

R2 Introduction Workshop

Basics Part 2

25-March-2024

Lieke Hoyng , on behalf of the R2 Team

Dept. CEMM | Location AMC

Amsterdam University Medical Centers (AUMC)

University of Amsterdam, the Netherlands

R2 Support: r2-support@amsterdamumc.nl

Jan Koster: jankoster@amsterdamumc.nl

r2platform.com

R2-Platform

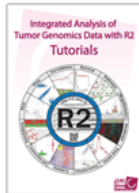
Correlations with a gene



Correlate with a gene

Go to: **Main**

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2



Download the R2
Tutorials Book

R2: Genomics Analysis and Visualization Platform

2,192,415 (2,030,474 unique) samples available

Choose single or multiple dataset analysis

- 1
- 2
- 3
 - View Gene(s)
 - View a Gene
 - View a Gene in groups
 - View multiple Genes
 - Correlate 2 Genes
 - Correlate Gene with track
 - View all Reporters for a Gene (Heatmap)
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Online Tutorial

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For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (<http://r2.amc.nl>)'.

Financial Supporter of R2



News

We are organising another **R2 Introduction Workshop**

Basics Part 1 and Basics Part 2
Thursday 22 & 29 June 2023.
For more info and registration, click [here](#)



News

Check out the new iTHER pediatric cancer precision medicine datascope. Now publicly available in R2 via the 'datascope' menu item.

[all news](#)

Correlate with a gene

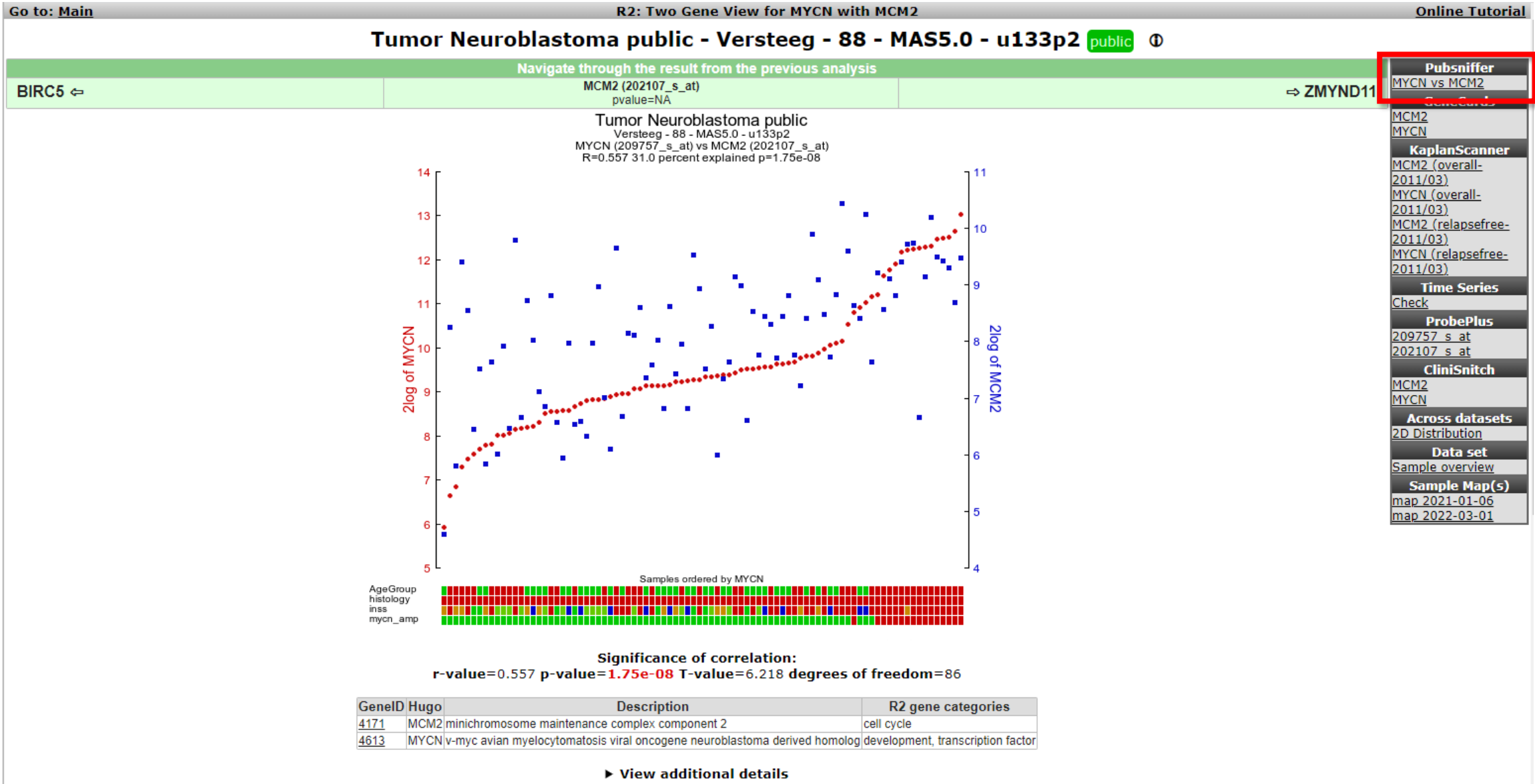
Search gene-set.

GS:cell cycle (537)

Name

Name	count
<input checked="" type="checkbox"/> Categories	18302
<input checked="" type="checkbox"/> base	18302
<input type="checkbox"/> DNA repair	247
<input type="checkbox"/> Oncogenesis	449
<input type="checkbox"/> transcription factor	945
<input type="checkbox"/> apoptosis	677
<input type="checkbox"/> cancer_gene_census	487
<input checked="" type="checkbox"/> cell cycle	537
<input type="checkbox"/> development	1696
<input type="checkbox"/> differentiation	718
<input type="checkbox"/> drugged_kinase	74
<input type="checkbox"/> drug target	1174
<input type="checkbox"/> kinase	700
<input type="checkbox"/> membrane	5599
<input type="checkbox"/> signal transduction	3385
<input type="checkbox"/> transcription regulator activation	1412
<input type="checkbox"/> transcription repressor activation	202

Two Gene View for MYCN with MCM2



Pub sniffer

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 - TAR literature
 - Change Data Scope ▶
 - User Options ▶
 - Help ▶
 - Contact / About R2

R2: PubSniffer

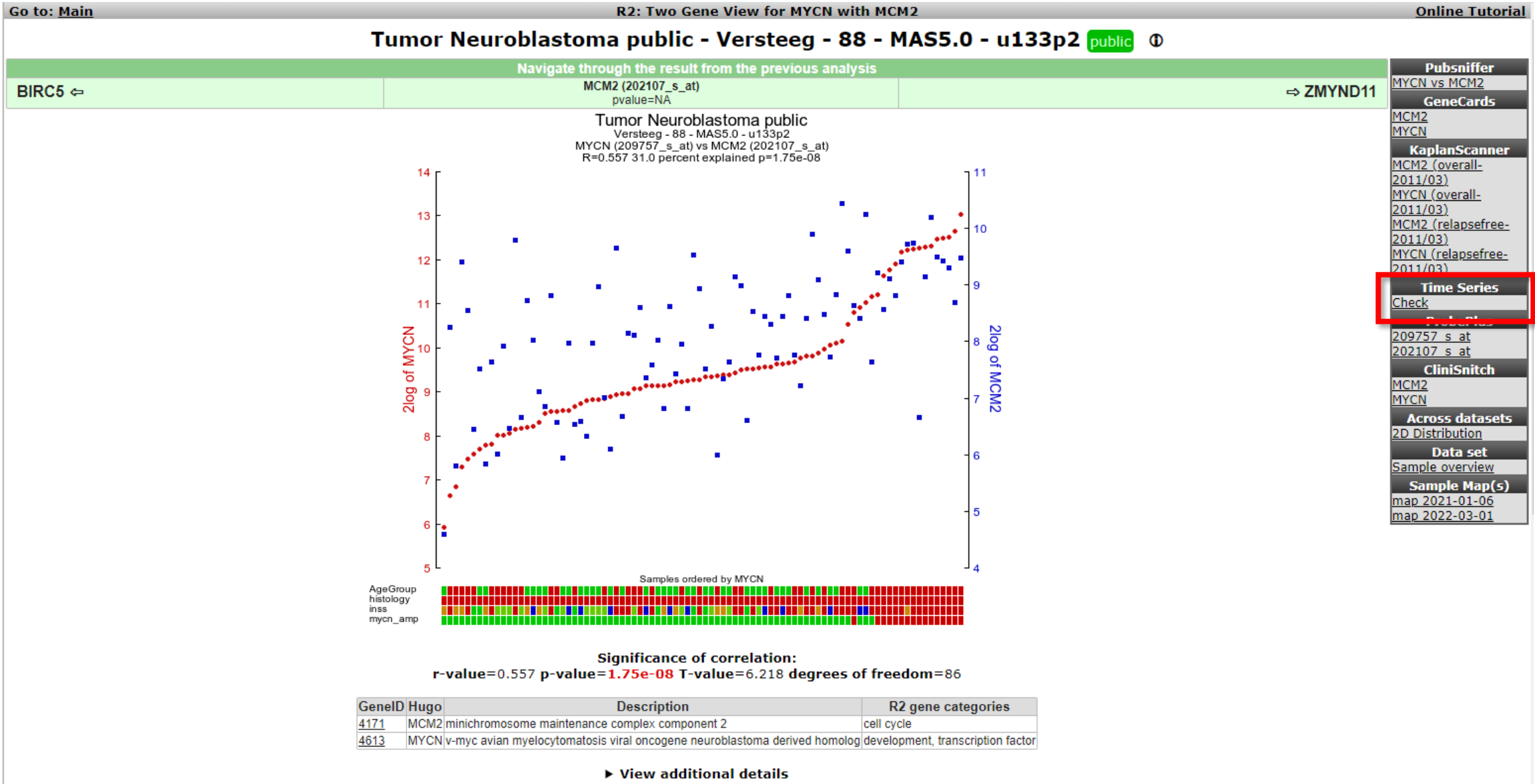
Checking NCBI PubMed for MYCN, MCM2

Query	# Articles	Outlink
'MYCN AND MCM2'	1	Pubreminer
'MYCN'	2934	Pubreminer
'MCM2'	1336	Pubreminer
'MYCN AND MCM2 AND cancer'	1	Pubreminer
'MYCN AND MCM2 AND development'	0	Pubreminer
'MYCN AND MCM2 AND neuroblastom'	1	Pubreminer
'MCM2 AND cancer'	665	Pubreminer
'MCM2 AND development'	199	Pubreminer
'MCM2 AND neuroblastom'	7	Pubreminer

Co-occurrences of "MYCN AND MCM2" within sentences of abstracts
 PubMed(7) MYCN was bound to the proximal promoters of the MCM2 to -8 genes

The screenshot shows the PubMed search results page. The search query is: `MCM2 AND CANCER AND (IMMUNOHISTOCHEMISTRY[MH]) AND (*2016[DP] OR *2017[DP]) OR`. The results are sorted by 'Most recent' and show 9 items. The first result is a review article from BMC Cancer (2018) with PMID 29463213. The second result is an Epub article from Hum Pathol (2017) with PMID 28302837. The search details section shows the query breakdown: `MCM2 [All Fields] AND ("Neoplasms"[MeSH Terms] OR "Neoplasms"[All Fields] OR "cancers"[All Fields]) AND "IMMUNOHISTOCHEMISTRY"[Me] AND`.

Two gene View for MYCN with MCM2



Regulated in timeseries experiments

Go to: [Main](#)

R2: Regulated in Experiments

[Online Tutorial](#)

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- User Options ▶
- Help ▶

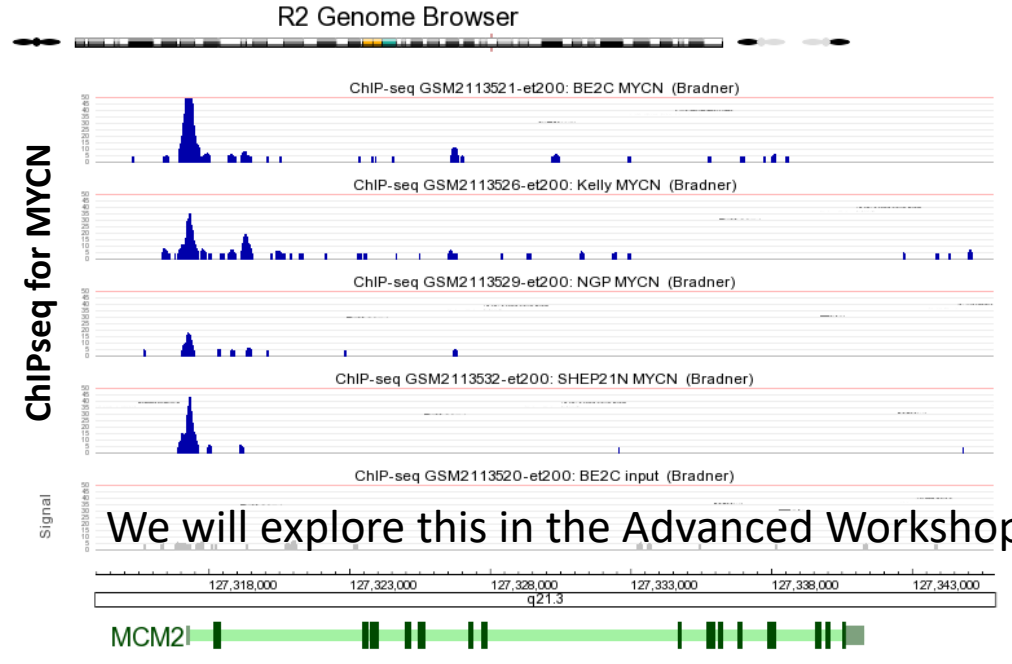
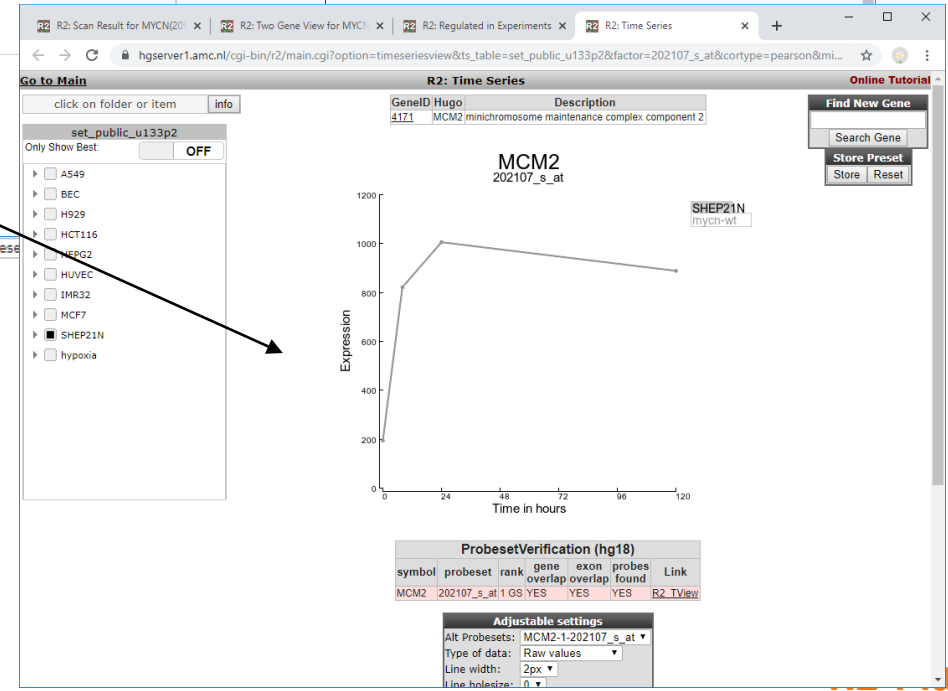
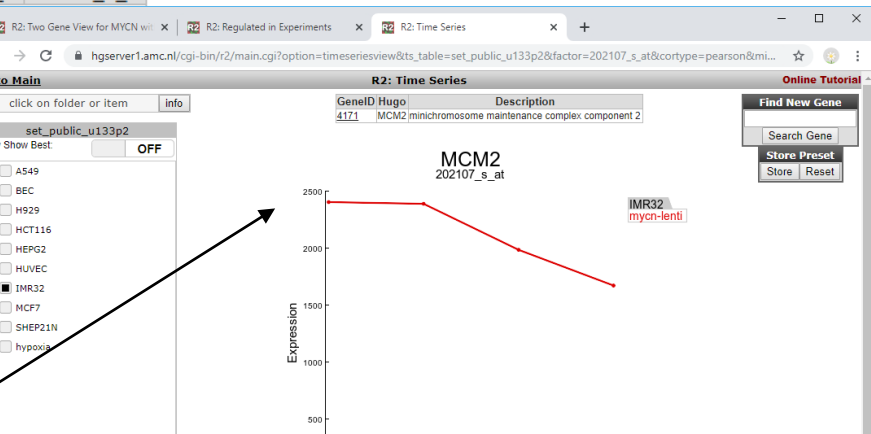
Regulated in Experiments (97 entries)

Experiment 202107_s_at209757_s_at

set_public_u1	
MCF7-egf_r1	5/11
MCF7-egf_r2	3/11
MCF7-hrg_r1	4/11
MCF7-hrg_r2	2/11
UCBMSC-lowserum	2/20

set_public_u1	
A549-TGFB_1	8/8
A549-TGFB_2	6/8
A549-TGFB_3	7/7
BEC-diff_donor1	4/7
BEC-diff_donor2	1/10
BEC-diff_donor3	5/10
HCT116-nocodazole	2/3
HEPG2-control	4/6
HEPG2-mir124	2/8
HUVEC-tnfa-wt	4/24
IMR32-mycn-lenti	3/3
IMR32-mycn-lenti_2	1/3
IMR32-notch3ic	6/8
IMR32-notch3ic-wt-c6	3/7
MCF7-control_1	1/2
MCF7-control_2	1/2
SHEP21N-mycn-wt	3/3
hypoxia-HT29	6/7
hypoxia-MCF7	4/7

NB. Only probesets that contain at least 1 pres



We will explore this in the Advanced Workshop

2d distribution

Go to: [Main](#) R2: Two Gene View for MYCN with MCM2 [Online Tutorial](#)

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public ⓘ

Navigate through the result from the previous analysis

BIRC5 ← MCM2 (202107_s_at)
pvalue=NA ⇒ ZMYND11

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
MYCN (209757_s_at) vs MCM2 (202107_s_at)
R=0.557 31.0 percent explained p=1.75e-08

Samples ordered by MYCN

AgeGroup
histology
ins
mycn_amp

Significance of correlation:
r-value=0.557 p-value=**1.75e-08** T-value=6.218 degrees of freedom=86

GeneID	Hugo	Description	R2 gene categories
4171	MCM2	minichromosome maintenance complex component 2	cell cycle
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

▶ [View additional details](#)

PubsNiffer
[MYCN vs MCM2](#)

GeneCards
[MCM2](#)
[MYCN](#)

KaplanScanner
[MCM2 \(overall-2011/03\)](#)
[MYCN \(overall-2011/03\)](#)
[MCM2 \(relapsefree-2011/03\)](#)
[MYCN \(relapsefree-2011/03\)](#)

Time Series
[Check](#)

ProbePlus
[209757 s at](#)
[202107 s at](#)

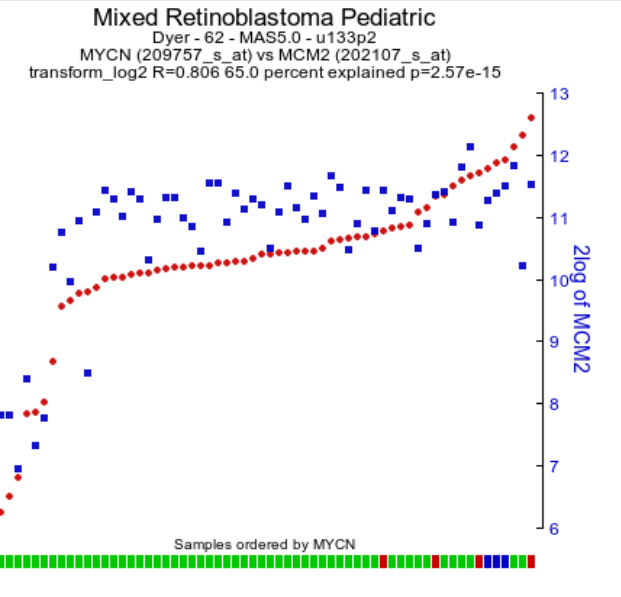
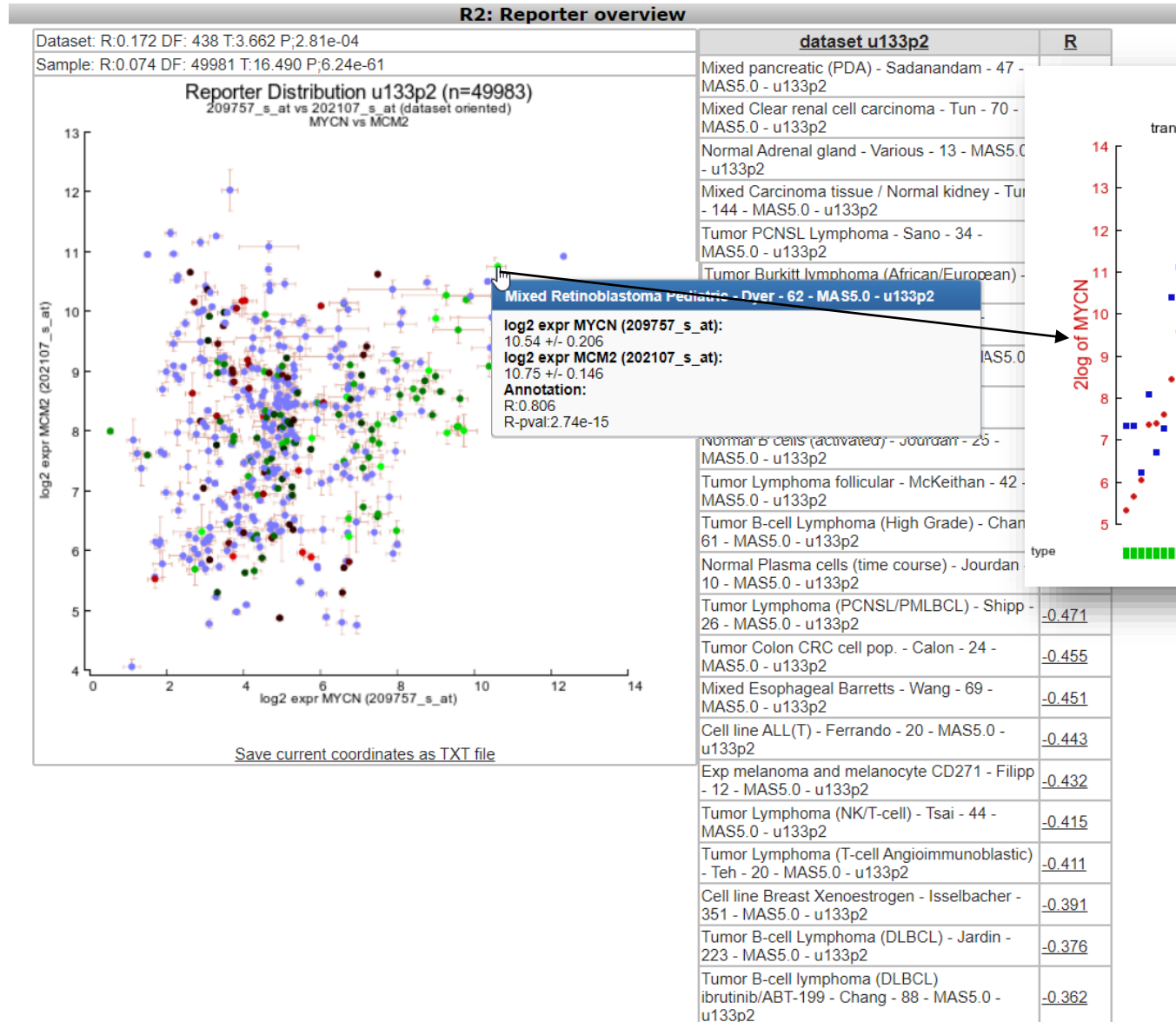
CliniSnitch
[MCM2](#)
[MYCN](#)

Across datasets
[2D Distribution](#)

