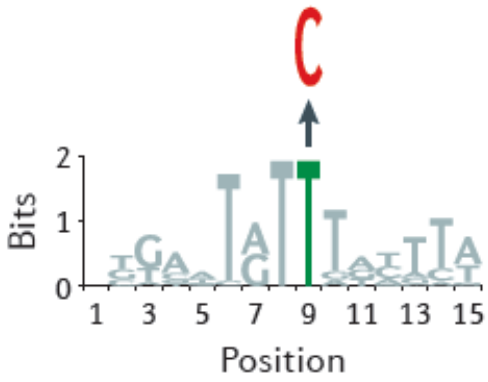


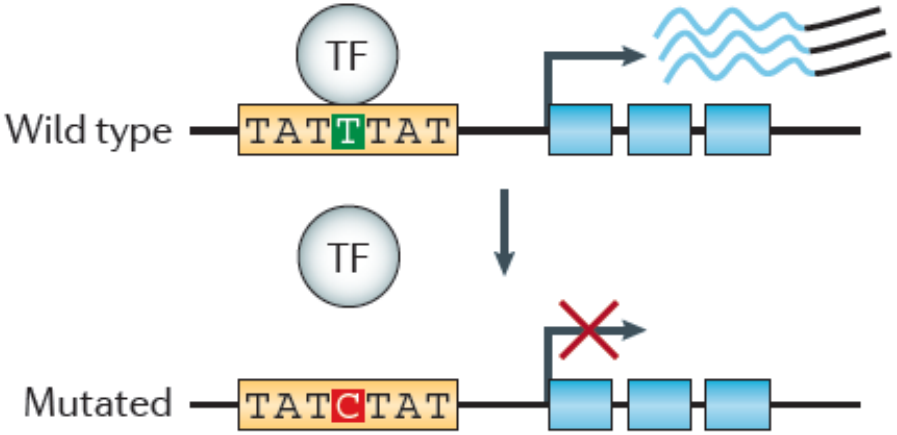
SNPs types functions at trascription factor binding sites:

