



R2 Introduction Workshop Pressure Part 1 21-May-2024

Computer login:
func_user
Welkom01

Lieke Hoyng and Richard Volckmann
on behalf of the R2 Team

Dept. CEMM | Location AMC

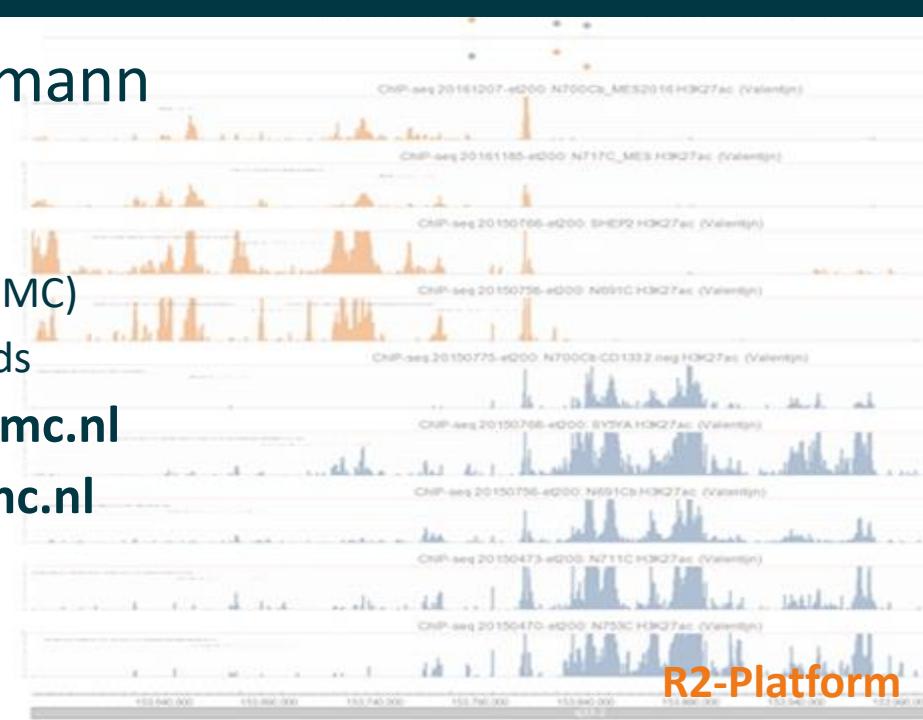
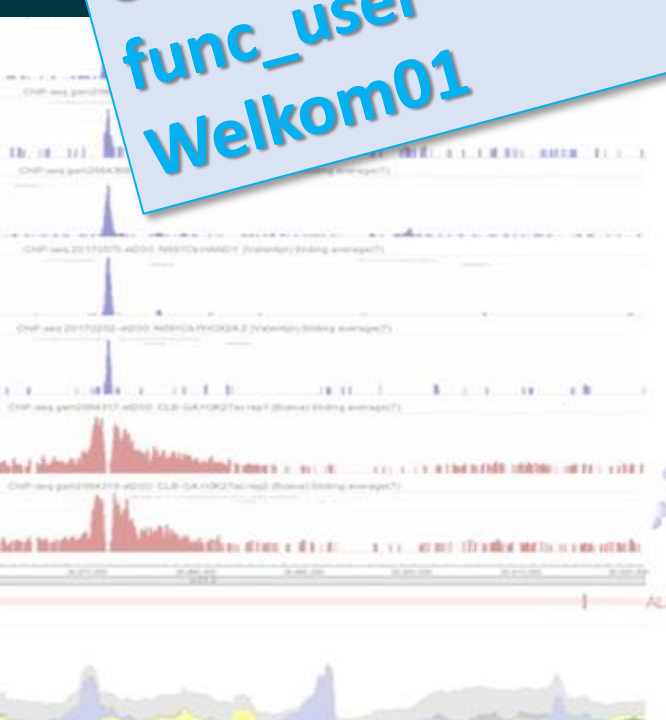
Amsterdam University Medical Centers (AUMC)

University of Amsterdam, the Netherlands

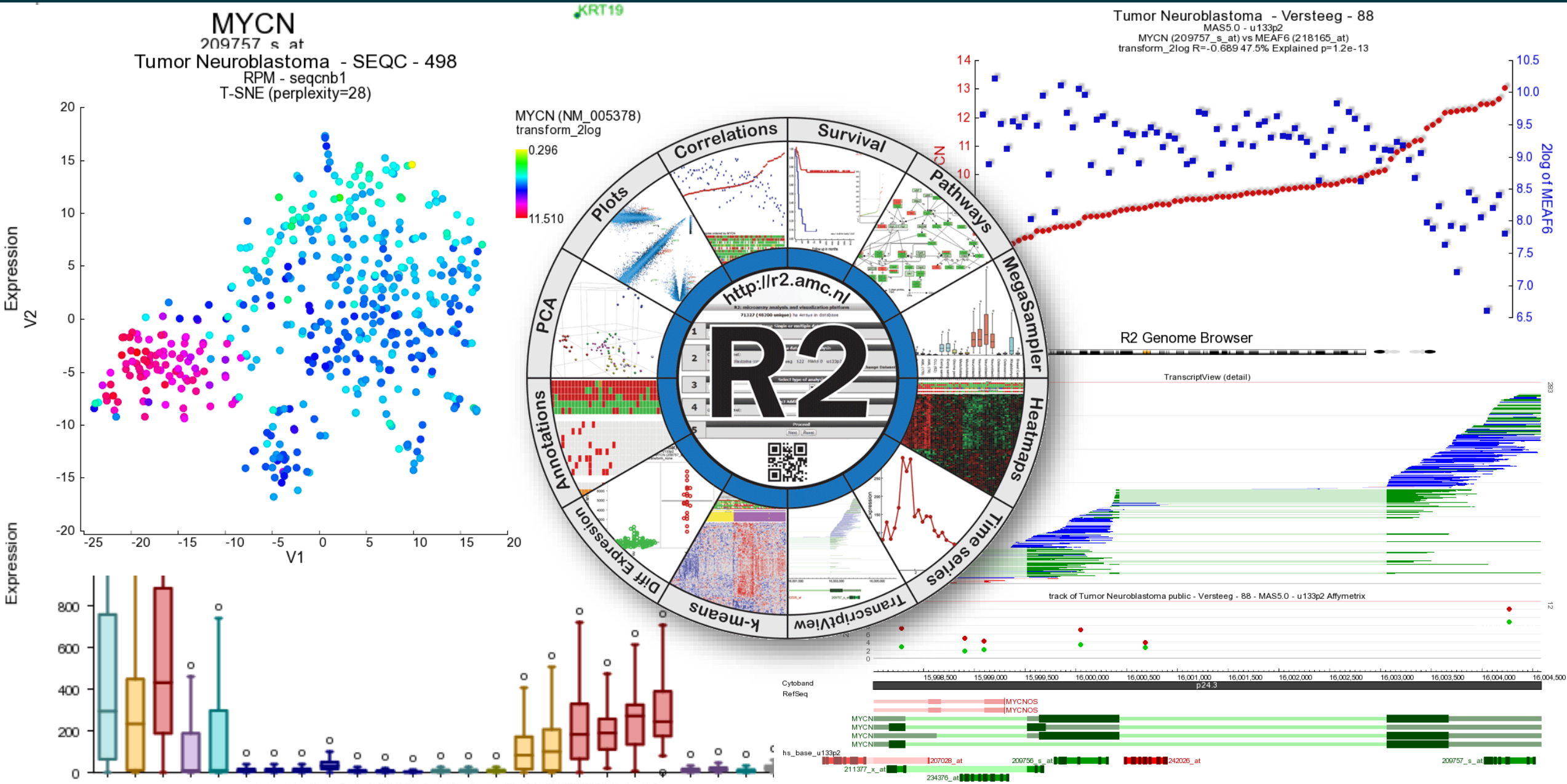
R2 Support: r2-support@amsterdamumc.nl

Jan Koster: jankoster@amsterdamumc.nl

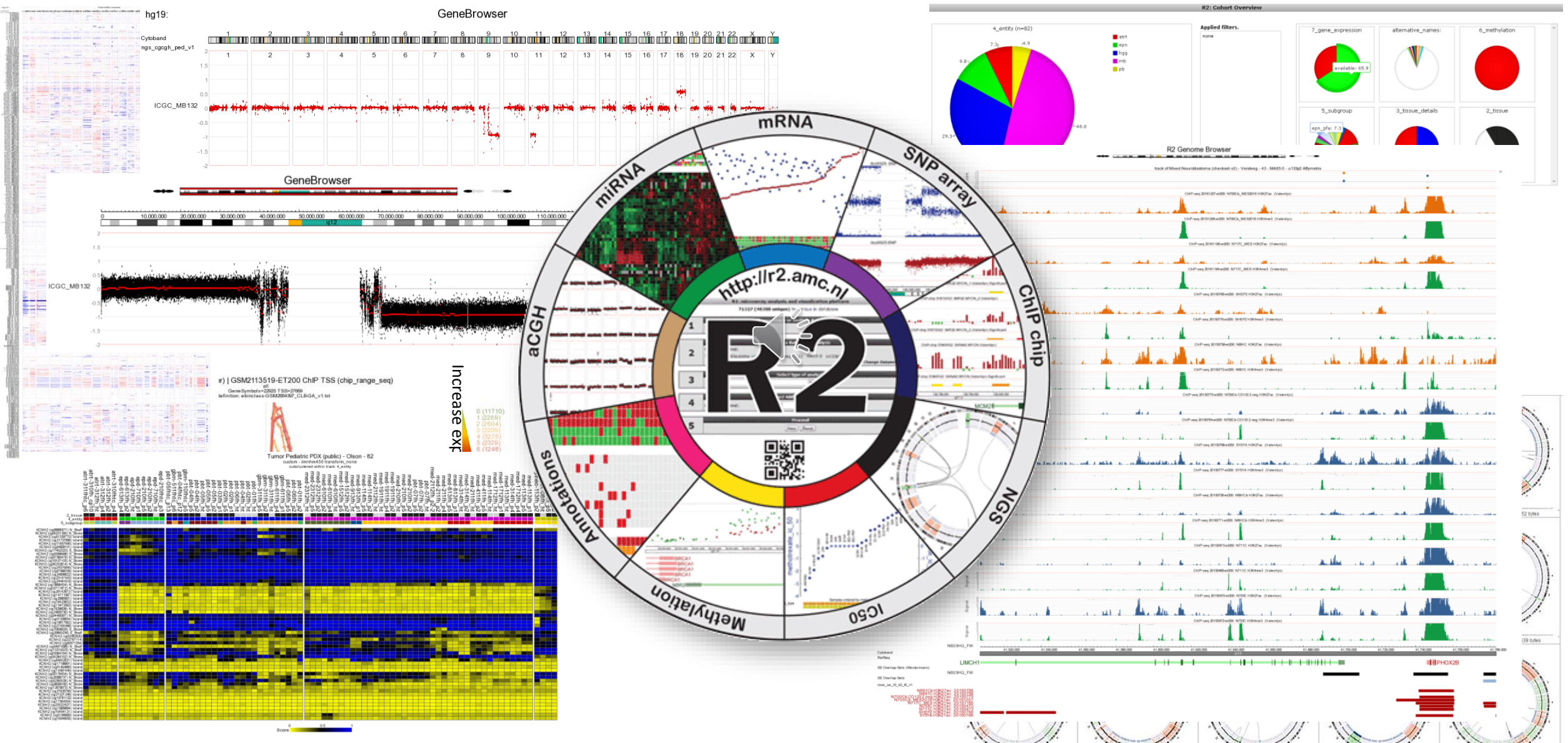
r2platform.com



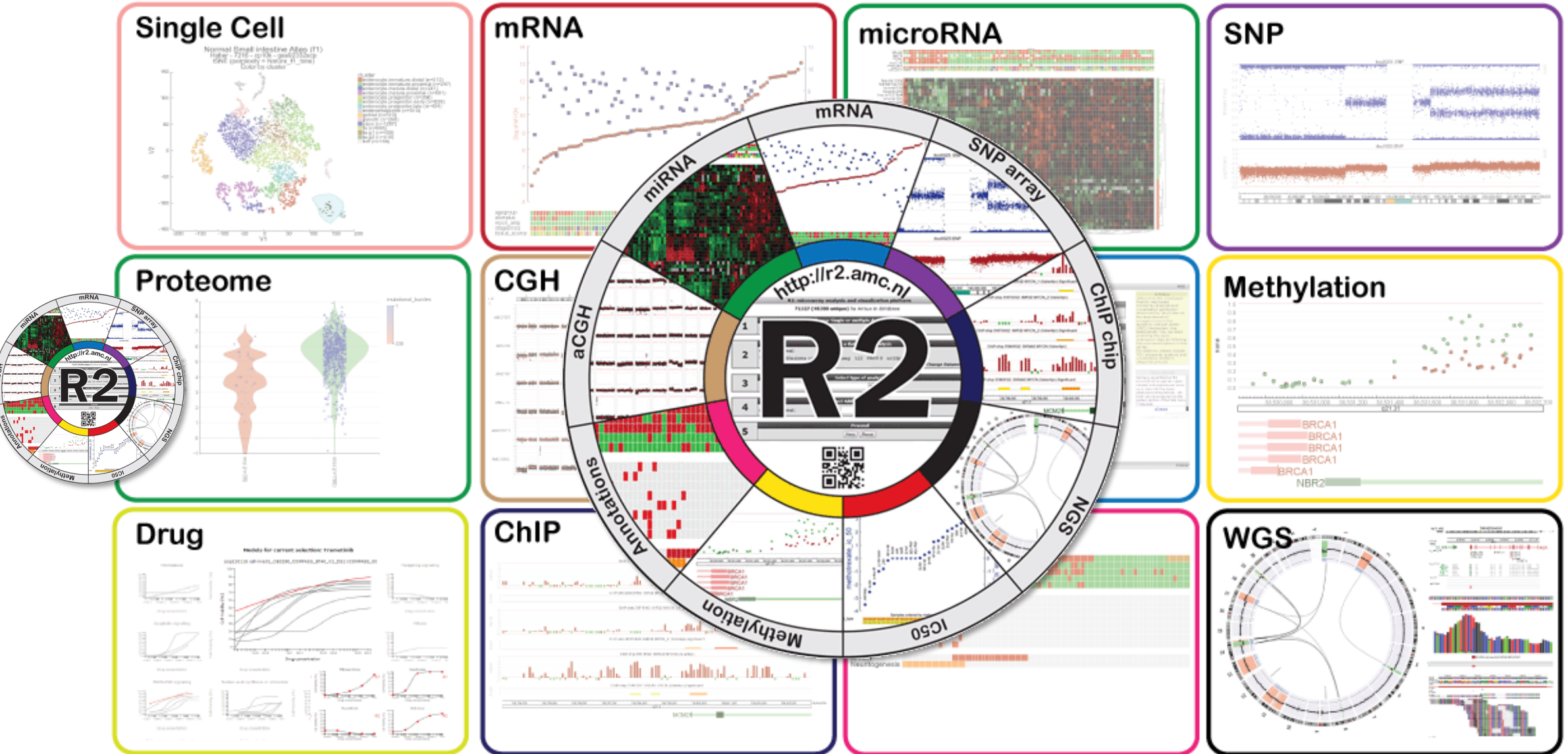
R2: Genomics Analysis and Visualization Platform



R2: Genomics Analysis and Visualization Platform



R2: Different types of Omics data available in the R2 Platform



R2: Usage statistics

Registered Users
11.760

Sessions
628.8

IP addresses
252.833

Pages
16.4

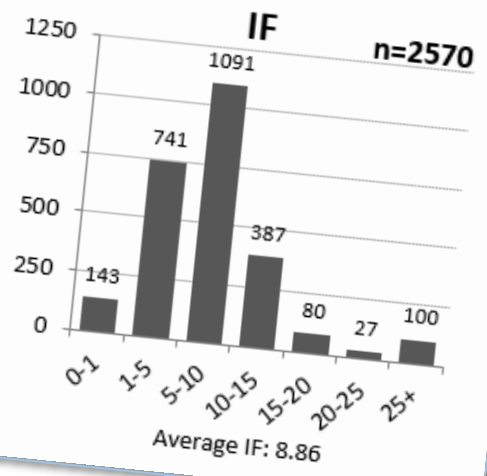
IF	Journal
60.72	Nat Rev Cancer (n=1)
56.27	JAMA (n=1)
54.91	Nat Biotechnol (n=2)
53.44	Nat Med (n=3)
53.24	Nat Rev Genet (n=1)
49.96	Nature (n=13)
47.73	Science (n=2)
44.54	J Clin Oncol (n=3)
41.58	Cell (n=6)
39.40	Cancer Discov (n=10)
38.33	Nat Genet (n=8)
31.74	Cancer Cell (n=22)
28.82	Nat Cell Biol (n=3)
27.40	Mol Cancer (n=16)
27.29	Cell Metab (n=3)
25.84	J Extracell Vesicles (n=1)
25.61	Nat Immunol (n=1)
25.47	Pharmacol Rev (n=1)
25.08	J Hepatol (n=2)
24.63	Cell Stem Cell (n=6)
23.06	Gut (n=4)
22.68	Gastroenterology (n=6)
22.11	Blood (n=11)
18.50	Drug Resist Updat (n=2)
18.19	Signal Transduct Target Ther (n=5)
17.97	Mol Cell (n=2)
17.96	Sci Transl Med (n=8)