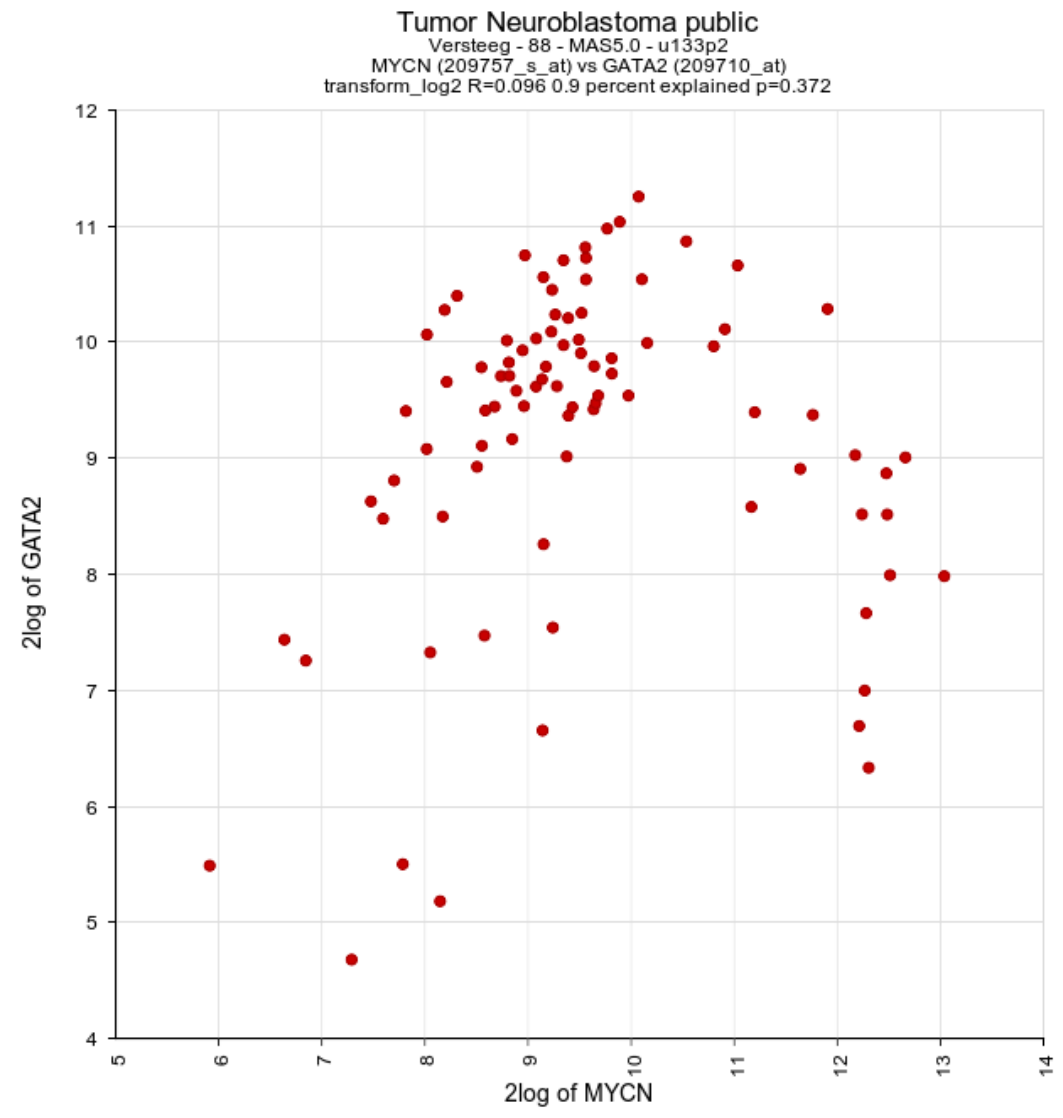
Data set
[Sample overview](#)

Sample Map(s)
[map 2021-01-06](#)
[map 2022-03-01](#)

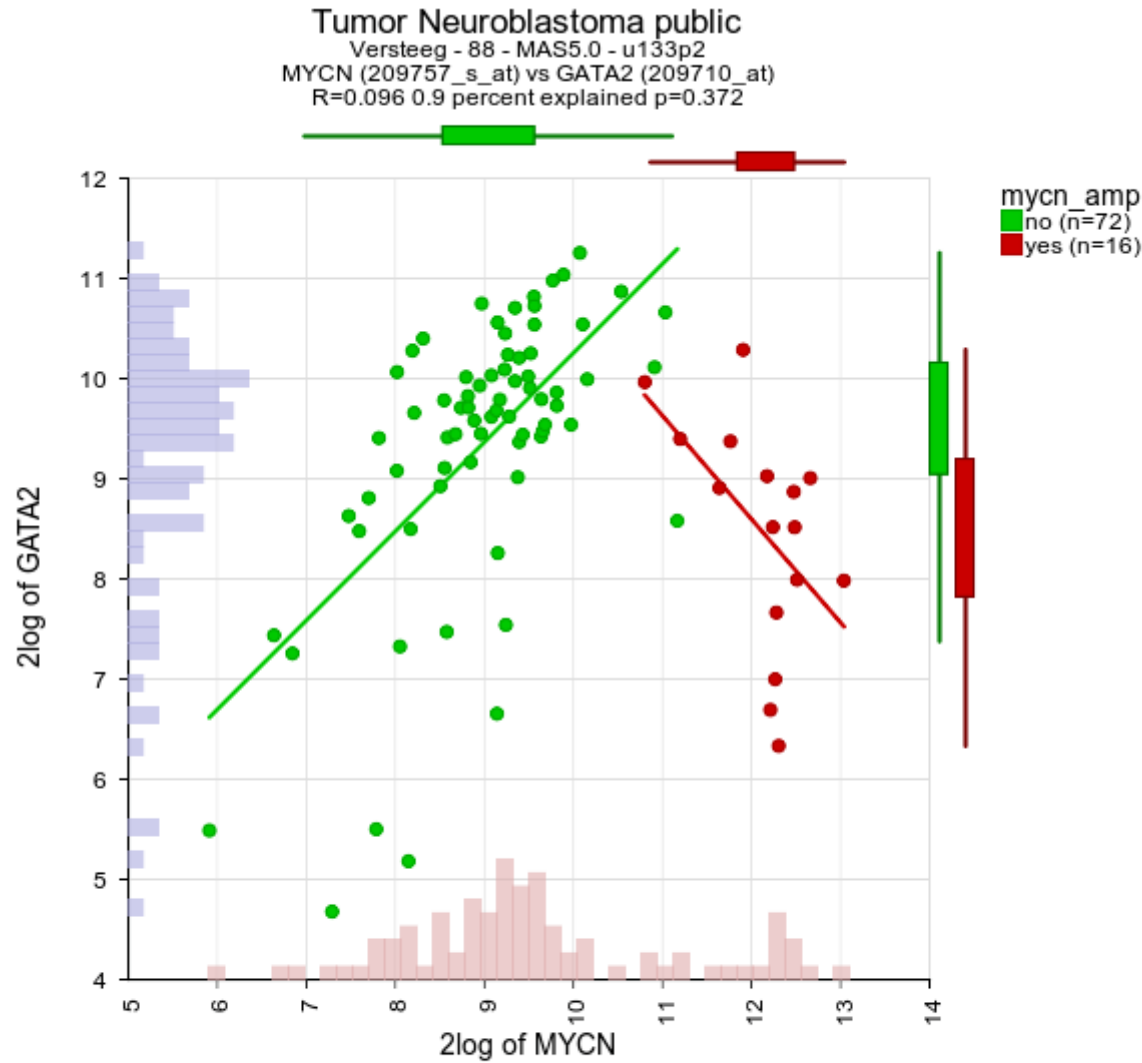
2d distribution



X-gene-view



X-gene-view



Trend lines		
group	r	rpval
no	0.617	8.06e-09
yes	-0.509	0.044

Adjustable settings

Analysis type:

Gene / Reporter 1:

Gene / Reporter 2:

Transformation:

Sample Filter

Subset track:

Selected sample subset: None

Graphics

Graph type:

Samples to mark:

Sample paths:

Color mode:

Color track:

Track Display Selection

More Settings

Min (X):

Max (X):

Color (X):

Min (Y):

Max (Y):

Color (Y):

Mark method:

Vector (SVG) output:

Draw height:

Dot size:

Add Boxplot per group:

Linear Fit:

Histogram:

fontsize_y:

fontsize_ruler:

fontsize_t1:



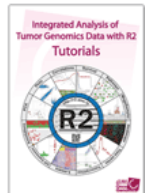
View multiple genes



View multiple genes

Go to: Main

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- User Options ▶
- Help ▶
- Contact / About R2



Download the R2 Tutorials Book

R2: Genomics Analysis and Visualization Platform

2,189,183 (2,027,339 unique) samples available

Choose single or multiple dataset analysis

1

Single Dataset

2

Select a dataset for analysis

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2

3

Select type of analysis

- View a Gene
- View Gene(s)
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Online Tutorial

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Financial Supporter of R2



News

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[all news](#)



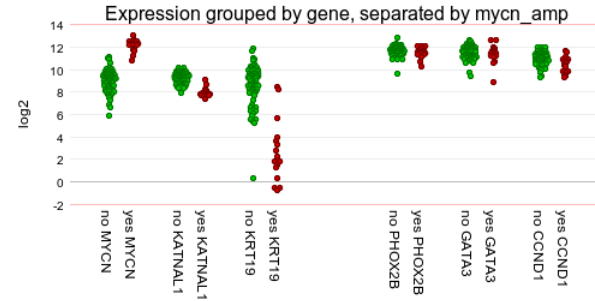
View multiple genes

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R2: View Multiple Genes

Tumor Neuroblastoma public
Versteeg - 88 - MASS.0 - u133p2



Adjustable settings

Genes/Reporters to include

- mycn
- katna11
- krt19
- phox2b

Gene label: Genesymbol

Track Separations

Track: mycn_amp (2 cat)

Handle groups by: lump by gene plot group

Coloring

Color by: Track

User defined color: FF8282

Sample Filter

Subset track:

Selected sample subset: None

Transformation: Log2

Plotting Options

Plot Type: Dot plot

(sub)panel height: 150

gene width: 15

gene space: 5

group separator width: 15

stroke width: 1

dot size (dotplot): 1

Samples to mark: comma separated sample names

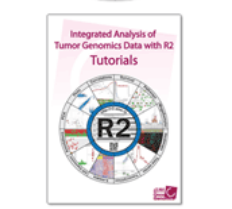
next Reset

Annotation Views



Annotation Views

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- 1 Single Dataset
- 2 Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2
- 3 Select type of analysis
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Relate 2 tracks

R2: Relate two tracks

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public ⓘ

Adjustable settings

Analysis type: track vs track ▼ ⓘ

X track: mycn_amp (2 cat) ▼ ⓘ

Y track: Alive (2 cat) ▼ ⓘ

Sample Filter

Subset track: ▼ ⓘ

Selected sample subset: None

Graphics

Graph type: XY plot ▼ ⓘ

Samples to mark: comma separated sample names ⓘ

Sample paths:

Group overlap as: Single samples ▼ ⓘ

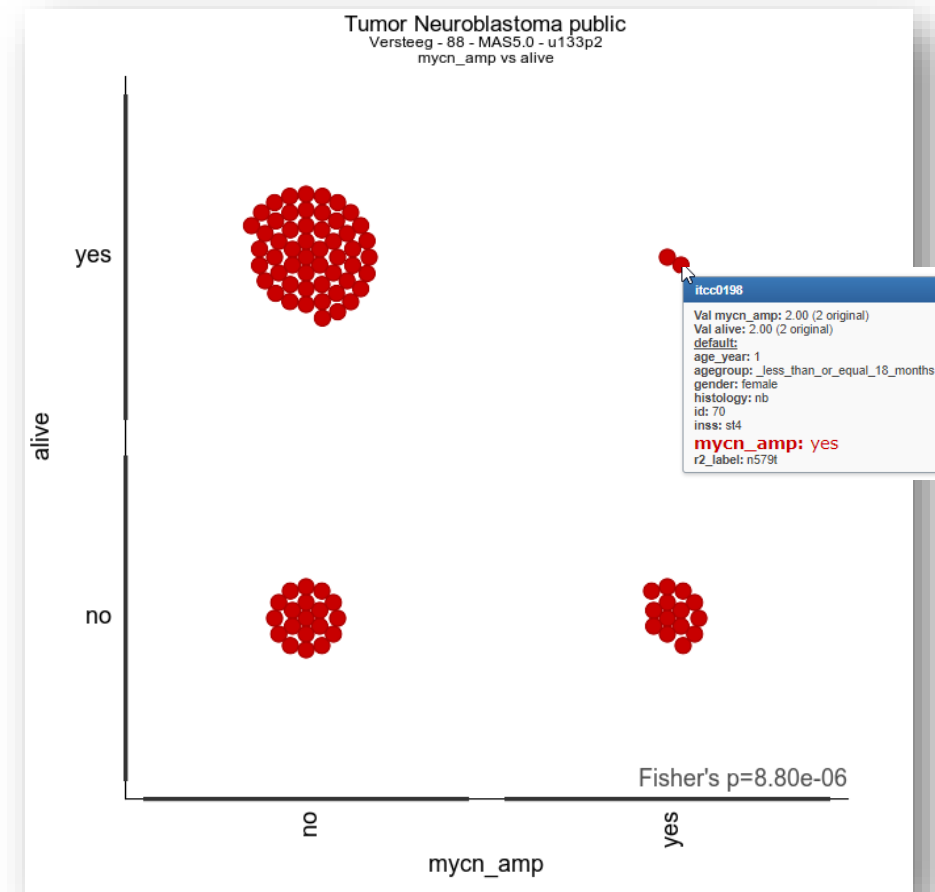
Color mode: Default Color ▼

Track Display Selection

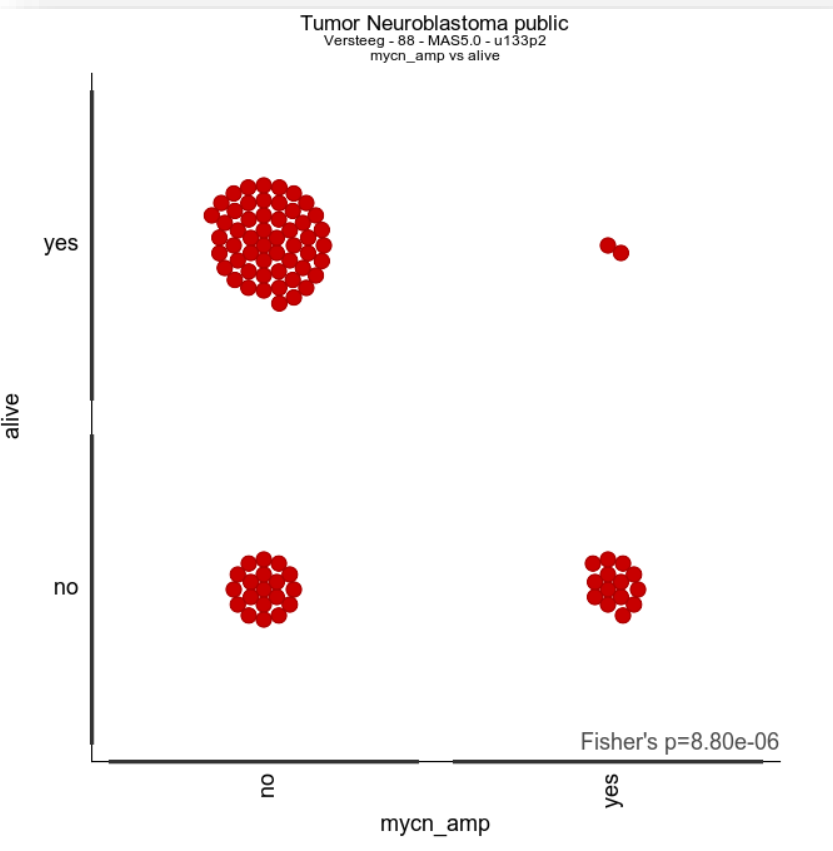
Select tracks

More Settings +

Submit



Relate 2 tracks



Adjustable settings

Analysis type: track vs track

X track: mycn_amp (2 cat)

Y track: Alive (2 cat)

Sample Filter

Subset track:

Selected sample subset: None

Graphics

Graph type: XY plot

Samples to mark: comma separated sample names

Sample paths:

Group overlap as: Single samples

Color mode: Color by a Track

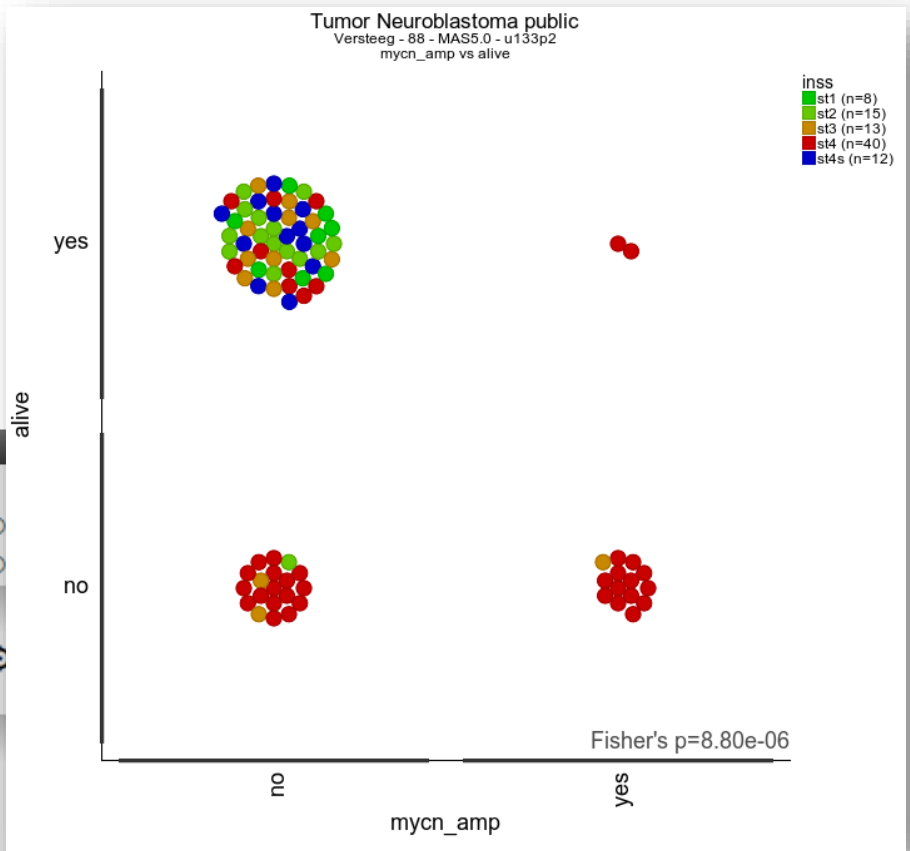
Color track: inss (5 cat)

Track Display Selection

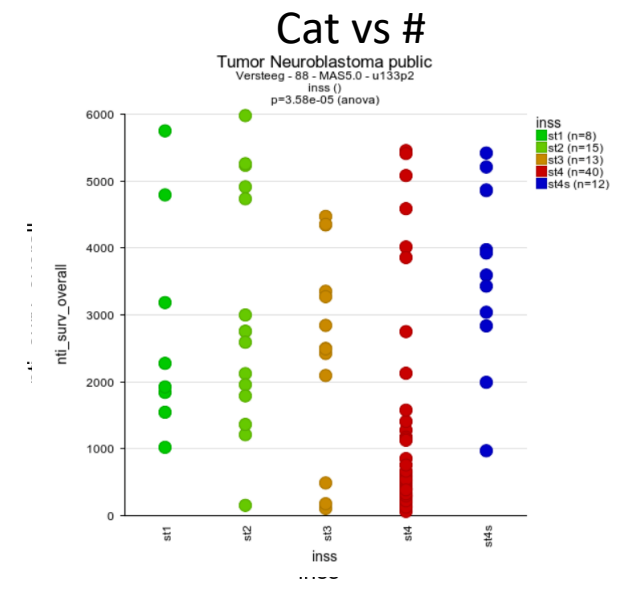
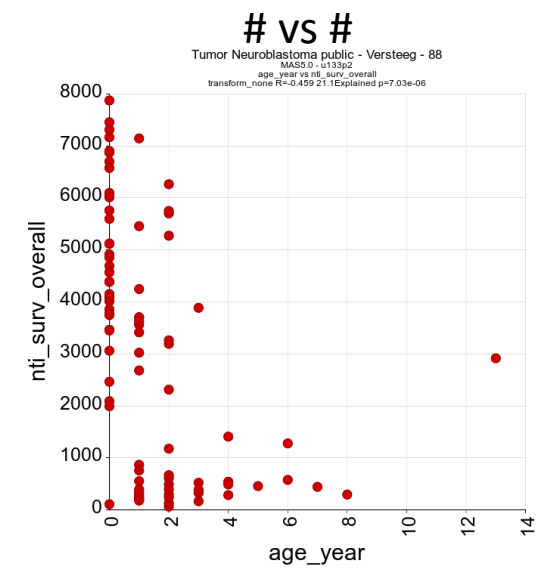
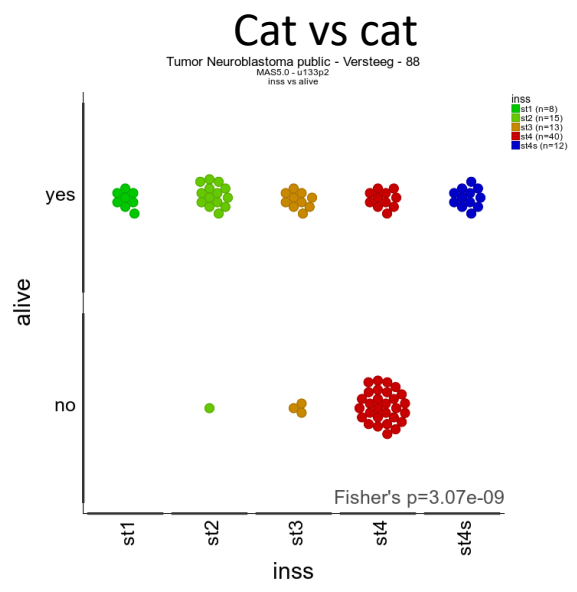
Select tracks

More Settings

Submit



Relate 2 tracks



Number of samples

Legend: (g) st1, (s) st2

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
88 samples
nti_surv_overall vs inss
p=3.58e-05 (anova)

Legend: inss (st1 n=8, st2 n=15, st3 n=13, st4 n=40, st4s n=12)

Tumor Neuroblastoma public - Versteeg - 88
MAS5.0 - u133p2
inss vs nti_surv_overall
transform_none
p=2.23e-07 (anova)

Expression nti_surv_overall

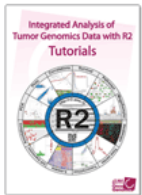
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
p=3.58e-05 (anova)

Alive
no (n=33)
yes (n=55)

Annotation Plotter

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Annotation Plotter

[Online Tutorial](#)

The annotation plotter allows you to generate track annotations for any dataset. Tracks to include in your image can be selected in the 'Track Display Selection'. You are able to define the order of samples by using the 'Track Sort Order' by dragging tracks into the right hand panel. The order of the tracks is also used in the sort order.

