

Assessing compound carcinogenicity *in vitro* using connectivity mapping

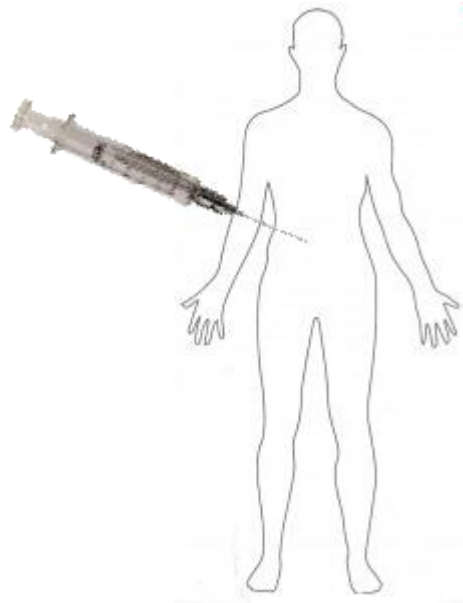
Florian Caiment



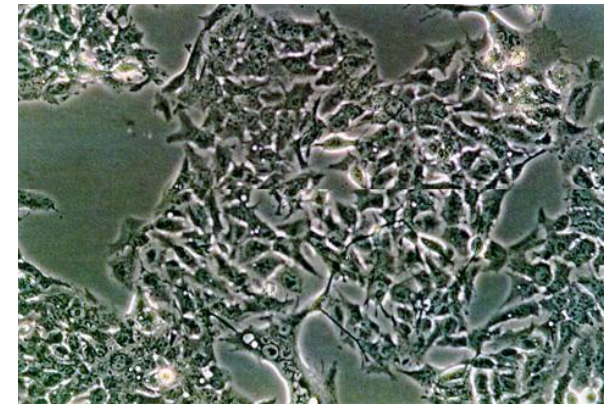
Alternative to animal testing



**Compound
X**



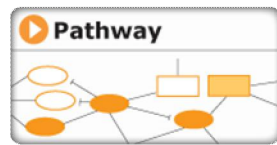
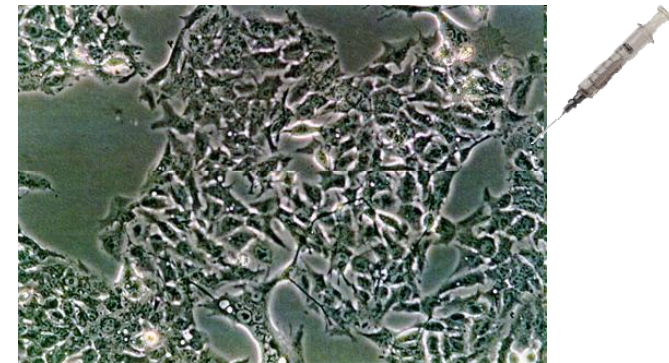
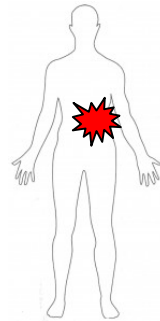
***in vitro* toxicogenomics**



60% accuracy

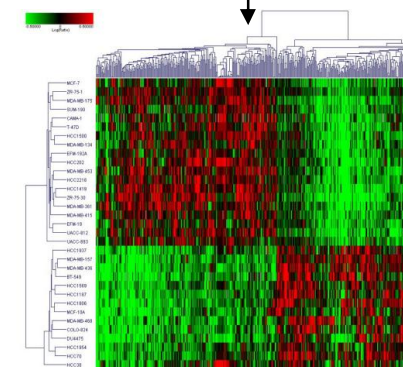
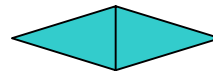
3R : Reduction, Refinement, Replacement of animal testing.

in vitro toxicogenomics as alternative



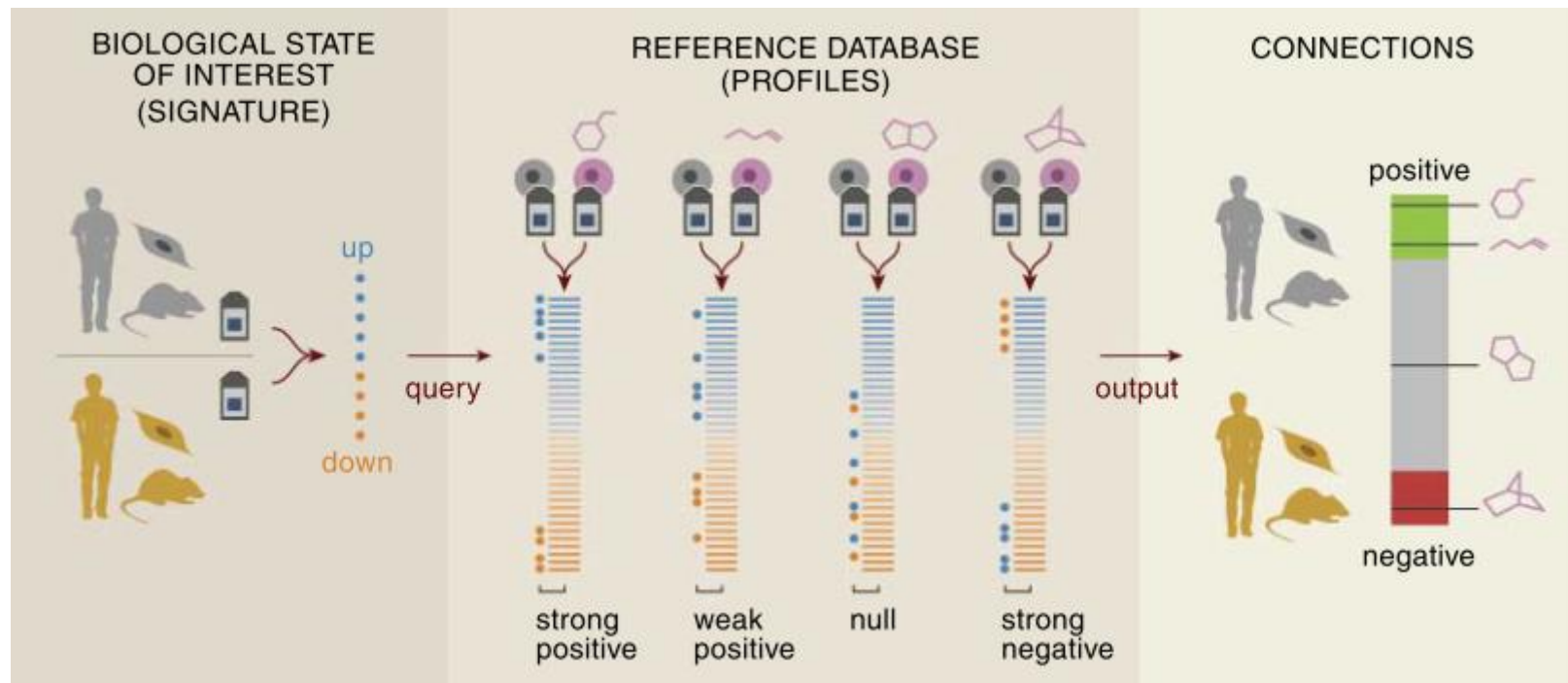
Symbol	
IGFBP3	
AGL	IL13RA1
BIRC3	IMPA2
AQP1	LGALS3BP
COL1A1	MMP2
COL5A2	PLN
CTBP2	POLRMT
DCK	SGCB
DCN	SP100
DPP4	VIM
EIF4EBP1	SRPX
FBN1	PROM1
FGFR2	NAT8
GJA1	HEPH

?