Count	Journal
114	Oncotarget (IF=3.765)
113	Cancers (Basel) (IF=6.639)
82	Oncogene (IF=9.867)
76	Cancer Res (IF=12.701)
63	Cell Death Dis (IF=8.469)
62	Int J Mol Sci (IF=5.923)
60	Sci Rep (IF=4.379)
54	Nat Commun (IF=14.919)
43	Front Oncol (IF=6.244)
38	J Exp Clin Cancer Res (IF=11.161)
37	PLoS One (IF=3.24)
33	Proc Natl Acad Sci U S A (IF=11.205)
32	Cell Rep (IF=9.423)

Data Sets
4.354

Single Cell
450

Samples (Bulk)
706.500



PubMed Citations
2.570

R2: Usage statistics (Public)

Registered
Users
11.760

Sessions
628.868

Data Sets
2.400

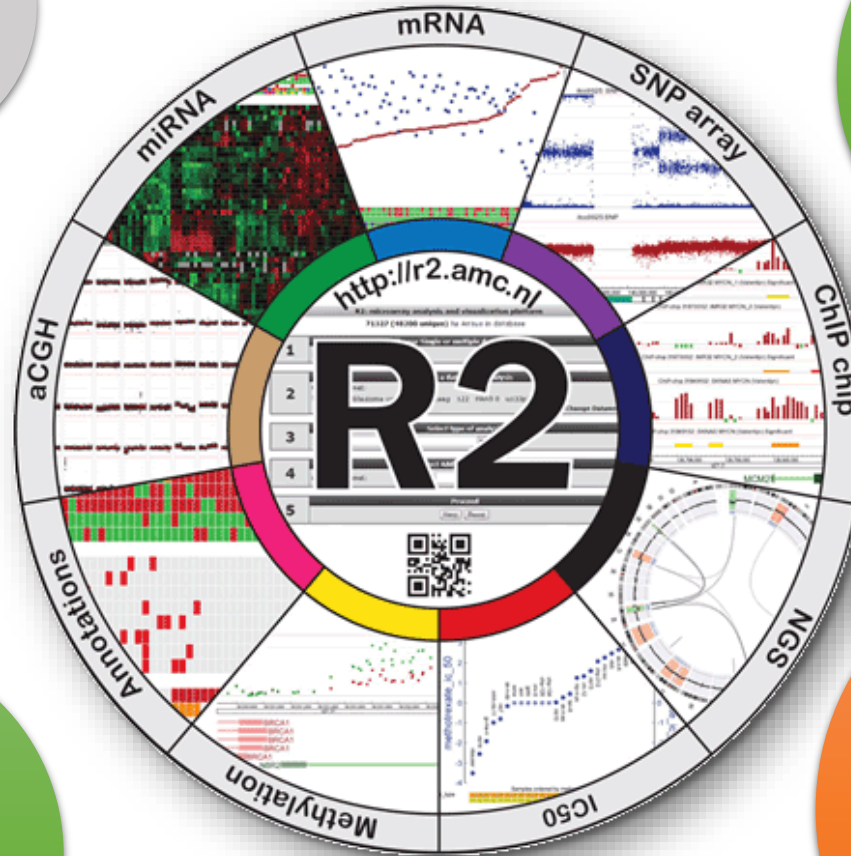
Single
Cell
220

IP addresses
252.833

Pages Served
16.414.469

PubMed
Citations
2.570

Samples
(Bulk)
441.000



Schedule (+/-)

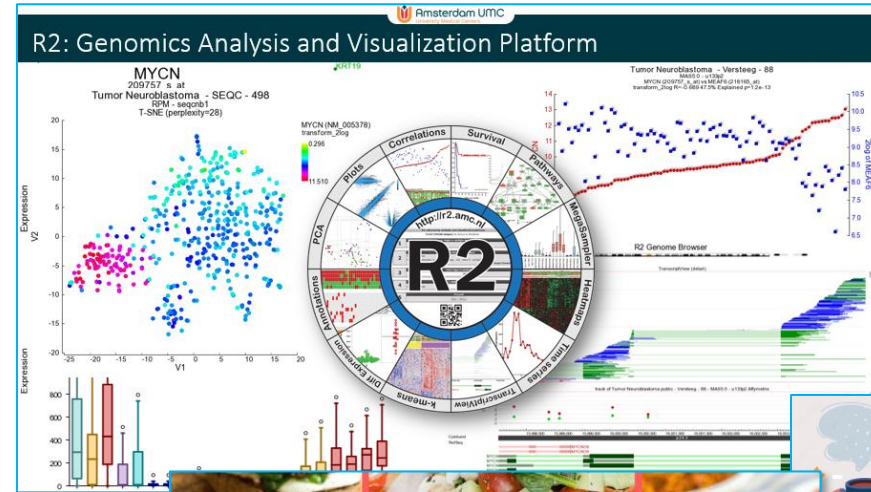
Today morning

- 9:30 - 11:00 Presentation Key Concepts
- 11:00 - 11:15 Tea / coffee
- 11:15 - 13:00 (Guided) R2 play time

--- LUNCH ---

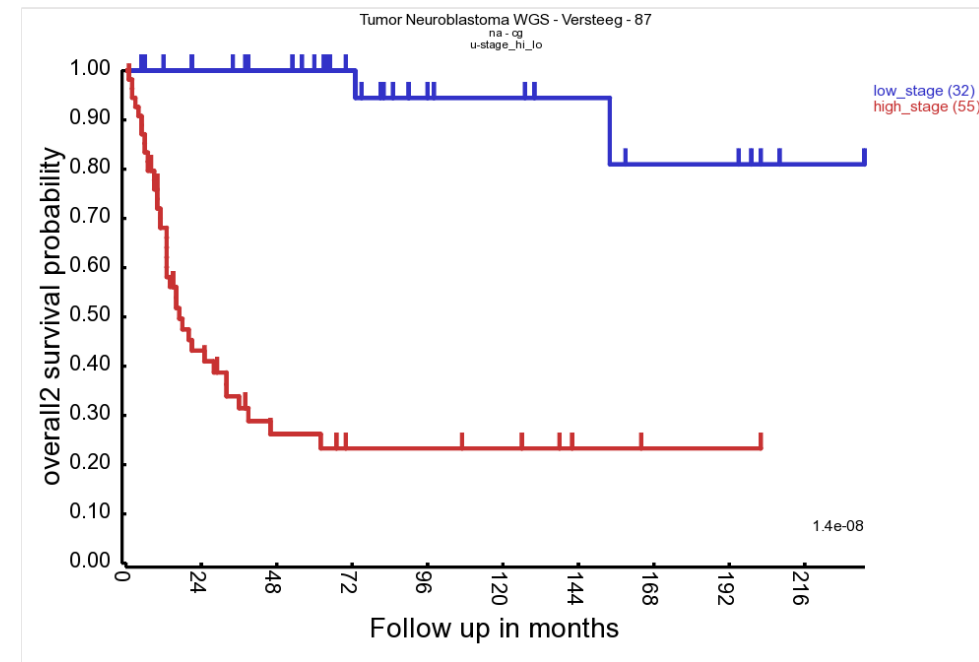
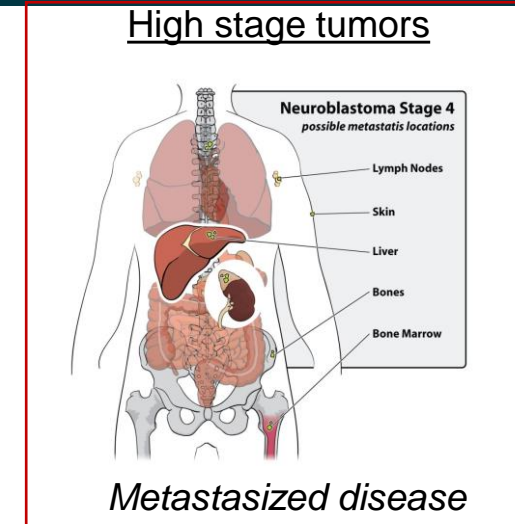
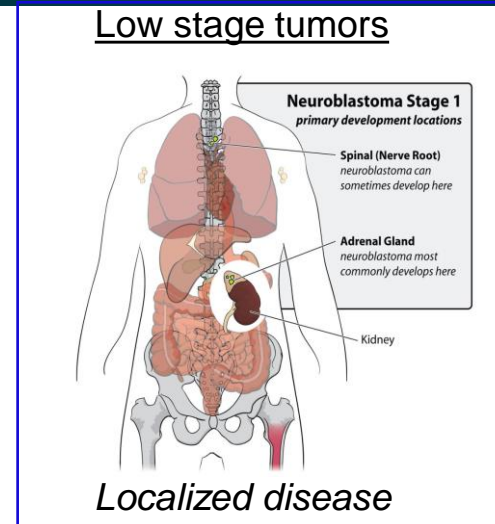
Today afternoon

- 13:45 - 15:30 Presentation Analysis Pipeline
- 15:30 - 15:45 Tea / coffee
- 15:45 - 17:00 (Guided) R2 play time



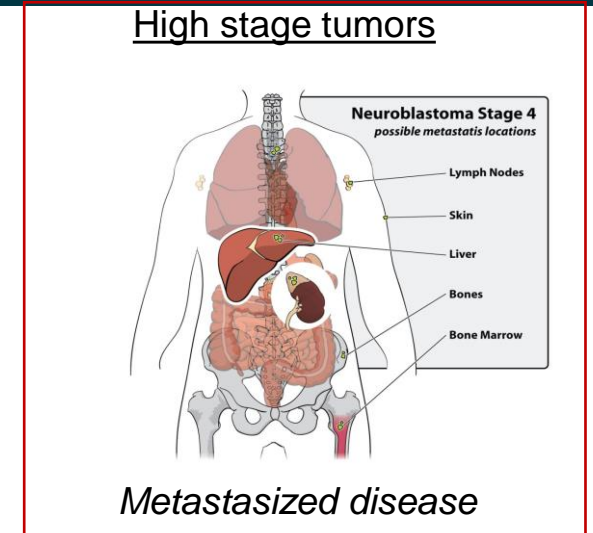
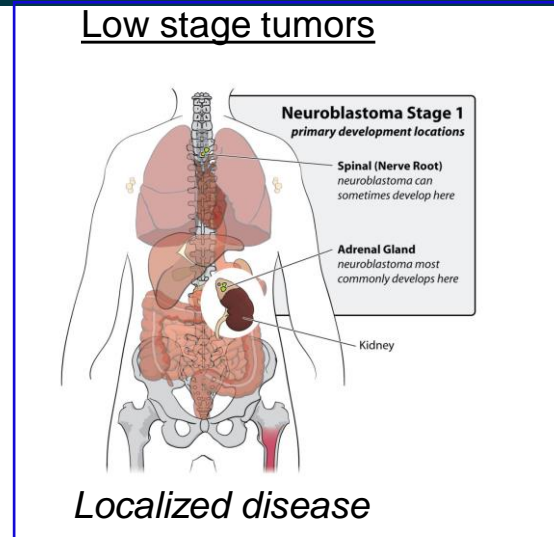
Neuroblastoma

- Childhood tumor
- Tumor of the peripheral sympathetic nervous system
- Incidence:
 - Children <15 years: 10% of all tumors
 - ~30 cases/year in The Netherlands
 - Peak incidence: 0-4 years, median age of 23 months
 - Responsible 15% of all tumor-related childhood deaths
- INSS stages
 - Stage 1,2,3,4, 4s (no progression)
 - Worst prognosis stage 4, no cure
 - Low stage vs high stage

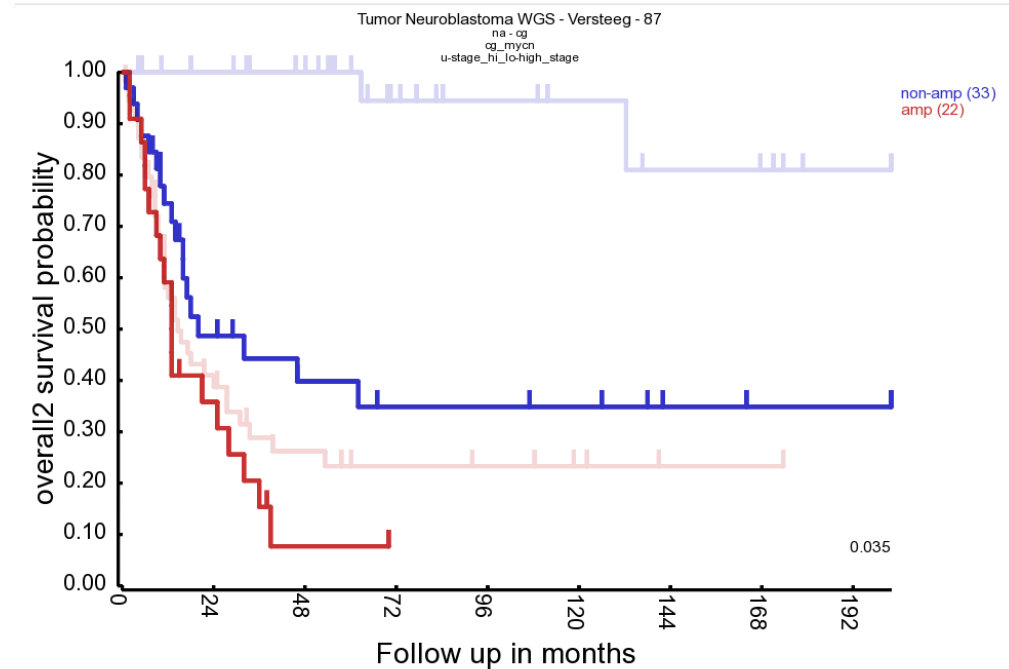


Neuroblastoma: MYCN amplification

- Neuroblastoma
 - **INSS** stages
 - Stage 1,2,3,4, 4s
 - Low stage vs high stage

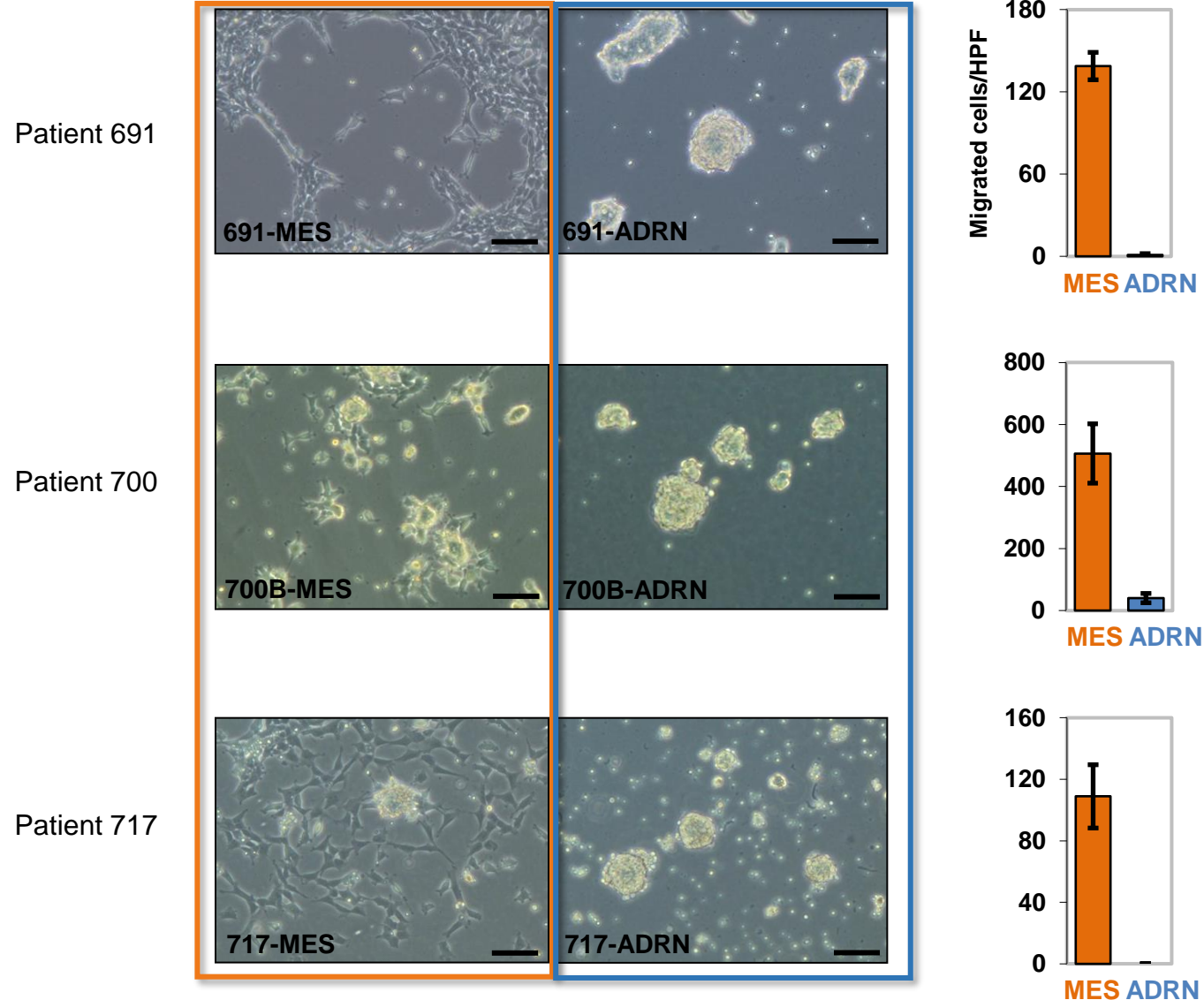


- **MYCN** oncogene amplified
 - 20% patients
 - ++ DNA copies
 - Bad prognosis on their survival

