

IntOGen: A novel framework for integration and data-mining of multidimensional oncogenomic data

Christian Pérez-Llamas

Biomedical Genomics Group
Universitat Pompeu Fabra



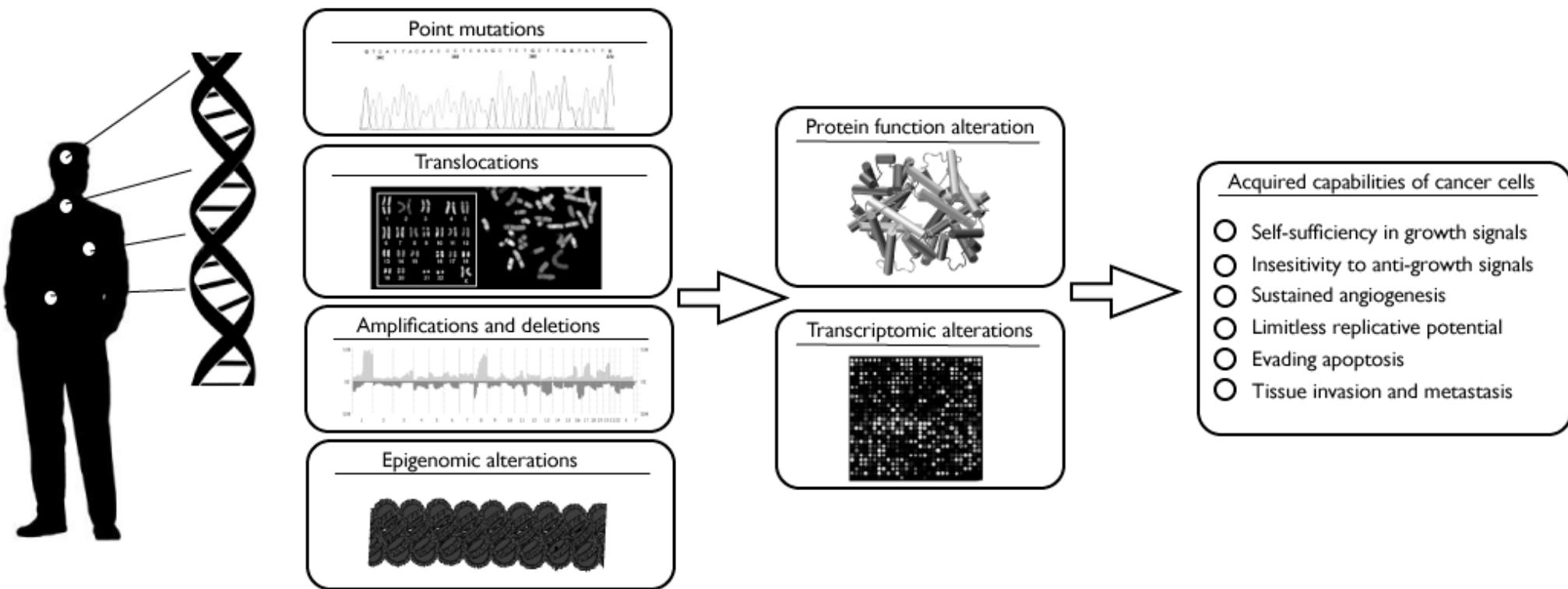
Parc de Recerca Biomedica de Barcelona



Genomic and epigenomic aberrations in cancer

consequences at the level of gene expression and protein function

Altered cell functions and uncontrolled growth





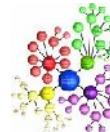
Oncogenomics Data

- Transcriptomic alterations
- Copy Number Variation alt.
- Mutations
- Epigenomic alterations



Clinical Annotations

International Classification
of Diseases for Oncology



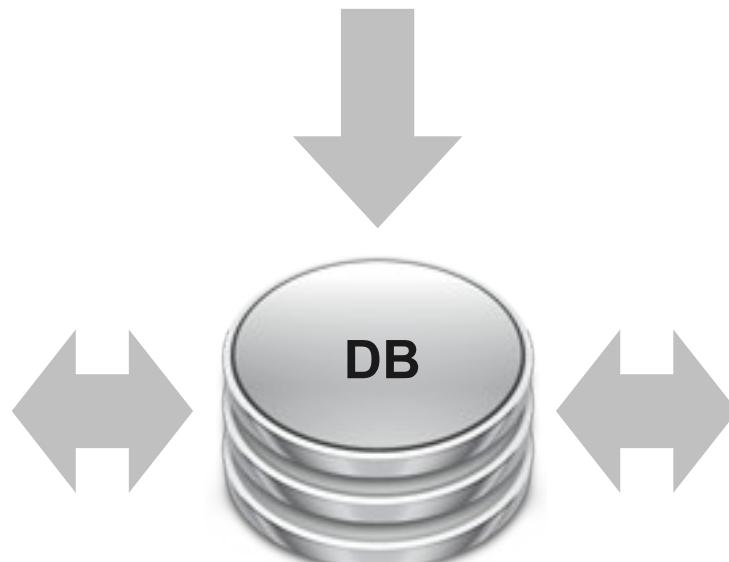
Genomic Annotations

- Ensembl
- GO
- KEGG
- ...



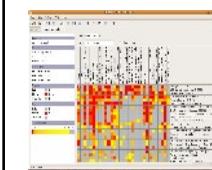
Statistics

- Raw data processing
- Cancer related genes identification
- Cancer related modules identification
- Combinations
- Correlations



Visualization & Exploration

www.intogen.org



GiTools

www.gitools.org



- BioMart service
- DAS server
- SOAP-WS



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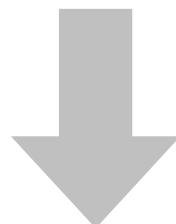
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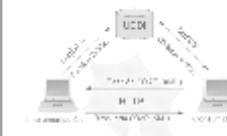
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Collation of Cancer Data

Transcriptomic Alterations

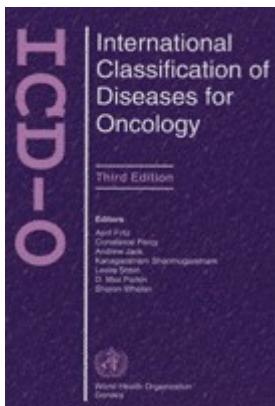
Copy Number Variations

Mutations

	Transcriptomic Alterations	Copy Number Variations	Mutations
 Gene Expression Omnibus	✓		
 ARRAYEXPRESS	✓		
 THE CANCER GENOME ATLAS	✓	✓	
		✓	
 Copy Number Analysis from Sanger Institute		✓	
			✓
 International Cancer Genome Consortium	⚙	⚙	⚙



Clinical Annotations of Patients and Samples



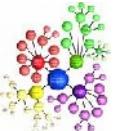
International Classification
of Diseases for Oncology

ICD-O {

- Topography
- Morphology

Prepared for any
type of annotations:

- Type of treatment
- Age of onset
- Gender
- Cell type
- ...