The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease

Justin Lamb,^{1*} Emily D. Crawford,^{1†} David Peck,¹ Joshua W. Modell,¹ Irene C. Blat,¹ Matthew J. Wrobel,¹ Jim Lerner,¹ Jean-Philippe Brunet,¹ Aravind Subramanian,¹ Kenneth N. Ross,¹ Michael Reich,¹ Haley Hieronymus,^{1,2} Guo Wei,^{1,2} Scott A. Armstrong,^{2,3} Stephen J. Haggarty,^{1,4} Paul A. Clemons,¹ Ru Wei,¹ Steven A. Carr,¹ Eric S. Lander,^{1,5,6} Todd R. Golub^{1,2,3,5,7*}



Liver Cancer



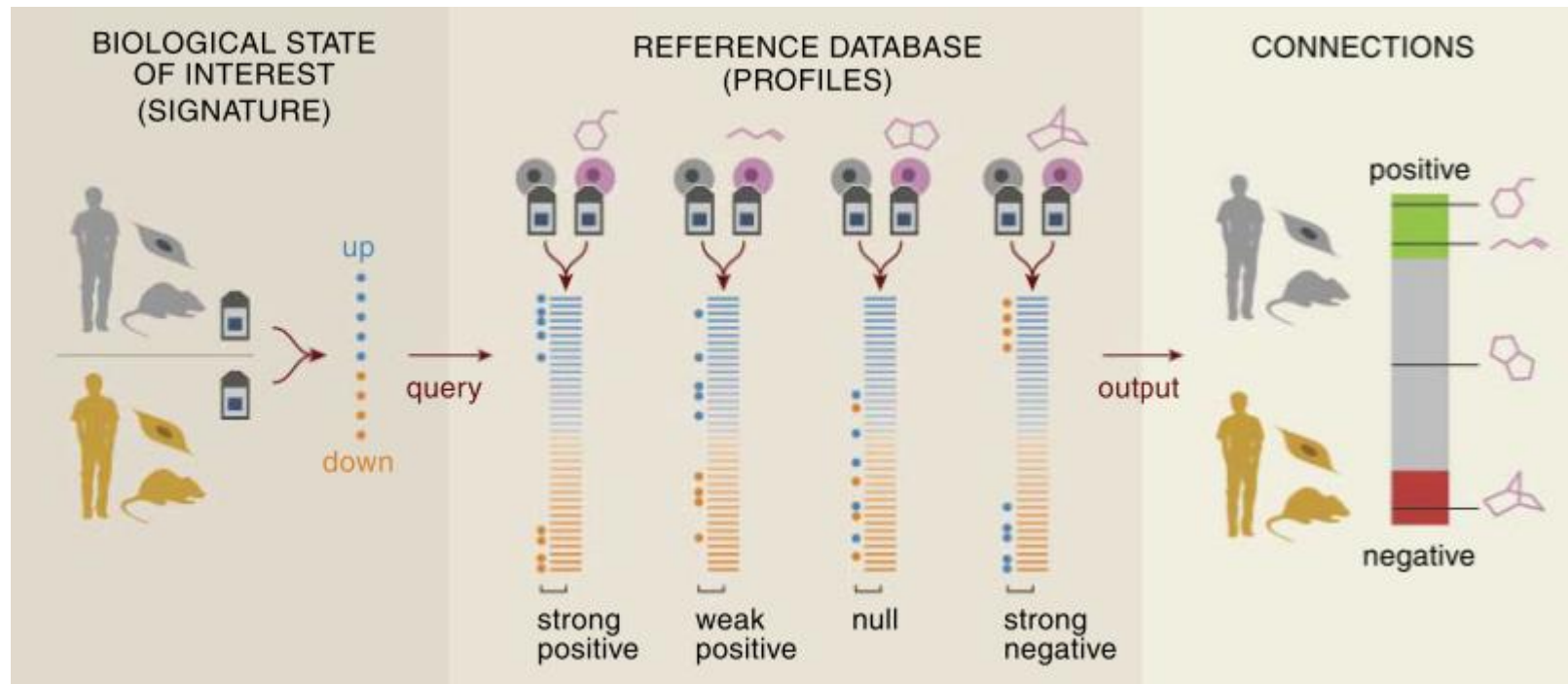
HepatoCellular Carcinoma (HCC)

- 5th most common cancer worldwide
- 3rd most common cause of cancer mortality
- Accounts for ~90% of primary liver cancers
- Induced either by hepatic viral infections (HBV/HVC) or hepatic cirrhosis (alcoholism)
Other known risks: AFB1, cigarette smoking, obesity, diet
- Complex process associated with accumulation of genetic & epigenetic changes that occur during initiation, promotion and progression of the disease

Connectivity Mapping

HCC signature

***in vitro* human liver**



Open TG-GATEs



このDBIについて

お知らせ

データ検索

公開データ一覧

利用許諾条件

お問い合わせ

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CompoundかPathologyのどちらか一つの検索条件を選択し[Search]をクリックしてください。

Compound List

select compound

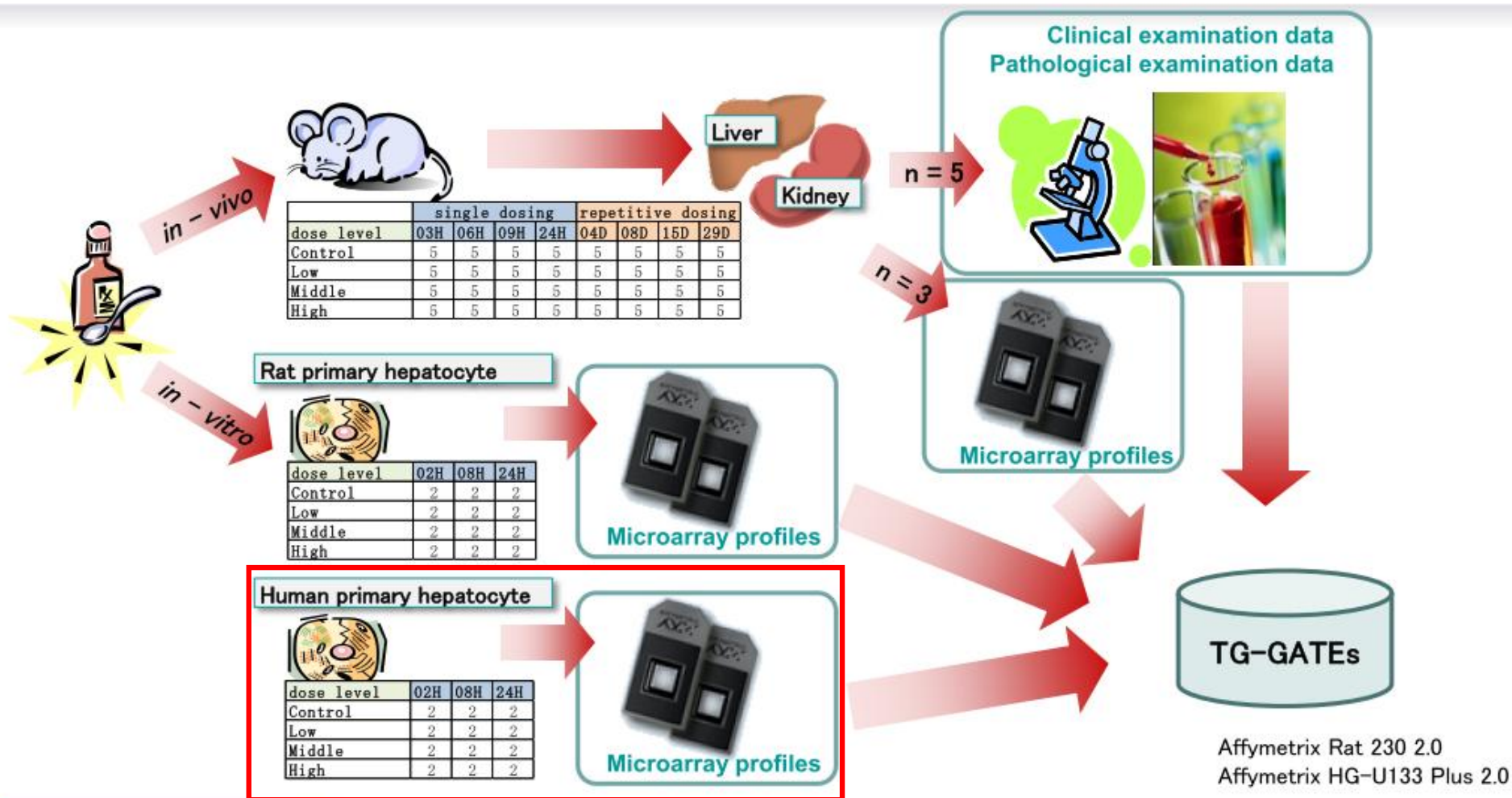
acarbose
acetamidofluorene
acetaminophen
acetazolamide
adapin
ajmaline
allopurinol
allyl alcohol
amiodarone
amitriptyline

上記化合物を一つ選択してください



生物種・実験条件の選択画面に進みます

Typical Experimental Design for Each Compound



Up to 240 microarray profiles for each compound

- 3 (n) x 8 (time-point) x 4 (dose-level) = 96 microarray profiles from vivo liver
- 3 (n) x 8 (time-point) x 4 (dose-level) = 96 microarray profiles from vivo kidney
- 2 (n) x 3 (time-point) x 4 (dose-level) = 24 microarray profiles from vitro rat hepatocyte
- 2 (n) x 3 (time-point) x 4 (dose-level) = 24 microarray profiles from vitro human hepatocyte

Open TG-GATes



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CompoundがPathologyのどちらか一つの検索条件を選択し[Search]をクリックしてください。

Compound List

select compound

acarbose
acetamidofluorene
acetaminophen
acetazolamide
adapin
ajmaline
allopurinol
allyl alcohol
amiodarone
amitriptyline