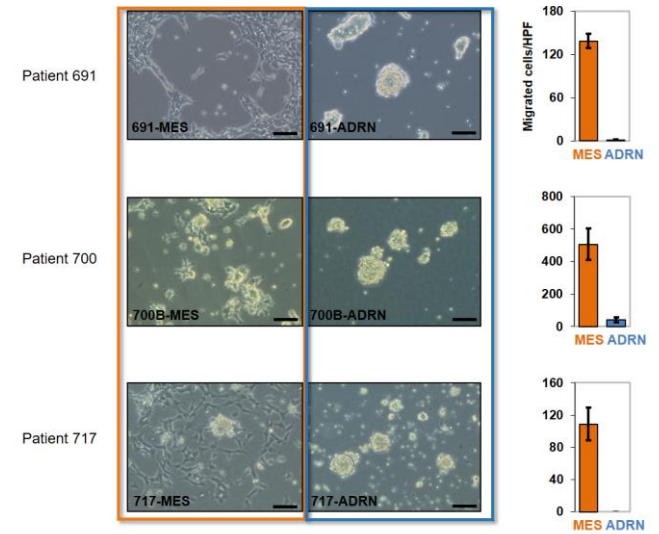
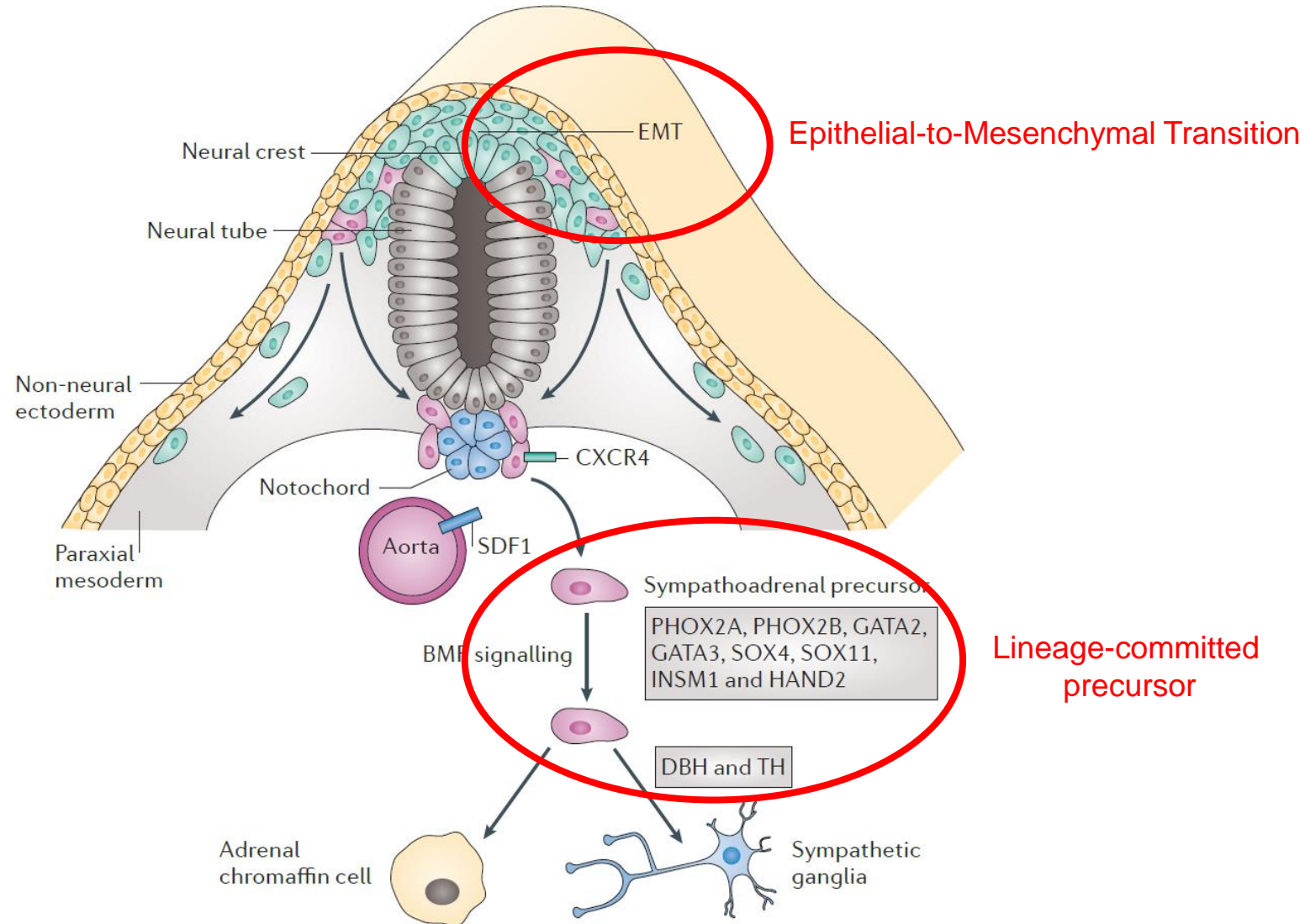


Neuroblastoma: intra-tumorheterogeneity, two cell types

- Identification of mesenchymal-type neuroblastoma cells *in vitro*

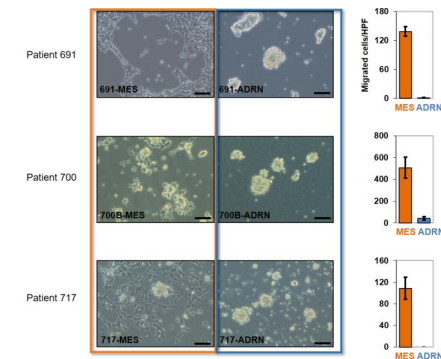
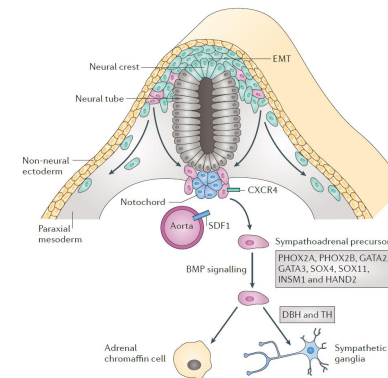
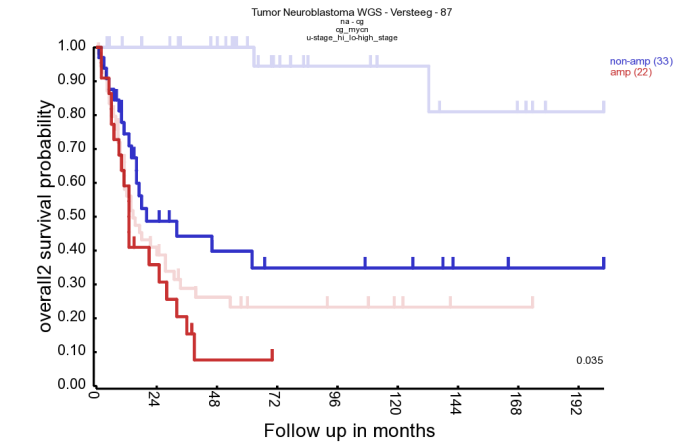
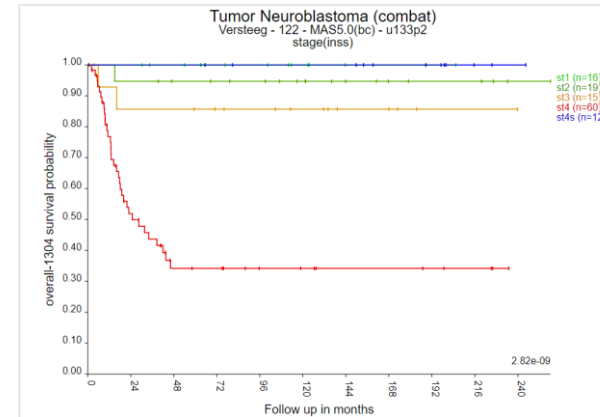


Development of the sympatho-adrenal lineage from the neural crest



Summary neuroblastoma

- **INSS stages**
 - High stage tumor: **stage 4**
- **MYCN** oncogene amplified
 - Bad prognosis on their survival
- **Two cell types: MES, ADRN**
- But R2 has ~2400 public cohorts / experiments and thousands of additional 'profiles'
 - e.g. ChIP / WES / WGS
 - Covering *many tissues / cancers / cell lines*
 - All types of data



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



YouTube

Integrated Analysis of Tumor Genomics Data with R2 Tutorials



Download the R2 Tutorials Book

R2: Genomics Analysis and Visualization Platform

2,191,770 (2,029,829 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 Proceed

[Online Tutorial](#)

What is R2?

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

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

Financial Supporter of R2

Cancer Center Amsterdam



News

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

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](#)

Are you: 

Then this workshop is for you!



R2 Support

Go to: **Main**

- Main
- Time series
- Survival (Kaplan-Meier/Cox)
- Sample maps (UMAP/TSNE)
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AUMC: CEMM

Online Documentation (RTD)

Tutorials Book (PDF)

Training Courses

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

R2 training courses

latest

Search docs

STUDENTS COURSE

- Investigating Intra-tumor Heterogeneity in Neuroblastoma

GRADUATE COURSE

- Investigating structural variants
- Investigating Intra-tumor Heterogeneity

ADDITIONAL COURSE MATERIALS

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

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Docs » R2 Training Courses: 2023-02-02

Edit on GitHub

R2 Training Courses: 2023-02-02

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

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Table of Contents

Students Course

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

Graduate Course

- 1. Investigating structural variants
 - 1.1. Introduction
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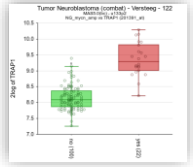
all news

Facebook

Twitter

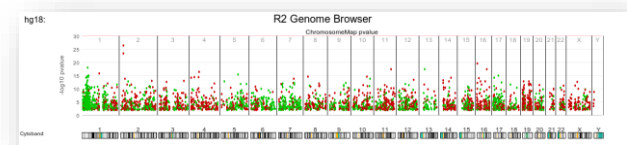
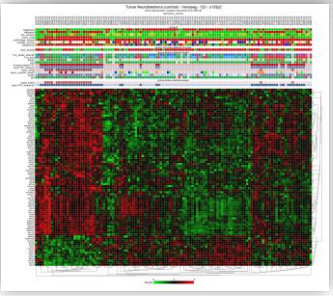
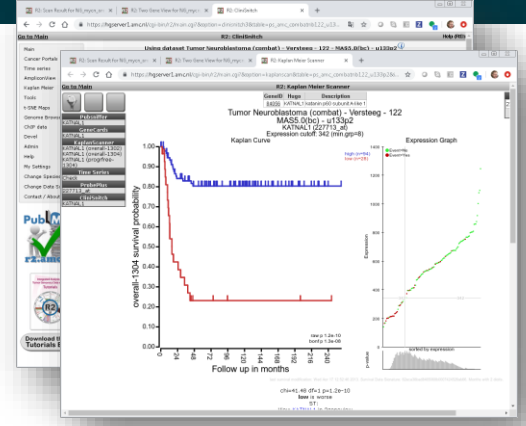
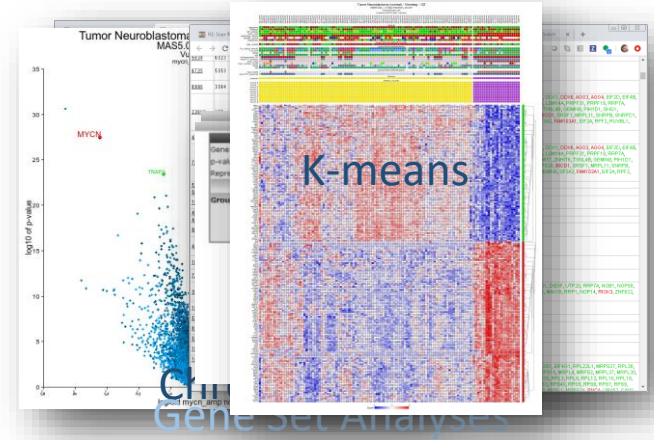
encca (2)

Example: Differential Expression Analysis



122 samples, transform_log, Prescaled=1
14988 combinations did not meet $p < 0.01$ and ≤ 1 minimal # of PresentCalls
3854 combinations meet your criteria (0 / 3854)
p-value correction for multiple testing: False Discovery Rate
Gene Hover Information is only added to the first 250 genes of a table

HUGO	FC	Genes	pval	FCsig
MYC	0.824	myc_mrn_101	1.5e-27	21
MYC	0.788	myc_mrn_101	3.22e-24	122
MYC	0.759	myc_mrn_101	2.71e-20	122
MYC	0.739	myc_mrn_101	5.13e-18	122
MYC	0.733	myc_mrn_101	3.18e-18	122
MYC	0.726	myc_mrn_101	4.65e-18	122
MYC	0.720	myc_mrn_101	8.22e-18	117
MYC	0.717	myc_mrn_101	3.88e-17	122
MYC	0.715	myc_mrn_101	4.55e-17	122
MYC	0.707	myc_mrn_101	7.56e-16	72
MYC	0.702	myc_mrn_101	3.47e-16	120
MYC	0.696	myc_mrn_101	3.18e-16	122
MYC	0.695	myc_mrn_101	8.05e-16	102
MYC	0.693	myc_mrn_101	1.26e-15	122
MYC	0.689	myc_mrn_101	2.25e-15	98
MYC	0.689	myc_mrn_101	2.95e-15	122
MYC	0.687	myc_mrn_101	3.24e-15	122
MYC	0.684	myc_mrn_101	3.51e-15	122
MYC	0.683	myc_mrn_101	4.01e-15	122
MYC	0.683	myc_mrn_101	4.29e-15	117
MYC	0.680	myc_mrn_101	6.95e-15	49
MYC	0.680	myc_mrn_101	8.15e-15	121
MYC	0.679	myc_mrn_101	8.99e-15	121
MYC	0.678	myc_mrn_101	7.91e-15	118
MYC	0.678	myc_mrn_101	8.20e-14	122
MYC	0.673	myc_mrn_101	1.94e-14	9
MYC	0.671	myc_mrn_101	1.92e-14	112
MYC	0.669	myc_mrn_101	1.94e-14	122
MYC	0.668	myc_mrn_101	4.75e-14	120
MYC	0.668	myc_mrn_101	4.75e-14	120
MYC	0.663	myc_mrn_101	8.06e-14	122
MYC	0.660	myc_mrn_101	1.92e-13	116



R2 Main Page (r2.amc.nl)

- Go to: **Main**
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 - Sample maps (UMAP/TSNE)
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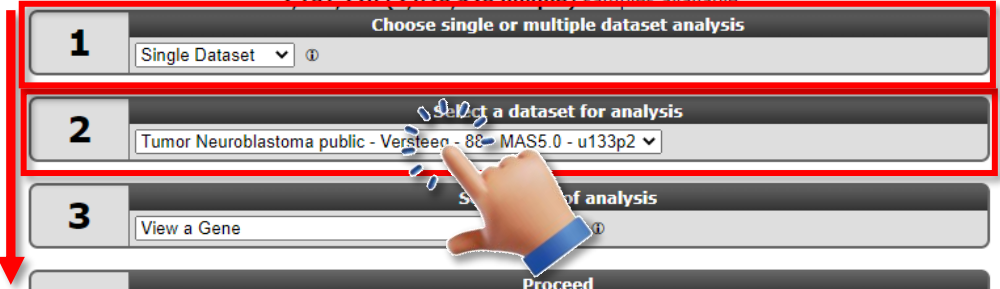

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1 Choose single or multiple dataset analysis
Single Dataset

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

3 Select a gene for analysis
View a Gene

4 Proceed
Next Reset



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○○○

News
Check out the new iTHER pediatric cancer precision medicine datascope. Now publicly available in R2 via the 'datascope' menu item.
[all news](#)



Dataset Selection

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

Species	Data type	Category	Tissue/Tumor	Author	N	Normalization	Platform	Comp...	Accession	Release da...	R2 date	Access	Favo...
hs	Expression data	Tumor	Neuroblastoma public	Versteeg	88	MAS5.0	u133p2	bulk	GSE16476	2012-03-08	2010-06-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Cell line	CCLE Cancer Cell Line Encyclopedia	Broad	917	MAS5.0	u133p2	bulk	GSE36133	2012-03-20	2012-04-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Normal	Adrenal Medulla development	Westermann	10739	tp10k	10x300hg19	single cell		2021-03-28	2021-03-28	public	<input checked="" type="checkbox"/>
hs	Expression data	Allograft	Kidney	Naesens	224	MAS5.0	u133p2	bulk	GSE147089	2020-11-10	2023-02-21	public	<input type="checkbox"/>
hs	Expression data	Cell line	ALL(T)	Ferrando	20	MAS5.0	u133p2	bulk	GSE48046	2013-06-18	2013-09-04	public	<input type="checkbox"/>
hs	Expression data	Cell line	B cell lymphoma (DLBCL)	Baden Holmes	29	leseq2_rlog	tpm109geo	bulk	GSE207388	2022-07-01	2023-06-16	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast	Hoeflich	51	MAS5.0	u133p2	bulk	GSE12777	2009-01-12	2009-08-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast HCC1143 32 kinase inhibitors	Douglass	184	leseq2_vst	geneid2011hs	bulk	GSE186341	2021-10-28	2022-12-01	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast MCF7 (methotrexate resistant)	Ciudad	5	MAS5.0	u133p2	bulk	GSE16070	2009-09-08	2015-12-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast Xenoestrogen	Isselbacher	351	MAS5.0	u133p2	bulk	GSE50705	2013-09-10	2013-10-14	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast Xenoestrogen	Isselbacher	351	RMA	u133p2	bulk	GSE50705	2013-09-10	2013-10-14	public	<input type="checkbox"/>

rows: 2098

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

Title: Integrated bioinformatic and wet-lab approach to identify potential oncogenic networks in neuroblastoma

Summary: mRNA profiles of thousands of human tumors are available, but methods to deduce oncogenic signaling networks from these data lag behind. It is especially challenging to identify main-regulatory routes, and to generalize conclusions obtained from experimental models. We designed the bioinformatic platform R2 in parallel with a wet-lab approach of neuroblastoma. Here we demonstrate how R2 facilitates an integrated analysis of our neuroblastoma data. Analysis of the MYCN pathway suggested important regulatory connections to the polyamine synthesis route, the Notch pathway and the BMP/TGF β pathway. A network of genes emerged connecting major oncogenes in neuroblastoma. Genes in the network carried strong prognostic values and were essential for tumor cell survival.

