CG920 Genomics
Lecture 10

High throughput approaches Systems biology

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Functional genomics and proteomics of plants,
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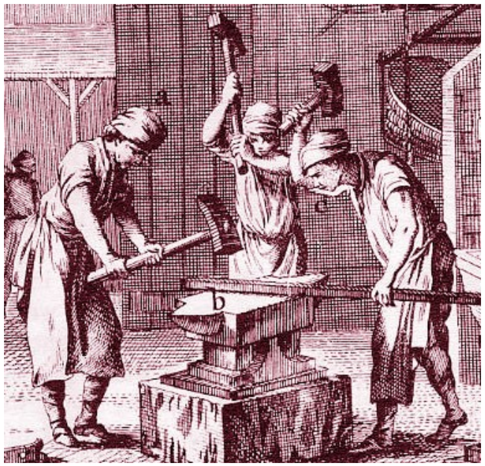
Overview

- High throughput biology
  - Automation
  - Omics
  - Transcriptomics and high throughput transcriptomics
  - High throughput interactomics and how to read it
  - High throughput of anything
  - 1000(+1) genomes, GWAS
  - ENCODE
  - Epigenenome and epitranscriptome
- Little about Systems biology
  - Omics
  - Holism and modules
  - Gene regulation in E. coli


COMPUTING
LABORATORY
DATA

Examples of automation in human history



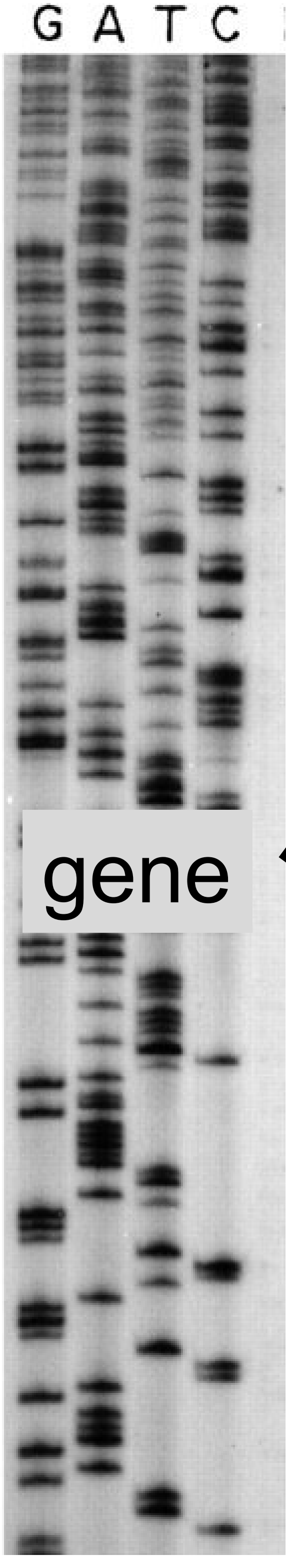
blacksmith

manufacture

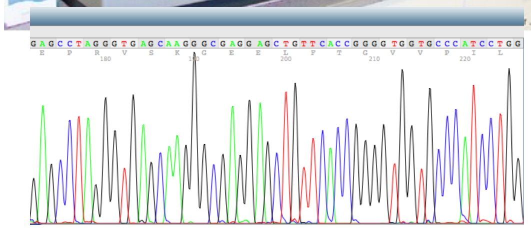
assembly line

robotic automation

High throughput sequencing

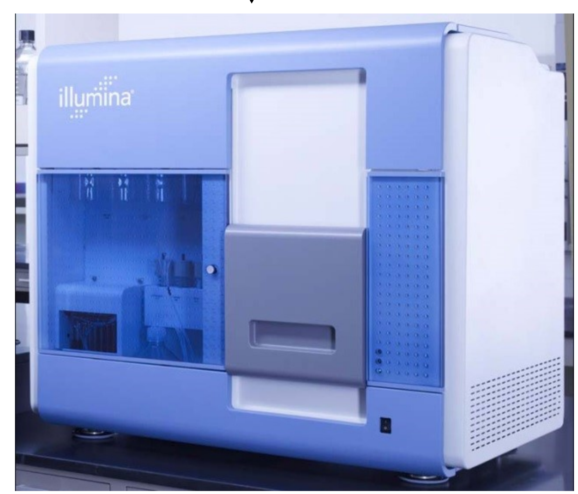


gene



genes

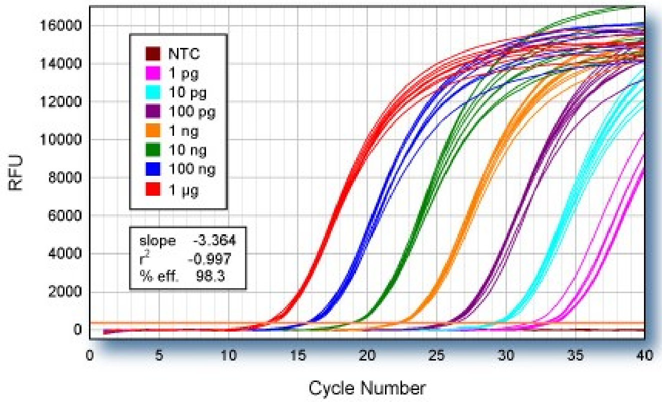
genome



genomes

ecosystems?