上記化合物を一つ選択してください



生物種・実験条件の選択画面に進みます

PHH

158 compounds

Affy_hg u133 plus 2

2 or 3 Times points :
(2h) - 8h, 24h

2 or 3 Doses :
(low)-Medium-High

Control and duplicates
=> 2605 arrays

Compound Classification



- **Human Liver Carcinogens** (C^{HL}) : 3
Sufficient data on *human* carcinogenicity on *liver* organ available
- **Rodent Liver Carcinogens** (C^{RL}) : 23
Sufficient data on *rodent* carcinogenicity on *liver* organ available
- **Non Liver Carcinogens** (C^{NL}) : 12
known human and/or rodent carcinogenic compounds in non-liver target organs
- **Non Carcinogens** (NC) : 15
Negative in all available carcinogenicity tests in rodents (often no available information about human studies)
- **Unknown Carcinogenicity** (UC) : 78
Unavailable / Unclear *in* all available carcinogenicity tests (mainly in rodents)

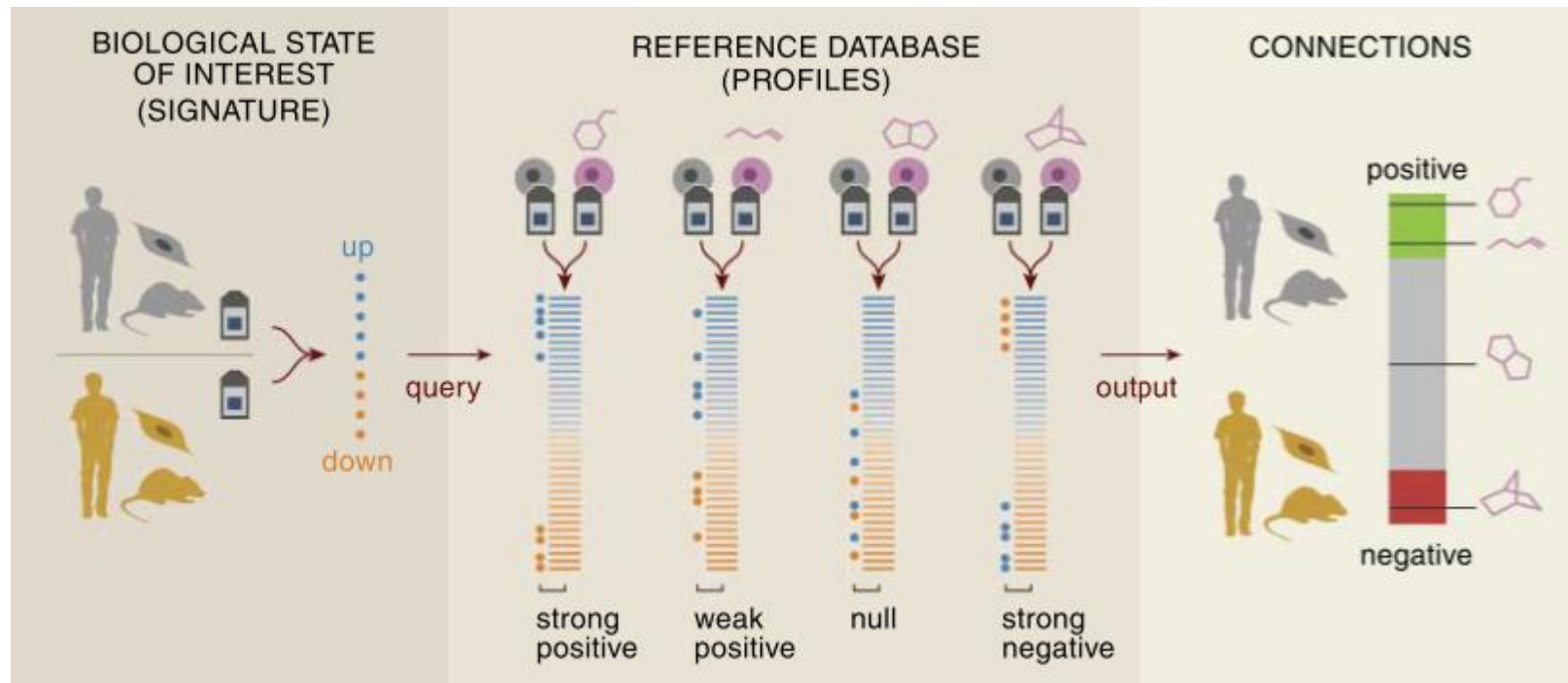
International Agency for Research on Cancer



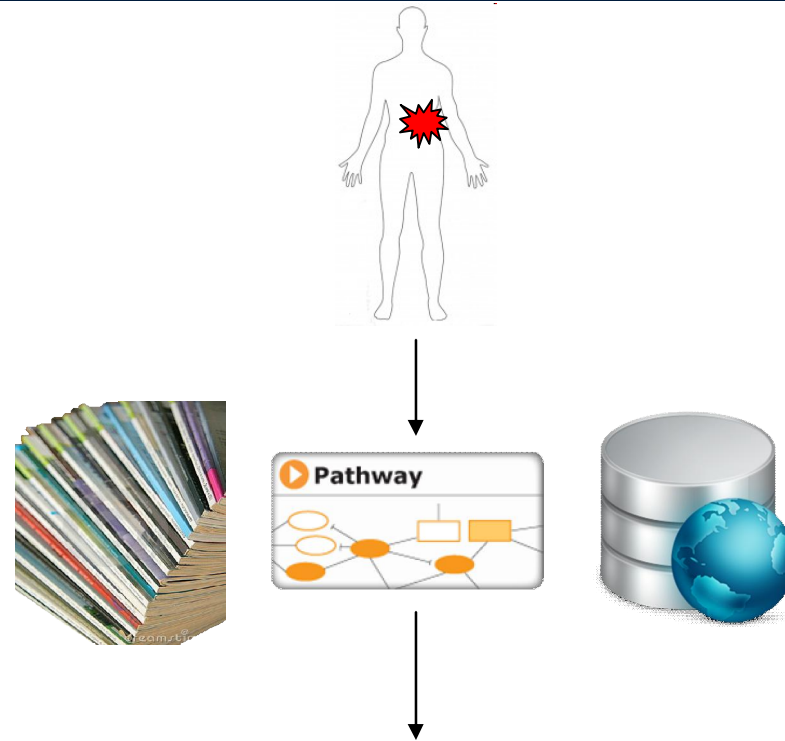
National Toxicology Program
Department of Health and Human Services

The Carcinogenic
Potency Project

Connectivity Mapping

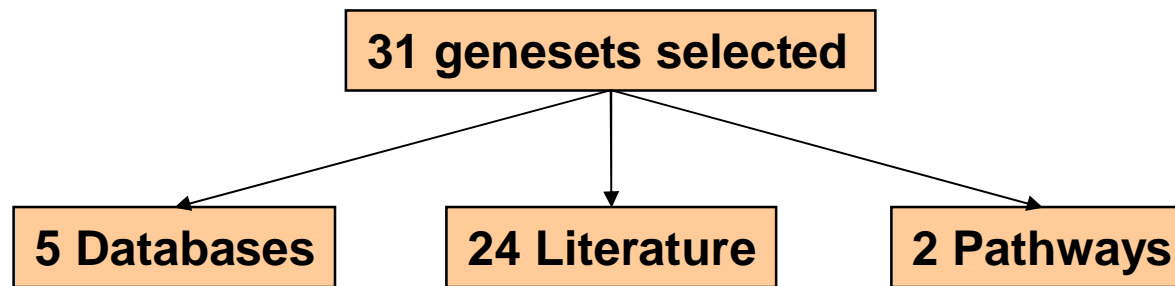
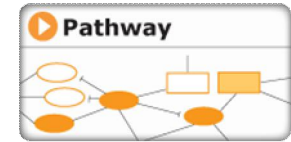


in vitro toxicogenomics as alternative ?