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R2:

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2



itcc0221 (n620t)

default:
agegroup: _more_than_18_months
alive: yes
histology: nb
inss: st4
mycn_amp: no

Adjustable settings

Sample annotation tracks

- ▼ default
- age_year
- agegroup
- alive
- death_cause
- gender
- histology
- id
- inss
- mycn_amp
- nti_event_overall
- nti_event_progfree

Selected tracks (drag here)

- agegroup
- alive
- histology
- inss
- mycn_amp

Sample Filter

Subset track: ⚙️ ℹ️

Selected sample subset: None

Graphics Settings

fontsize_t1:




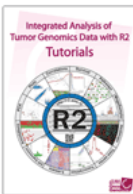
fontsize_tsub:

fontsize_tracks:

Cohort Overview

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Select a dataset for analysis

2 Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2

Select type of analysis

3 View a Gene

4

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[all news](#)

Cohort Overview

Go to: [Main](#) R2: Cohort Overview [Online Tutorial](#)

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public

Main

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Tumor Neuroblastoma public agegroup (n=88)

Legend: ■ _less_than_or_equal_18_months, ■ _more_than_18_months, ■ nd

Applied filters:

none

histology

inss

death_cause

mycn_amp

Filter by "Click"

- default
- samplenames
- link

samplenames	agegroup	alive	histology	inss	mycn_amp	age_year	death_cause	gender	nti_event_overall	nti_event_agree	...	
ITCC0001	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd		no	7876	7876	n
ITCC0002	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd		no	4914	4914	n
ITCC0003	_less_than_or_equal_18_months	yes	nb	st4s	no	0	nd		yes	7457	97	n
ITCC0008	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd		no	6904	6904	n
ITCC0009	_less_than_or_equal_18_months	yes	nb	st2	no	1	nd		yes	7146	161	n
ITCC0010	_less_than_or_equal_18_months	yes	nb	st4	no	0	nd		no	7168	7168	n
ITCC0013	_more_than_18_months	no	nb	st4	no	2	tumor		yes	488	456	n
ITCC0015	_more_than_18_months	no	nb	st4	yes	6	tumor		yes	1277	549	n
ITCC0017	_more_than_18_months	no	nb	st4	no	6	tumor		yes	576	511	n
ITCC0018	_more_than_18_months	no	nb	st4	no	2	tumor		yes	609	445	n
ITCC0020	_more_than_18_months	no	nb	st4	yes	1	tumor	male	yes	340	340	n

Filter in table

Build a track from table

Build a track

Sort Ascending

Sort Descending

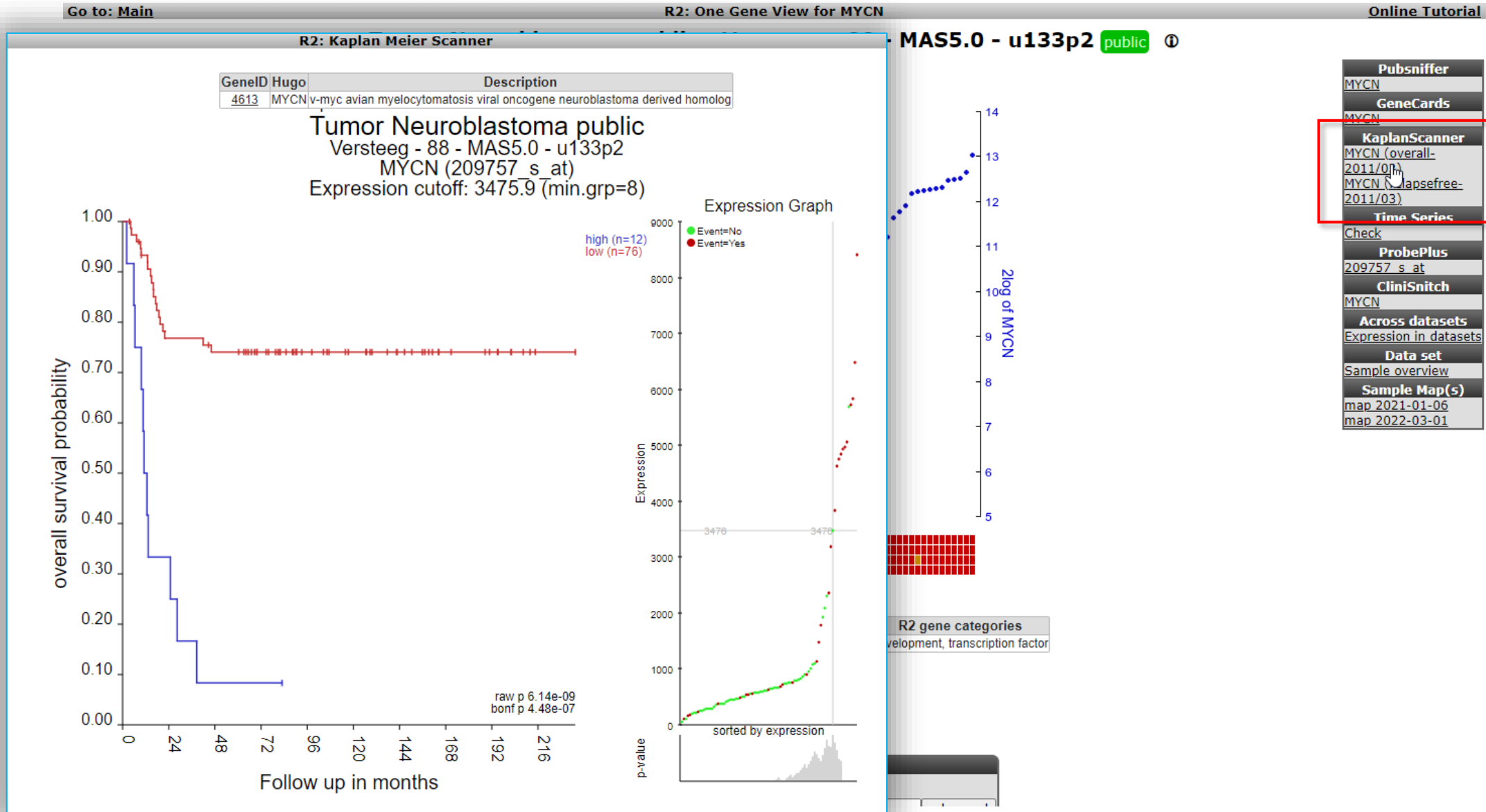
Remove Sort

Show rows where:

- (Select All)
- nd
- toxic
- tumor


Filter Clear

Recap Result page panel for follow-up analyses



Survival analysis (Kaplan)

Go to: [Main](#)

- Main
- Time series
- Survival (Kaplan-Meier/Cox) 
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

R2: Kaplan-Meier

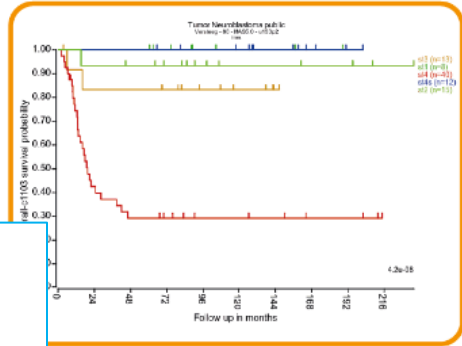
[Online Tutorial](#)

Kaplan-Meier analysis using a data set

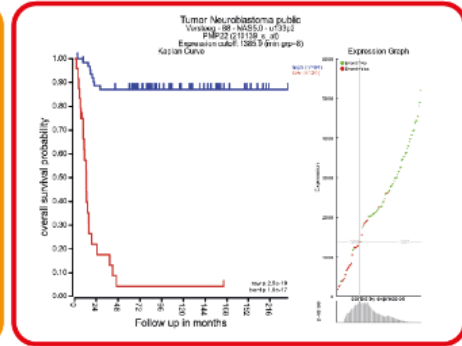
Data set: ▼

Separate by: ▼

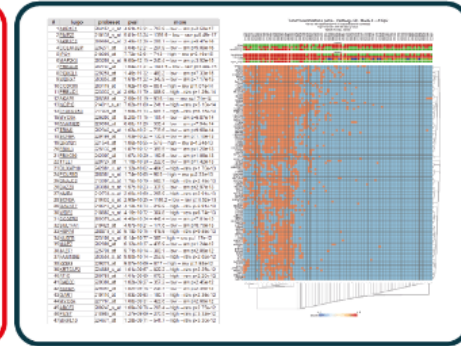
Most common survival analyses in R2 separate by:




categorical track



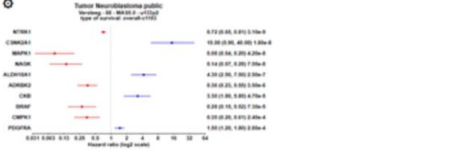
expression of a gene



multiple genes

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 

88 samples




name	survival_type	reporter	beta	HR	HR_low	HR_high	wald	pvalue	-Y	kaplan
NRXN1	overall-c1103	208605_at	-0.32	0.72	0.65	0.81	35	3.1e-9	50%	50%
C19K2A1	overall-c1103	213072_at	2.7	15	5.9	40	32	1.6e-9	50%	50%
MAPK1	overall-c1103	224623_at	-2.5	0.694	0.629	0.7	30	4.2e-9	50%	50%
MAPK8	overall-c1103	216371_at	-2	0.64	0.567	0.73	29	7e-9	50%	50%
ALDH3B1	overall-c1103	225418_at	1.5	4.3	2.5	7.5	27	3.5e-7	50%	50%
ADRM2	overall-c1103	228771_at	-1	0.36	0.23	0.55	22	0.000035	50%	50%
CRB	overall-c1103	209884_at	1.2	3.3	1.8	5.8	17	0.00047	50%	50%
BRAP	overall-c1103	226391_at	-1.3	0.28	0.15	0.52	14	0.00073	50%	50%
CRNK1	overall-c1103	217670_at	-1.1	0.35	0.2	0.61	13	0.0024	50%	50%
PDGFRA	overall-c1103	203131_at	0.36	1.5	1.2	1.8	13	0.0028	50%	50%

Survival analysis (Kaplan)

Go to: [Main](#)

R2: Kaplan-Meier

[Online Tutorial](#)

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- User Options ▶
- Help ▶
- Contact / About R2

Kaplan-Meier analysis using a data set

Data set: Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2

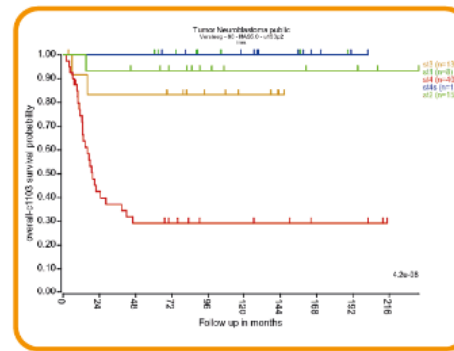
Separate by:
 a categorical track
 a categorical track
 a numerical track
 a single gene
 multiple genes
 Hazard_ratio for a gene
 Hazard_ratio for multiple genes

in multiple data sets

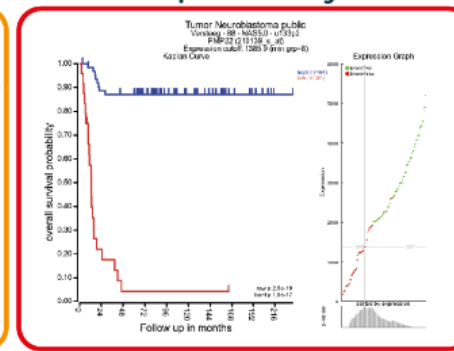
custom data

Most common survival analyses in R2

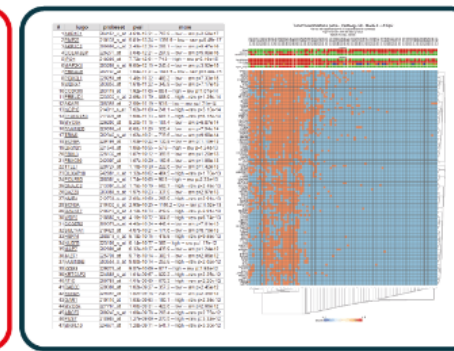
separate by:



categorical track



expression of a gene



multiple genes

Kaplan Meier by categorical track

R2: Kaplan Meier

Using dataset Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 ⓘ

Adjustable settings

Survival

Type of Survival: ▾

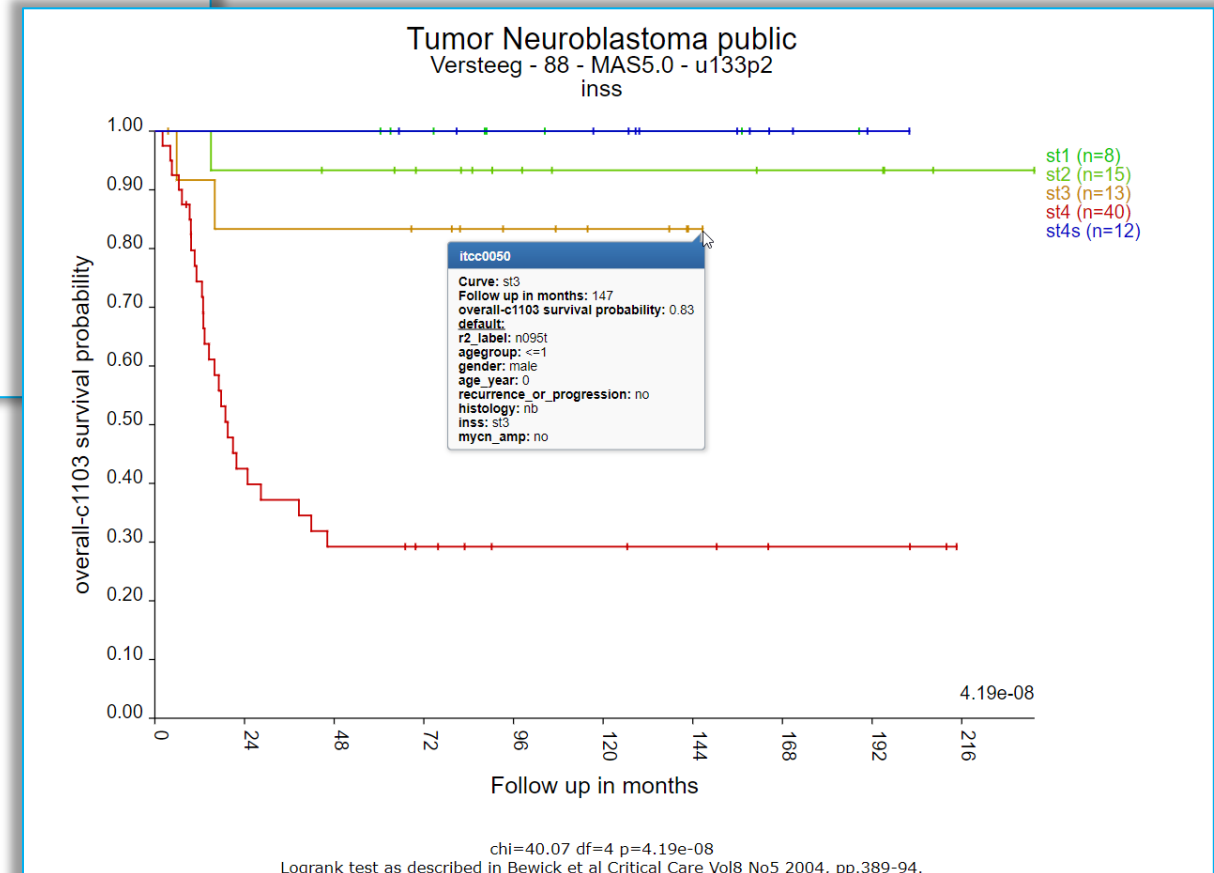
Separate by: ▾

Track: ▾ ⓘ

Sample Filter

Subset track: ▾ ⚙️ ⓘ

Selected sample subset: None



KaplanScan

- Go to: Main**
- Main
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 - Survival (Kaplan-Meier/Cox)
 - Sample maps (UMAP/tsNE)
 - Small Tools
 - DataGrabber
 - Genome Browser
 - ChIP data
 - TAR literature
 - Change Data Scope ▶
 - User Options ▶
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R2: Kaplan-Meier

[Online Tutorial](#)

Kaplan-Meier analysis using a data set

Data set: Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2

Separate by: **a single gene**

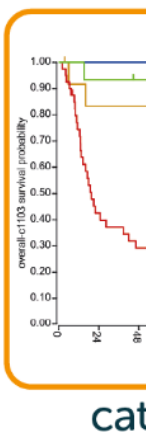
- a single gene
- a categorical track
- a numerical track
- a single gene**
- multiple genes
- Hazard_ratio for a gene
- Hazard_ratio for multiple genes

in multiple data sets

custom data

Most common survival analyses in R2

R2: Kaplan-Meier Scanner



Kaplan Meier Scanner:

Gene / Reporter: PMP22 210139_s_at advanced

Cutoff mode: scan

- scan
- median
- average
- first_quartile
- last_quartile
- first_vs_last_quartile
- curtain

Subset track: [dropdown]

Selected sample subset: [dropdown]

Type of Survival: [dropdown]

Minimal group size: 8

Next

KaplanScan

Go to: [Main](#)
R2: Kaplan Meier Scanner Online Tutorial

Pubsniiffer

PMP22

GeneCards

PMP22

KaplanScanner

PMP22 (overall-2011/03)

PMP22 (relapsefree-2011/03)

Time Series

Check

ProbePlus

210139_s_at

CliniSnitch

PMP22

Sample Map(s)

map 2021-01-06 ⓘ

GeneID	Hugo	Description
5376	PMP22	peripheral myelin protein 22

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 1385.9 (min.grp=8)
Kaplan Curve

high (n=64)
low (n=24)

itcc0221

Curve: high

Follow up in months: 76

overall survival probability: 0.87

default:

age_year: 2

agegroup: _more_than_18_months

gender: male

histology: nb

id: 73

inss: st4

mycn_amp: no

r2_label: n620t

raw p 2.5e-19

bonf p 1.8e-17

Expression Graph

● Event=No
● Event=Yes

Red = event
Green = censored

Click to use that as a cutoff

P-values hill plot

Click to use that as a cutoff

chi=80.80 df=1 p=2.5e-19
low is worse
ST:
View [PMP22](#) in 2geneview

TrackSaver

Store Settings

Adjustable settings

Gene / Reporter: PMP22 | 210139_s_at | advanced

Cutoff mode: scan

Cutoff: 24 - 661.6: raw p: 2.5e-19 (bonf. 1.8e-17)

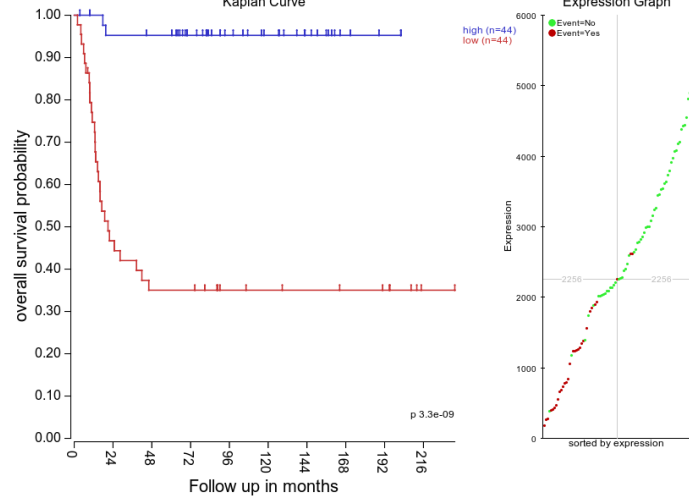
Sample Filter

Subset track: ⓘ

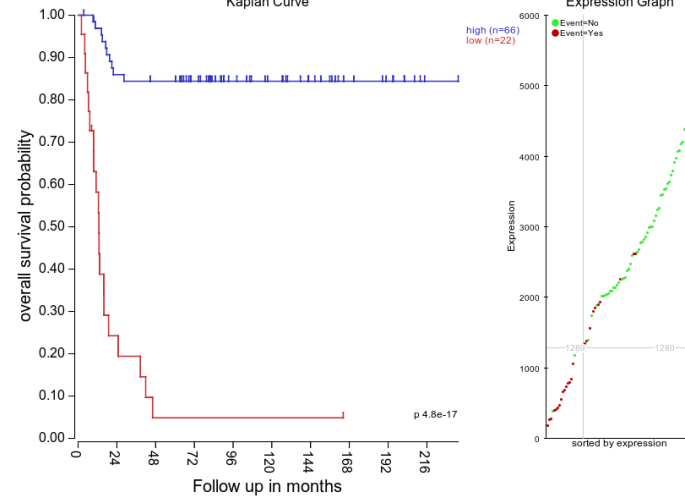
Selected sample subset: None

Other separation methods

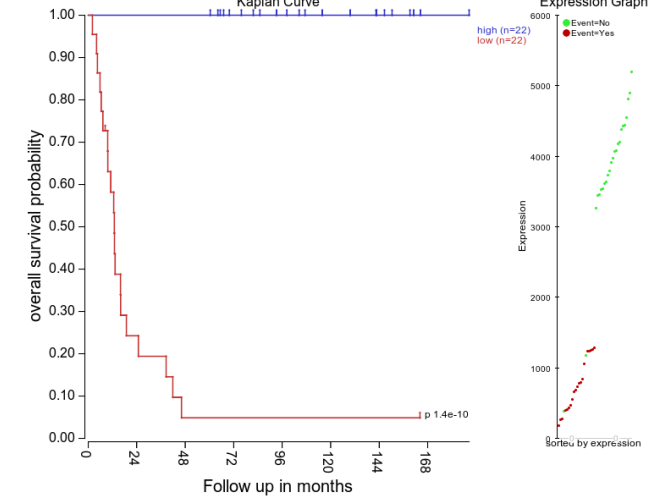
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 2255.8



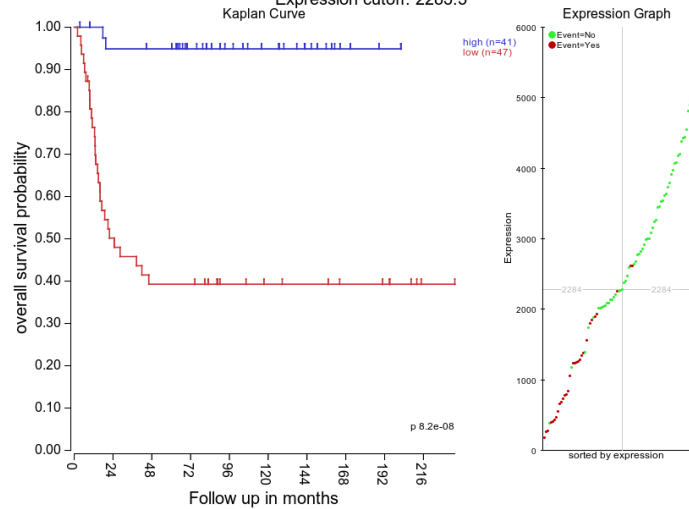
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 1279.5



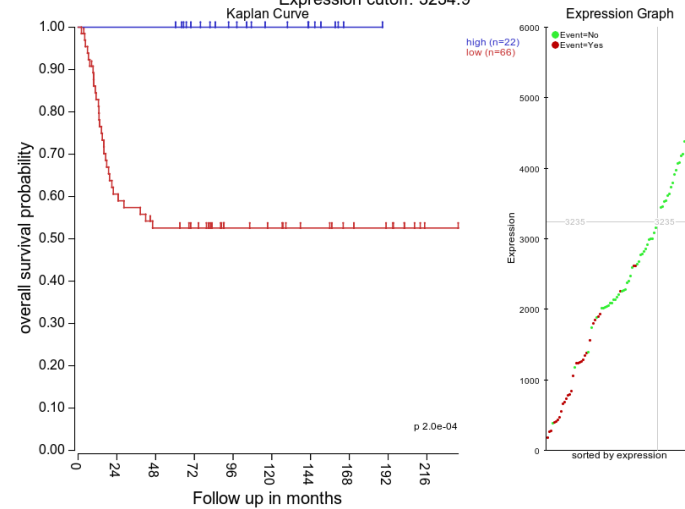
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff:



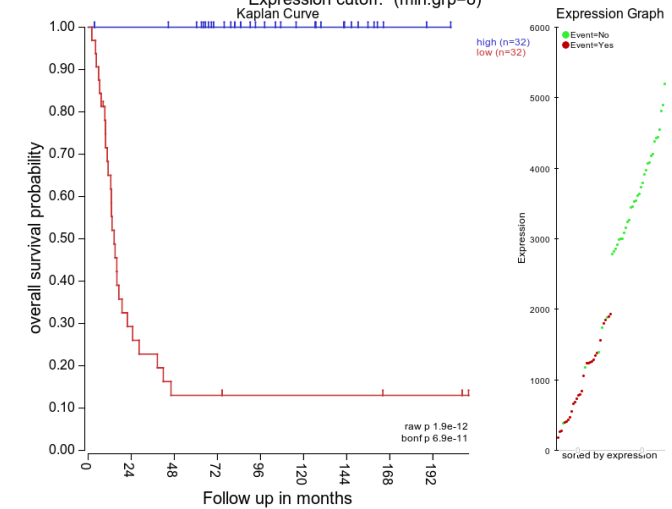
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 2283.5



Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 3234.9



Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: (min.grp=8)



KaplanScan

Go to: [Main](#)
Online Tutorial

Pubsntiffer

PMP22

GeneCards

PMP22

KaplanScanner

PMP22 (overall-2011/03)

PMP22 (relapsefree-2011/03)

Time Series

Check

ProbePlus

210139_s_at

CliniSnitch

PMP22

Sample Map(s)

map 2021-01-06 ⓘ

R2: Kaplan Meier Scanner

GeneID	Hugo	Description
5376	PMP22	peripheral myelin protein 22

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 1385.9 (min.grp=8)
Kaplan Curve

overall survival probability

Follow up in months

raw p 2.5e-19
bonf p 1.8e-17

Expression Graph

Expression

sorted by expression

high (n=64)
low (n=24)

chi=80.80 df=1 p=2.5e-19
low is worse
ST:
View [PMP22](#) in 2geneview

TrackSaver **Store Settings**

store as track Store Reset

Adjustable settings

Gene / Reporter: PMP22 210139_s_at advanced

Cutoff mode: scan

Cutoff: 24 - 661.6: raw p: 2.5e-19 (bonf: 1.8e-17)

Sample Filter

Subset track: ⓘ

Selected sample subset: None

itcc0147:	high
itcc0148:	high
itcc0150:	high
itcc0151:	high
itcc0155:	high
itcc0169:	low
itcc0170:	high
itcc0172:	high
itcc0174:	low
itcc0175:	high
itcc0181:	high
itcc0183:	high
itcc0184:	low
itcc0189:	low
itcc0191:	high
itcc0193:	high
itcc0194:	low
itcc0195:	low
itcc0198:	high
itcc0217:	high
itcc0219:	high
itcc0221:	high
itcc0284:	high
itcc0285:	high
itcc0288:	low
itcc0302:	high
itcc0380:	high
itcc0382:	high
itcc0383:	low
itcc0385:	high
itcc0387:	low
itcc0390:	low
itcc0391:	high
itcc0392:	low
itcc0398:	high

Groups
C:2 / N: / U:

Group 'high': high DD0000

Group 'low': low 00DD00

Track Settings

Track name: Temporary (24hrs)

Show as track: Temporary (24hrs)

Where: **personal track**

Community: student

Community: student_breast

Build set Reset

KaplanScanner multiple genes

R2: Kaplan-Meier

Kaplan-Meier analysis using a data set

Search gene-set.