Automation in transcriptomics

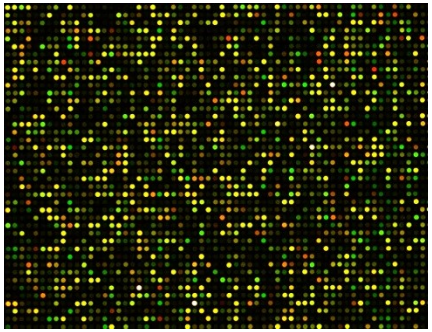


qRT-PCR

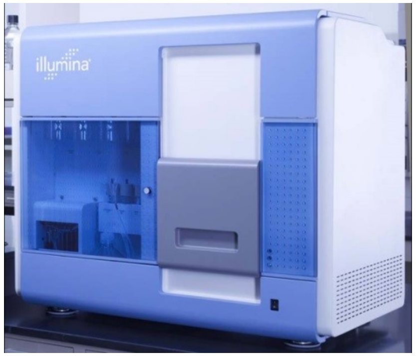
multichannel pipette

bigger multichannel pipette

pipetting robot

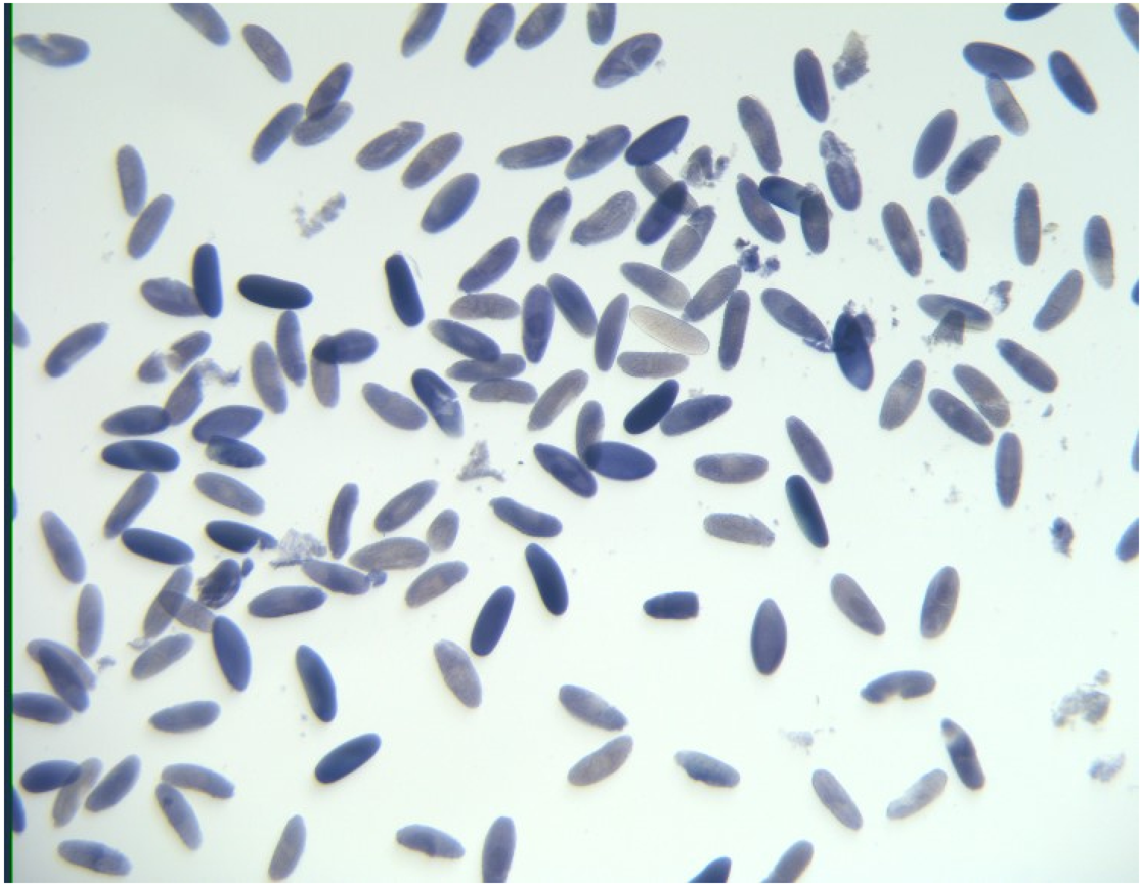


microarray



transcriptome sequencing

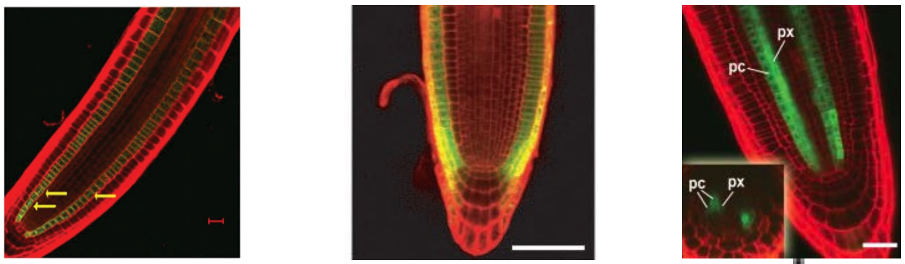
Fl(2)D gene in Drosophila embryos

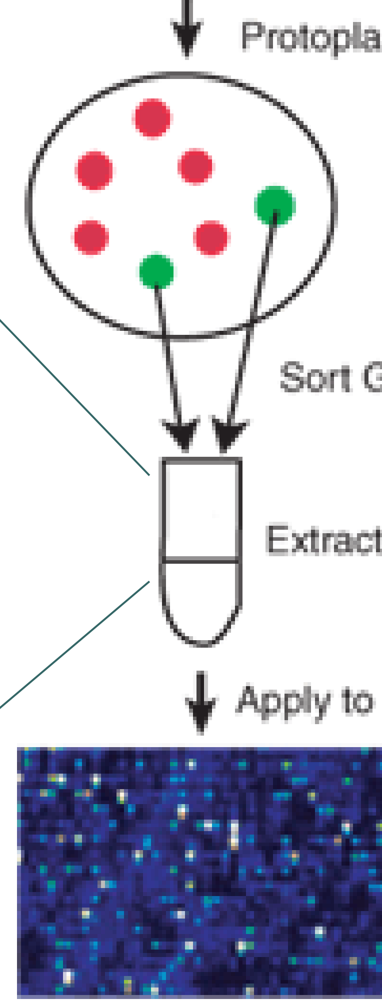


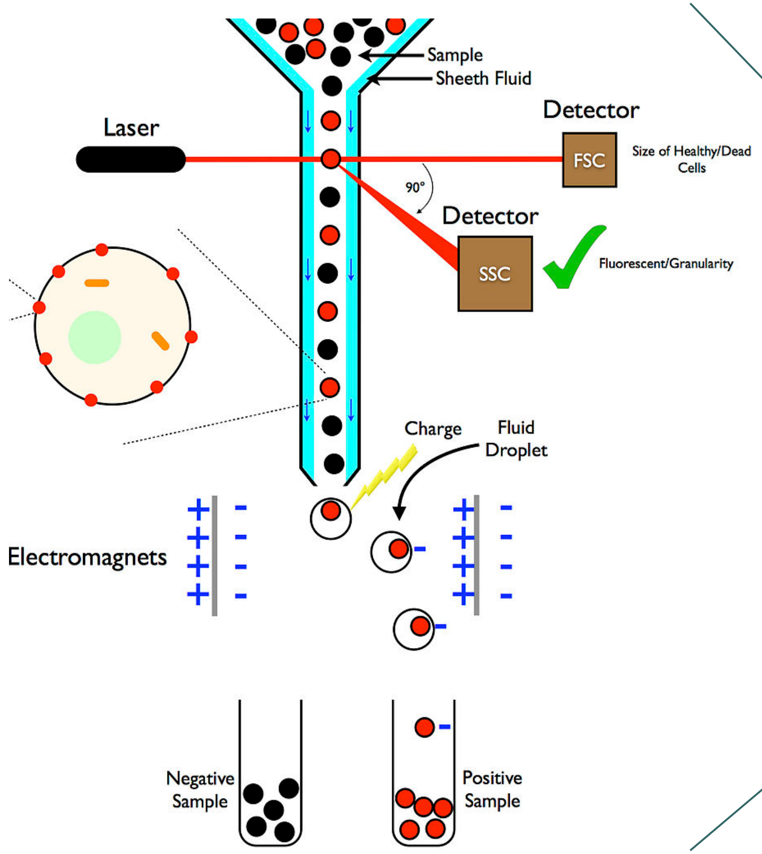
insitu.fluitfly.org

KIAA1841 in mouse expressed in neurons

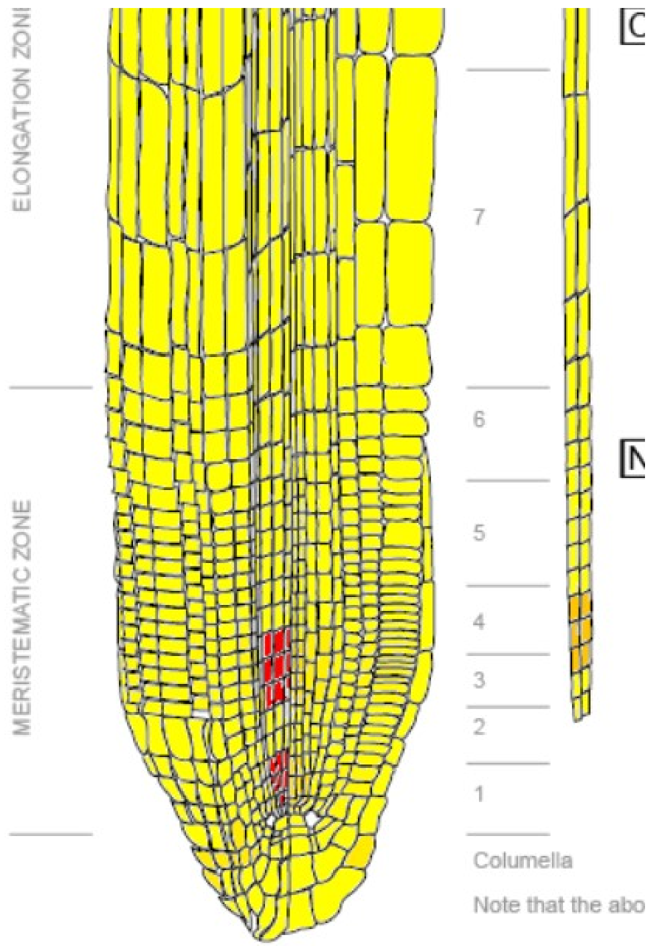
Protoplasting/cell sorting

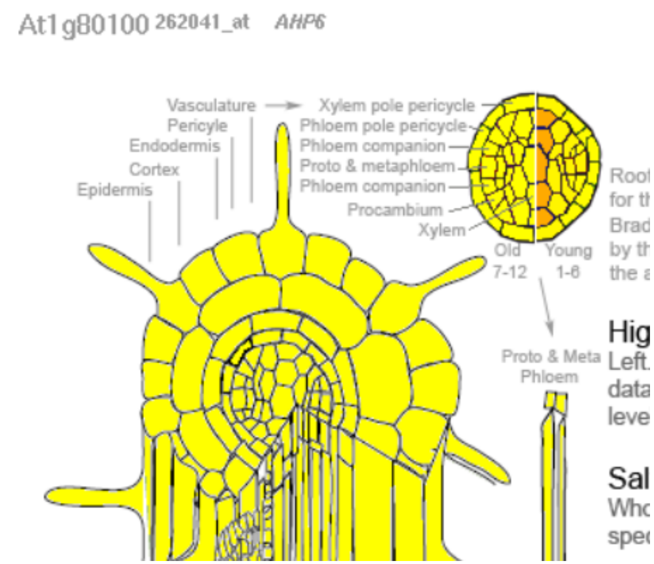






eFP browser

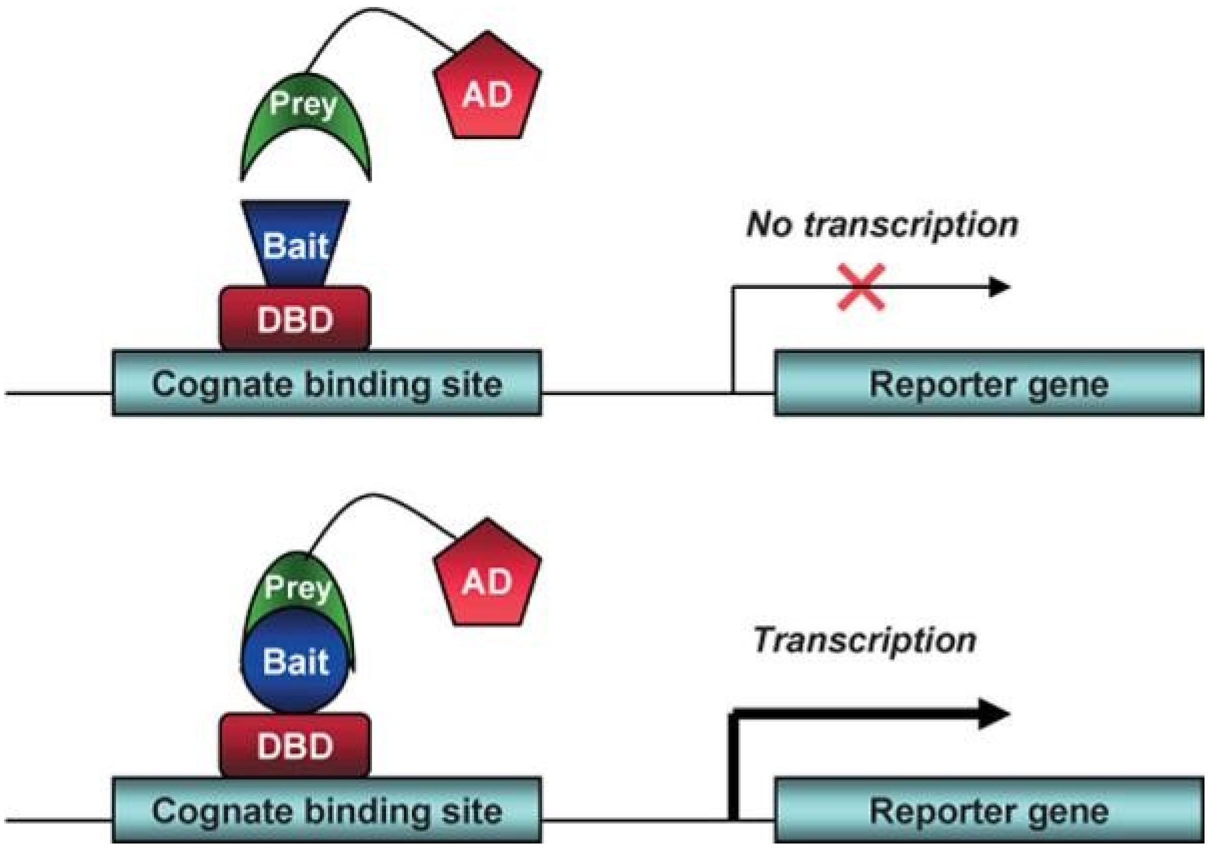




http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi

Yeast two-hybrid (Y2H) summary

protein-protein interaction hunt



High throughput yeast two hybrid for various organisms

articles

A comprehensive analysis of protein–protein interactions in *Saccharomyces cerevisiae*

(2000)

Peter Uetz*†, Loic Giot*‡, Gerard Cagney†, Traci A. Mansfield‡, Richard S. Judson‡, James R. Knight‡, Daniel Lockshon†, Vaibhav Narayan‡, Maithreyan Srinivasan‡, Pascale Pochart‡, Alia Qureshi-Emili†§, Ying Li‡, Brian Godwin‡, Diana Conover†§, Theodore Kalbfleisch‡, Govindan Vijayadamodar‡, Meijia Yang‡, Mark Johnston†‖, Stanley Fields†§ & Jonathan M. Rothberg‡

A Protein Interaction Map of *Drosophila melanogaster*

L. Giot,[1]* J. S. Bader,[1]*† C. Brouwer,[1]* A. Chaudhuri,[1]*
B. Kuang,[1] Y. Li,[1] Y. L. Hao,[1] C. E. Ooi,[1] B. Godwin,[1] E. Vitols,[1]
G. Vijayadamodar,[1] P. Pochart,[1] H. Machineni,[1] M. Welsh,[1]
Y. Kong,[1] B. Zerhusen,[1] R. Malcolm,[1] Z. Varrone,[1] A. Collis,[1]
M. Minto,[1] S. Burgess,[1] L. McDaniel,[1] E. Stimpson,[1] F. Spriggs,[1]
J. Williams,[1] K. Neurath,[1] N. Ioime,[1] M. Agee,[1] E. Voss,[1]
. Furtak,[1] R. Renzulli,[1] N. Aanensen,[1] S. Carrolla,[1]
ickelhaupt,[1] Y. Lazovatsky,[1] A. DaSilva,[1] J. Zhong,[2]
tanyon,[2] R. L. Finley Jr.,[2] K. P. White,[3] M. Braverman,[1]
rvie,[1] S. Gold,[1] M. Leach,[1] J. Knight,[1] R. A. Shimkets,[1]
M. P. McKenna,[1] J. Chant,[1]‡ J. M. Rothberg[1]

Evidence for Network Evolution in an *Arabidopsis* Interactome Map

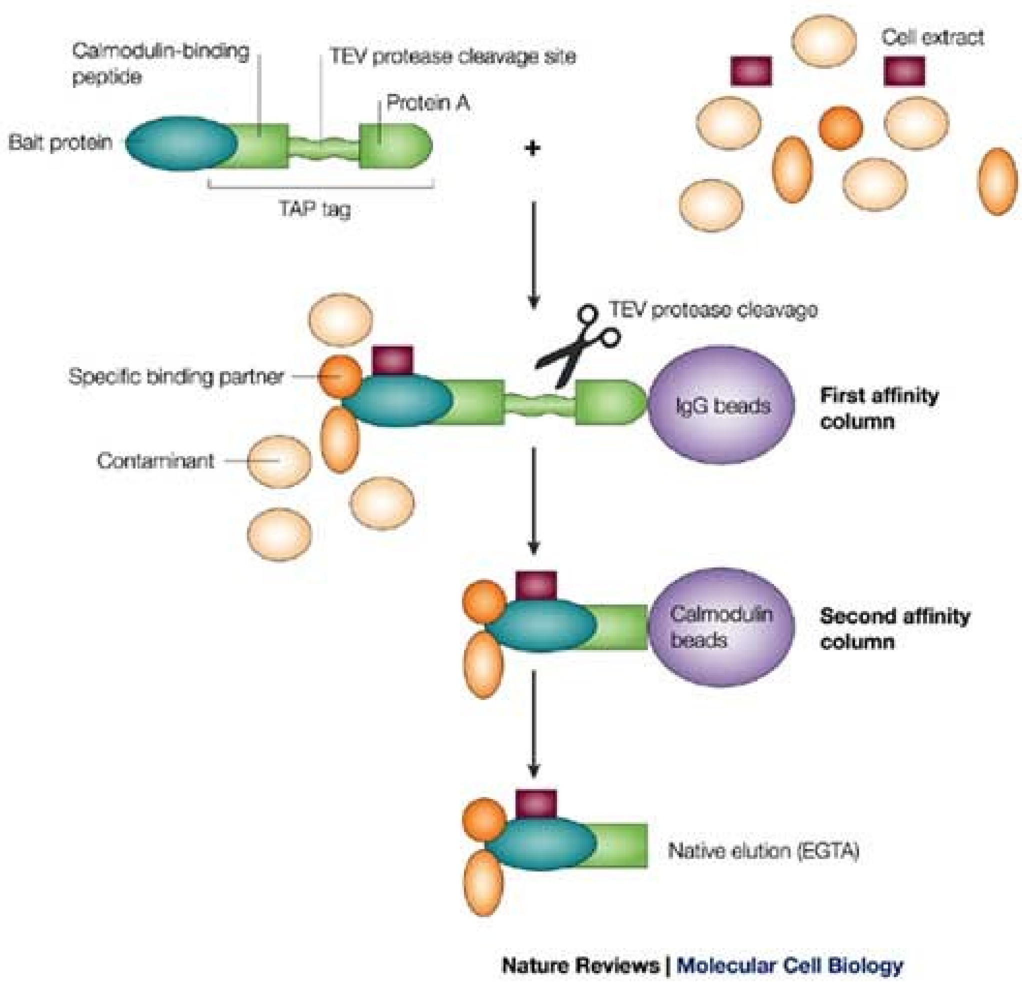
Arabidopsis Interactome Mapping Consortium*†

(2009)

(2005)

TAP purification

affinity purification interaction hunt



↓

MALDI-TOF

So, far high throughput affinity purification approach slightly less popular

Functional organization of the yeast proteome by systematic analysis of protein complexes (2002)

Anne-Claude Gavin*, Markus Bösche*, Roland Krause*, Paola Grandi*, Martina Marzioch*, Andreas Bauer*, Jörg Schultz*, Jens M. Rick*, Anne-Marie Michon*, Cristina-Maria Cruciat*, Marita Remor*, Christian Höfert*, Malgorzata Schelder*, Miro Brajenovic*, Heinz Ruffner*, Alejandro Merino*, Karin Klein*, Manuela Hudak*, David Dickson*, Tatjana Rudi*, Volker Gnau*, Angela Bauch*, Sonja Bastuck*, Bettina Huhse*, Christina Leutwein*, Marie-Anne Heurtier*, Richard R. Copley†, Angela Edelmann*, Erich Querfurth*, Vladimir Rybin*, Gerard Drewes*, Manfred Raida*, Tewis Bouwmeester*, Peer Bork†, Bertrand Seraphin†‡, Bernhard Kuster*, Gitte Neubauer* & Giulio Superti-Furga*†

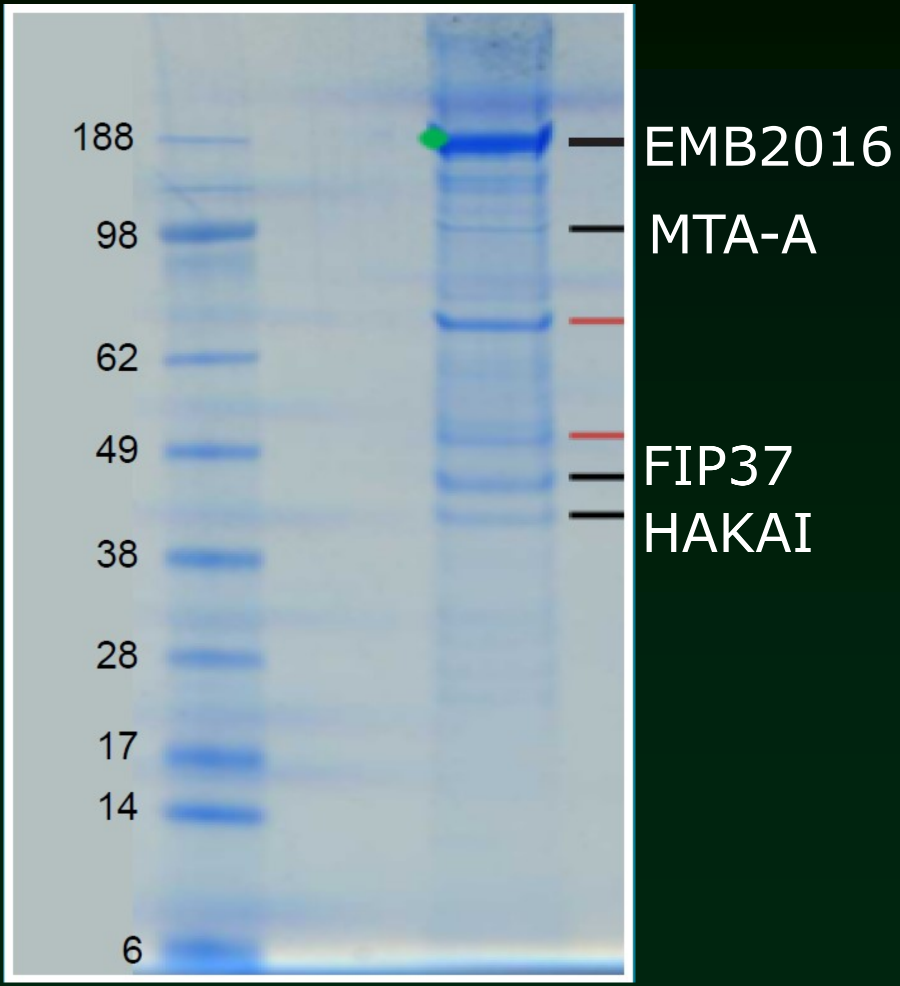
A Protein Complex Network of *Drosophila melanogaster* (2011)

K.G. Guruharsha,[1,4] Jean-François Rual,[1,4] Bo Zhai,[1,4] Julian Mintseris,[1,4] Pujita Vaidya,[1] Namita Vaidya,[1] Chapman Beekman,[1] Christina Wong,[1] David Y. Rhee,[1] Odise Cenaj,[1] Emily McKillip,[1] Saumini Shah,[1] Mark Stapleton,[2] Kenneth H. Wan,[2] Charles Yu,[2] Bayan Parsa,[2] Joseph W. Carlson,[2] Xiao Chen,[2] Bhaveen Kapadia,[2] K. VijayRaghavan,[3] Steven P. Gygi,[1] Susan E. Celniker,[2] Robert A. Obar,[1,*] and Spyros Artavanis-Tsakonas[1,*]

thebiogrid.org - highly relevant for searching for interactors, but look also elsewhere!

Interactors of EMB2016

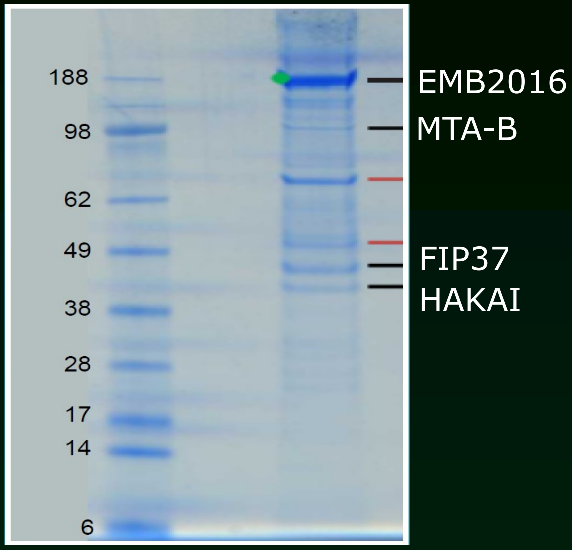
use databases if you have a conserved complex



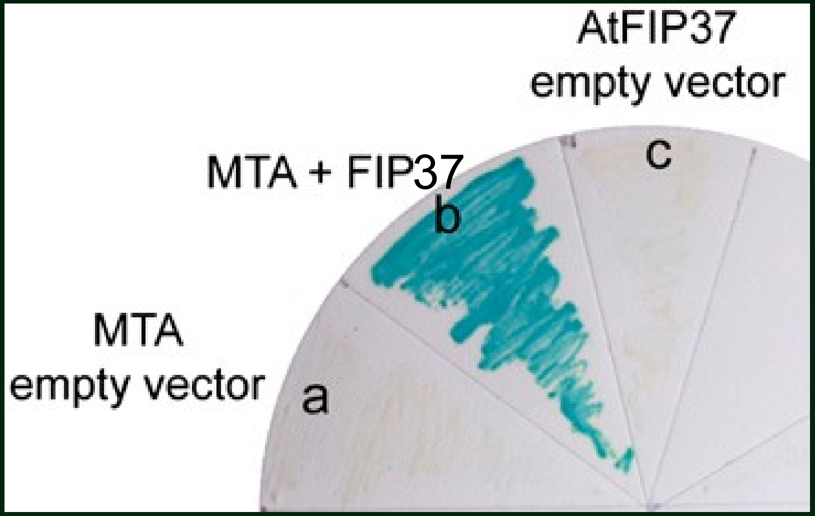
tandem affinity purification

Geert de Jaeger lab

EMB2016 interactors – RNA methylase



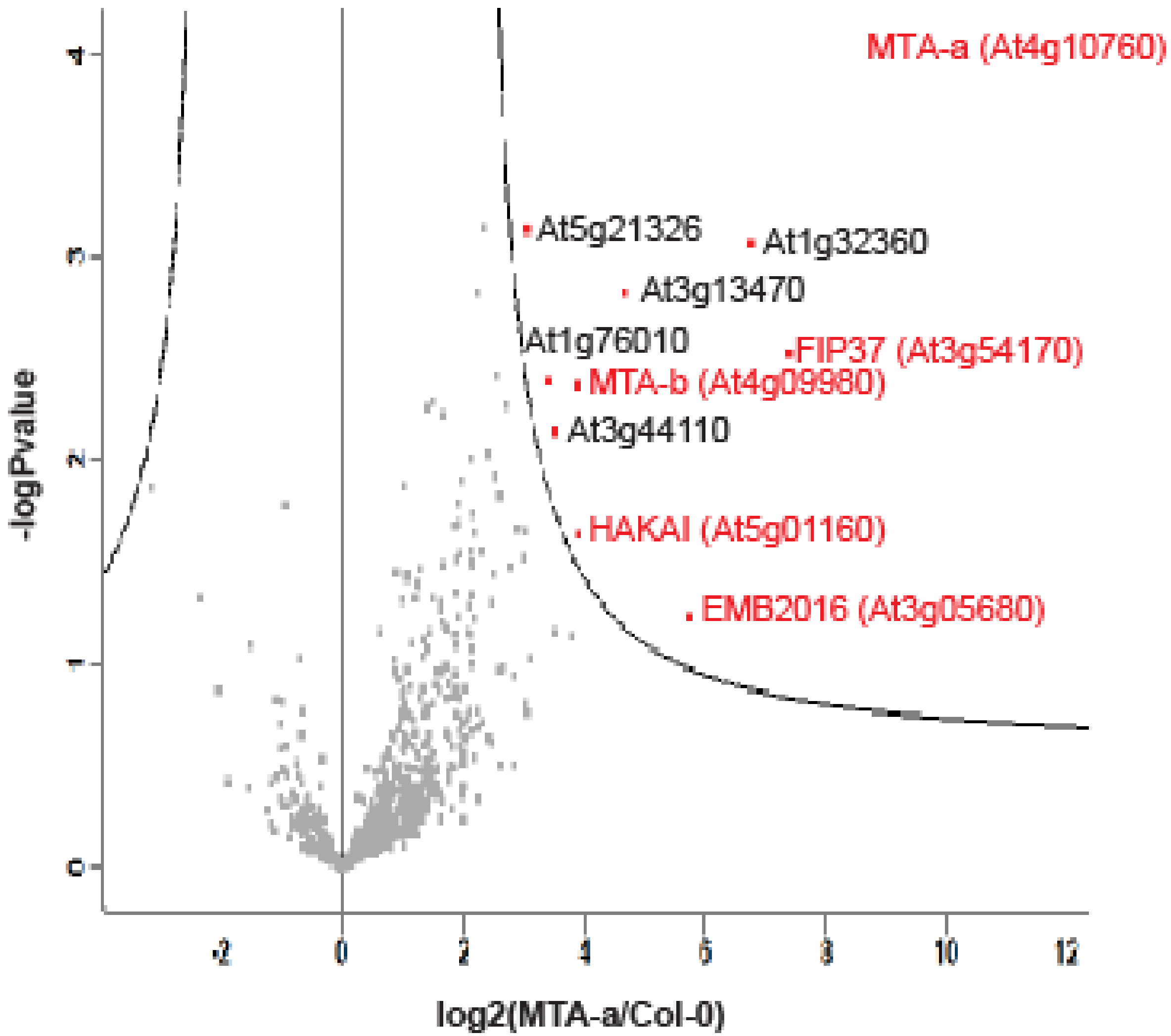
RING finger/HAKAI was also shown to associate with splicing factors (human)