Sources of Knowledge





Oncogenomics Data

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Clinical Annotations

International Classification
of Diseases for Oncology



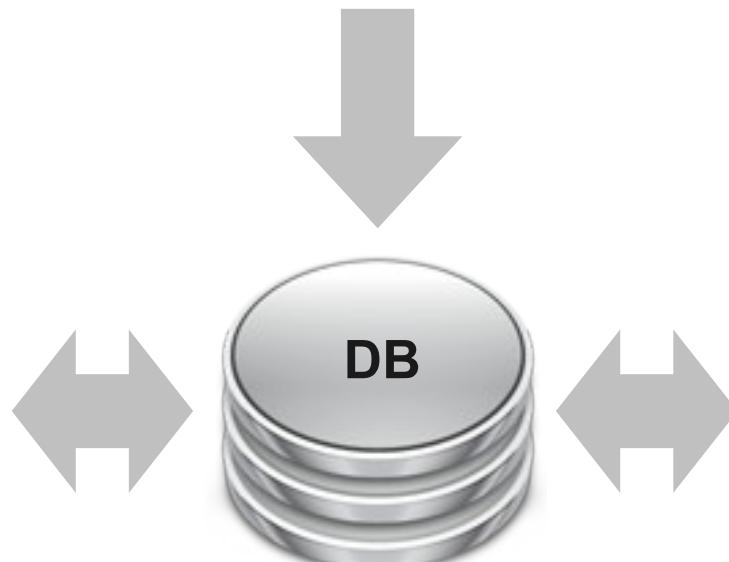
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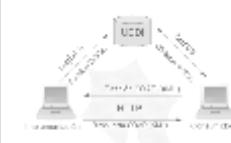
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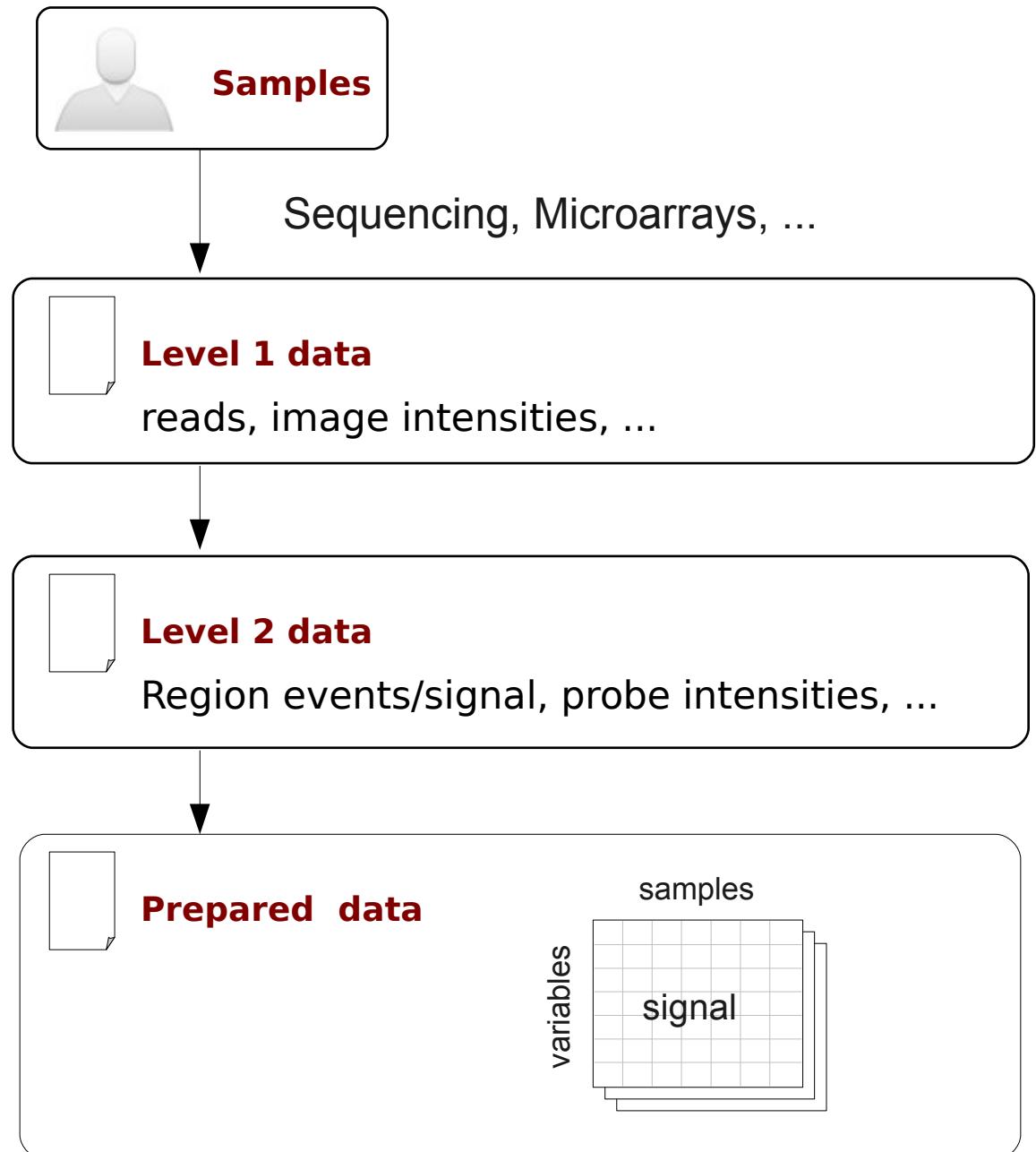
Raw data processing

Cancer related genes identif.

Cancer related modules identif.