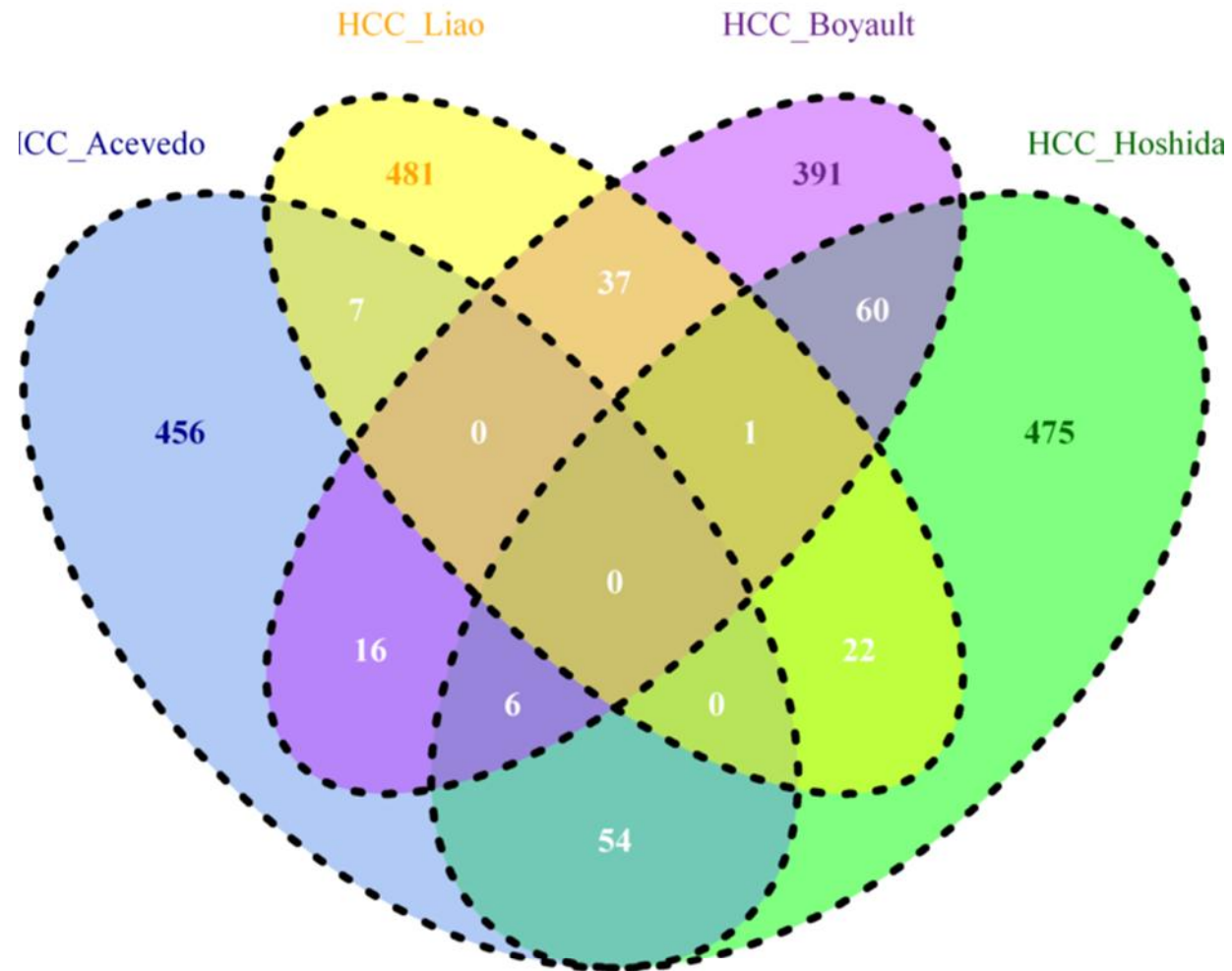


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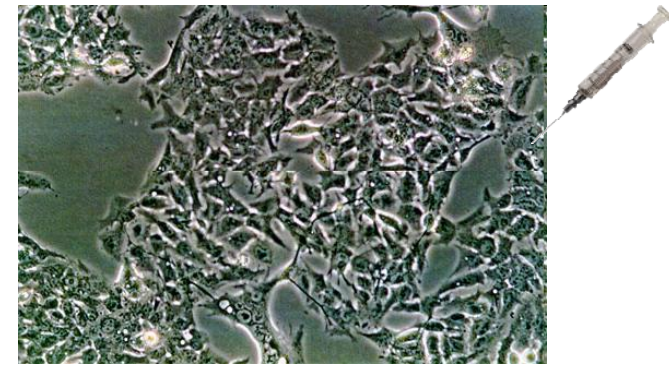
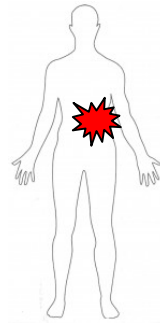
Query signature : genesets



Genesets Overlap

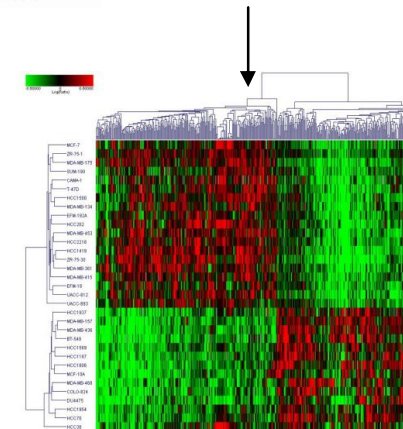
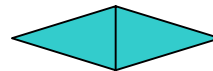


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?



Array Express *in vivo* HCC data



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Examples: [E-MEXP-31](#), [cancer](#), [p53](#), [Genetics](#)

ArrayExpress - functional genomics data

ArrayExpress is a database of functional genomics experiments that can be queried and the data downloaded. It includes gene expression data from microarray and high throughput sequencing studies. Data is collected to [MIAME](#) and [MINSEQE](#) standards. Experiments are submitted directly to ArrayExpress or are imported from the NCBI GEO database.

Data Content

Updated today at 06:00

- 38392 experiments
- 1104757 assays
- 14.21 TB of archived data

Latest News

5 Mar 2013 - **New ArrayExpress interface**

ArrayExpress, along with the EBI website, has a new look and feel. Click the [experiment tab](#) to see our new layout or [read about the new design](#). We have preserved the previous functionality to maintain a consistent query experience and we would love to hear what you think. Please use our [Feedback](#) to provide comments.

Links

Information about how to search ArrayExpress, understand search results, how to submit data and FAQ can be found in our [Help section](#).

Find out more about the [Functional Genomics group](#).

Tools and Access

[ArrayExpress Bioconductor package](#): an R package to access ArrayExpress and build data structures.

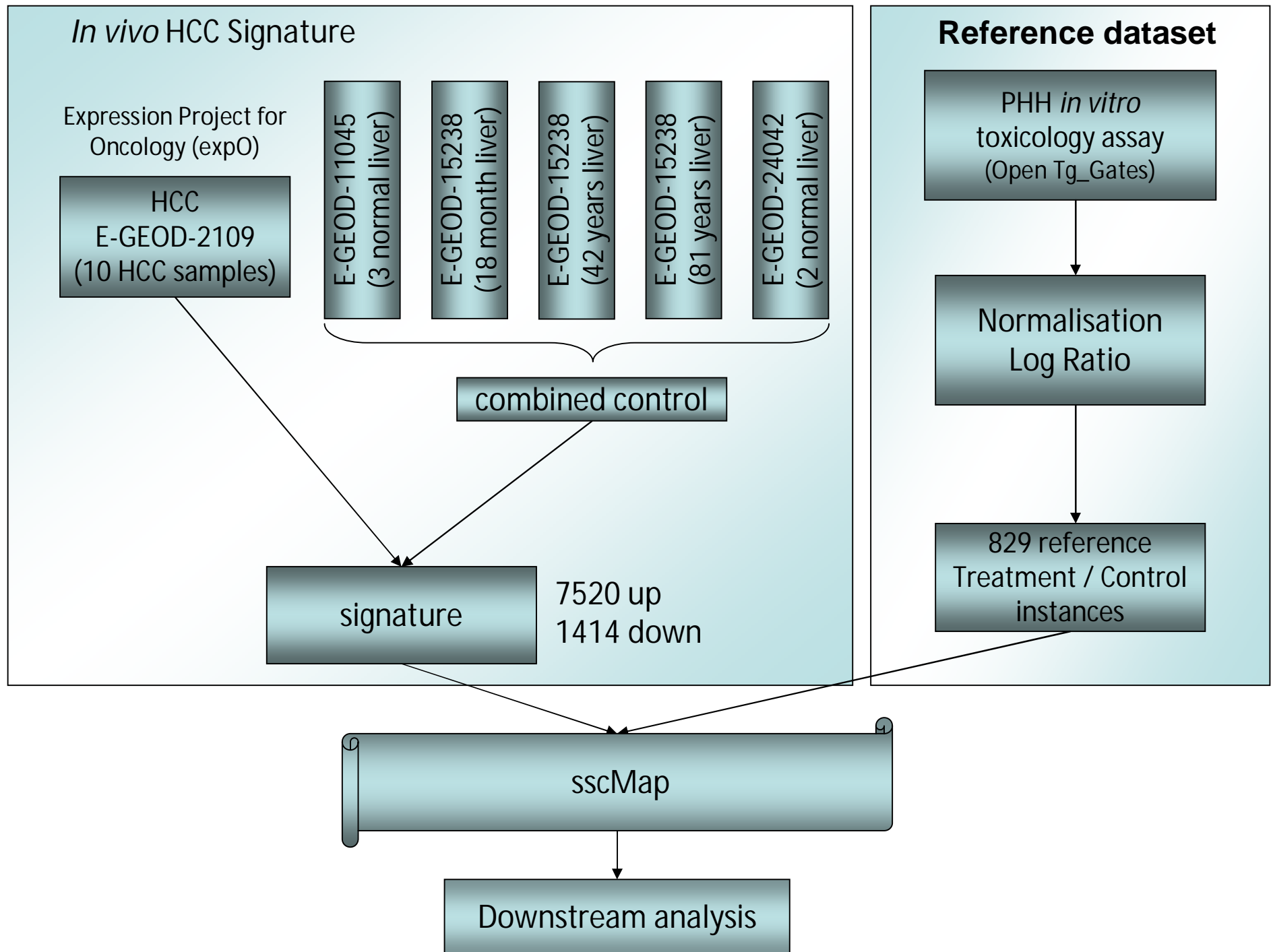
[Programmatic access](#): query and download data using web services or JSON.