MTA-A – homolog of MTA

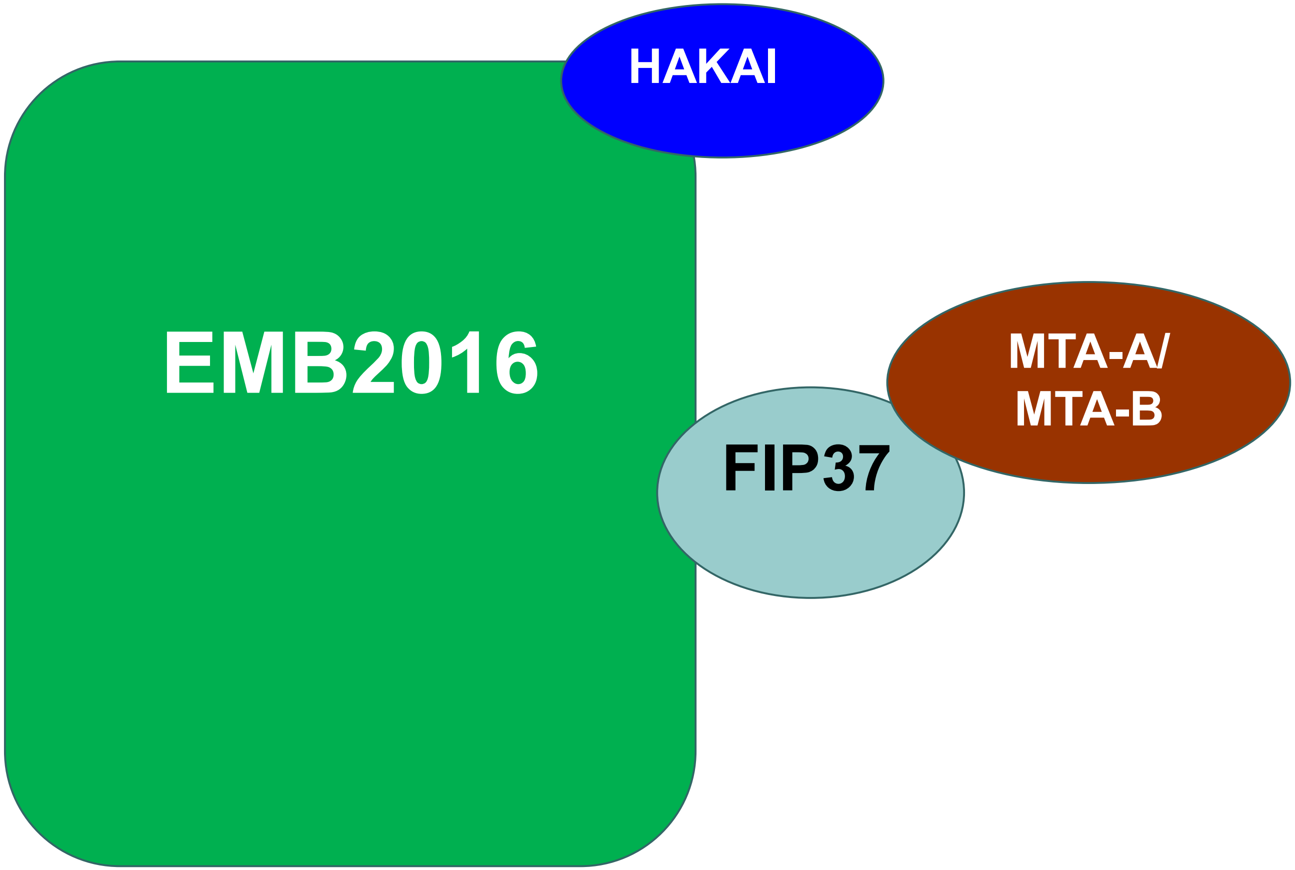
Zhong et al. 2009

All guys back here when using MTA-A as bait

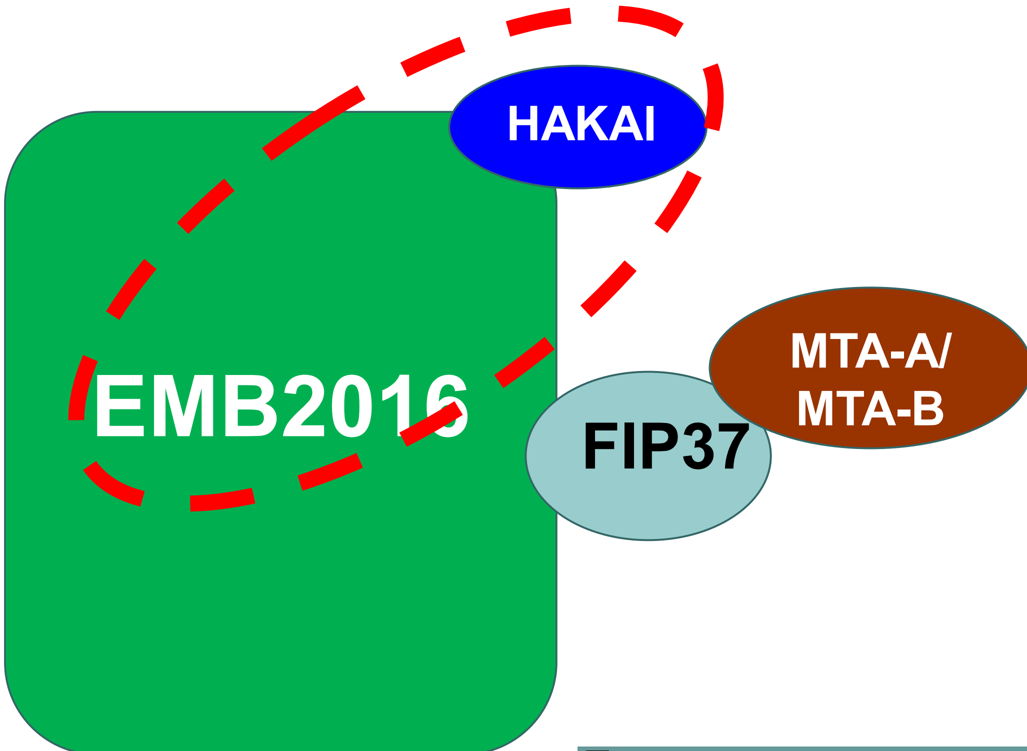


(Immunoprecipitation)

Inferred protein complex



Inferred protein complex

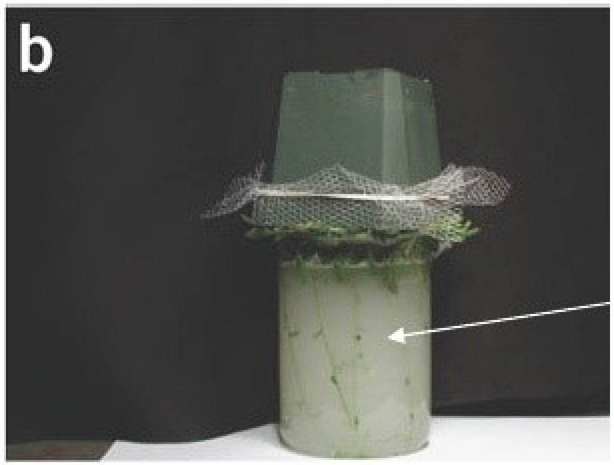


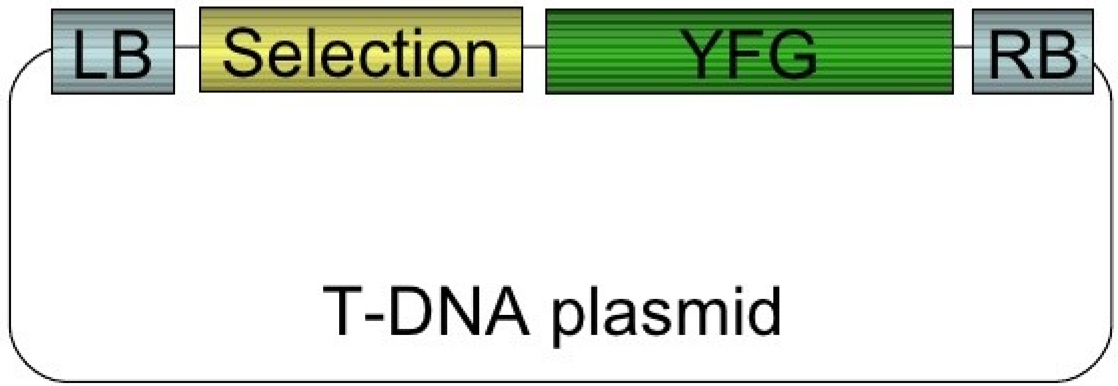
Flybase: EMB2016 interacts with HAKAI (no data on Biogrid)

Summary of Physical Interactions

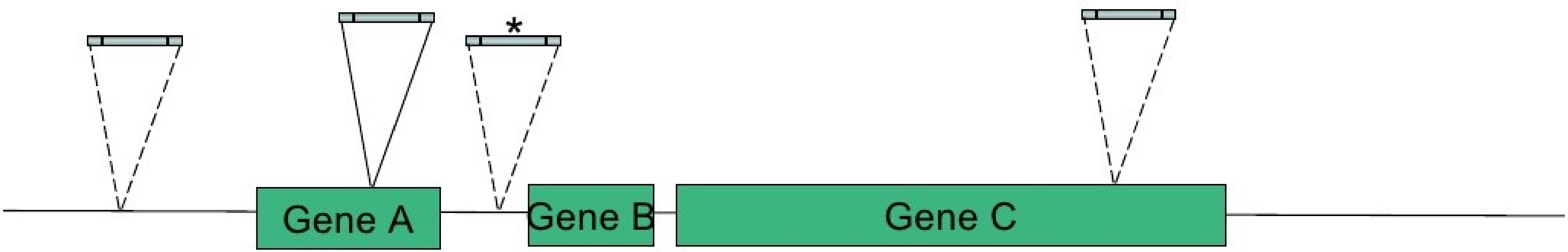
Interacting group	Assay	References
RNA-protein		
vir - stau	anti bait coimmunoprecipitation, partial dna sequence identification by hybridization	(*Laver et al., 2013*)
protein-protein		
vir - CG7358	experimental knowledge based	(*Guruharsha et al., 2011*)
vir - Hakai	experimental knowledge based	(*Guruharsha et al., 2011*)
vir - fl(2)d	experimental knowledge based	(*Guruharsha et al., 2011*)

T-DNA insertion at random locations in the genome

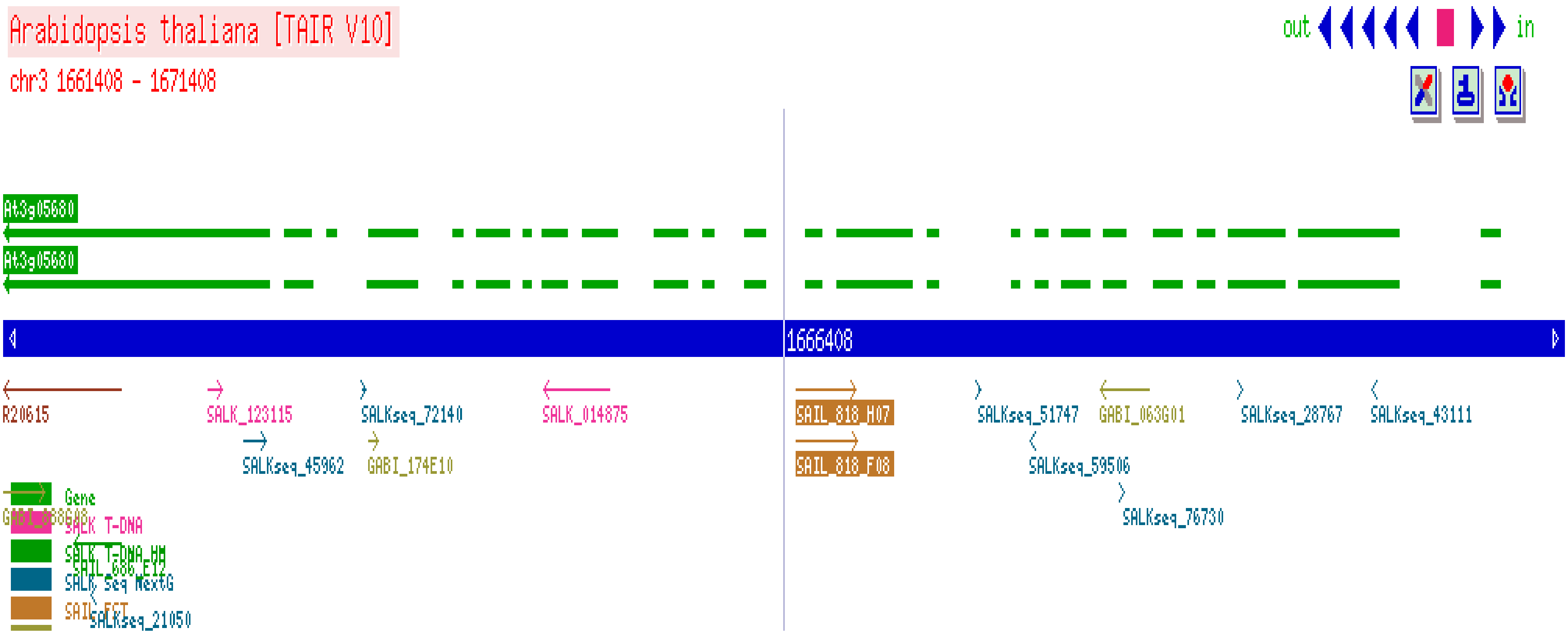




Examples of possible insertions:



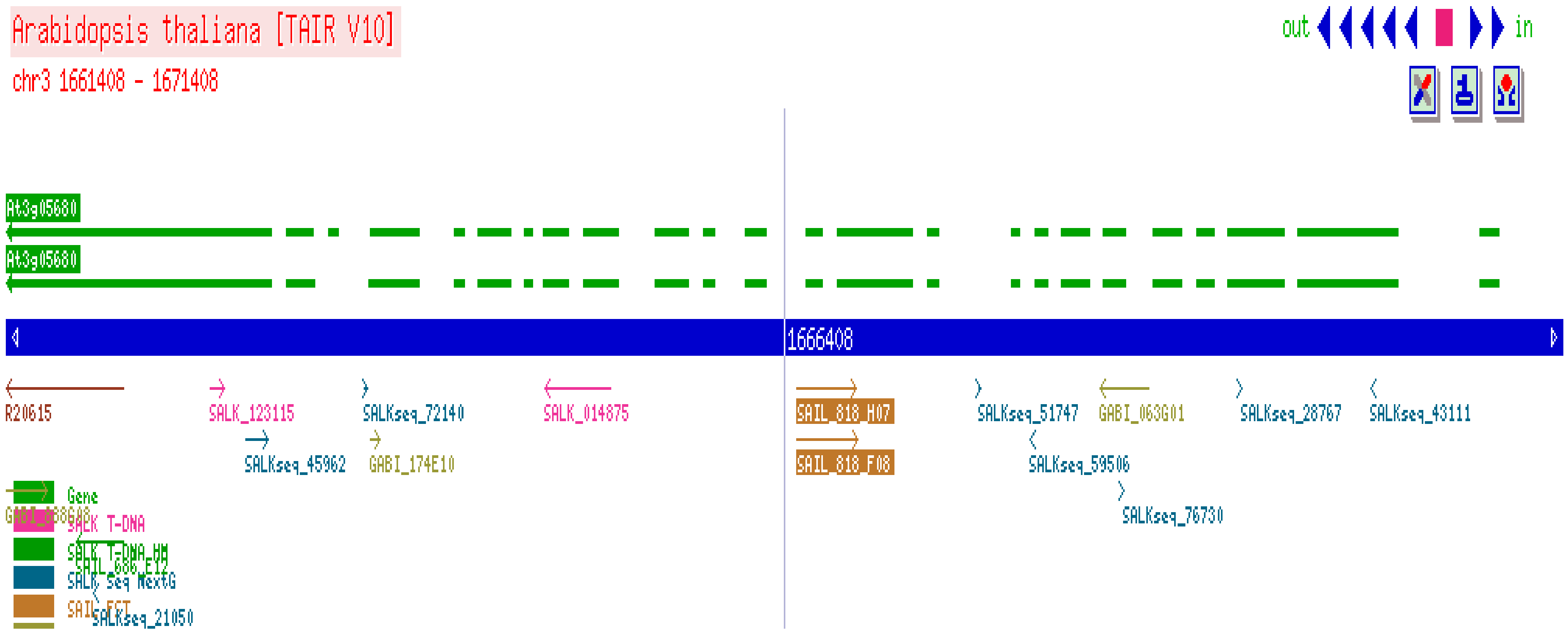
You can order your mutant from the stock center



the same for Drosophila, mouse, worm etc.

