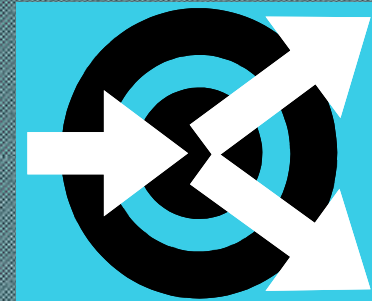


Computing offtarget-effect by cross-  
analysis of transcriptome-level data  
from ~~1,118~~ 1,380 studies

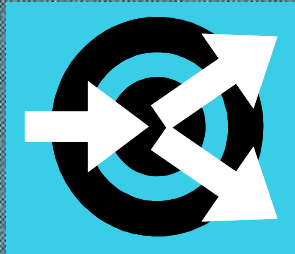


Balázs Györfy

MTA TTK Lendület Cancer Biomarker Research Group  
Semmelweis University 2<sup>nd</sup> Dept. of Pediatrics



# Side effects of molecular targeted therapy

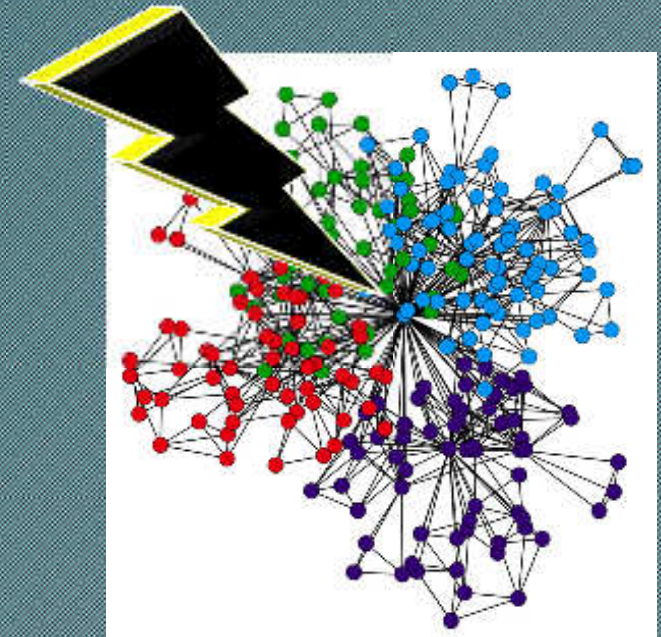


## On-target effect:

- EGFR inhibitors -> skin rash
- VEGFR2 blockers -> vasoconstriction -> hypertonia

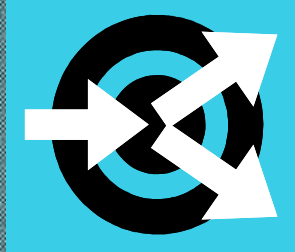
## Off-target effect:

- HER2 inhibitors -> heart failure
- mTOR inhibitors -> high cholesterol
- BRAF inhibitors -> epithelial tumors





# Therapy



## 1. Drug treatment

- Approved medicines
- Agents of preclinical studies

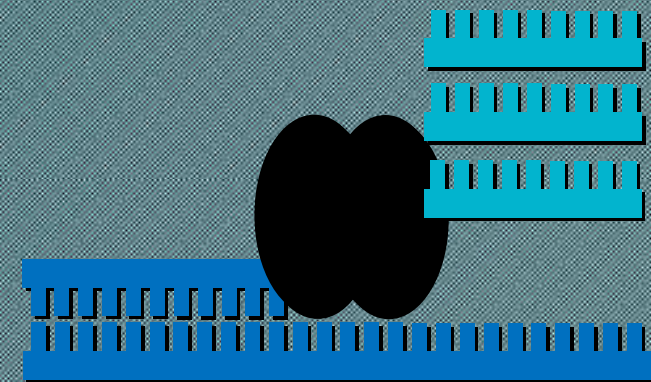
## 2. RNA interference

- double-stranded RNA
- "interfere" with the translation of protein
- degradation of mRNA at specific sequences



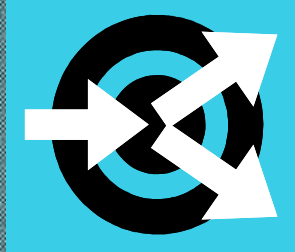
## 3. Overexpression

- Experimentally induced excessive expression of a gene





# Therapy -> Off-target effects



*General approach:*

treatment



off-target effect

*Reversed question:*

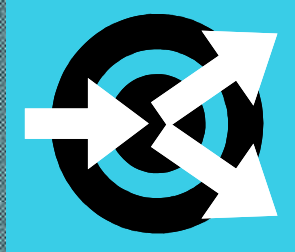
off-target effect



which treatment?