Combinations

Correlations



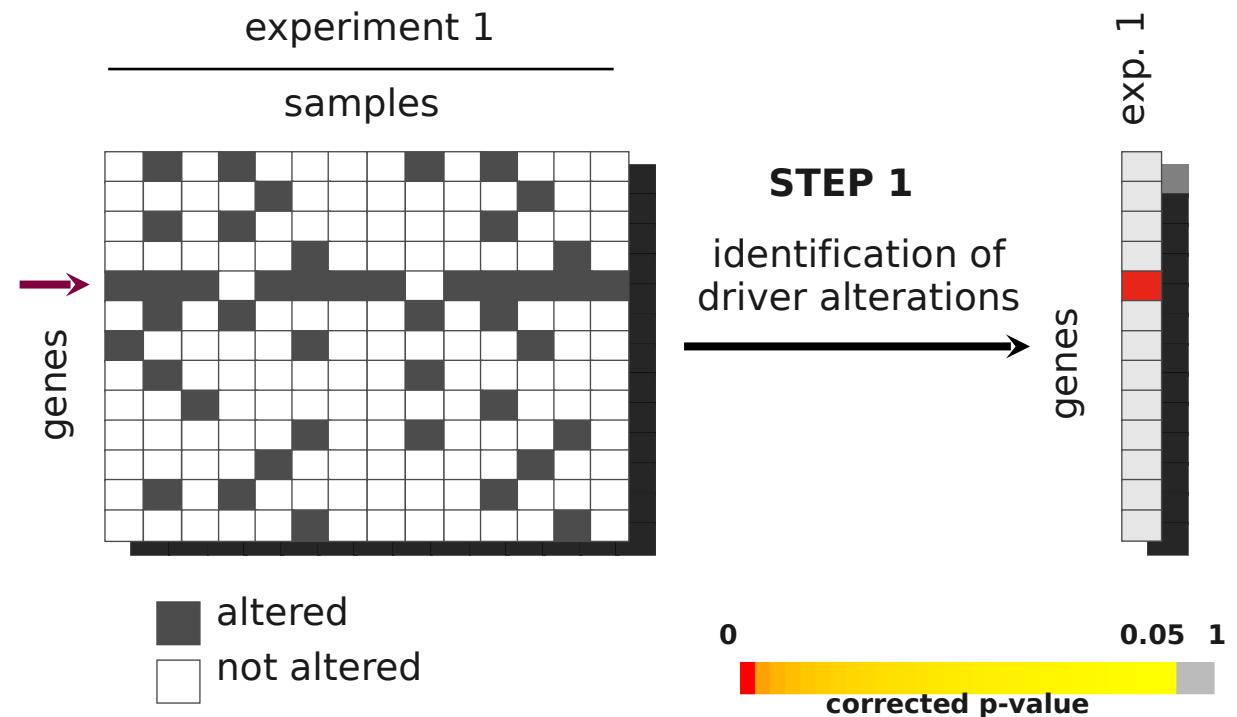
Raw data processing

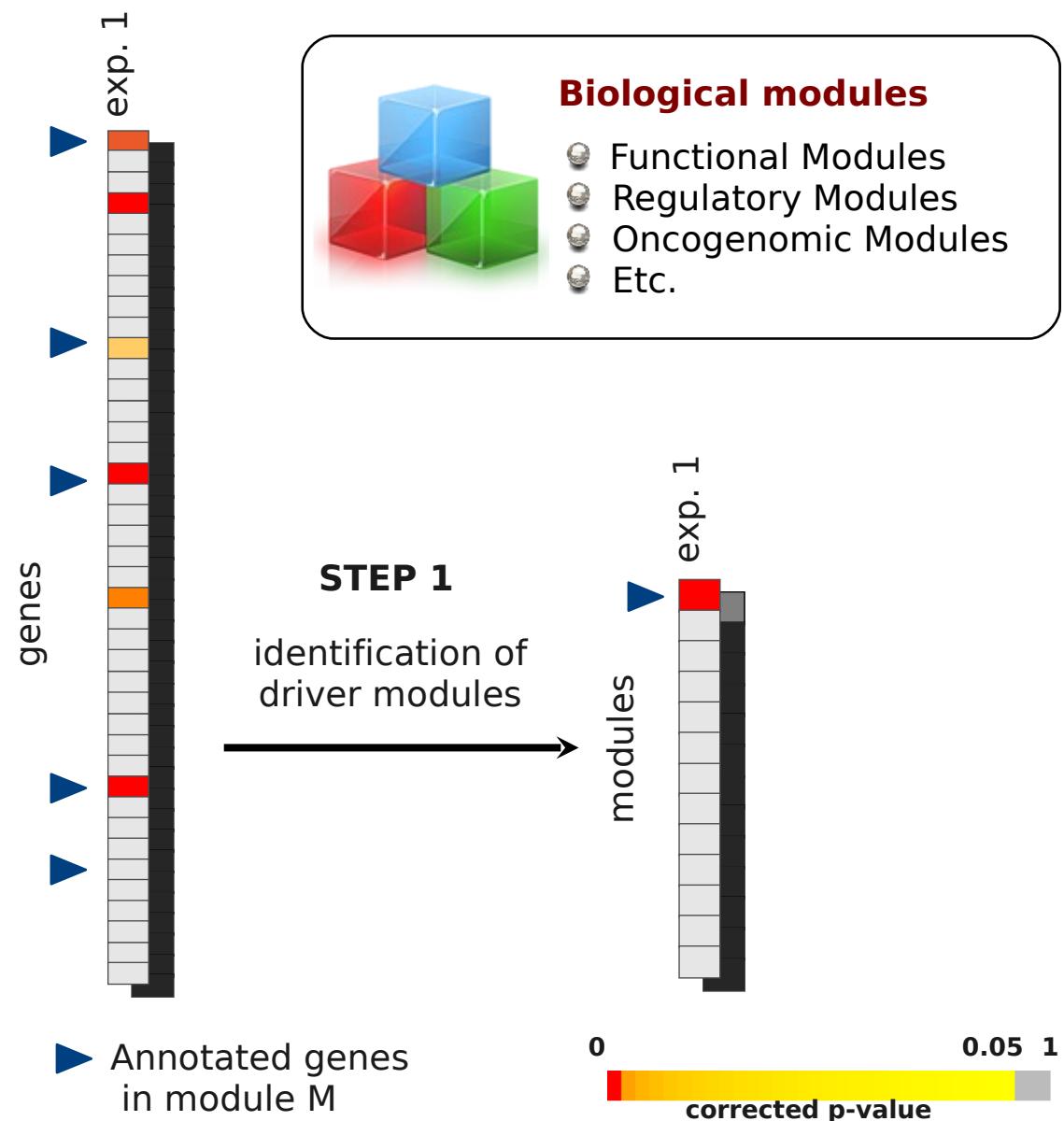
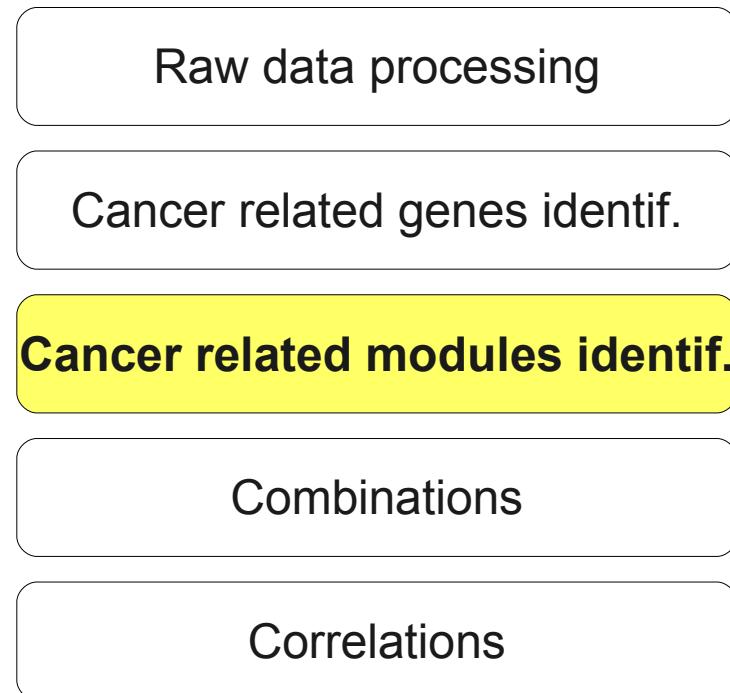
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Combinations

