



R2 Introduction Workshop

PRESSURE Part 2

21-May-2024

Computer login:
func_user
Welkom01

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

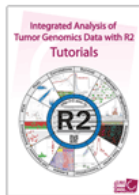
r2platform.com

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

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
Find Correlated Genes with a single Gene

4 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)

Correlate Genes
Correlate 2 Genes
Find Correlated Genes with a single Gene
Correlate with a track

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

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



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. x

GS:cell cycle (537)

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

Reset selected

Use selected

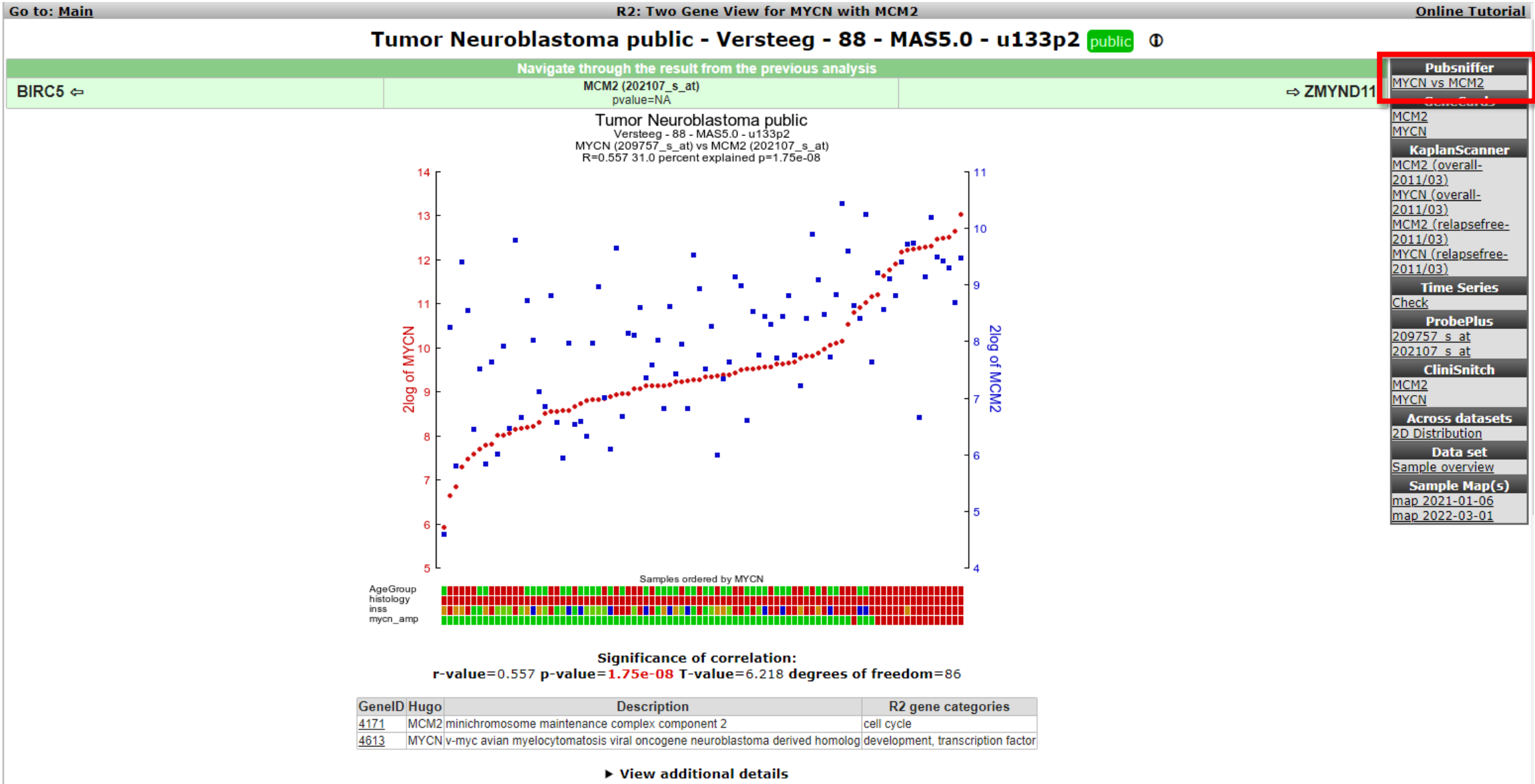
Correlate with a gene

Go to: !

View	Gene	R	P	Presence
	KATNB1	0.63	2.35e-8	88/88
	H2AFX	0.575	7.36e-7	88/88
	CHEK1	0.565	0.00000115	83/88
	CHAF1A	0.561	0.00000119	80/88
	RUVBL1	0.56	0.00000106	86/88
	MCM2	0.557	0.00000117	88/88
	Gene details			81/88
	Gene symbol: MCM2 (GeneID: 4171)			88/88
	Description: minichromosome maintenance complex component 2			73/88
	Alternative names: • MCM2 • BM28 • CCNL1 • CDCL1 • D3S3194 • MITOTIN • cdc19			80/88
	Other designations: • DNA replication licensing factor MCM2 • MCM2 minichromosome maintenance deficient 2, mitotin • cell division cycle-like 1 • cyclin-like 1 • minichromosome maintenance deficient 2 (mitotin) • minichromosome maintenance protein 2 homolog • nuclear protein BM28			79/88
	Ontology data: • cell cycle			88/88

View	Gene	R	P	Presence
	CDC42	-0.621	2.57e-8	87/88
	SEPT4	-0.524	0.00000828	86/88
	SEPT8	-0.507	0.0000197	88/88
	SEPT7	-0.494	0.0000337	88/88
	CDKN2D	-0.483	0.0000563	81/88
	MAPK1	-0.482	0.0000562	88/88
	PTP4A1	-0.418	0.000516	88/88
	CLIP1	-0.416	0.000539	88/88
	LIG4	-0.403	0.00085	88/88
	TACC1	-0.395	0.00104	88/88
	AHR	-0.388	0.00132	88/88
	PAFAH1B1	-0.379	0.00165	88/88
	DMTF1	-0.374	0.00192	88/88
	ING4	-0.364	0.00262	88/88
	CYLD	-0.359	0.00301	88/88
	RASSF4	-0.358	0.00302	88/88
	MAD2L2	-0.33	0.00736	88/88

Two Gene View for MYCN with MCM2



Pub sniffer

- Go to: **Main**
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 - AmpliconView
 - Kaplan-Meier
 - Sample maps
 - Small Tools
 - DataGrabber
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 - Change Data Scope ▶
 - User Options ▶
 - Help ▶
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R2: PubSniffer

Checking NCBI PubMed for MYCN, MCM2

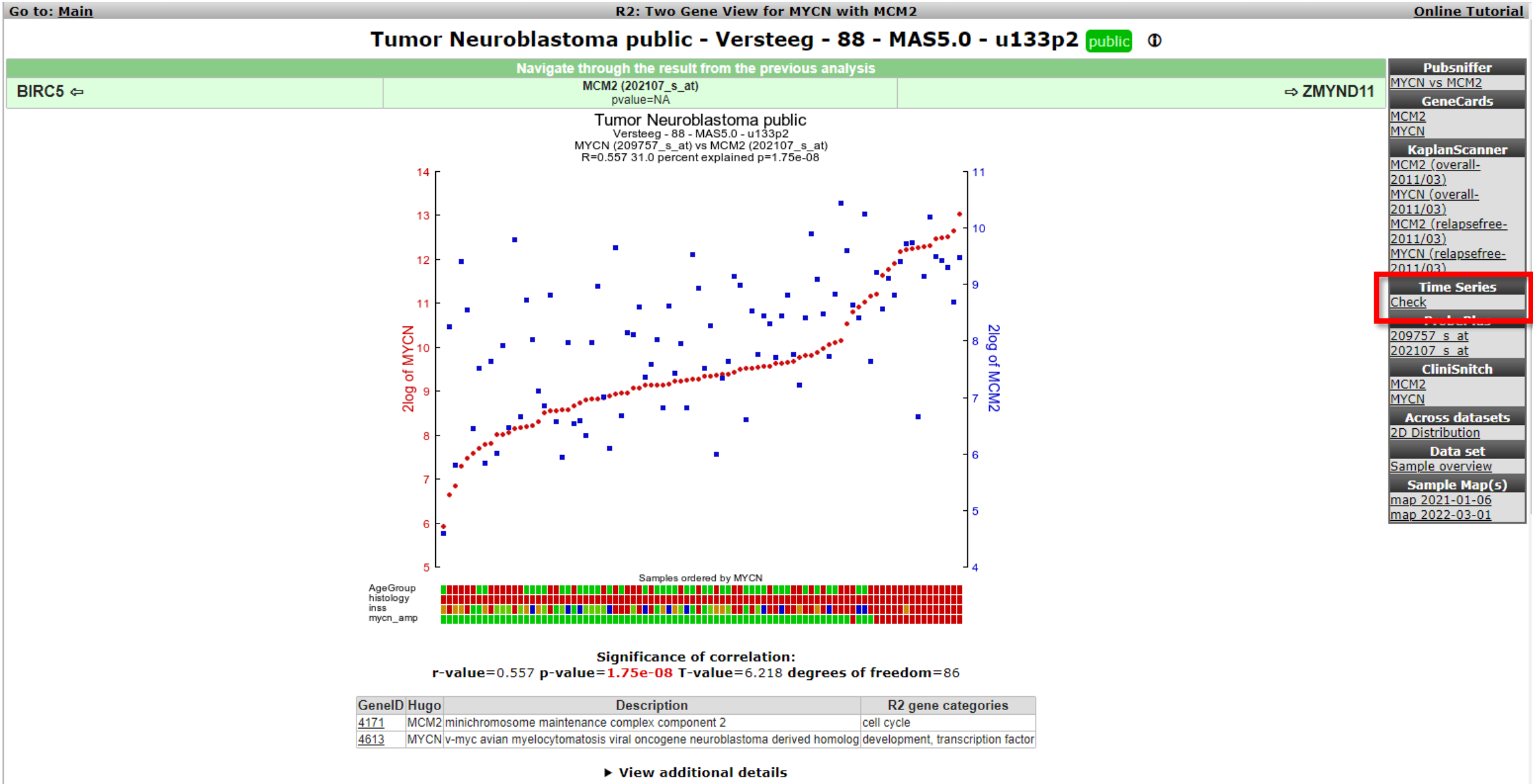
Query	# Articles	Outlink
'MYCN AND MCM2'	1	Pubreminer
'MYCN'	2934	Pubreminer
'MCM2'	1336	Pubreminer
'MYCN AND MCM2 AND cancer'	1	Pubreminer
'MYCN AND MCM2 AND development'	0	Pubreminer
'MYCN AND MCM2 AND neuroblastom'	1	Pubreminer
'MCM2 AND cancer'	665	Pubreminer
'MCM2 AND development'	199	Pubreminer
'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 displays the R2 PubSniffer interface with the following details:

- Search Query:** MCM2 AND CANCER AND (IMMUNOHISTOCHEMISTRY[MH]) AND (*2016[DP] OR *2017[DP] OR *2018[DP])
- Search Results:** 9 items found, sorted by Most Recent.
- Article 1:** MCM family in HCC: MCM6 indicates adverse tumor features and poor outcomes and promotes S/G2 cell cycle progression. *BMC Cancer*. 2018 Feb 20;18(1):200. doi: 10.1186/s12885-018-4056-8. Review. PMID: 29482213. Free PMC Article.
- Article 2:** MCM2 expression in serrated polyps demonstrates aberrant cellular proliferation. Fortuna D, Boman B, O'Neill R, Palazzo J. *Hum Pathol*. 2017 May;63:177-183. doi: 10.1016/j.humpath.2017.02.020. Epub 2017 Mar 14. PMID: 28302337.
- Article 3:** Characterization and clinical validation of MCM2 and TOP2A monoclonal antibodies in the BD Endo™ C assay: An immunobassay which detects aberrant S-phase induction in cervical tissue. Dixon EP, King LM, Nelson R, Simkins SG, Knapp SL, Brough GH, Lenz KL, Henderson DT, Whitehead CM, Hessling J, Brown CA, Malinowski DP. *J Immunol Methods*. 2017 Mar;442:35-41. doi: 10.1016/j.jim.2017.01.002. Epub 2017 Jan 16. PMID: 28092271.
- Article 4:** Diagnostic and Prognostic Value of ProEx C and GLUT1 in Melanocytic Lesions. Yan S, Coffing BN, Li Z, Xie H, Brennick JB, Beg HA, Froehlich HM, Wells WA. *Anticancer Res*. 2016 Jun;36(6):2871-80. PMID: 27272799.
- Article 5:** Systematic cytological evaluation and immunocytochemistry of minichromosome maintenance protein 2 and p53 significantly improve cytological diagnosis of pancreaticobiliary adenocarcinoma. Abe N, Matsuo K, Kamatsubo T, Naka K, Hashimoto S, Takemura T, Fujiwara M, Ito Y, Nakata R, Hashimoto T, Makuuchi M, Soejima Y, Sawada M. *J Med Dent Sci*. 2016;63(1):19-27. doi: 10.11480/jmids.630103. PMID: 27181487. Free Article.

Two gene View for MYCN with MCM2



Regulated in timeseries experiments

- Go to: **Main**
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 - User Options
 - Help

R2: Regulated in Experiments

Online Tutorial

Regulated in Experiments (97 entries)

Experiment 202107_s_at209757_s_at

Experiment	Count
set_public_u1	5/1
MCF7-egf_r1	3/17
MCF7-egf_r2	4/1
MCF7-hrg_r1	2/1
MCF7-hrg_r2	2/2
UCBMSC-lowserum	8/8
A549-TGFB_1	6/8
A549-TGFB_2	7/7
A549-TGFB_3	4/7
BEC-diff_donor1	1/10
BEC-diff_donor2	5/10
BEC-diff_donor3	2/3
HCT116-nocodazole	4/6
HEPG2-control	2/8
HEPG2-mir124	4/24
HUVEC-tnfa-wt	3/3
IMR32-mycn-lenti	1/3
IMR32-mycn-lenti_2	6/8
IMR32-notch3ic	3/7
IMR32-notch3ic-wt-c6	1/2
MCF7-control_1	1/2
MCF7-control_2	3/3
SHEP21N-mycn-wt	6/7
hypoxia-HT29	4/7
hypoxia-MCF7	

set_public_u133p2

Only Show Best: OFF

GeneID Hugo Description
4171 MCM2 minichromosome maintenance complex component 2

MCM2
202107_s_at

IMR32 mycn-lenti

R2 Genome Browser

ChIP-seq GSM2113521-et200: BE2C MYCN (Bradner)

ChIP-seq GSM2113526-et200: Kelly MYCN (Bradner)

ChIP-seq GSM2113529-et200: NGP MYCN (Bradner)

ChIP-seq GSM2113532-et200: SHEP21N MYCN (Bradner)

ChIP-seq GSM2113520-et200: BE2C input (Bradner)

Signal

127,318,000 127,323,000 127,328,000 127,333,000 127,338,000 127,343,000

MCM2

We will explore this in the Advanced Workshop

R2: Scan Result for MYCN(20)

GeneID Hugo Description
4171 MCM2 minichromosome maintenance complex component 2

MCM2
202107_s_at

SHEP21N mycn-wt

ProbesetVerification (hg18)

symbol	probeset	rank	gene	exon	probes	overlap	found	Link
MCM2	202107_s_at	1	GS	YES	YES	YES		R2 View

Adjustable settings

Alt Probesets: MCM2-1-202107_s_at

Type of data: Raw values

Line width: 2px

Line boldsize: 0

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

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](#)

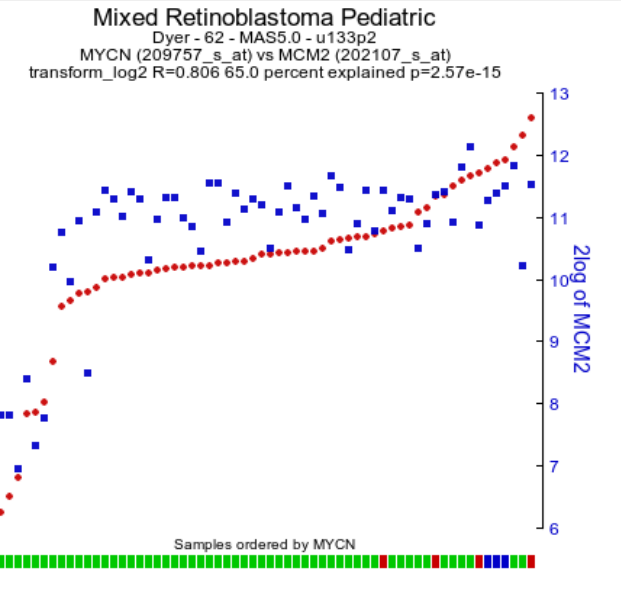
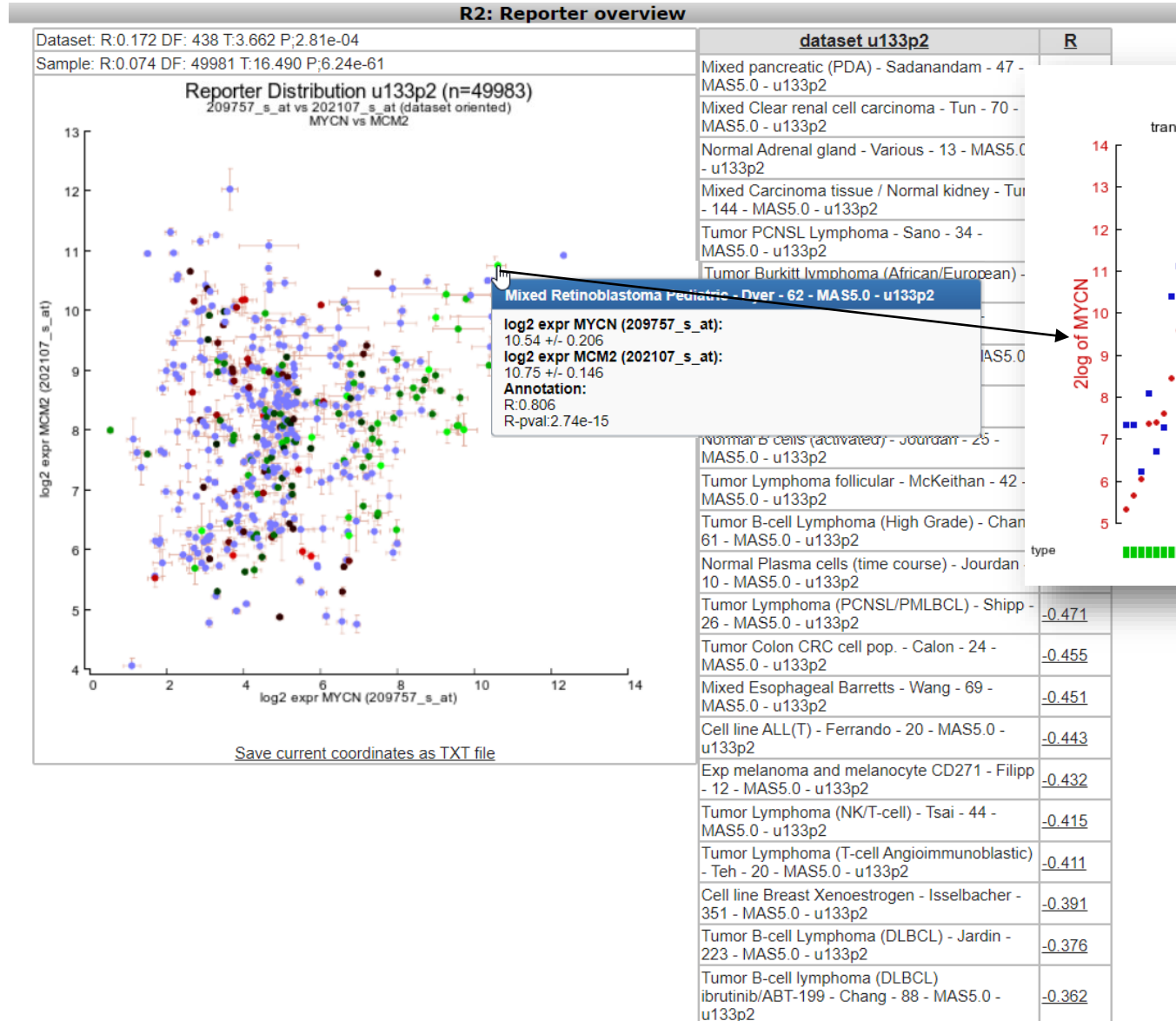
CliniSnitch
[MCM2](#)
[MYCN](#)

Across datasets
[2D Distribution](#)

Data set
[Sample overview](#)

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

2d distribution



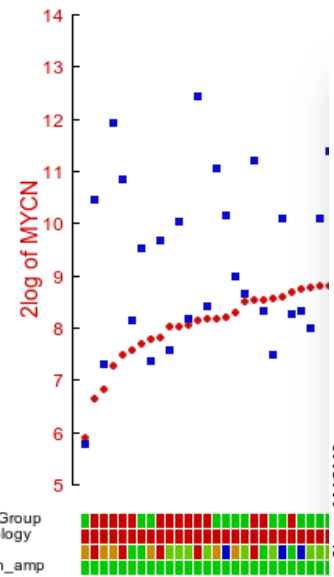
X-gene-view

R2: Two Gene View for MYCN with MCM2

[Online Tutorial](#)

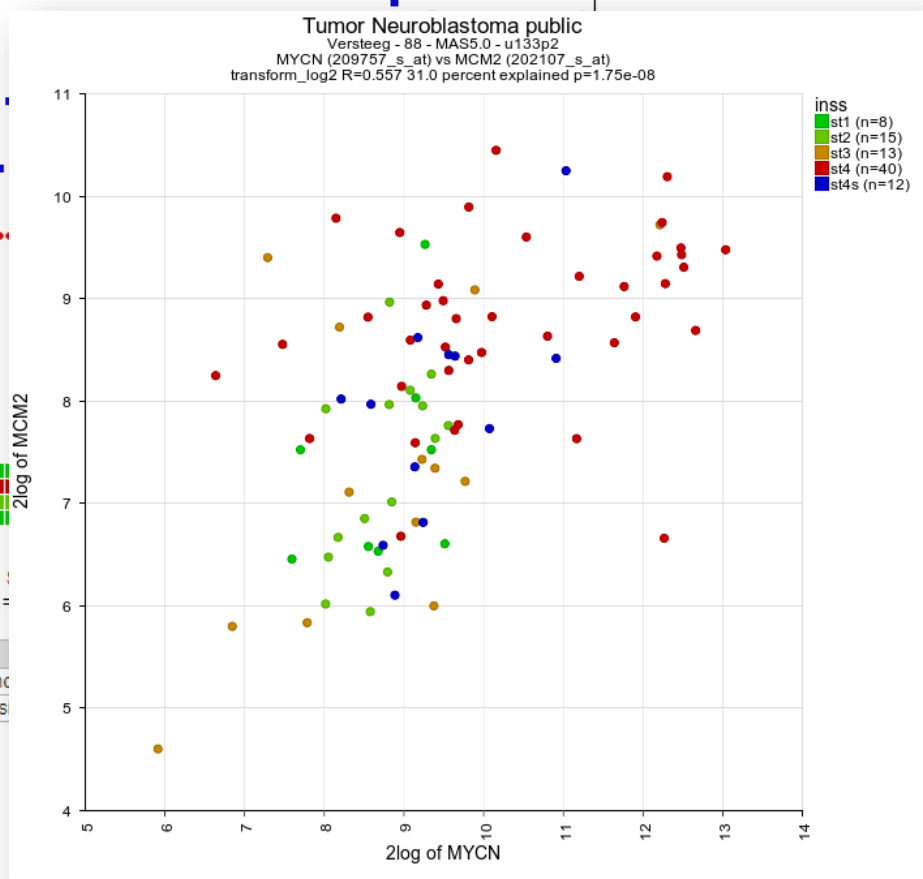
Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public ⓘ