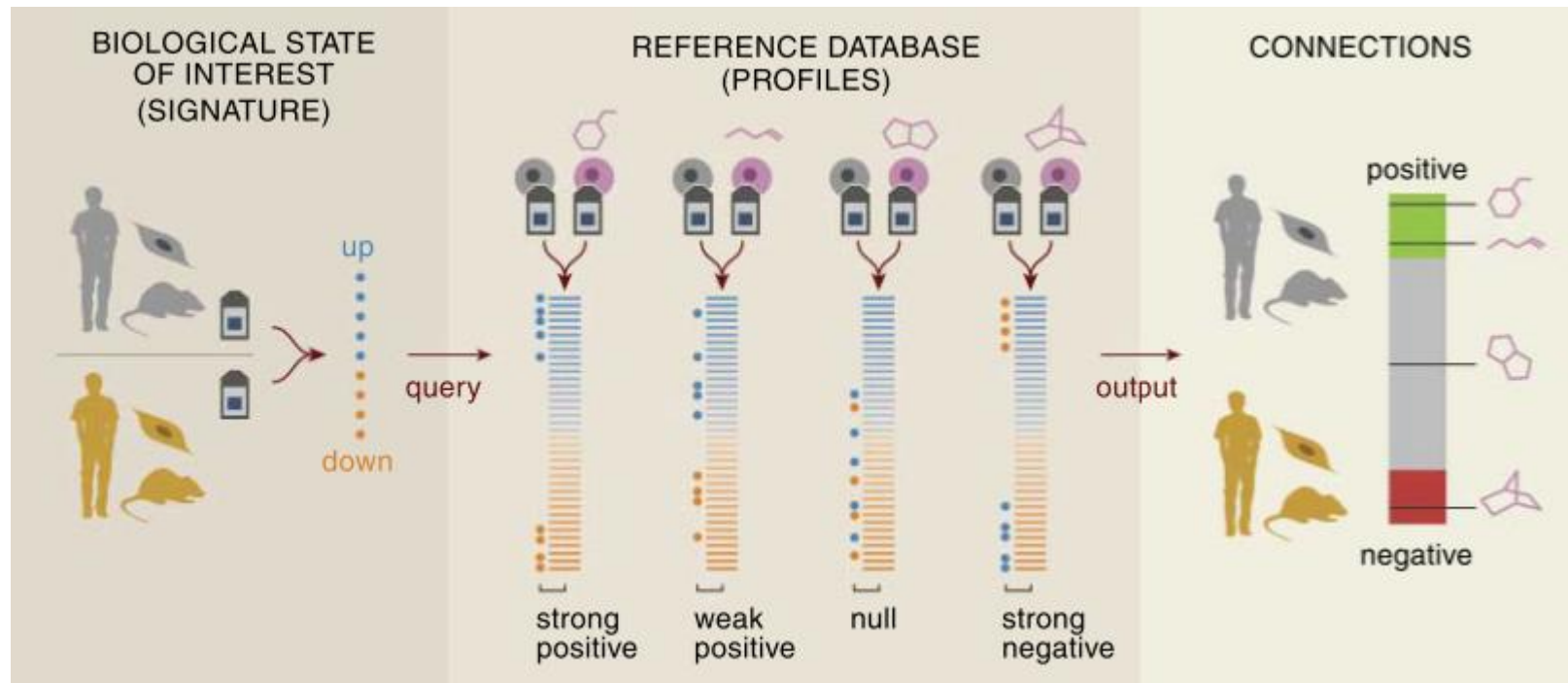
[FTP access](#): data can be downloaded directly from our FTP site.

Related Projects

Discover up and down regulated genes in numerous experimental conditions in the [Expression Atlas](#).

Explore the [Experimental Factor Ontology](#) used to support queries and annotation of ArrayExpress data.