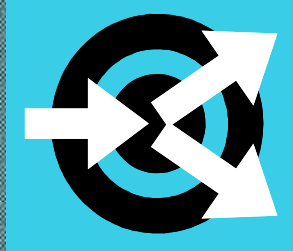
## Study aim



Establish a framework to identify off-target effects for a large number of agents on a genomic scale.



# Methods 1/3: database setup



**GEO search: all cell culture experiments, 2005-2014, n=145,693**

Raw data (CEL file) available  
n=134,289

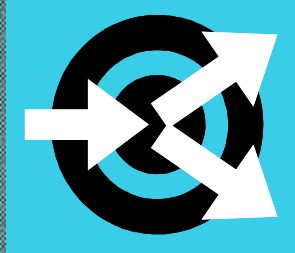
Treatment-control pairs  
n=68,108



The database in numbers	n
Datasets	1,380
Cell lines	1,823
Drugs	1,920
Silenced / overexpressed genes	759



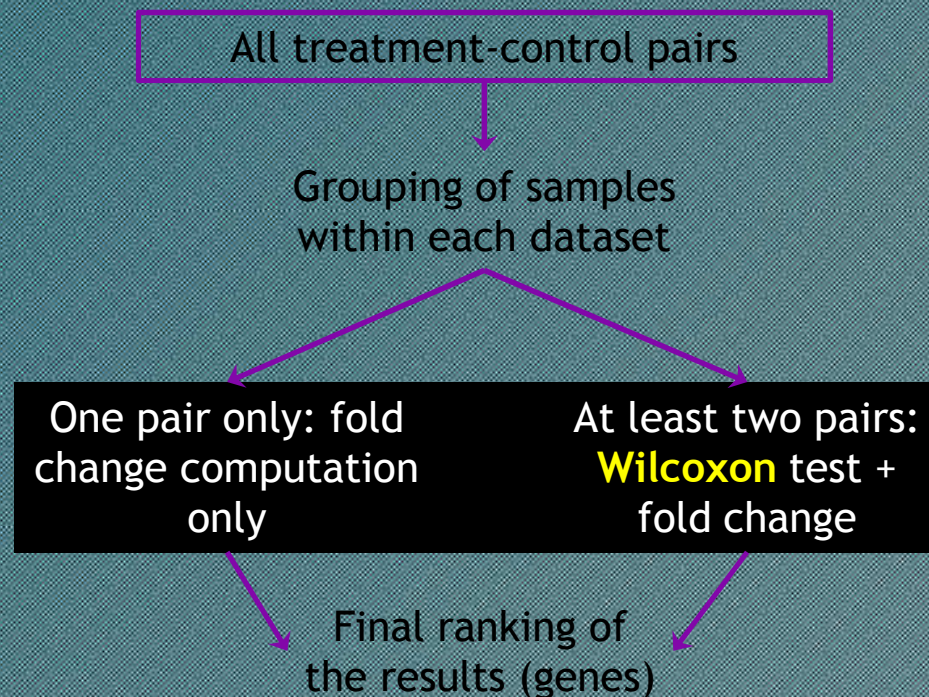
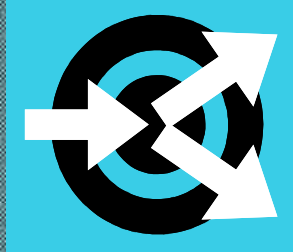
## Methods 2/3: data processing



- **Platforms:** Affymetrix HGU133A, HGU133plus2, HGU133Av2
- **R environment**
- **Normalization:** MAS5
- **Quality control:** Affy whitepaper
- **Probe sets:** JetSet (n=12,209)