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



r-value=0.557 p-value=

GeneID	Hugo	
4171	MCM2	minichromosome maintenanc
4613	MYCN	v-myc avian myelocytomas



- 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

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:

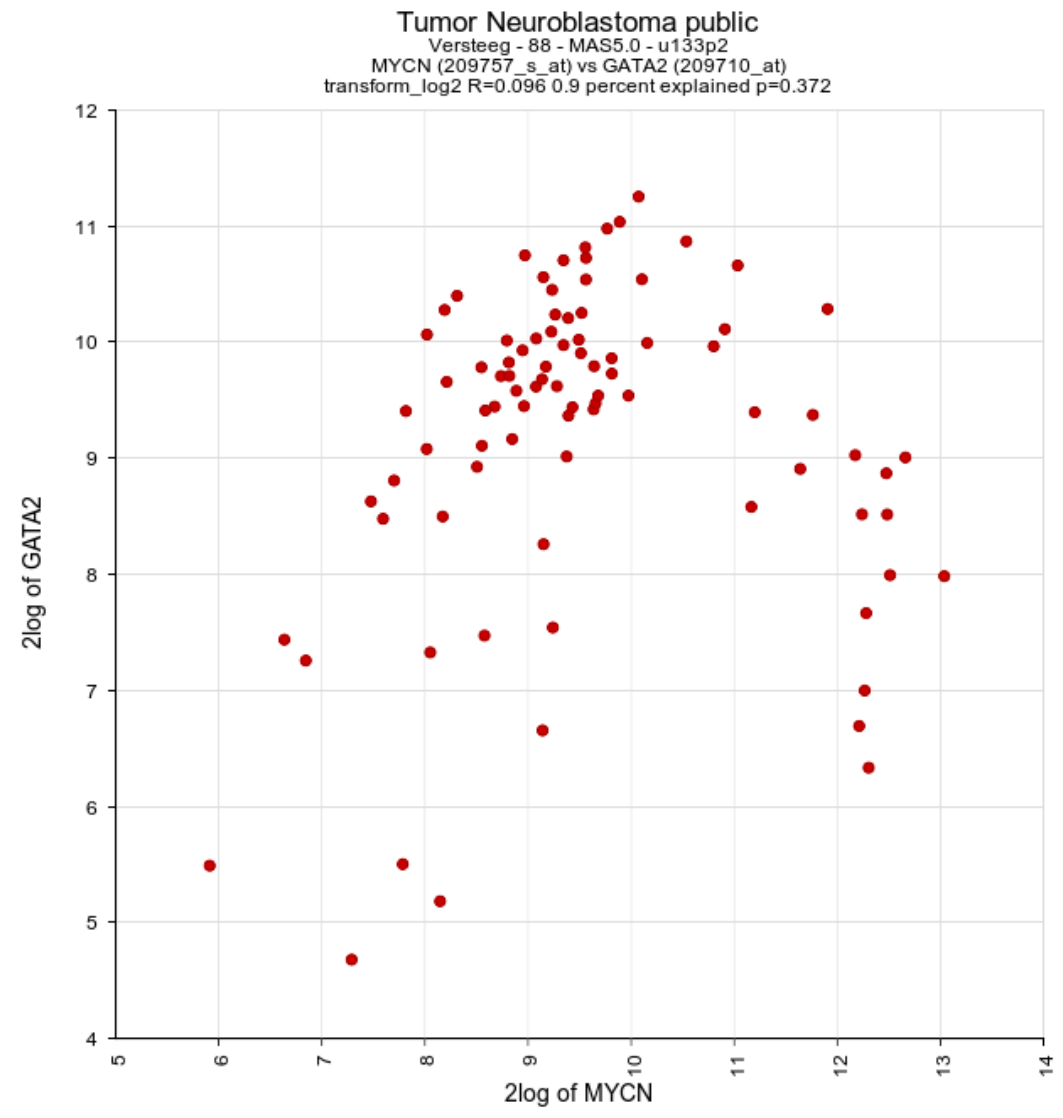
Color mode:

Color track:

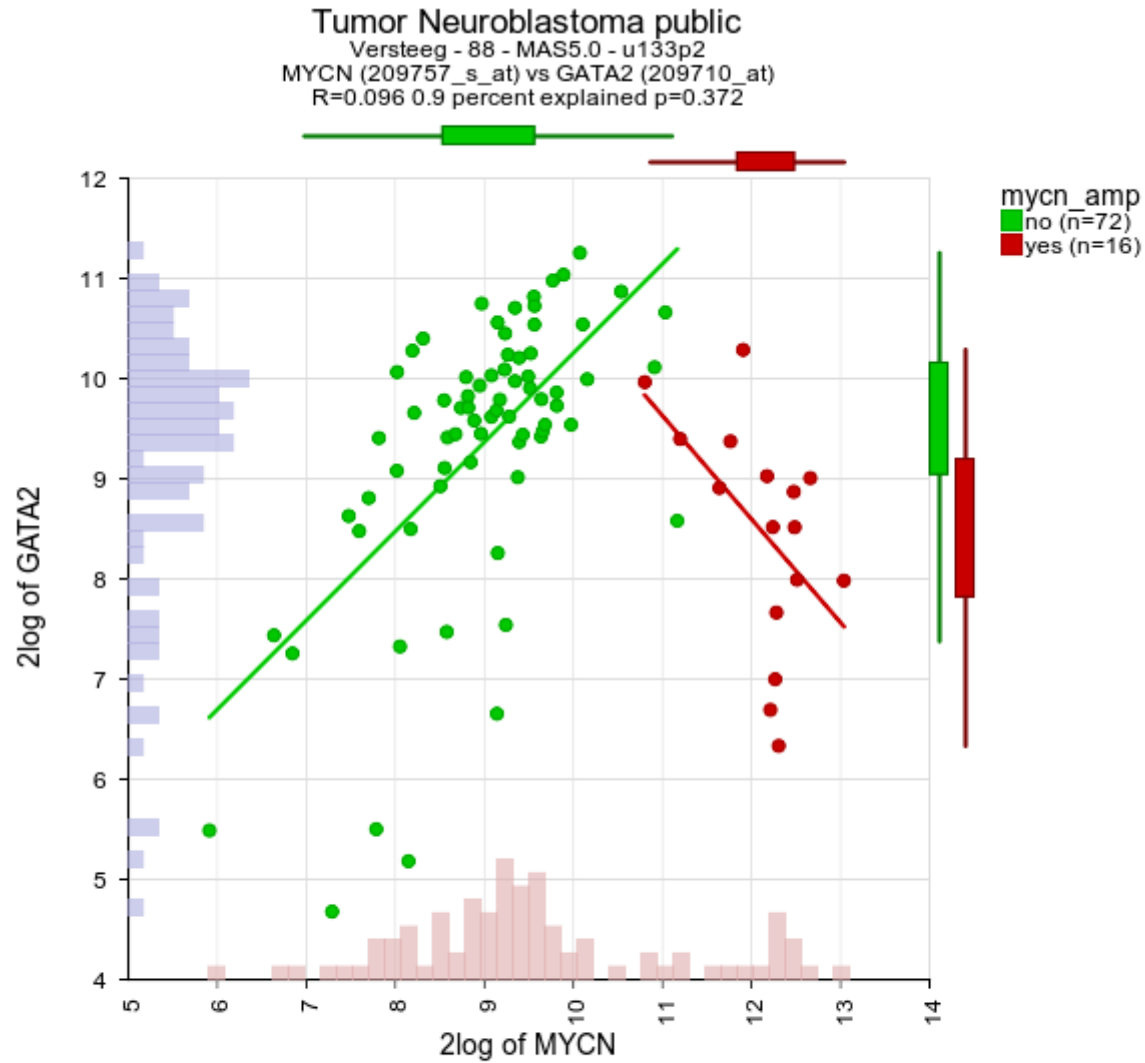
Track Display Selection

More Settings

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

Select tracks

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:



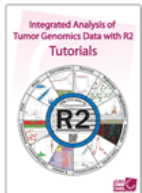
View multiple genes



View multiple genes

Go to: Main

- Main
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R2: Genomics Analysis and Visualization Platform

2,189,183 (2,027,339 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)
 - Correlate Genes
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 - Annotation_plotter
 - Cohort SunBurst plotter
 - Sample overview
 - Cohort Overview
 - Relate 2 tracks
 - Differential Expression
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- 4

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[all news](#)



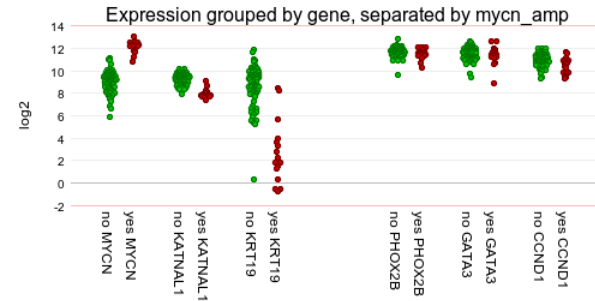
View multiple genes

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R2: View Multiple Genes

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - 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: [empty]

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

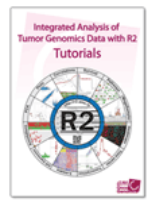
next Reset

Annotation Views



Annotation Views

- Go to: Main**
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[all news](#)



Relate 2 tracks

R2: Relate two tracks

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

Adjustable settings

Analysis type: ⓘ

X track: ⓘ

Y track: ⓘ

Sample Filter

Subset track: ⓘ

Selected sample subset: None

Graphics

Graph type: ⓘ

Samples to mark: ⓘ

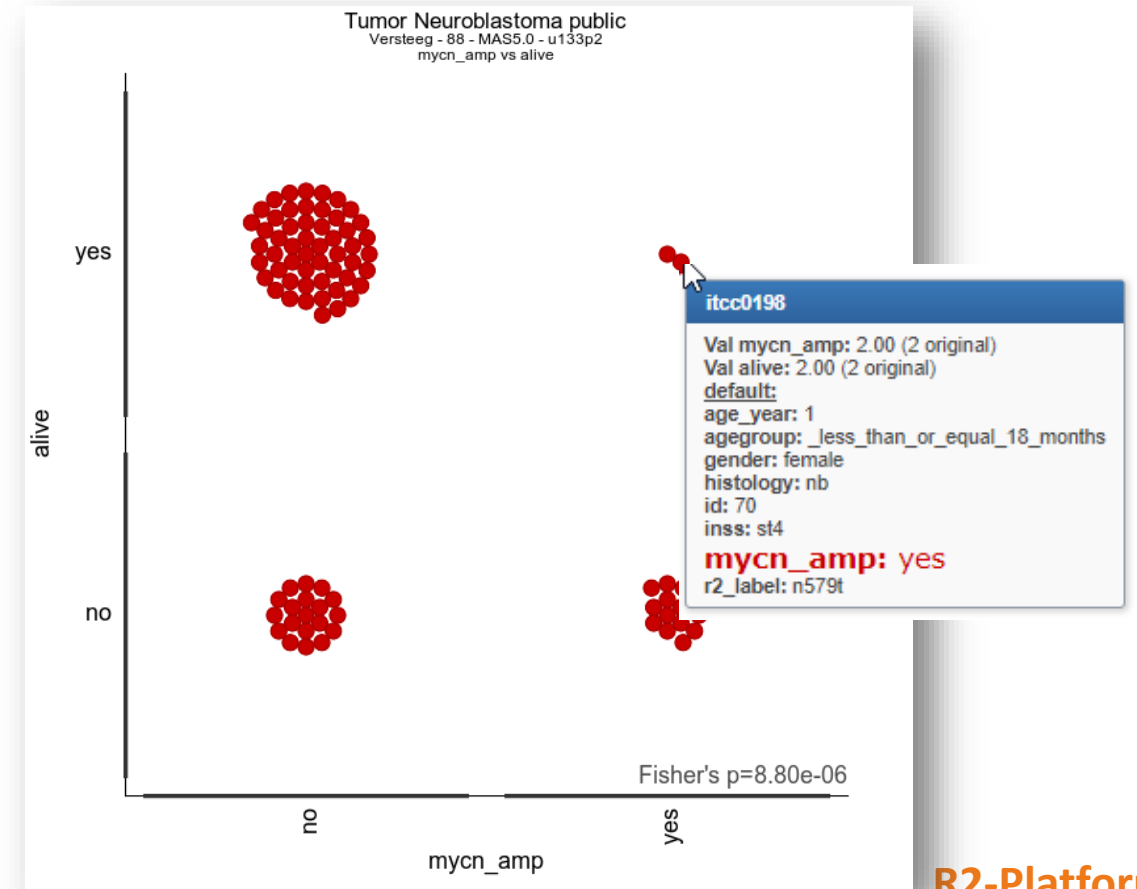
Sample paths:

Group overlap as: ⓘ

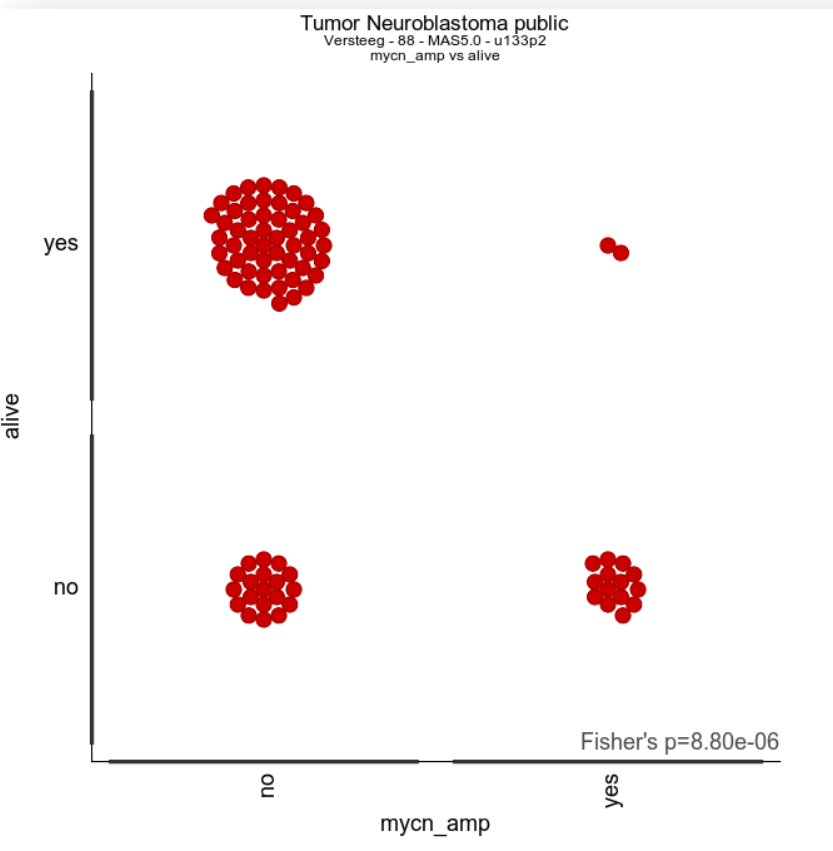
Color mode:

Track Display Selection

More Settings +



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

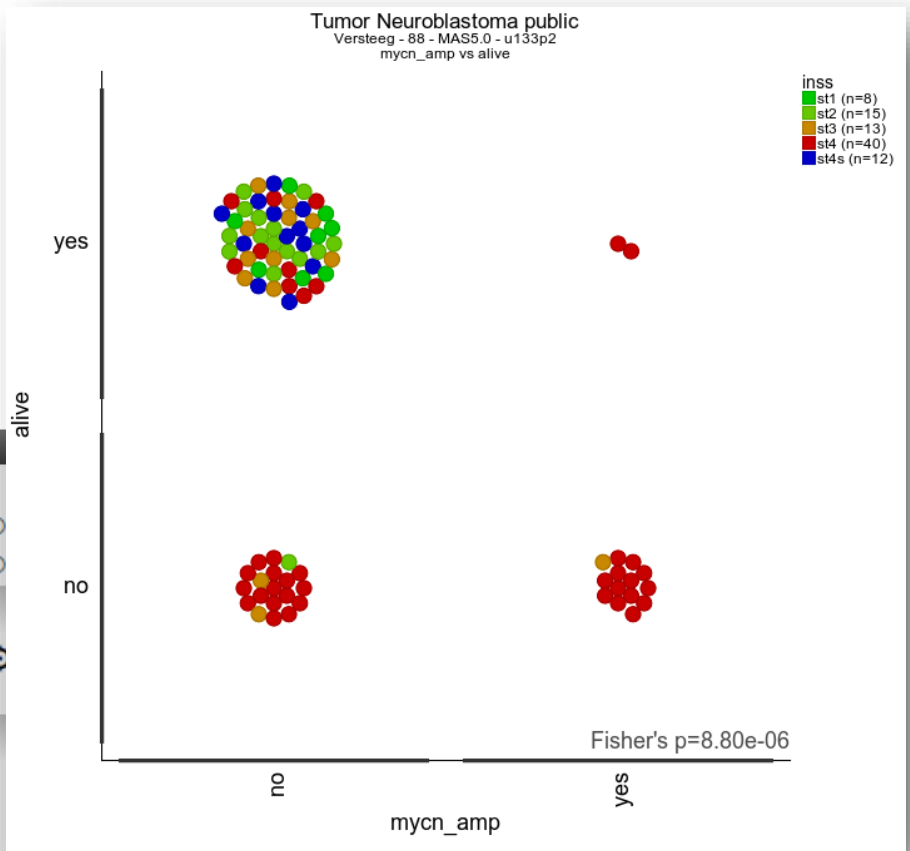
Color track: inss (5 cat)

Track Display Selection

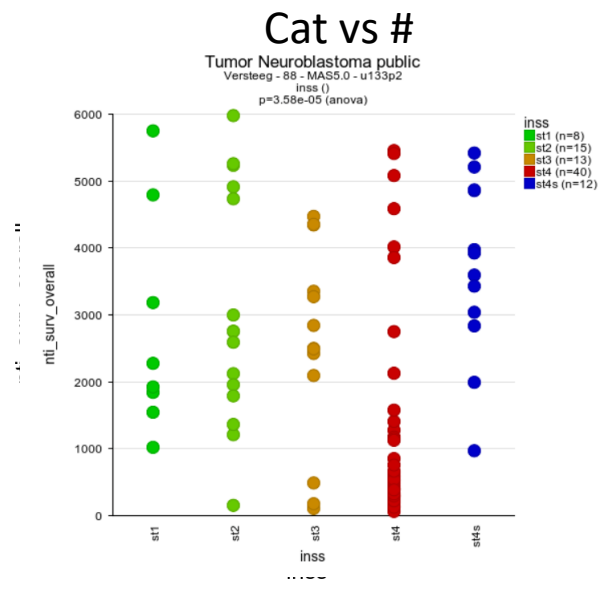
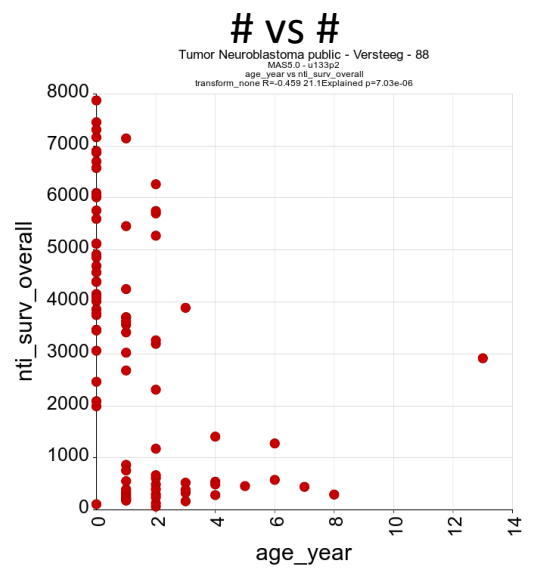
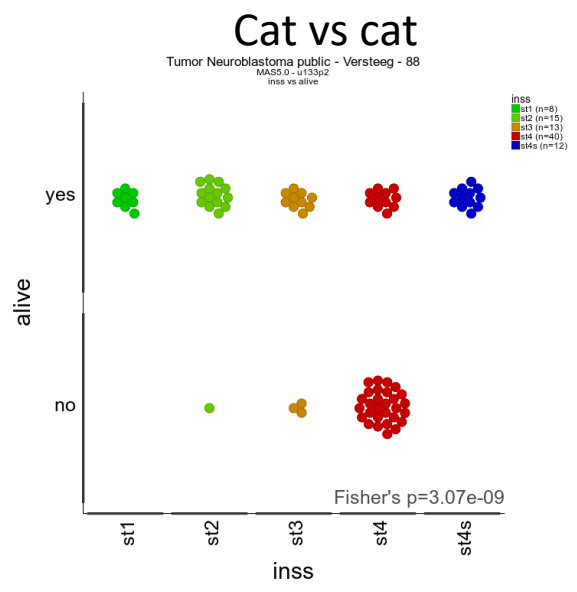
Select tracks

More Settings

Submit



Relate 2 tracks



Tumor Neuroblastoma public

Versteeg - 88 - MAS5.0 - u133p2

88 samples

nti_surv_overall vs inss
p = 3.58e-5 (anova)

Number of samples

(g) st1 (8)

(g) st2 (15)

(g) st3 (13)

(g) st4 (40)

(g) st4s (12)

Tumor Neuroblastoma public

Versteeg - 88 - MAS5.0 - u133p2

88 samples

nti_surv_overall vs inss
p = 3.58e-5 (anova)

nti_surv_overall

inss

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

st1 st2 st3 st4 st4s

Tumor Neuroblastoma public

Versteeg - 88 - MAS5.0 - u133p2

p = 3.58e-5 (anova)

Alive

no (n=33)

yes (n=55)

st1 (n=8)

st2 (n=15)

st3 (n=13)

st4 (n=40)

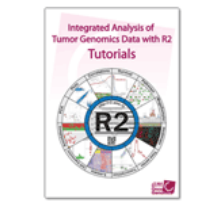
st4s (n=12)

nti_surv_overall

Annotation Plotter

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
2,189,195 (2,027,351 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

4 [Dropdown menu open]

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)

Correlate Genes

- Correlate 2 Genes
- Find Correlated Genes with a single Gene
- Correlate with a track

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

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

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

[all news](#)



Annotation Plotter

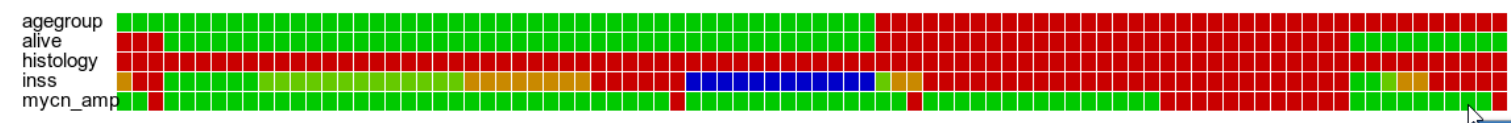
[Online Tutorial](#)

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.