GS:Oncogenesis (449)

Name

Categories

- base
 - DNA repair
 - Oncogenesis
 - transcription
 - apoptosis
 - cancer_gene
 - cell cycle
 - development
 - differentiation
 - drugged_kin
 - drug target
 - kinase
 - membrane
 - signal trans

Reset selected

Use selected

Adjustable settings

Cutoff mode: scan

Gene Filters

Chromosome: All

Gene ontology: All Search GO

Gene set: GS:Oncogenesis (449) Search GS

Manual list: none

Sample Filter

Subset track:

Selected sample subset: None

Survival Data

Type of Survival: overall-c1103

Statistics

P-value: 0.05

Corr. multiple testing: False Discovery Rate

Filter results: no

Graphics Settings

Draw heatmap: yes

Heatmap data: zscore

Heatmap gene weight: no

Next Reset

	count
	18302
	18302
	247
	449
	945
	677
	487
	537
	1696
	718
	74
	1174
	700
	5599
	2385

KaplanScanner multiple genes

Go to: [Main](#)

[Kaplan start](#) [Adapt settings](#)

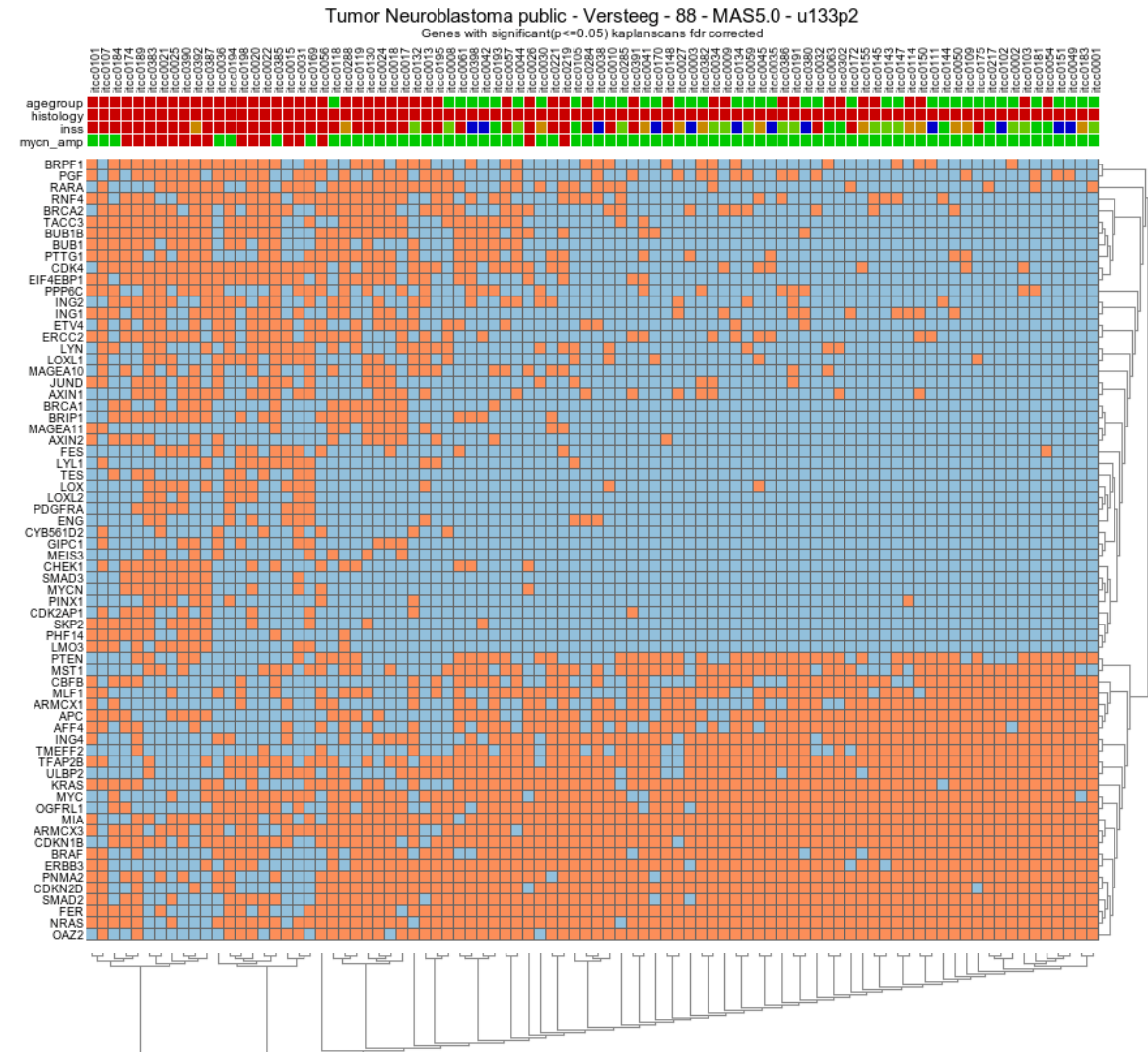
R2: Kaplan Meier Scanner Pro

[Online Tutorial](#)

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public ⓘ

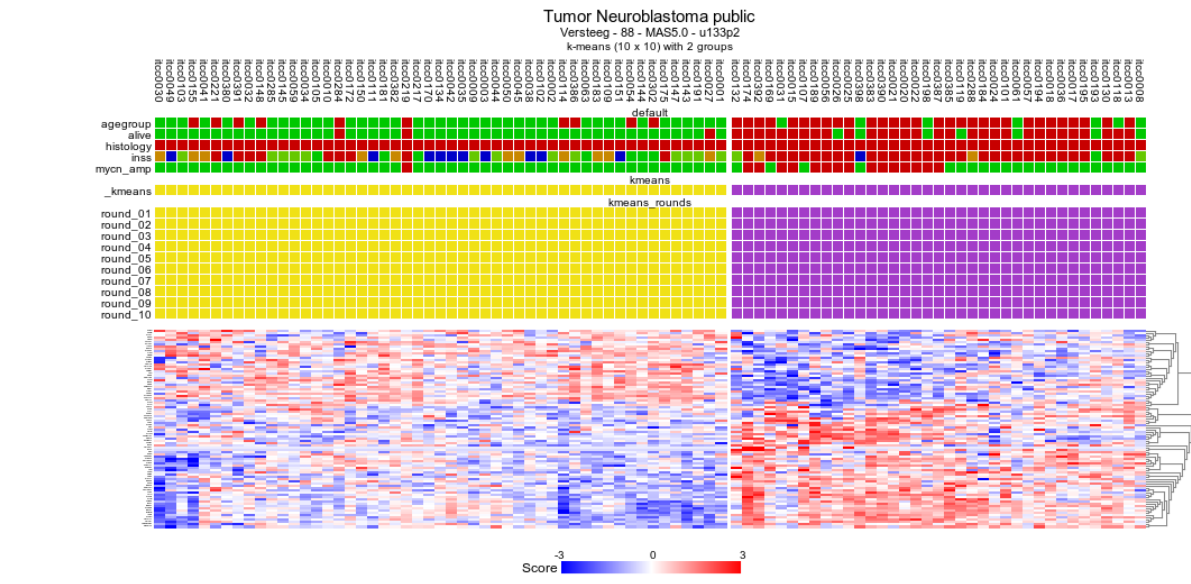
88 samples, gene set: Oncogenesis
Results corrected for multiple gene testing by fdr
68 out of 315 genes found where $p < 0.05$

#	hugo	probeset	pval	more
1	QAZ2	201365_at	2.74e-08	14 -- 283.5 -- low -- raw p=8.69e-11
2	LMO3	204424_s_at	4.65e-08	76 -- 68.1 -- high -- raw p=2.95e-10
3	EIF4EBP1	221539_at	5.25e-08	56 -- 284.3 -- high -- raw p=5.00e-10
4	SKP2	203625_x_at	7.06e-08	74 -- 511.2 -- high -- raw p=8.96e-10
5	PHF14	228095_at	7.29e-07	77 -- 866.7 -- high -- raw p=1.16e-08
6	TMEFF2	223557_s_at	4.63e-06	37 -- 457.2 -- low -- raw p=8.83e-08
7	PINX1	223907_s_at	8.11e-06	79 -- 115.3 -- high -- raw p=1.80e-07
8	ERBB3	226213_at	8.44e-06	19 -- 3.3 -- low -- raw p=2.41e-07
9	CDK4	202246_s_at	9.20e-06	47 -- 723.3 -- high -- raw p=2.34e-07
10	FER	227579_at	1.31e-05	11 -- 214.6 -- low -- raw p=4.58e-07
11	CDKN1B	209112_at	1.39e-05	9 -- 917.4 -- low -- raw p=4.42e-07
12	MYCN	209757_s_at	2.03e-05	76 -- 3475.9 -- high -- raw p=7.72e-07
13	MEIS3	228327_x_at	6.23e-05	80 -- 234 -- high -- raw p=2.57e-06
14	ULBP2	238542_at	7.27e-05	22 -- 22.6 -- low -- raw p=3.23e-06
15	SMAD3	218284_at	1.03e-04	79 -- 101.6 -- high -- raw p=4.92e-06
16	ETV4	1554576_a_at	1.19e-04	63 -- 16.7 -- high -- raw p=6.07e-06
17	ING4	48825_at	1.60e-04	27 -- 149.4 -- low -- raw p=8.66e-06
18	BUB1	209642_at	1.70e-04	63 -- 133.5 -- high -- raw p=9.73e-06
19	APC	203525_s_at	1.96e-04	26 -- 318.7 -- low -- raw p=1.18e-05
20	AXIN2	222696_at	2.02e-04	72 -- 158.8 -- high -- raw p=1.28e-05
21	OGFRL1	226810_at	2.87e-04	18 -- 274.7 -- low -- raw p=1.91e-05
22	BUB1B	203755_at	3.09e-04	54 -- 294 -- high -- raw p=2.16e-05
23	TACC3	218308_at	4.81e-04	56 -- 133 -- high -- raw p=3.51e-05
24	MAGEA10	210295_at	6.26e-04	65 -- 54 -- high -- raw p=4.77e-05
25	ARMCX3	222444_at	7.39e-04	9 -- 374.6 -- low -- raw p=5.87e-05
26	CHEK1	205394_at	9.15e-04	71 -- 142.3 -- high -- raw p=7.84e-05
27	CYB561D2	209665_at	9.38e-04	80 -- 101.2 -- high -- raw p=7.74e-05
28	MIA	206560_s_at	9.55e-04	8 -- 14.7 -- low -- raw p=8.49e-05
29	PDGFRA	203131_at	9.77e-04	79 -- 920.6 -- high -- raw p=8.99e-05
30	SMAD2	203075_at	1.13e-03	13 -- 409.9 -- low -- raw p=1.11e-04
31	BRAF	226391_at	1.14e-03	20 -- 240.7 -- low -- raw p=1.15e-04
32	BRIP1	235609_at	1.15e-03	64 -- 327.5 -- high -- raw p=1.10e-04
33	RNF4	212696_s_at	1.19e-03	48 -- 253.3 -- high -- raw p=1.28e-04
34	CDKN2D	210240_s_at	1.19e-03	16 -- 55.2 -- low -- raw p=1.24e-04
35	ING1	208415_x_at	1.19e-03	60 -- 154.9 -- high -- raw p=1.33e-04
36	ERCC2	235399_at	1.55e-03	56 -- 41.3 -- high -- raw p=1.78e-04
37	CDK2AP1	201938_at	2.09e-03	78 -- 2456.8 -- high -- raw p=2.46e-04
38	BRPF1	204481_at	2.77e-03	49 -- 107.9 -- high -- raw p=3.34e-04
39	AXIN1	212849_at	3.34e-03	64 -- 56.7 -- high -- raw p=4.13e-04
40	BRCA1	204531_s_at	3.54e-03	73 -- 382.4 -- high -- raw p=4.49e-04
41	JUND	203752_s_at	3.79e-03	68 -- 1944.3 -- high -- raw p=4.93e-04
42	FES	205418_at	3.88e-03	73 -- 61.9 -- high -- raw p=5.17e-04
43	TFAP2B	214451_at	4.51e-03	16 -- 683.8 -- low -- raw p=6.16e-04
44	GIPC1	207525_s_at	9.63e-03	78 -- 121.3 -- high -- raw p=1.38e-03
45	LYN	210754_s_at	9.71e-03	62 -- 129.4 -- high -- raw p=1.36e-03
46	OX1	203570_at	0.010	65 -- 129.4 -- high -- raw p=1.56e-03



Add-on analyses on the list of genes

- Correlate the results with dataset
- use genes in k-means with dataset
- Save current selection as TXT file
- Gene set analysis
- Known interactions
- Store result as custom gene set
- Chromosome Map
- Gene Ontology Analysis
- DataAdder



GoPath	BP	#	p_value	Gold_Desc	GeneSymbols
5928	18	5	3.4e-42	1. DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator (7.6)	CHEK2, MUC1, BRCA1, BRCA2, TP53
42722	19	5	5.6e-40	1. DNA damage response, signal transduction resulting in transcription (6.8)	CHEK2, MUC1, BRCA1, BRCA2, TP53
50681	43	7	5.0e-36	2. androgen receptor binding (7.8)	DAXX, DDIX, FOXO1, SMARCA4, BRCA1, NCOA1, CCNE1
20241	83	8	2.9e-32	1. androgen receptor signaling pathway (6.10)	DAXX, DDIX, FOXO1, SMARCA4, BRCA1, NCOA1, CCNE1, MED12
212	24	5	1.3e-31	2. DNA secondary structure binding (6.6)	MSH6, MEN1, BLM, WRN, RECQL4
32392	82	9	2.0e-31	1. DNA geometric change (7.7)	DBP2, ERCC2, HMGAT1, HNRNP2B1, BLM, TP53, WRN, BRIP1, RECQL4
3114	396	20	1.4e-30	1. response to radiation (4.4)	CHEK2, CREB1, DDX1, DNMT3A, ERCC2, FANCD2, OGAQ, MSH6, KRAS, MEN1, MYC, NTRK1, PIK3R1, CND1, BLM, BRCA1, BRAF, BRCA2, TP53, WRN
726	25	5	3.7e-29	1. strand displacement (5.9)	BLM, BRCA1, BRCA2, WRN, BRIP1
13332	53	7	4.8e-29	1. response to gamma radiation (6.6)	CHEK2, FANCD2, MEN1, MYC, BRCA2, TP53, WRN
44402	784	27	4.7e-26	3. chromosome pair (4.9)	CDK4, CHEK2, CREB1, DAXX, DDIX, DNMT3A, MSH6, HMGAT1, HNRNP2B1, APC, MEN1, MUC1, MYC, MYCN, CCNE1, RARA, BLM, SMARCA4, BRCA1, BRCA2, TP53, BUB1B, TP53, TPR, WRN, NCOA1, RECQL4
6259	897	29	7.3e-26	1. DNA metabolic process (5.7)	CHEK2, DBP2, DNMT3A, ERCC2, FANCA, FANCD2, FANCF, MSH6, HMGAT1, HNRNP2B1, MEN1, MYC, NFIB, NONO, PDGFRA, CENPF, BLM, MAP2K4, SET, BRCA1, BRCA2, TCF3, TFR3, WHSC1, WRN, BRIP1, CCNE1, RECQL4
5584	904	29	1.3e-25	3. chromosome (5.6)	CDK4, CHEK2, CREB1, DAXX, DDIX, DNMT3A, FANCD2, MSH6, HMGAT1, HNRNP2B1, APC, MEN1, MUC1, MYC, MYCN, CCNE1, RARA, BLM, SMARCA4, BRCA1, BRCA2, TCF3, BUB1B, TP53, TPR, WHSC1, WRN, NCOA1, RECQL4
15212	148	11	1.4e-25	1. response to ionizing radiation (5.5)	CHEK2, DNMT3A, FANCD2, MEN1, MYC, CND1, BLM, BRCA1, BRCA2, TP53, WRN
30518	128	10	1.9e-24	1. intracellular steroid hormone receptor signaling pathway (5.9)	DAXX, DDIX, FOXO1, SMARCA4, BRCA1, RUNX1, NCOA1, CFBF, CCNE1, MED12
6111	130	10	4.9e-24	1. response to UV (6.6)	DBP2, ERCC2, MSH6, MEN1, MYC, PIK3R1, CND1, BRCA2, TP53, WRN
3884	85	7	1.7e-23	2. damaged DNA binding (6.6)	DBP2, MSH6, BLM, BRCA1, TP53, WRN, RECQL4
8133	261	14	9.3e-23	1. response to light stimulus (5.5)	CREB1, DBP2, ERCC2, OGAQ, MSH6, KRAS, MEN1, MYC, PIK3R1, CND1, BRAF, BRCA2, TP53, WRN
6503	34	5	3.1e-22	2. ATP-dependent DNA helicase activity (5.11)	ERCC2, BLM, WRN, BRIP1, RECQL4
35690	306	15	3.0e-22	1. cellular response to drug (5.5)	CDK4, CHEK2, DAXX, DNMT3A, OGAQ, MYB, MYC, NTRK1, PTEN, BLM, BRCA1, BRAF, TFR3, TP53, NCOA1
33233	619	22	5.6e-22	1. cellular response to hormone stimulus (5.6)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DDIX, FOXO1, OGAQ, APC, MEN1, MSN, PIK3R1, PTEN, RARA, SMARCA4, BRCA1, BRIP1, RUNX1, NCOA1, CFBF, CCNE1, MED12
72035	91	8	6.5e-22	2. purine NTP-dependent helicase activity (9.9)	DDIX, DDIX, DDIX, ERCC2, BLM, WRN, BRIP1, RECQL4
49835	1497	38	1.1e-21	1. positive regulation of nucleotide-containing compound metabolic process (5.7)	NCOA2, CHEK2, CREB1, DAXX, ERCC2, ETV4, CANT1, MSH6, HMGAT1, HNRNP2B1, LYL1, MEN1, MUC1, MYB, MYC, MYCN, NFIB, PAX5, PDGFRA, PIK3R1, RARA, BLM, MAP2K4, SMARCA4, BRCA1, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, RUNX1, NCOA1, CFBF, CCNE1, MED12
10504	2640	50	1.2e-21	1. positive regulation of macromolecule metabolic process (4.6)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DDIX, ERF15, ERCC2, ETV4, CANT1, MSH6, HMGAT1, HNRNP2B1, APC, B1E1, KRAS, LYL1, MEN1, MSN, MUC1, MYB, MYC, MYCN, NFIB, NTRK1, PAX5, PDGFRA, PIK3R1, FEV, PTEN, RARA, CND1, BLM, MAP2K4, SMARCA4, BRCA1, BRAF, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, ASPSCR1, RUNX1, NCOA1, CFBF, FUBP1, CCNE1, MED12
32527	144	10	1.7e-21	2. nuclear hormone receptor binding (5.6)	NCOA2, DAXX, DDIX, FOXO1, HMGAT1, SMARCA4, BRCA1, NCOA1, CCNE1, MED12
8726	857	26	2.9e-21	1. response to hormone (4.5)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DDIX, DNMT3A, FOXO1, OGAQ, APC, KRAS, MEN1, MSN, PIK3R1, PTEN, RARA, CND1, SMARCA4, BRCA1, BRAF, BRIP1, RUNX1, NCOA1, CFBF, CCNE1, MED12
42483	175	10	3.0e-21	1. steroid hormone mediated signaling pathway (5.8)	DAXX, DDIX, FOXO1, RARA, SMARCA4, BRCA1, RUNX1, NCOA1, CFBF, CCNE1, MED12
32508	72	7	4.0e-21	1. DNA duplex unwinding (6.8)	DBP2, ERCC2, HMGAT1, BLM, WRN, BRIP1, RECQL4
6874	754	24	7.3e-21	1. cellular response to DNA damage stimulus (5.5)	CHEK2, DBP2, DDIX, ERCC2, FANCA, FANCD2, FANCF, MSH6, HMGAT1, APC, MEN1, MUC1, MYC, NONO, PIK3R1, CND1, BLM, BRCA1, BRCA2, TP53, WHSC1, WRN, BRIP1, RECQL4
8993	2818	51	1.0e-20	1. positive regulation of metabolic process (3.5)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DDIX, ERF15, ERCC2, ETV4, CANT1, MSH6, HMGAT1, HNRNP2B1, APC, B1E1, KRAS, LYL1, MEN1, MSN, MUC1, MYB, MYC, MYCN, NFIB, NTRK1, PAX5, PDGFRA, PIK3R1, FEV, PTEN, RARA, CND1, BLM, MAP2K4, SMARCA4, BRCA1, BRAF, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, ASPSCR1, BLCRA3, RUNX1, NCOA1, CFBF, FUBP1, CCNE1, MED12
15658	875	26	1.1e-20	2. sequence-specific DNA binding (6.6)	NCOA2, CREB1, ETV4, CANT1, FOXO1, HMGAT1, HNRNP2B1, HODT1, LYL1, MUC1, MYB, MYC, MYCN, NFIB, NONO, PAX5, FEV, RARA, BLM, SMARCA4, TP53, TP53, WHSC1, WRN, RUNX1, MED12
51223	1077	29	2.9e-20	1. chromosome organization (5.5)	DAXX, DBP2, DNMT3A, ERCC2, FANCD2, MSH6, HMGAT1, HNRNP2B1, APC, MEN1, MUC1, MYC, PAX5, CCNE1, BLM, SET, SMARCA4, BRCA1, BRCA2, BUB1B, TP53, TPR, WHSC1, WRN, BRIP1, NCOA1, CCNE1, RECQL4

KaplanScanner Custom Data

R2: Kaplan-Meier

Kaplan-Meier analysis using a data set

Data set: ⓘ

Separate by: ▾

R2: KaplanScan on UserDefined Data

KaplanScan:

Paste Survival information `samplename; survtime(days); event(1/0/YES/NO); expression_value (tab or ; separated)`

#Copy your data below the #H: line.
 #H:samplename;survival_time;event;Gene_x

GSM1542334	7876	no	11.03011533
GSM1542335	4914	no	11.67083326
GSM1542336	7457	no	11.22562922
GSM1542337	6904	no	10.44429021
GSM1542338	7146	no	11.08308037
GSM1542339	7168	no	10.98299357
GSM1542340	488	yes	10.28262513
GSM1542341	1277	yes	10.30309576
GSM1542342	576	yes	10.03974158
GSM1542343	609	yes	11.35524096
GSM1542344	340	yes	10.27484403
GSM1542345	296	yes	9.412993173
GSM1542346	394	yes	8.68474862
GSM1542347	1408	yes	9.510170751
GSM1542348	196	yes	8.737416366
GSM1542349	2916	no	11.14140469
GSM1542350	108	no	11.44315076
GSM1542351	4013	no	12.34396294
GSM1542352	866	yes	10.85447883
GSM1542353	6872	no	10.8752886
GSM1542354	5458	no	11.21170582
GSM1542355	6013	no	11.59091447
GSM1542356	165	yes	9.62516088
GSM1542357	5759	no	11.81750335
GSM1542358	5118	no	11.43728393
GSM1542359	4693	no	11.54530237
GSM1542360	4152	no	10.97806689

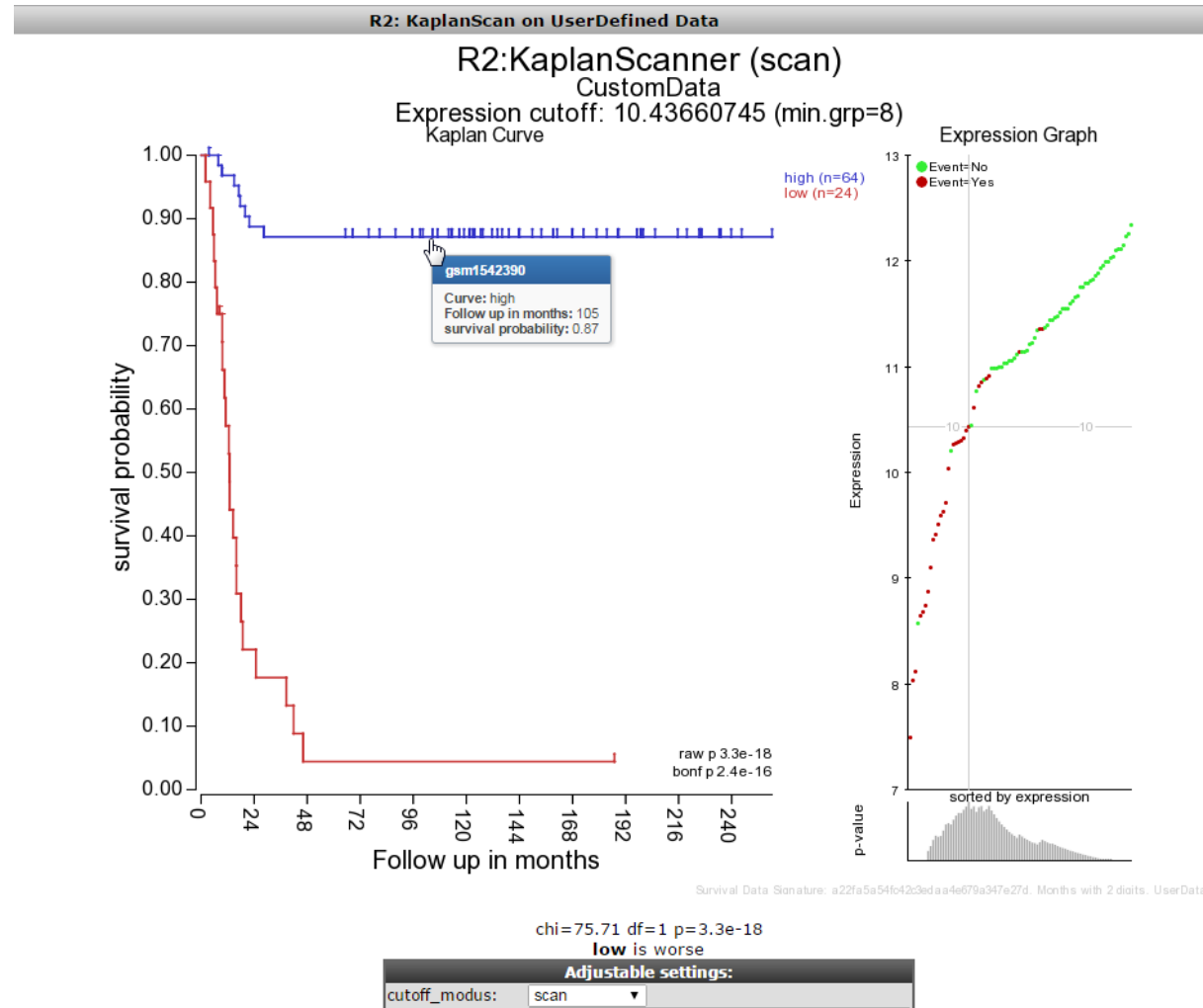
Cutoff mode: ▾

Survival time
In days

Event
yes/no/0/1

Numerical values
e.g. Expression Gene X

KaplanScanner Custom Data

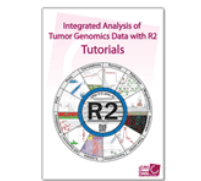


View a GeneSet (Heatmap)



View a GeneSet

- Go to: Main**
- Main
 - Time series
 - AmpliconView
 - Kaplan-Meier
 - Sample maps
 - Small Tools
 - DataGrabber
 - Genome Browser
 - ChIP data
 - TAR literature
 - Change Data Scope >
 - User Options >
 - Help >
 - Contact / About R2



Download the R2 Tutorials Book

R2: Genomics Analysis and Visualization Platform

1018043 (881501 unique) samples available

- 1** Choose single or multiple dataset analysis
Single Dataset
- 2** Select a dataset for analysis
Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2
- 3** Select type of analysis
View Geneset (Heatmap)
- 4** [Action button]

Online Tutorial

What is R2?
Welcome to R2; a biologist friendly web based genomics analysis and visualization application developed by Jan Koster at the department of Oncogenomics in the Academic Medical Center (AMC) Amsterdam, the Netherlands. You can start exploring the gene expression data by following the numbered options in the center.
For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (http://r2.amc.nl)'.