Ba Gain of motif

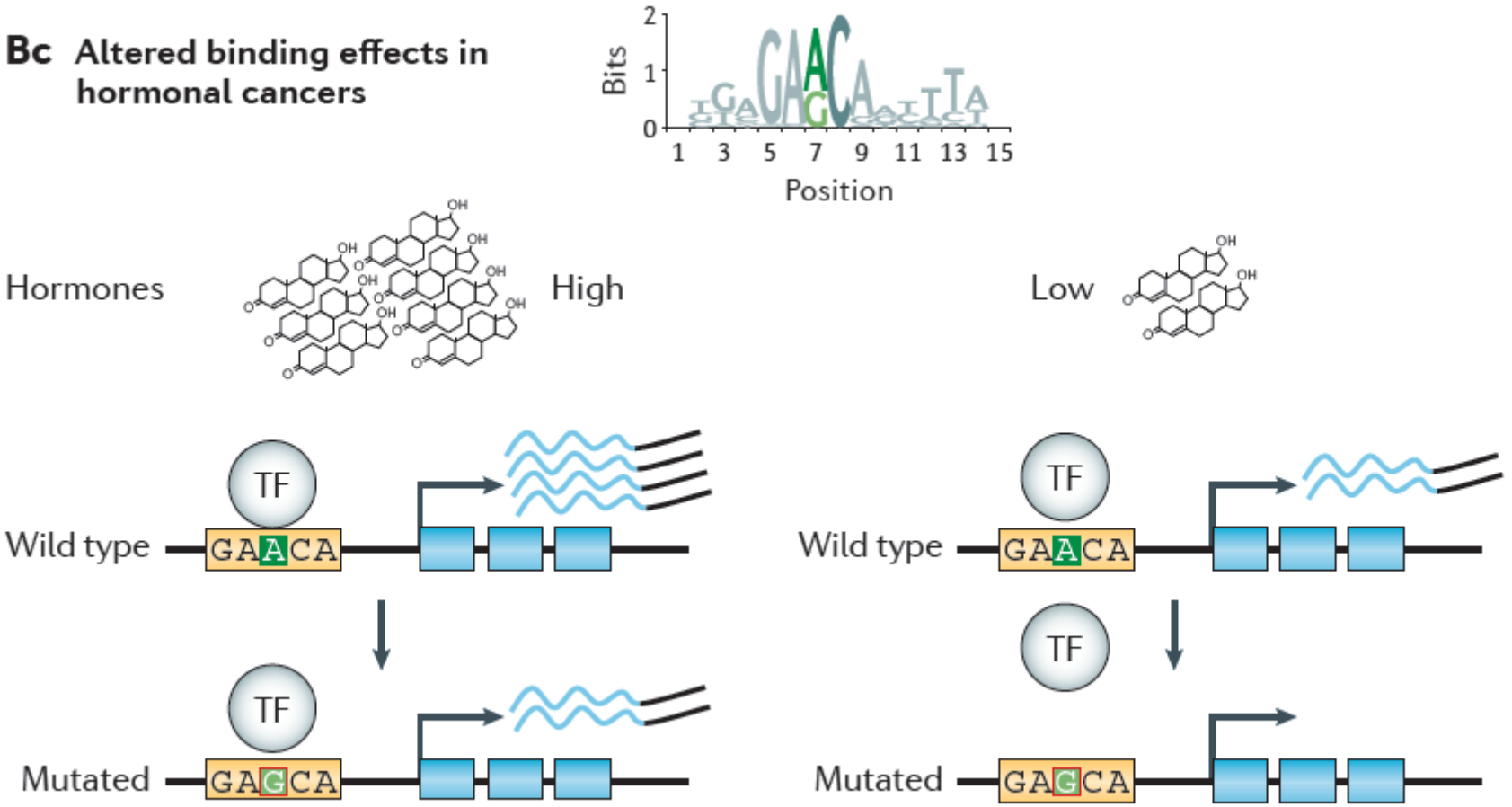


Bb Loss of motif

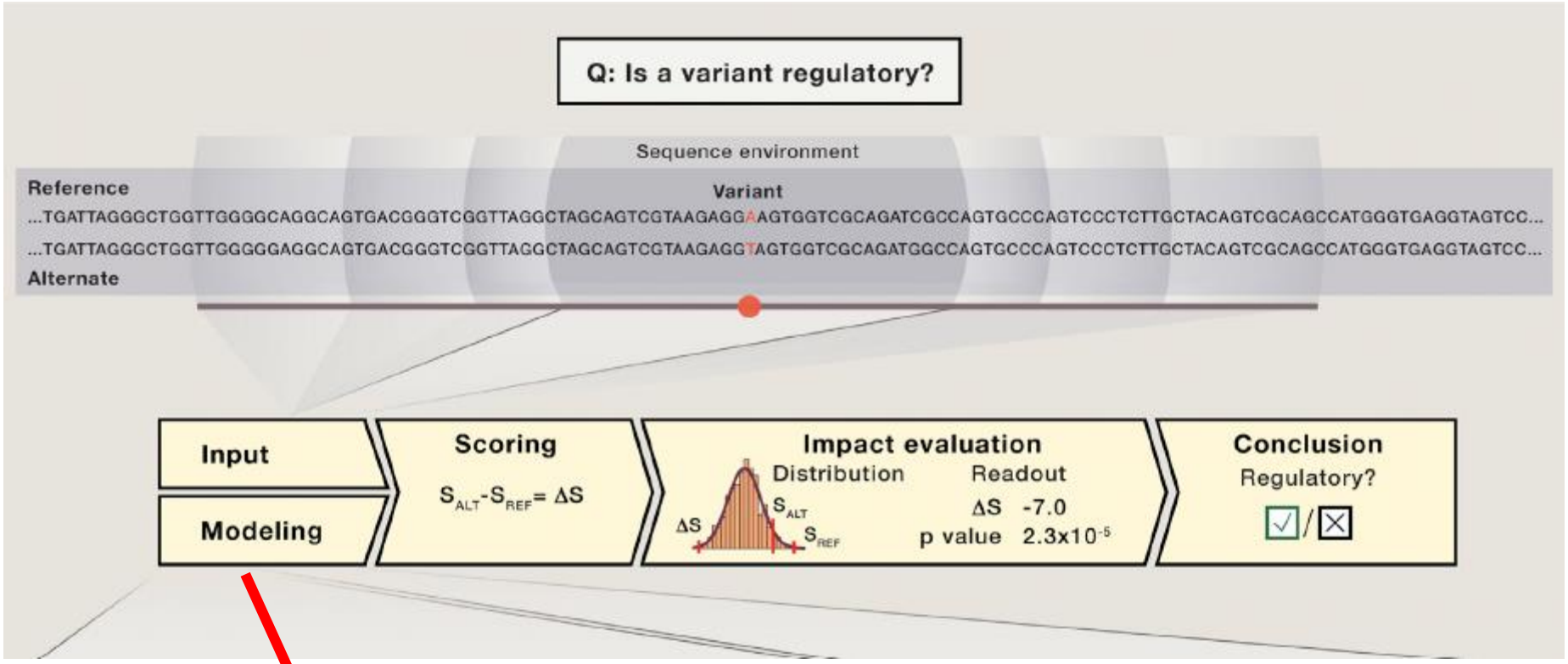


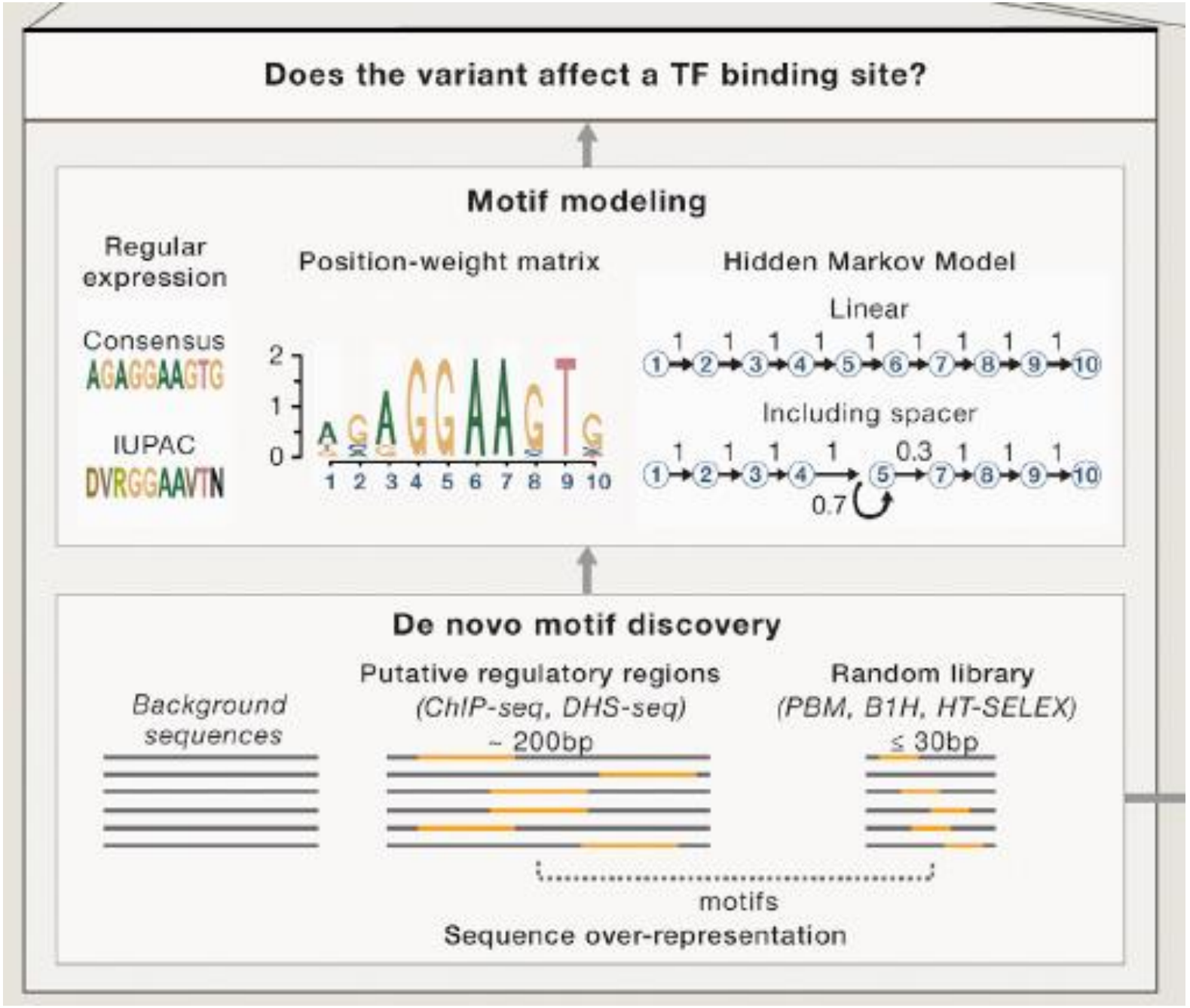


SNPs types functions on hormone responce:

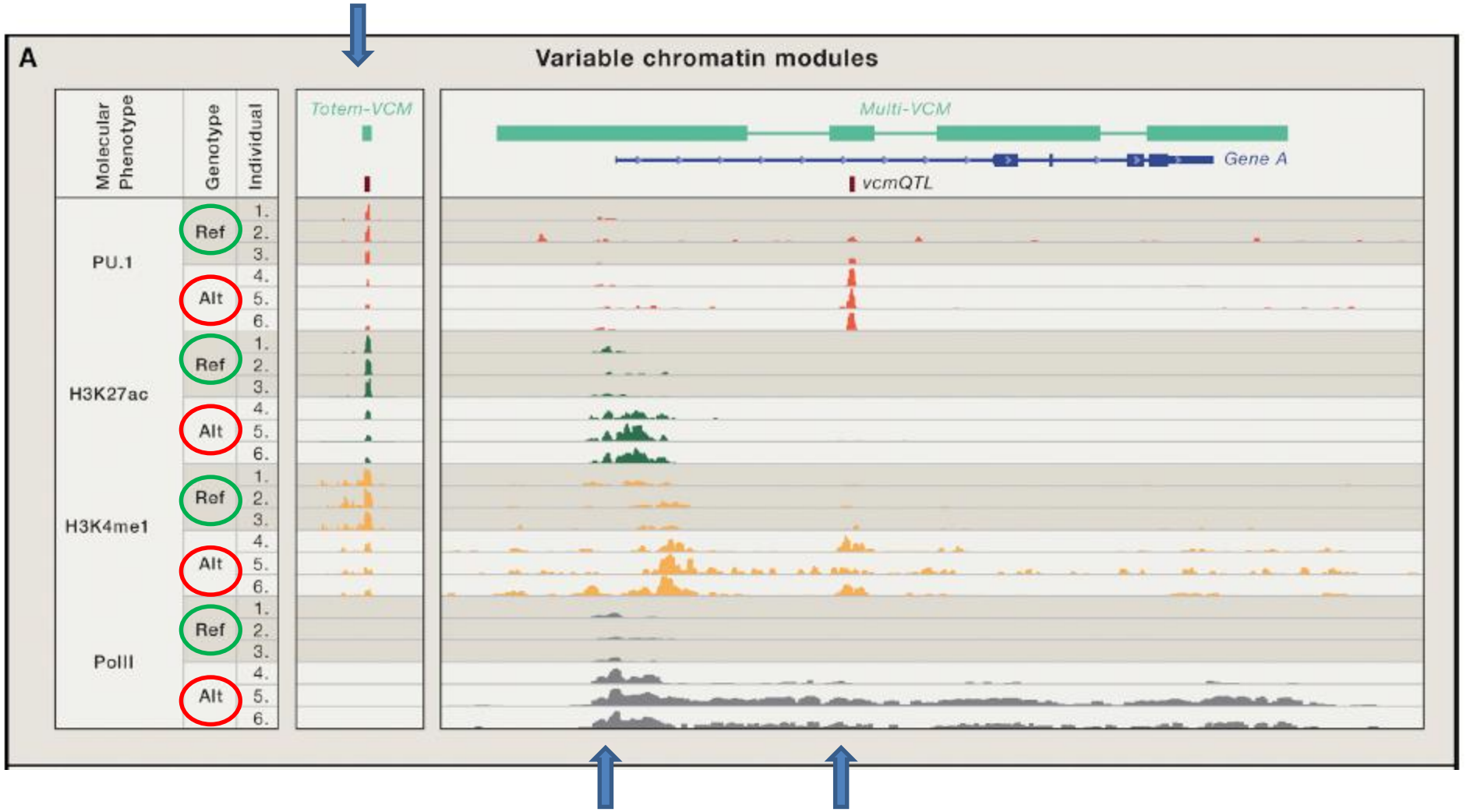


SNPs in the genomic regulatory regions DEFINITION



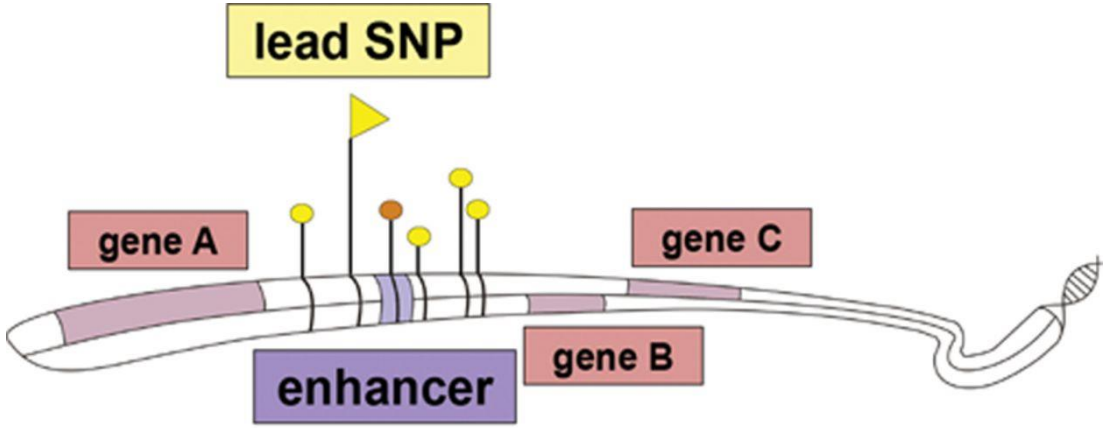

Does the variant affect a TF binding site?
Motif modeling
Regular expression
Consensus
AGAGGAAGTG
IUPAC
DVRGGAAVTN
Position-weight matrix
2
1
0
1 2 3 4 5 6 7 8 9 10
Hidden Markov Model
Linear
1 1 1 1 1 1 1 1 1 1
1 2 3 4 5 6 7 8 9 10
Including spacer
1 1 1 1 0.3 1 1 1
1 2 3 4 5 7 8 9 10
0.7
De novo motif discovery
Background sequences
Putative regulatory regions
(ChIP-seq, DHS-seq)
~ 200bp
Random library
(PBM, B1H, HT-SELEX)
≤ 30bp
motifs
Sequence over-representation