Design: 88 human Neuroblastoma samples were analyzed.

Available tracks in R2:

- age_year: (#) 0 - 13
- agegroup: <=1, >1
- alive: no, yes
- death_cause: nd, toxic, tumor
- gender: female, male
- histology: nb

Adjustments: MAS5.0 normalization was performed in GCOS with trimmed mean 96 set to 100 (alpha1=0.04, alpha2=0.06).

Available on R2 since: 2010-06-10

Platform: u133p2

Species: hs

Number of samples: 88

Source: GEO ID: GSE16476 Date: 2012-03-08

Dataset Selection

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

Species	Data type	Category	Issue/Tumor	Author	N	Normalization	Platform	Comp...	Accession	Release da...	R2 date	Access	Favo...
hs	Expression data	Tumor	Neuroblastoma public	Versteeg	88	MAS5.0	u133p2	bulk	GSE16476	2012-03-08	2010-06-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Cell line	CCLC Cancer Cell Line Encyclopedia	Broad	917	MAS5.0	u133p2	bulk	GSE36133	2012-03-20	2012-04-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Normal	Adrenal Medulla development	Westermann	10739	cp10k	10x300hg19	single cell		2021-03-28	2021-03-28	public	<input checked="" type="checkbox"/>
hs	Expression data	Allograft	Kidney	Naesens	224	MAS5.0	u133p2	bulk	GSE147089	2020-11-10	2023-02-21	public	<input type="checkbox"/>
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hs	Expression data	Cell line	Breast	Hoeflich	51	MAS5.0	u133p2	bulk	GSE12777	2009-01-12	2009-08-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast HCC1143 32 kinase inhibitors	Douglass	184	deseq2_vst	geneid2011hs	bulk	GSE186341	2021-10-28	2022-12-01	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast MCF7 (methotrexate resistant)	Ciudad	6	MAS5.0	u133p2	bulk	GSE16070	2009-09-08	2015-12-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast Xenoestrogen	Isselbacher	351	MAS5.0	u133p2	bulk	GSE50705	2013-09-10	2013-10-14	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast Xenoestrogen	Isselbacher	351	FRMA	u133p2	bulk	GSE50705	2013-09-10	2013-10-14	public	<input type="checkbox"/>

[Confirm selection](#)

rows: 2098

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

Title: Integrated bioinformatic and wet-lab approach to identify potential oncogenic networks in neuroblastoma

Summary: mRNA profiles of thousands of human tumors are available, but methods to deduce oncogenic signaling networks from these data lag behind. It is especially challenging to identify main-regulatory routes, and to generalize conclusions obtained from experimental models. We designed the bioinformatic platform R2 in parallel with a wet-lab approach of neuroblastoma. Here we demonstrate how R2 facilitates an integrated analysis of our neuroblastoma data. Analysis of the MYCN pathway suggested important regulatory connections to the polyamine synthesis route, the Notch pathway and the BMP/TGF β pathway. A network of genes emerged connecting major oncogenes in neuroblastoma. Genes in the network carried strong prognostic values and were essential for tumor cell survival.

Design: 88 human Neuroblastoma samples were analyzed.

Available tracks in R2:

- age_year: (#) 0 - 13
- agegroup: <=1, >1
- alive: no, yes
- death_cause: nd, toxic, tumor
- gender: female, male
- histology: nb

Adjustments: MAS5.0 normalization was performed in GCOS with trimmed mean 96 set to 100 (alpha1=0.04, alpha2=0.06).

Available on R2 since: 2010-06-10

Platform: u133p2

Species: hs

Number of samples: 88

Source: GEO ID: GSE16476 Date: 2012-03-08

Dataset Selection

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

Species	Data type	Category	Tissue/Tumor	Author	N	Normalization	Platform	Comp...	Accession	Release da...	R2 date	Access	Favo...
hs	Expression data	Tumor	Neuroblastoma public	Versteeg	88	MAS5.0	u133p2	bulk	GSE16476	2012-03-08	2010-06-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Cell line	CCLC Cancer Cell Line Encyclopedia	Broad	91	MAS5.0	u133p2	bulk	GSE36133	2012-03-20	2012-04-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Normal	Adrenal Medulla development	Westermann	1073	cp10k	10x300hg19	single cell		2021-03-28	2021-03-28	public	<input checked="" type="checkbox"/>
hs	Expression data	Allograft	Kidney	Naesen	224	MAS5.0	u133p2	bulk	GSE147089	2020-11-10	2023-02-21	public	<input type="checkbox"/>
hs	Expression data	Cell line	ALL(T)	Ferrando	20	MAS5.0	u133p2	bulk	GSE48046	2013-06-18	2013-09-04	public	<input type="checkbox"/>
hs	Expression data	Cell line	B cell lymphoma (DLBCL)	Baden Holmes	29	diseq2_rlog	tmm109geo	bulk	GSE217388	2022-07-01	2023-06-16	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast	Hoeflich	51	MAS5.0	u133p2	bulk	GSE12777	2009-01-12	2009-08-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast HCC1143 32 kinase inhibitors	Douglas	184	diseq2_vst	geneid2011hs	bulk	GSE186341	2022-10-28	2022-12-01	public	<input type="checkbox"/>

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

Title: Integrated bioinformatic analysis of neuroblastoma data

Summary: mRNA profiles of thousands of human tumors are available, but methods to deduce oncogenic signaling networks from these data lag behind. It is especially challenging to identify main-regulatory routes, and to generalize conclusions obtained from experimental models. We designed the bioinformatic platform R2 in parallel with a wet-lab approach of neuroblastoma. Here we demonstrate how R2 facilitates an integrated analysis of our neuroblastoma data. Analysis of the MYCN pathway suggested important regulatory connections to the polyamine synthesis route, the Notch pathway and the BMP/TGF β pathway. A network of genes emerged connecting major oncogenes in neuroblastoma. Genes in the network carried strong prognostic values and were essential for tumor cell survival.

Design: 88 human Neuroblastoma samples were analyzed.

Available tracks in R2:

- age_year: (#) 0 - 13
- agegroup: <=1, >1
- alive: no, yes
- death_cause: nd, toxic, tumor
- gender: female, male
- histology: nb

Adjustments: MAS5.0 normalization was performed in GCOS with trimmed mean 96 set to 100 (alpha1=0.04, alpha2=0.06).

Available on R2 since: 2010-06-10

Platform: u133p2

Species: hs

Number of samples: 88

Source: GEO ID: [GSE16476](#) **Date:** 2012-03-08

Pubmed link: [22367537](#)

R2 internal identifier: ps_avgpres_nbadam88_u133p2

Dataset Selection

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

Species	Data type	Category	Tissue/Tumor	Author	N	Normalization	Platform	Comp...	Accession	Release da...	R2 date	Access	Favo...
hs	Expression data	Tumor	Neuroblastoma public	Versteeg	88	MAS5.0	u133p2	bulk	GSE16476	2012-03-08	2010-06-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Cell line	CCLC Cancer Cell Line Encyclopedia	Broad	917	MAS5.0	u133p2	bulk	GSE36133	2012-03-20	2012-04-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Normal	Adrenal Medulla development	Westermann	10739	cp10k	10x300hg19	single cell		2021-03-28	2021-03-28	public	<input checked="" type="checkbox"/>
hs	Expression data	Allograft	Kidney	Naesens	224	MAS5.0	u133p2	bulk	GSE147089	2020-11-10	2023-02-21	public	<input type="checkbox"/>
hs	Expression data	Cell line	ALL(T)	Ferrando	20	MAS5.0	u133p2	bulk	GSE48046	2013-06-18	2013-09-04	public	<input type="checkbox"/>
hs	Expression data	Cell line	B cell lymphoma (DLBCL)	Baden Holmes	29	deseq2_rlog	tpm109geo	bulk	GSE207388	2022-07-01	2023-06-16	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast	Hoeflich	51	MAS5.0	u133p2	bulk	GSE12777	2009-01-12	2009-08-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast HCC1143 32 kinase inhibitors	Douglass	184	deseq2_vst	geneid2011hs	bulk	GSE186341	2021-10-28	2022-12-01	public	<input type="checkbox"/>

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

Title: Integrated bioinformatic and wet-lab approach to identify potential oncogenic networks in neuroblastoma

Summary: mRNA profiles of thousands of human tumors are available, but methods to deduce oncogenic signaling networks from these data lag behind. It is especially challenging to identify main-regulatory routes, and to generalize conclusions obtained from experimental models. We designed the bioinformatic platform R2 in parallel with a wet-lab approach of neuroblastoma. Here we demonstrate how R2 facilitates an integrated analysis of our neuroblastoma data. Analysis of the MYCN pathway suggested important regulatory connections to the polyamine synthesis route, the Notch pathway and the BMP/TGF β pathway. A network of genes emerged connecting major oncogenes in neuroblastoma. Genes in the network carried strong prognostic values and were essential for tumor cell survival.

Design: 88 human Neuroblastoma samples were analyzed.

Available tracks in R2:

- age_year: (#) 0 - 13
- agegroup: <=1, >1
- alive: no, yes
- death_cause: nd, toxic, tumor
- gender: female, male
- histology: nb

Adjustments: MAS5.0 normalization was performed in GCOS with trimmed mean 96 set to 100 (alpha1=0.04, alpha2=0.06).

Available on R2 since: 2010-06-10

Platform: u133p2

Species: hs

Number of samples: 88

Source: GEO ID: [GSE16476](#) **Date:** 2012-03-08

Pubmed link: [22367537](#)

R2 internal identifier: ps_avgpres_nbadam88_u133p2

Dataset Tracks: annotation

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

Species	Data type	Category	Tissue/Tumor
hs	Expression data	Tumor	Neuroblastoma public
hs	Expression data	Cell line	CCLC Cancer Cell Line Encyclopedia
hs	Expression data	Normal	Adrenal Medulla development
hs	Expression data	Allograft	Kidney
hs	Expression data	Cell line	ALL(T)
hs	Expression data	Cell line	B cell lymphoma (DLBCL)
hs	Expression data	Cell line	Breast
hs	Expression data	Cell line	Breast HCC1143 32 kinase inhibitors

samplenames	agegroup	inss	mycn_amp	age_year	alive	death_cause	gender
ITCC0001	<=1	st2	no	0	yes	nd	female
ITCC0002	<=1	st2	no	0	yes	nd	male
ITCC0003	<=1	st4s	no	0	yes	nd	female
ITCC0008	<=1	st2	no	0	yes	nd	male
ITCC0009	>1	st2	no	1	yes	nd	female
ITCC0010	<=1	st4	no	0	yes	nd	male
ITCC0013	>1	st4	no	2	no	tumor	female
ITCC0015	>1	st4	yes	6	no	tumor	female
ITCC0017	>1	st4	no	6	no	tumor	female
ITCC0018	>1	st4	no	2	no	tumor	female
ITCC0020	>1	st4	yes	1	no	tumor	male
ITCC0021	>1	st4	yes	1	no	tumor	male
ITCC0022	>1	st4	yes	1	no	tumor	female
ITCC0024	>1	st4	no	4	no	tumor	female
ITCC0025	>1	st4	yes	1	no	tumor	male
ITCC0026	>1	st4	yes	13	yes	nd	male
ITCC0027	<=1	st3	no	0	no	toxic	male
ITCC0030	<=1	st3	no	0	yes	nd	male

Species	Favo...
hs	<input checked="" type="checkbox"/>
hs	<input checked="" type="checkbox"/>
hs	<input checked="" type="checkbox"/>
hs	<input type="checkbox"/>
hs	<input type="checkbox"/>
hs	<input type="checkbox"/>
hs	<input type="checkbox"/>
hs	<input type="checkbox"/>
hs	<input type="checkbox"/>

Title: Integrated bioinformatic and wet-lab approach to identify potential oncogenic networks

Summary: mRNA profiles of thousands of human tumors are available, but methods to deduce models. We designed the bioinformatic platform R2 in parallel with a wet-lab approach to identify connections to the polyamine synthesis route, the Notch pathway and the BMP/TGF- β survival.

Design: 88 human Neuroblastoma samples were analyzed.

Available tracks in R2:

- age_year: (#) 0 - 13
- agegroup: <=1, >1
- alive: no, yes
- death_cause: nd, toxic, tumor
- gender: female, male
- histology: nb

Adjustments: MAS5.0 normalization was performed in GCOS with trimmed mean 96 set to 1

Available on R2 since: 2010-06-10

Platform: u133p2

Species: hs

Number of samples: 88

Source: GEO ID: [GSE16476](#) Date: 2012-03-08

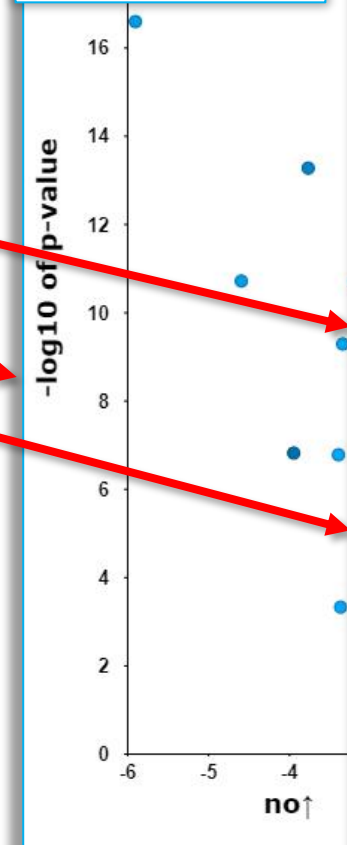
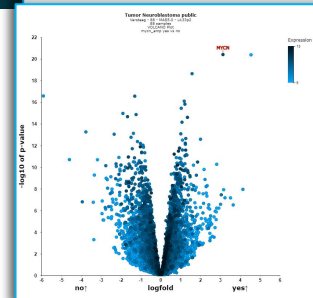
Pubmed link: [22367537](#)

R2 internal identifier: ps_avgpres_nbadam88_u133p2

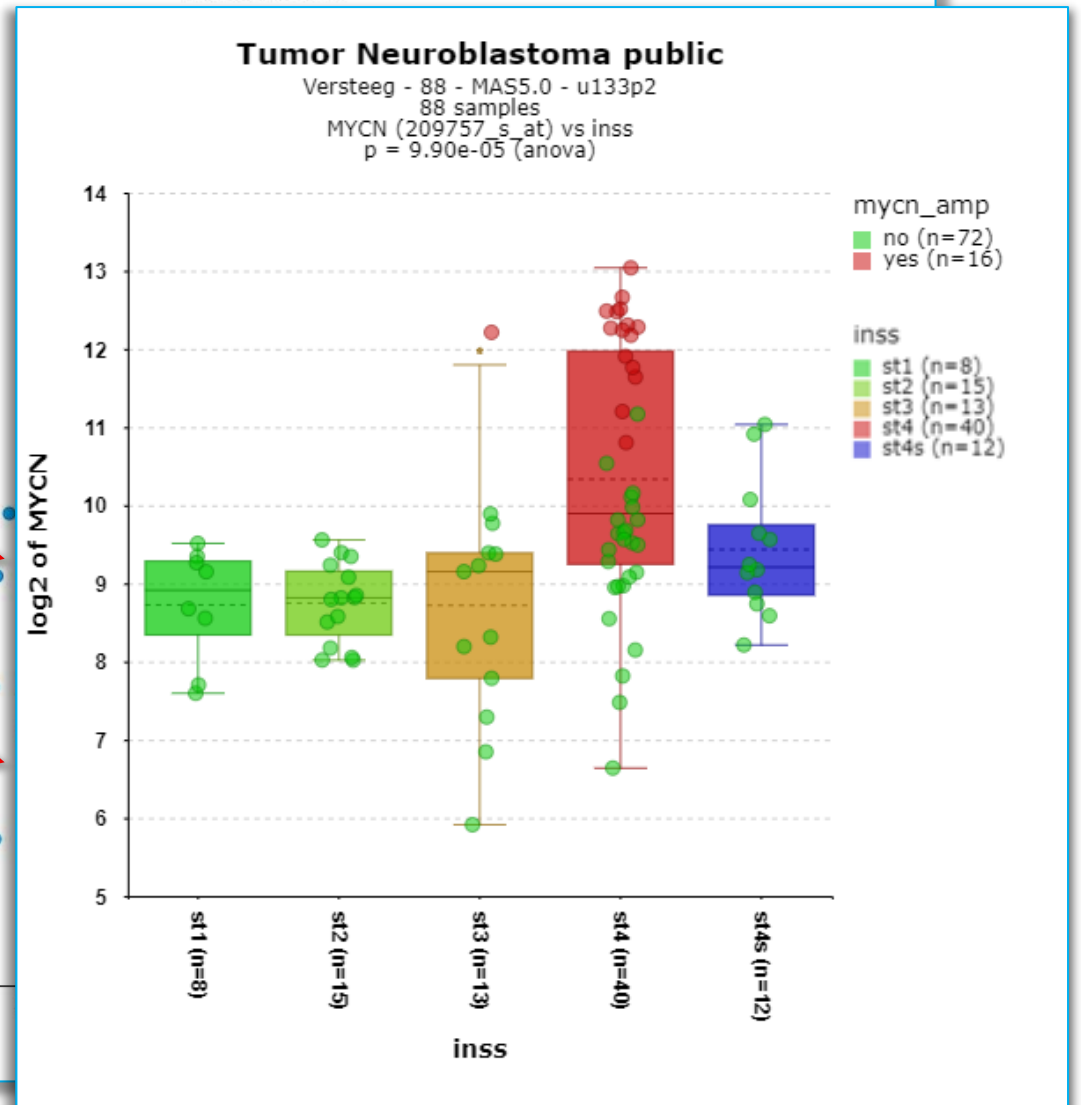
ns obtained from experimental suggested important regulatory b were essential for tumor cell