- 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:

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:

Selected sample subset: None

Graphics Settings

fontsize_t1:

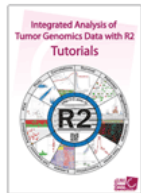
fontsize_tsub:

fontsize_tracks:

Cohort Overview

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

2,189,224 (2,027,380 unique) samples available

Choose single or multiple dataset analysis

1 Single Dataset

Select a dataset for analysis

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

Select type of analysis

3 View a Gene

- View Gene(s)**
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- Annotation**
- Annotation_plotter
- Cohort SunBurst plotter
- Sample overview
- Cohort Overview**
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[Online Tutorial](#)

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Financial Supporter of R2



News

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

[all news](#)



Cohort Overview

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

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

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

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

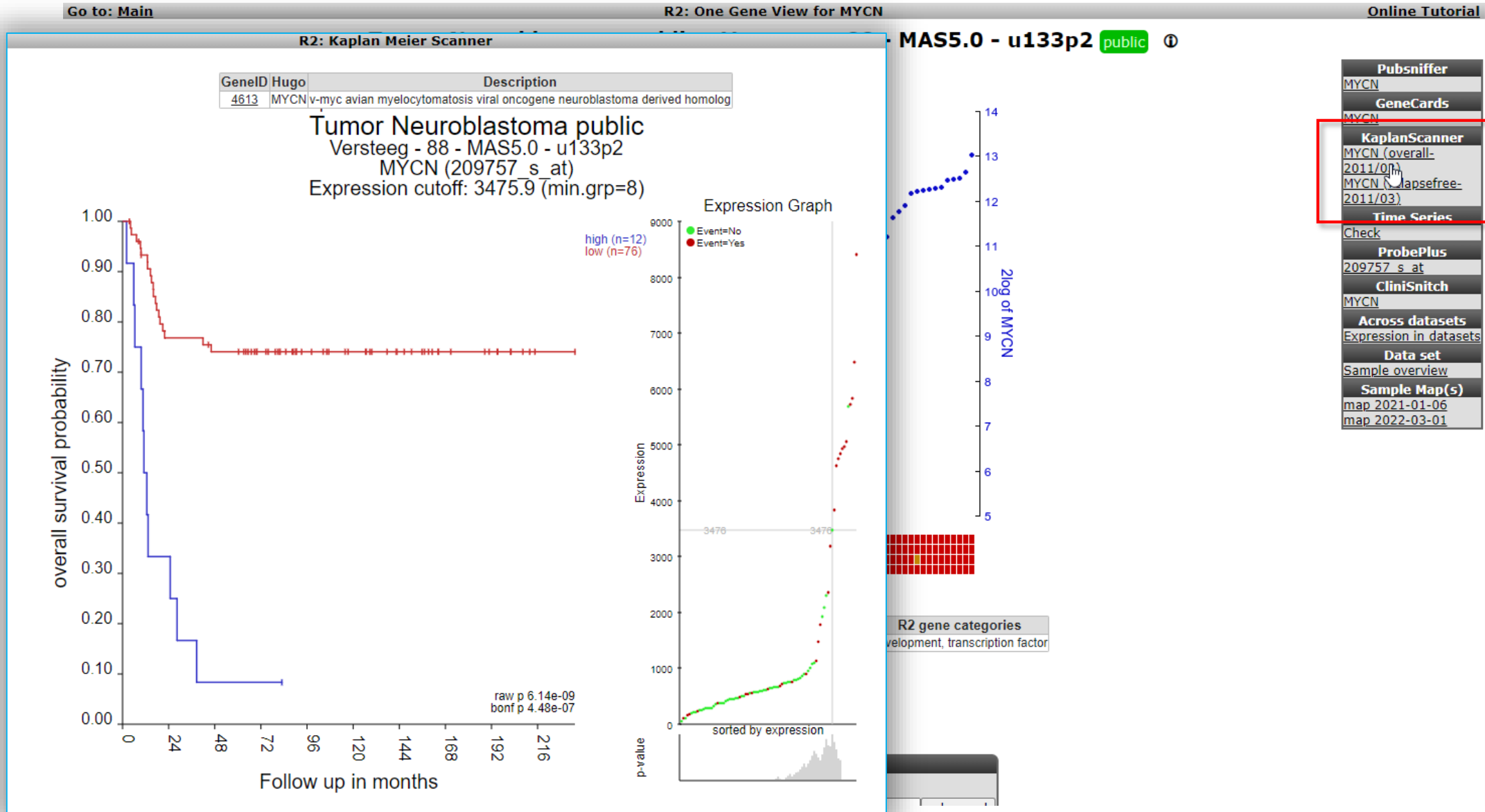
samplenames	agegroup	alive	histology	inss	mycn_amp	age_year	death_cause	gender	nti_event_overall	nti_event_agree	
ITCC0001	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd		no	7876	7876
ITCC0002	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd		no	4914	4914
ITCC0003	_less_than_or_equal_18_months	yes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

Filter in table

Build a track


Build a track from table

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

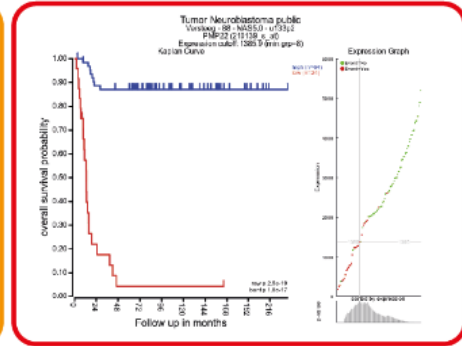
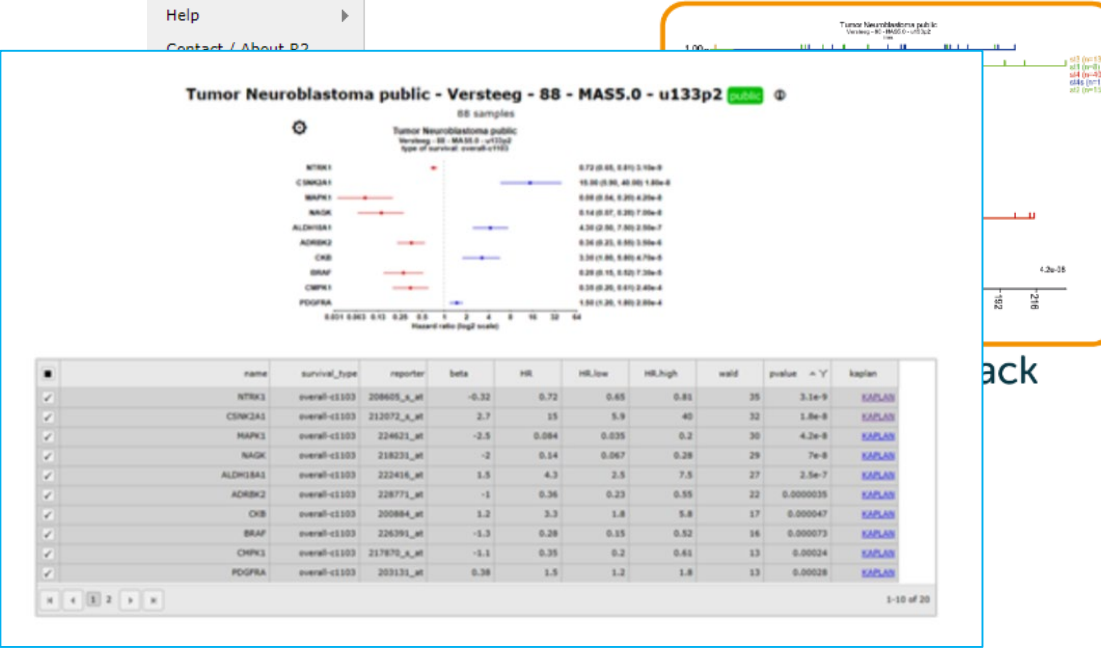
[Online Tutorial](#)

Kaplan-Meier analysis using a data set

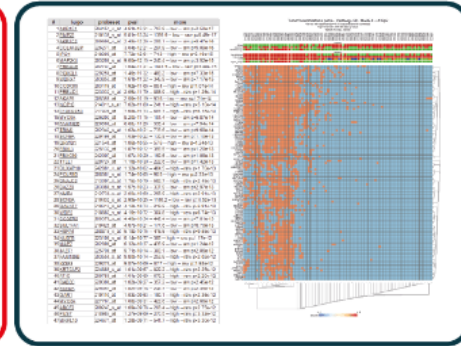
Data set:

Separate by:

Most common survival analyses in R2 separate by:



expression of a gene




multiple genes

Survival analysis (Kaplan)

Go to: [Main](#)

R2: Kaplan-Meier

[Online Tutorial](#)

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

Kaplan-Meier analysis using a data set

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

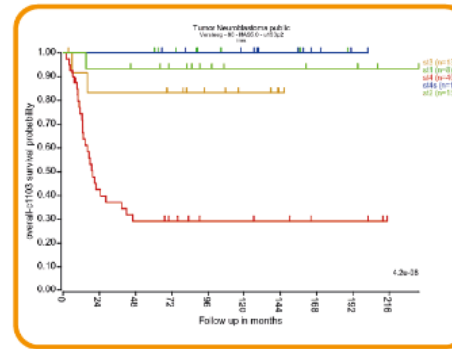
Separate by: a categorical track ▼

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

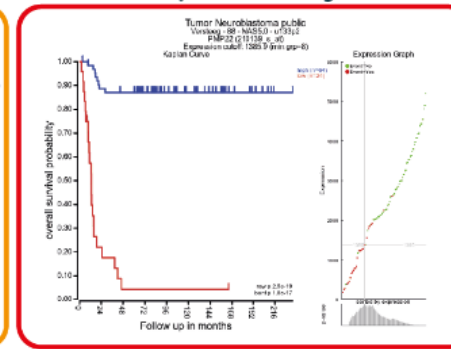
in multiple data sets custom data

Most common survival analyses in R2

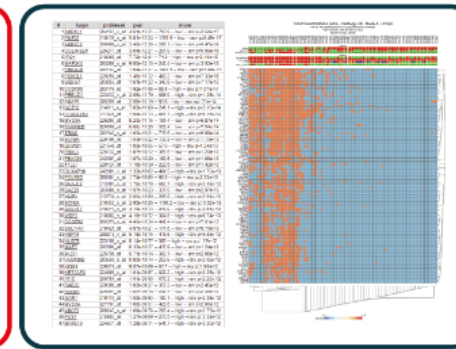
separate by:



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: ▾

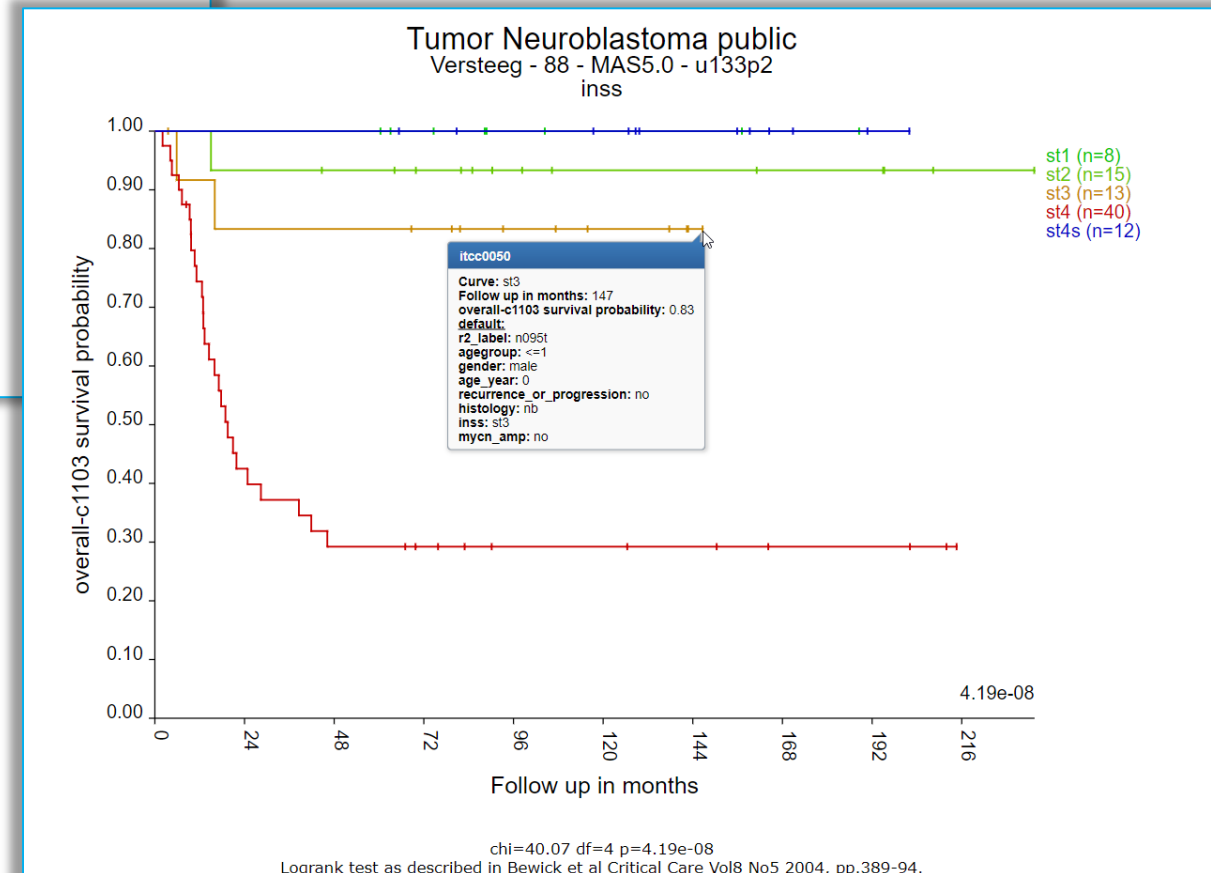
Separate by: ▾

Track: ▾ ⓘ

Sample Filter

Subset track: ▾ ⚙ ⓘ

Selected sample subset: None



KaplanScan

- Go to: Main**
- Main
 - Time series
 - Survival (Kaplan-Meier/Cox)
 - Sample maps (UMAP/tsNE)
 - Small Tools
 - DataGrabber
 - Genome Browser
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 - 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: Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2

Separate by: **a single gene**

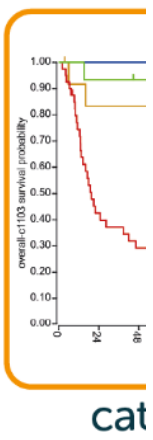
- a single gene
- a categorical track
- a numerical track
- a single gene**
- multiple genes
- Hazard_ratio for a gene
- Hazard_ratio for multiple genes

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:

Selected sample subset:

Type of Survival:

Minimal group size: 8

Next

KaplanScan

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

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

Expression Graph

● Event=No
● Event=Yes

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

Expression

sorted by expression

Red = event
Green = censored

Click to use that as a cutoff

P-values hill plot
Click to use that as a cutoff

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

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)

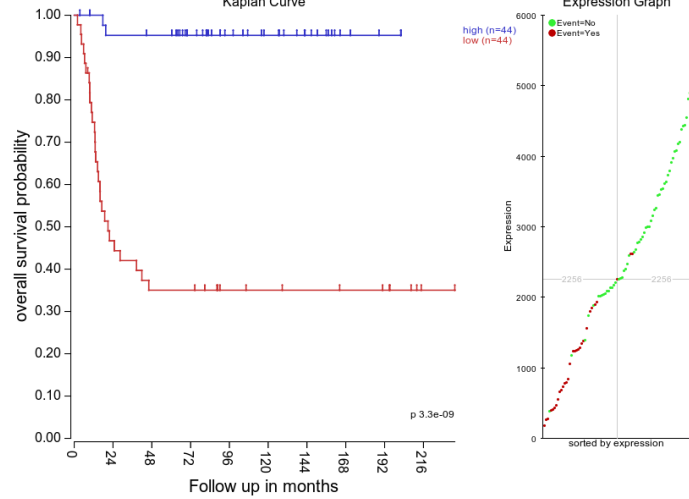
Sample Filter

Subset track: ⓘ

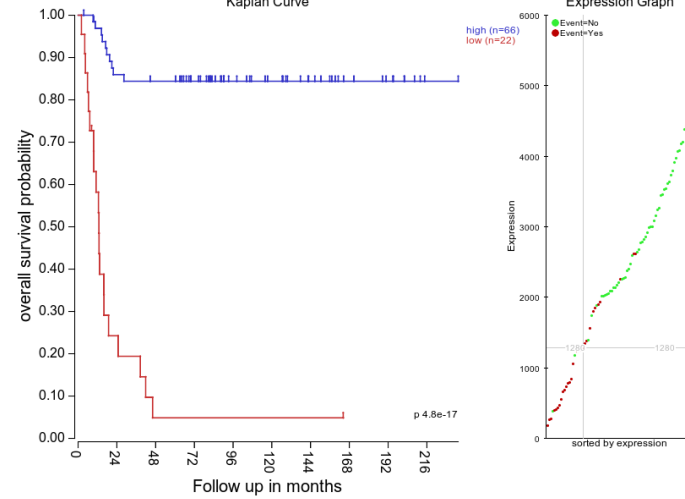
Selected sample subset: None

Other separation methods

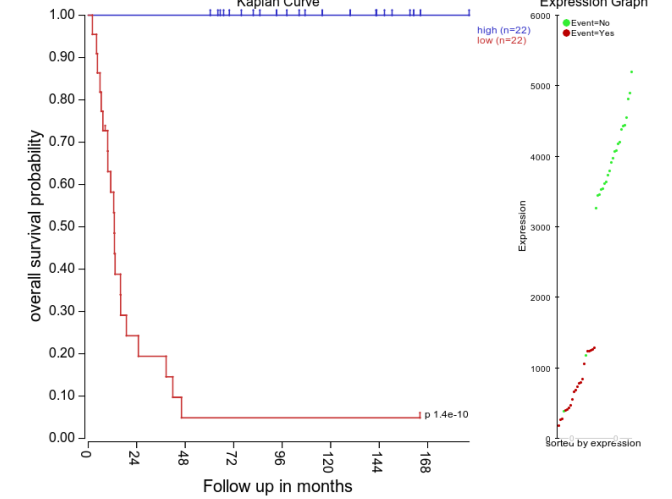
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 2255.8



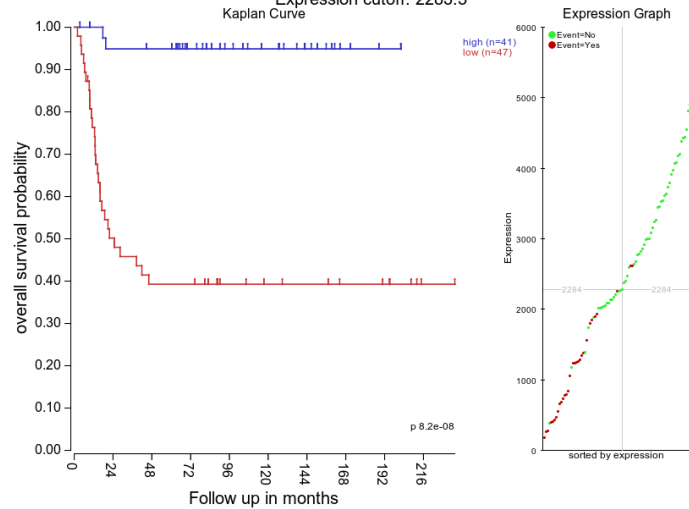
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 1279.5



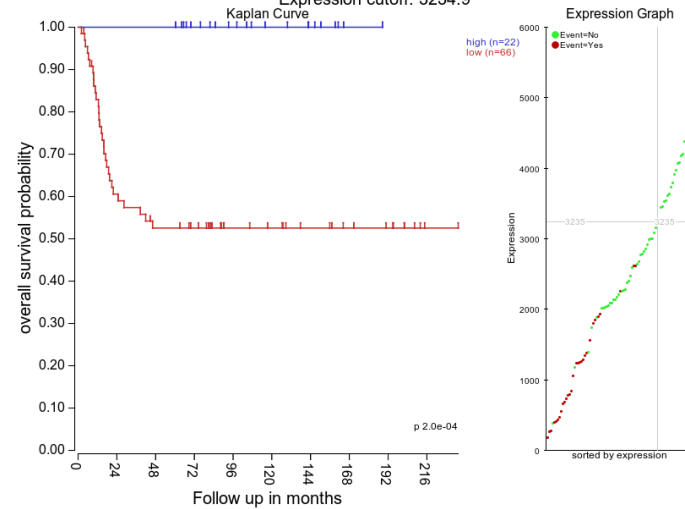
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff:



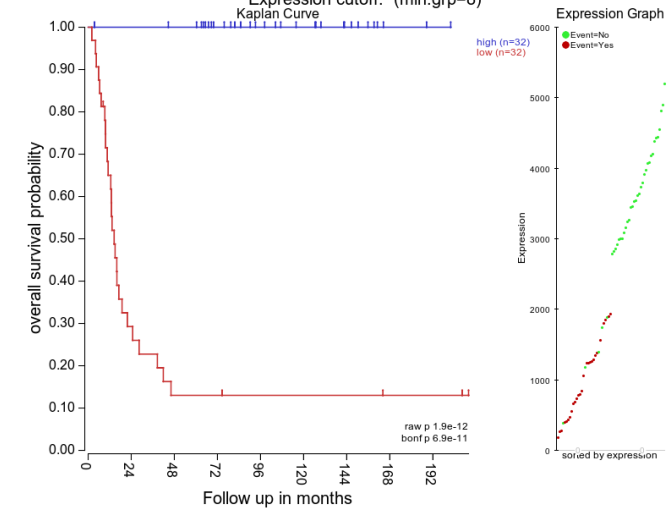
Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
PMP22 (210139_s_at)
Expression cutoff: 2283.5



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

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

Show as track: **Temporary (24hrs)**

Where: **Temporary (24hrs)**

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

Gene set: GS:Oncogenesis (449)

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

	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](#)