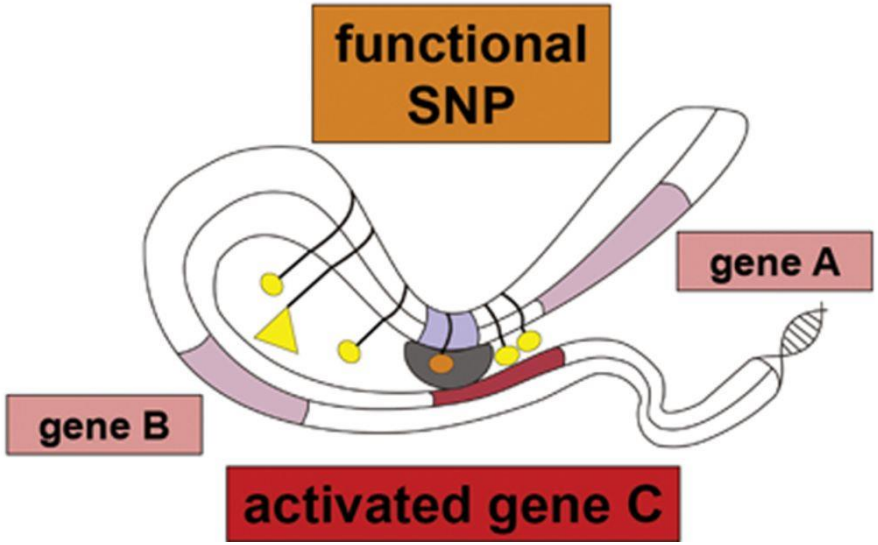
SNPs in the genomic regions may alter a binding site of a specific TFs, such as PU.1 and chromatin states change in the same region



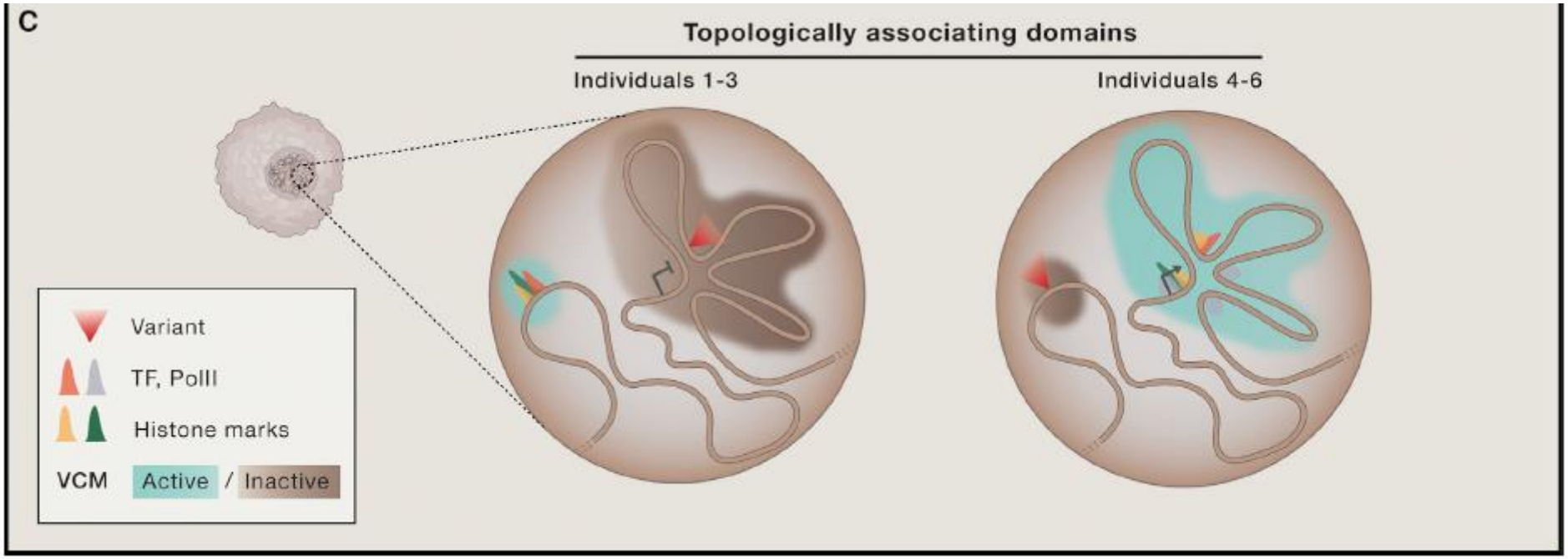
SNPs in the genomic regions may alter a binding site of a specific TFs, such as PU.1 while chromatin states change a whidespread regio