Financial Supporter of R2

[all news](#)



cluster

Search gene-set.

HALLMARK_MYC_TARGETS_V2 (58)

<input type="checkbox"/> HALLMARK_IL2_STAT5_SIGNALING	200
<input type="checkbox"/> HALLMARK_IL6_JAK_STAT3_SIGNALING	87
<input type="checkbox"/> HALLMARK_INFLAMMATORY_RESPONSE	200
<input type="checkbox"/> HALLMARK_INTERFERON_ALPHA_RESPONSE	97
<input type="checkbox"/> HALLMARK_INTERFERON_GAMMA_RESPONSE	200
<input type="checkbox"/> HALLMARK_KRAS_SIGNALING_DN	200
<input type="checkbox"/> HALLMARK_KRAS_SIGNALING_UP	200
<input type="checkbox"/> HALLMARK_MITOTIC_SPINDLE	199
<input type="checkbox"/> HALLMARK_MTORC1_SIGNALING	200
<input type="checkbox"/> HALLMARK_MYC_TARGETS_V1	200
<input checked="" type="checkbox"/> HALLMARK_MYC_TARGETS_V2	58
<input type="checkbox"/> HALLMARK_MYOGENESIS	200
<input type="checkbox"/> HALLMARK_NOTCH_SIGNALING	32
<input type="checkbox"/> HALLMARK_OXIDATIVE_PHOSPHORYLATION	200
<input type="checkbox"/> HALLMARK_P53_PATHWAY	200
<input type="checkbox"/> HALLMARK_PANCREAS_BETA_CELLS	40
<input type="checkbox"/> HALLMARK_PEROXISOME	104
<input type="checkbox"/> HALLMARK_PI3K_AKT_MTOR_SIGNALING	105
<input type="checkbox"/> HALLMARK_PROTEIN_SECRETION	96
<input type="checkbox"/> HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	49
<input type="checkbox"/> HALLMARK_SPERMATOGENESIS	135

Clear selection

Confirm selection

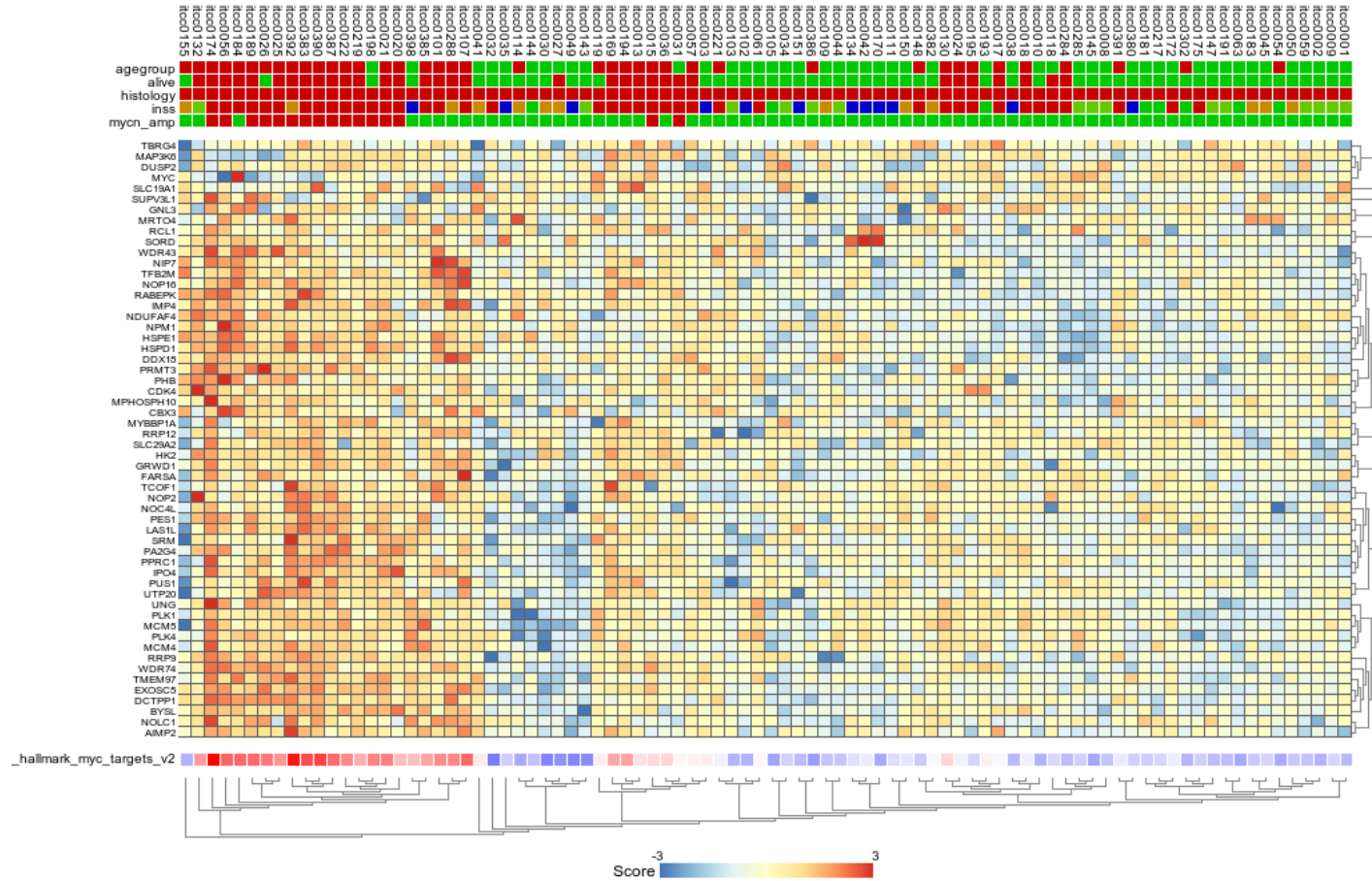
R2: GeneSet (Detail)

Tumor Neuroblastoma public

Versteeg - 88 - MAS5.0 - u133p2

db:geneset_broad_2019_h_hallmark

.HALLMARK_MYC_TARGETS_V2



distance:e; linkage:a;
Sort Order Listing
DetailView hyperlink settings
Transformation: ⓘ

Gene set values

Cluster multiple gene sets

Search gene-set.

HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY

HALLMARK_TGF_BETA_SIGNALING (54)

HALLMARK_WNT_BETA_CATENIN_SIGNALING (42)

HALLMARK_MYOGENESIS

HALLMARK_NOTCH_SIGNALING

HALLMARK_OXIDATIVE_PHOSPHORYLATION

HALLMARK_P53_PATHWAY

HALLMARK_PANCREAS_BETA_CELLS

HALLMARK_PEROXISOME

HALLMARK_PI3K_AKT_MTOR_SIGNALING

HALLMARK_PROTEIN_SECRETION

HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY

HALLMARK_SPERMATOGENESIS

HALLMARK_TGF_BETA_SIGNALING

HALLMARK_TNFA_SIGNALING_VIA_NFKB

HALLMARK_UNFOLDED_PROTEIN_RESPONSE

HALLMARK_UV_RESPONSE_DN

HALLMARK_UV_RESPONSE_UP

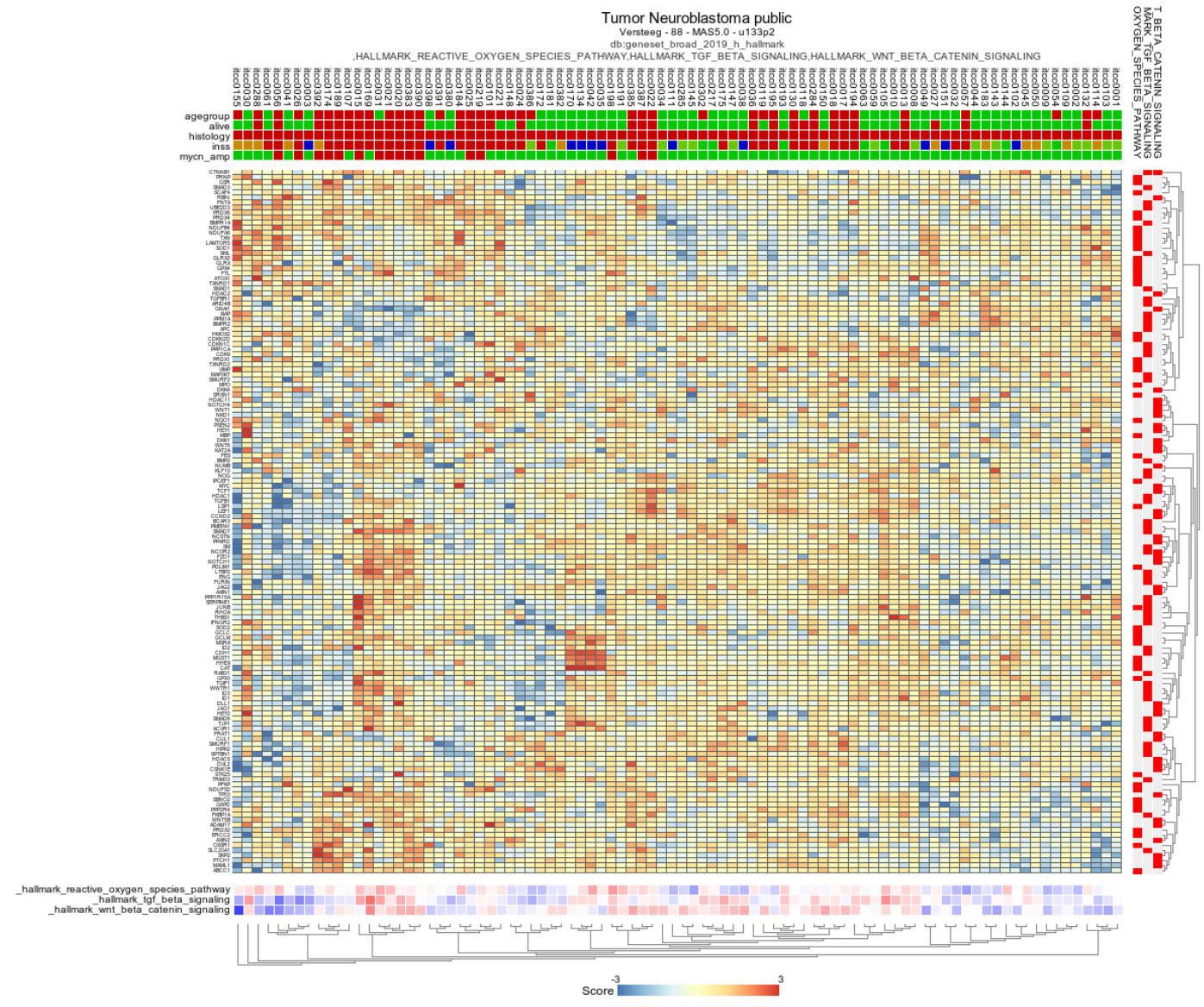
HALLMARK_WNT_BETA_CATENIN_SIGNALING

HALLMARK_XENOBIOTIC_METABOLISM

Broad 2020 09 archived

Clear selection

Confirm selection



Sub-cluster by track

Go to: [Main](#)

R2: Gene Set View

[Online Tutorial](#)

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public ⓘ

Adjustable settings

Gene selection
Gene set Collection:

Sample Filter
Subset track:
Selected sample subset: None

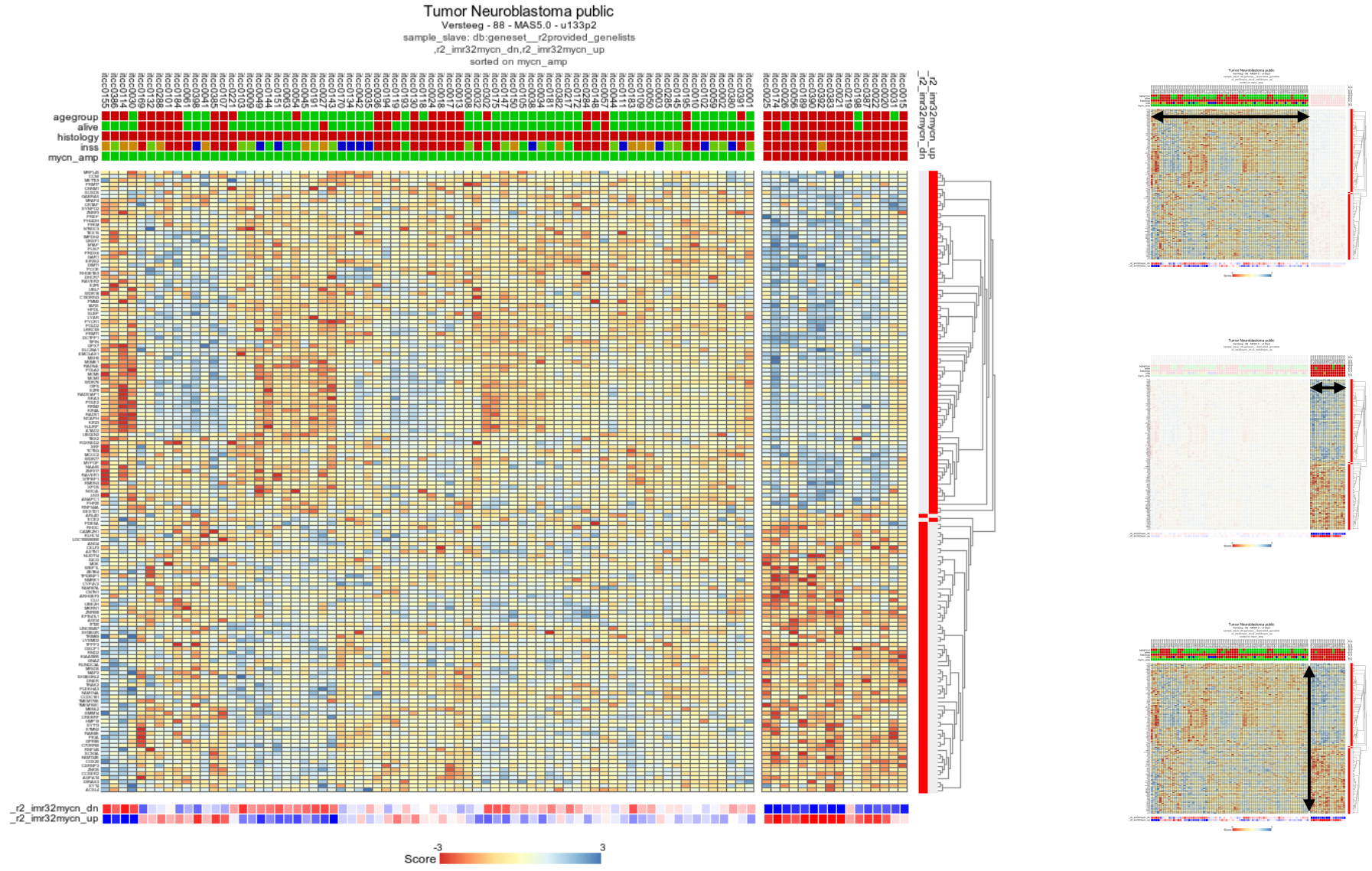
Sample ordering
Order samples by:
clustering
a track
expression of a gene
user defined order

Search for:

genesets containing a gene:
Search for:

Gene Set View
GeneSetView will generate a heatmap of a collection of genes represented within a gene set. Please use the dropdown menu to select a collection, or use the search boxes to find either a gene or geneset name.

Sub-cluster by track



Cohort subgroups



Exploratory dataset analyses

- Finding / visualizing subgroups within a dataset often performed on cohorts
- Different ways to do this in R2
 - Hierarchical clustering
 - K-means clustering
 - Principle component analysis
 - t-SNE/ UMAP maps

Toplister

- Go to: Main**
- Main
 - Time series
 - Survival (Kaplan-Meier/Cox)
 - Sample maps (UMAP/tSNE)
 - Small Tools
 - DataGrabber
 - Genome Browser
 - ChIP data
 - TAR literature
 - Change Data Scope ▶
 - User Options ▶
 - Help ▶
 - Contact / About R2



R2: Genomics Analysis and Visualization Platform

2,192,455 (2,030,514 unique) samples available

1 Choose single or multiple dataset analysis
Single Dataset

2 Select a dataset for analysis
Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2

3 Select type of analysis
View a Gene
meta analyses
Parametric analysis of geneset enrichment (PAGE)
Geneset maps (GSM)
K-means
Principle Component Analysis (PCA)
T-SNE
Sample Correlation Map (SCM)
View Geneset (Heatmap)
TopLister (Gene filter stdev)
Geneset vs Genesets Correlations
Track(#) vs Genesets Correlations
Venn Diagram of GeneCategories

4 Personalized Genomics
Static circos files (v3)
Somatic Mutations (v3)
Variants Overlap Counter
Pers. Med. OncoPrint (dynamic data)
Pers. Med. OncoPrint (fixed data)
CliniSnitch (Track vs som. mutation)
Find a Sample on omics criteria

Toplister

Go to: [Main](#) R2: TopLister [Online Tutorial](#)

Tumor Medulloblastoma PLoS One - Kool - 62 - MAS5.0 - u133p2 [public](#)
 Top 100 standard_deviation normal
 , transform_log2, present>=1

Adjustable settings

Which set: Standard Deviation (SD)

Modus: normal

How many genes: 100

Floor value: 0

Transformation: Log2

Sample Filter

Subset track:

Selected sample subset: None

Gene Filters

HugoOnce mode: yes

Min. # Present calls: 1

Minimal maximum value:

Minimal range size: 0

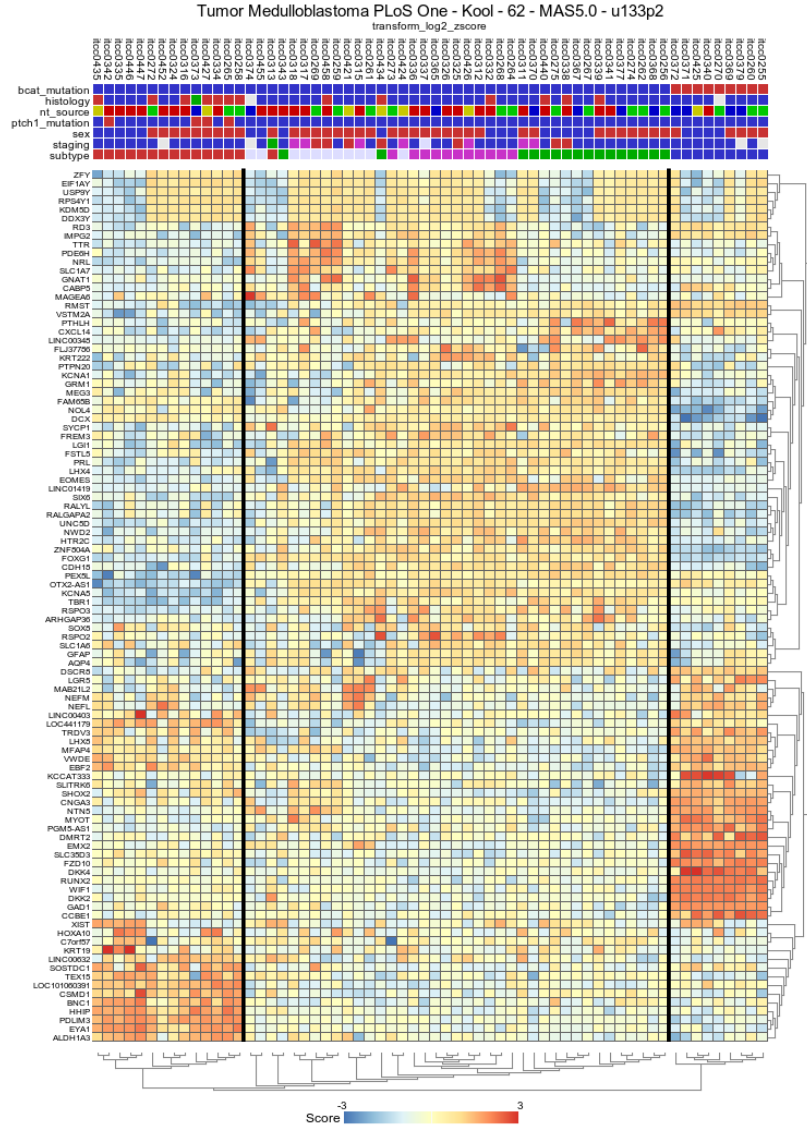
Chromosome: All

Gene ontology: All

Gene set:

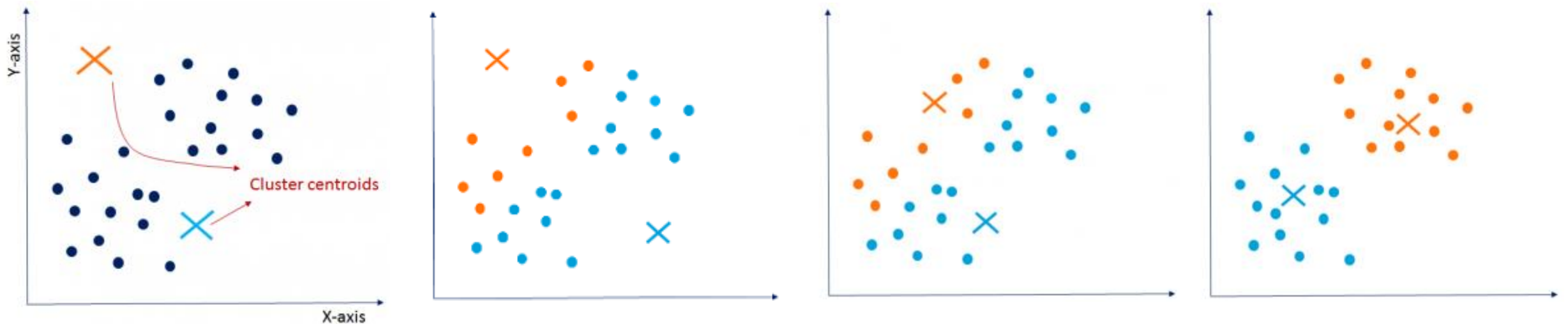
Manual list: none

View	Rank	Gene	Reporter	Value
<input type="button" value="i"/>	1	LINC01419	1559213_at	5,2946...
<input type="button" value="i"/>	2	XIST	224588_at	4,3756...
<input type="button" value="i"/>	3	FOXP1	206018_at	4,3274...
<input type="button" value="i"/>	4	RPS4Y1	201909_at	4,1058...
<input type="button" value="i"/>	5	RALGAP2	234314_at	4,0906...
<input type="button" value="i"/>	6	RALYL	213967_at	3,9871...
<input type="button" value="i"/>	7	SHOX2	210135_s_at	3,8976...
<input type="button" value="i"/>	8	LHX8	1569469_a_at	3,8847...
<input type="button" value="i"/>	9	GAD1	205278_at	3,7782...
<input type="button" value="i"/>	10	DDX3Y	205000_at	3,7024...
<input type="button" value="i"/>	11	WIF1	204712_at	3,6922...
<input type="button" value="i"/>	12	HTR2C	207307_at	3,6730...
<input type="button" value="i"/>	13	EMX2	221950_at	3,6010...
<input type="button" value="i"/>	14	EOMES	231776_at	3,5940...
<input type="button" value="i"/>	15	DKK2	219908_at	3,5496...
<input type="button" value="i"/>	16	RMST	229782_at	3,5128...
<input type="button" value="i"/>	17	MFAP4	212713_at	3,4545...
<input type="button" value="i"/>	18	EIF1A1	204409_s_at	3,4509...
<input type="button" value="i"/>	19	PTPN20	215172_at	3,4277...
<input type="button" value="i"/>	20	USP9Y	228492_at	3,4212...
<input type="button" value="i"/>	21	FSTL5	232010_at	3,4148...
<input type="button" value="i"/>	22	CNGA3	207261_at	3,4119...
<input type="button" value="i"/>	23	IMPG2	241856_at	3,3991...
<input type="button" value="i"/>	24	TRDV3	216191_s_at	3,3744...
<input type="button" value="i"/>	25	KCNA5	206762_at	3,3582...
<input type="button" value="i"/>	26	PDE6H	206841_at	3,3328...
<input type="button" value="i"/>	27	SLC1A6	1554593_s_at	3,3287...
<input type="button" value="i"/>	28	NEFM	205113_at	3,3048...
<input type="button" value="i"/>	29	LINC00348	233170_at	3,2960...
<input type="button" value="i"/>	30	LGR5	213880_at	3,2935...
<input type="button" value="i"/>	31	C7ORF57	1557636_a_at	3,2496...