signal.salk.edu

You can order your mutant from the stock center



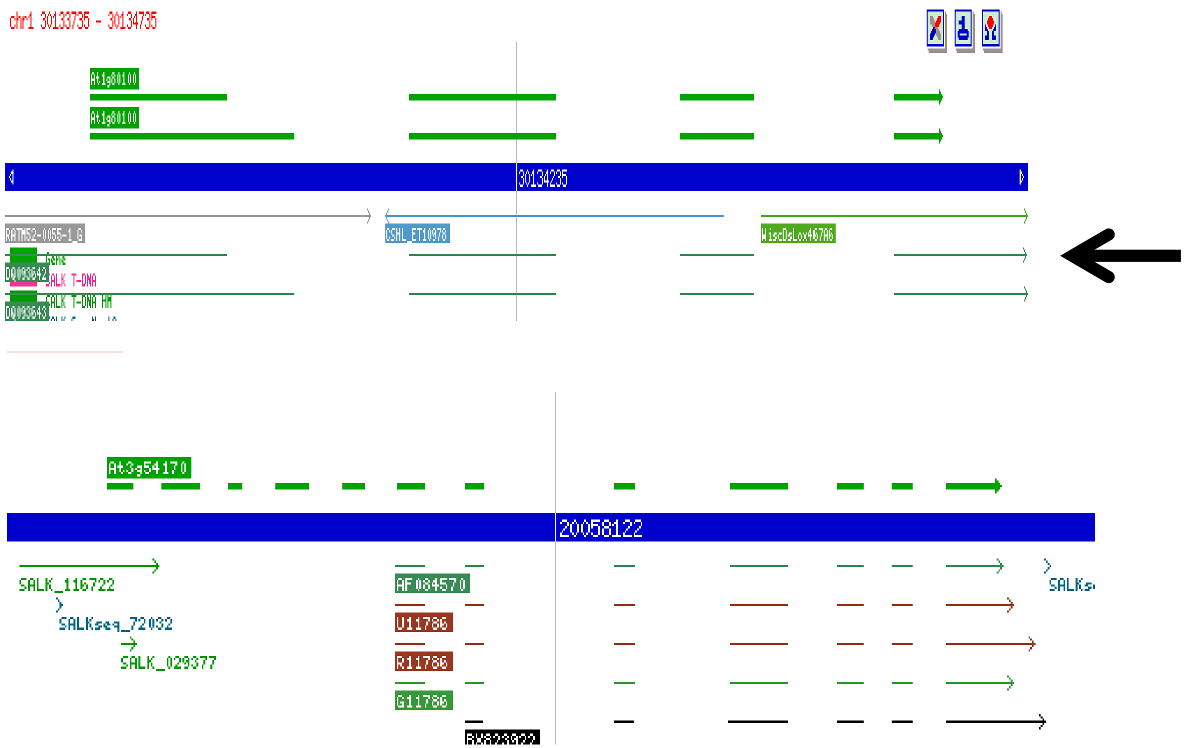
the same for Drosophila, mouse, worm etc.

What to do if you cannot find insertion line for your gene?

signal.salk.edu

- RNAi/amiRNA (can be also ordered)
- CRISPR

You can order your cDNA clone from the stock center



the same for yeast, Drosophila, mouse etc.

signal.salk.edu

You can order even various constructs regarding your gene from stock centers

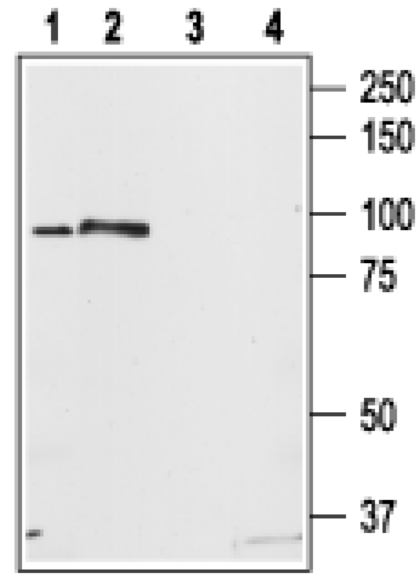
even basic fusions (GFP, myc, TAP etc.) often ready for you

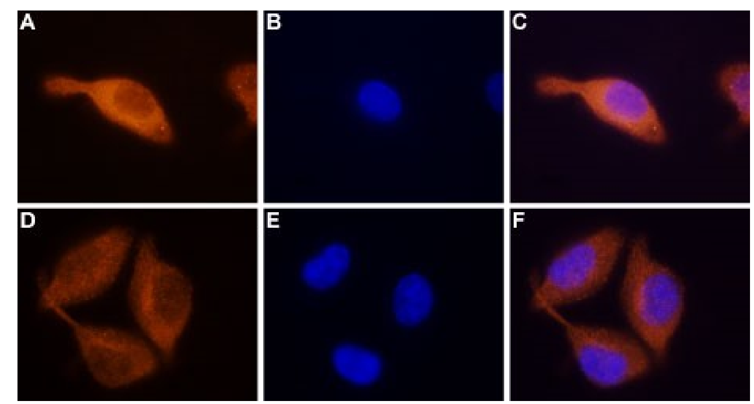
signal.salk.edu

You can order antibodies against your protein

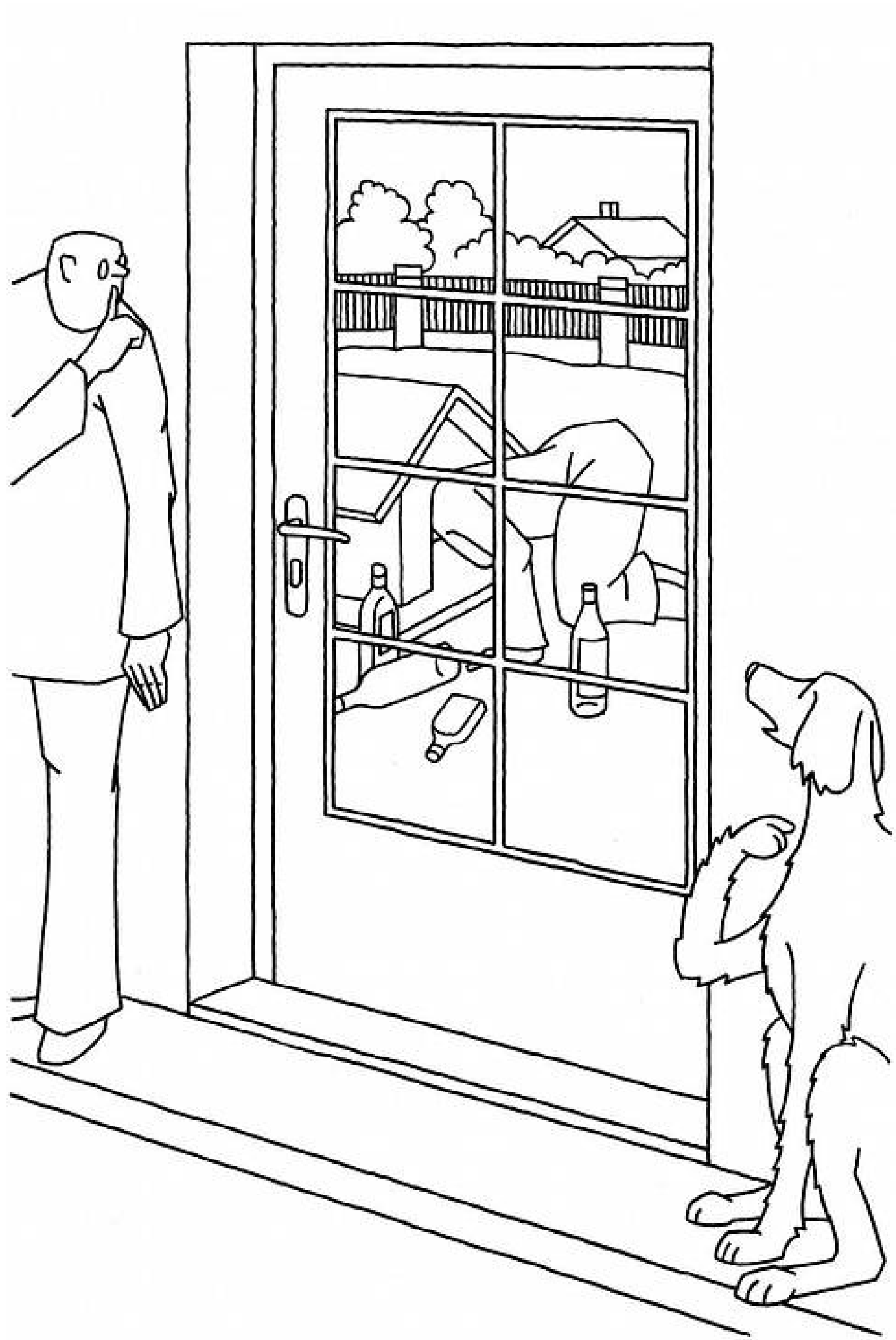
several human proteins providers:
http://www.scbt.com/
www.acris-antibodies.com/
etc.

- even get western and immunocytochemistry in advance



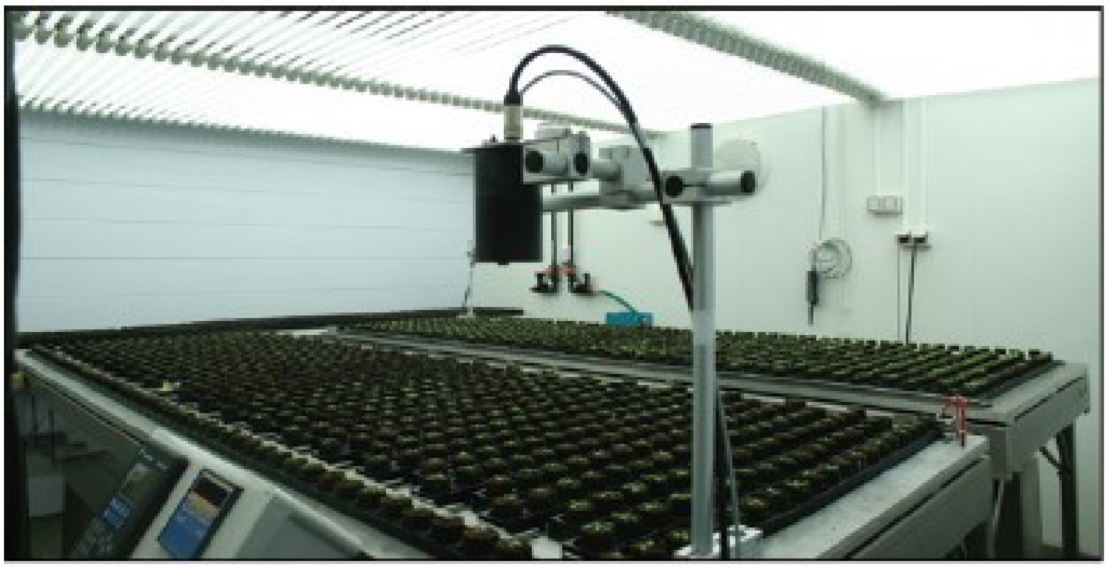


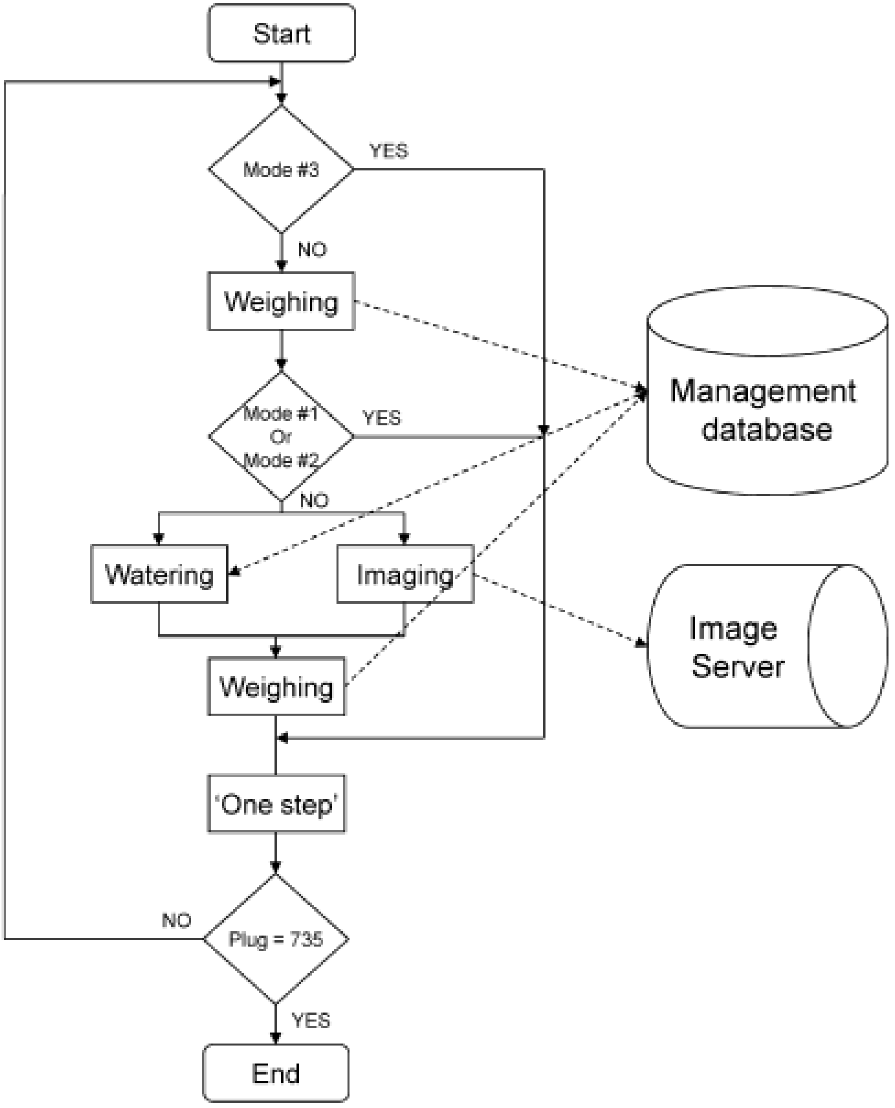
Arabidopsis so far lagging – agrisera.com perhaps little bit.
Rather commercial service.



Phenoscope

(a)