Single nucleotide variants in genomic regulatory regions



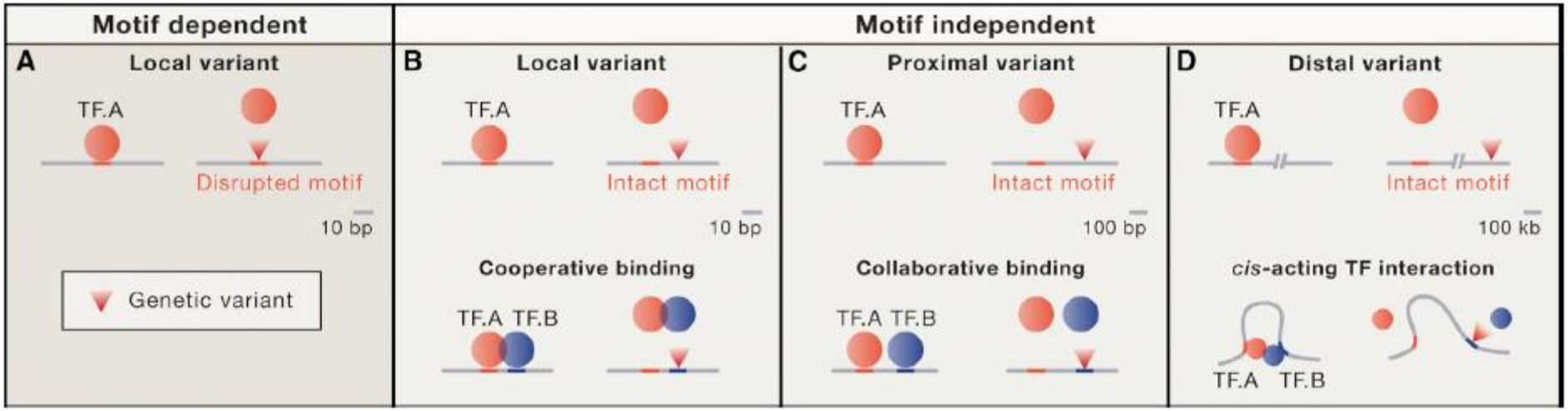


SNPs may change long range interactions



Deplancke et al., 2016

SNPs mechanims for alteration of regulatory transcrption factors complexes



Deplancke et al., 2016

SNPs roles in the genomic regulatory regions are:

- Changing the transcription factor binding site
- Disrupting long range interaction
- Inhibition of interaction between transcription factors
- Changing epigenetic modifications

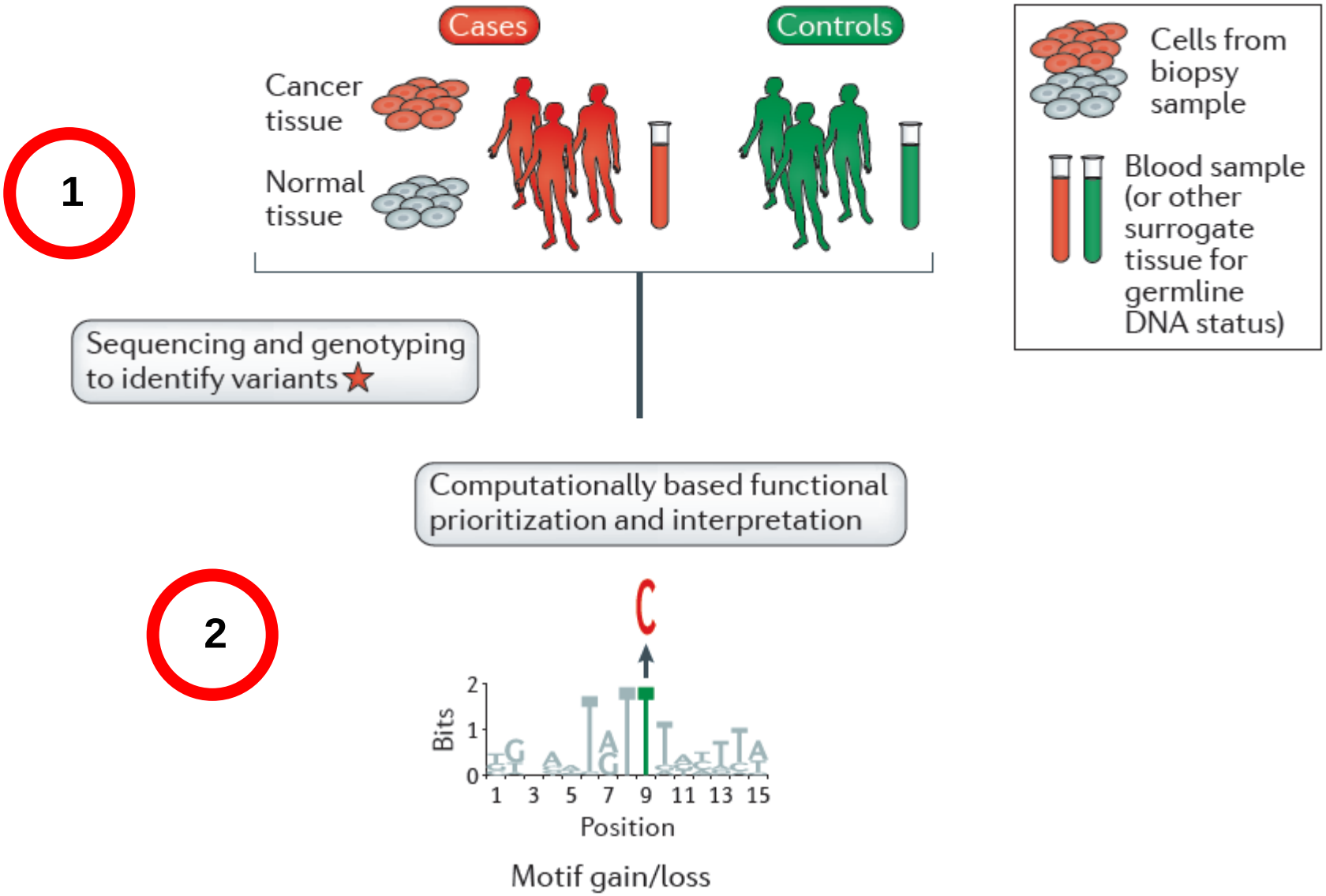
Role of non-coding sequence variants in cancer

Ekta Khurana[1–4], Yao Fu[5], Dimple Chakravarty[2,6], Francesca Demichelis[2,3,7], Mark A. Rubin[1,2,6] and Mark Gerstein[8–10]

Abstract | Patients with cancer carry somatic sequence variants in their tumour in addition to the germline variants in their inherited genome. Although variants in protein-coding regions have received the most attention, numerous studies have noted the importance of non-coding variants in cancer. Moreover, the overwhelming majority of variants, both somatic and germline, occur in non-coding portions of the genome. We review the current understanding of non-coding variants in cancer, including the great diversity of the mutation types — from single nucleotide variants to large genomic rearrangements — and the wide range of mechanisms by which they affect gene expression to promote tumorigenesis, such as disrupting transcription factor-binding sites or functions of non-coding RNAs. We highlight specific case studies of somatic and germline variants, and discuss how non-coding variants can be interpreted on a large-scale through computational and experimental methods.