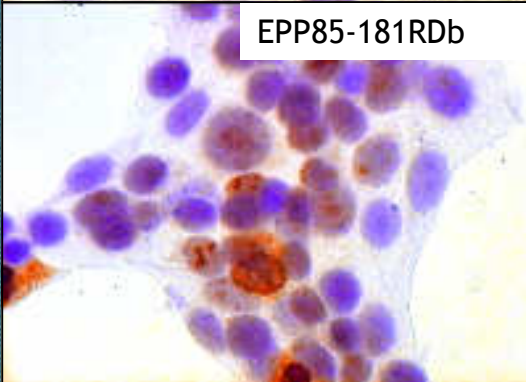
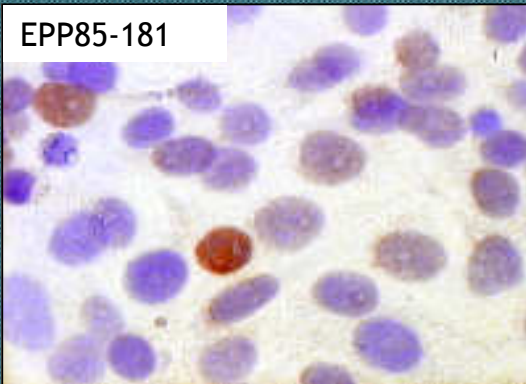
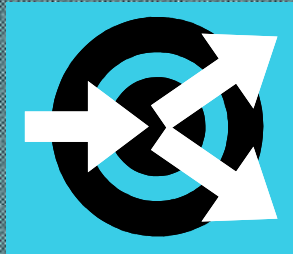


# Methods 3/3: statistical analysis

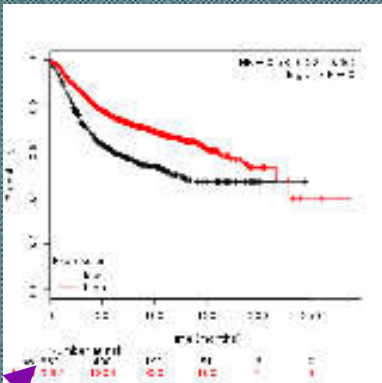
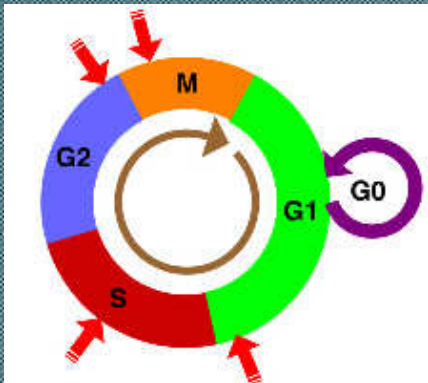




# Results 1/3: proliferation (breast cancer)



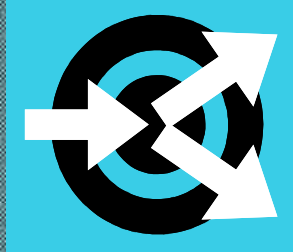
**MKI67**  
(212023\_s\_at)



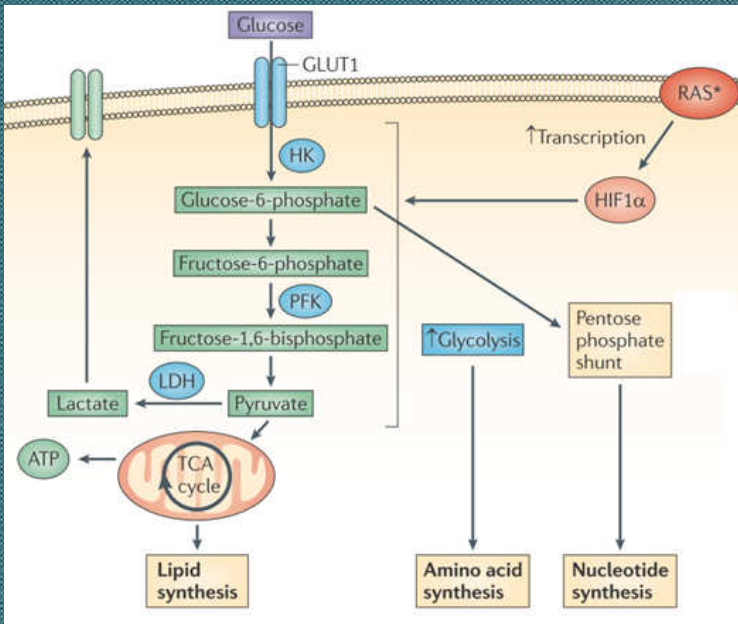
Treatment	Type	P value	Fold change	Datasets
ESR2	Overexpression	1E-16	0.62	GSE9936
Resveratrol	Drug	3E-08	0.43	CMAP
MTX	Drug	1.5E-05	0.45	CMAP
Estrogen	Drug	1.1E-04	1.68	GSE11324, GSE8640