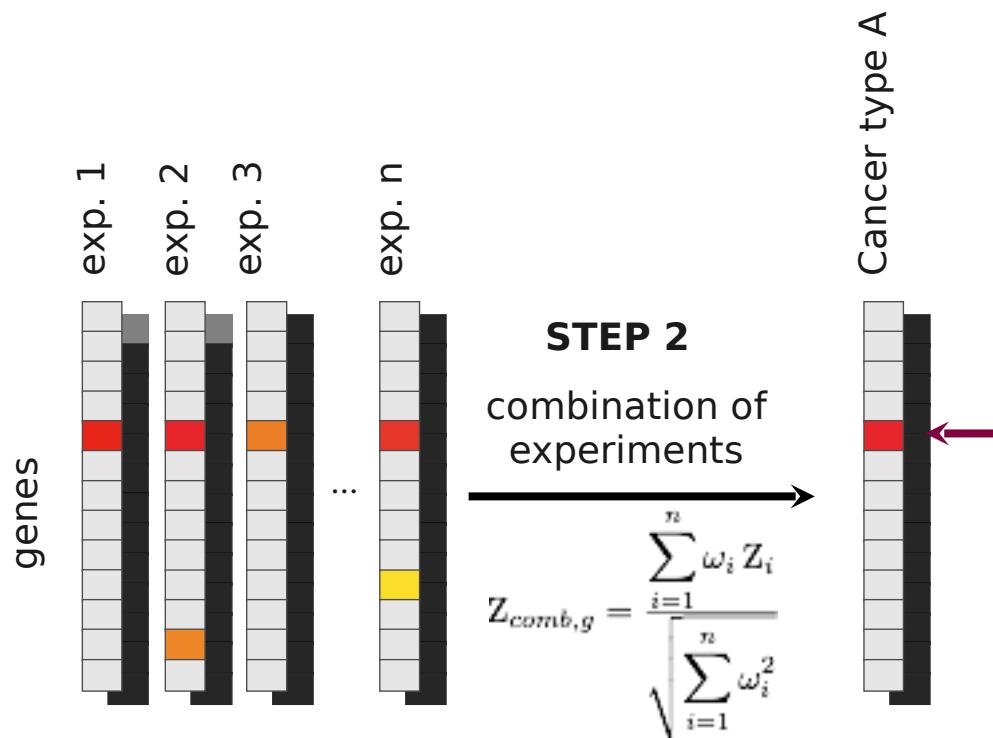
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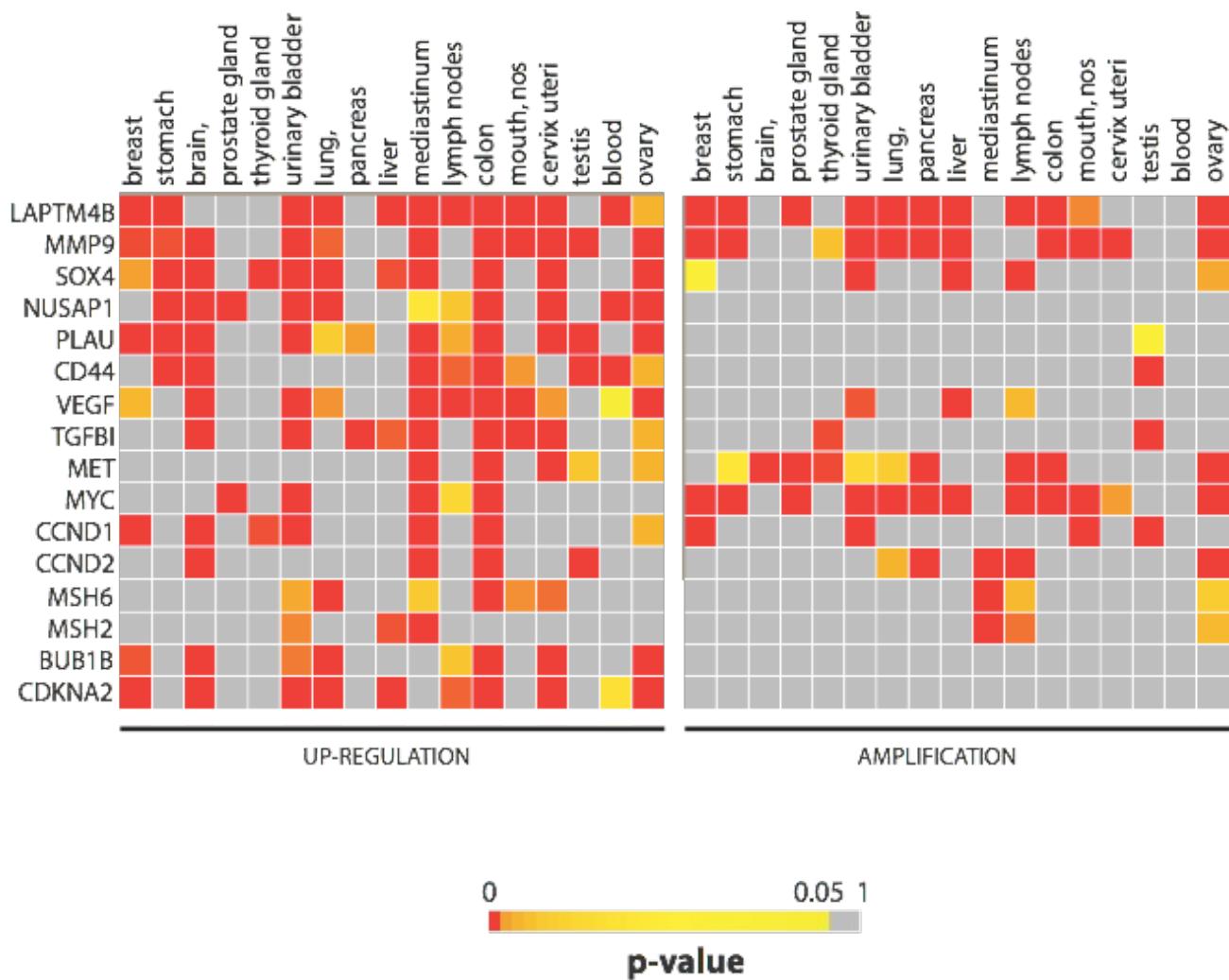
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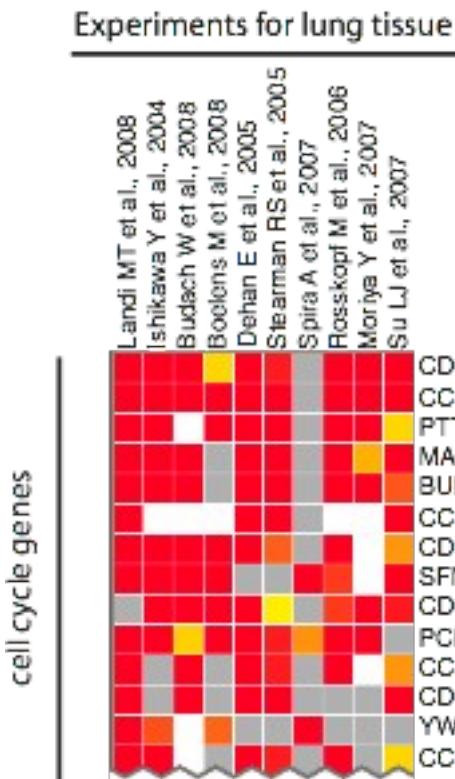
Correlations





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Analysis at different levels



Biological modules

Functional Modules

Regulatory Modules
Oncogenomic Modules

...