SNPs with an impact in tumorigenesis

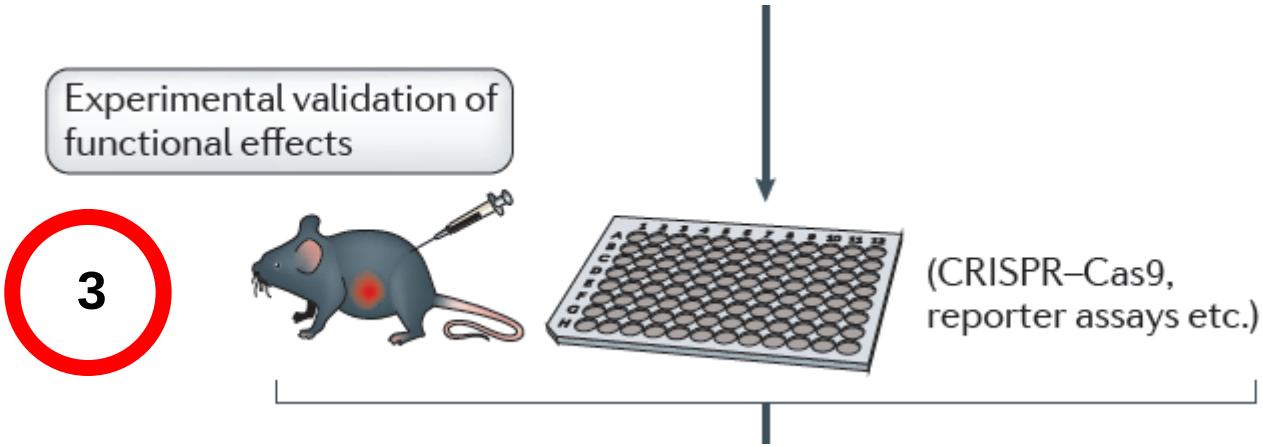
Steps for studying the role of SNP



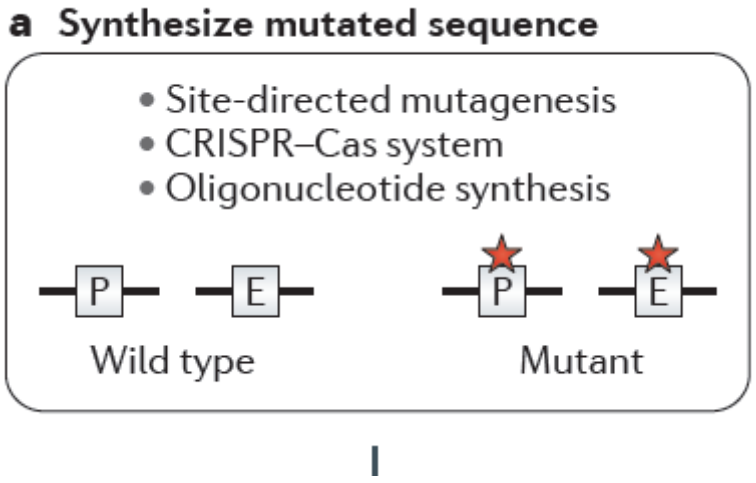
SNPs may have an impact in tumorigenesis