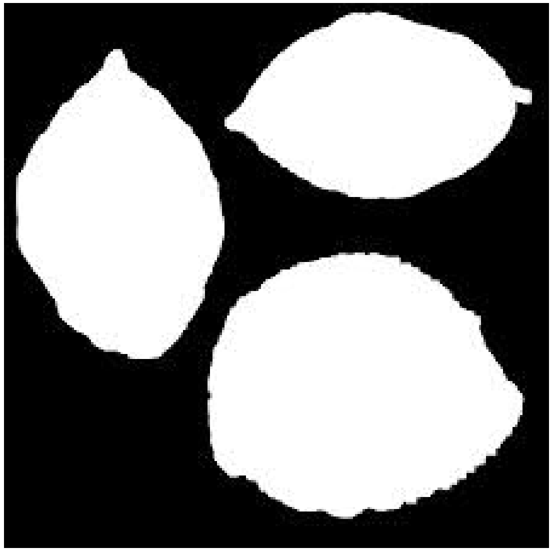


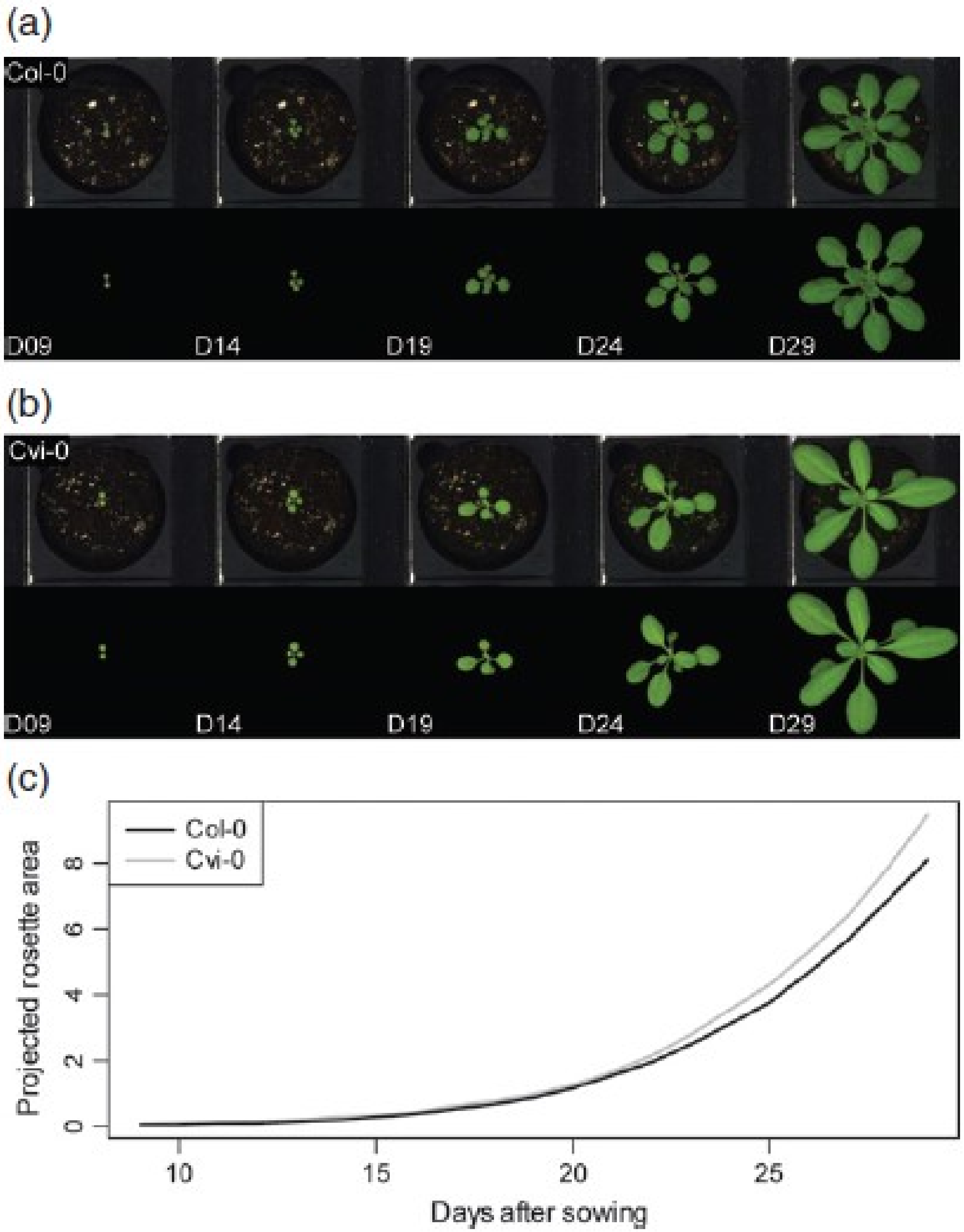


PHENOSCOPE: an automated large-scale phenotyping platform

Thisne et al. 2013

Phenoscope





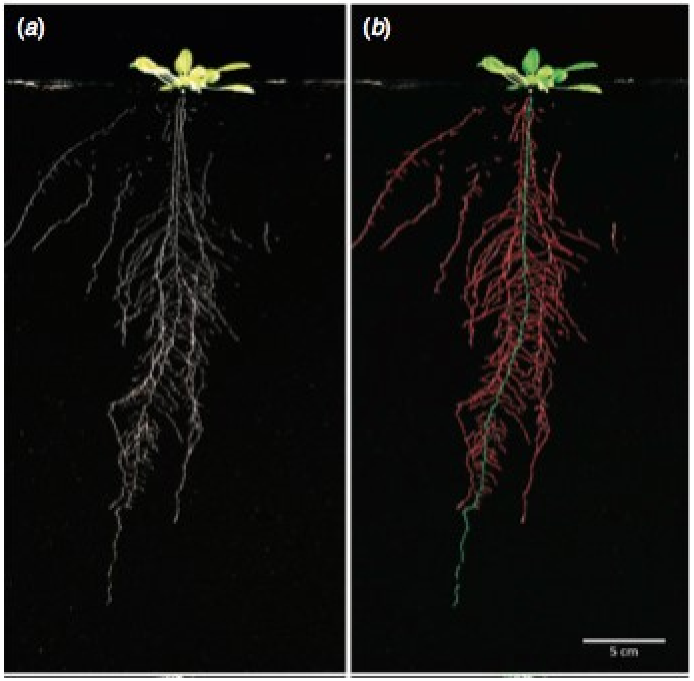
(a)
Col-0
D09
D14
D19
D24
D29
(b)
Cvi-0
D09
D14
D19
D24
D29
(c)
Col-0
Cvi-0
Projected rosette area
0
2
4
6
8
10
15
20
25
Days after sowing

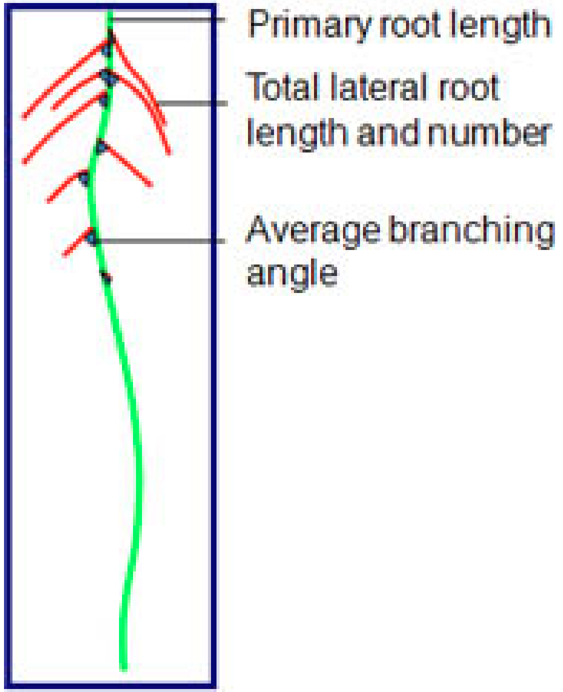
Phenoscope

- leaf area (camera)
- photosynthesis (spectra)
- weight
- temperature (thermo camera)
- in a dynamic manner
- …
- various ecotypes only, so far
- commercially promising

Phenoscope – perhaps in future

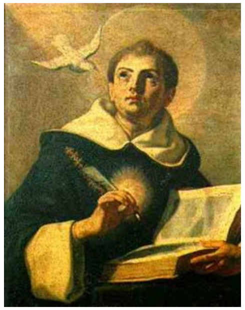
adaptation on other growth conditions





GrowScreen-Root software

Check your phenotype online

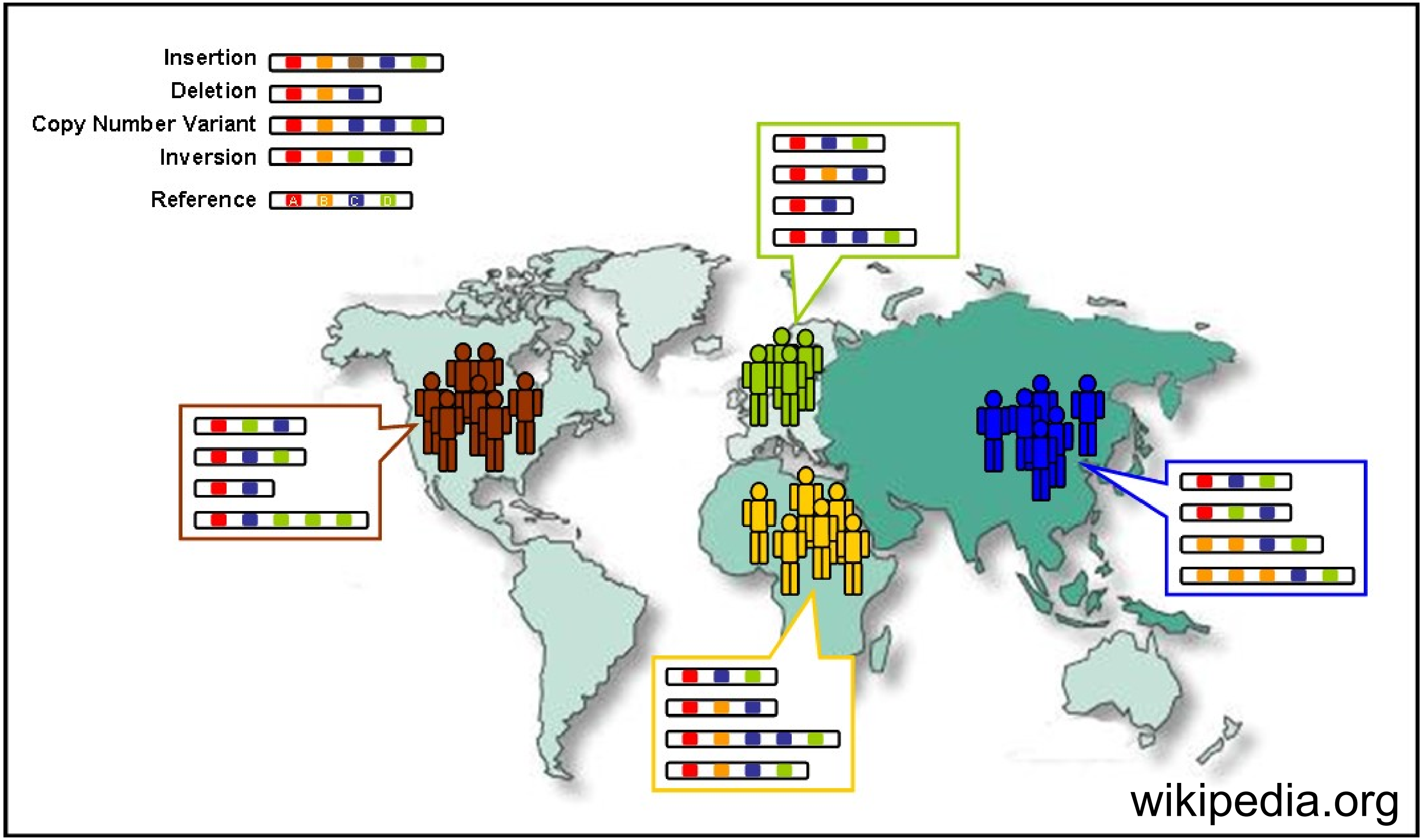


seedgenes.org
– database of plant embryonic mutants (in-dept)

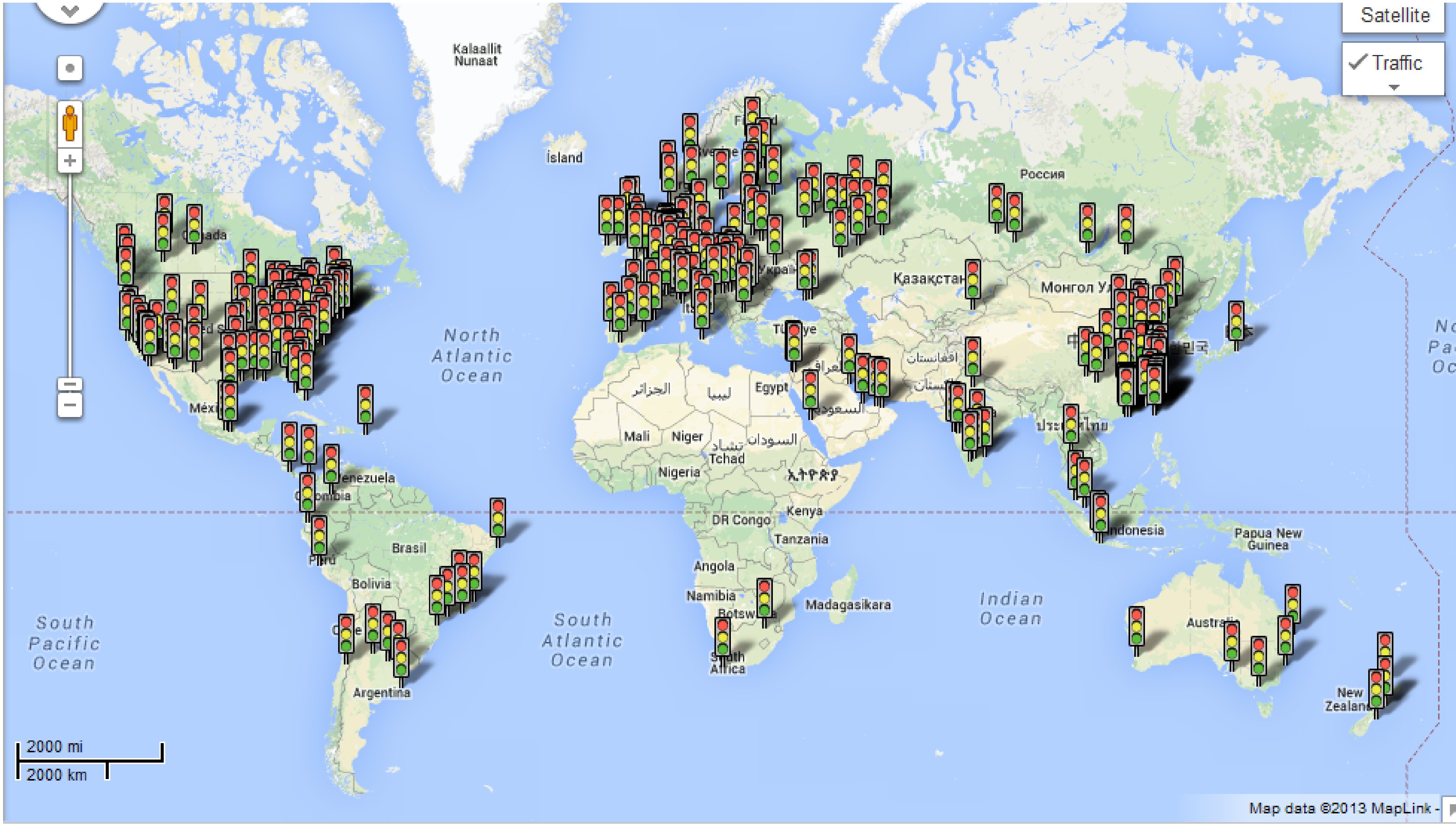
http://rarge.psc.riken.jp/phenome/
- RIKEN Arabidopsis Phenome Information Database (kind of attempt on adult plant)

1000 genomes

1000 human genomes sequenced over the world



1001 genomes - Arabidopsis



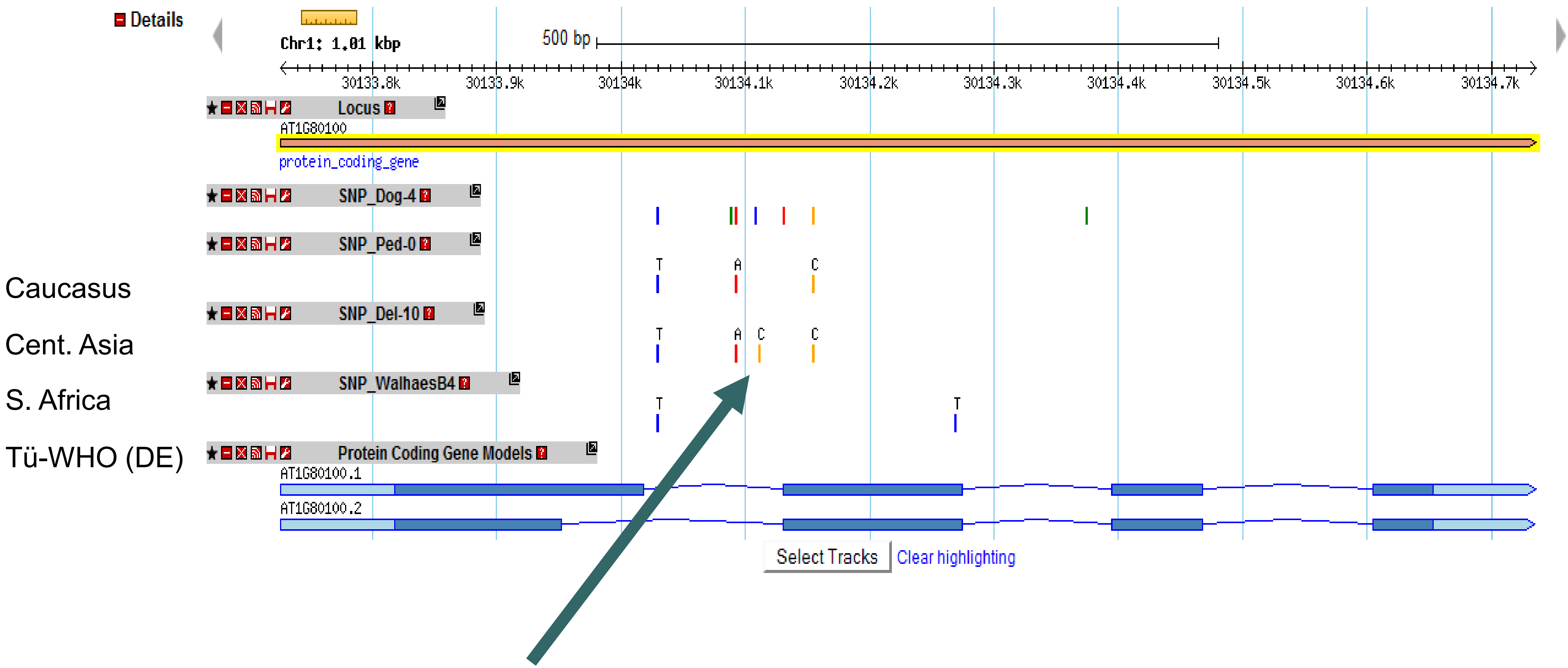
http://1001genomes.org/

in both cases, much more lines already sequenced

How the ecotypes are collected

Olivier Loudet web page

1001 genomes user interface



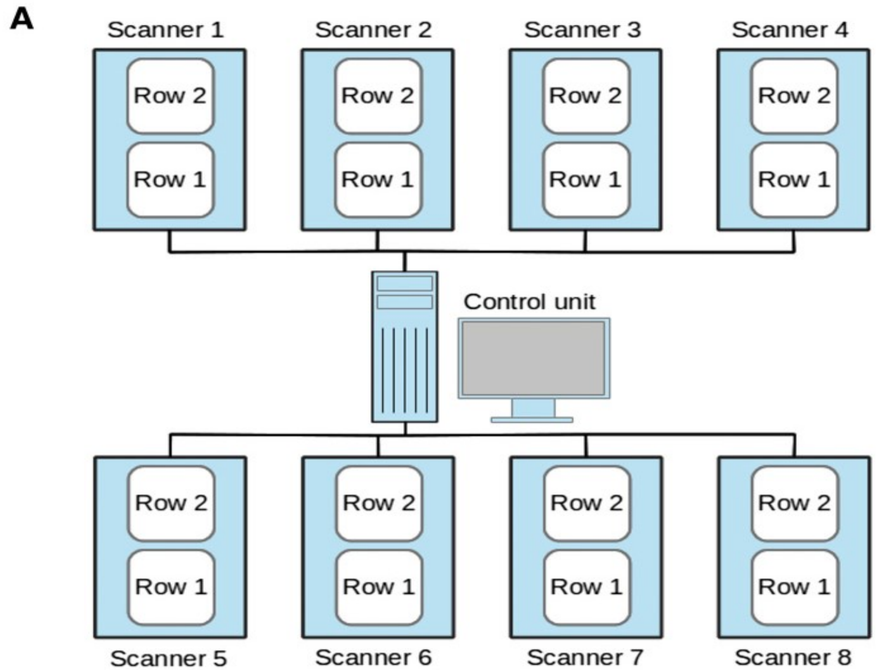
several single nucleotide polymorphisms (**SNP**) in the selected gene