MODULE ANALYSIS

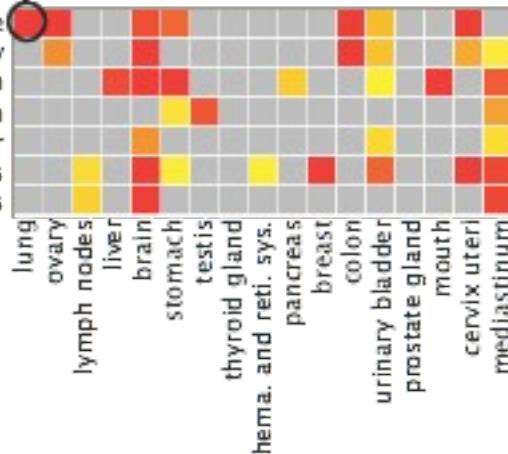
→ Cell cycle



COMBINATION

Cell cycle
p53 signalling pathway
ECM-receptor interaction
Antigen processing and presentation
Bladder cancer
Systemic lupus erythematosus
Type I diabetes mellitus

pathways



Correlation between cancer types

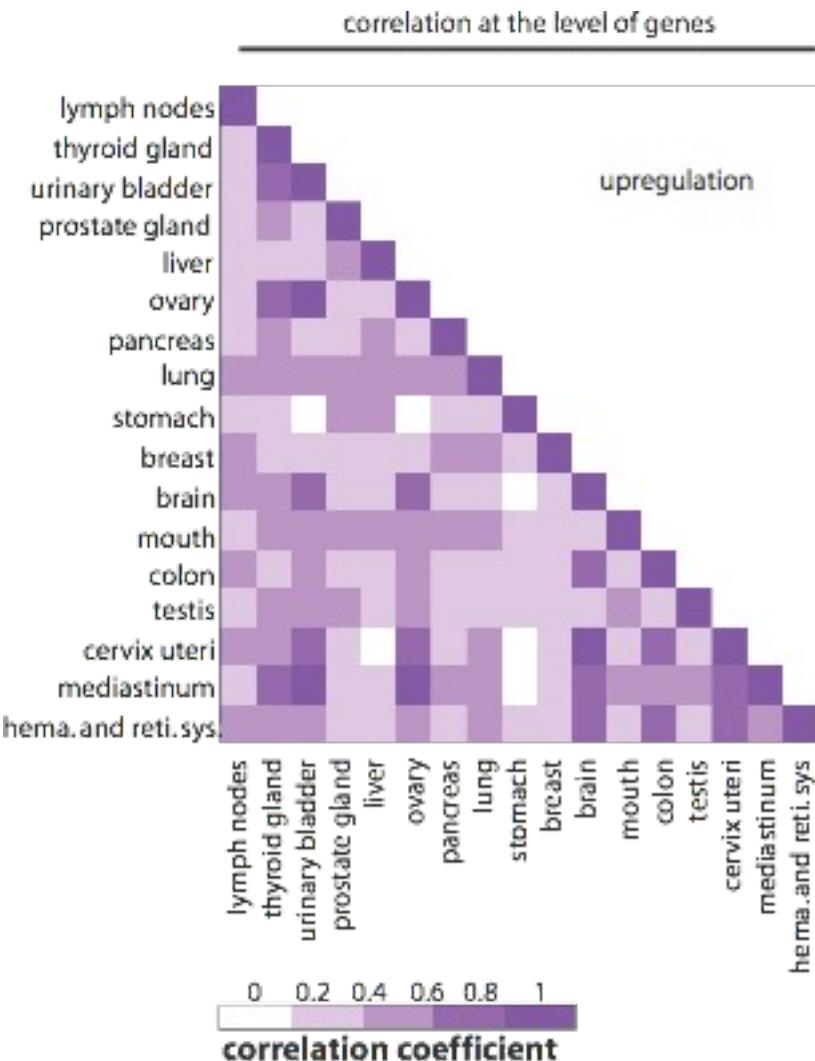
Raw data processing

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Correlations



Correlation between cancer types

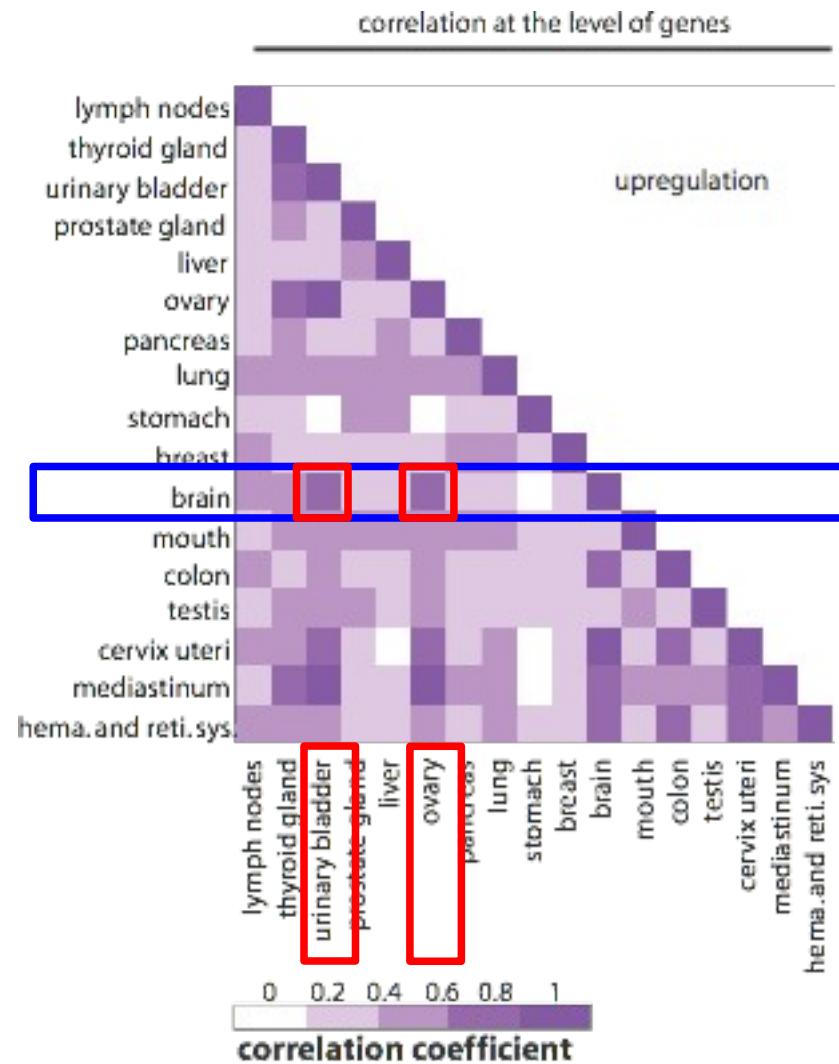
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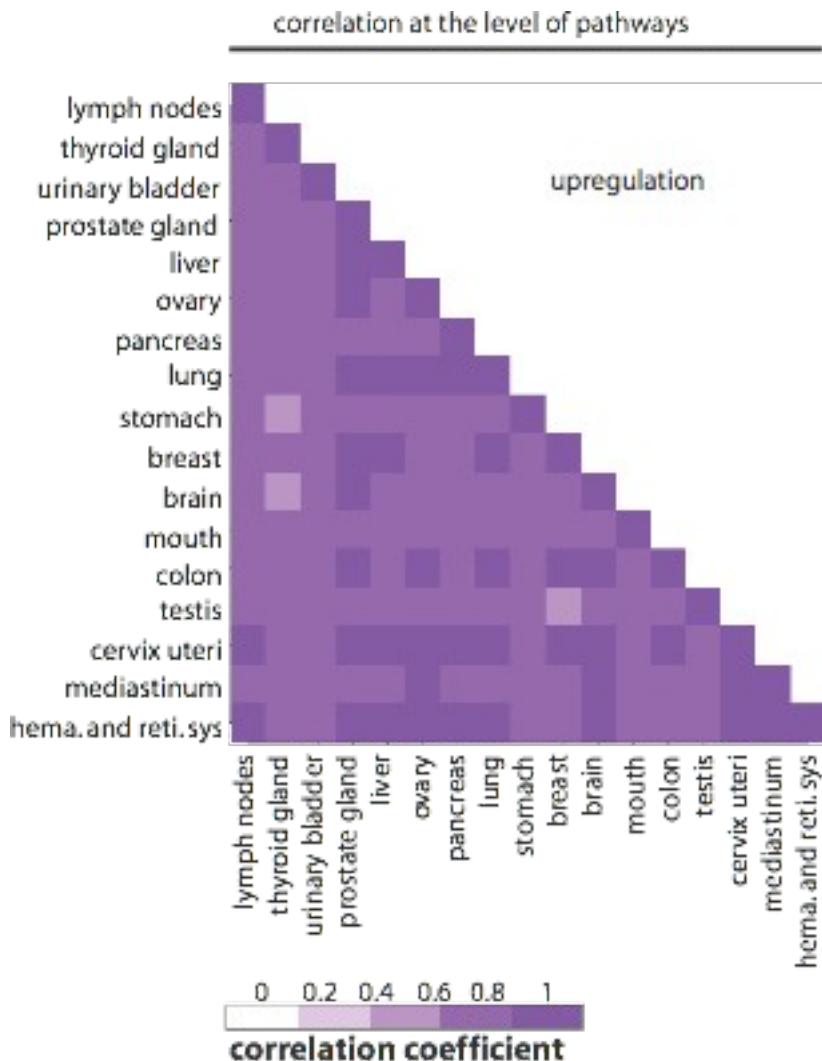
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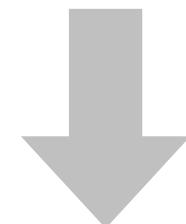
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Integrative
Onco
Genomics