Dataset Tracks: annotation

samplenames	agegroup	inss	mycn_amp	age_year	alive	death_cause	gender
ITCC0001	<=1	st2	no	0	yes	nd	female
ITCC0002	<=1	st2	no	0	yes	nd	male
ITCC0003	<=1	st4s	no	0	yes	nd	female
ITCC0008	<=1	st2	no	0	yes	nd	male
ITCC0009	>1	st2	no	1	yes	nd	female
ITCC0010	<=1	st4	no	0	yes	nd	male
ITCC0013	>1	st4	no	2	no	tumor	female
ITCC0015	>1	st4	yes	6	no	tumor	female
ITCC0017	>1	st4	no	6	no	tumor	female
ITCC0018	>1	st4	no	2	no	tumor	female
ITCC0020	>1	st4	yes	1	no	tumor	male
ITCC0021	>1	st4	yes	1	no	tumor	male
ITCC0022	>1	st4	yes	1	no	tumor	female
ITCC0024	>1	st4	no	4	no	tumor	female
ITCC0025	>1	st4	yes	1	no	tumor	male
ITCC0026	>1	st4	yes	13	yes	nd	male
ITCC0027	<=1	st3	no	0	no	toxic	male
ITCC0030	<=1	st3	no	0	yes	nd	male

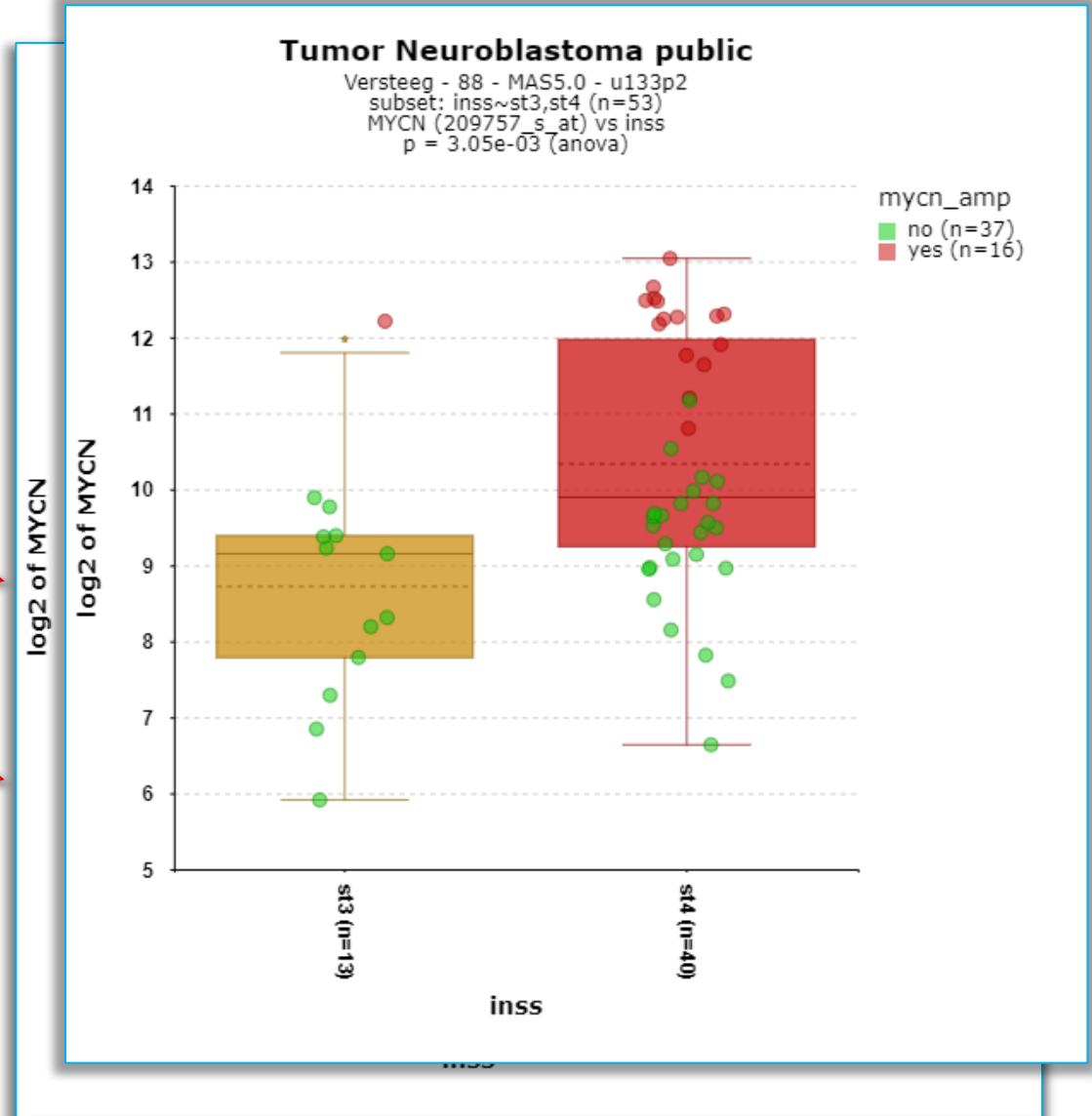
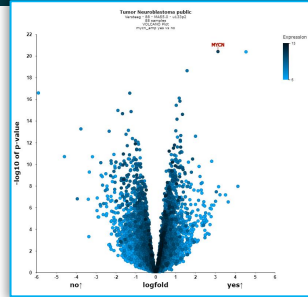


Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
88 samples
VOLCANO Plot
mycn_amp yes vs no



Dataset Tracks: annotation

samplenames	agegroup	inss	mycn_amp	age_year	alive	death_cause	gender
ITCC0001	<=1	st2	no	0	yes	nd	female
ITCC0002	<=1	st2	no	0	yes	nd	male
ITCC0003	<=1	st4s	no	0	yes	nd	female
ITCC0008	<=1	st2	no	0	yes	nd	male
ITCC0009	>1	st2	no	1	yes	nd	female
ITCC0010	<=1	st4	no	0	yes	nd	male
ITCC0013	>1	st4	no	2	no	tumor	female
ITCC0015	>1	st4	yes	6	no	tumor	female
ITCC0017	>1	st4	no	6	no	tumor	female
ITCC0018	>1	st4	no	2	no	tumor	female
ITCC0020	>1	st4	yes	1	no	tumor	male
ITCC0021	>1	st4	yes	1	no	tumor	male
ITCC0022	>1	st4	yes	1	no	tumor	female
ITCC0024	>1	st4	no	4	no	tumor	female
ITCC0025	>1	st4	yes	1	no	tumor	male
ITCC0026	>1	st4	yes	13	yes	nd	male
ITCC0027	<=1	st3	no	0	no	toxic	male
ITCC0030	<=1	st3	no	0	yes	nd	male



Dataset Selection

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

Species	Data type	Category	Tissue/Tumor	Author	N	Normalization	Platform	Comp...	Accession	Release da...	R2 date	Access	Favo...
hs	Expression data	Tumor	Neuroblastoma public	Versteeg	88	MAS5.0	u133p2	bulk	GSE16476	2012-03-08	2010-06-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Cell line	CCLC Cancer Cell Line Encyclopedia	Broad	917	MAS5.0	u133p2	bulk	GSE36133	2012-03-20	2012-04-10	public	<input checked="" type="checkbox"/>
hs	Expression data	Normal	Adrenal Medulla development	Westermann	10739	cp10k	10x300hg19	single cell		2021-03-28	2021-03-28	public	<input checked="" type="checkbox"/>
hs	Expression data	Allograft	Kidney	Naesens	224	MAS5.0	u133p2	bulk	GSE147089	2020-11-10	2023-02-21	public	<input type="checkbox"/>
hs	Expression data	Cell line	ALL(T)	Ferrando	20	MAS5.0	u133p2	bulk	GSE48046	2013-06-18	2013-09-04	public	<input type="checkbox"/>
hs	Expression data	Cell line	B cell lymphoma (DLBCL)	Baden Holmes	29	deseq2_rlog	tpm109geo	bulk	GSE207388	2022-07-01	2023-06-16	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast	Hoeflich	51	MAS5.0	u133p2	bulk	GSE12777	2009-01-12	2009-08-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast HCC1143 32 kinase inhibitors	Douglass	184	deseq2_vst	geneid2011hs	bulk	GSE186341	2021-10-28	2022-12-01	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast MCF7 (methotrexate resistant)	Ciudad	6	MAS5.0	u133p2	bulk	GSE16070	2009-09-08	2015-12-11	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast Xenoestrogen	Isselbacher	351	MAS5.0	u133p2	bulk	GSE50705	2013-09-10	2013-10-14	public	<input type="checkbox"/>
hs	Expression data	Cell line	Breast Xenoestrogen	Isselbacher	351	FRMA	u133p2	bulk	GSE50705	2013-09-10	2013-10-14	public	<input type="checkbox"/>

rows: 2098

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

Title: Integrated bioinformatic and wet-lab approach to identify potential oncogenic networks in neuroblastoma

Summary: mRNA profiles of thousands of human tumors are available, but methods to deduce oncogenic signaling networks from these data lag behind. It is especially challenging to identify main-regulatory routes, and to generalize conclusions obtained from experimental models. We designed the bioinformatic platform R2 in parallel with a wet-lab approach of neuroblastoma. Here we demonstrate how R2 facilitates an integrated analysis of our neuroblastoma data. Analysis of the MYCN pathway suggested important regulatory connections to the polyamine synthesis route, the Notch pathway and the BMP/TGF β pathway. A network of genes emerged connecting major oncogenes in neuroblastoma. Genes in the network carried strong prognostic values and were essential for tumor cell survival.

Design: 88 human Neuroblastoma samples were analyzed.

Available tracks in R2:

- age_year: (#) 0 - 13
- agegroup: <=1, >1
- alive: no, yes
- death_cause: nd, toxic, tumor
- gender: female, male
- histology: nh

Adjustments: MAS5.0 normalization was performed in GCOS with trimmed mean 96 set to 100 (alpha1=0.04, alpha2=0.06).

Available on R2 since: 2010-06-10

Platform: u133p2

Species: hs

Number of samples: 88

Source: GEO ID: GSE16476 Date: 2012-03-08

R2 Main Page (r2.amc.nl)

- Go to: [Main](#)
- Main
 - Time series
 - Survival (Kaplan-Meier/Cox)
 - Sample maps (UMAP/tSNE)
 - Small Tools
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r2.amc.nl



Video training



YouTube



Integrated Analysis of Tumor Genomics Data with R2 Tutorials



R2

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R2: Genomics Analysis and Visualization Platform

2,191,770 (2,029,829 unique) samples available

Choose single or multiple dataset analysis

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- 2 **Select a dataset for analysis**
- 3 **Select type of analysis**
 ⓘ
- 4 **Proceed**

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

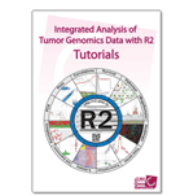
Check out the new iTHER pediatric cancer precision medicine datascope. Now publicly available in R2 via the 'datascope' menu item.

[all news](#)



View a Gene

- Go to: **Main**
- Main
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 - AmpliconView
 - Kaplan-Meier
 - Sample maps
 - Small Tools
 - DataGrabber
 - Genome Browser
 - ChIP data
 - TAR literature
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R2: Genomics Analysis and Visualization Platform

2,008,352 (1,846,508 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** Proceed

Online Tutorial

What is R2?
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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** on Friday the **7th of October 2022**. For more info and registration click [here](#)

[all news](#)



View a Gene: Gene / Reporter required

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

Adjustable settings

Analysis type:

Gene / Reporter:

Transformation: ⓘ

Sample Filter

Subset track: ⓘ ⓘ

Selected sample subset: None

Graphics

Graph type: ⓘ

Extra Graph Option: ⓘ

Samples to mark: ⓘ

Color mode:

Track Display Selection

More Settings +

View a Gene pre-settings: Advanced gene search

- 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

Analysis type:

Gene / Reporter:

Transformation: ⓘ

Sample Filter

Subset track: ⓘ

Selected sample subset: None

Graphics

Graph type: ⓘ

Extra Graph Option: ⓘ

Samples to mark: ⓘ

Color mode:

Track Display Selection

More Settings

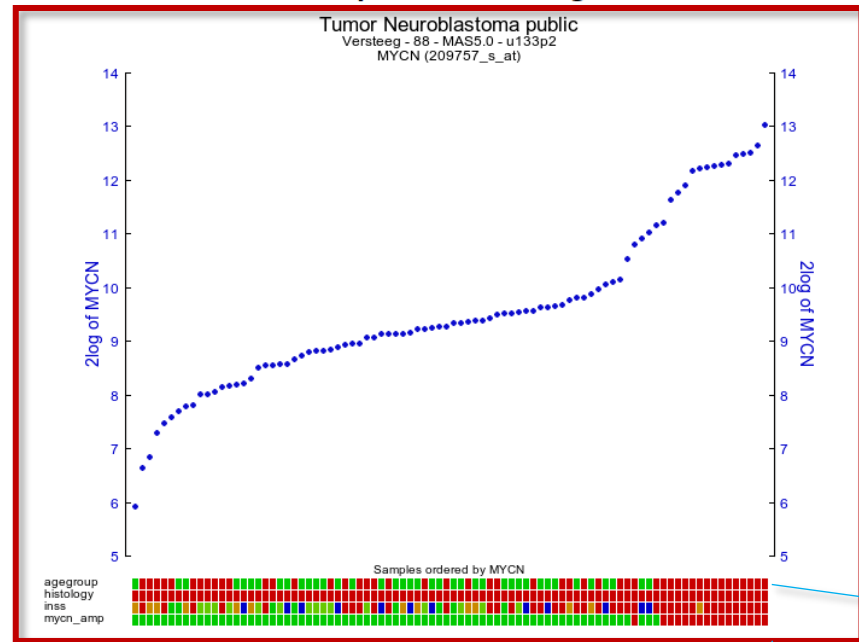
View a Gene: page overview

Go to: [Main](#)

R2: One Gene View for MYCN

[Online Tutorial](#)

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



default

agegroup

- <= 1
- > 1

histology

- nb

inss

- st1
- st2
- st3
- st4
- st4s

mycn_amp

- no
- yes

Pubsniffer

MYCN

GeneCards

MYCN

KaplanScanner

MYCN (overall-2011/03)
MYCN (relapsefree-2011/03)

Time Series

Check

ProbePlus

209757_s_at

CliniSnitch

MYCN

Across datasets

Expression in datasets

Data set

Sample overview

Sample Map(s)

map 2021-01-06
map 2022-03-01

GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

[View additional details](#)

[View data table](#)

Analysis type:

Gene / Reporter:

Transformation:

Sample Filter

Subset track:

Selected sample subset: None

Graphics

Graph type:

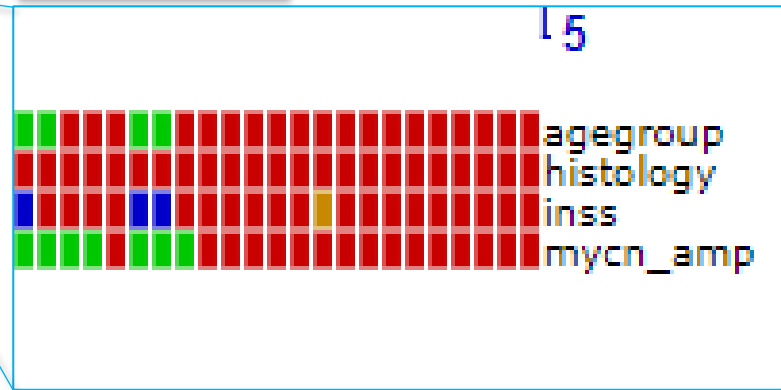
Extra Graph Option:

Samples to mark:

Color mode:

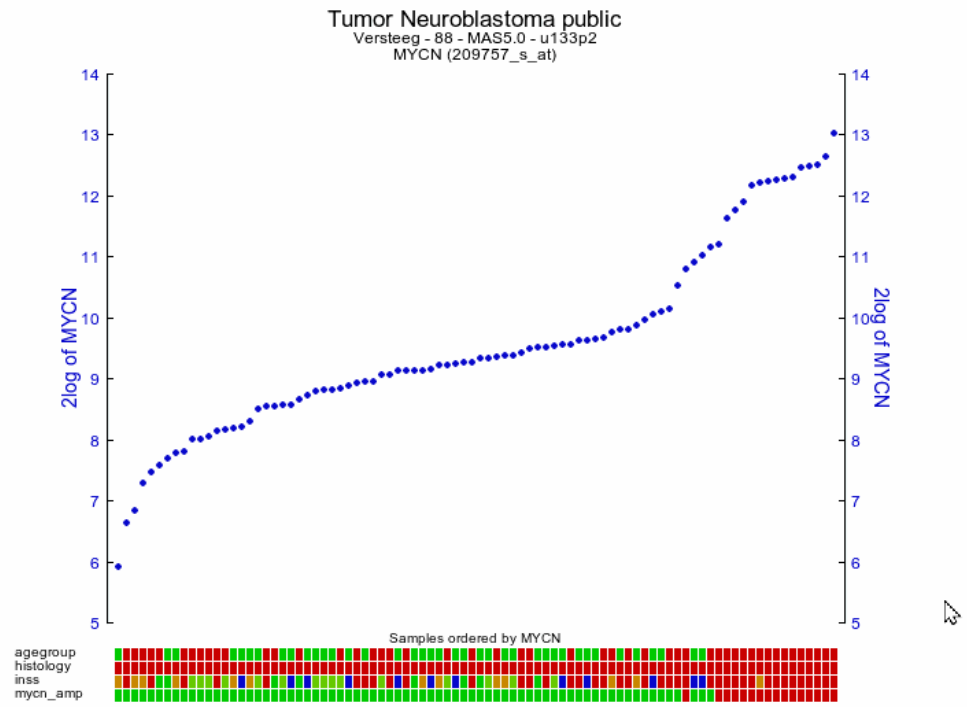
Track Display Selection

More Settings



View a Gene: hover over the plot

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



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

► [View additional details](#)

[View data table](#)

Adjustable settings

Analysis type: single gene ▼

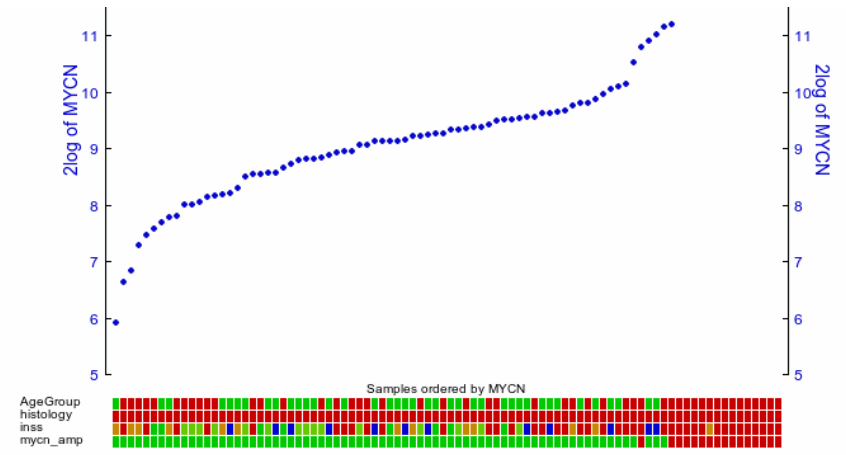
Gene / Reporter: MYCN 209757_s_at advanced

Transformation: Log2 ▼ ⓘ

Sample Filter

Subset track: ▼ ⓘ ⓘ

View a Gene: page overview



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

► View additional details

View data table

Adjustable settings

Analysis type: single gene

Gene / Reporter: MYCN 209757_s_at advanced

Transformation: Log2

Subset track: Log2

Selected sample subset: Log2 z-score

Graph type: Center

Extra Graph Option: Log2 center

Samples to mark: Rank

Color mode: Log2 grouped z-score

Track Display Selection

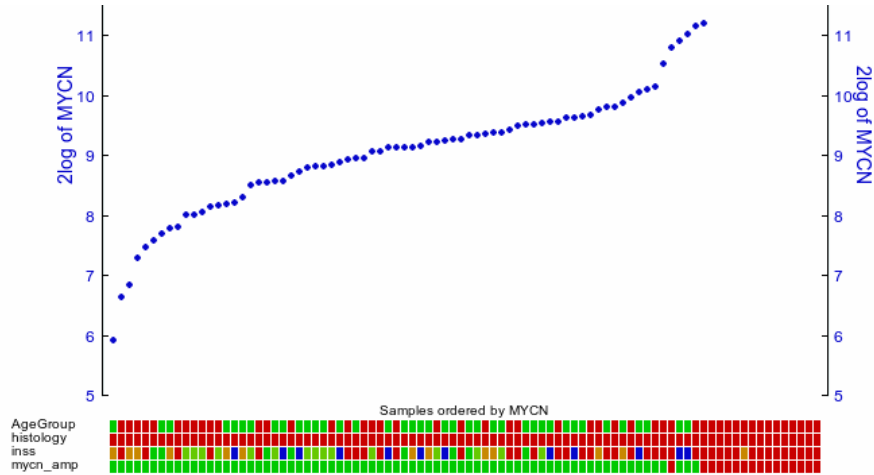
Select tracks

More Settings

Submit

Store Preset

Sample filters



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

► View additional details

View data table

Adjustable settings

Analysis type: ▼

Gene / Reporter: advanced

Transformation: ⓘ

Sample Filter

Subset track: ⚙️ ⓘ

Selected sample subset: None

Graphics

Graph type: ⓘ

Extra Graph Option: ⓘ

Samples to mark: ⓘ

Color mode: ⓘ

Track Display Selection

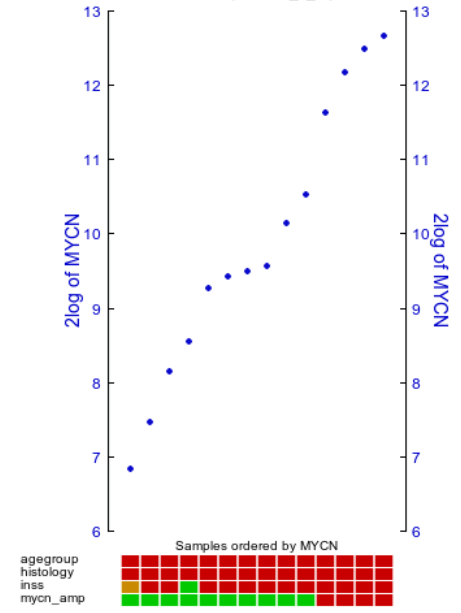
More Settings +

Store Preset

Sample filters: advanced selection

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

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
gender=female|age_year>=2 (n=14)
MYCN (209757_s_at)



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

▶ [View additional details](#)

[View data table](#)

Adjustable settings

Analysis type: single gene

Gene / Reporter: MYCN 209757_s_at advanced

Transformation: Log2

Sample Filter

Subset track: ⚙️ ❌ ⓘ

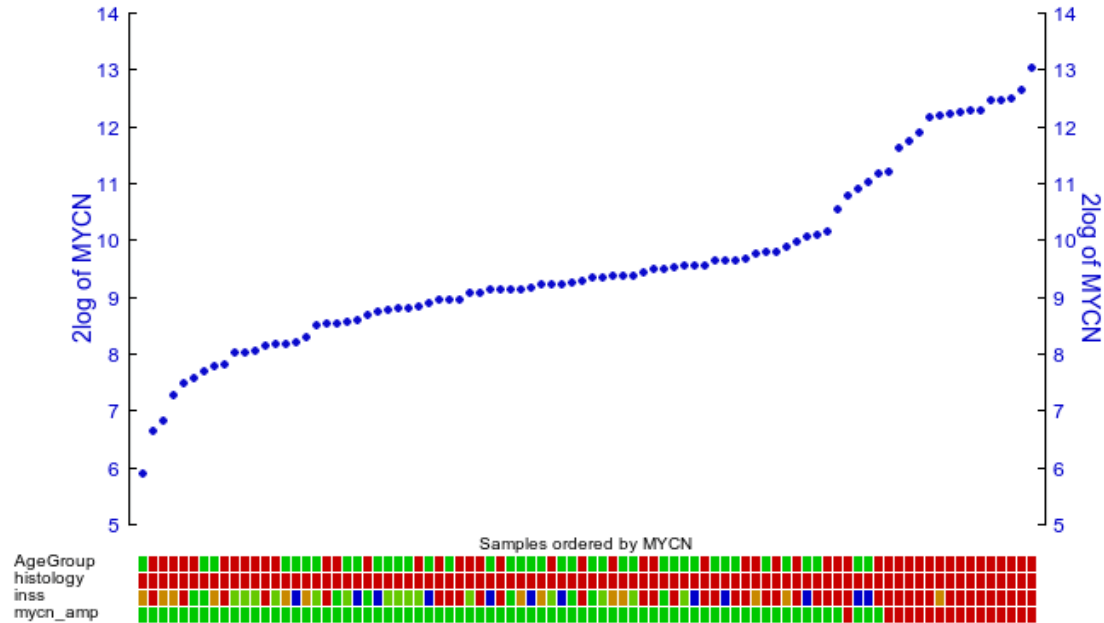
Number of samples in subset: n=14

- Pubsniiffer**
- MYCN
- GeneCards**
- MYCN
- KaplanScanner**
- MYCN (overall-2011/03)
- MYCN (relapsefree-2011/03)
- Time Series**
- Check
- ProbePlus**
- 209757_s_at
- CliniSnitch**
- MYCN
- Across datasets**
- Expression in datasets
- Data set**
- Sample overview
- Sample Map(s)**
- map 2021-01-06
- map 2022-03-01

View a Gene: Side menu

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

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
MYCN (209757_s_at)



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

► [View additional details](#)

[View data table](#)

- Pubsniiffer**
[MYCN](#)
- GeneCards**
[MYCN](#)
- KaplanScanner**
[MYCN \(overall-2011/03\)](#)
[MYCN \(relapsefree-2011/03\)](#)
- Time Series**
[Check](#)
- ProbePlus**
[209757_s_at](#)
- CliniSnitch**
[MYCN](#)
- Across datasets**
[Expression in datasets](#)
- Data set**
[Sample overview](#)
- Sample Map(s)**
[map 2021-01-06](#)
[map 2022-03-01](#)

Go to: [Main](#)

R2: clinisnitch (by values)

[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

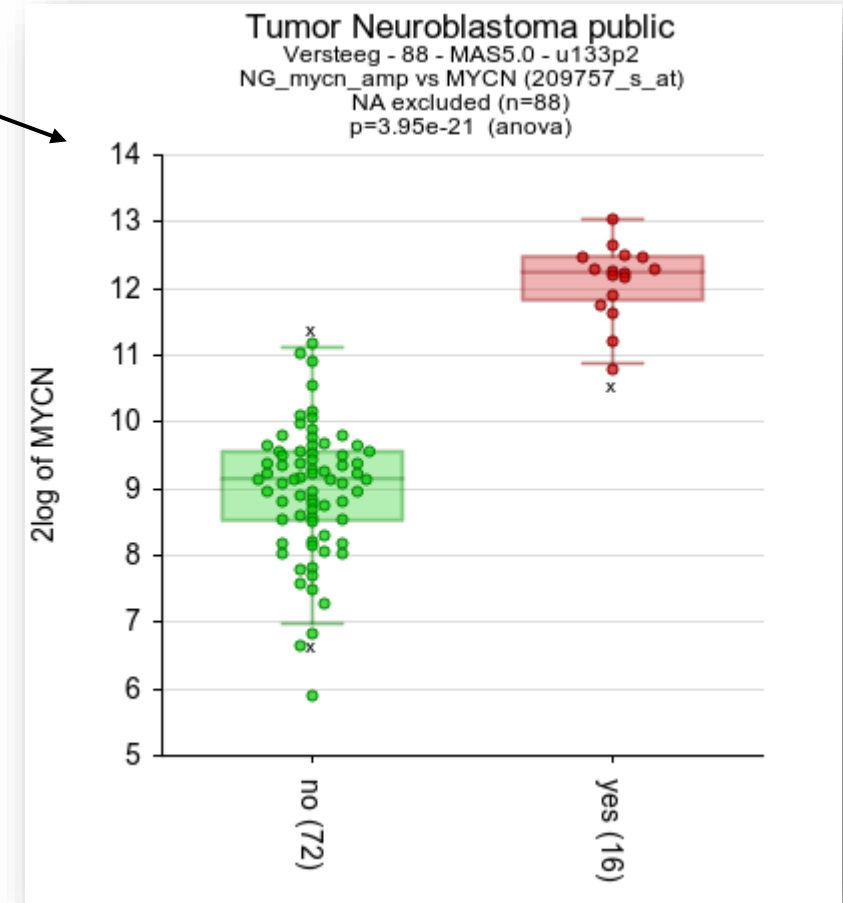
Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public ⓘ

MYCN (209757_s_at)

catvsnum	
track	pvalue
histology	1 group
r2_label	test failed
samplenames	test failed
mycn_amp (View)	3.95e-21
nti_event_overall (View)	9.55e-05
inss (View)	9.90e-05
recurrence_or_progression (View)	1.58e-04
nti_event_progfree (View)	1.88e-04
alive (View)	5.66e-04
agegroup (View)	0.014
death_cause (View)	0.155
gender (View)	0.726

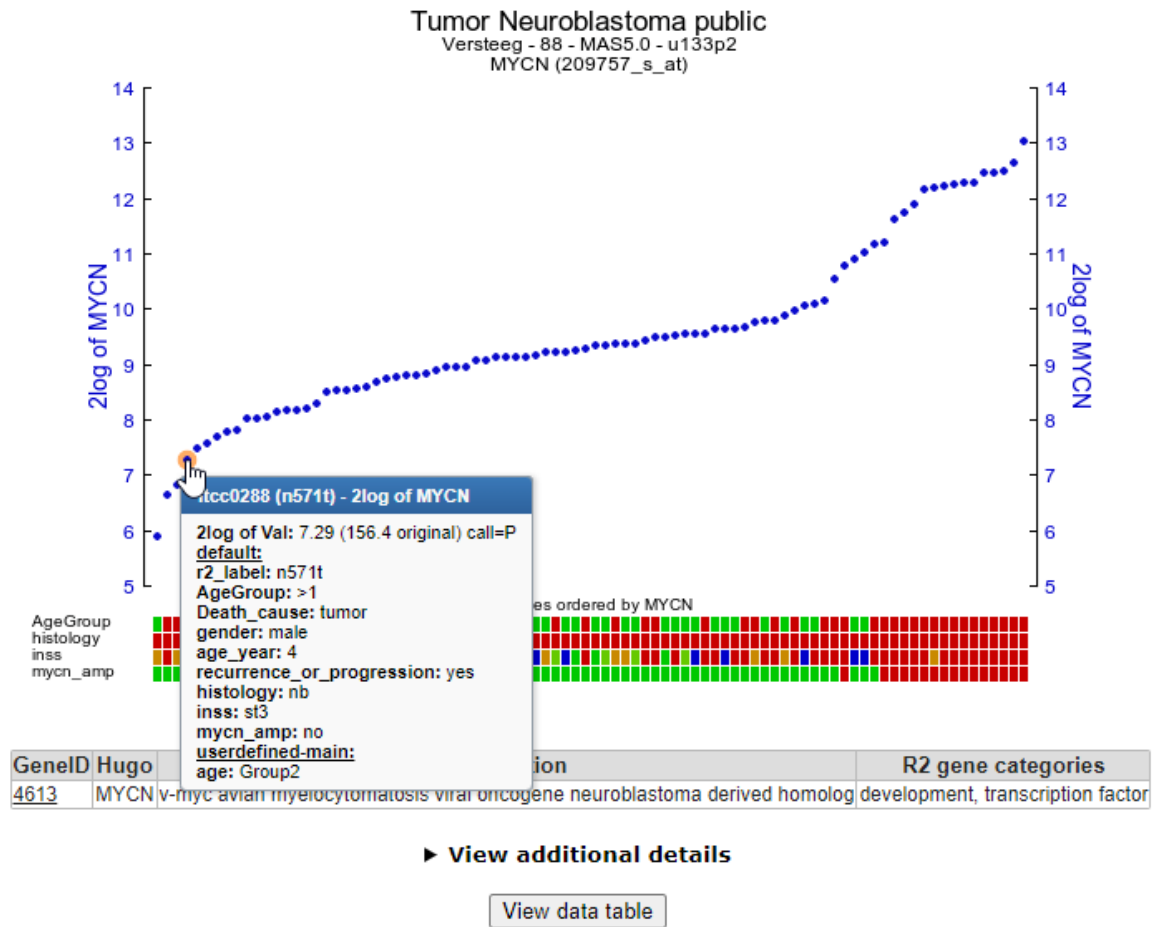
numvsnum	
track	pvalue
nti_surv_progfree (View)	0.00813204967822536
nti_surv_overall (View)	0.010917082155167
age_year (View)	0.202454009051515
id (View)	0.630681656951703