K-means clustering

- You tell the algorithm to subdivide a dataset in a predefined number of groups
- Algorithm has a random start, which may impact the results
 - Keep best solution out of 10 draws
 - Repeat the procedure to assess stability (10X10)



K-means

- Go to: **Main**
- Main
 - Time series
 - AmpliconView
 - Kaplan-Meier
 - Sample maps
 - Small Tools
 - DataGrabber
 - Genome Browser
 - ChIP data
 - TAR literature
 - Change Data Scope ▶
 - User Options ▶
 - Help ▶
 - Contact / About R2






R2: Genomics Analysis and Visualization Platform

1018043 (881501 unique) samples available

- 1** Choose single or multiple dataset analysis
Single Dataset
- 2** Select a dataset for analysis
Tumor Medulloblastoma PLoS One - Kool - 62 - MAS5.0 - u133p2
- 3** Select type of analysis
K-means
- 4** [Dropdown menu open]

- 2 Groups Plotter
- Fold over Fold Plotter
- PathwayFinder
 - KEGG PathwayFinder by Groups
 - KEGG PathwayFinder by Gene correlation
- Meta analyses
 - Parametric analysis of geneset enrichment (PAGE)
 - Geneset maps (GSM)
 - K-means
 - Principle Component Analysis (PCA)
 - T-SNE
 - Sample Correlation Map (SCM)
 - View Geneset (Heatmap)
 - TopLister (Gene filter stdev)
 - Geneset vs Genesets Correlations
 - Track(#) vs Genesets Correlations
 - Venn Diagram of GeneCategories
- Personalized Genomics
 - Static circo files (v3)
 - Somatic Mutations (v3)

Online Tutorial

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Financial Supporter of R2



Amsterdam UMC

[all news](#)




Using HGserver1(7)

K-means

R2: K-means

Tumor Medulloblastoma PLoS One - Kool - 62 - MAS5.0 - u133p2 public

Adjustable settings

Floor value: ⓘ

Transformation: ⓘ

Sample Filter

Subset track: ⓘ

Selected sample subset: None

Gene Filters

Min. # Present calls: ⓘ

Minimal maximum value: ⓘ

Minimal range size: ⓘ

highest SD genes: ⓘ

Chromosome: ⓘ

Gene ontology:

Gene set:

Manual list: ⓘ

Clustering

Number of groups: ⓘ

Number of passes: ⓘ

Number of rounds: ⓘ

Graphics

Draw heatmap: ⓘ

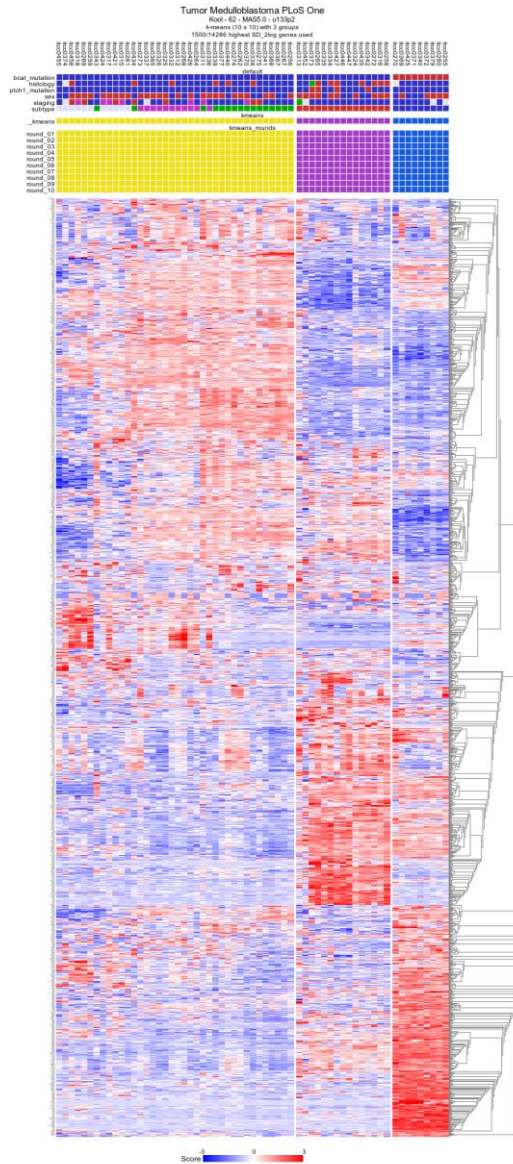
Color scheme: ⓘ

Label track: ⓘ

Heatmap Options

Cell width: ⓘ

Cell height: ⓘ



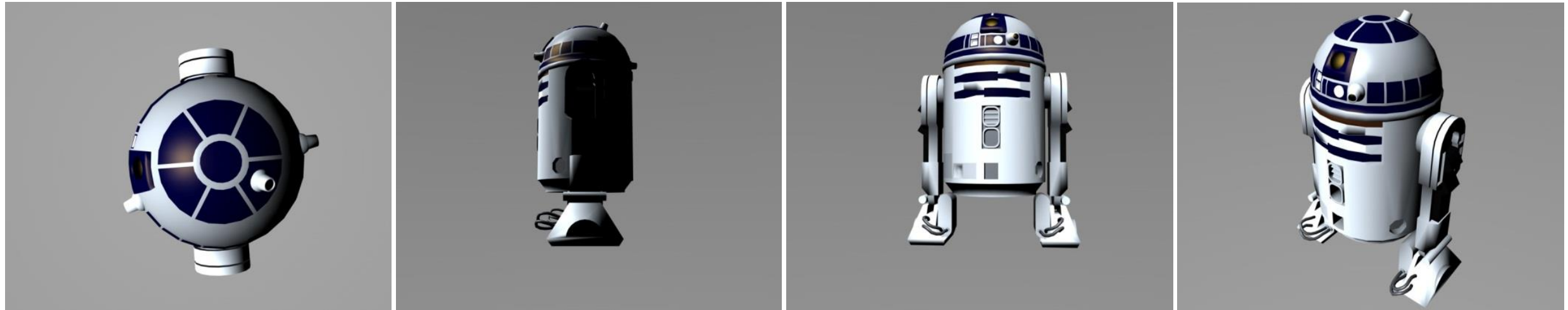
kmeans group vs annotation tracks
Chi-square tests with Yates correction (if 2x2) and Fisher's Exact tests (#groups<30)
NA or ND values are skipped and test is only performed on 'cat' variables

Source track: _kmeans

track	chi_pvalue	chisquare	df	fisher's exact
round_01	7.47e-26	124.000	4	7.89e-24
round_03	7.47e-26	124.000	4	7.89e-24
round_04	7.47e-26	124.000	4	7.89e-24
round_05	7.47e-26	124.000	4	7.89e-24
round_07	7.47e-26	124.000	4	7.89e-24
round_08	7.47e-26	124.000	4	7.89e-24
round_09	7.47e-26	124.000	4	7.89e-24
round_10	7.47e-26	124.000	4	7.89e-24
round_02	7.47e-26	124.000	4	7.89e-24
round_06	7.47e-26	124.000	4	7.89e-24
subtype	4.94e-23	124.000	8	7.89e-24
bcat_mutation	3.44e-14	62.000	2	4.93e-11
ptch1_mutation	1.23e-03	13.398	2	4.93e-03
histology	0.016	12.141	4	8.92e-03
staging	0.080	14.057	8	0.063
nt_source	0.212	8.378	6	0.195
samplenames	0.433	124.000	122	too many groups(186)
sex	0.763	0.540	2	0.747

Principal Components Analysis (PCA)

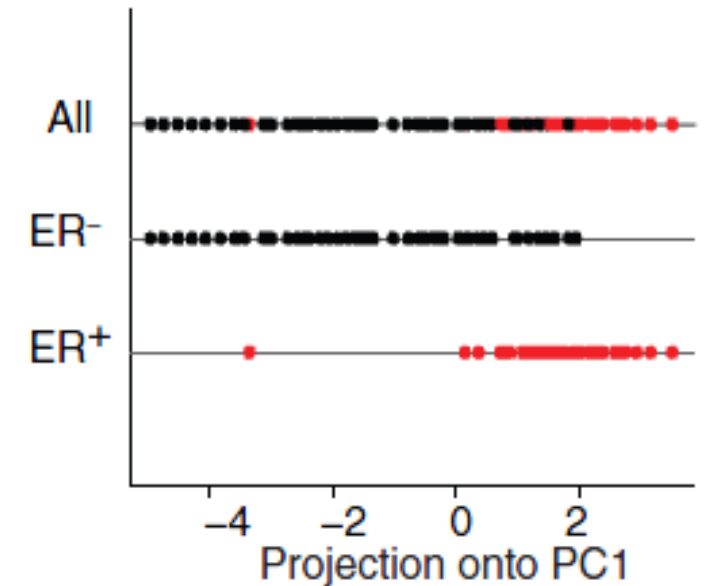
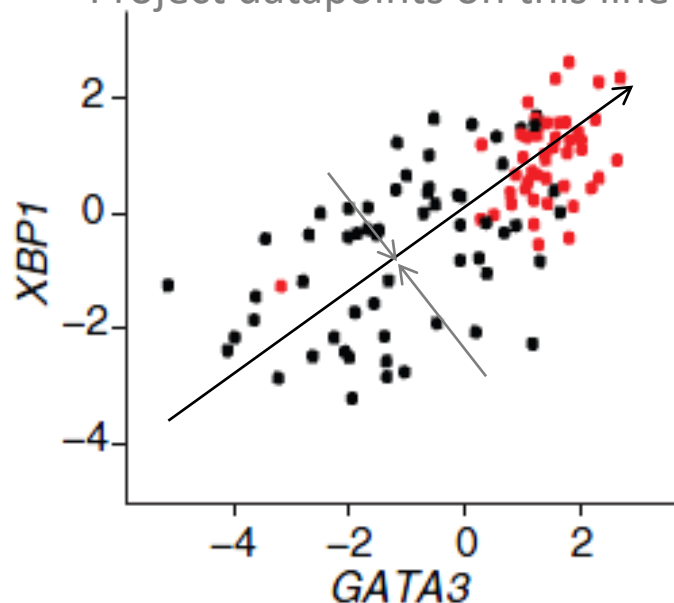
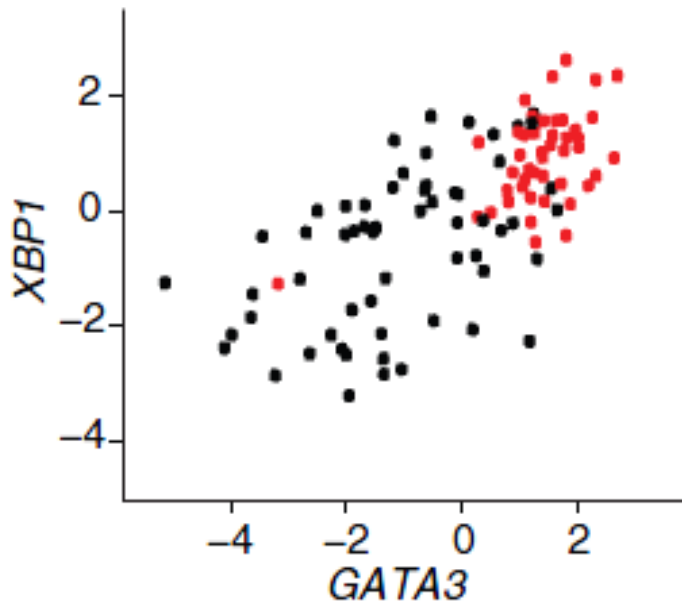
- Describe samples by a very limited number of variables
- Samples that are similar 'cluster' closer together
- Mathematical procedure orthogonal projection (Mathematical procedure) for data reduction
- Nice way of visualizing subgroups



Principal Components Analysis (PCA)

- Describe samples by a very limited number of variables
- Samples that are similar 'cluster' closer together
- Mathematical procedure orthogonal projection (Mathematical procedure) for data reduction
- Nice way of visualizing subgroups



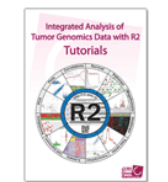

Draw the longest possible line
Through the data = max. variance
Project datapoints on this line



Principal Components Analysis (PCA)

Go to: [Main](#)

- Main
- Time series
- AmpliconView
- Kaplan-Meier
- Sample maps
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

R2: Genomics Analysis and Visualization Platform

1018043 (881501 unique) samples available

1 Choose single or multiple dataset analysis

Single Dataset ⓘ

2 Select a dataset for analysis

Tumor Medulloblastoma PLoS One - Kool - 62 - MAS5.0 - u133p2 ⓘ

3 Select type of analysis

Principle Component Analysis (PCA) ⓘ

- Annotation**
- Annotation_plotter
- Cohort SunBurst plotter
- Sample overview
- Cohort Overview
- Relate 2 tracks
- Differential Expression**
- Differential expression between two groups
- Differential expression between multiple groups
- 2 Groups Plotter
- Fold over Fold Plotter
- PathwayFinder**
- KEGG PathwayFinder by Groups
- KEGG PathwayFinder by Gene correlation
- Meta analyses**
- Parametric analysis of geneset enrichment (PAGE)
- Geneset maps (GSM)
- K-means
- Principle Component Analysis (PCA)**
- T-SNE

4 [Empty field]


Online Tutorial

What is R2?



Welcome to R2; a biologist friendly web based genomics analysis and visualization application developed by Jan Koster at the department of Oncogenomics in the Academic Medical Center (AMC) Amsterdam, the Netherlands. You can start exploring the gene expression data by following the numbered options in the center.

For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (<http://r2.amc.nl>)'.

Financial Supporter of R2



[all news](#)

Using:HGserver1(7)

Principal Components Analysis (PCA)

Go to: [Main](#)

R2: Principle Component Analysis (PCA)

[Online Tutorial](#)

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

Adjustable settings

Transformation: ⓘ

Use Scaling within PCA: ⓘ

Gene Filter

Min. # Present calls: ⓘ

Chromosome: ⓘ

Gene ontology:

Gene set:

Manual list: ⓘ

Sample Filter

Subset track: ⓘ

Selected sample subset: None

Graphics

Sample Paths: , separated

Dot size: ⓘ

Vector (SVG) output: ⓘ

Color mode:

Principal Components Analysis (PCA)

Go to: **Main**

R2: Principle Component Analysis (PCA)

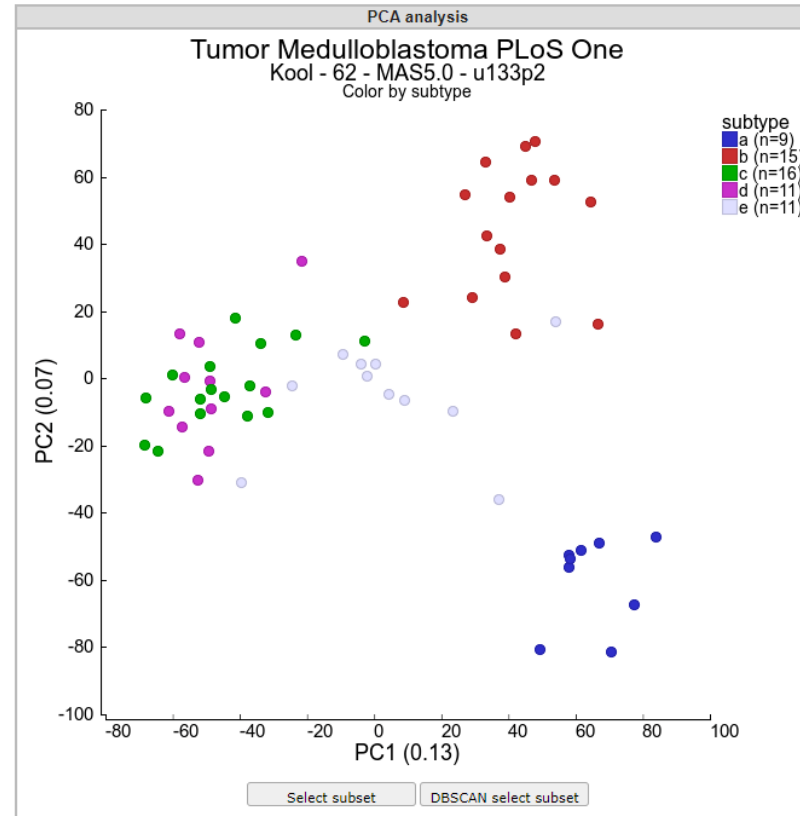
Online Tutorial

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- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope >
- User Options >
- Help >
- Contact / About R2

Projection

PCA Projection: PC1:PC2

Next



Adjustable settings

Transformation: Log2 z-score

Gene Filter

Min. # Present calls: 1

Chromosome: All

Gene ontology: All

Gene set:

Search GO

Search GS



Principal Components Analysis (PCA)

Go to: [Main](#)

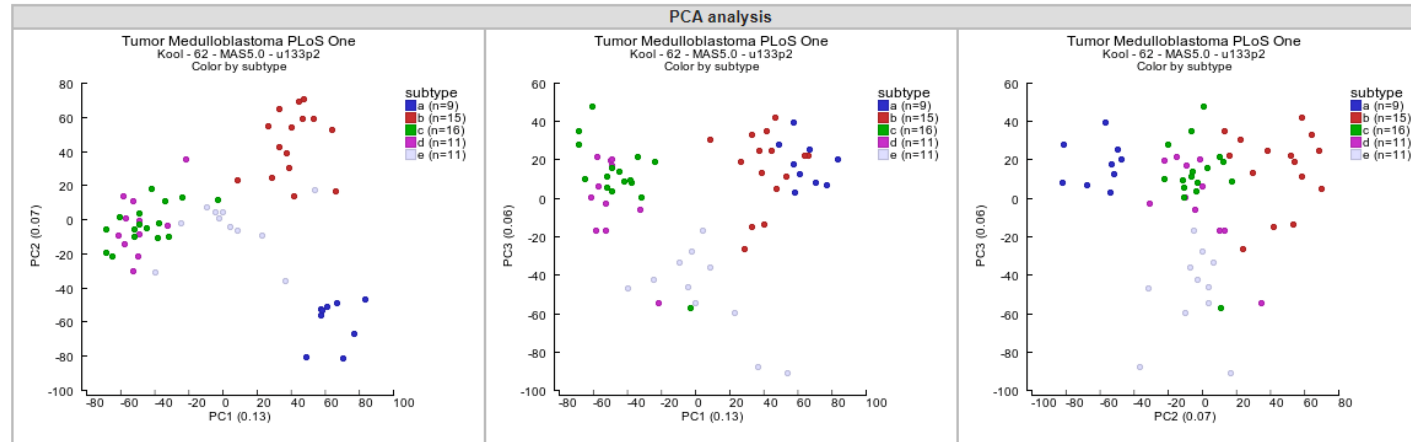
R2: Principle Component Analysis (PCA)

[Online Tutorial](#)

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- Genome Browser
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- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

Projection

PCA Projection:



Adjustable settings

Transformation: ⓘ

Gene Filter

Min. # Present calls: ⓘ

Chromosome: ⓘ

Gene ontology:

Gene set:

Manual list: ⓘ

Sample Filter

Subset track: ⓘ

Selected sample subset: None

Graphics

Sample Paths: , separated

Dot size: ⓘ

Vector (SVG) output: ⓘ

Color mode:

Color track: ⓘ

Principal Components Analysis (PCA)

Go to: **Main**
R2: Principle Component Analysis (PCA)
Online Tutorial

Go to: **Main**

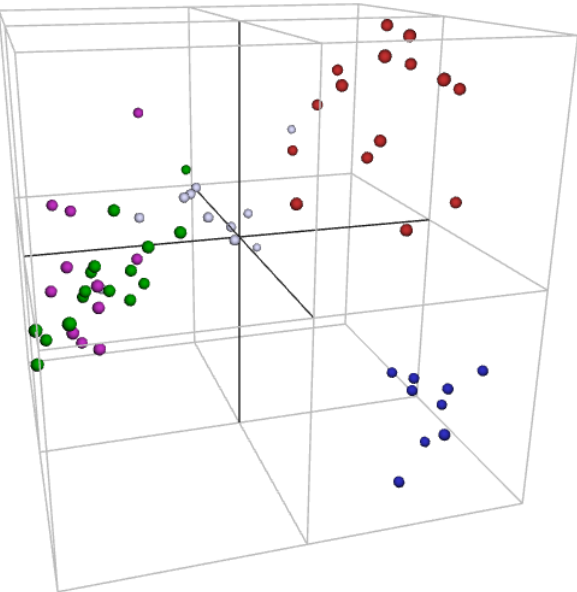
- Main
- Time series
- AmpliconView
- Kaplan-Meier
- Sample maps
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope >
- User Options >
- Help >
- Contact / About R2

Projection

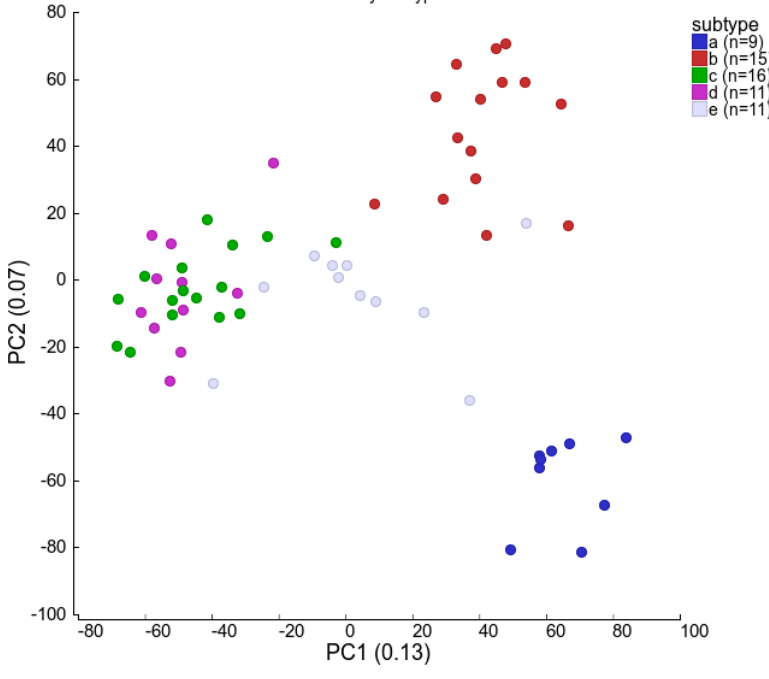
PCA Projection: PC1.PC2.PC3-3D

Next

PCA analysis



Tumor Medulloblastoma PLoS One
Kool - 62 - MAS5.0 - u133p2
Color by subtype



subtype
■ a (n=9)
■ b (n=15)
■ c (n=16)
■ d (n=11)
■ e (n=11)

Adjustable settings

Transformation: Log2 z-score ⓘ

Gene Filter

Min. # Present calls: 1 ⓘ

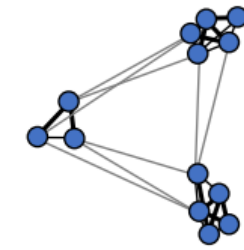
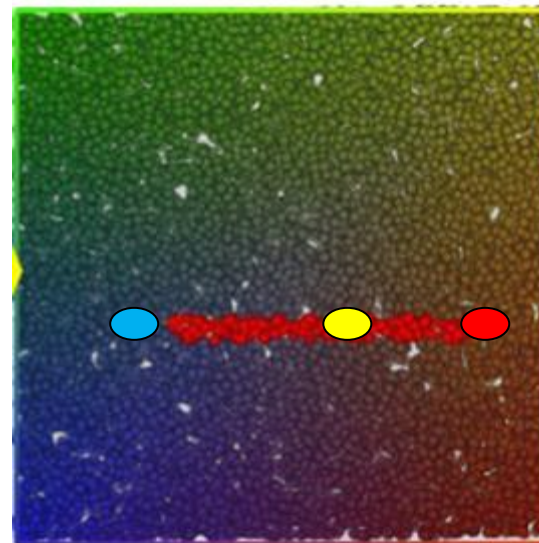
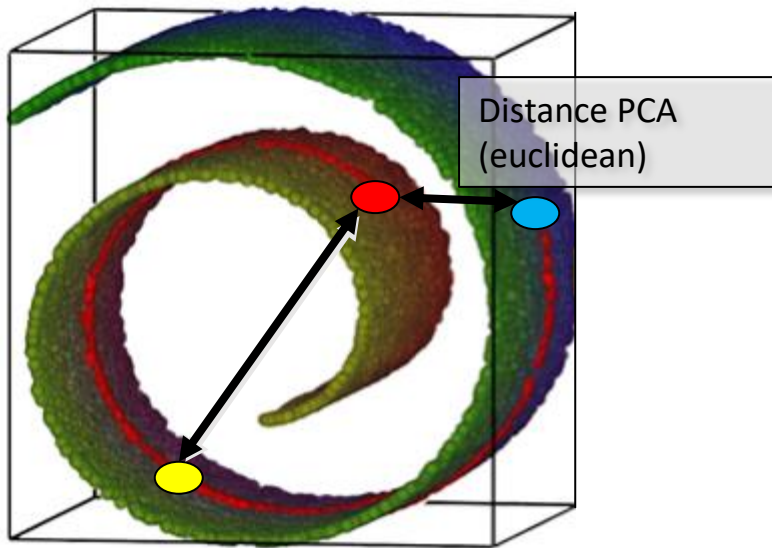
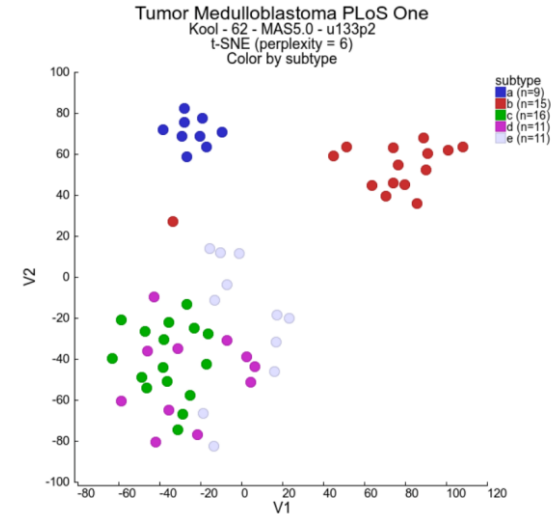
Chromosome: All ⓘ