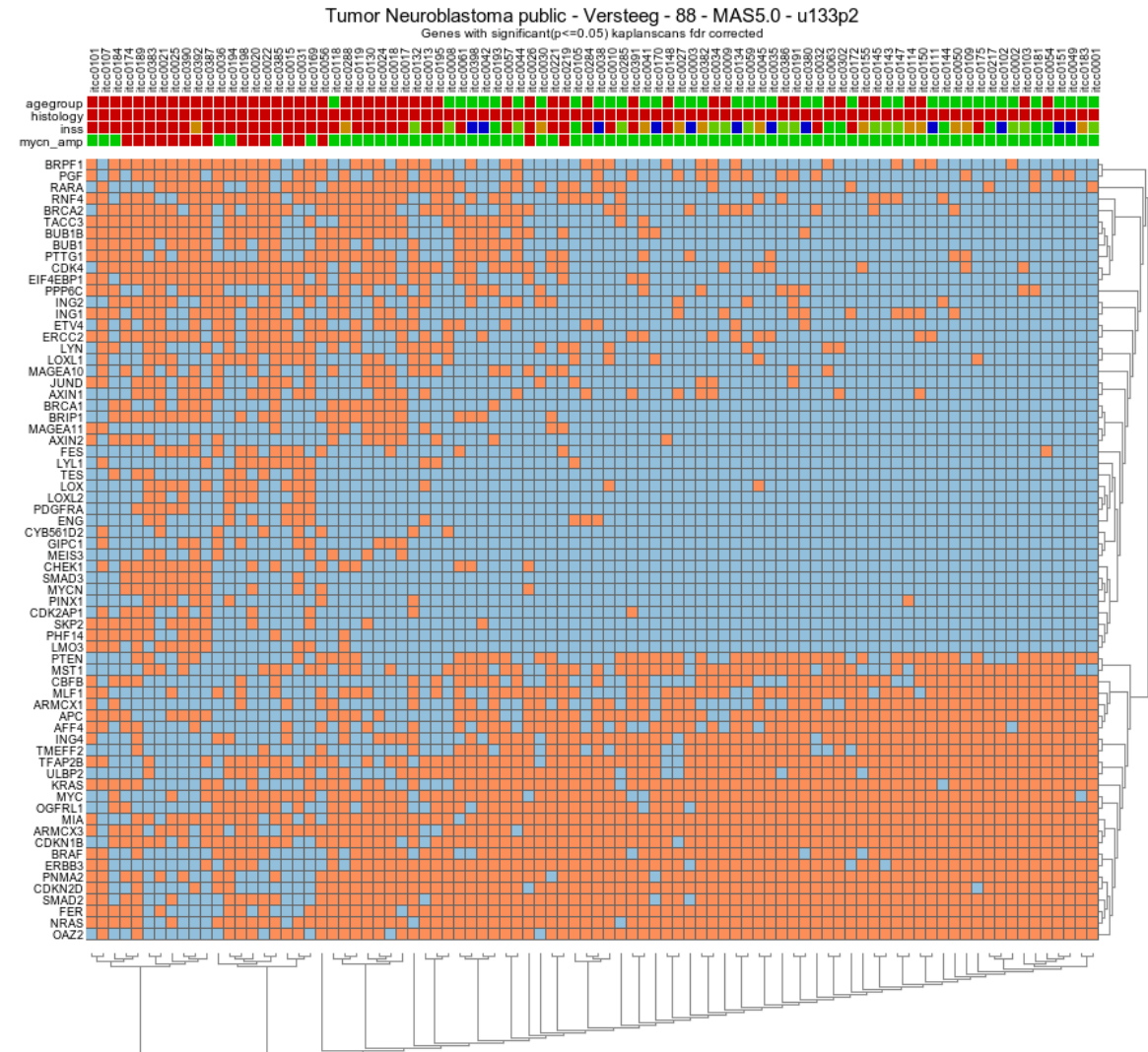
R2: Kaplan Meier Scanner Pro

[Online Tutorial](#)

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

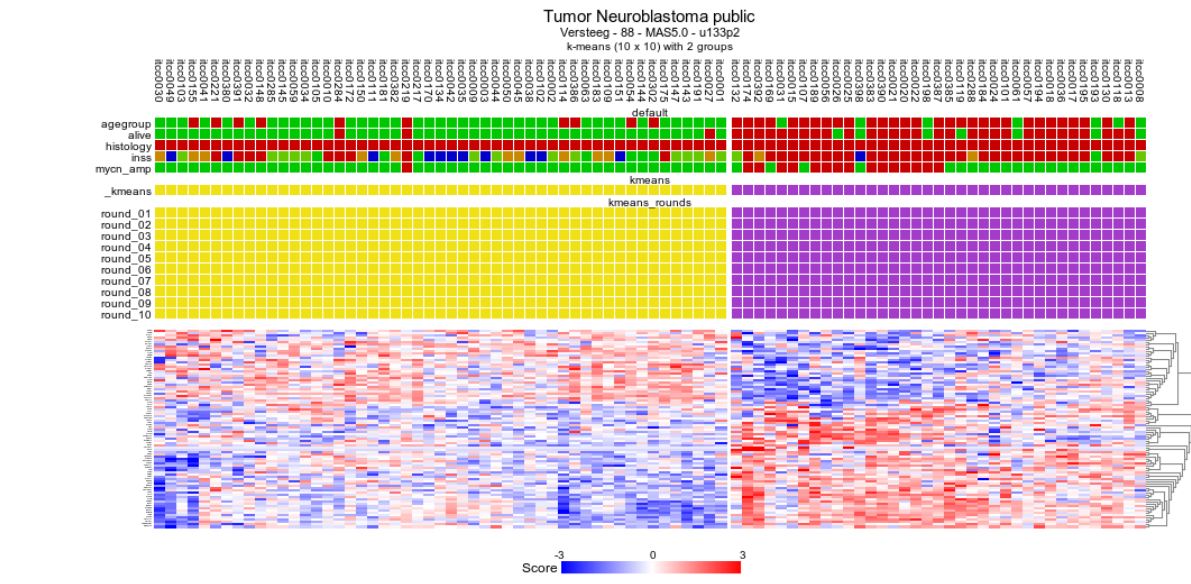
88 samples, gene set: Oncogenesis
Results corrected for multiple gene testing by fdr
68 out of 315 genes found where $p < 0.05$