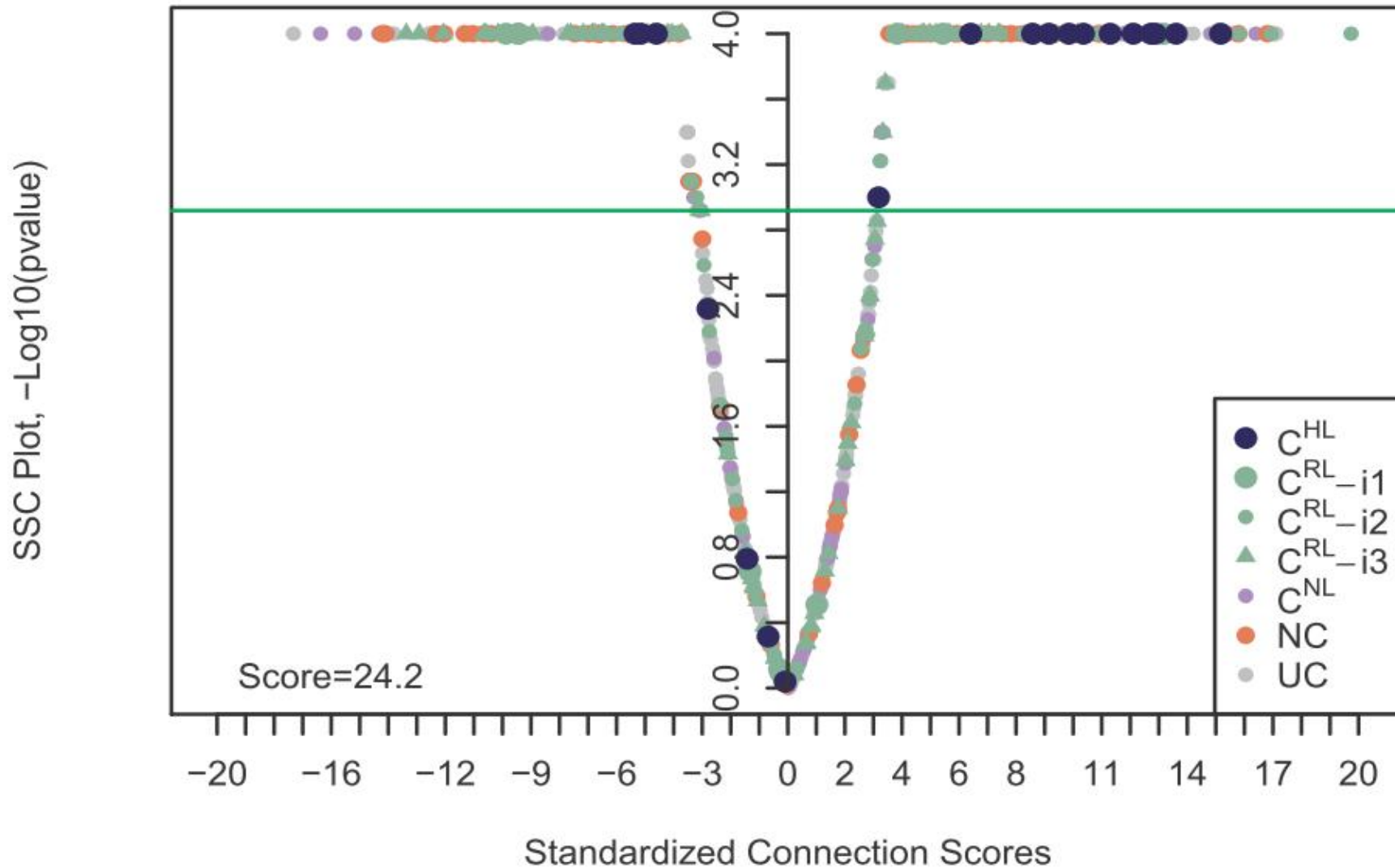




sscMap results



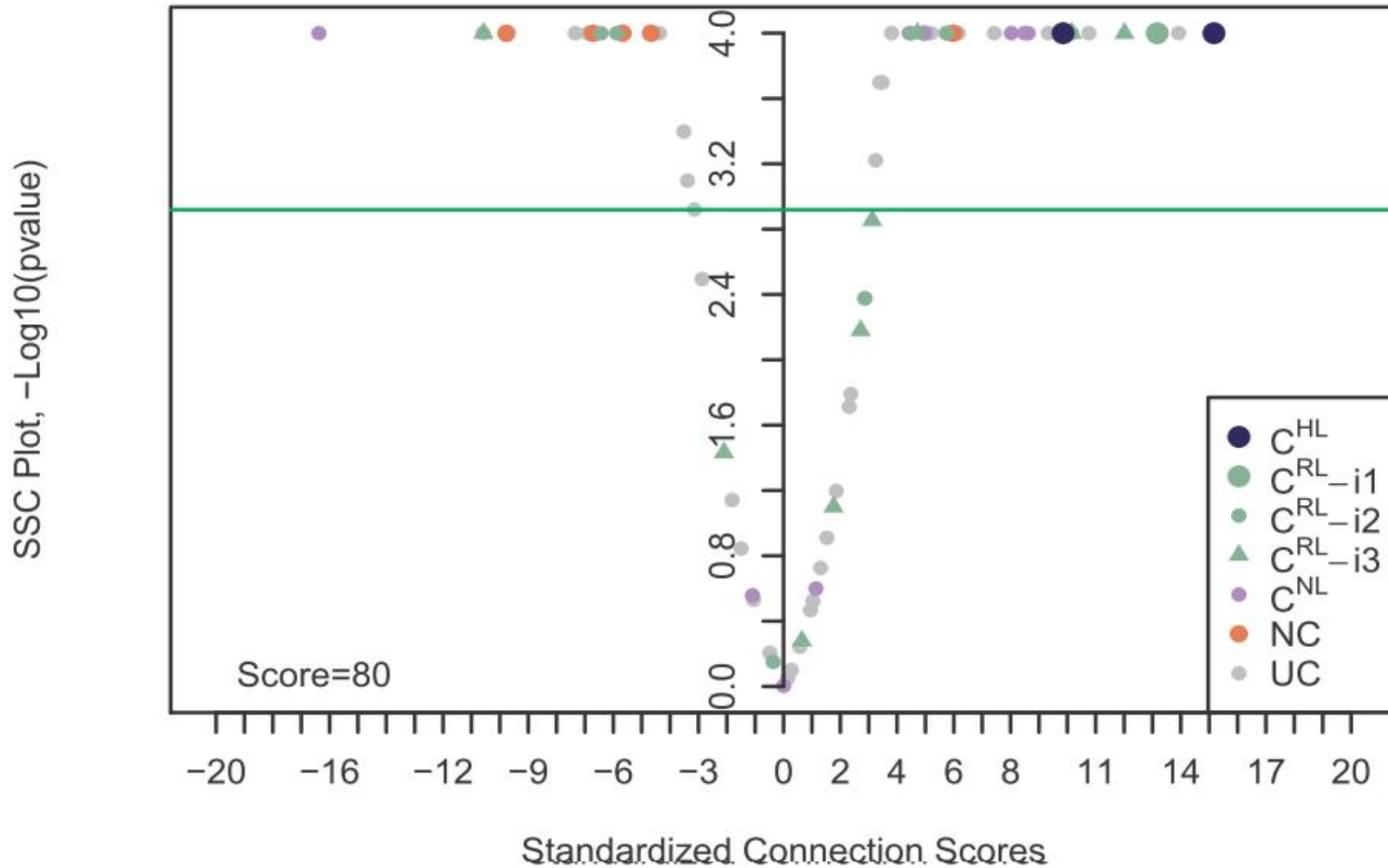
All doses and time points



sscMap results



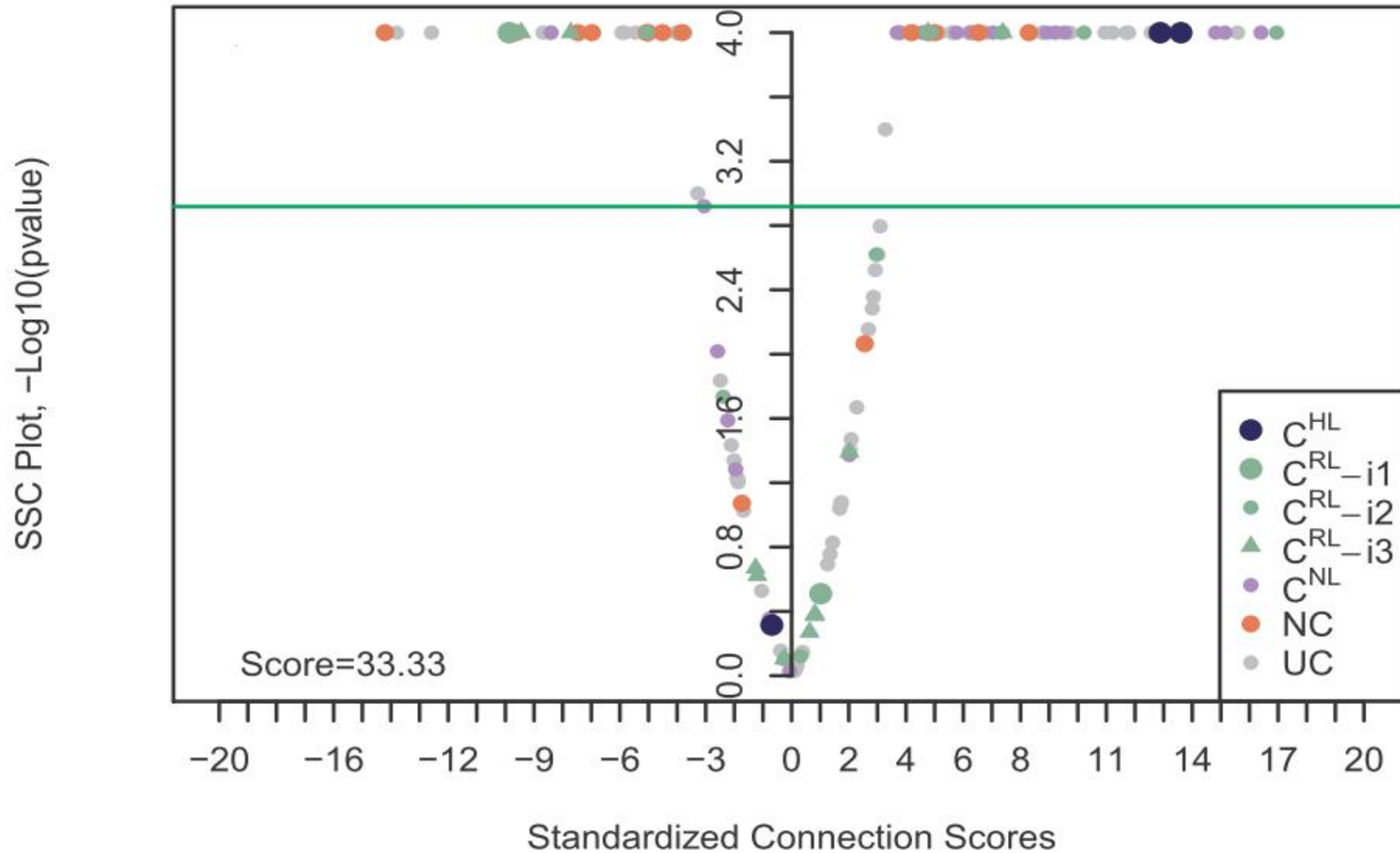
Low dose and 24 hours exposure



sscMap results



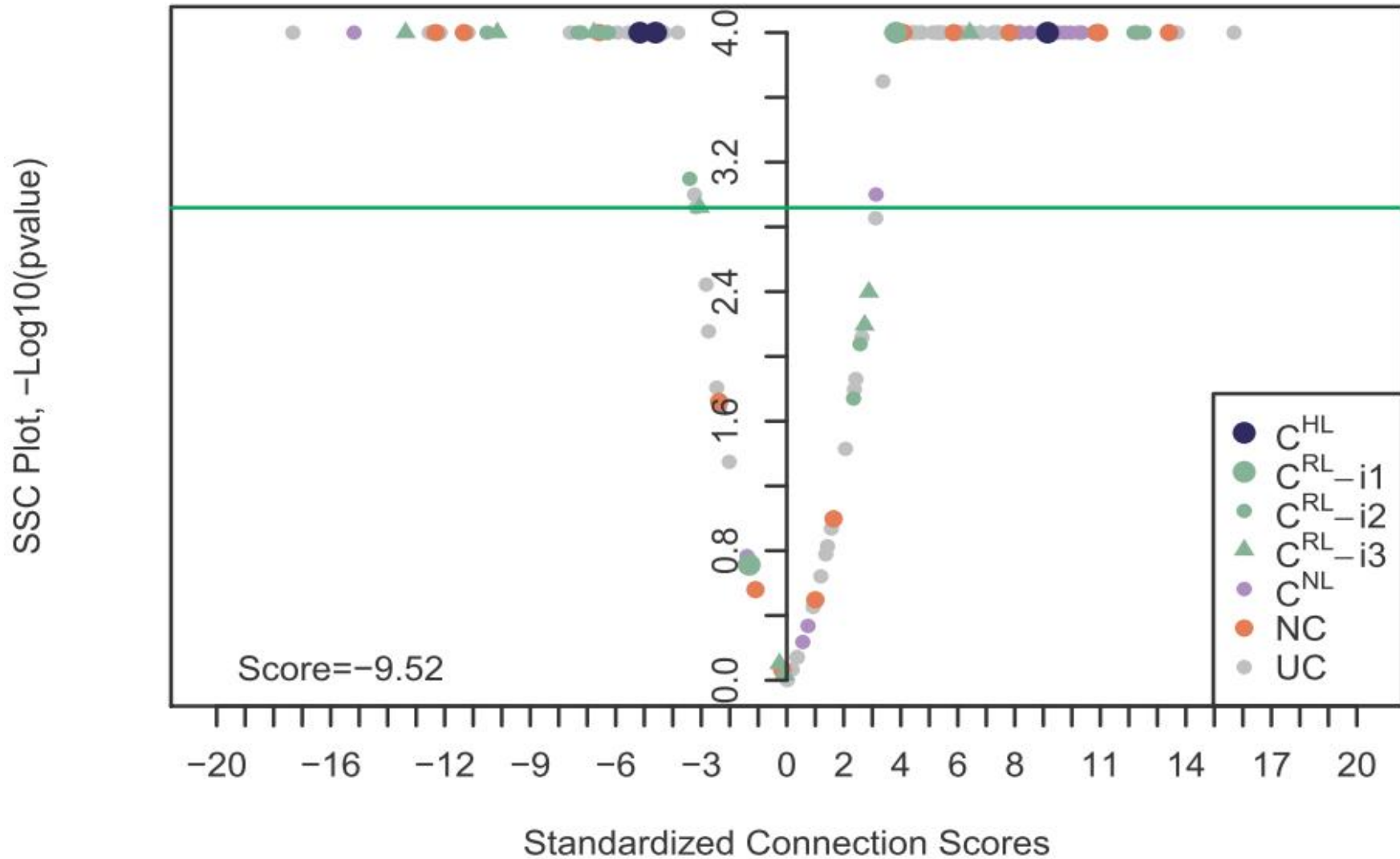
High dose and 24 hours exposure



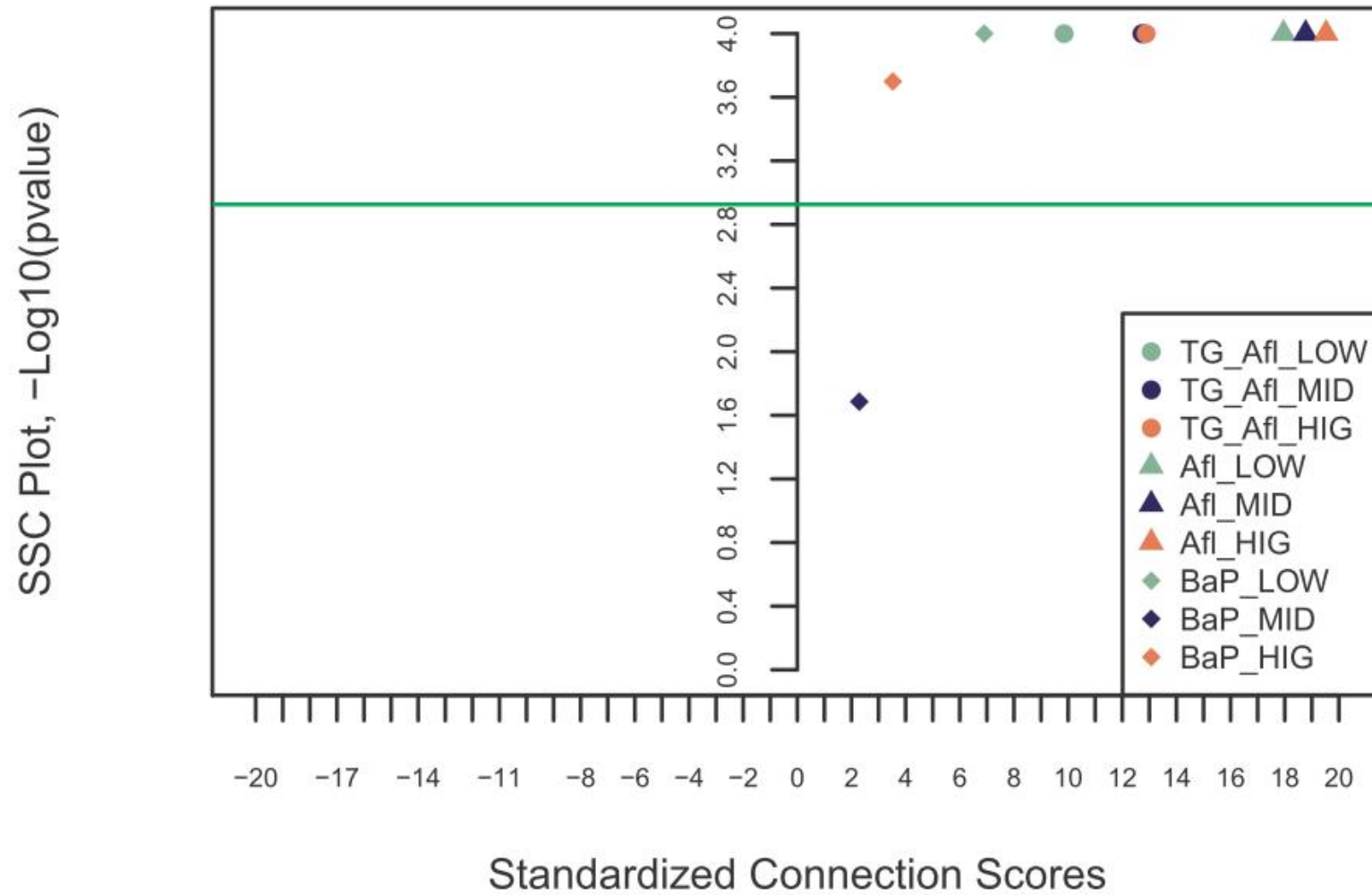
sscMap results



High dose and 8 hours exposure



validation set



Conclusion:

- *in vivo* HHC signature with many genes
- best classification at low dose and 24h
- better classification at 24h than 8h
- classification accuracy decrease with concentration

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Advance Access publication August 12, 2013