Home Browser Help About

Integrative OncoGenomics

IntOGen, a discovery tool for cancer researchers, is a resource that integrates multidimensional OncoGenomics Data for the identification of genes and groups of genes (biological modules) involved in cancer development.

Please note: IntOGen is **UNDER DEVELOPMENT**. The results shown are preliminary and the browser is a beta version, errors may be found and we are currently working to fix them.

If you are interested in using IntOGen and would like to be informed when new options are added [subscribe to the IntOGen mailing list](#).

Explore IntOGen



GENE
SEARCH



EXPERIMENT
SEARCH



TUMOR TYPE
SEARCH



CANCER
GENE
PRIORITIZATION



COMBINE
EXPERIMENTS



ANALYZE
YOUR MODULES



Discovery tool for cancer research



Gene Search

Search for a gene of interest and have a wide view of the implication of this gene in cancer



Experiment search

Search for a experiment and identify the most significant genes and modules altered



Tumor type search

Search for a cancer type of interest and discover the most significant altered genes and modules



Cancer Gene Prioritization

Prioritize a list of candidate genes based on CGPrio probabilities and oncogenomic alterations



Combine experiments

Choose a group of experiments and combine the statistics to obtain combined significant genes and modules



Analyze your modules

Load your own modules and find out if they are enriched for genes significantly altered in different cancer types

Experiments

all

Tumor type

all

Genes / Modules

all > Genes > CDKN2A

Details

Tumor type

Experiments

<<

Search

Filters

p-value



Export

[CSV file](#)

Tumor type	Alterations			
	Mutations	CNA	Transcrip	
	+ Fnd / Std	+ Loss	+ Gain	+ Down
cervix uteri	36 / 504			
breast	33 / 604			
brain, nos	329 / 1543			
ovary	70 / 657			
lung	300 / 1896			
colon, nos	9 / 273			
liver	88 / 656			
lymph nodes				
stomach	43 / 526			
stomach	0 / 8			
urinary bladder	226 / 1371			
thyroid gland	22 / 174			
hematopoietic and reticuloendothelial systems	603 / 4051			
mouth, nos				
pancreas	208 / 623			
testis	0 / 33			
mediastinum				
prostate gland	11 / 280			
cerebellum				
nervous system, nos				
tonsil				
pharynx, nos				
unspecified digest. organs				
larynx				
pituitary gland	0 / 71			
adrenal glands	1 / 46			

Showing 1 to 26 of 54

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Experiments

all

Tumor type

breast

all > breast

Genes / Modules

all > Genes > CDKN2A

Details

Tumor type

Experiments

<<

Search

Filters

p-value



Experiment and platform					Alterations				
+ Authors	+ Title	+ Year	+ Ref	+ Platform	CNA	?	Transcriptomic	?	
					+ Loss	+ Gain	+ N	+ N	
Yu K et al.	A precisely regulate...	2008	GSE5364	Affymetrix Gene...					183
Finak G et al.	Stromal gene express...	2008	GSE9014	Agilent-012391 ...					52
Richardson A et al.	Expression data fro...	2007	GSE7904	Affymetrix Gene...					43
Richardson AL et al.	X chromosomal abnorm...	2006	GSE3744	Affymetrix Gene...					40
Weigelt B et al.	Molecular portraits ...	2005	GSE2741	Agilent Human 1...					64
Weigelt B et al.	Molecular portraits ...	2005	GSE2741	Agilent-012097 ...					55
Mostafavi, ZB et al.	Gene Expression Anal...	2008	GSE4122	Affymetrix Gene...					53
Casey T et al.	Molecular signatures...	2008	GSE10797	Affymetrix Gene...					28
Davis SR et al.	Gene Expression and ...	2008	GSE7882	NCI Qiagen Homo...					54
Radvanyi L et al.	The gene associated ...	2005	GSE1477	Protein Design ...					51
Persson K et al.	Chromosomal aberrati...	1999	10337995	CGH					27
Hwang KT et al.	Genomic copy number ...		18649361	aCGH					62
Aubele M et al.	Intratumoral heterog...	1999	10214356	CGH					23
Weber-Mangal S et al.	Breast cancer in you...		14520696	CGH					85
Fridlyand J et al.	Breast tumor copy nu...		16620391	aCGH					67
Gronwald J et al.	Comparison of genomi...		15540206	CGH					45
Jones C et al.	Comparative genomic ...		12533827	CGH					28
Jones C et al.	Molecular cytogeneti...		11141494	CGH					24
Fung LF et al.	Genetic imbalances i...	2001	11165323	CGH					40
Vincent-Salomon A et al.	Identification of ty...		17417968	aCGH					59
Ried T et al.	Comparative genomic ...		7585611	CGH					20
Teixeira MR et al.	Evaluation of breast...	2001	11494114	CGH					37
van Beers EH et al.	Comparative genomic ...		15705879	CGH					132
Moore E et al.	Widespread chromosom...	1999	10398098	CGH					23
Park SC et al.	Genetic changes in b...		17380298	CGH					32
Hwang ES et al.	Clonality of lobular...		15197797	CGH					48

Showing 1 to 26 of 31

<<< 1 2 >>>

Experiments

all

Tumor type

breast

all > breast

Genes / Modules

all > Genes > CDKN2A

Details

Tumor type

Experiments

<<

Search

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Authors	Title	Year	Ref	Platform	Alterations				
					CNA	Transcriptomic	Loss	Gain	N
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Showing 1 to 26 of 31