#	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	R#	n_value	Gold Desc	Gene Symbols
9978	18	5	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	1. DNA damage response, signal transduction resulting in transcription (6.8)	CHEK2, MUC1, BRCA1, BRCA2, TP53
50681	43	7	2. androgen receptor binding (7.8)	DXDX, DD3, FOXP1, SMARCA4, BRCA1, NCOA1, CCNE1
20241	83	8	1. androgen receptor signaling pathway (8.10)	DAXX, DD3, FOXF1, SMARCA4, BRCA1, NCOA1, CCNE1, MED12
217	24	5	2. DNA secondary structure binding (6.6)	MSH6, MEN1, BLM, WRN, RECQL4
22382	82	9	1. DNA geometric change (7.7)	DBP2, ERCC2, HMG1A1, HNRNP2B1, BLM, TP53, WRN, BRIP1, RECQL4
2114	396	20	1. response to radiation (4.4)	CHEK2, CREB1, DDX1, DNMT3A, ERCC2, FANCD2, GNAQ, MSH6, KRAS, MEN1, MYC, NTRK1, PIK3R1, CCND1, BLM, BRCA1, BRAF, BRCA2, TP53, WRN
126	25	5	1. strand displacement (5.9)	BLM, BRCA1, BRCA2, WRN, BRIP1
13332	53	7	1. response to gamma radiation (6.6)	CHEK2, FANCD2, MEN1, MYC, BRCA2, TP53, WRN
44427	784	27	3. chromosomal part (4.9)	CDK4, CHEK2, CREB1, DAXX, DD3, DNMT3A, MSH6, HMG1A1, HNRNP2B1, APC, MEN1, MUC1, MYC, MYCN, CCNB1P1, RARA, BLM, SMARCA4, BRCA1, BRCA2, TCF3, BUB1B, TP53, TPR, WRN, NCOA1, RECQL4
6258	897	29	1. DNA metabolic process (5.7)	CHEK2, DBP2, DNMT3A, ERCC2, FANCA, FANCD2, FANCF, MSH6, HMG1A1, HNRNP2B1, MEN1, MYC, NFB, NONO, PDGFRA, CCNB1P1, BLM, MAP2K4, SET, BRCA1, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, BRIP1, CCNE1, RECQL4
5994	904	29	3. chromosome (5.8)	CDK4, CHEK2, CREB1, DAXX, DD3, DNMT3A, FANCD2, MSH6, HMG1A1, HNRNP2B1, APC, MEN1, MUC1, MYC, MYCN, CCNB1P1, RARA, BLM, SMARCA4, BRCA1, BRCA2, TCF3, BUB1B, TP53, TPR, WHSC1, WRN, NCOA1, RECQL4
19212	148	19	1. response to ionizing radiation (5.5)	CHEK2, DNMT3A, FANCD2, MEN1, MYC, CCND1, BLM, BRCA1, BRCA2, TP53, WRN
39538	128	10	1. intracellular steroid hormone receptor signaling pathway (5.9)	DAXX, DD3, FOXF1, SMARCA4, BRCA1, RUNX1, NCOA1, CFB, CCNE1, MED12
8411	130	10	1. response to UV (6.6)	DBP2, ERCC2, MSH6, MEN1, MYC, PIK3R1, CCND1, BRCA2, TP53, WRN
3884	85	7	2. damaged DNA binding (6.6)	DBP2, MSH6, BLM, BRCA1, TP53, WRN, RECQL4
2415	289	14	1. response to light stimulus (5.5)	CREB1, DBP2, ERCC2, GNAQ, MSH6, KRAS, MEN1, MYC, PIK3R1, CCND1, BRAF, BRCA2, TP53, WRN
6501	34	5	2. ATP-dependent DNA helicase activity (5.11)	ERCC2, BLM, WRN, BRIP1, RECQL4
13580	306	19	1. cellular response to drug (5.5)	CDK4, CHEK2, DAXX, DNMT3A, GNAQ, MYB, MYC, NTRK1, PTEN, BLM, BRCA1, BRAF, TFR3, TP53, NCOA1
23232	619	22	1. cellular response to hormone stimulus (5.6)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DD3, FOXF1, GNAQ, APC, MEN1, MSN, PIK3R1, PTEN, RARA, SMARCA4, BRCA1, BRIP1, RUNX1, NCOA1, CFB, CCNE1, MED12
20035	91	8	2. purine NTP-dependent helicase activity (9.9)	DD3, DD3, DD3, ERCC2, BLM, WRN, BRIP1, RECQL4
45935	1497	36	1. positive regulation of nucleosome-containing compound metabolic process (9.7)	NCOA2, CHEK2, CREB1, DDX3, ERCC2, ETV4, CANT1A1, MSH6, HMG1A1, HNRNP2B1, LY1, MEN1, MUC1, MYB, MYC, MYCN, NFB, PAX5, PDGFRA, PIK3R1, RARA, BLM, MAP2K4, SMARCA4, BRCA1, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, RUNX1, NCOA1, CFB, CCNE1, MED12
10694	2640	50	1. positive regulation of macromolecule metabolic process (4.0)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DD3, ERF15, ERCC2, ETV4, CANT1A1, MSH6, HMG1A1, HNRNP2B1, APC, BUB1, KRAS, LY1, MEN1, MSN, MUC1, MYB, MYC, MYCN, NFB, NTRK1, PAX5, PDGFRA, PIK3R1, FEV, PTEN, RARA, CCND1, BLM, MAP2K4, SMARCA4, BRCA1, BRAF, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, ASPSCR1, RUNX1, NCOA1, CFB, FUBP1, CCNE1, MED12
32527	144	10	2. nuclear hormone receptor binding (5.6)	NCOA2, DAXX, DD3, FOXF1, HMG1A1, SMARCA4, BRCA1, NCOA1, CCNE1, MED12
8724	857	26	1. response to hormone (4.5)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DD3, DNMT3A, FOXF1, GNAQ, APC, KRAS, MEN1, MSN, PIK3R1, PTEN, RARA, CCND1, SMARCA4, BRCA1, BRAF, BRIP1, RUNX1, NCOA1, CFB, CCNE1, MED12
42463	179	3	1. steroid hormone mediated signaling pathway (5.8)	DAXX, DD3, FOXF1, RARA, SMARCA4, BRCA1, RUNX1, NCOA1, CFB, CCNE1, MED12
22588	72	7	1. DNA duplex unwinding (8.8)	DBP2, ERCC2, HMG1A1, BLM, WRN, BRIP1, RECQL4
6974	754	24	1. cellular response to DNA damage stimulus (5.5)	CHEK2, DBP2, DDX3, ERCC2, FANCA, FANCD2, FANCF, MSH6, HMG1A1, APC, MEN1, MUC1, MYC, NONO, PIK3R1, CCND1, BLM, BRCA1, BRCA2, TP53, WHSC1, WRN, BRIP1, RECQL4
8993	2918	51	1. positive regulation of metabolic process (3.5)	CDK4, NCOA2, CHEK2, CREB1, DAXX, DD3, ERF15, ERCC2, ETV4, CANT1A1, MSH6, HMG1A1, HNRNP2B1, APC, BUB1, KRAS, LY1, MEN1, MSN, MUC1, MYB, MYC, MYCN, NFB, NTRK1, PAX5, PDGFRA, PIK3R1, FEV, PTEN, RARA, CCND1, BLM, MAP2K4, SMARCA4, BRCA1, BRAF, BRCA2, TCF3, TFR3, TP53, WHSC1, WRN, ASPSCR1, RUNX1, NCOA1, CFB, FUBP1, CCNE1, MED12
12565	875	26	2. sequence-specific DNA binding (6.6)	NCOA2, CREB1, ETV4, CANT1A1, FOXF1, HMG1A1, HNRNP2B1, HOD1, LYL1, MUC1, MYB, MYC, MYCN, NFB, NONO, PAX5, FEI1, RARA, BLM, SMARCA4, TCF3, TP53, WHSC1, WRN, RUNX1, MED12
51235	1077	29	1. chromosome organization (5.5)	DAXX, DBP2, DNMT3A, ERCC2, FANCD2, MSH6, HMG1A1, HNRNP2B1, APC, MEN1, MUC1, MYB, MYC, MYCN, NFB, CCNB1P1, 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
```

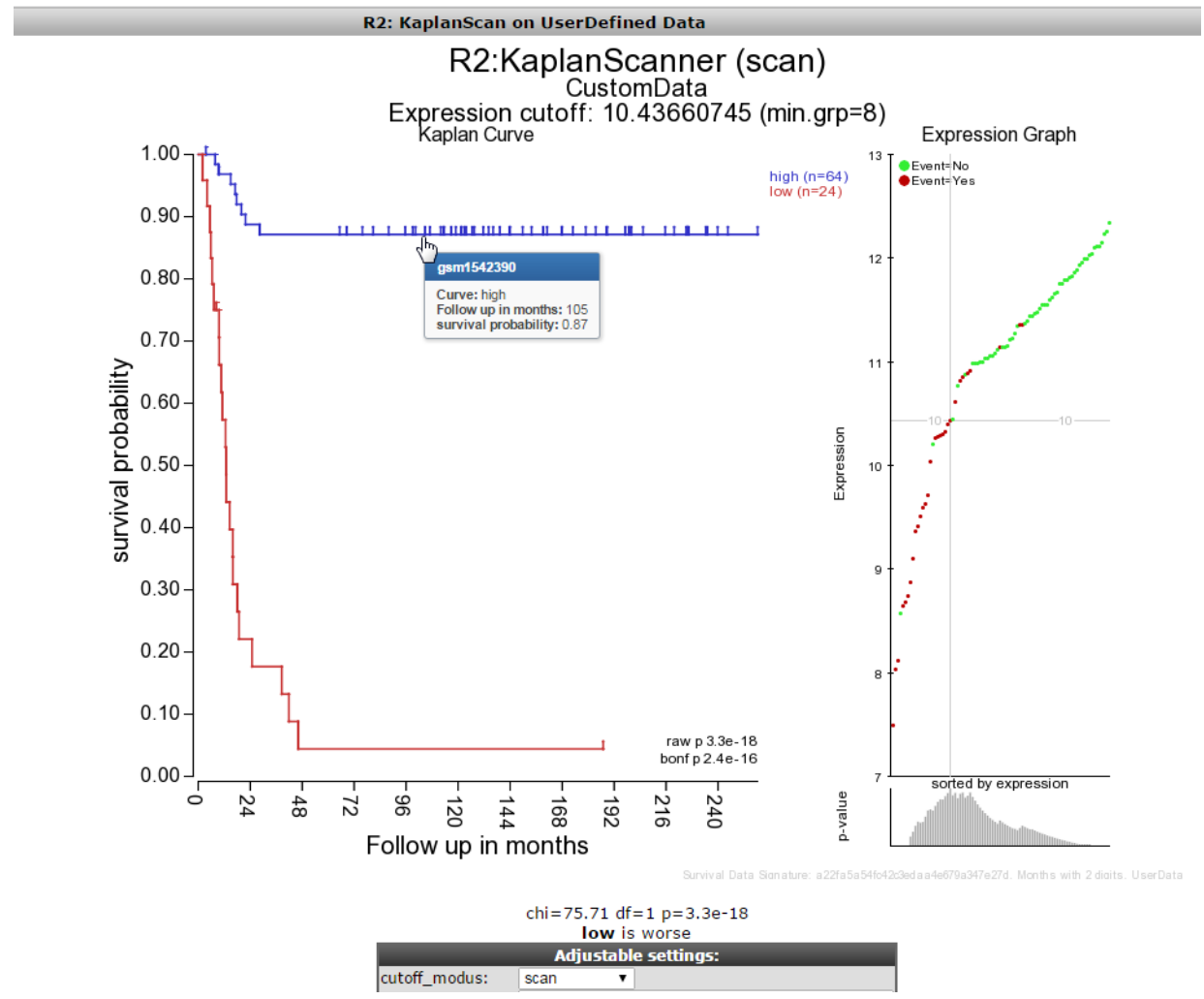
Cutoff mode: ▾

Survival time
In days

Event
yes/no/0/1

Numerical values
e.g. Expression Gene X

KaplanScanner Custom Data

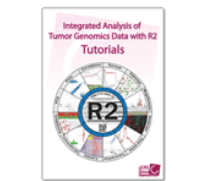


View a GeneSet (Heatmap)



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]

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