Gene ontology: All

Gene set:

tSNE/UMAP Analysis

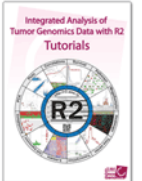
- t-Distributed Stochastic Neighbor Embedding (t-SNE)
 - a technique for dimensionality reduction that is particularly well suited for the visualization of high-dimensional datasets.
 - Has an almost magical ability to create 2-dimensional ‘maps’ of data with thousands of dimensions
 - Non-linear
- Graph based dimensionality reduction: connected points in graph
- UMAP



tSNE/UMAP Analysis

- Go to: Main
- Main
 - Time series
 - Survival (Kaplan-Meier/Cox)
 - Sample maps (UMAP/tSNE)
 - Small Tools
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All access levels
pre-generated **fast**



Download the R2 Tutorial Book

R2: Genomics Analysis and Visualization Platform
2,192,455 (2,030,514 unique) samples available

1 Choose single or multiple dataset analysis
Single Dataset

2 Select a dataset for analysis
Tumor Medulloblastoma PLoS One - Kool - 62 - MASS.0 - u133p2

3 Select type of analysis
T-SNE

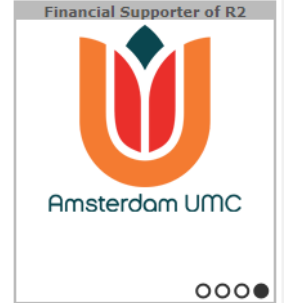
4

- Sample overview
- Cohort Overview
- Relate 2 tracks
- Differential Expression
 - Differential expression between two groups
 - Differential expression between multiple groups
 - 2 Groups Plotter
 - Fold over Fold Plotter
- PathwayFinder
 - KEGG PathwayFinder by Groups
 - KEGG PathwayFinder by Gene correlation
- Meta analyses
 - Parametric analysis of geneset enrichment (PAGE)
 - Geneset maps (GSM)
 - K-means
 - Principle Component Analysis (PCA)
 - T-SNE
 - Sample Correlation Map (SCM)
 - View Geneset (Heatmap)
 - Tool lister (Gene filter, stdev)

Collaborator or higher
Generate new maps **slow**

Online Tutorial

What is R2?
Welcome to R2; a biologist friendly web based genomics analysis and visualization application developed by Jan Koster at the department of Oncogenomics in the Academic Medical Center (AMC) Amsterdam, the Netherlands. You can start exploring the gene expression data by following the numbered options in the center.
For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (<http://r2.amc.nl>)'.



News
We are organising another **R2 Introduction Workshop**
Basics Part 1 and Basics Part 2
Thursday 22 & 29 June 2023.
For more info and registration, click [here](#)



News
Check out the new iTHER pediatric cancer precision medicine datascope. Now publicly available in R2 via the 'datascope' menu item.

[all news](#)



tSNE/UMAP Analysis: select pregenerated sample maps

Go to: **Main**

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)**
- Small tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

R2: t-SNE / UMAP Generated Map Collection

Select	Info	Dataset Class	Dataset Author	Dataset Samples	Dataset Norm.	Dataset Platform	Map Type	Created	Favourit
<input type="checkbox"/>	<input type="checkbox"/>	ccl			Select Filter ▼	Select Filter ▼	Select Filter ▼	<input type="checkbox"/>	<input type="checkbox"/>
Select	i	Cell line CCLE Cancer Cell Line Encyclopedia 21q4	Broad	1389	tpm	gencode19a		2022-02-19	<input type="checkbox"/>
Select	i	Cell line CCLE Cancer Cell Line Encyclopedia	Broad	917	MASS.0	u133p2	t-SNE	2020-11-24	<input type="checkbox"/>
Select	i	Cell line CCLE Cancer Cell Line Encyclopedia	Broad	917	MASS.0	u133p2	UMAP	2021-01-08	<input type="checkbox"/>
Select	i	Cell line CCLE Cancer Cell Line Encyclopedia	Broad	917	MASS.0	u133p2	t-SNE	2017-03-28	<input type="checkbox"/>
Select	i	Cell line CCLE Cancer Cell Line Encyclopedia	Broad	917	MASS.0	u133p2		2021-02-11	<input type="checkbox"/>
Select	i	Cell line CCLE gene effects	Broad	1086	custom	depmapgid		2022-09-22	<input type="checkbox"/>
Select	i	Cell line Colon cancer CCLE (CRC)	Broad	69	tpm	gencode19a		2022-02-26	<input type="checkbox"/>
Select	i	Cell line CCLE Cancer Cell Line Encyclopedia 21q4	Broad	1389	tpm	gencode19a	UMAP	2021-12-16	<input type="checkbox"/>

Go to page: Show rows: 1-8 of 8

Online Tutorial

Info

Welcome to the t-Distributed Stochastic Neighbor Embedding (T-SNE) module of R2. T-SNE models each high-dimensional object by a two-dimensional point in such a way that similar objects are modeled by nearby points and dissimilar objects are modeled by distant points.

An important parameter in T_SNE is the 'perplexity', a value which kind of reflect the number of close neighbours. R2 will scan a whole range of these and allow you to 'browse' through them. Because of this, a T-SNE run can take a long time to finish (up to an hour for ~500 samples). Within R2, a fixed seed (fixed random number) is used to generate reproducible results.

T-SNE plots often look pretty, however be sure to understand some of the basic properties before you interpret the result. We can warmly recommend the following blog post on T-SNE behaviour [here](#)

In this section, only datasets for which a complete analysis has been executed are listed for visualization and inspection. Depending on your access rights, t-SNE can also be executed from box3.

Cell line CCLE Cancer Cell Line Encyclopedia 21q4 - Broad - 1389 - tpm - gencode19a

Title:

Sample Map info: Data set: Cell line CCLE Cancer Cell Line Encyclopedia 21q4 - Broad - 1389 - tpm - gencode19a Filters: best reporter per gene; present in at least 1 sample(s) Transformations: log2_zscore

Summary:

Design: RNAseq TPM gene expression data for all genes using RSEM. Log2 transformed, using a pseudo-count of 1

Available tracks in R2:

- age: (#) 0 - 92
- cas9_activity: (#) 23 - 99.6
- ccl_name: 1389 entities
- cell_line_name: 1342 entities
- cell_line_nnmd: (#) -6.562238824 - 0.005954845
- culture_type: 11 entities

Adjustments: expression_full set ids converted to gencode19a

Available on R2 since: 2021-12-16

Platform: gencode19a

Species: hs

Number of samples: 1389

Source: website ID: Date: 2021-12-16

Pubmed link:

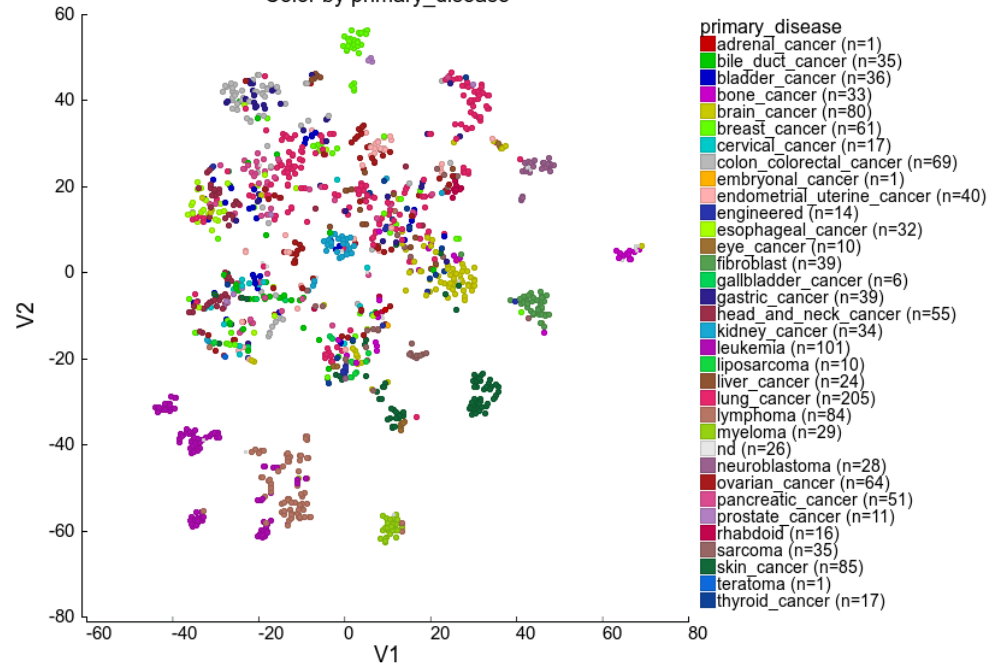
R2 internal identifier: ps_avgpres_ccl21q4a1389_gencode19a

tSNE Analysis result

R2: Sample map Viewer

Cell line CCLE Cancer Cell Line Encyclopedia 21q4 - Broad - 1389 - tpm - gencode19a public

Cell line CCLE Cancer Cell Line Encyclopedia 21q4
Broad - 1389 - tpm - gencode19a
t-SNE (perplexity = 15)
Color by primary_disease



Select subset DBSCAN select subset

View interactive plot

Perplexity (~# neighbours)
A variable that can be varied
Select 'All' to assess stability and/or
optimal representation

Adjustable settings

Perplexity: 15

Image size: 500

Dot size: 2

Samples to mark: comma separated sample names

Mark method: dot

Samples paths: comma separated sample names

Vector (SVG) output: false

tSNE Analysis: perplexity all

Go to: [Main](#) R2: Sample map Viewer [Online Tutorial](#)

Cell line CCL6 Cancer Cell Line Encyclopedia 21q4 - Broad - 1389 - tpm - gencode19a [public](#)

- Main
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- User Options
- Help
- Contact / About R2

[View interactive plot](#)

Adjustable settings

Perplexity:

Image size:

Dot size:

Samples to mark:

Mark method:

Samples paths:

Vector (SVG) output:

Enable hovering:

x: min: max:

y: min: max:

Color mode:

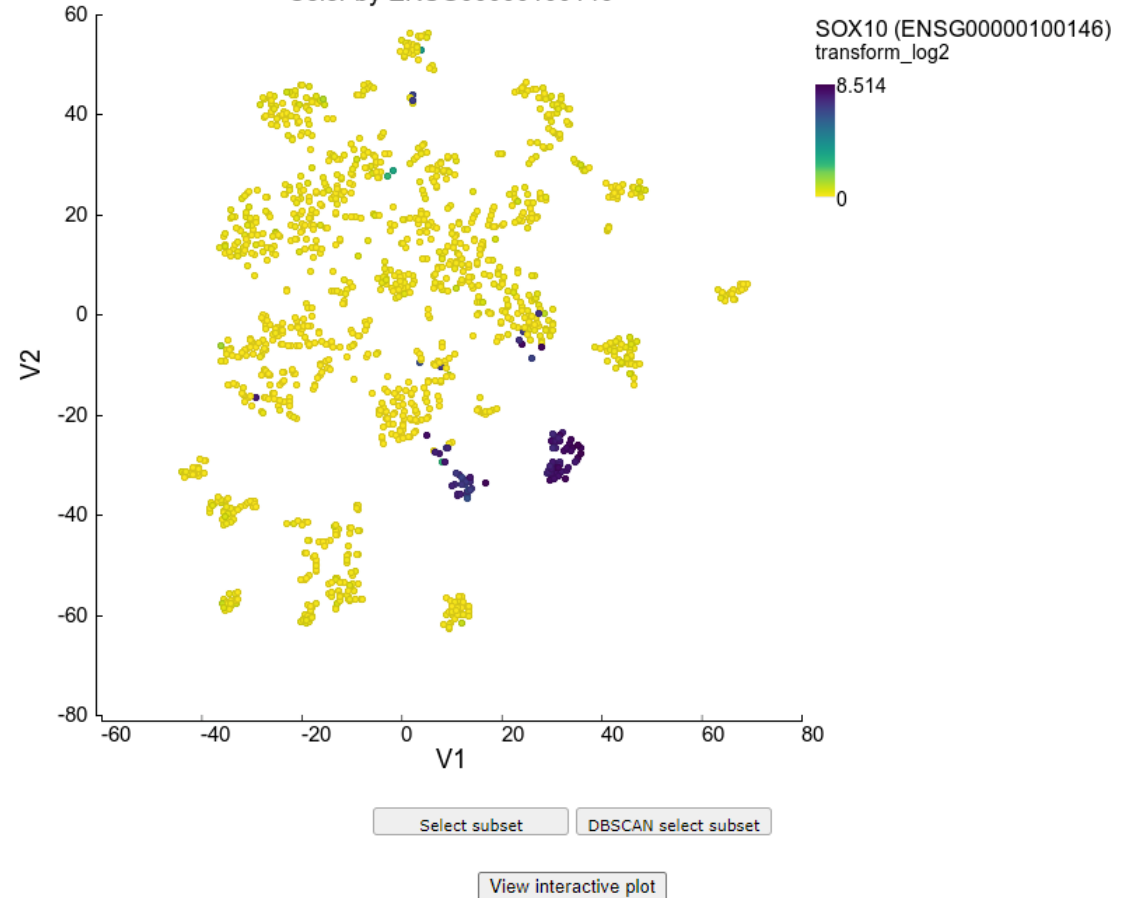
Color track:

tSNE Analysis: color by gene expression

R2: Sample map Viewer

Cell line CCLE Cancer Cell Line Encyclopedia 21q4 - Broad - 1389 - tpm - gencode19a public

Cell line CCLE Cancer Cell Line Encyclopedia 21q4
Broad - 1389 - tpm - gencode19a
t-SNE (perplexity = 15)
Color by ENSG00000100146



Adjustable settings

Perplexity: 15

Image size: 500

Dot size: 2

Samples to mark: comma separated sample names

Mark method: dot

Samples paths: comma separated sample names

Vector (SVG) output: false

Enable hovering: yes

x: min: max:

y: min: max:

Color mode: Color by Gene

Color source: Cell line CCLE Cancer Cell Line Encyclopedia 21q4 - Broad - 1389 - tpm - gencode19a

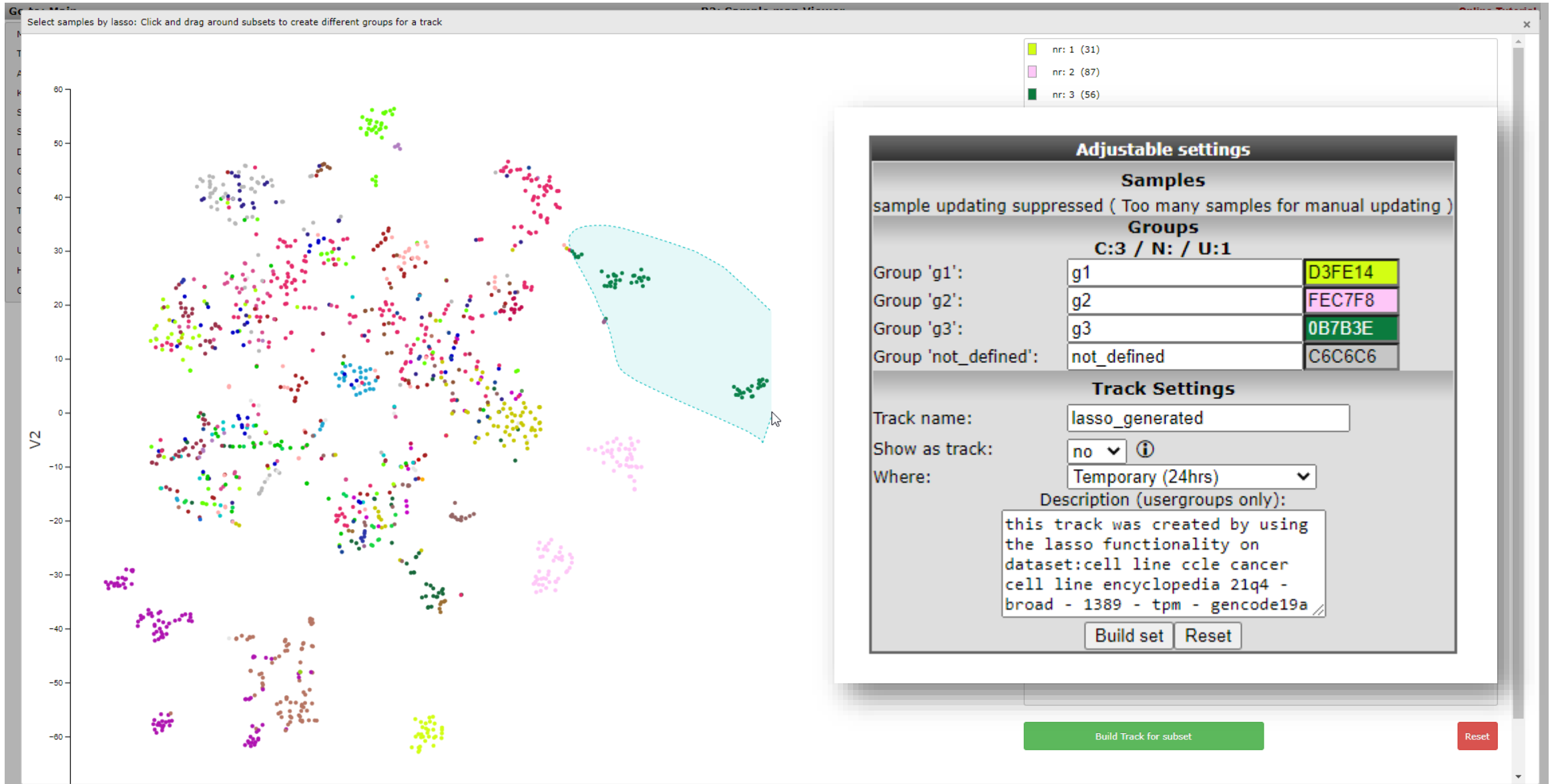
Gene / Reporter: SOX10 ENSG00000100146 advanced

Transformation: Log2

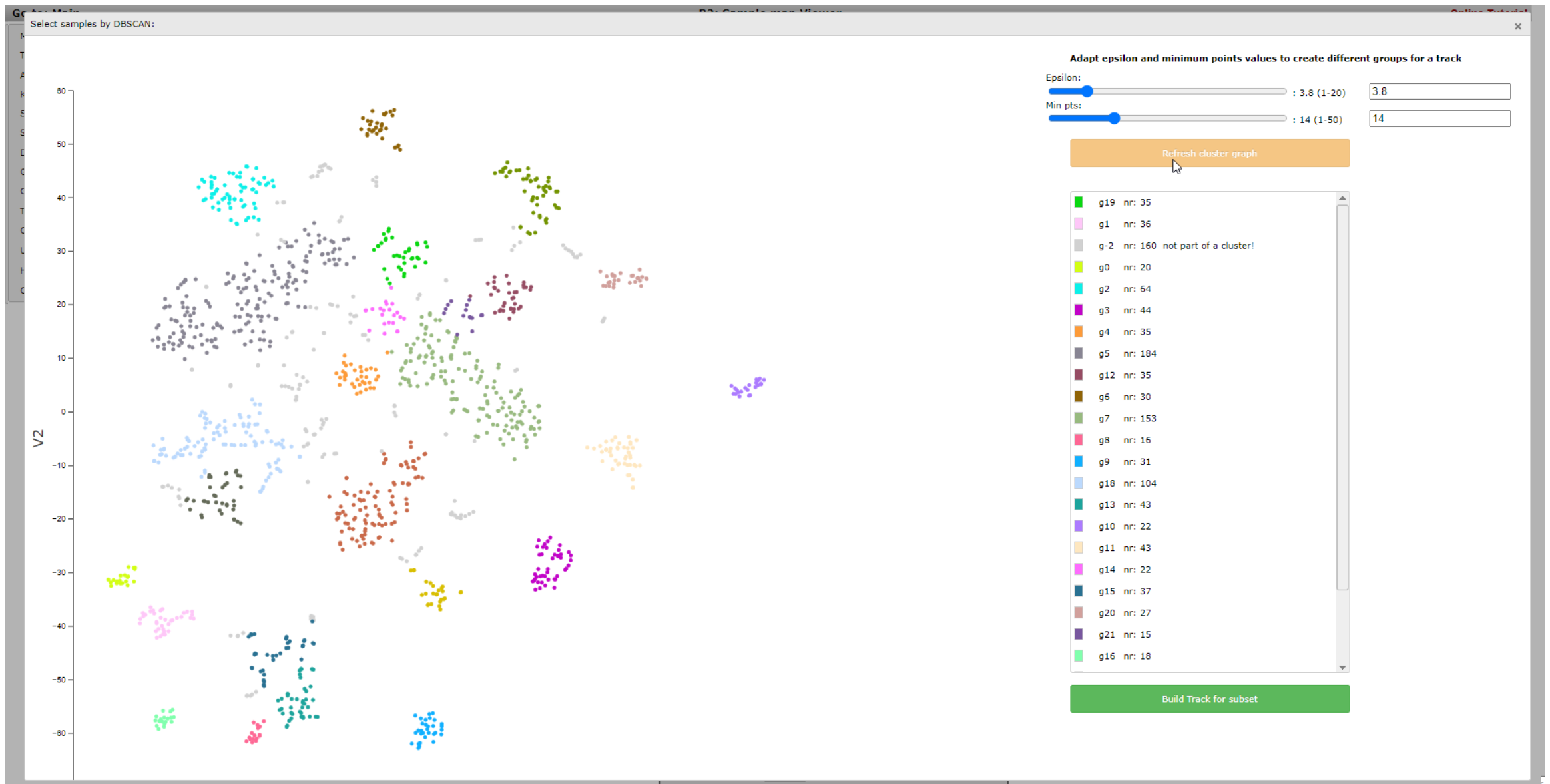
Color scheme: viridis

Submit

tSNE Analysis: lasso



tSNE Analysis



In multi omics sets 'color by gene'

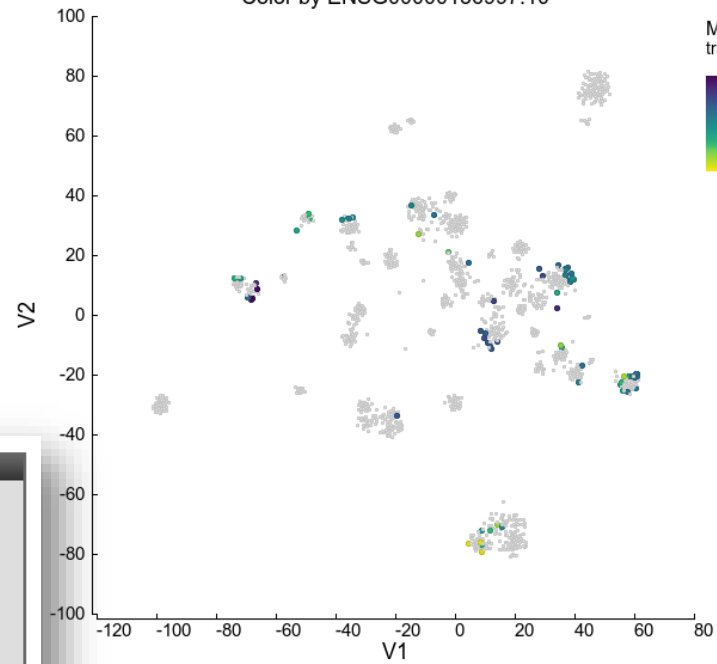
- Go to: **Main**
- Main
 - ITCC-P4 (IMI2)
 - Cancer Portals
 - Time series
 - AmpliconView
 - Kaplan-Meier
 - Sample maps
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R2: Sample map Viewer

Online Tutorial

Tumor Pediatric_PDX (with_reference) - ITCC-P4 - 1507 - custom - ilmnhm450 private

Tumor Pediatric_PDX (with_reference)
ITCC-P4 - 1507 - custom - ilmnhm450
tSNE (perplexity = perplexity_unkn)
Color by ENSG00000136997.10



MYC (ENSG00000136997.10)*
transform_log2
12.209
0

Partially overlapping mRNA dataset

[Direct link to View](#)

Adjustable settings

Perplexity:

Image size:

Dot size:

Samples to mark:

Mark method:

Samples paths:

Vector (SVG) output:

Enable hovering:

x: min: max:

y: min: max:

Color mode:

Color source:

Gene / Met_id:

Transformation:

Color scheme:

Select subset DBSCAN select subset

[View interactive plot](#)

[Direct link to View](#)

Adjustable settings

Perplexity:

Image size:

Dot size:

Samples to mark:

Mark method:

Samples paths:

Vector (SVG) output:

DataScopes



DataScopes (Landing pages with subsection of datasets)

Go to: **Main**

R2: DataScopes available in R2

[Online Tutorial](#)

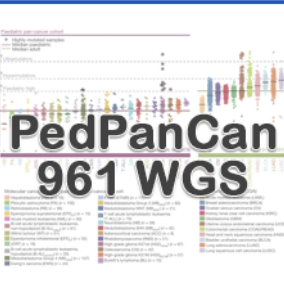
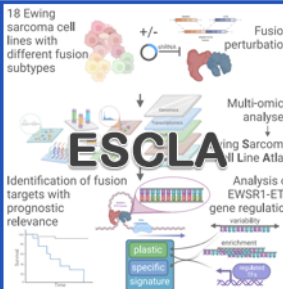
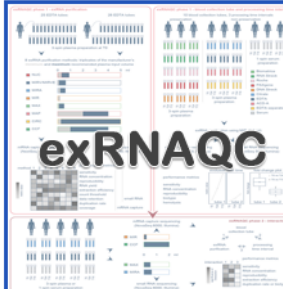
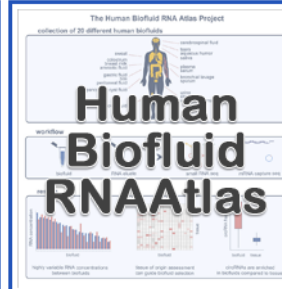


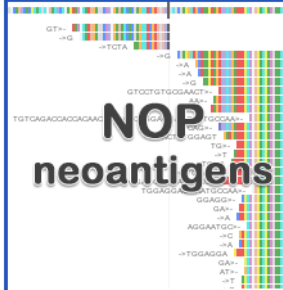


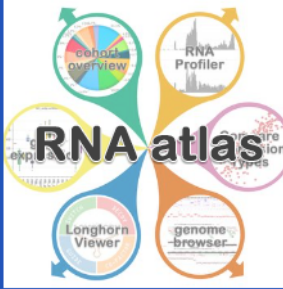

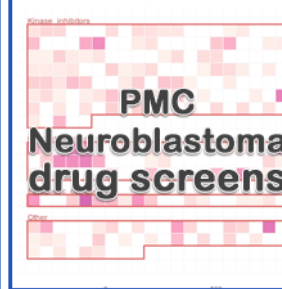
- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope**
- User Options
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- resources
- tumor

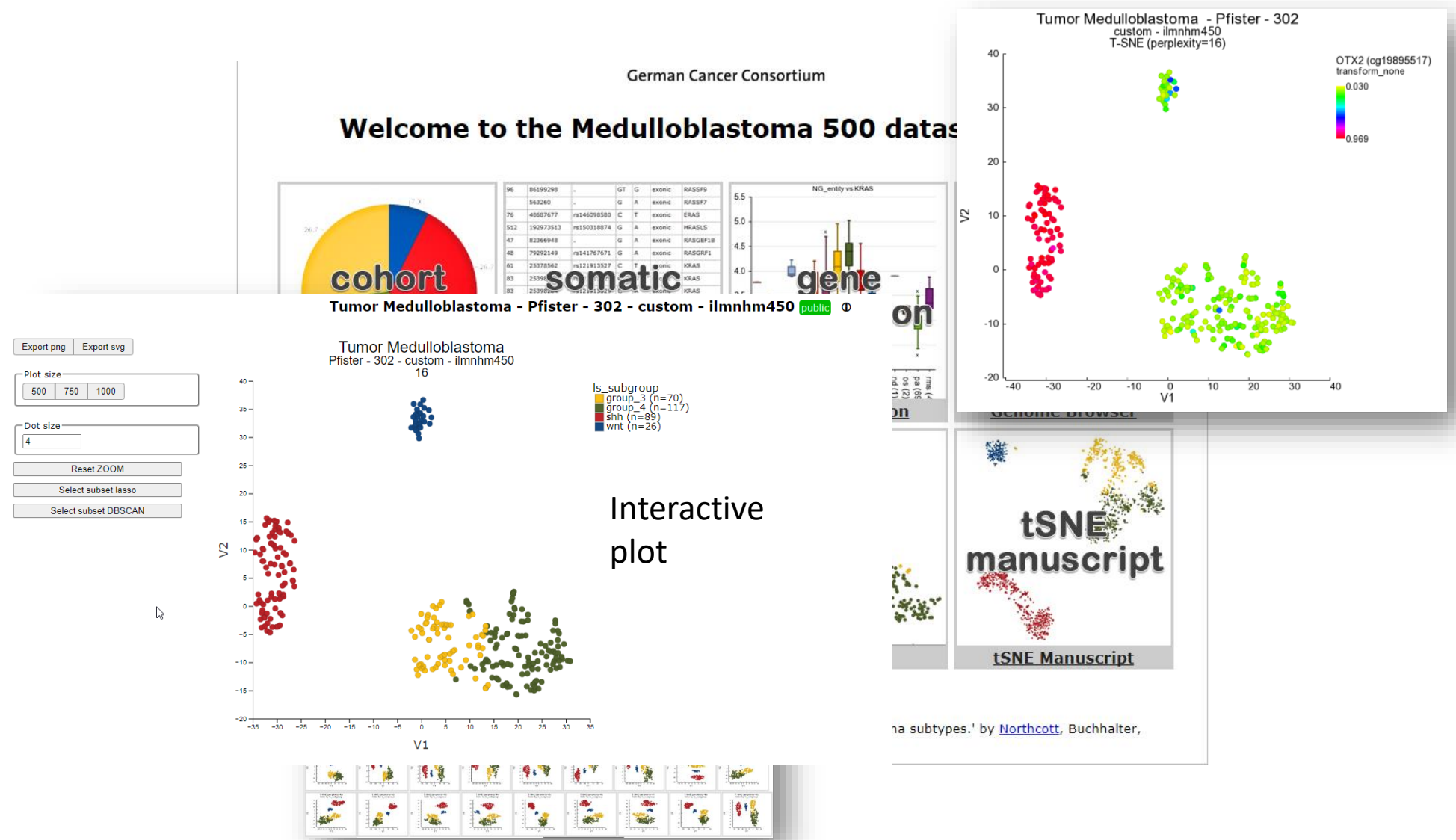
Welcome to the data scopes index in R2

Data scopes are dedicated 'landing pages' from where predefined jumps into analyses are presented. These data scopes often are parts of projects / consortia, but can also define a focus for a particular tumor entity (the tumor scopes). Please click on one of the tiles available to your access profile to proceed to the respective landing page.

resources

 <p>PedPanCan 961 WGS</p> <p>Pediatric Pan Cancer(DKFZ)</p>	 <p>ESCLA Ewing Sarcoma Cell Line Atlas</p> <p>Ewing Sarcoma Cell Line Atlas</p>	 <p>exRNAQC</p> <p>exRNAQC</p>	 <p>Human Biofluid RNAAtlas</p> <p>HumanBiofluidRNAAtlas</p>
 <p>Northcott Medulloblastoma 500 WGS</p> <p>Medulloblastoma 500</p>	 <p>HighRisk nrbl CGH (Preter)</p> <p>HR NB CGH cohort (Preter)</p>	 <p>NOP neoantigens</p> <p>NOP neoantigens</p>	 <p>Pediatric PDX (Olson)</p> <p>Pediatric PDX (Olson)</p>
 <p>PPTC PDX cohort</p>	 <p>RNA atlas</p>	 <p>iTHER2.0 Precision medicine</p>	 <p>PMC Neuroblastoma drug screens</p>

WGS of 500 medulloblastoma tumors



Northcott Nature 2017

WGS of 1000 pediatric patients

R2: Genomics analysis and visualization platform

dkfz.
German Cancer Consortium

Welcome to the DKFZ Pediatric Pan-Cancer dataset

cohort overview

ID	chr	start	end	GT	G	A	exonic	RASFS
96	86199298	.	.	GT	G	exonic	RASSF9	
563260	.	.	.	G	A	exonic	RASSF7	
76	48687677	rs146098580	C	T	exonic	ERAS		
512	192973513	rs150318874	G	A	exonic	HRASLS		
47	82366948	.	.	G	A	exonic	RASGEF1B	
48	79292149	rs141767671	G	A	exonic	RASGEF1		
61	25378562	rs121913527	C	T	exonic	KRAS		
83	25398	.	.	C	T	exonic	KRAS	
83	25398	rs121913527	C	T	exonic	KRAS		
546	141336348	.	.	TA	T	exonic	RASA2	
39	1558	.	.	CA	C	exonic	RASAL3	
657	206795661	.	.	CA	C	exonic	RASSF5	
26	82366727	.	.	C	T	exonic	RASGEF1B	
84	25398285	rs121913530	C	G	exonic	KRAS		
743	115258744	rs121434596	C	T	exonic	NRAS		
746	115258747	rs121913237	C	T	exonic	NRAS		
747	115258748	rs121913250	C	T	exonic	NRAS		

gene expression

genome browser

1,000 WGS

The data presented here belong to the manuscript 'The landscape of somatic mutations in pediatric cancer', Groebner et al, 2017.

GeneBrowser

ICGC_MB132

556 Neuroblastoma CGH samples

Genome Browser (Preter) Help (R)

Distal 6q loss: novel markers for poor high-risk neuroblastoma patients.

Sample Sorter

Genome Browser

CGH TSNE Plotter

CGH Reporter Viewer

Other Analyses

Genomic amplifications and distal 6q loss: novel markers for poor survival in high-risk neuroblastoma patients [et al., 2018](#).

PDX explorer linked to genomic data

R2: Pediatric PDX (Olson)
R2: Genomics analysis and visualization platform

Welcome to the Pediatric PDX data

cohort overview

Cohort Overview

Sample ID	Variant ID	Ref	Alt	Gene	Effect	
96	86199298	-	GT	G	exonic	RASSF9
563260		G	A	exonic	RASSF7	
76	48687677	rs146098580	C	T	exonic	ERAS
512	192973513	rs150318874	G	A	exonic	HRASLS
47	82366940		G	A	exonic	RASGEF1B
48	79292149	rs141767671	G	A	exonic	RASGRF1
61	25378962	rs121913527	C	T	exonic	KRAS
83	25398285		C	T	exonic	KRAS
546	141376548		T	C	exonic	RASA2
39	15566480		T	C	exonic	RASA3
657	206756661		C	A	exonic	RASSF5
26	82366727		C	T	exonic	RASGEF1B
84	25398285	rs121913530	C	G	exonic	KRAS
743	115258744	rs121434596	C	T	exonic	NRAS
746	115258747	rs121913237	C	T	exonic	NRAS
747	115258748	rs121913250	C	T	exonic	NRAS

somatic variants

Somatic Variants Table

PDX explorer

PDX Explorer

gene expression

Gene Expression

methy gene

Methyl

circos overview

R2: Single Sample Circos Overview

genomic data table

R2: Single Sample Circos Overview

cell line diagram

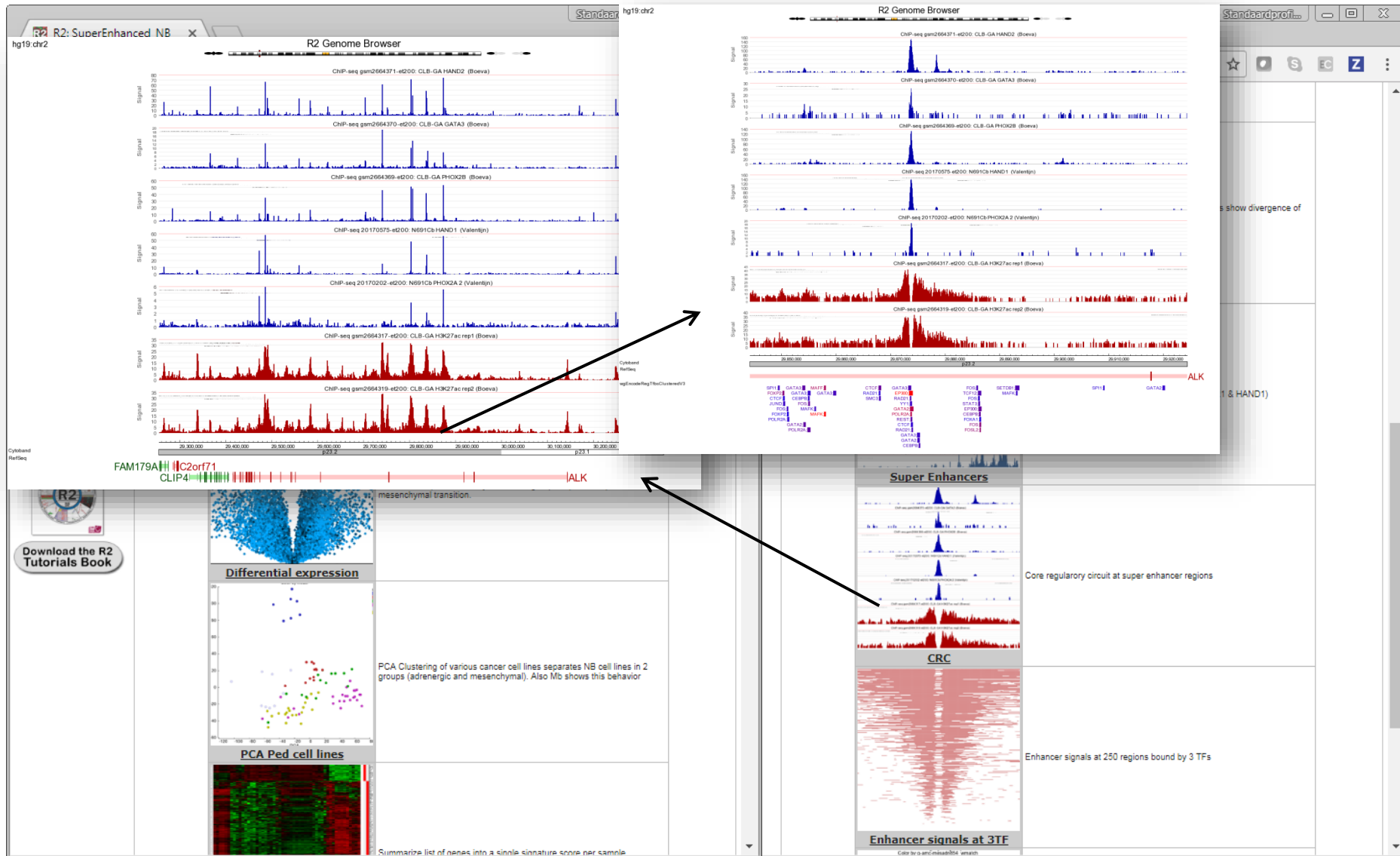
Cell Line for Passing in Tissue Culture

NO5 subgroup vs CDKN1A

Mixed Pediatric PDX (public) - Olson - 55

The data presented here belong to the manuscript 'A brain pediatric brain tumors' by Brabetz et al, 2017.

Links to interactive analyses (like Super Enhancers)




Personalized Medicine programs


R2: INFORM
R2: Genomics analysis and visualization platform

dkfz.
German Cancer Consortium

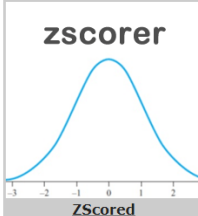
Welcome to the DKFZ INFORM section.



Circos



Genome Browser




ZScored

R2: iTHER
R2: Genomics analysis and visualization platform

prinsesMÁXIMA
centrum voor kinderoncologie


Welcome to the iTHER section of R2.



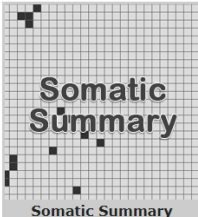
Circos

96	36189208	.	GT	G	bcwng	BSGDP9
146320		G	A	bcwng	BSGDP7	
40667677	1614009050	C	T	bcwng	ERAS	
1321927813	1619311874	G	A	bcwng	HRAGLB	
82388668		G	A	bcwng	BSGDP18	
79261449	1614767671	G	A	bcwng	BSGDP1	
25378962	1612613557	C	A	bcwng	HRAS	
25378962	1612613557	C	A	bcwng	HRAS	
25378962	1612613557	C	A	bcwng	HRAS	
1417957		T	C	bcwng	HRAS2	
15917000		T	C	bcwng	HRAS3	
200700861		CA	C	bcwng	HRAS1	
92366727		C	T	bcwng	BSGDP18	
25380281	1612613550	C	G	bcwng	HRAS	
1321927813	1612613550	C	T	bcwng	HRAS	
1321927813	1612613550	C	T	bcwng	HRAS	
1321927813	1612613550	C	T	bcwng	HRAS	

Somatic Variants Table



Genome Browser



Somatic Summary

Interested?

- If you are interested in having a datascope for your group / consortium?
 - Get in touch with us via r2-support@amsterdamumc.nl

R2 communities

- Users working together on 1 project may want to share
 - MegaSampler presets
 - Tracks
 - Gene Sets
- R2 Community feature
 - Any user can start user groups (as many as you like)
 - Invite other users
 - Share
 - Tracks
 - MegaSampler presets
 - Gene Categories
 - GenomeBrowser profiles



R2 communities

Go to: [Main](#)

R2: Communities Center

From this panel you can manage/create communities and see of which groups you are a member

You are a member of the following communities:


r2

[Communities Center](#)

[Start a new Community](#)

[Community updates](#)

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope ▶
- User Options ▶
- Help ▶
- Contact / About R2

- Account
- MegaSampler Presets
- Custom gene sets
- Tracks ▶
- Community 
- Cohort Annotation
- Upload New Dataset
- Logout

R2: Communities Center

From this panel you can manage/create communities and see of which groups you are a member

You are a member of the following communities:

r2, student, student_breast

[Communities Center](#)

[Start a new Community](#)

[Community updates](#)

[Manage student](#)

[Manage student breast](#)

Recap R2 Support

Go to: **Main**

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/TSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope
- User Options
- Help
- Contact / About R2

PubMed

r2.amc.nl

Video training

Integrated Analysis of Tumor Genomics Data with R2 Tutorials

Download the R2 Tutorials Book

AUMC: CEMM

r2-training-courses.readthedocs.io/en/latest/

R2 training courses

latest

Search docs

STUDENTS COURSE

- Investigating Intra-tumor Heterogeneity in Neuroblastoma

GRADUATE COURSE

- Investigating structural variants
- Investigating Intra-tumor Heterogeneity

ADDITIONAL COURSE MATERIALS

- Differential gene expression in micro-array colon cancer data
- Finding causes in Neuroblastoma genomics data
- Investigating structural variants
- BMS38: Computer Practicals

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Docs » R2 Training Courses: 2023-02-02

Edit on GitHub

R2 Training Courses: 2023-02-02

This contains a collection of training courses for R2; a biologist friendly, web based genomics analysis and visualization application developed by Jan Koster at the department of Oncogenomics in the Academic Medical Center (AMC) Amsterdam, the Netherlands. For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (<http://r2.amc.nl> <http://r2platform.com>)'

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Table of Contents

Students Course

- 1. Investigating Intra-tumor Heterogeneity in Neuroblastoma
 - 1.1. Introduction
 - 1.2. Tumors and origins: a first impression of your data
 - 1.3. Urgency of research: patient material
 - 1.4. Which genes make a difference? Creating signatures
 - 1.5. Identifying groups: using signatures to classify other datasets
 - 1.6. Using scores for further characterization
 - 1.7. Finding causes: homing in on transcription factors
 - 1.8. Proving causes: manipulating cell lines
 - 1.9. Creating hypotheses: relating to chromatin modification data
 - 1.10. Suggesting therapy
 - 1.11. Final remarks / future directions

Graduate Course

- 1. Investigating structural variants
 - 1.1. Introduction
 - 1.2. Exploring the dataset
 - 1.3. Pie Charts
 - 1.4. Somatic mutations in neuroblastoma
 - 1.5. Further use of WGS data; structural variants
 - 1.6. Chromothripsis
 - 1.7. Locations of structural variants, hotspots?

Online Tutorial

What is R2?

Welcome to R2; a biologist friendly web based genomics analysis and visualization application developed by Jan Koster at the department of Oncogenomics in the Academic Medical Center (AMC) Amsterdam, the Netherlands. You can start exploring the gene expression data by following the numbered options in the center.

For citations, please include the following website: 'R2: Genomics Analysis and Visualization Platform (<http://r2.amc.nl>)'.

Financial Supporter of R2

Cancer Center Amsterdam

News

Check out the new iTHER pediatric cancer precision medicine datascopes. Now publicly available in R2 via the 'datascopes' menu item.

all news

Genome Browser

Genomics Analysis & Visualization Platform

Genome Browser

Genomics Analysis & Visualization Platform

Genome Browser

Genomics Analysis & Visualization Platform

encca (2)

R2-Platform

Fun things to do:

Tutorial

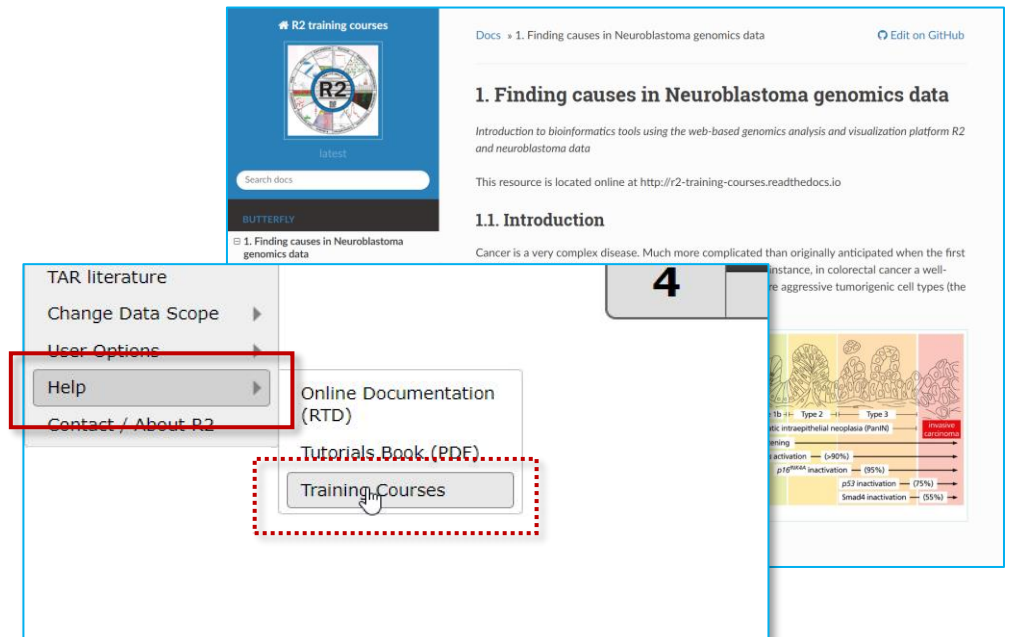
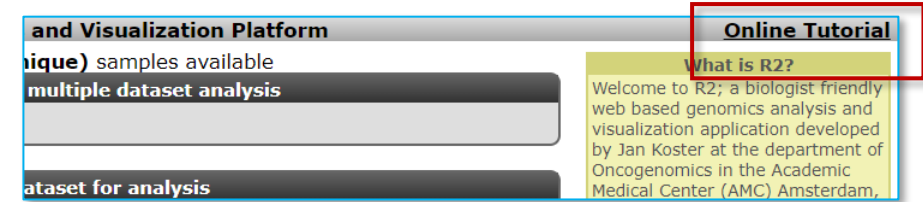
- Go to a chapter of interest and follow the examples
- Toy around with a similar pipeline on a different dataset
- Perform a follow up analysis from the tutorial

R2 Butterfly Training Courses

- Help => Training Courses => Butterfly
- Read carefully and follow the research line step by step
- Feel free to toy around
 - Who knows

Do your own research

- Find a dataset of your interest
- Think about a good biological research question
- Try to find the analyses that can help you gain insight



R2 Platform Team

Romeo Willinge Prins

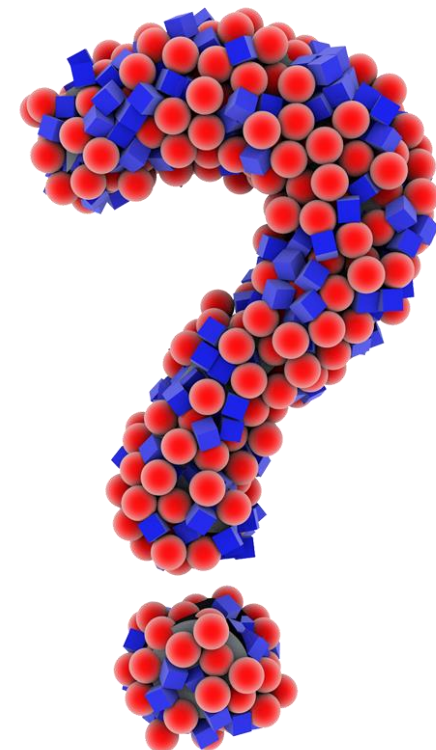
Danny Zwijnenburg

Richard Volckmann

Christian Griffioen

Lieke Hoyng

Jan Koster



http://twitter.com/r2_platform
<http://facebook.com/r2platform>

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