<< < 1 2 > >>

Experiments

all > Agilent-012391 / Finak G

Tumor type

breast

infiltrating duct

all > breast > infiltrating duct carcinoma, nos

Genes / Modules

all > Genes > CDKN2A

Details

Experiment and platform

- Authors: Finak G et al. (2008)
- Title: Stromal gene expression predicts clinical outcome in breast cancer. (pubmed. [18438415](#))
- Journal: Nature medicine
- Database: GEO Reference: GSE9014
- Platform: Agilent-012391 Whole Human Genome Oligo Microarray G4112A (Feature Number version) Type: mRNAexpr

CGPrio predictions

Type	Oncogene	Suppressor
PC-GS	0.361	0.308
PC-GS-PI	0.969	0.942
PC-GS-PD	0.314	0.328
PC-GS-RD	0.55	0.273
PC-GS-PD-PI-RD	0.86	0.941

Transcriptomic Alterations

	Upreg	Downreg
Q-Value	1.466E-17	1.048
P-Value	6.738E-19	1
Observed	46	0
Expected	15.175	14.007
Deviation	3.278	3.199
Samples	52	

Cancer Gene Census

- Cancer Somatic Mutated: yes
- Cancer Germline Mutated: yes
- TumourTypes (Somatic Mutations): melanoma, multiple other tumour types
- TumourTypes (Germline Mutations): melanoma, pancreatic
- Cancer Syndrome: Familial malignant melanoma
- Tissue Type: L, E, M, O
- Cancer Molecular Genetics: Rec

Ensembl Genes

- Ensembl ID: [ENSG00000147889](#)
- Symbol: CDKN2A
- Chromosome: 9
- Band: p21.3
- Description: Cyclin-dependent kinase inhibitor 2A, isoform 4 (p14ARF) (p19ARF)

Tumor type

- Morphology: infiltrating duct carcinoma, nos
- Topography: breast

Experiments

all

Tumor type

lung

all > lung

Genes / Modules

all > Genes

Details

Genes

Modules...

Tumor type

Experiments

<<

 Search

Filters

Filter Ensembl...
[Upload filter...](#)

Predictions



p-value



Export

[CSV file](#)

Ensembl Genes	CGC	Alterations						
		Predictions		Mutations		CNA	Transcrip	
		+ Onco	+ Supp	+ Fnd / Std	+ Loss	+ Gain	+ Down	- Up
ENSG00000138413 IDH1	Dom			0 / 11				
ENSG00000147889 CDKN2A	Rec			300 / 1896				
ENSG00000136718 IMP4								
ENSG00000168542 COL3A1								
ENSG00000135446 CDK4	Dom			0 / 70				
ENSG00000145604 SKP2				0 / 11				
ENSG00000146648 EGFR	Dom			4312 / 16115				
ENSG00000135763 KIAA0133								
ENSG00000066248 NGEF				0 / 12				
ENSG00000121879 PIK3CA	Dom			29 / 964				
ENSG00000196712 NF1	Rec			0 / 154				
ENSG00000081479 LRP2								
ENSG00000139687 RB1	Rec							
ENSG00000141510 TP53	Rec			18 / 23				
ENSG00000146350 C6orf170								
ENSG00000165953 SERPINA12				1 / 11				
ENSG00000128641 MYO1B								
ENSG00000146247 PHIP								
ENSG00000162761 LMX1A								
ENSG00000175065 DSG4								
ENSG00000174586 ZNF497								
ENSG00000104499 GML				0 / 11				
ENSG00000198822 GRM3								
ENSG00000159387 IRX6								
ENSG00000169432 SCN9A								
ENSG00000171862 PTEN	Rec			48 / 548				

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Prototype

Experiments

all

Tumor type

breast

all > lung

Genes / Modules

all > Genes

Details

Genes

Modules...

Tumor type

Experiments

<<

Search

Filters

[Upload filter...](#)

Predictions



p-value



Export

[CSV file](#)

move

<<<

<<

<

>

>>

zoom in

1.5x

3x

10x

base

zoom out

1.5x

3x

10x

position/search chrX:149,829,362-152,627,668

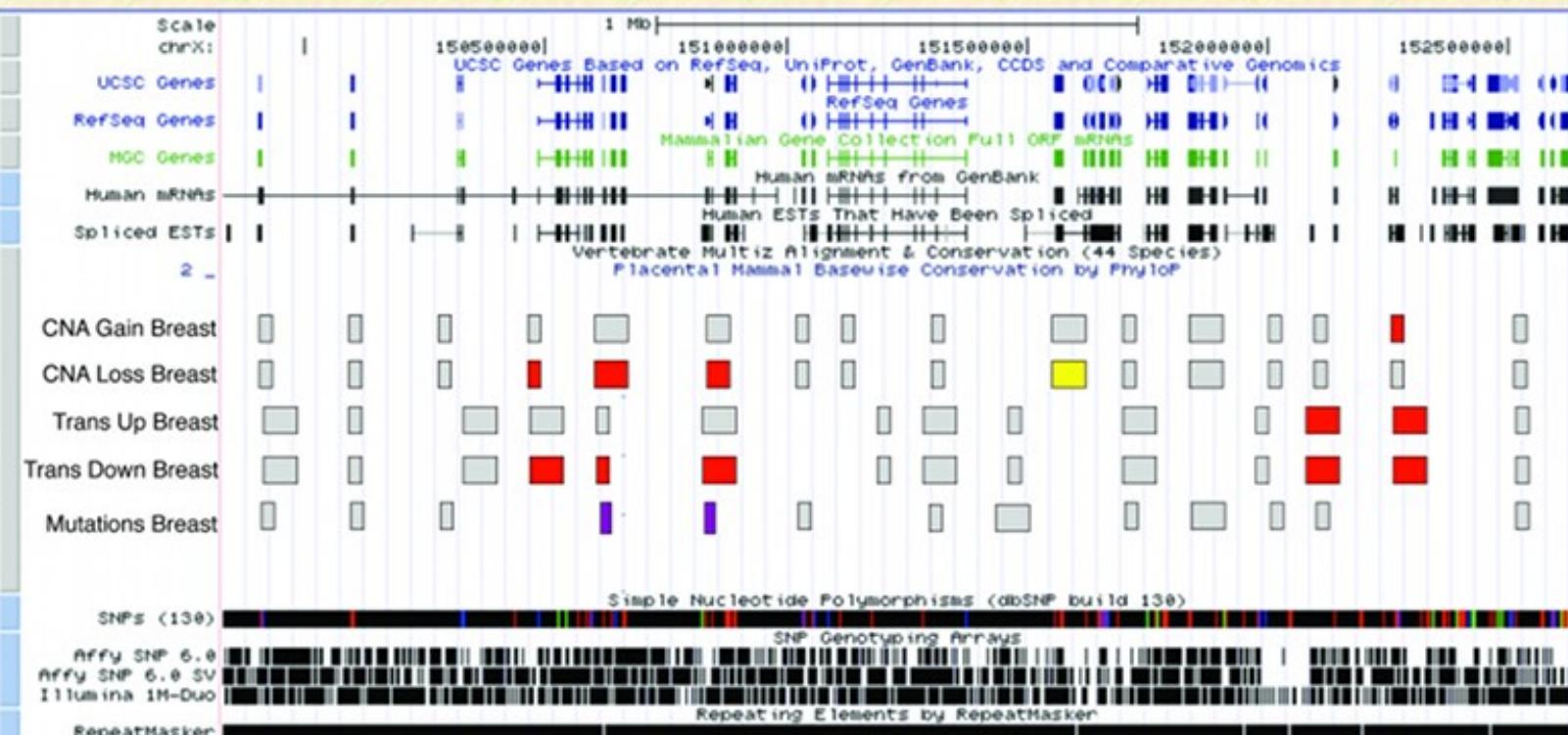
jump

clear

size 2,798,307 bp.