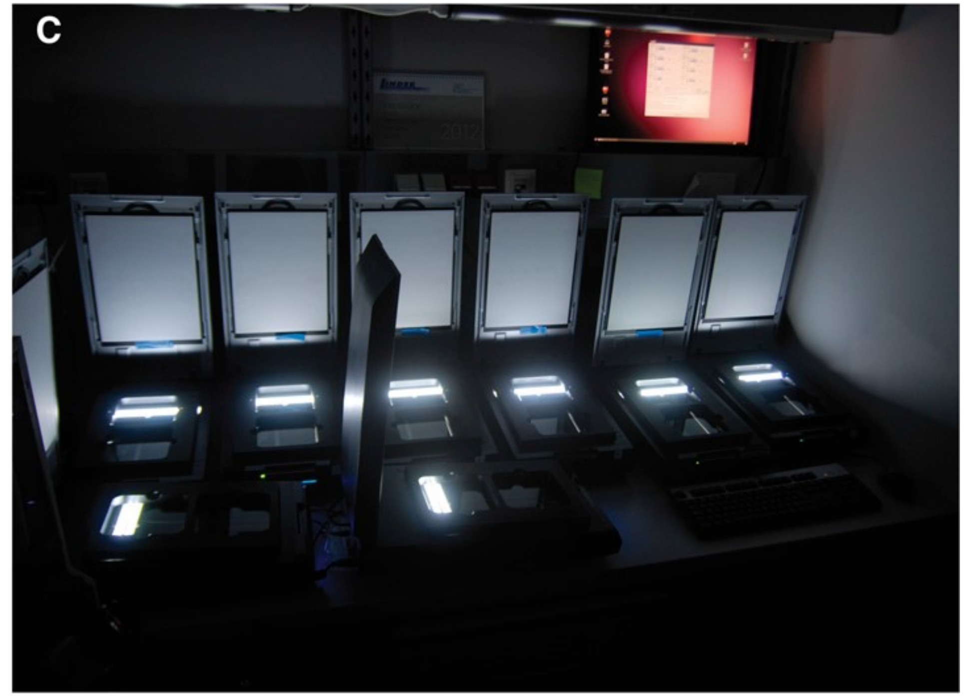
What could be natural variation good for?

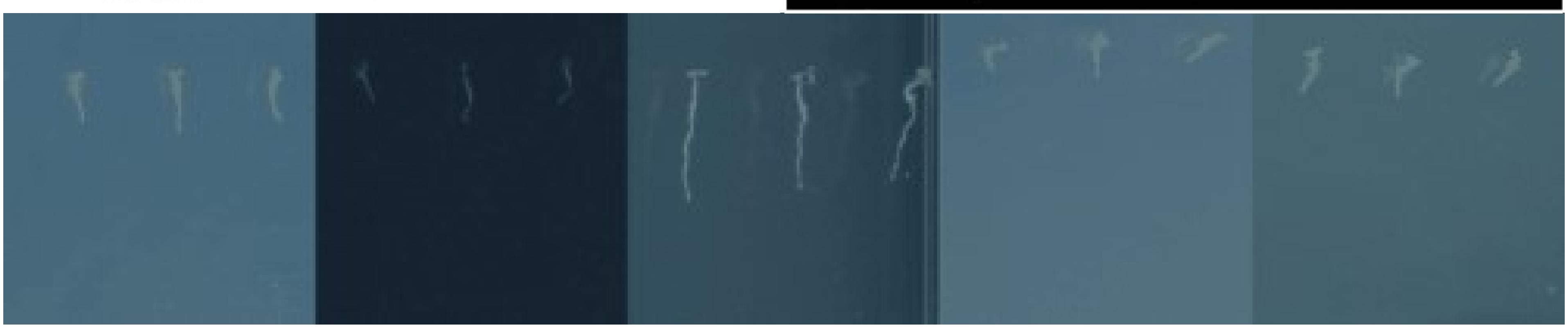
Quantitative trait loci (QTL)

- nature makes genetic screen for you
- QTL is analogous to gene in genetic screen

Genome wide association studies (GWAS)







Slovak et al. 2014, Busch lab, Vienna

Genome wide association studies (GWAS)

Trait No.	Trait
1	Total length
2	Euclidian length
3	Root tortuosity
4	Root growth rate
5	Relative root growth rate
6	Root angle
7	Root direction index
8	Root horizontal index
9	Root vertical index
10	Root linearity
11	Average root width
12	Root width 20
13	Root width 40
14	Root width 60
15	Root width 80
16	Root width 100

163 accessions (ecotypes), several replicates (8 x 3)

↓

searching for those different (say how different they might be!)

Slovak et al. 2014

Genome wide association studies (GWAS)

Trait No.	Trait
1	Total length
2	Euclidian length
3	Root tortuosity
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5	Relative root growth rate
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11	Average root width
12	Root width 20
13	Root width 40
14	Root width 60
15	Root width 80
16	Root width 100

163 accessions (ecotypes), several replicates (8 x 3)

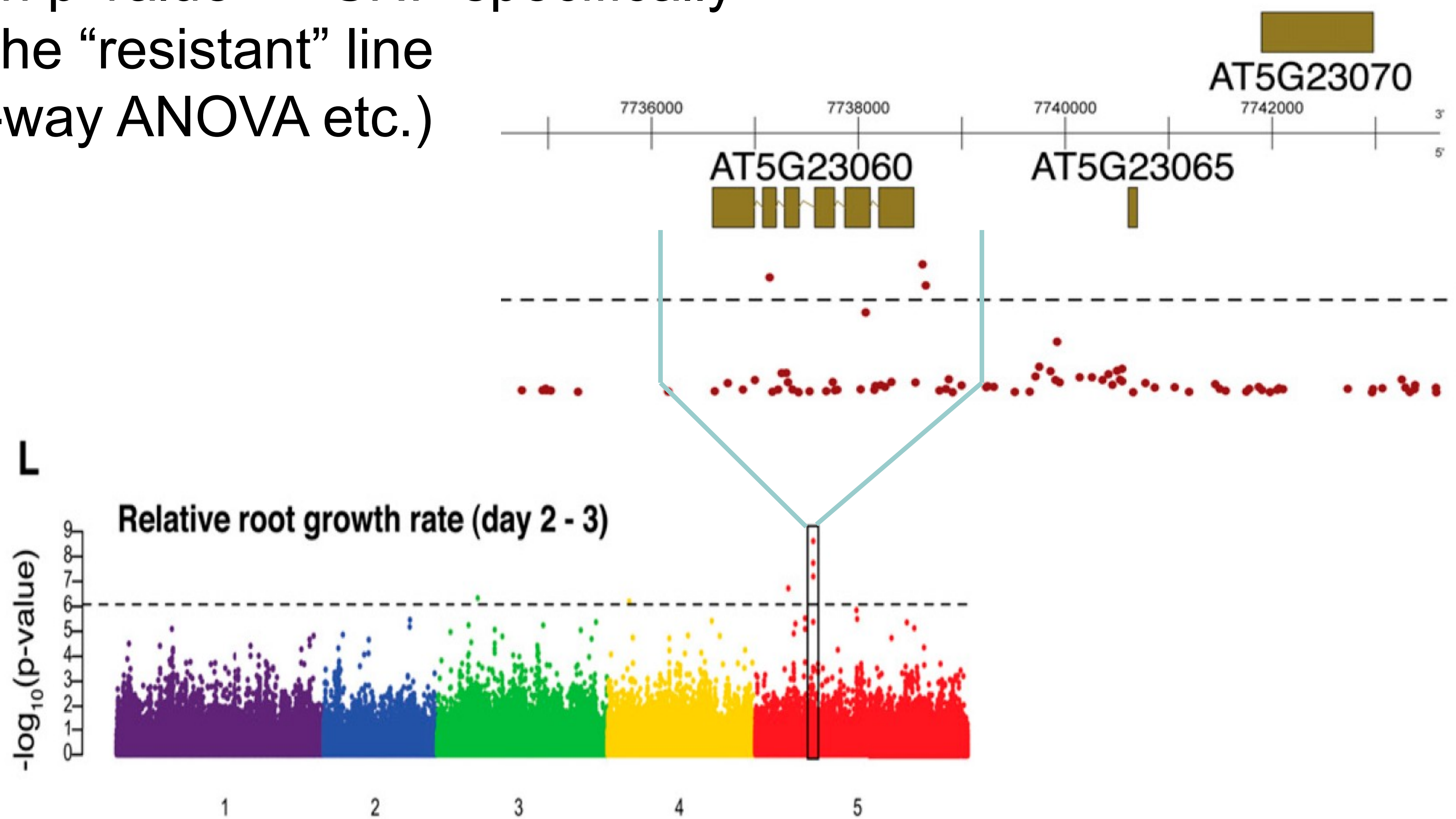
↓

searching for those different (e. g. root growth, slim root, resistant to exogenous treatment)

Slovak et al. 2014

Genome wide association studies (GWAS)

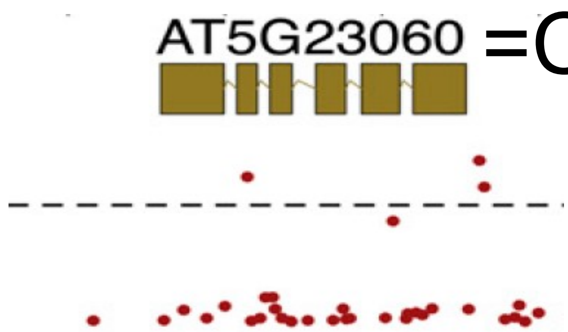
high p-value => SNP specifically in the “resistant” line (*N*-way ANOVA etc.)



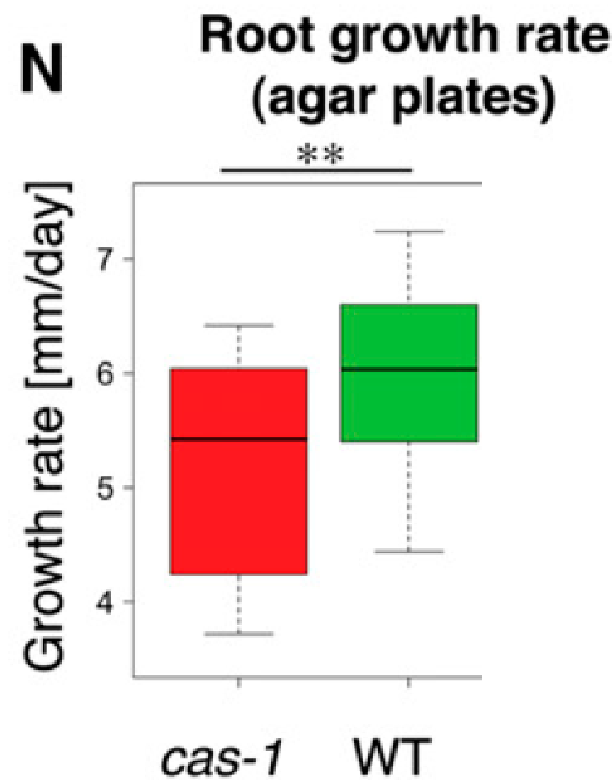
chromosome (locus)

Genome wide association studies (GWAS)

In contrast to human:
- how to test it?



=CaS

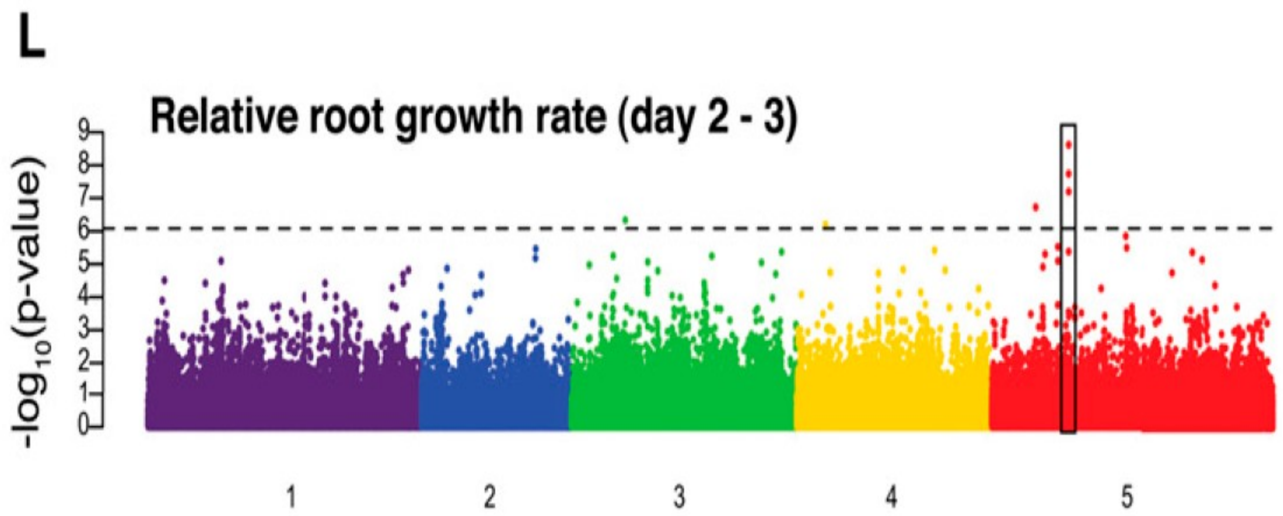


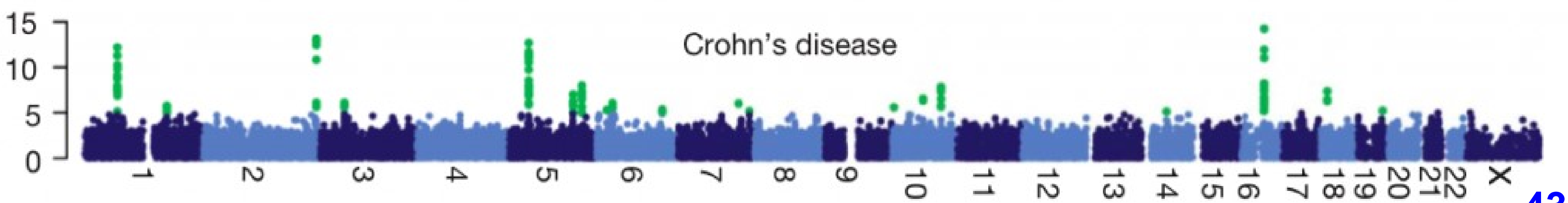
cas-1 mutant has indeed shorter root

Slovak et al. 2014

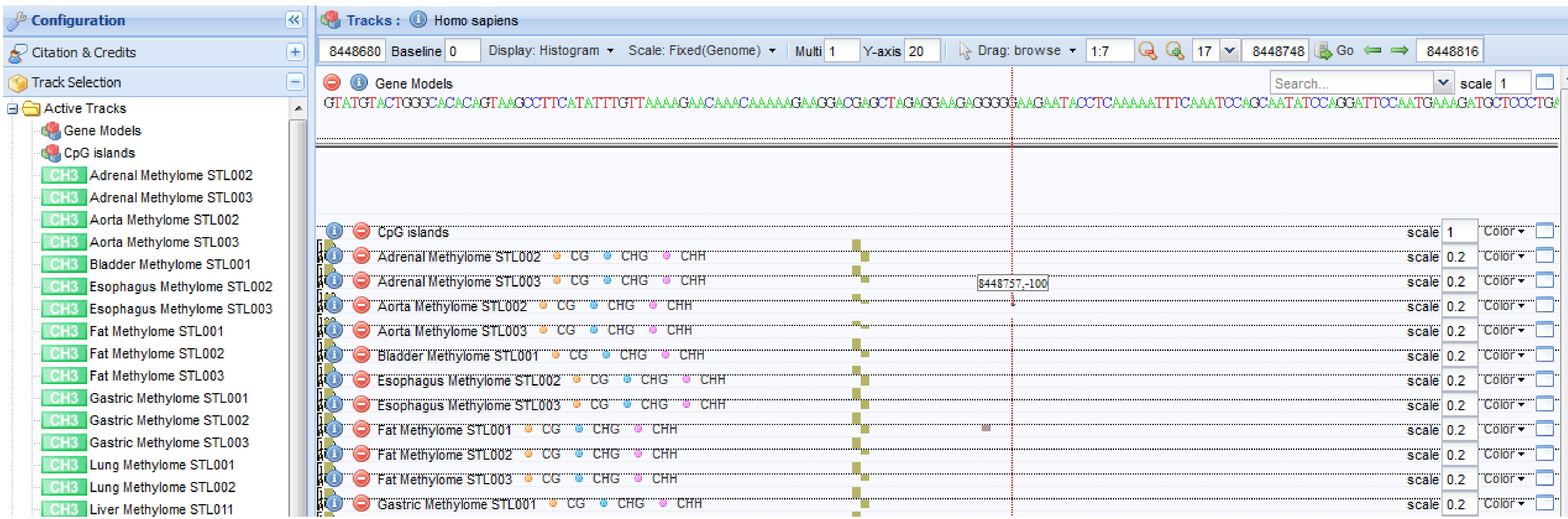
Genome wide association studies (GWAS)

Manhattan plot by human





Status of cytosine methylations in various tissues can be explored in various tissues (human)