CliniSnitch (Historic)
Execute it the old way



Sample Overview

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



Find extreme genes for a patient (itcc0288)

PubSniffer	
MYCN	
GeneCards	
MYCN	
KaplanScanner	
MYCN (overall-2011/03)	
MYCN (relapsefree-2011/03)	
Time Series	
Check	
ProbePlus	
209757 s at	
CliniSnitch	
MYCN	
Across datasets	
Expression in datasets	
Data set	
Sample overview	
Sample Map(s)	
map 2021-01-06	
map 2022-03-01	

Sample Overview

nti_surv_progfree	387
recurrence_or_progression	yes
samplenames	ITCC0288

Expression Binner

Select Datasource for Binner

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

Obtain expression extremes (compared to the rest of the dataset) for the current sample

Get Extremes for ITCC0288

Sample Filter

Subset track: ▼

Selected sample subset: None

Gene Filters

Chromosome: All ▼

Gene ontology: All ▼

Gene set:

Manual list: none ▼

Statistics

Absolute zscore cutoff: 2.24

Sample Extremes

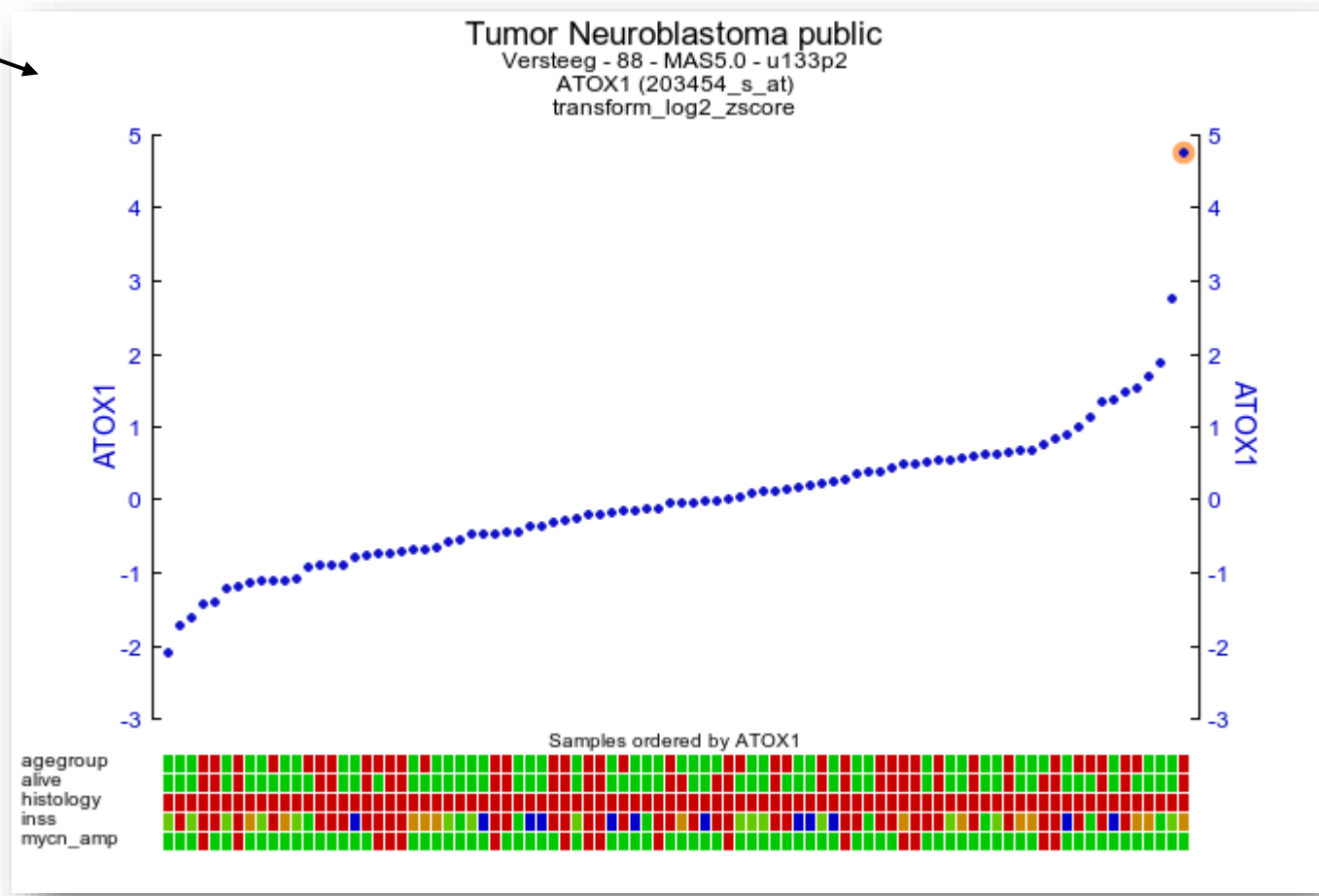
Go to: [Main](#)

R2: Sample Extremes

[Online Tutorial](#)

Genes with extreme expression values(zscore>2.24) for itcc0288

Z-score	Gene	Express	Z-score	Gene	Express
-6.46	RUFY2	2.2	4.76	ATOX1	1701.1
-5.98	PDE9A	1.8	4.34	TOR3A	392.5
-5.95	PAIP2B	3.4	4.33	PIK3C3	981.7
-5.91	DNMBP	1.9	4.18	SERPINI1	1520.7
-5.70	LOC102725022	6.5	4.03	MRPL51	2049.0
-5.28	NIPSNAP3B	7.4	3.85	NR1H3	632.7
-5.15	TH	1.5	3.85	GTSF1	1084.3
-5.12	INPP5A	56.5	3.78	GMPR2	501.4
-5.07	ATP2B2	1.7	3.74	VOPP1	1401.1
-4.90	TPPP	13.9	3.72	ZNHIT1	1231.3
-4.89	LOC100133039	3.3	3.69	PSMC3IP	625.2
-4.81	DDC	4.6	3.67	NUAK1	1142.5
-4.80	DBH	1.1	3.59	GRM3	225.9
-4.80	BAIAP2-AS1	4.0	3.57	MGC70870	230.1
-4.78	UNC5C	3.9	3.49	C19ORF70	736.6
-4.76	PELI2	5.4	3.47	TFRC	3780.7
-4.61	TTCT7A	4.1	3.45	SDCCAG3	337.7
-4.60	NTNG2	0.7	3.41	WDR34	673.1
-4.57	VAV2	23.4	3.38	LSM1	1220.9
-4.55	FURIN	2.5	3.37	RTP1	103.3
-4.52	JPH3	7.5	3.36	POLR2H	1105.7
-4.48	ZNF383	3.1	3.33	TCTEX1D2	919.1
-4.38	PKD1P1	3.8	3.28	EIF2B5	363.4
-4.34	QPR146	2.3	3.26	UBAC1	464.5
-4.33	FRMD6-AS1	4.1	3.24	NEDD8	2786.2
-4.27	LINC00260	1.6	3.23	MRPL47	2266.3
-4.26	TSHZ3	24.4	3.22	ST6GALNAC3	1020.5
-4.16	IRX1	0.2	3.22	RPS19BP1	794.9
-4.11	DYRK1B	1.7	3.21	ACTL6A	974.5
-4.07	PEG3	18.7	3.21	PPIH	657.9
-4.05	H6PD	6.0	3.20	FBXO8	1213.8
-4.00	ABLIM1	49.4	3.17	LYPD6B	125.8
-3.99	ZDHHC11	7.7	3.15	SOX5	735.3
-3.96	PXK	52.9	3.14	DFNB59	112.3
-3.95	LINC00942	2.2	3.14	TMEM138	473.9
-3.94	ARSD	13.4	3.13	BUD31	1361.6
-3.94	LINC00664	0.7	3.12	ZMYND19	364.6
-3.94	ADARB1	10.1	3.10	AKAP12	3905.2
-3.91	LOC101927043	1.2	3.08	PAGE1	90.0
-3.88	SAXO2	0.5	3.08	PLA2G7	1524.8
-3.87	PLCD4	1.9	3.07	GRM1	362.1
-3.86	GTF2IP20	1.5	3.07	ZPR1	365.6
-3.84	SYT16	0.4	3.05	DPCD	355.3
-3.82	SLC37A1	3.1	3.05	SDHD	1271.4
-3.81	LOC101928590	0.4	3.04	ATP6V1F	2255.2
-3.80	RTKN	1.2	3.04	ZNHIT6	417.4
-3.77	ETS2	40.7	3.04	PARL	685.3
-3.77	ANP32A-IT1	4.2	3.04	CHMP1A	426.8
-3.77	ZSCAN20	2.5	3.03	SSBP1	3211.1
-3.76	SPOCK1	75.9	3.00	NUDT1	559.4
-3.75	SLC25A35	1.4	2.97	CFDP1	1676.9
-3.75	C1ORF226	13.3	2.97	MRPS21	3102.3
-3.72	ARSK	3.0	2.97	SSNA1	193.6



Sample Extremes

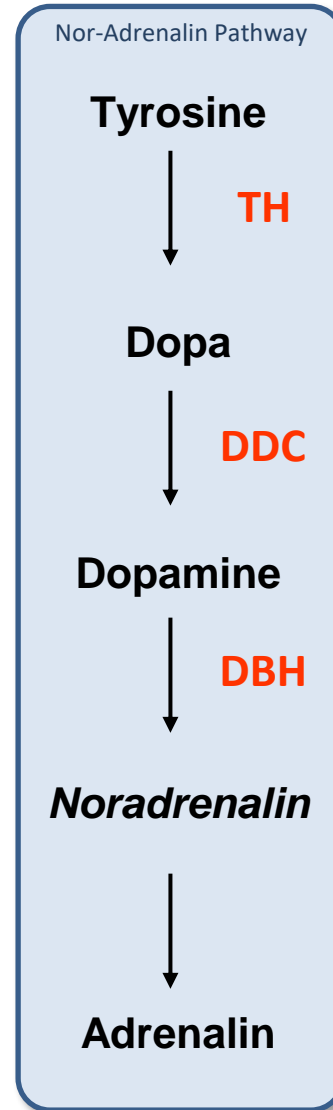
Go to: [Main](#)

R2: Sample Extremes

[Online Tutorial](#)

Genes with extreme expression values (zscore > 2.24) for itcc0288

Z-score	Gene	Express	Z-score	Gene	Express
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-4.55	FURIN	2.5	3.37	RTP1	103.3
-4.52	JPH3	7.5	3.36	POLR2H	1105.7
-4.48	ZNF383	3.1	3.33	TCTEX1D2	919.1
-4.38	PKD1P1	3.8	3.28	EIF2B5	363.4
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-4.07	PEG3	18.7	3.21	PPIH	657.9
-4.05	H6PD	6.0	3.20	FBXO8	1213.8
-4.00	ABLIM1	49.4	3.17	LYPD6B	125.8
-3.99	ZDHHC11	7.7	3.15	SOX5	735.3
-3.96	PXK	52.9	3.14	DFNB59	112.3
-3.95	LINC00942	2.2	3.14	TMEM138	473.9
-3.94	ARSD	13.4	3.13	BUD31	1361.6
-3.94	LINC00664	0.7	3.12	ZMYND19	364.6
-3.94	ADARB1	10.1	3.10	AKAP12	3905.2
-3.91	LOC101927043	1.2	3.08	PAGE1	90.0
-3.88	SAXO2	0.5	3.08	PLA2G7	1524.8
-3.87	PLCD4	1.9	3.07	GRM1	362.1
-3.86	GTF2IP20	1.5	3.07	ZPR1	365.6
-3.84	SYT16	0.4	3.05	DPCCD	355.3
-3.82	SLC37A1	3.1	3.05	SDHD	1271.4
-3.81	LOC101928590	0.4	3.04	ATP6V1F	2255.2
-3.80	RTKN	1.2	3.04	ZNHIT6	417.4
-3.77	ETS2	40.7	3.04	PARL	685.3
-3.77	ANP32A-IT1	4.2	3.04	CHMP1A	426.8
-3.77	ZSCAN20	2.5	3.03	SSBP1	3211.1
-3.76	SPOCK1	75.9	3.00	NUDT1	559.4
-3.75	SLC25A35	1.4	2.97	CFDP1	1676.9
-3.75	C1ORF226	13.3	2.97	MRPS21	3102.3
-3.72	ARSK	3.0	2.97	SSNA1	193.6



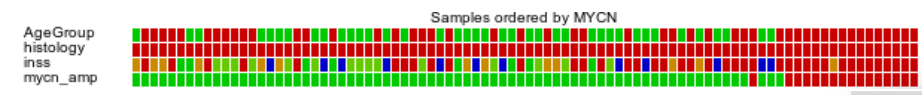
Nor-Adrenalin Pathway
controlled by Homeobox
transcription Factor

PHOX2B

Mutated in
ITCC0288



View all reporters



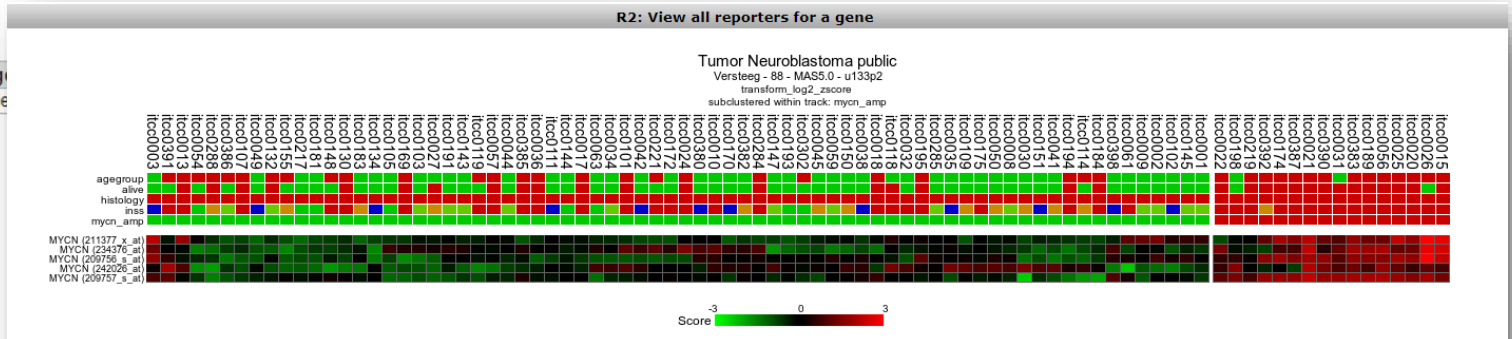
GeneID	Hugo	Description	R2 g
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	developme

[View additional details](#)
[View data table](#)