2

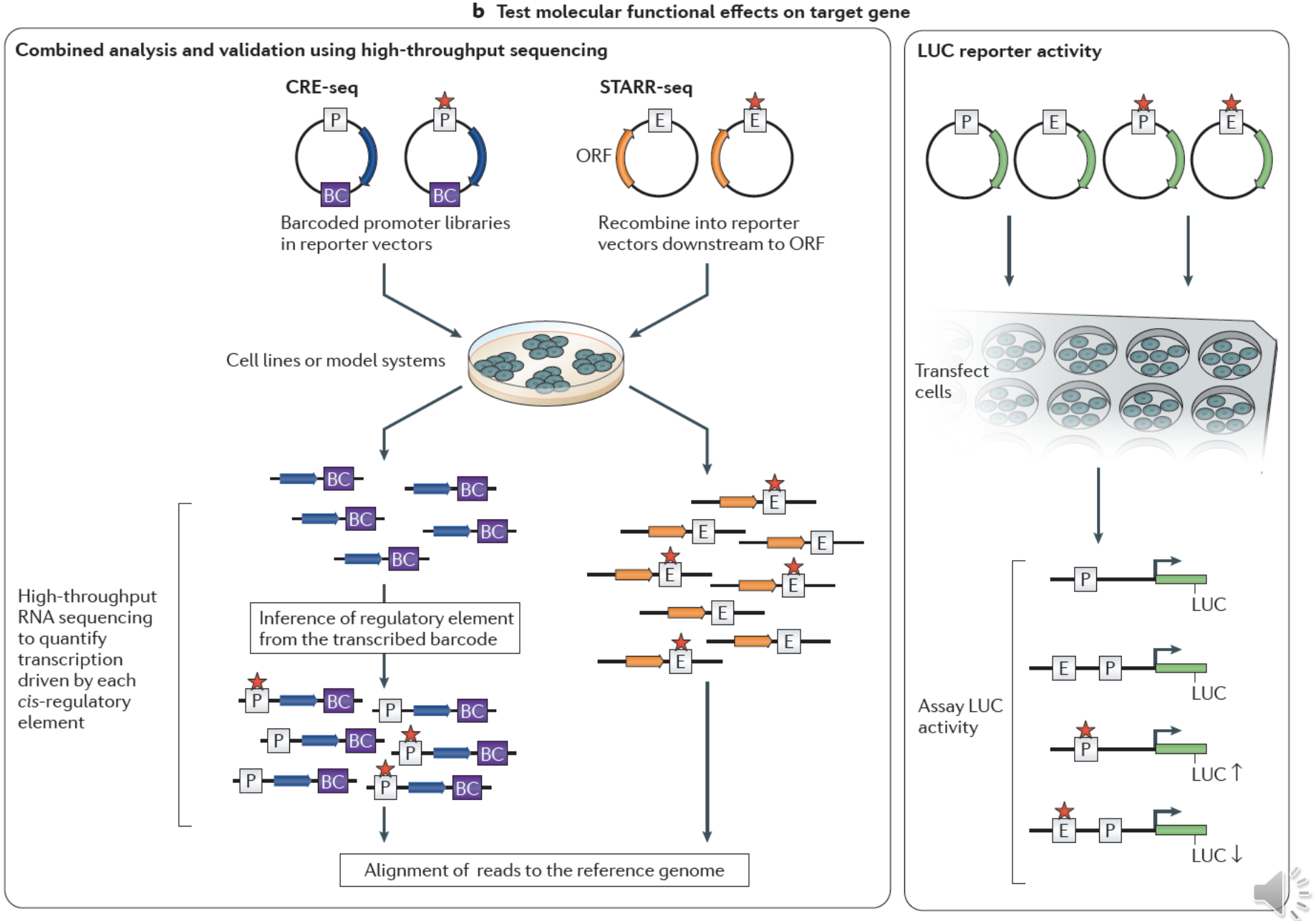
FUNCTIONAL ANNOTATION OF SNPs



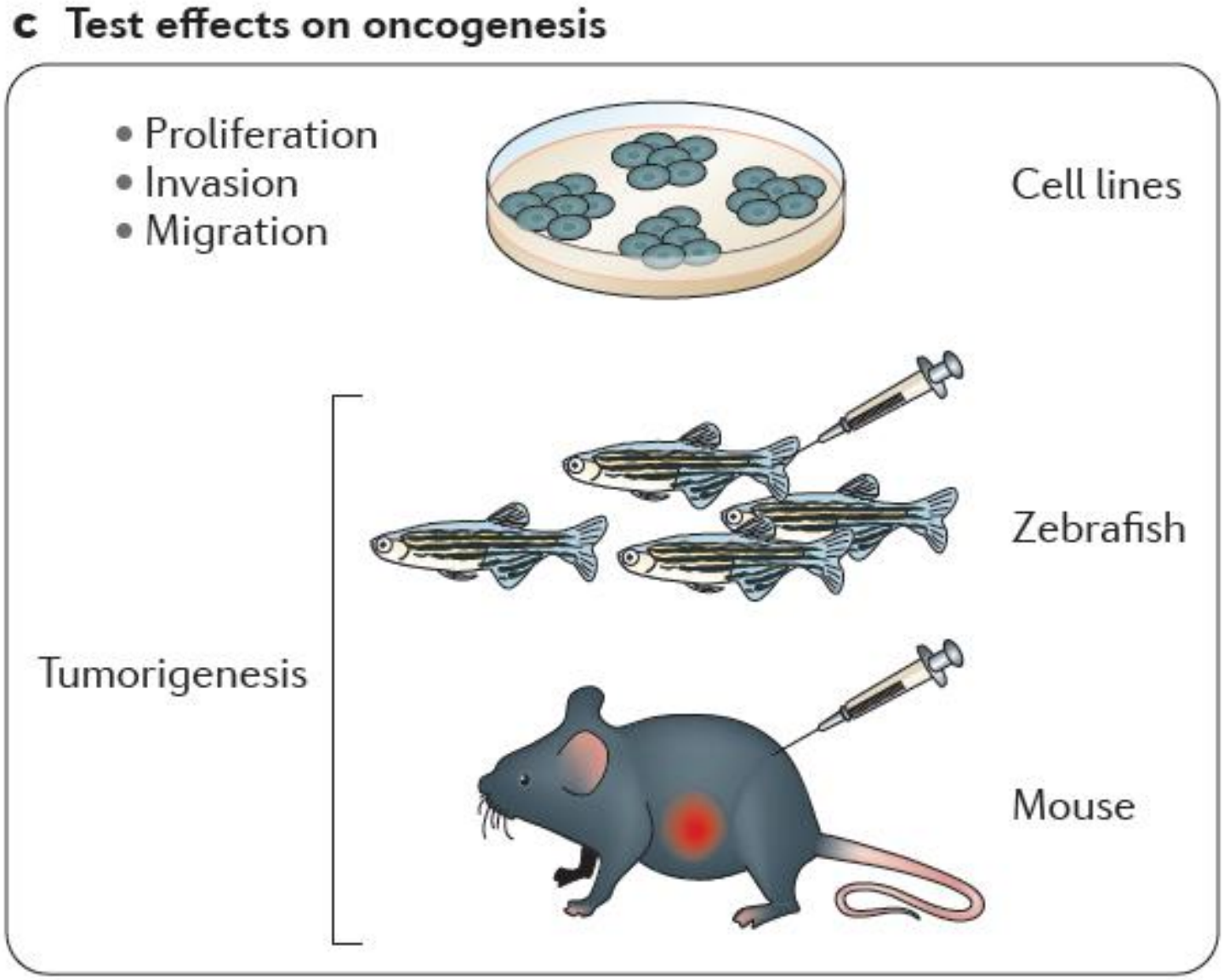
SNPs ESPERIMENTAL VALIDATIONS



MOLECULAR FUNCTIONAL EFFECTS



BIOLOGICAL FUNCTION TESTS



Framework for interpretation of individual disease-associated variants

- Single nucleotide polymorphisms (SNPs) is the nucleotide variations associated with disease

- Genome-wide association studies (GWAS) have successfully identified thousands of common genetic variants associated with complex diseases (http://www.ebi.ac.uk/gwas/)

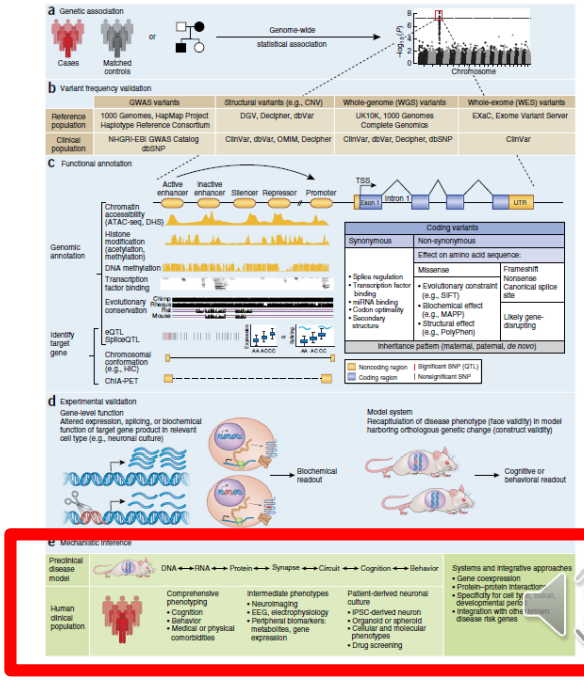
- Functional annotation: to define genomic regulatory regions by genome-wide integration data