# Results 2/3: energy metabolism (drug)



**HIF1A**  
(200989\_at)



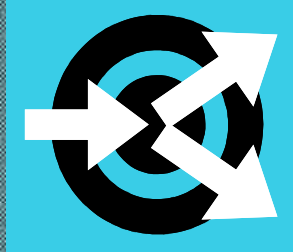
Treatment	Type	P value	Fold change	Datasets
Camptothecin	Drug	0.00049	0.52	GSE1417
PLX4032	Drug	0.016	0.7	GSE20051

Vemurafenib

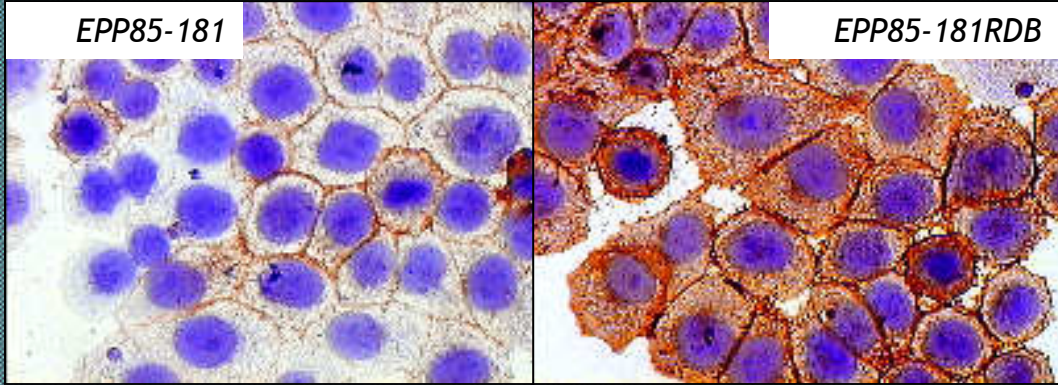
Topoisomerase inhibitor



# Results 3/3: multidrug resistance (**silencing**)



**ABCB1**  
(209993\_at)

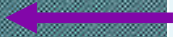


repair of DNA double strand breaks



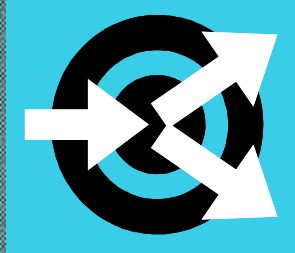
Treatment	Type	P value	Fold change	Datasets
RAD51	Silencing	0.022	5.6	GSE56940
Cyclin T	Silencing	9.6E-05	6.31	GSE11462
PSIP1	Silencing	0.0039	0.15	GSE7508
NFKB1	Silencing	0.024	0.14	GSE31912

PI3K-Akt signaling pathway





# Summary



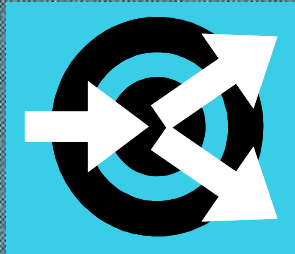
Established a database and a bioinformatic framework to process a large volume of curated experimental data.

is useful to:

1. We can identify the treatment inhibiting/activating any selected gene as its off-target effect.
2. We can select the most reliable preclinical model for a validation study.



# Acknowledgements



## Database construction



Gyöngyi Munkácsy PhD



Bence Bán

Nóra Szarvas



Péter Herman



Zsófia Pényváltó PhD



Zsófia Sztupinszki MD



Boglárka Weltz

Tamás Szabó Miklós