Assessing compound carcinogenicity *in vitro* using connectivity mapping

Florian Caiment*, Maria Tsamou, Danyel Jennen and
Jos Kleinjans

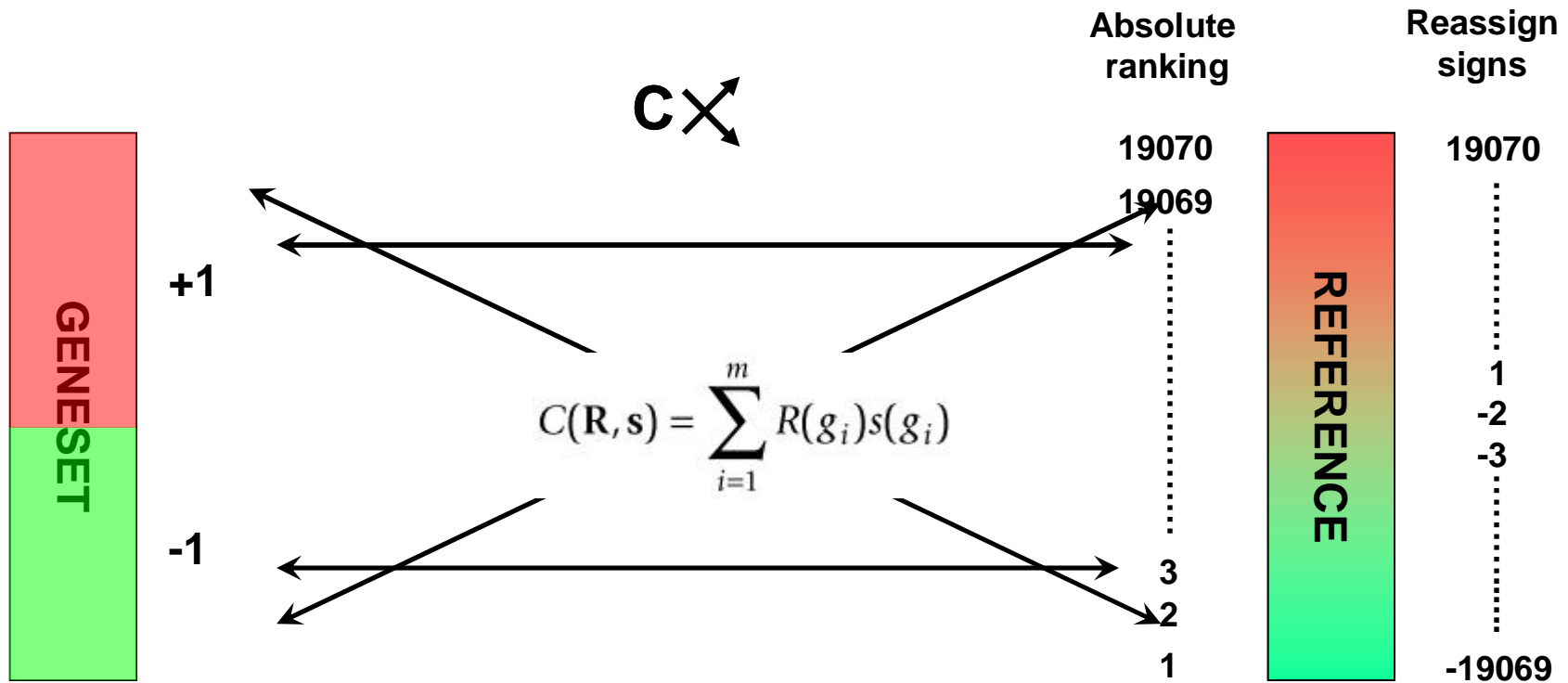
Acknowledgment



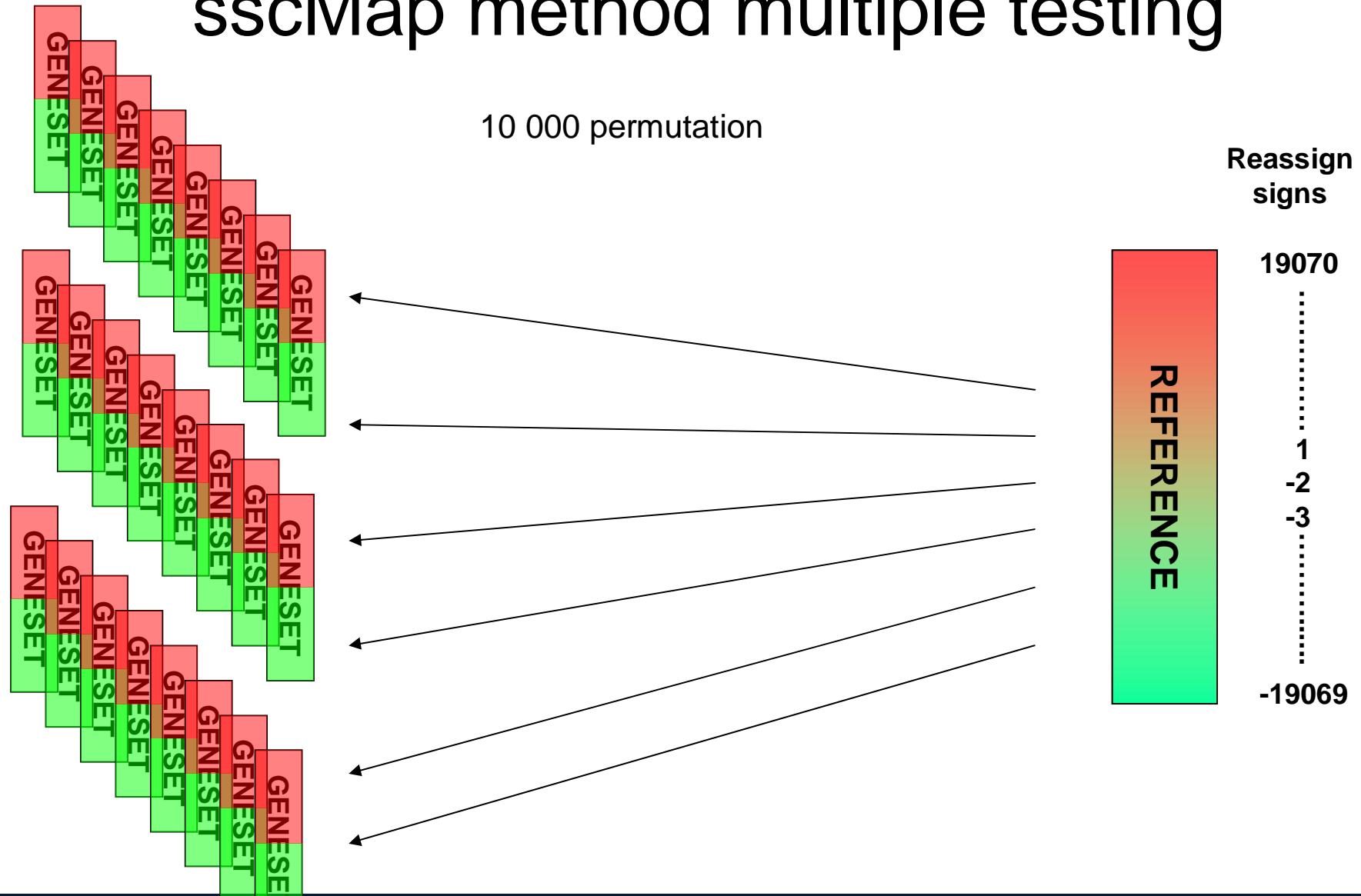
- Maria Tsamou
- Danyel Jennen
- Jos Kleijnans

QUESTIONS?

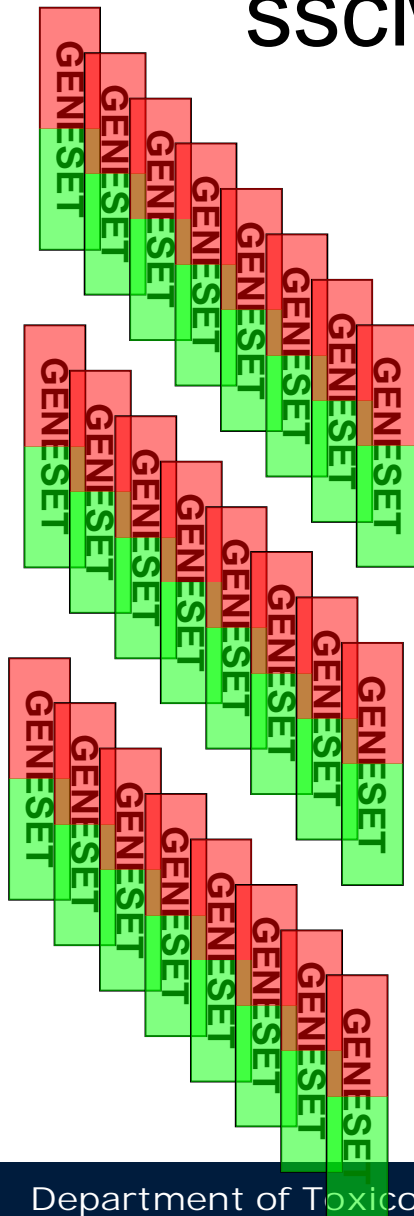
sscMap method



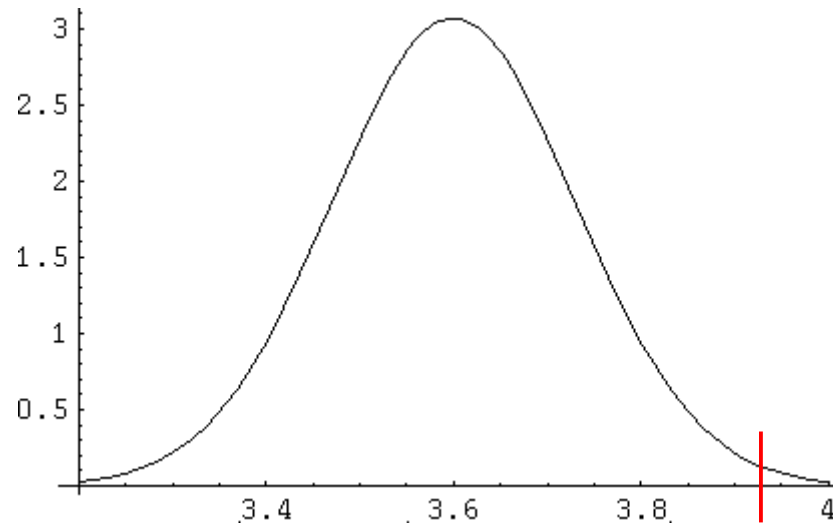
sscMap method multiple testing



sscMap method multiple testing



10 000 permutation



Reassign signs