- Experimental validation

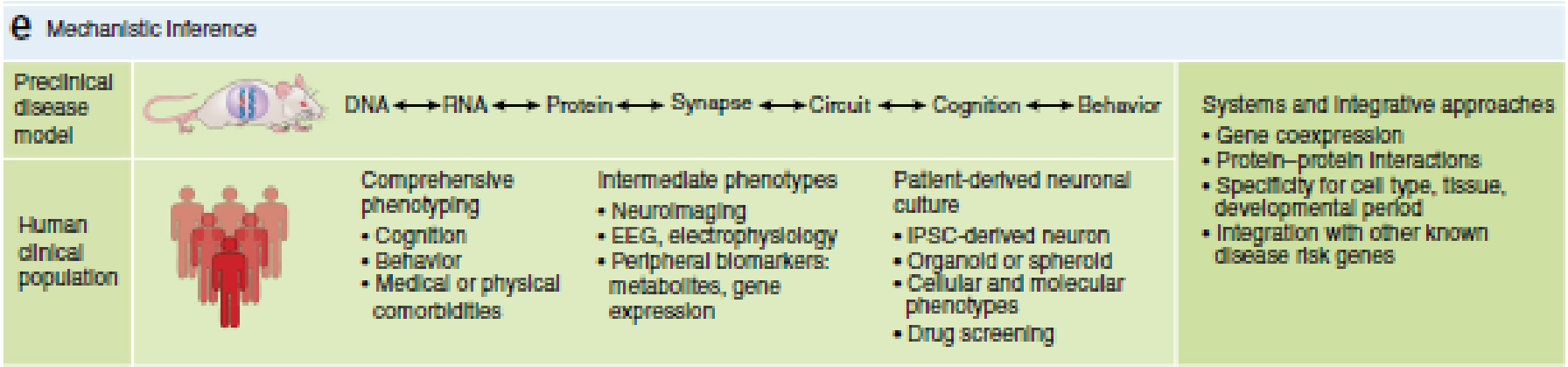
- Disease Animal models

- Correlation between molecular mechanisms and disease symptoms

- Drug Discovery



Correlation of SNP/functions with several clinical analysis

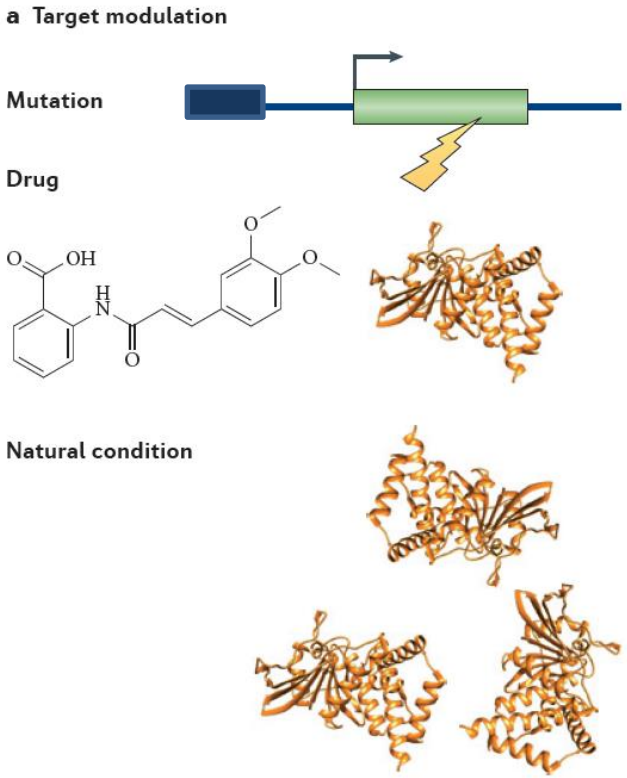


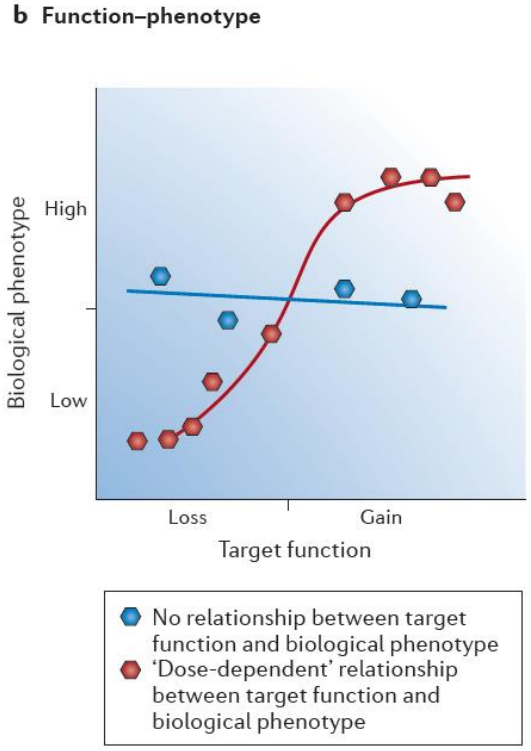
How can we use these knowledge?

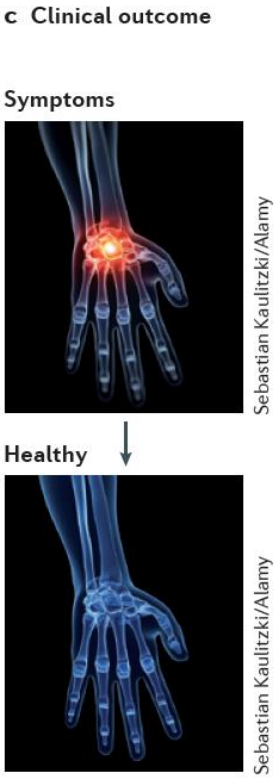
EXAMPLE

Gene expression alteration in disease May be used as BIOMARKERS (molecules acting as sensor of disease)

Gene expression alteration in disease May be used as DRUG TARGET (drug discovery to stop disease and restore health)







In Summary:

- **Functional genomics is a field of molecular biology based on genome-wide sequencing data.**
- **Genome-wide sequencing data describe genomic regulatory regions that control gene expression**
- **SNPs-involved in gene expression disregulation can be linked to the disease**
- **Understanding molecular mechanisms of disease outcome opens the way to discovery drug and identify biomarkers**