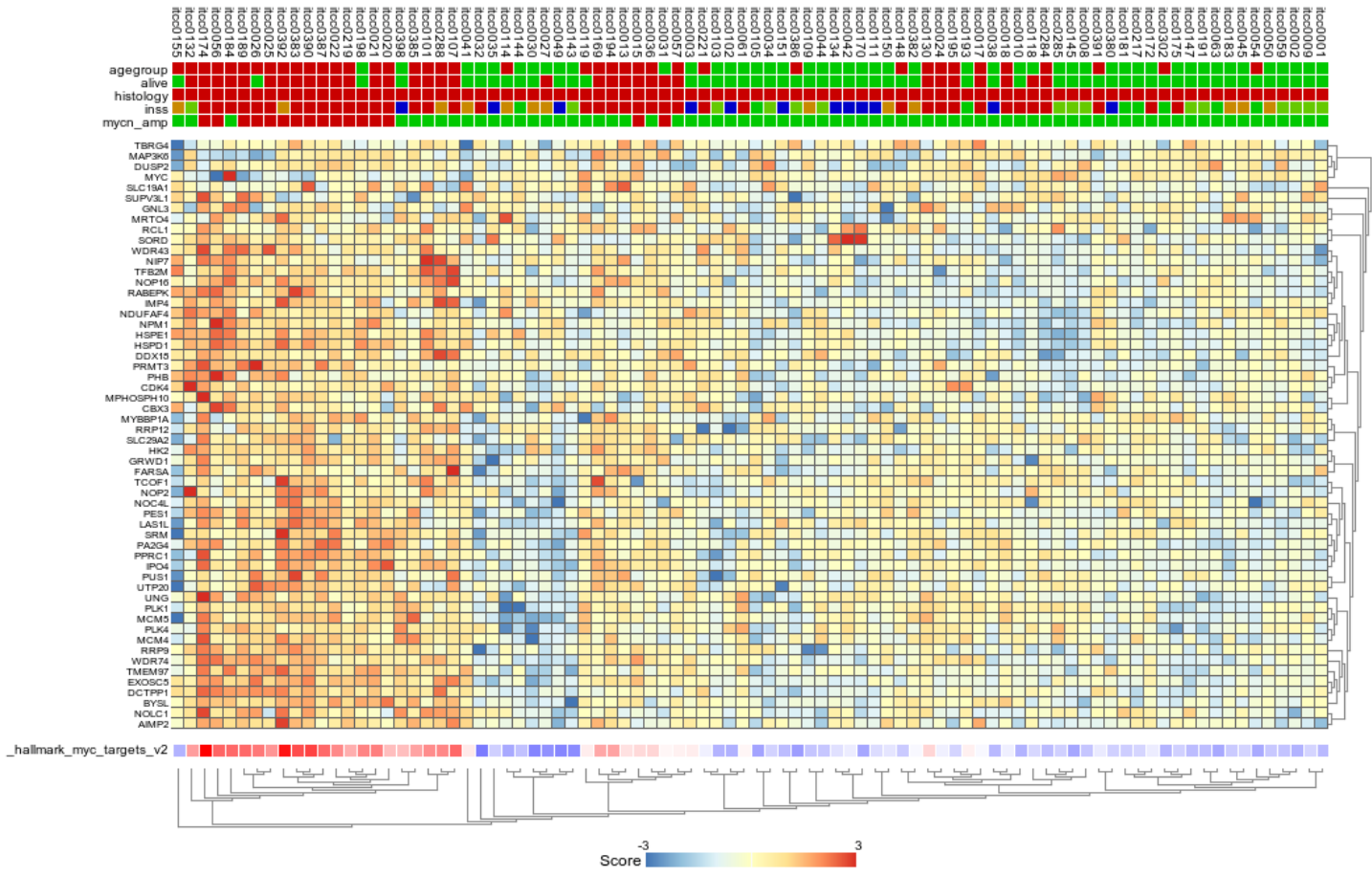
Clear selection

Confirm selection

cluster

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

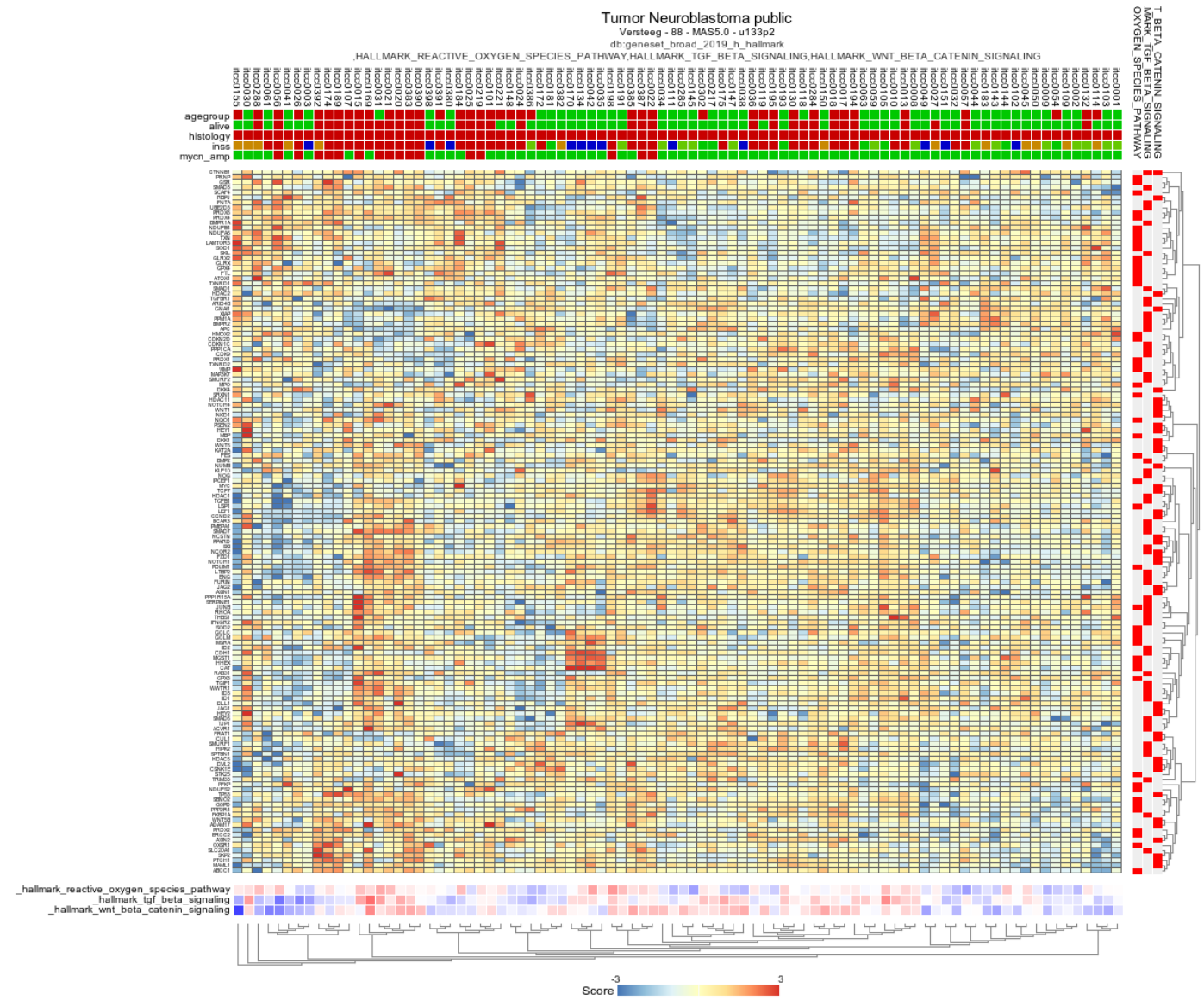
HALLMARK_WNT_BETA_CATENIN_SIGNALING

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:

- a track
- clustering
- a track
- expression of a gene
- user defined order

Search for:

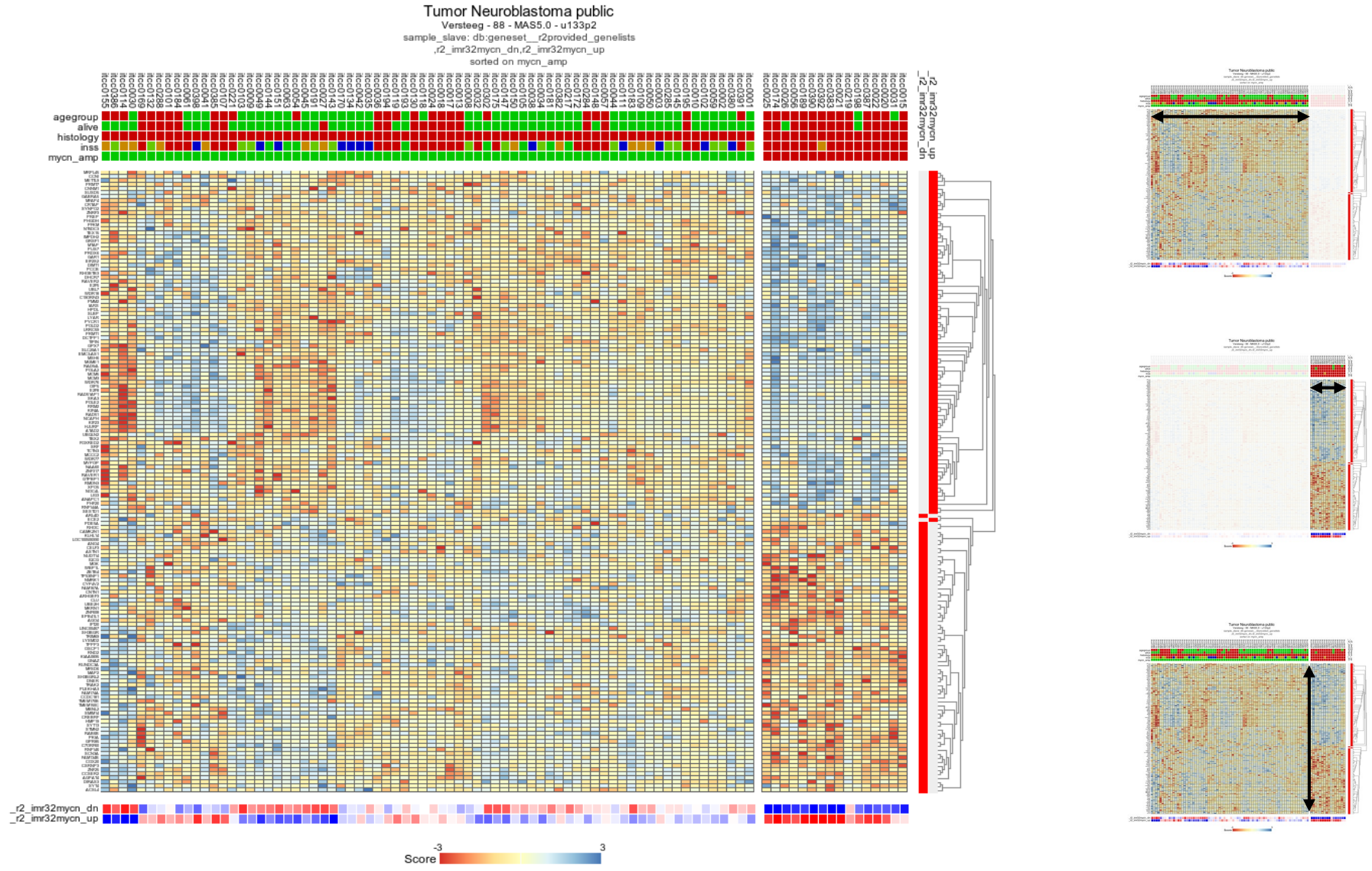
genesets containing a gene:

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

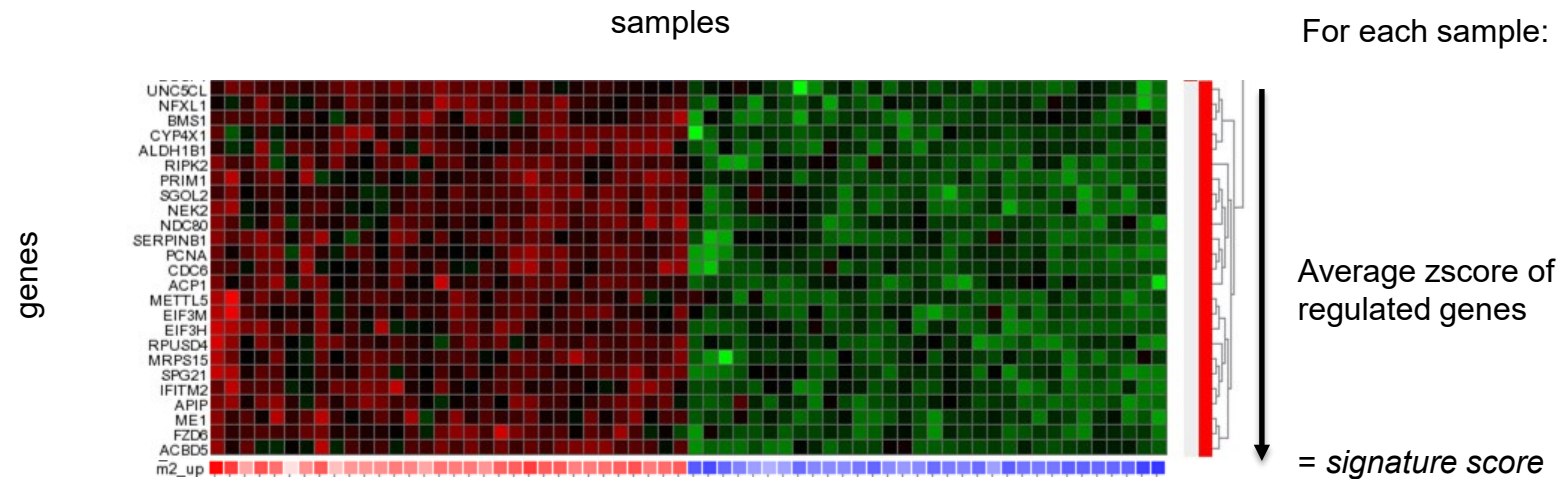


Metagenes

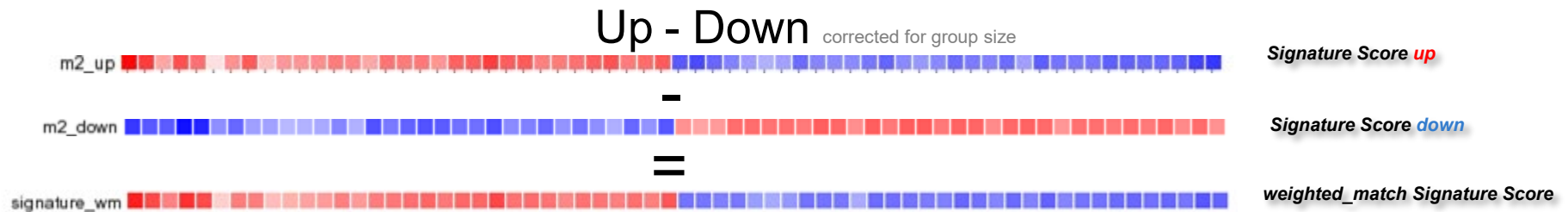
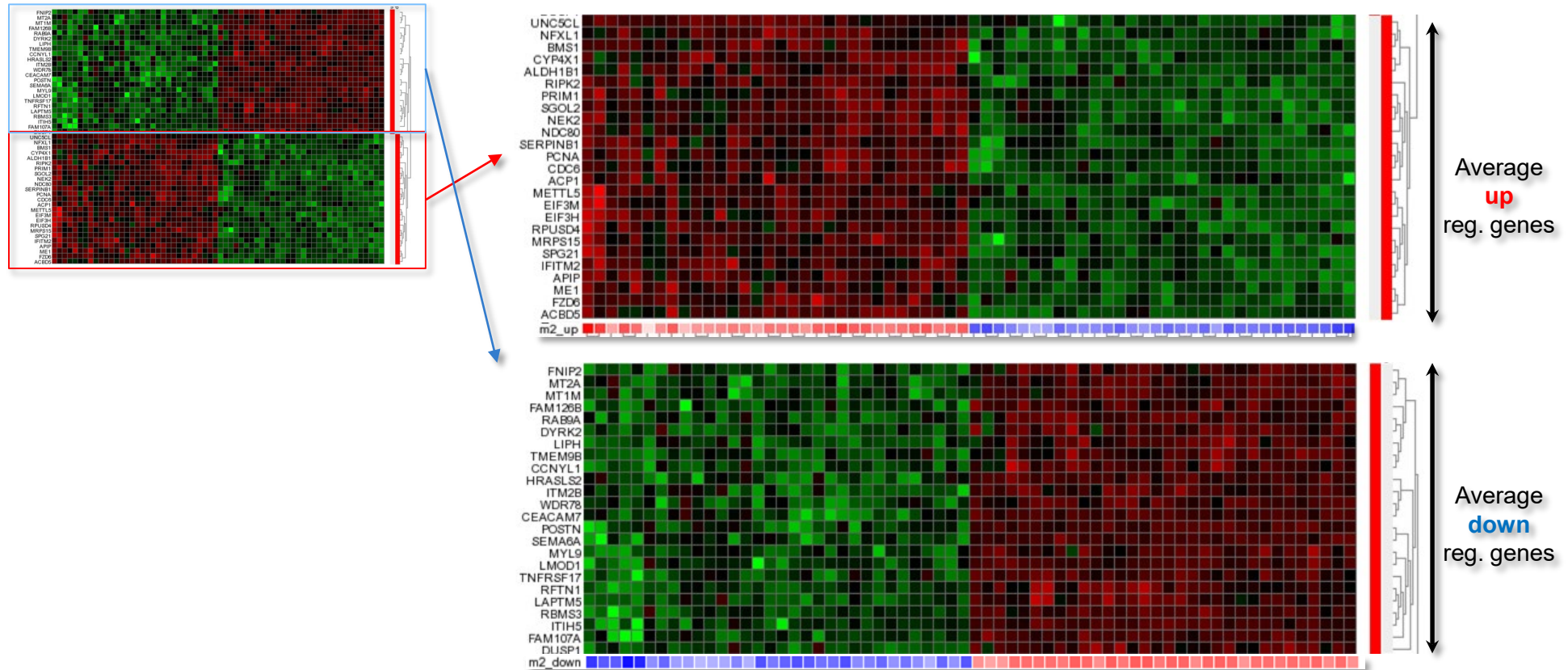
- Convert any list of genes (signature) into a single value, a *signature score*
 - a “summary expression value” of a group of genes for each sample of a dataset
 - Source can be any group of genes (e.g. genecategory)
 - Can be used as if it is one gene (=metagene) to represent a pathway activity for example

Metagene

- How does it work?
 - When all genes in your signature have a common direction



Signature scores are generated in the 'view a geneset' module



Store Signature Scores as Tracks in R2

The screenshot shows the R2 GeneSet (Detail) interface. The main heatmap displays gene expression data for various genes, with a color scale from -3 (green) to 3 (red). Below the heatmap, there are tracks for signature scores: 'r2_imr32mycn_down' (blue), 'r2_imr32mycn_up' (red), and 'r2_imr32mycn_wmatch' (white). A red box highlights the 'r2_imr32mycn_down' and 'r2_imr32mycn_up' tracks, with an arrow pointing to a table of gene set values.

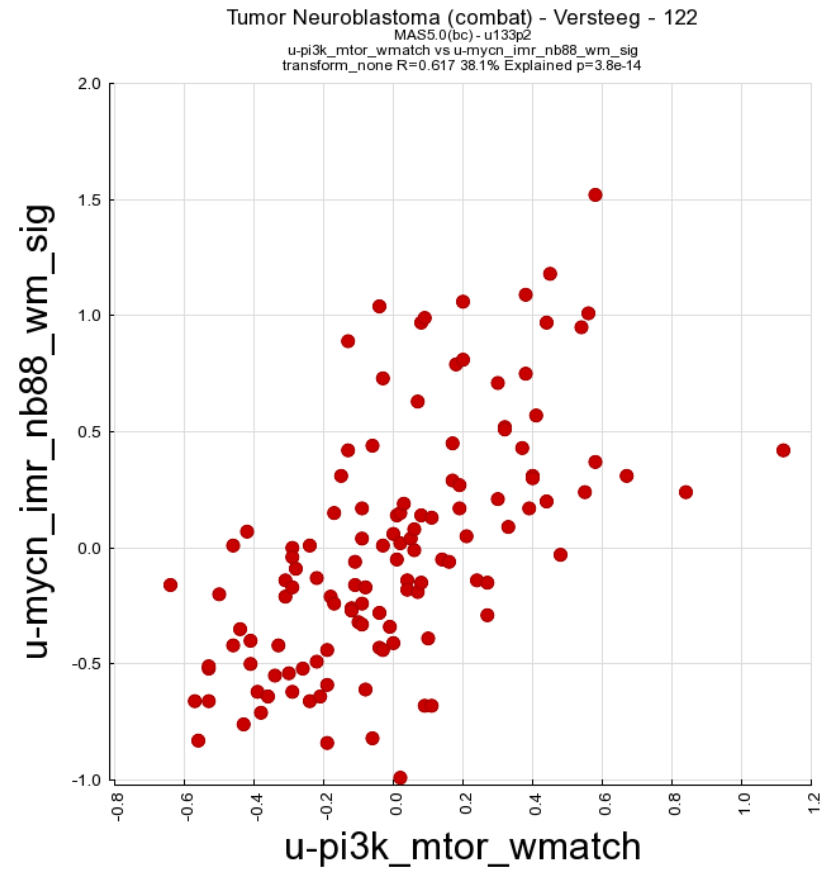
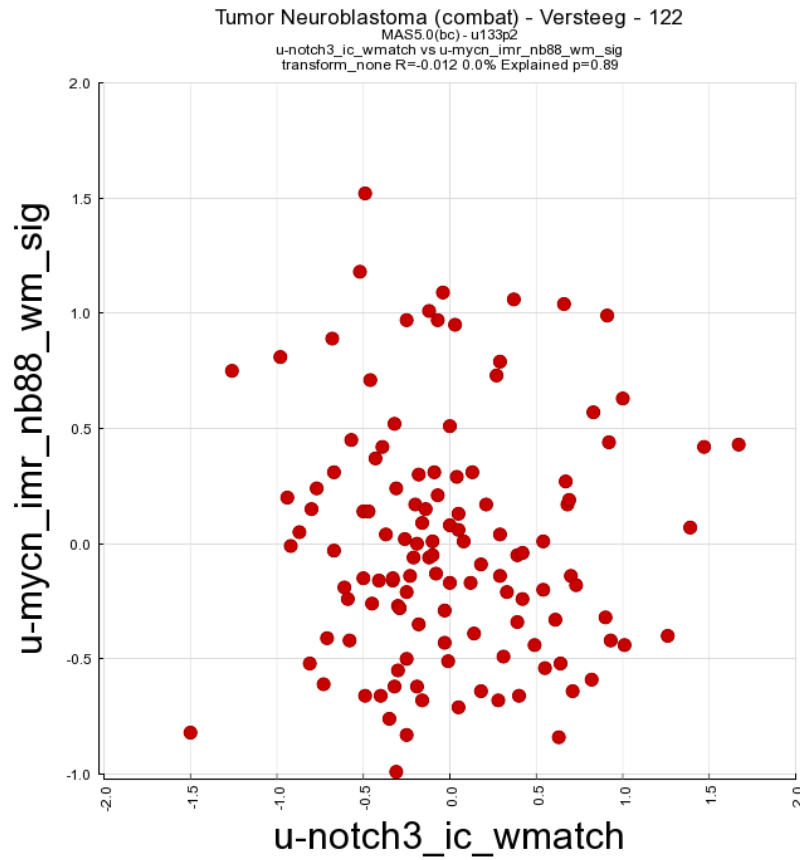
distance:e; linkage:a;
Sort Order Listing
DetailView hyperlink settings
Transform: zscore

Gene set values

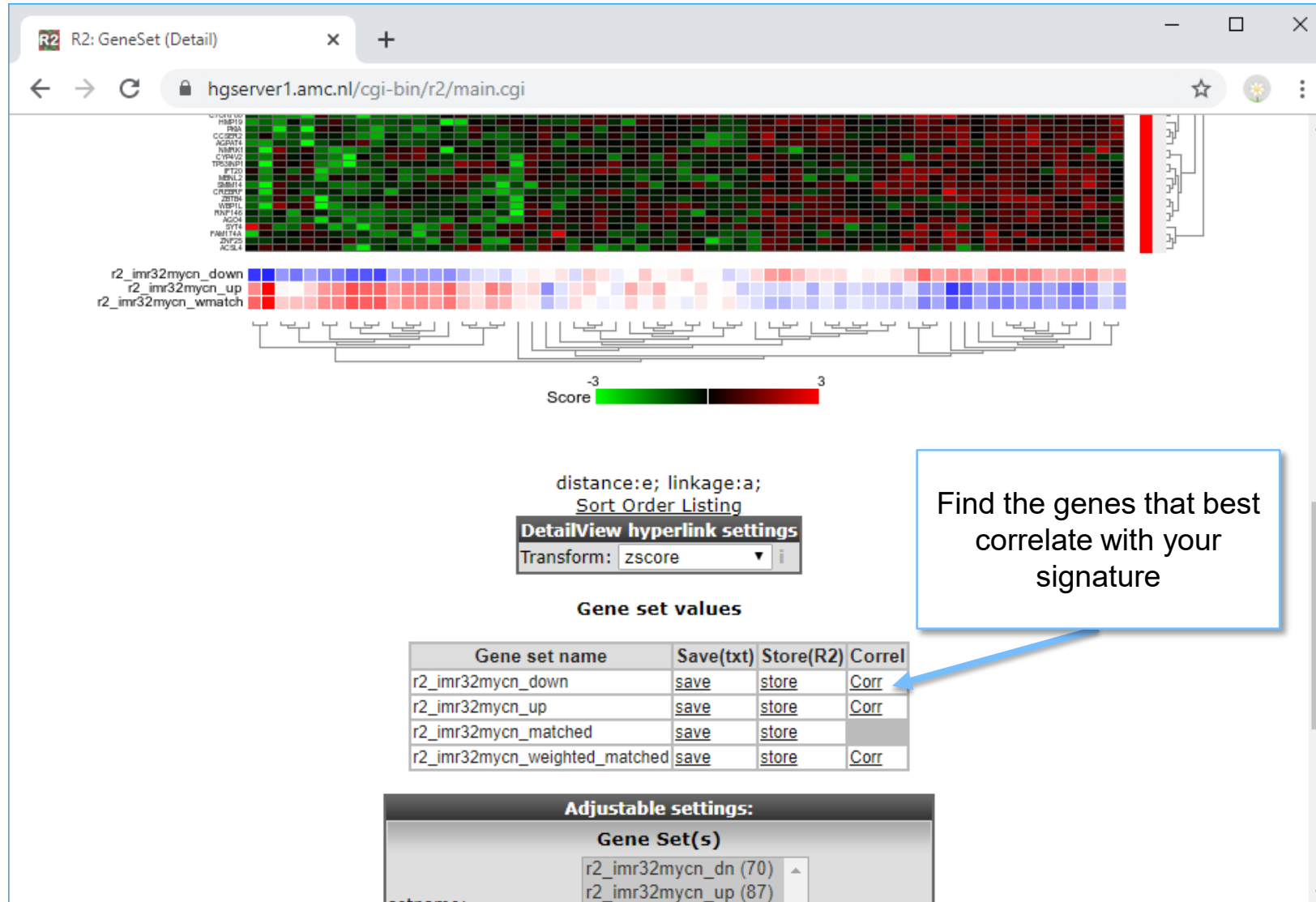
Gene set name	Save(txt)	Store(R2)	Correl
r2_imr32mycn_down	save	store	Corr
r2_imr32mycn_up	save	store	Corr
r2_imr32mycn_matched	save	store	Corr
r2_imr32mycn_weighted_matched	save	store	Corr

Signature scores can be **stored as tracks** in R2 and then used as if they are one gene

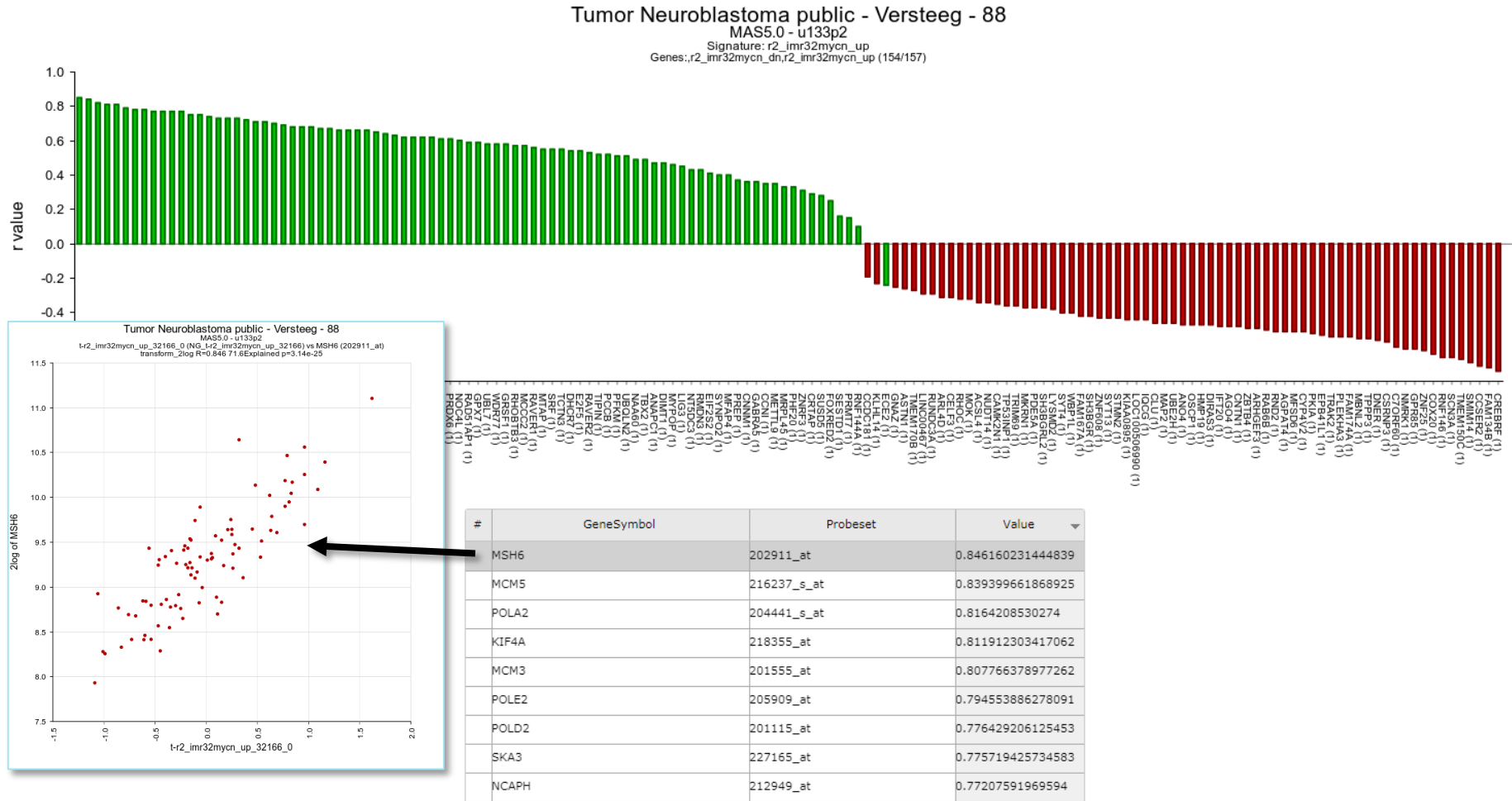
Compare 2 signatures (via relate 2 tracks)



Find best matching signature gene



Signature(s) vs signature genes



Cohort subgroups



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: None ⓘ

Selected sample subset: None

Gene Filters

HugoOnce mode: yes ⓘ

Min. # Present calls: 1 ⓘ

Minimal maximum value: 0 ⓘ

Minimal range size: 0 ⓘ

Chromosome: All ⓘ

Gene ontology: All Search GO

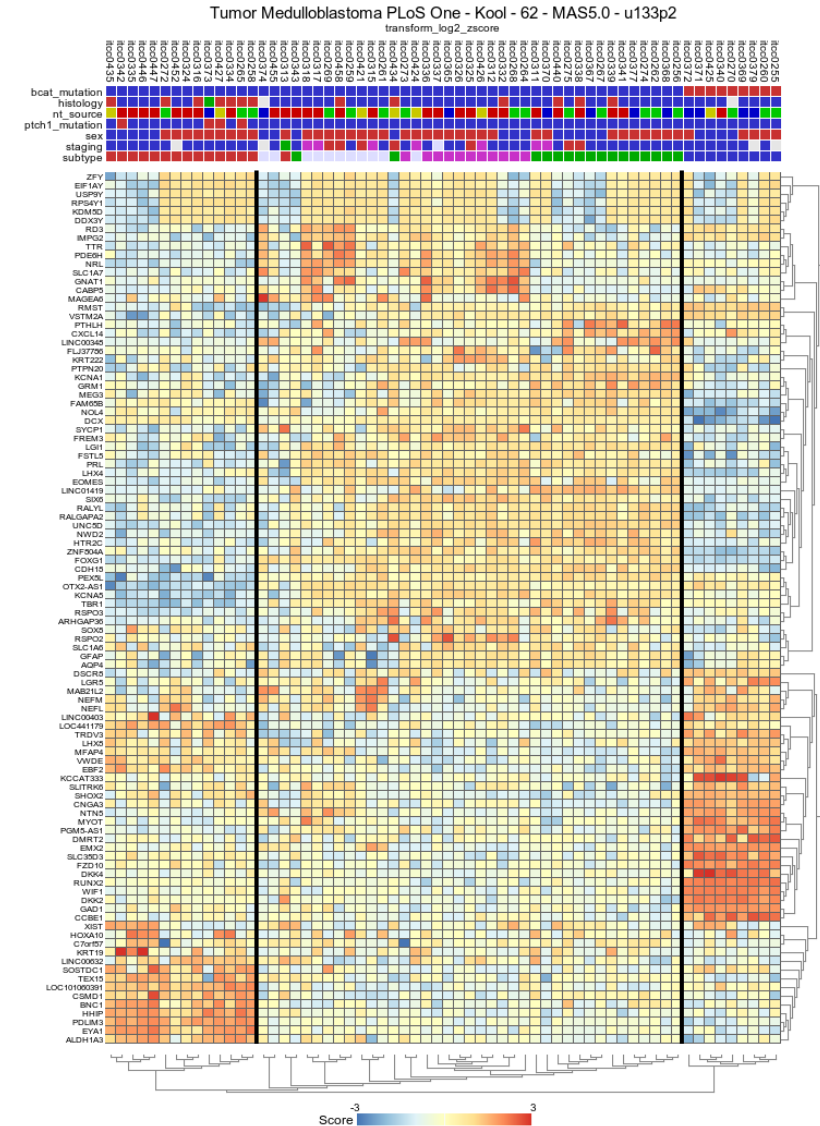
Gene set: Search GS

Manual list: none ⓘ

Next Reset

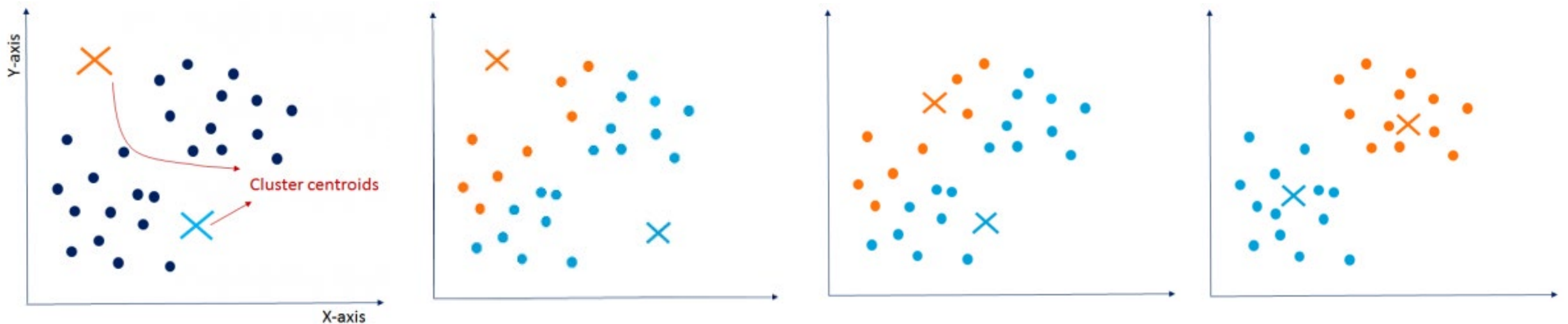
View	Rank	Gene	Reporter	Value
	1	LINC01419	1559213_at	5,2946...
	2	XIST	224588_at	4,3756...
	3	FOXP1	206018_at	4,3274...
	4	RPS4Y1	201909_at	4,1058...
	5	RALGAP2	234314_at	4,0906...
	6	RALYL	213967_at	3,9871...
	7	SHOX2	210135_s_at	3,8976...
	8	LHX8	1569469_a_at	3,8847...
	9	GAD1	205278_at	3,7782...
	10	DDX3Y	205000_at	3,7024...
	11	WIF1	204712_at	3,6922...
	12	HTR2C	207307_at	3,6730...
	13	EMX2	221950_at	3,6010...
	14	EOMES	231776_at	3,5940...
	15	DKK2	219908_at	3,5496...
	16	RMST	229782_at	3,5128...
	17	MFAP4	212713_at	3,4545...
	18	EIF1AY	204409_s_at	3,4509...
	19	PTPN20	215172_at	3,4277...
	20	USP9Y	228492_at	3,4212...
	21	FSTL5	232010_at	3,4148...
	22	CNGA3	207261_at	3,4119...
	23	IMPG2	241856_at	3,3991...
	24	TRDV3	216191_s_at	3,3744...
	25	KCNA5	206762_at	3,3582...
	26	PDE6H	206841_at	3,3328...
	27	SLC1A6	1554593_s_at	3,3287...
	28	NEFM	205113_at	3,3048...
	29	LINC00348	233170_at	3,2960...
	30	LGR5	213880_at	3,2935...
	31	C7ORF57	1557636_a_at	3,2496...

- Save current selection as TXT file
- Heatmap(zscore)
- Gene Ontology Analysis
- Store result as custom gene set



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
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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** PathwayFinder

- 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

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



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: ⓘ

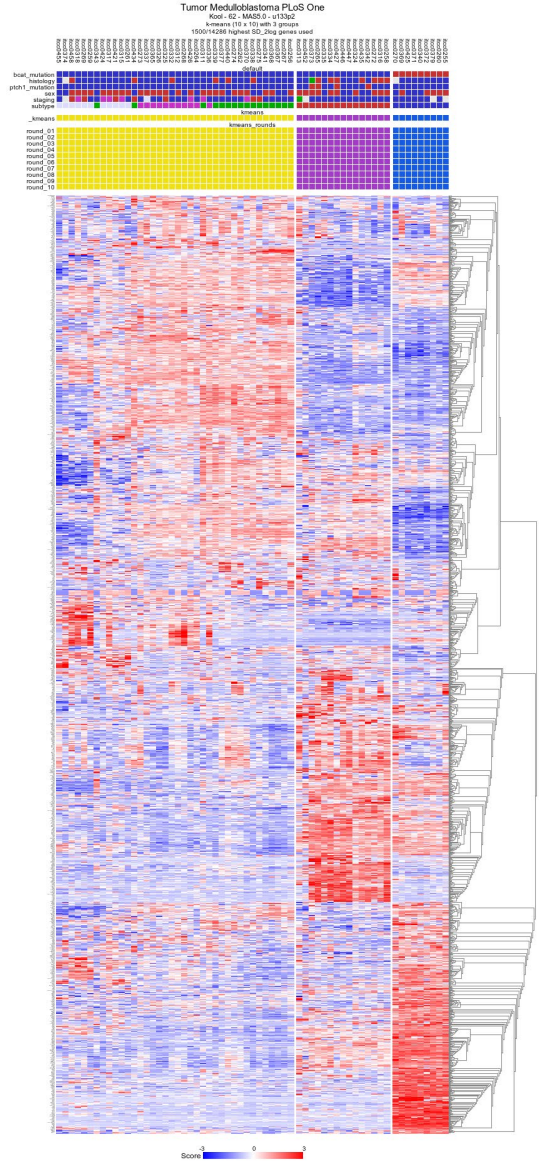
Color scheme: ⓘ

Label track: ⓘ

Heatmap Options

Cell width: ⓘ

Cell height: ⓘ



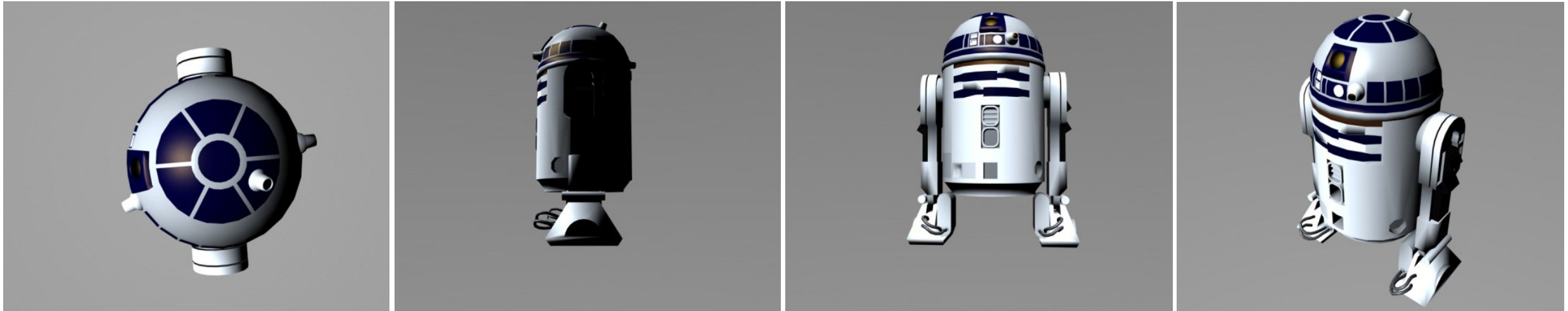
kmeans group vs annotation tracks
Chi-square tests with Yates correction (if 2x2) and Fisher's Exact tests (#groups<30)
NA or ND values are skipped and test is only performed on 'cat' variables

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)

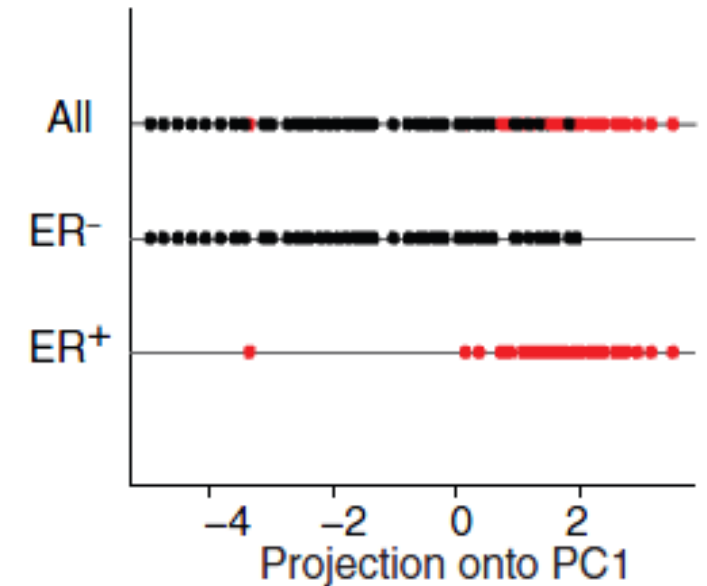
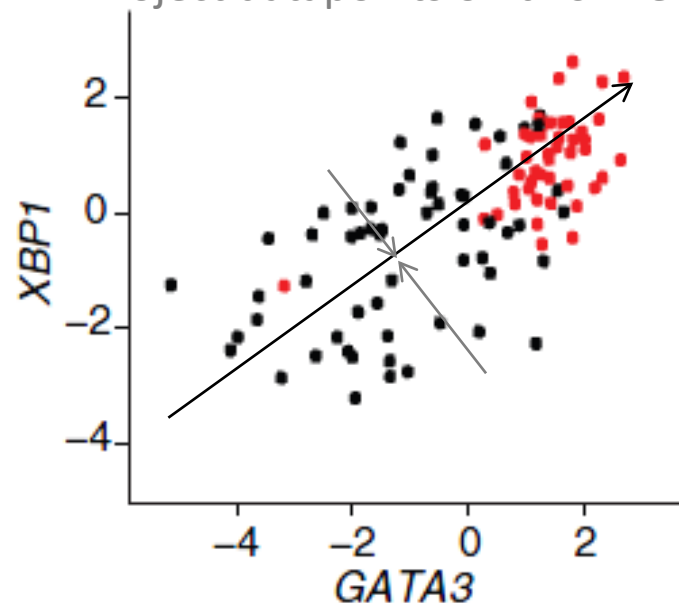
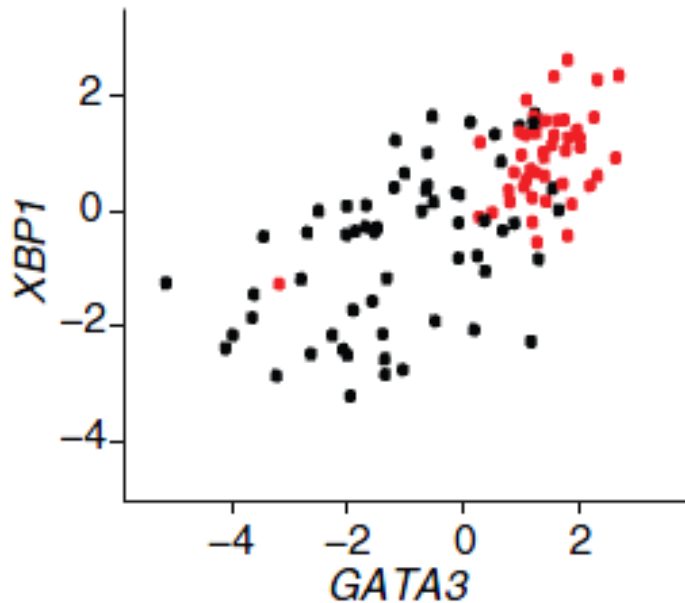
- Describe samples by a very limited number of variables
- Samples that are similar 'cluster' closer together
- Mathematical procedure orthogonal projection (Mathematical procedure) for data reduction
- Nice way of visualizing subgroups



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
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- Genome Browser
- ChIP data
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- 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?

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Financial Supporter of R2



**Individualized
PaediatricCure**

[all news](#)

Using:HGserver1(7)



PubMed



r2.amc.nl



**Video
training**



YouTube



**Integrated Analysis of
Tumor Genomics Data with R2
Tutorials**

**Download the R2
Tutorials Book**

Principal Components Analysis (PCA)

Go to: **Main**

R2: Principle Component Analysis (PCA)

[Online Tutorial](#)