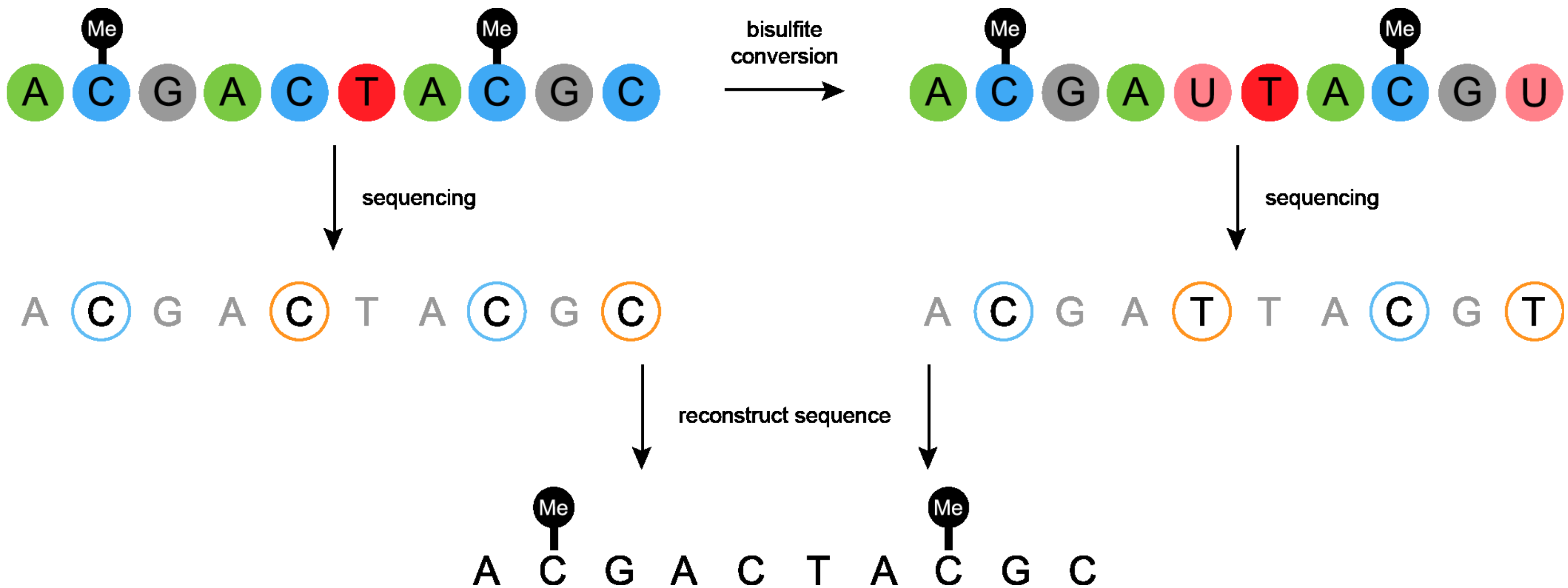


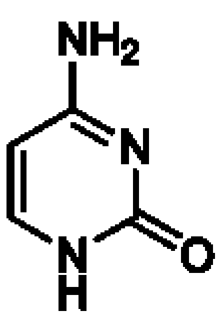
Epigenetic modifications

How to find methylated bases in genome?

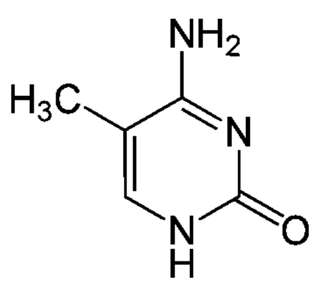
Which bases are methylated?

How to sequence methylation of genome?



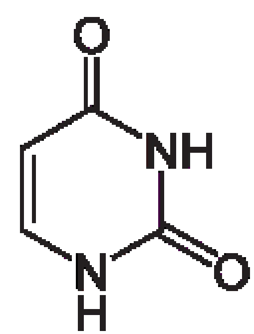


cytosine



5-methylcytosine

bisulfite sequencing



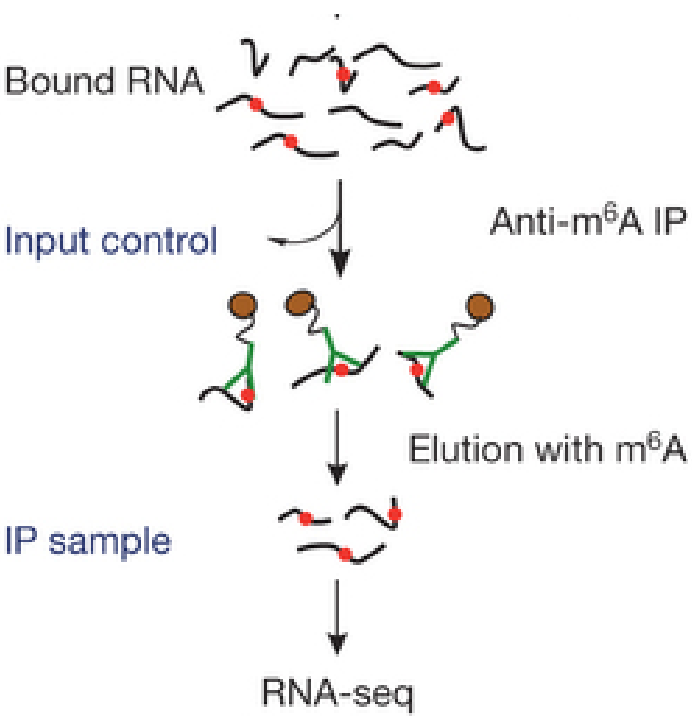
uracil

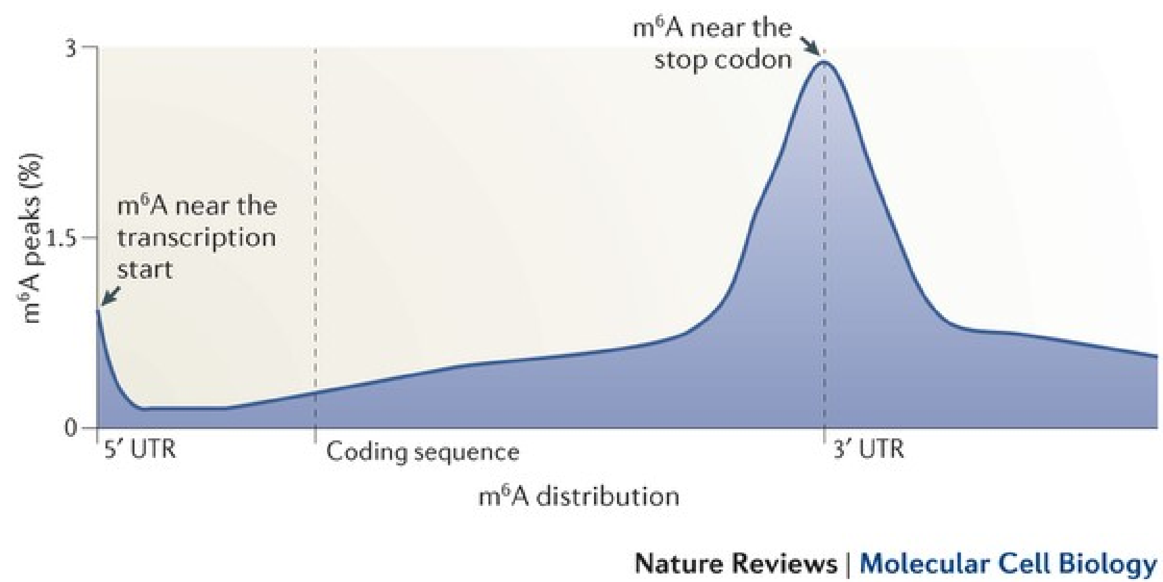
What is methylation of cytosine good for?

Are there other covalent modifications?

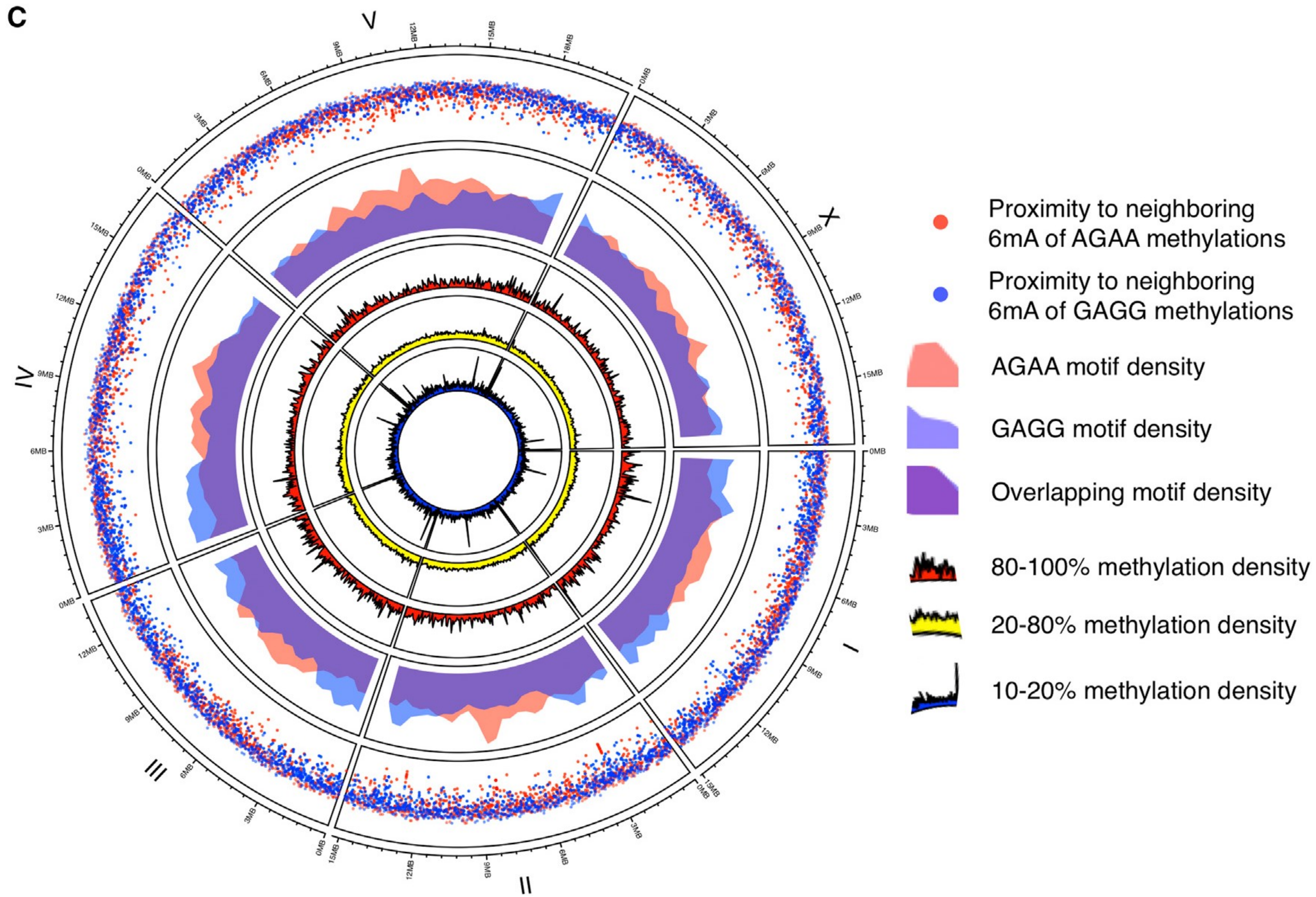
>100 base modification detected in nucleic acids, incl. RNA
N6-methyl adenosine most common in mRNA
(0.5 – 5 % adenosines methylated)

MeRIP – detecting adenine methylation on RNA

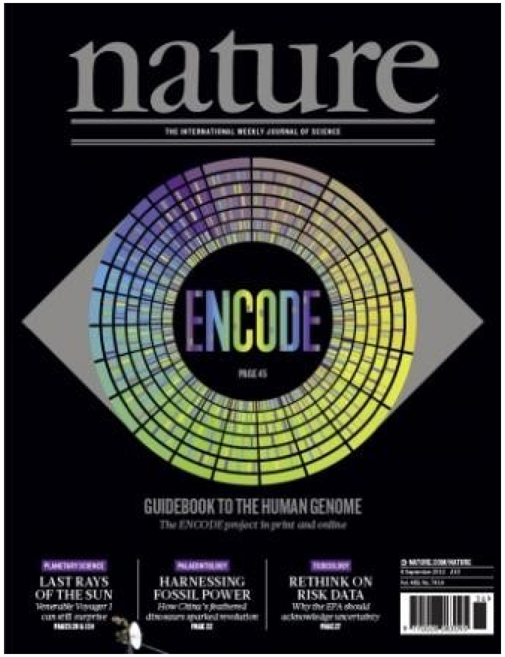




Similar technique also adapted on DNA in C. elegans



Greer et al. DNA Methylation on N6-Adenine in C. elegans, Cell 2015



The ENCODE project

The Encyclopedia of DNA Elements

Is really only ~1 % human genome functional?

1 % = gene coding regions

September 2012

ENCODE – think big

- 80 million dollars
- 1,640 data sets
- 147 cell types
- Nature (6), Genome Biology (18), Genome Research (6 papers)

The ENCODE project

Mainly cancer cells, lymphocytes etc.

RNA transcribed regions:
RNA-seq, CAGE, RNA-PET and manual annotation

Protein-coding regions:
mass spectrometry

Transcription-factor-binding sites:
ChIP-seq, DNase-seq

Chromatin structure:
DNase-seq, FAIRE-seq, histone ChIP-seq and MNase-seq

DNA methylation sites:
RRBS assay (cheaper version of bisulfite seq)

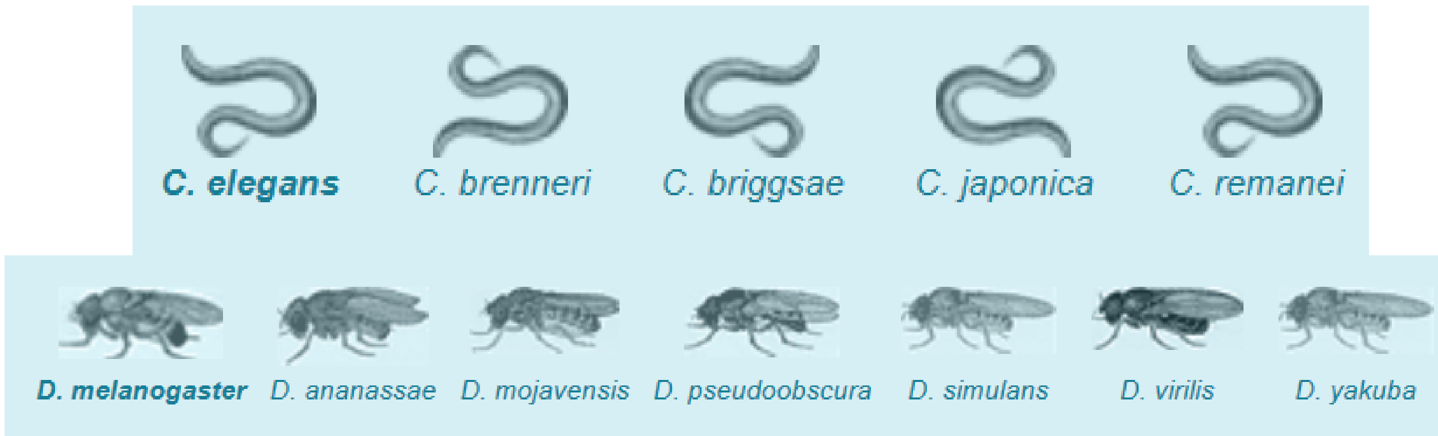
ENCODE - summary

~80 % genome associated with biochemical function:

- enhancers, promoters
- transcribed to non-coding RNA
- 75 % genome transcribed, at least little bit
- number of recognition sequences of DNA binding proteins doubled

E. g. 75 % meaningful number?

ModENCODE on the way



Drosophila tissue sources:

Adult eclosion + several days
Adult female
Adult male
Embryos 0-1, 0-2, 0-12, 10-12 hr etc
Larvae in various instars
Pupae in various stages
Mated males or females
etc.

http://www.modencode.org/

Question: where do you see the limits of high throughput biology?

Cons

- sometimes low quality data or artifacts
- occasionally data missing
- biological material is quite complex
- what to do with so many data?
- where is the idea?

What is systems biology

- next name for something between biology and chemistry?
  biochemistry -> proteomics
  molecular biology -> (functional) genomics
- a real new concept?