configure

chrX (q26) 22.2 q21.1 22.3 q23 24 Xq25 Xq26

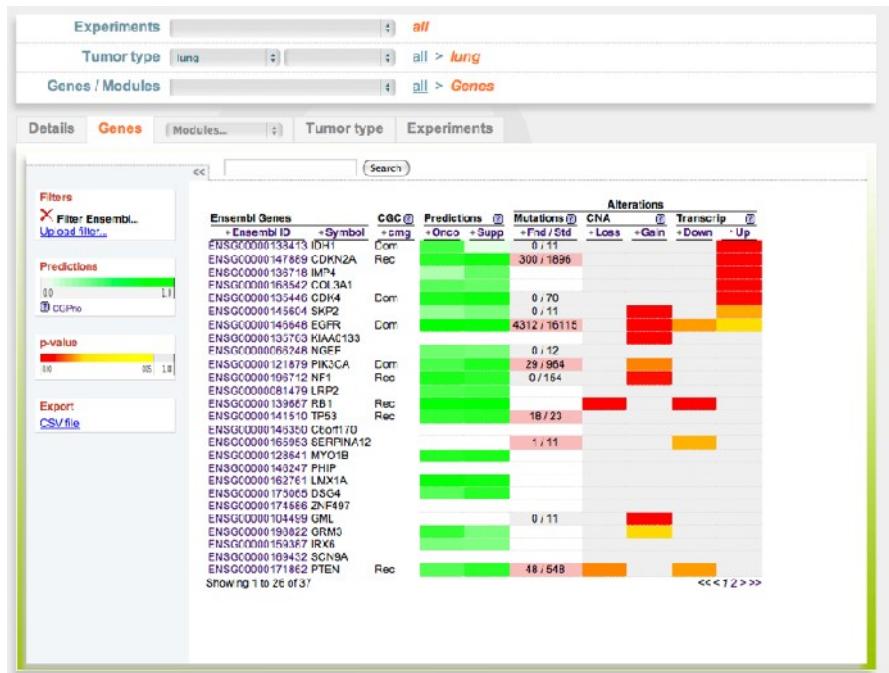


move start Click on a feature for details. Click or drag in the base position track to zoom in. Click move end

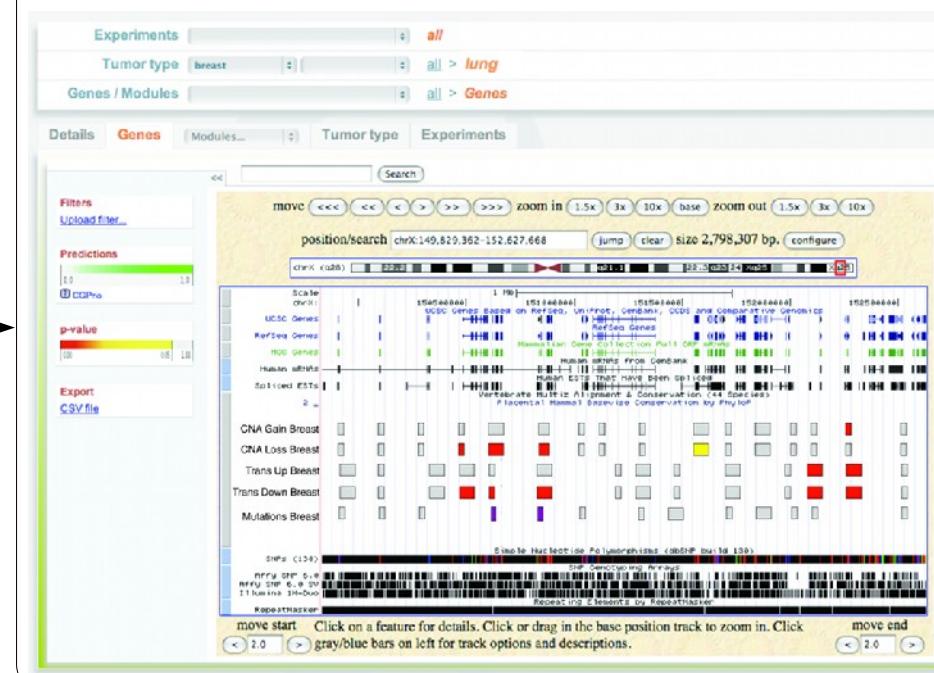
< 2.0 > gray/blue bars on left for track options and descriptions.

< 2.0 >

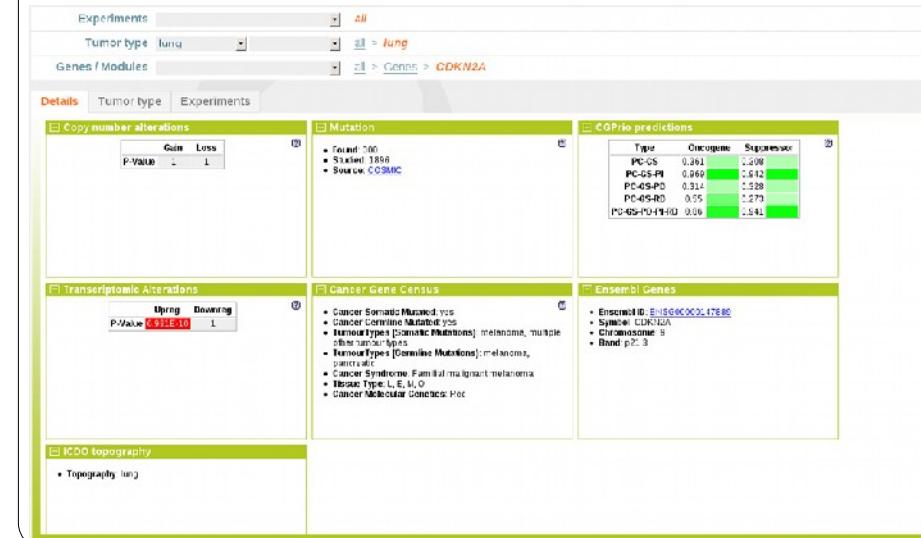
Table view



Genome view



Details view



- IntOGen is a novel framework for **Oncogenomics data** integration and analysis
- It **integrates** many tumor types and different types of alterations in a common framework
- It explores the data at **different levels**, from individual experiments to combinations of experiments, and from individual genes to biological modules
- The system is updatable, **flexible** and extensible
- It incorporates an intuitive web system designed to be a **discovery tool** for cancer researchers (www.intogen.org)
- It will allow to store, analyze and visualize data coming from **next generation sequencing** technologies

Acknowledgements



Biomedical Genomics Group

Nuria López-Bigas

Gunes Gundem

Jordi Deu-Pons

Alba Jené-Sanz

Khademul Islam

Michael Schroeder

Sergi Hernandez

Simon J Furney
(University College London)