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- Sample maps (UMAP/tSNE)
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- ChIP data
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- Help ▶
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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**

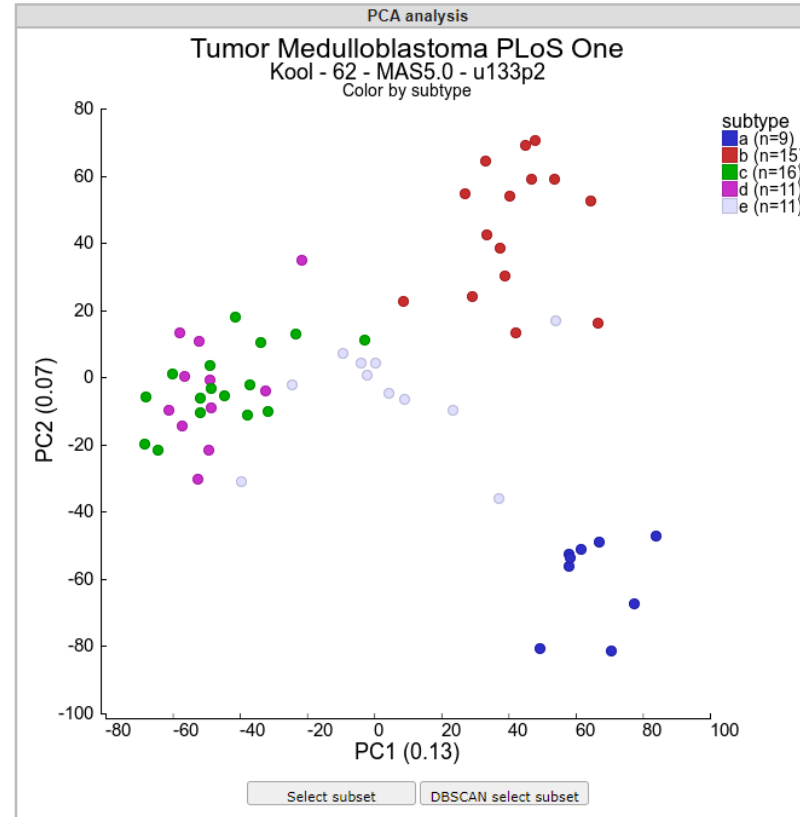
R2: Principle Component Analysis (PCA)

Online Tutorial

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- 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:



Principal Components Analysis (PCA)

Go to: [Main](#)

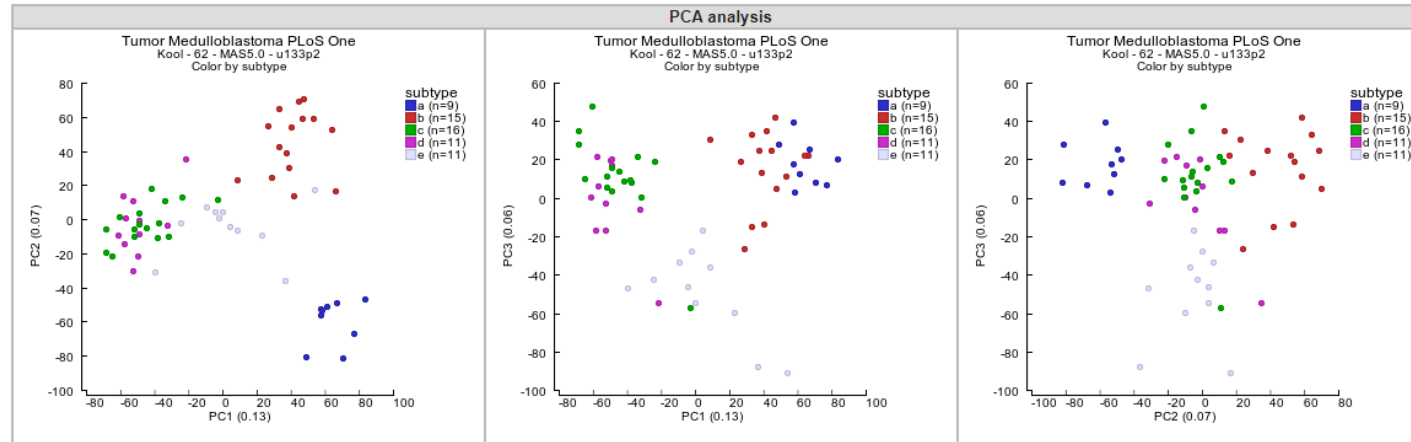
R2: Principle Component Analysis (PCA)

[Online Tutorial](#)

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- Kaplan-Meier
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- Small Tools
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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**

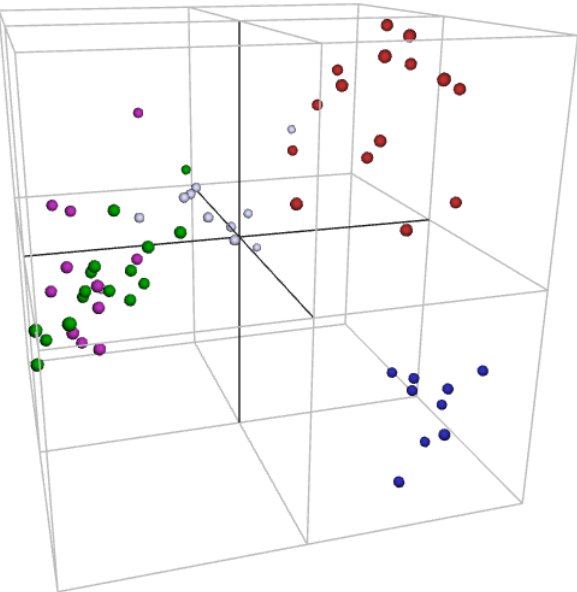
- Main
- Time series
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- ChIP data
- TAR literature
- Change Data Scope >
- User Options >
- Help >
- Contact / About R2

Projection

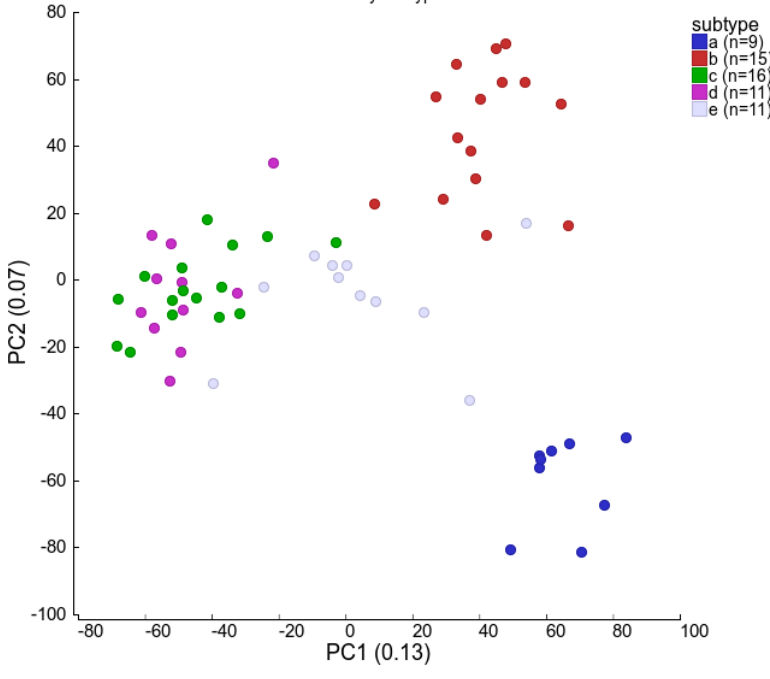
PCA Projection: PC1.PC2.PC3-3D

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 ⓘ

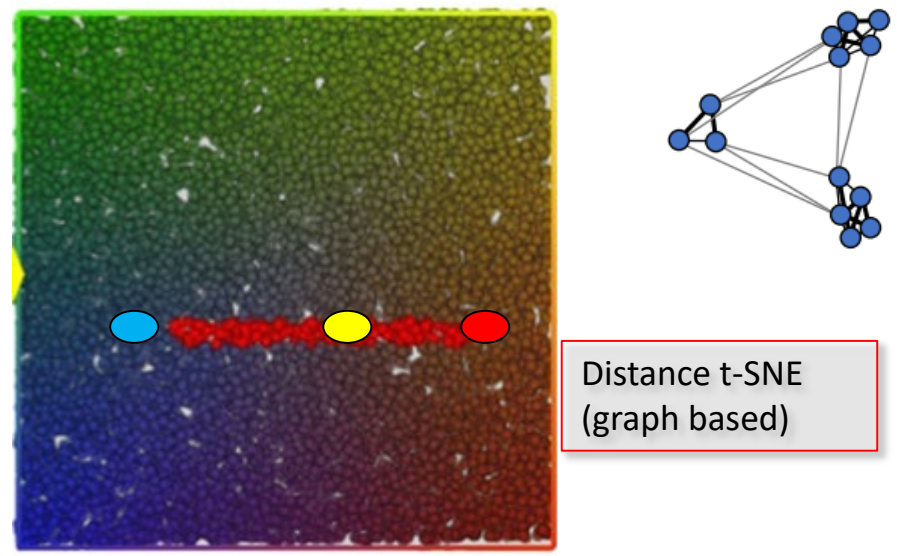
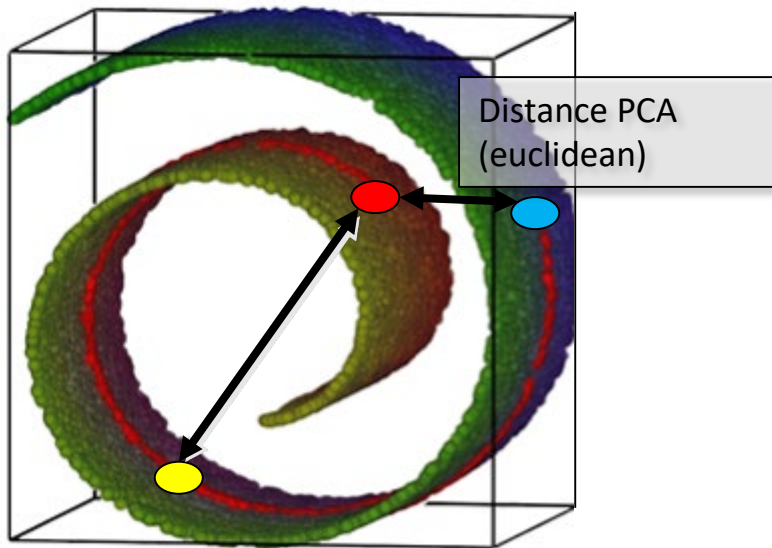
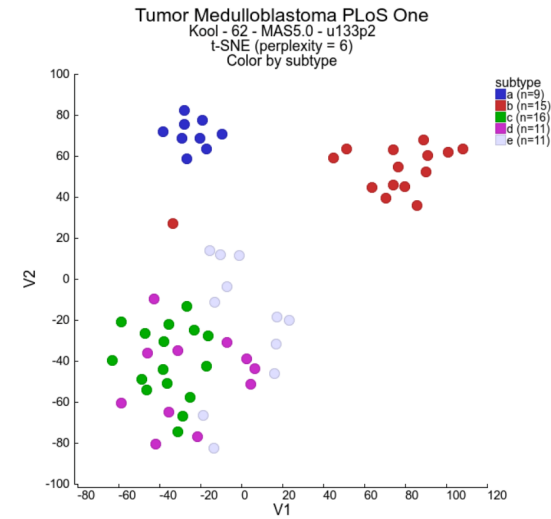
Chromosome: All ⓘ

Gene ontology: All

Gene set:

tSNE/UMAP Analysis

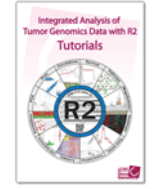
- t-Distributed Stochastic Neighbor Embedding (t-SNE)
 - a technique for dimensionality reduction that is particularly well suited for the visualization of high-dimensional datasets.
 - Has an almost magical ability to create 2-dimensional ‘maps’ of data with thousands of dimensions
 - Non-linear
- Graph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



tSNE/UMAP Analysis

- Go to: Main**
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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

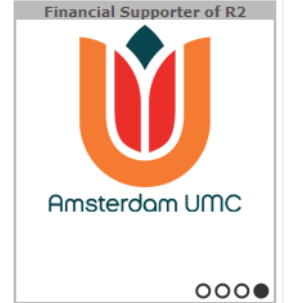
3 Select type of analysis
T-SNE

4 [Additional options in the dropdown menu]

Collaborator or higher
Generate new maps **slow**

Online Tutorial

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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**

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- User Options ▶
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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:

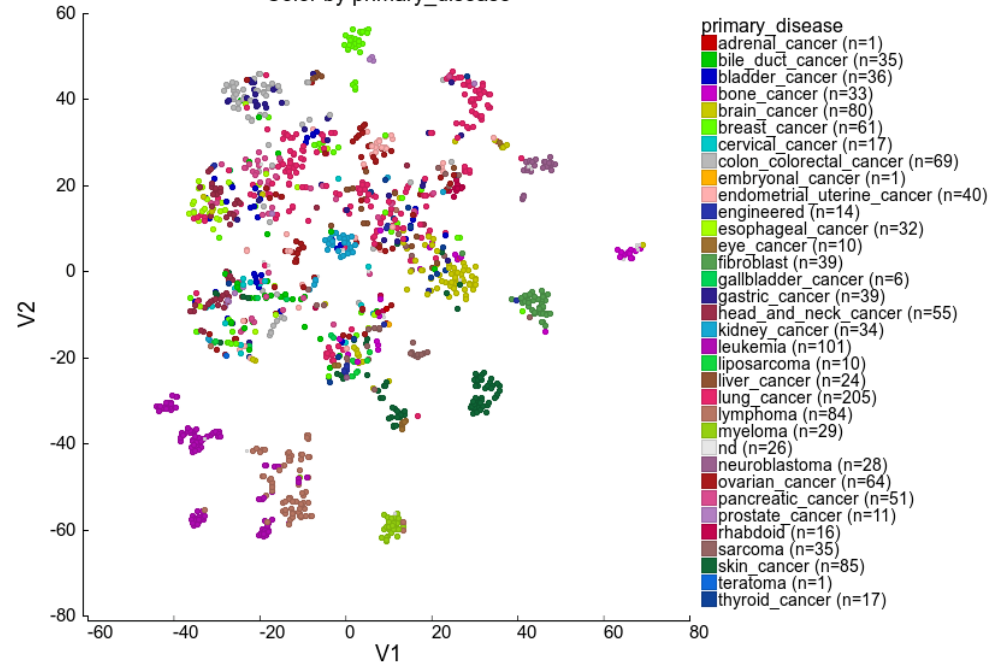
R2 internal identifier: ps_avgpres_ccl21q4a1389_gencode19a

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

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- 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

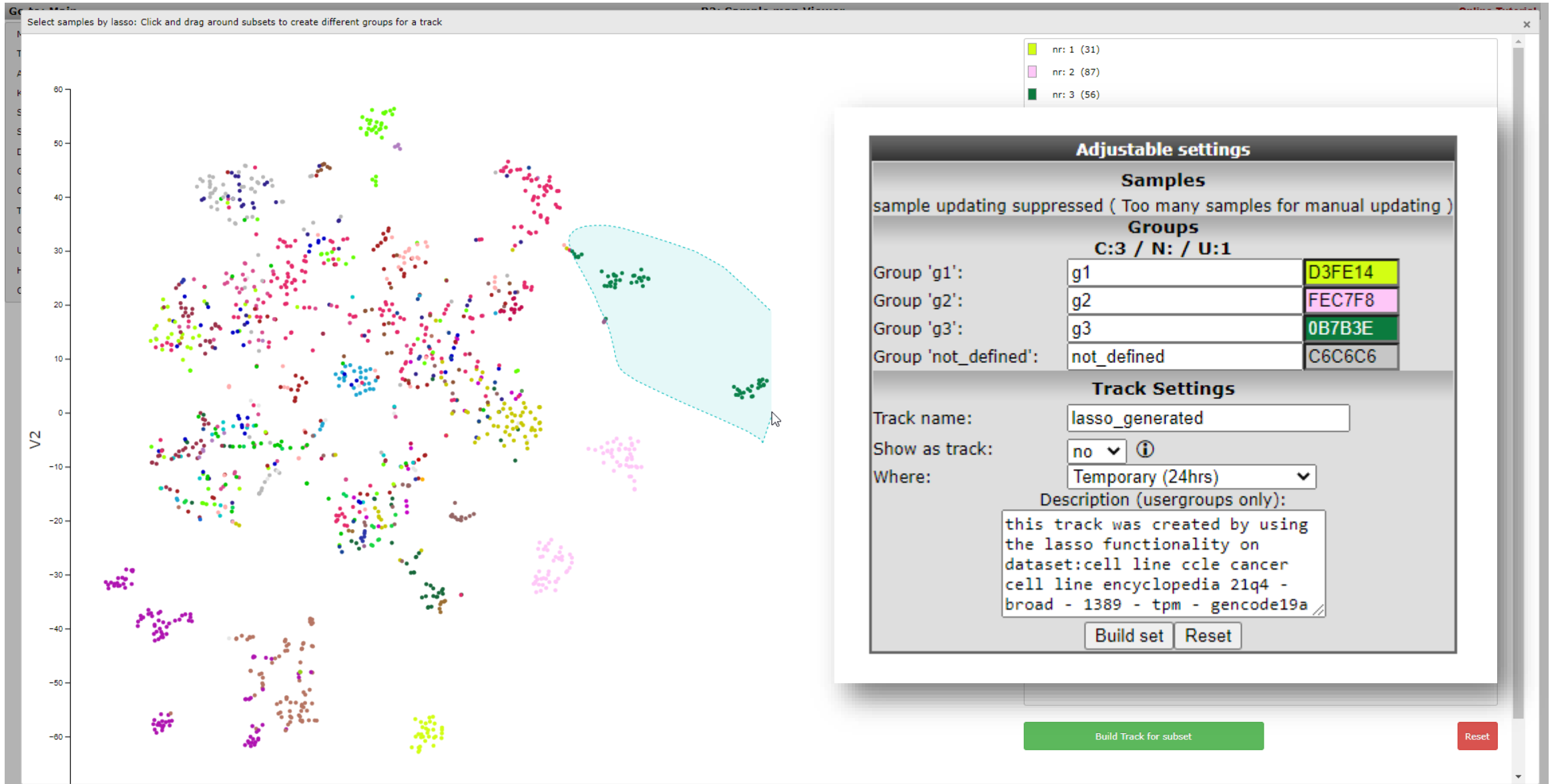
Gene / Reporter: SOX10 ENSG00000100146 advanced

Transformation: Log2

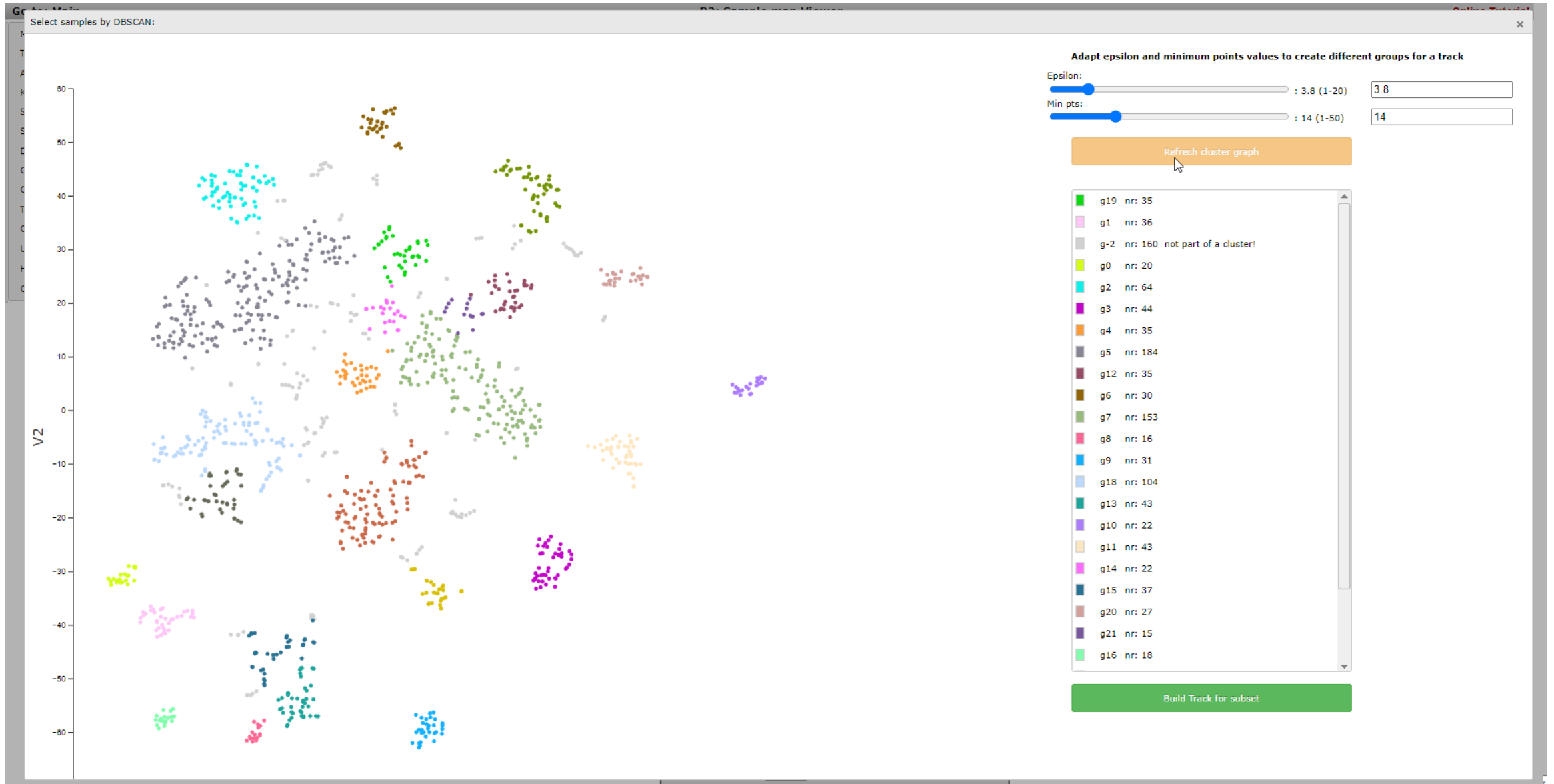
Color scheme: viridis

Submit

tSNE Analysis: lasso



tSNE Analysis



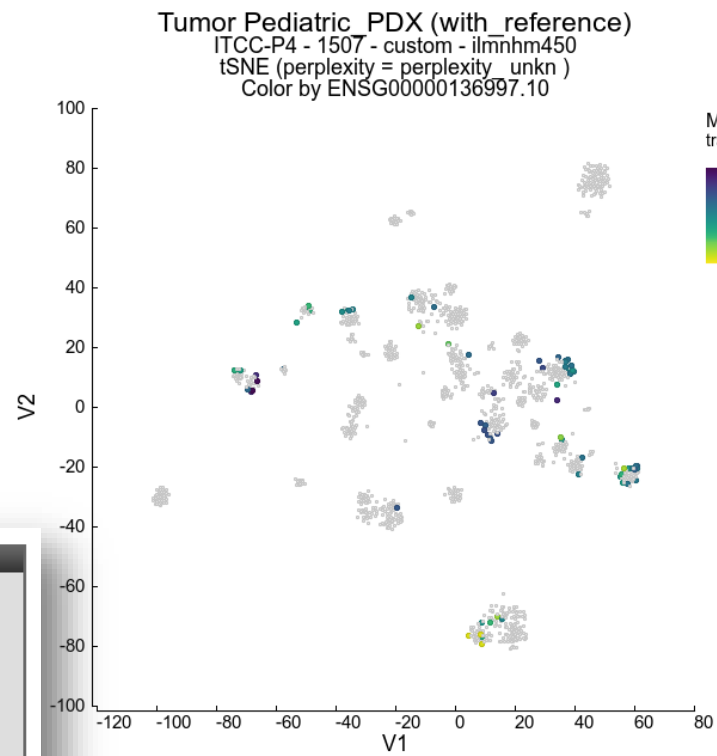
In multi omics sets 'color by gene'

- Go to: **Main**
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R2: Sample map Viewer

Online Tutorial

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



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)

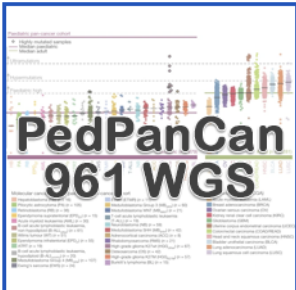
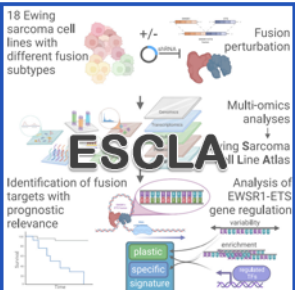
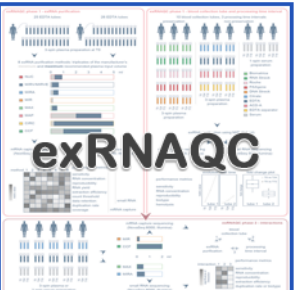
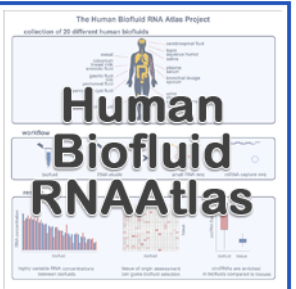

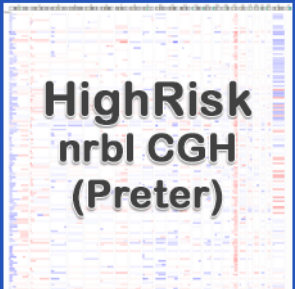
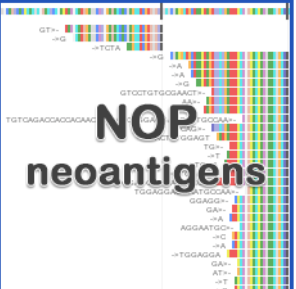


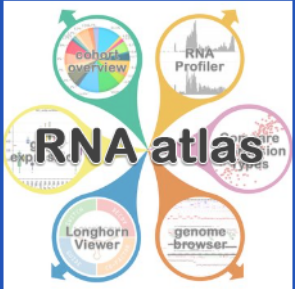

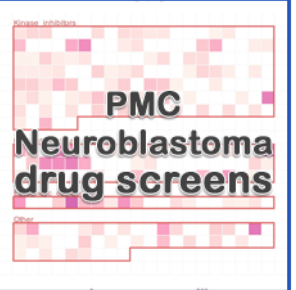
- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/tSNE)
- Small Tools
- DataGrabber
- Genome Browser
- ChIP data
- TAR literature
- Change Data Scope**
- User Options
- Help
- Contact / About R2

- resources
- tumor

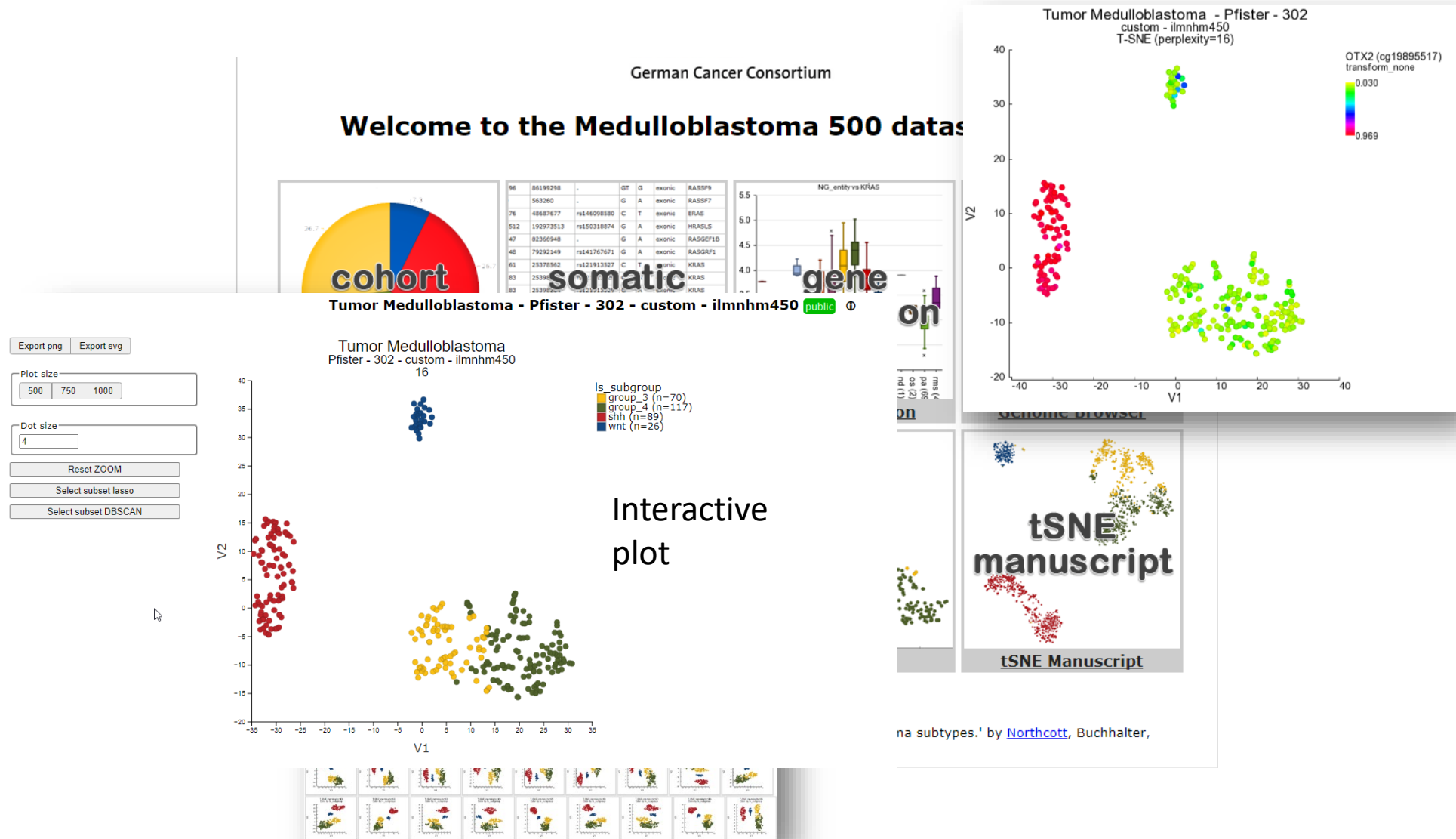
Welcome to the data scopes index in R2

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



WGS of 1000 pediatric patients

R2: Genomics analysis and visualization platform

dkfz.
German Cancer Consortium

GeneBrowser

hg19: Cytoband SV Pediatric Cancer SOM Pediatric Cancer

Welcome to the DKFZ Pediatric Pan-Cancer dataset section

cohort overview

Cohort Overview

96	86199298	.	GT	G	exonic	RASSF9
563260	.	G	A	exonic	RASSF7	
76	46687677	rs146098580	C	T	exonic	ERAS
512	192973513	rs150318874	G	A	exonic	HRASLS
47	82366948	.	G	A	exonic	RASGEF1B
48	79292149	rs141767671	G	A	exonic	RASGRF1
61	25378562	rs121913527	C	T	exonic	KRAS
83	25398225	rs121913528	C	T	exonic	KRAS
83	25398225	rs121913528	C	T	exonic	KRAS
546	141376648	.	T	A	exonic	RASA2
39	155675661	.	C	A	exonic	RASAL3
657	206756561	.	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

gene expression

Gene Expression

genome browser

Genome Browser

1,000 WGS

GeneBrowser

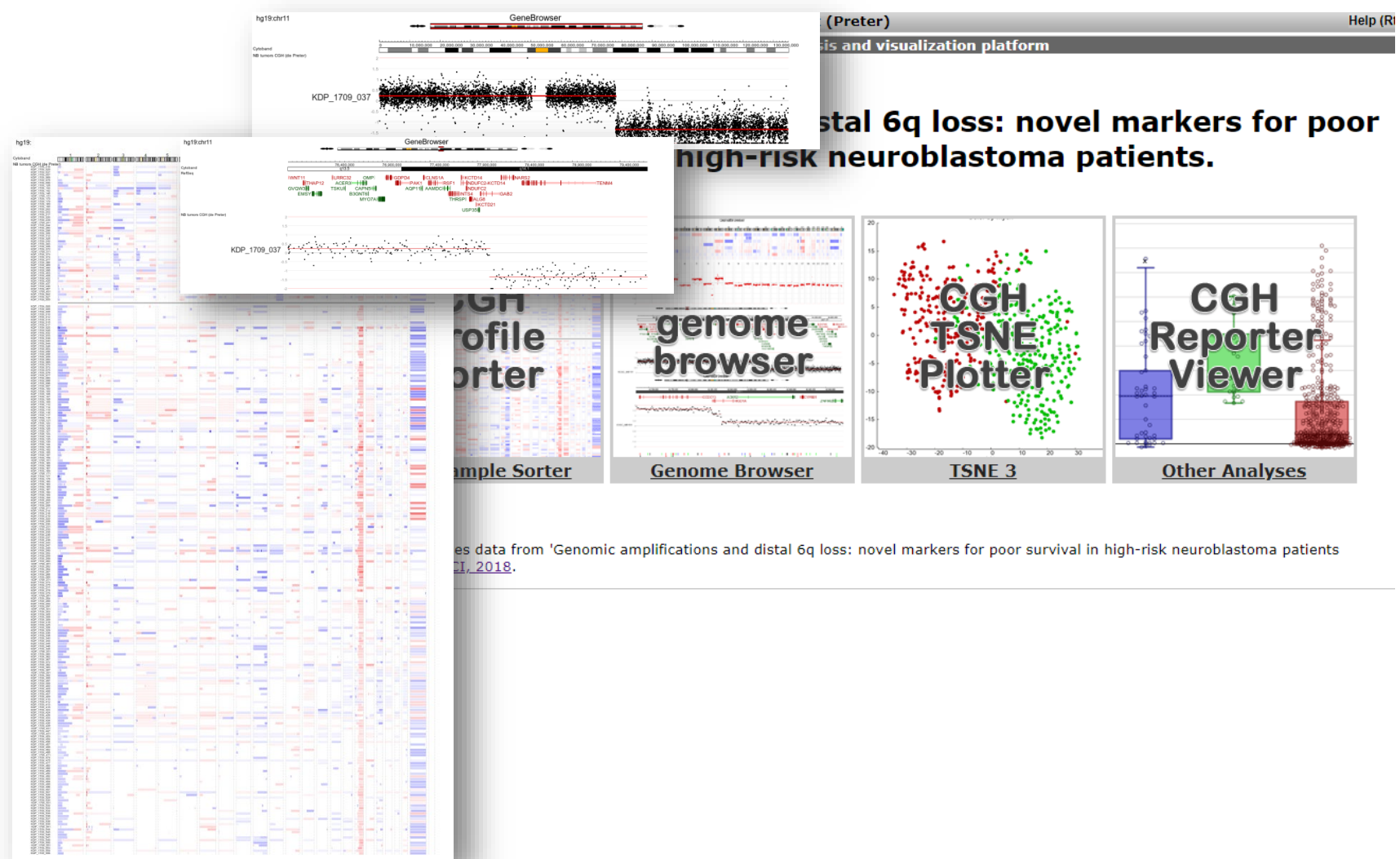
hg19: Cytoband ngs_logph_ped_v1 ICGC_MB132

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

GeneBrowser

ICGC_MB132

556 Neuroblastoma CGH samples



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

RNA Atlas (300 polyA / RiboDepl / Small)

R2: RNA Atlas
R2: Genomics analysis and visualization platform

Online Tutorial

Welcome to the RNA Atlas datascope.

cohort overview

Cohort Overview

gene expression

Gene Expression

LongHorn Viewer

LongHorn

genome browser

R2 Genome Browser

Compare Expression

Compare Expression

RNA Profiler

Home Profiles

Co-factor(TR) Decoy(MRNAIRBP)(PTR) Decoy(TF)(TR) Guide(TR)

Dataset Extender Correlation

Source: Mixed RNA Atlas Combined - Mestbagh_294
Target: Mixed RNA Atlas Combined - Mestbagh_294