“Multidimensional biology”

- Genomics
- Epigenomics
- Transcriptomics
- Epitranscriptomics
- Translatomics / Proteomics
- Metabolomics
- Interactomics

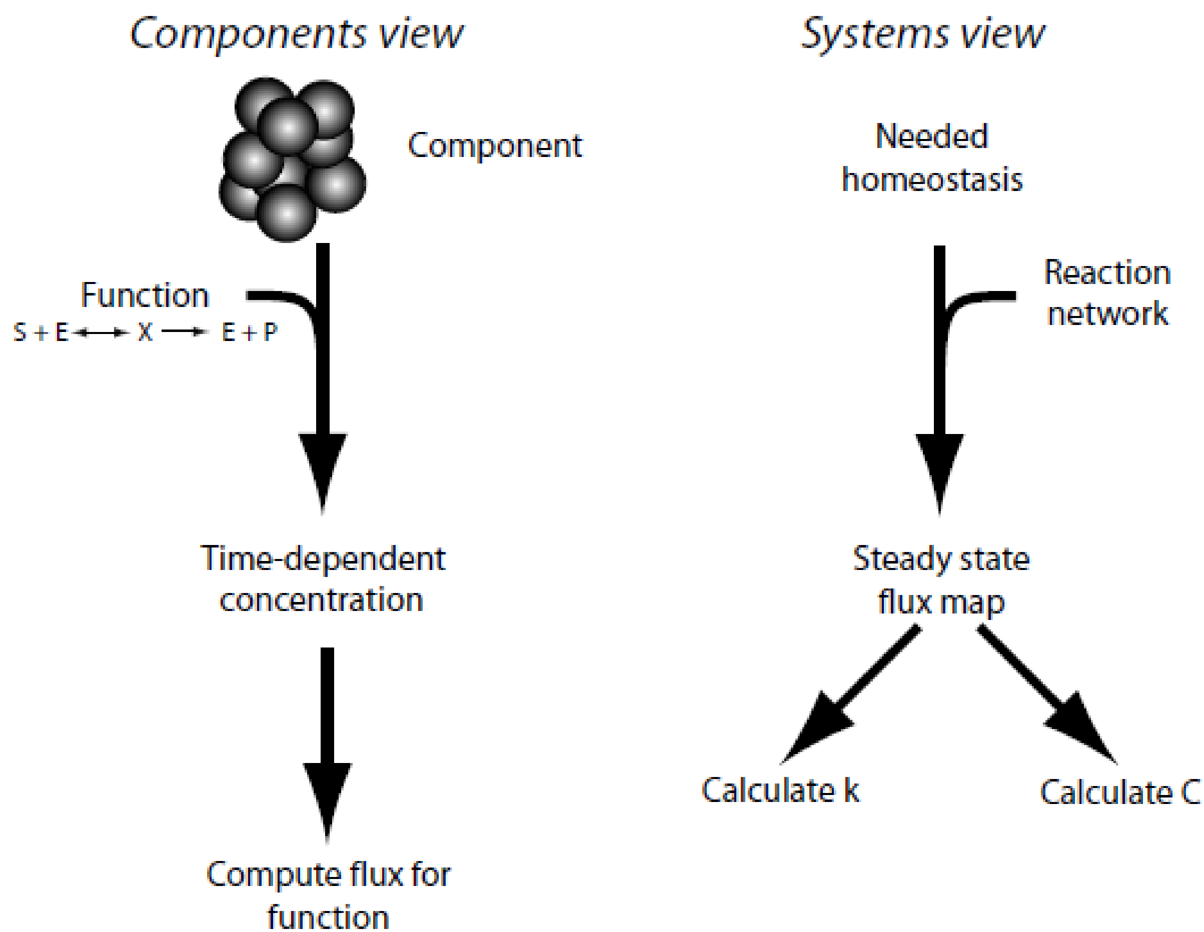
- Fluxomics
- NeuroElectroDynamics
- Phenomics
- Biomics

Systems theory

Forget about **reductionism**, think **holistically**.

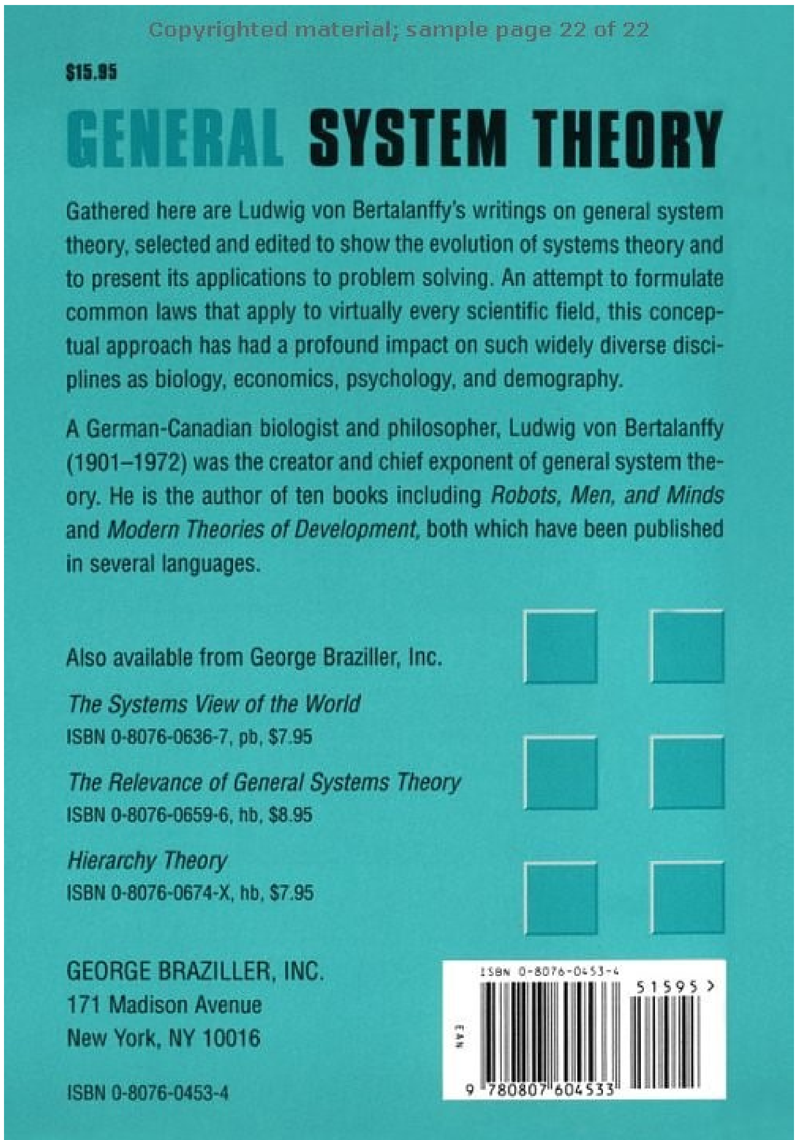
ὅλος [ho:'los] – greek. all, the whole, entire, complete

Reductionism vs. holism



Ludwig von Bertalanffy

(1901-1972)



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GENERAL SYSTEM THEORY

Gathered here are Ludwig von Bertalanffy's writings on general system theory, selected and edited to show the evolution of systems theory and to present its applications to problem solving. An attempt to formulate common laws that apply to virtually every scientific field, this conceptual approach has had a profound impact on such widely diverse disciplines as biology, economics, psychology, and demography.

A German-Canadian biologist and philosopher, Ludwig von Bertalanffy (1901–1972) was the creator and chief exponent of general system theory. He is the author of ten books including *Robots, Men, and Minds* and *Modern Theories of Development*, both which have been published in several languages.

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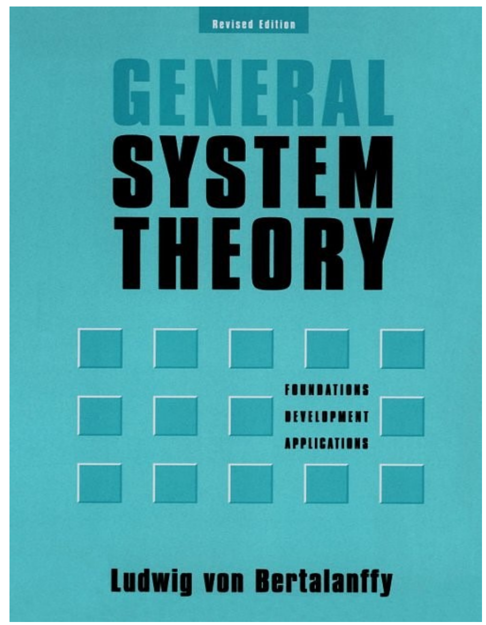
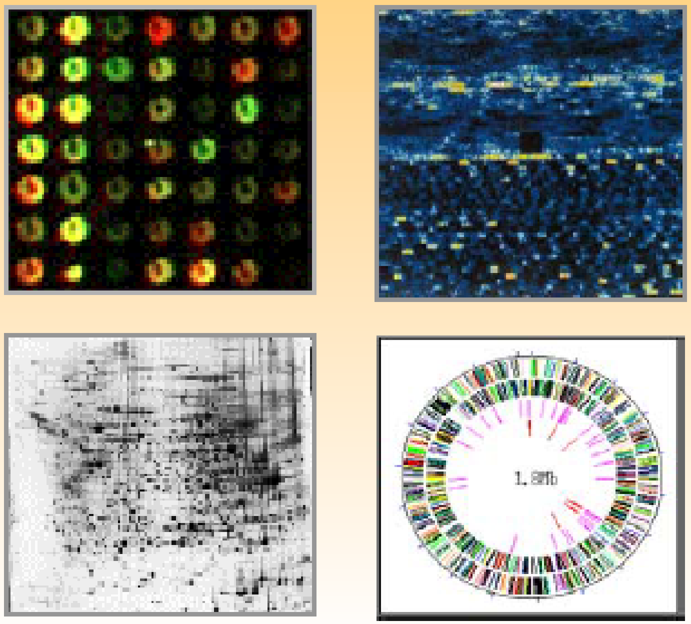


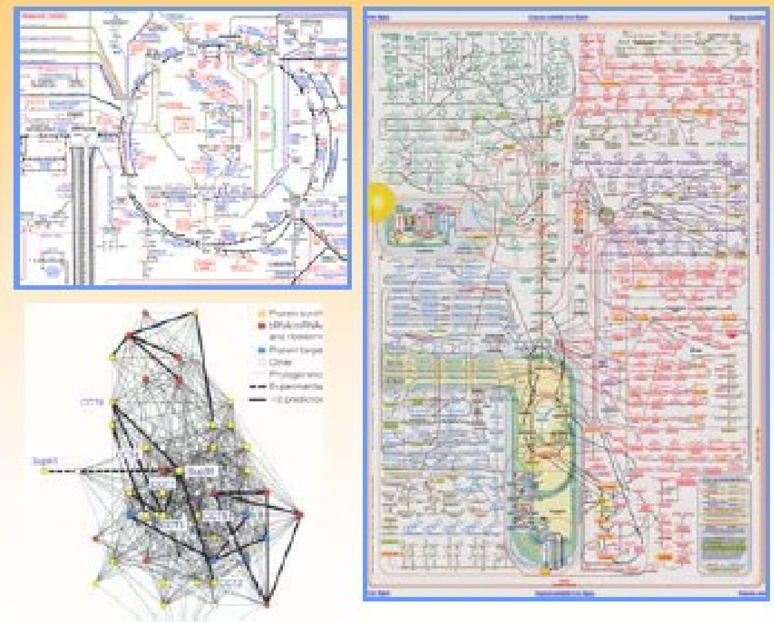
xiv

Omics-revolution shifts paradigm to large systems

High Throughput Data

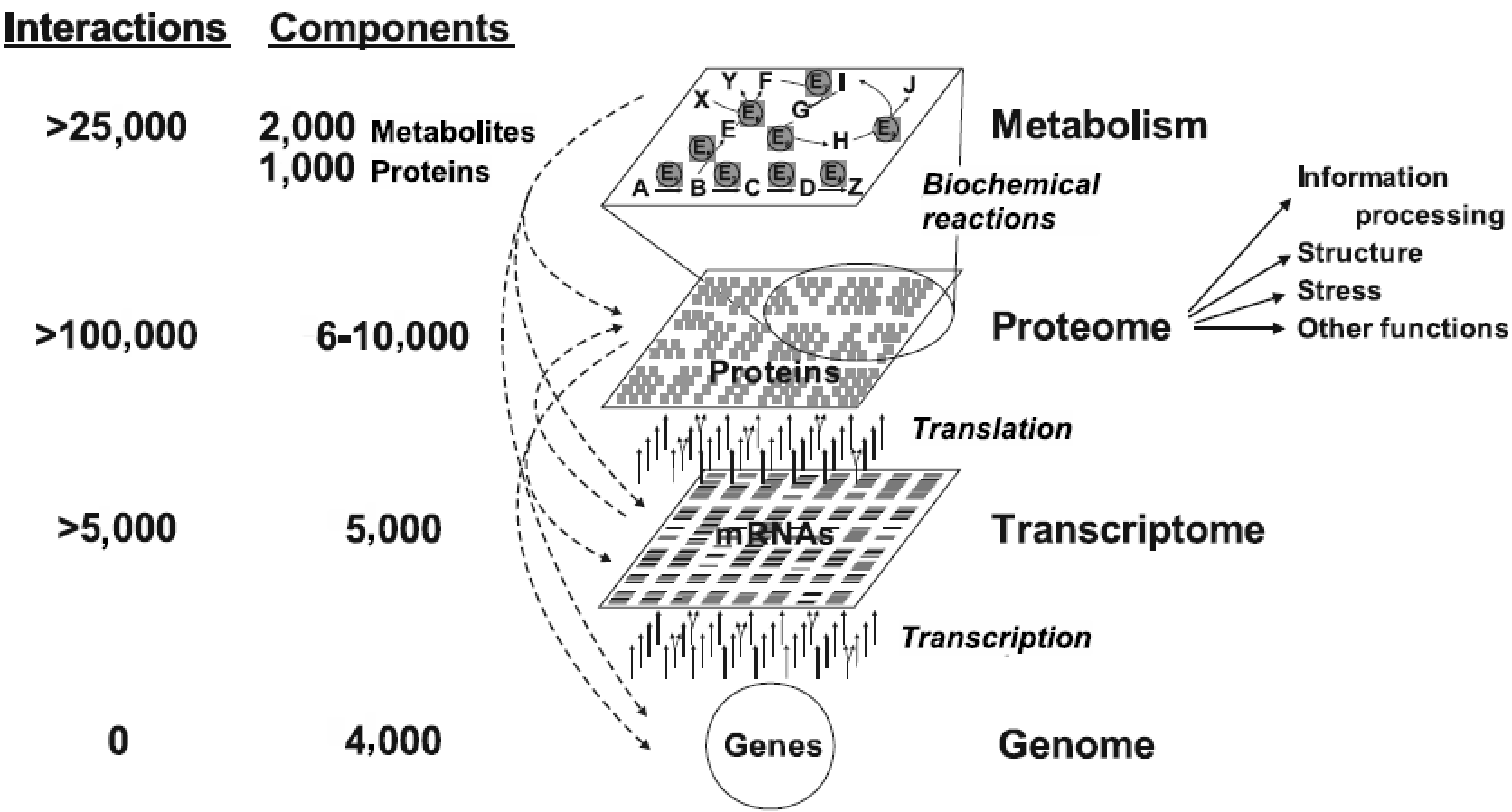


Cellular Complexity

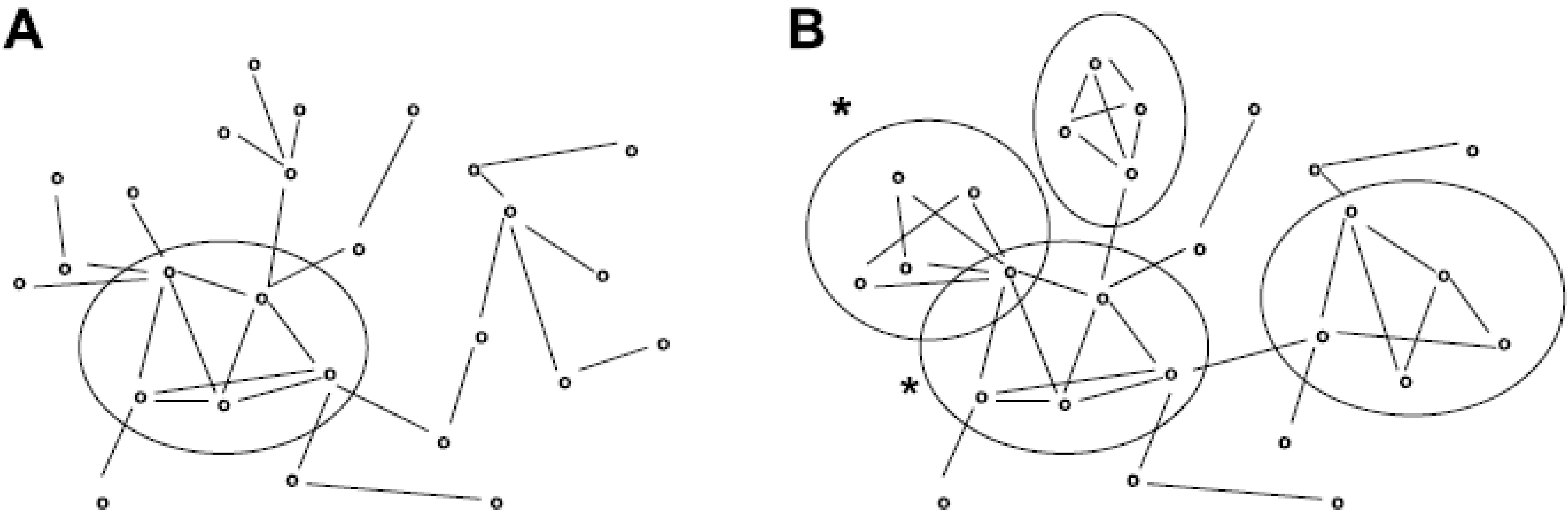


- Integrative bioinformatics
- (Network) modeling

E. coli genome and proteome is small



Reductionism within holism



Lets e.g. assume that transcription and translation is one module.

Conclusions – systems biology

- computing capacities allow handling large data sets
- fashionable
- modelling whole cell processes in silico?
- story frequently missing, there will be always question marks

Great web sites for organismal models

http://www.yeastgenome.org/	*S. cerevisiae*
http://www.pombase.org/	*S. pombe*
http://flybase.org/	*Drosophila*
http://www.wormbase.org/	*C. elegans*
http://www.arabidopsis.org/	*A. thaliana*

Also nice web sites

http://encodeproject.org/
http://www.thebiogrid.org/
http://www.genemania.org/
http://string-db.org/
…and many others
…pay attention, if they are kept alive and curated

Additional literature

- Venter, J.C. (2008). A life decoded: my genome, my life (London: Penguin).
- Albert-László Barabási (2002) Linked. (Perseus Publishing)
- http://www.youtube.com/watch?v=Z__BHVFP0Lk and further – excellent talks about systems biology from Uri Alon (Weizman Institute) – absolutely best
- http://www.pnas.org/content/110/29/11952 (paper which challenges something conclusions in ENCODE)