LineFs: high: 0.292 p=2.1E-11, low: 0.084 p=0.002, not: 0.106 p=0.208

t=0.25-att2_35297
high (n=75)
low (n=75)
not (n=144)

Trendlines:
group: F: Fval
high: -0.252 0.11
low: -0.054 0.08
not: -0.106 0.08

Mixed RNA Atlas Combined - Mestbagh - 294
Mixed RNA Atlas Combined - Mestbagh - 294

biological_source
organ_system
type

SAMSON
CDK6

Regulator vs Target
Mediator
Other Mediator(s)

Score: -1 to 1

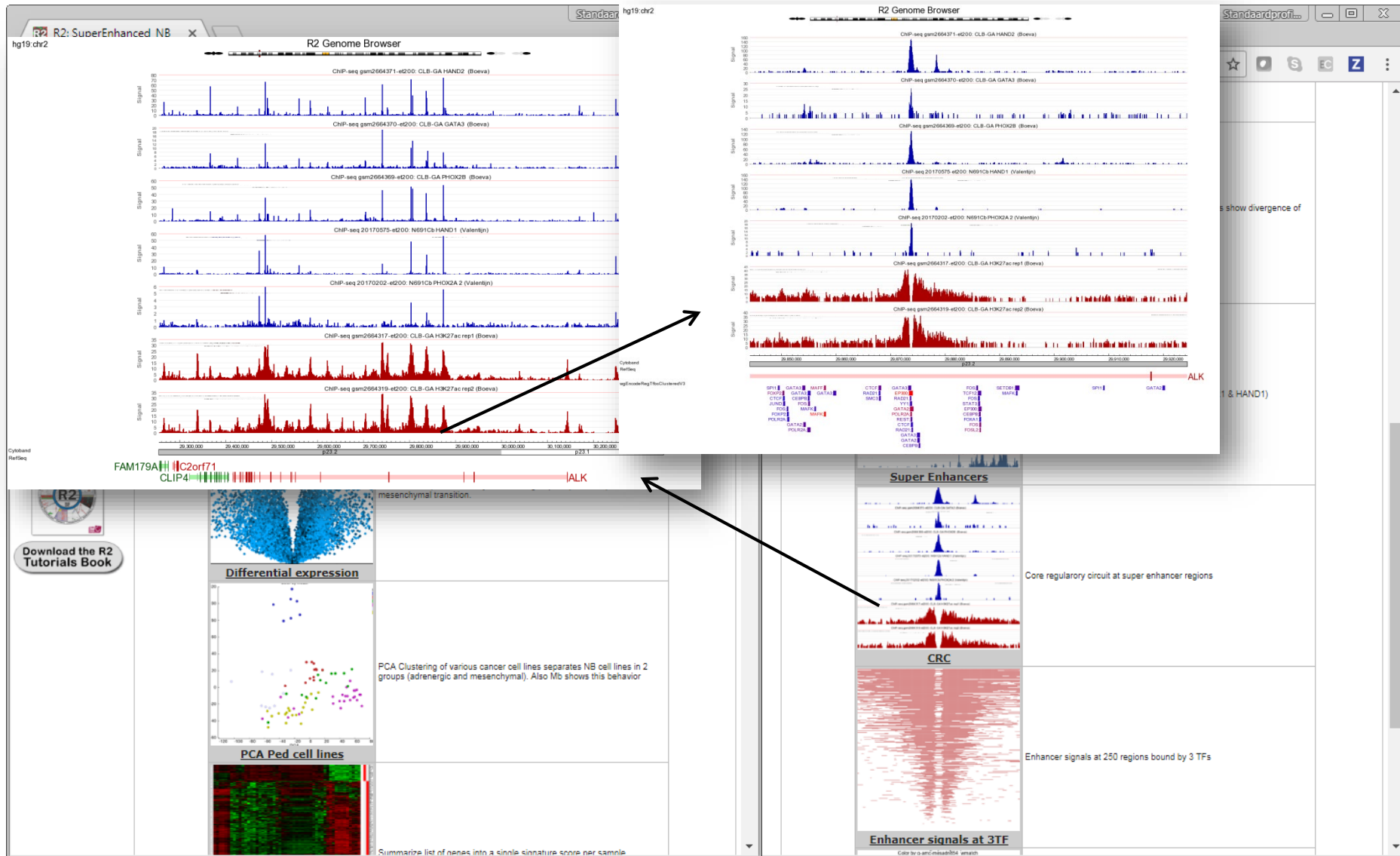
hg38:chr18
ma_atd43 GEex
RNA-seq ma_atd43_1 HT28 RNAseq polyA (RNA Atlas)
RNA-seq ma_atd43_1 HT28 RNAseq Total (RNA Atlas)

Cytband
RefSeq

maefus_chr_18
maefus_chr_18
maefus_chr_18
maefus_chr_18

MSTRG 4242.63
MSTRG 4242.64
MSTRG 4242.65
MSTRG 4242.66
MSTRG 4242.67
MSTRG 4242.68
MSTRG 4242.69
MSTRG 4242.70
MSTRG 4242.71
MSTRG 4242.72
MSTRG 4242.73
MSTRG 4242.74
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MSTRG 4242.91
MSTRG 4242.92
MSTRG 4242.93
MSTRG 4242.94
MSTRG 4242.95
MSTRG 4242.96
MSTRG 4242.97
MSTRG 4242.98
MSTRG 4242.99
MSTRG 4243.00

Links to interactive analyses (like Super Enhancers)

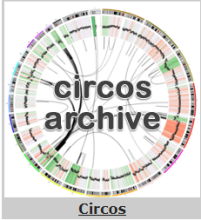


Personalized Medicine programs

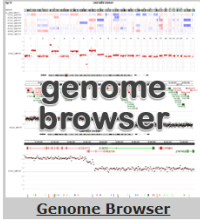
R2: INFORM
R2: Genomics analysis and visualization platform

dkfz.
German Cancer Consortium

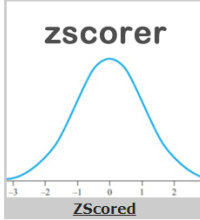
Welcome to the DKFZ INFORM section.



Circos



Genome Browser

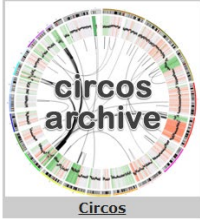


ZScorer

R2: IThER
R2: Genomics analysis and visualization platform

prinsesMÁXIMA
centrum voor kinderoncologie

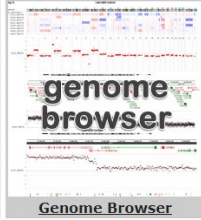
Welcome to the iThER section of R2.



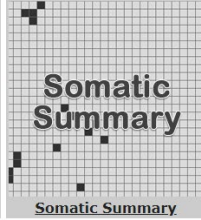
Circos

96	38119239	.	GT	G	rs94916	BAADP9
160366			G	A	rs49491	BAADP7
48467677	rs144049580	C	T	rs49491	IKAS	
182979813	rs103118874	G	A	rs49491	IKASL3	
82268448		G	A	rs49491	BAADP15	
79521149	rs147167671	G	A	rs49491	BAADP11	
25378862	rs123161927	C	T	rs49491	IKAS	
25122889					IKAS	
25122889					IKAS	
14112512					IKAS2	
151150161					IKASAL3	
206759561		C	A	rs49491	BAADP9	
62961677		C	T	rs49491	BAADP13	
21396085	rs123161930	C	G	rs49491	IKAS	
11328744	rs123161930	C	T	rs49491	IKAS	
11328747	rs123161930	C	T	rs49491	IKAS	
11328748	rs123161930	C	T	rs49491	IKAS	

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

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](#)

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

- 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

Upstream: Celebrating open source. WATCH NOW

Ad by EthicalAds

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>)'

Copyright (c) 2006-2023 Jan Koster

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 datascope. Now publicly available in R2 via the 'datascope' menu item.

all news

Genome Browser

Genomics Analysis & Visualization Platform

Genome Browser

Genomics Analysis & Visualization Platform

Genome Browser

Genomics Analysis & Visualization Platform

encca (2)

Fun things to do:

R2 MSCA-DN Training Courses

- Help => Training Courses => PRESSURE
 - **USE hgserver2!**
- 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 in R2 dataset grid
 - **Tissue/Tumor: "Esoph" => 21 public sets!**
 - **Author: Bijlsma | Zalm (access rights?)**
- Think about a good biological research question
- Try to find the analyses that can help you gain insight

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

Datascopees

- Look for datascopees that have similar type of data as yours and look at the kind of analyses that were done for inspiration

Computer login:
func_user
Welkom01

The screenshot shows the R2 training courses interface. The top navigation bar includes 'R2 training courses', 'Search docs', and 'MSCA-DN'. A sidebar menu on the left has 'Help' highlighted with a red box, and 'Training Courses' highlighted with a red dashed box. The main content area shows a document titled '1.3. Different expression patterns between subgroups and the underlying biology' with a graph showing 'Relapse' over 'Time' and a 'Detection limit' line.

The screenshot shows the R2-Platform interface. The top navigation bar includes 'and Visualization Platform' and 'Online Tutorial'. The 'Online Tutorial' button is highlighted with a red box. The main content area shows a document titled 'What is R2?' with a welcome message.

What's next?

R2 MSCA-DN Training Courses

- Help => Training Courses => PRESSURE

Do your own research with available datasets in the grid

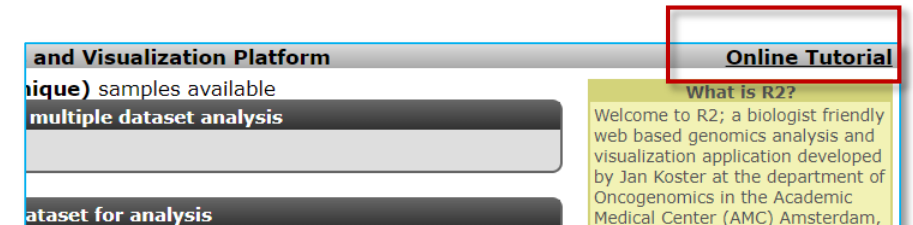
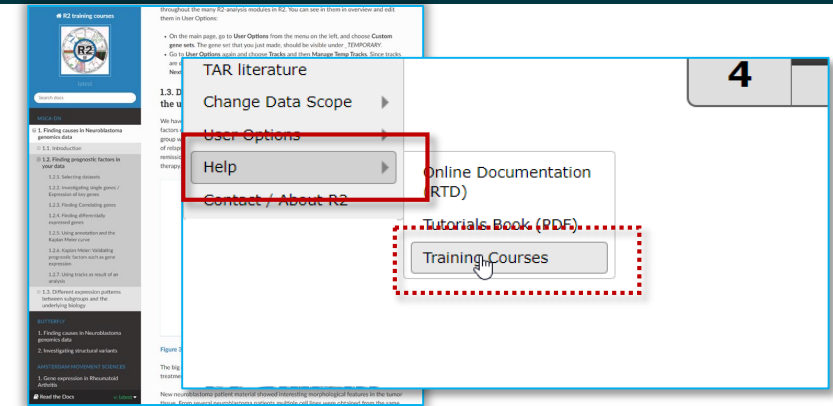
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- Try to find the analyses that can help you gain insight

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

Next:

- Look into other courses in the course material
- Datascope
 - Look for datascope that have similar type of data as yours and look at the kind of analyses that were done for inspiration
- **Find publicly available datasets and email us to get them uploaded**
- **Create you own data and email us to upload**



r2-support@amsterdamumc.nl

R2 Platform Team

Romeo Willinge Prins

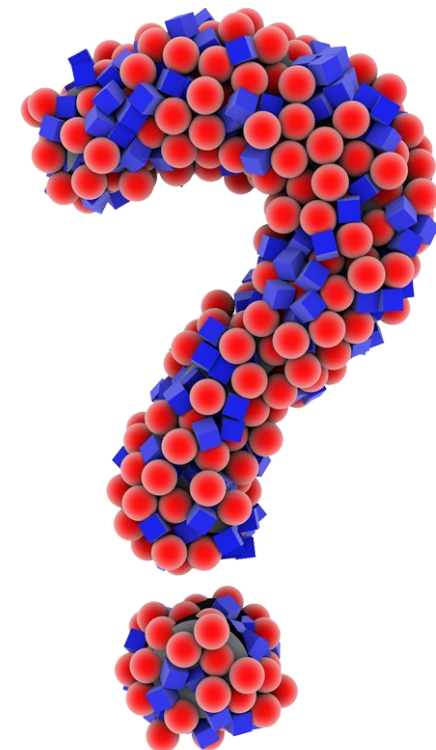
Danny Zwijnenburg

Richard Volckmann

Christian Griffioen

Lieke Hoyng

Jan Koster



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

Koster J(151) Johnsen JI(18) Zhang F(6) Li M(14) Yang W(7) Li Z(32) Faber AC(7) Stallings RL(14) Capper D(9) Li Y(36)
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 Pfister SM(67) Sun C(8) Sahm F(11) Eggert A(28) Wang F(14) He Y(6) Locatelli F(15) Bachmann AS(15)
 ... (many more names and counts)