▼ View additional details

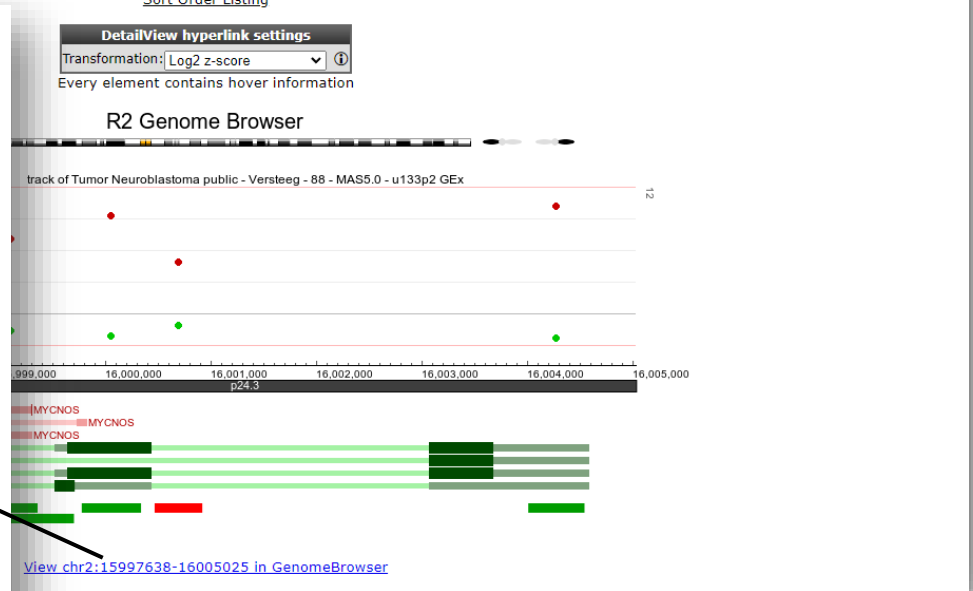
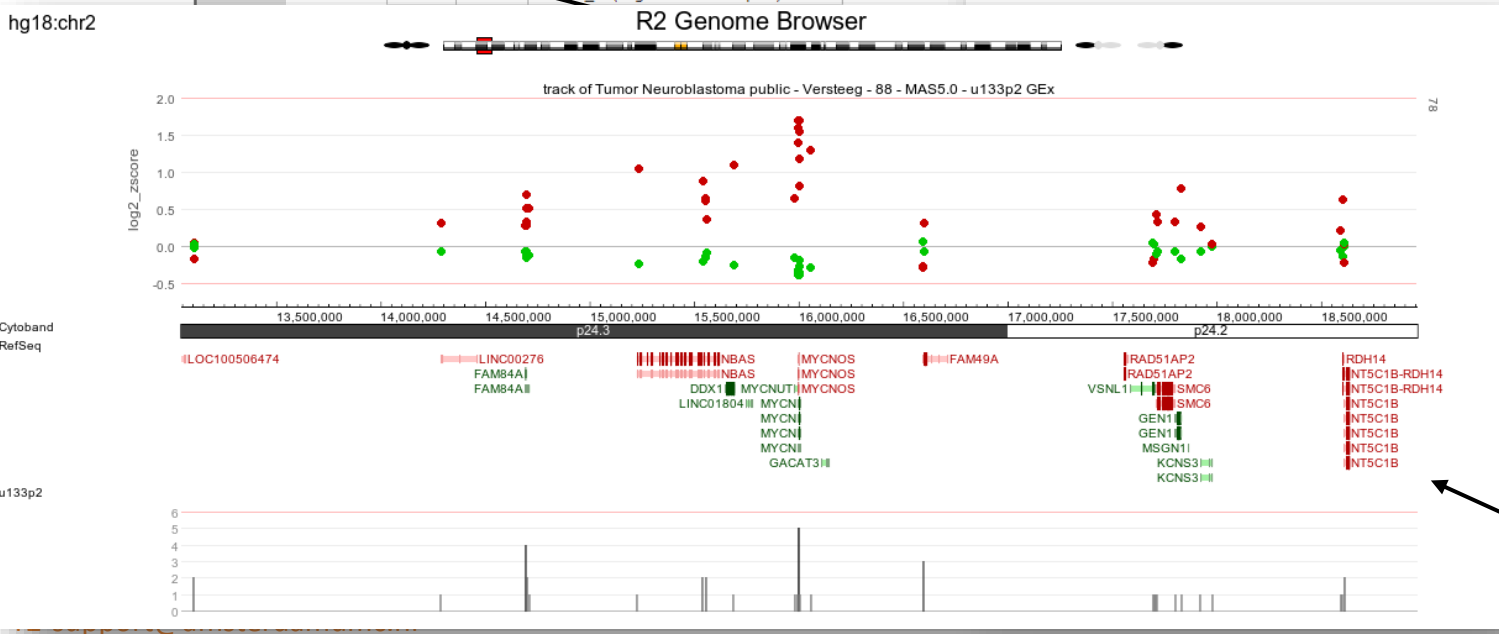
Alternative Reporters

Symbol Number	Reporter
MYCN	209757_s_at (avg 1369.7 in 88 samples)
	209756_s_at (avg 235.6 in 14 samples)
	211377_x_at (avg 158.8 in 5 samples)
	234376_at (avg 71.7 in 3 samples)
	242026_at (avg 22.8 in 5 samples)



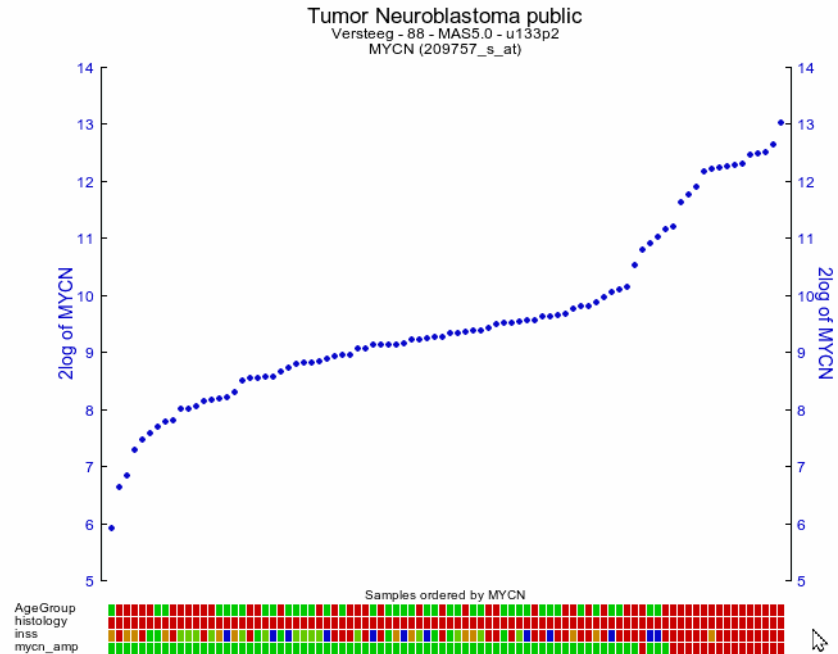
Sort Order Listing

DetailView hyperlink settings
 Transformation: [?](#)
 Every element contains hover information



View a Gene: Toggle tracks visualization

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



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

► View additional details

View data table

Adjustable settings

Analysis type:

Gene / Reporter:

Transformation: ⓘ

Sample Filter

Subset track: ⓘ ⓘ

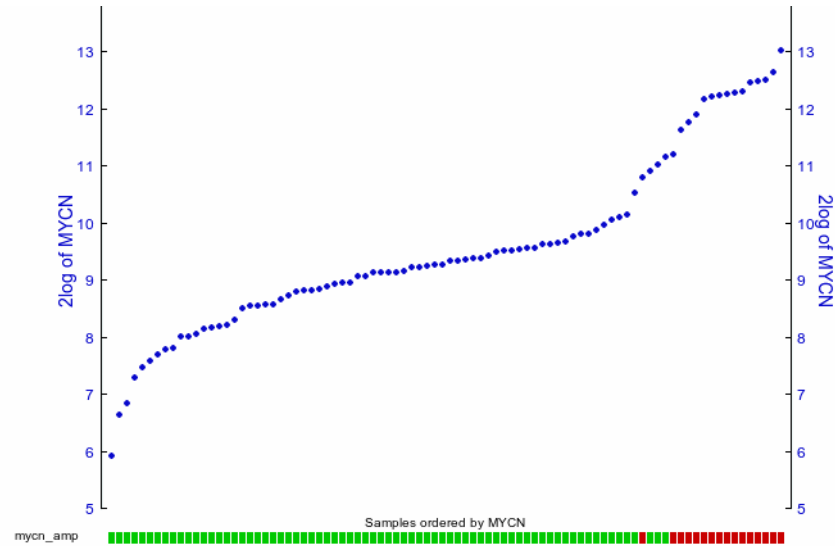
Selected sample subset: None

Graphics

Graph type: ⓘ

Extra Graph Option: ⓘ

View a Gene: Color by Track



GeneID	Hugo	Description	R2 gene categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog	development, transcription factor

► View additional details

View data table

Adjustable settings

Analysis type:

Gene / Reporter:

Transformation:

Sample Filter

Subset track:

Selected sample subset: None

Graphics

Graph type:

Extra Graph Option:

Samples to mark:

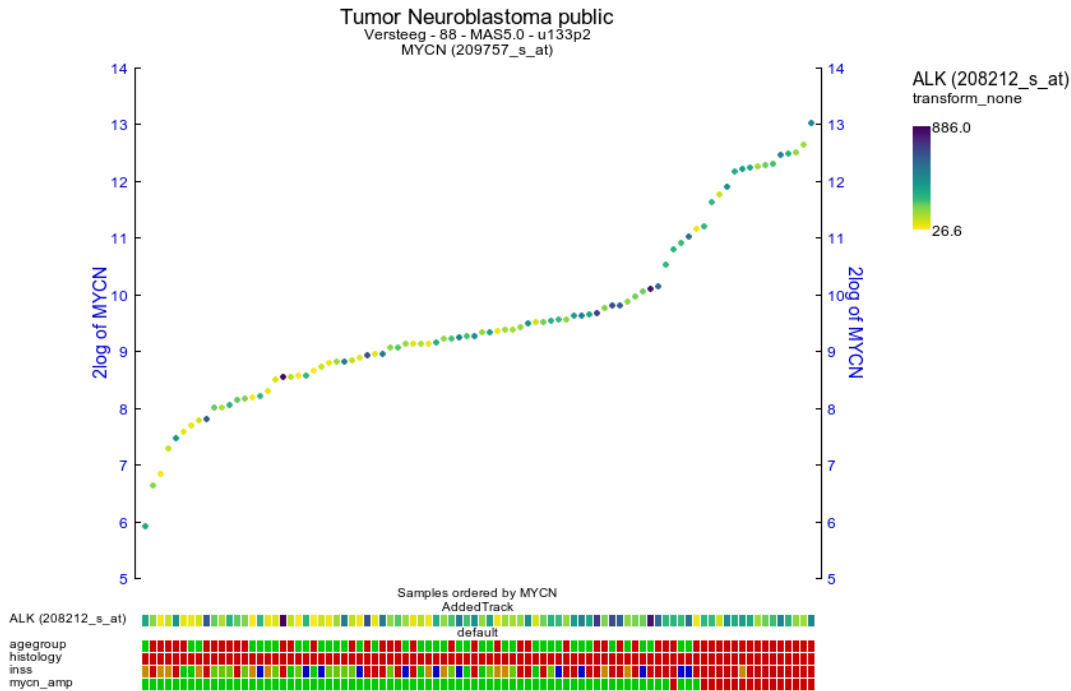
Color mode:

Track Display Selection

More Settings +

View a Gene: Color by Gene

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



Adjustable settings

Analysis type: ▾

Gene / Reporter: advanced

Transformation: ▾ ⓘ

Sample Filter

Subset track: ▾ ⓘ

Selected sample subset: None

Graphics

Graph type: ▾ ⓘ

Extra Graph Option: ▾ ⓘ

Samples to mark: ⓘ

Color mode: ▾

Color source: ▾

Gene / Reporter: advanced

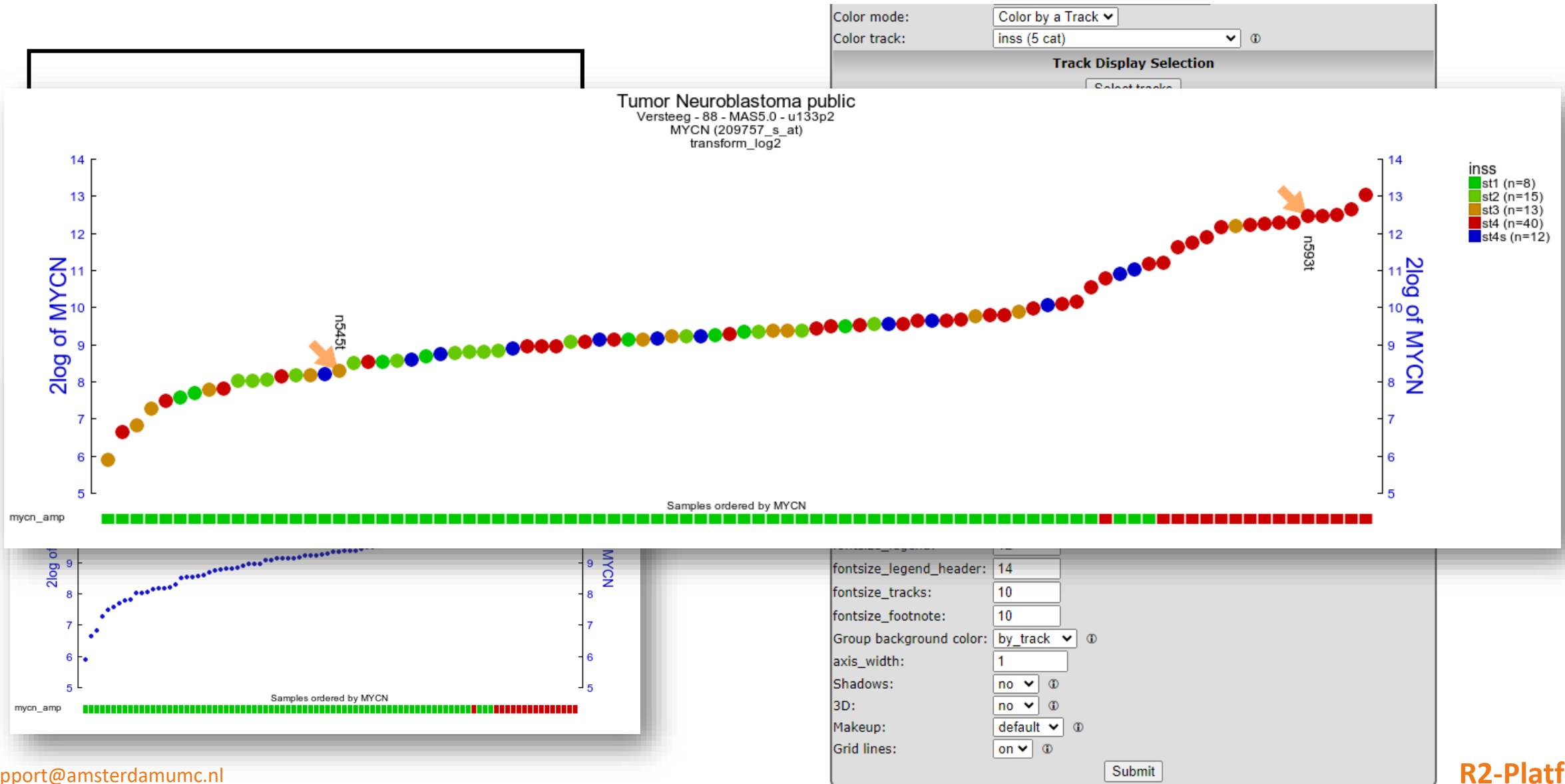
Transformation: ▾ ⓘ

Color scheme: ▾

Track Display Selection

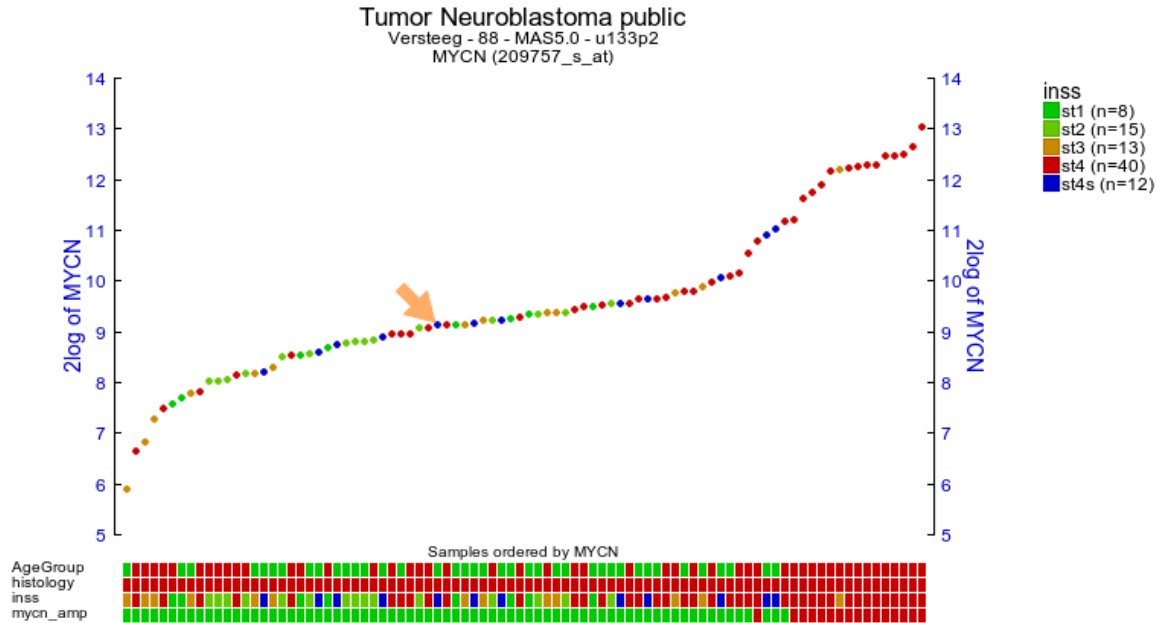
More Settings +

Graphics settings



Graphics settings

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



vector

GeneID	Hugo	Description	Categories
4613	MYCN	v-myc avian myelocytomatosis viral oncogene ne...	transcription factor

View additional data

Adjustable

Analysis type: single gene

Gene / Reporter: MYCN

Transformation: Log2

Block element...

Inspect

Color mode: Color by a Track

Color track: inss (5 cat)

Track Display Selection

Select tracks

More Settings

Min (X):

Max (X):

Color (X):

Min (Y):

Max (Y):

Color (Y):

Mark method: arrow

Vector (SVG) output: true

Draw height: 400

GapSize Groups: 10

Dot size: 3pt

Annot Graph: no

Draw legend: no

fontsize_y: 14

fontsize_ruler: 12

fontsize_t1: 17

fontsize_tsub: 12

fontsize_legend: 12

fontsize_legend_header: 14

fontsize_tracks: 10

fontsize_footnote: 10

Group background color: by_track

axis_width: 1

Shadows: no

3D: no

Makeup: default

Grid lines: on

Submit

plot options

Save General Marked

png svg copy

redraw plot

plot options

Save General Marked

Height ⓘ

min/max reporter:

Gene color: ⓘ

Dot size (pt): ⓘ ▾

font-size Y:

font-size Ruler:

font-size Title:

font-size sub-title rows:

Axis width:

fontsize_tracks:

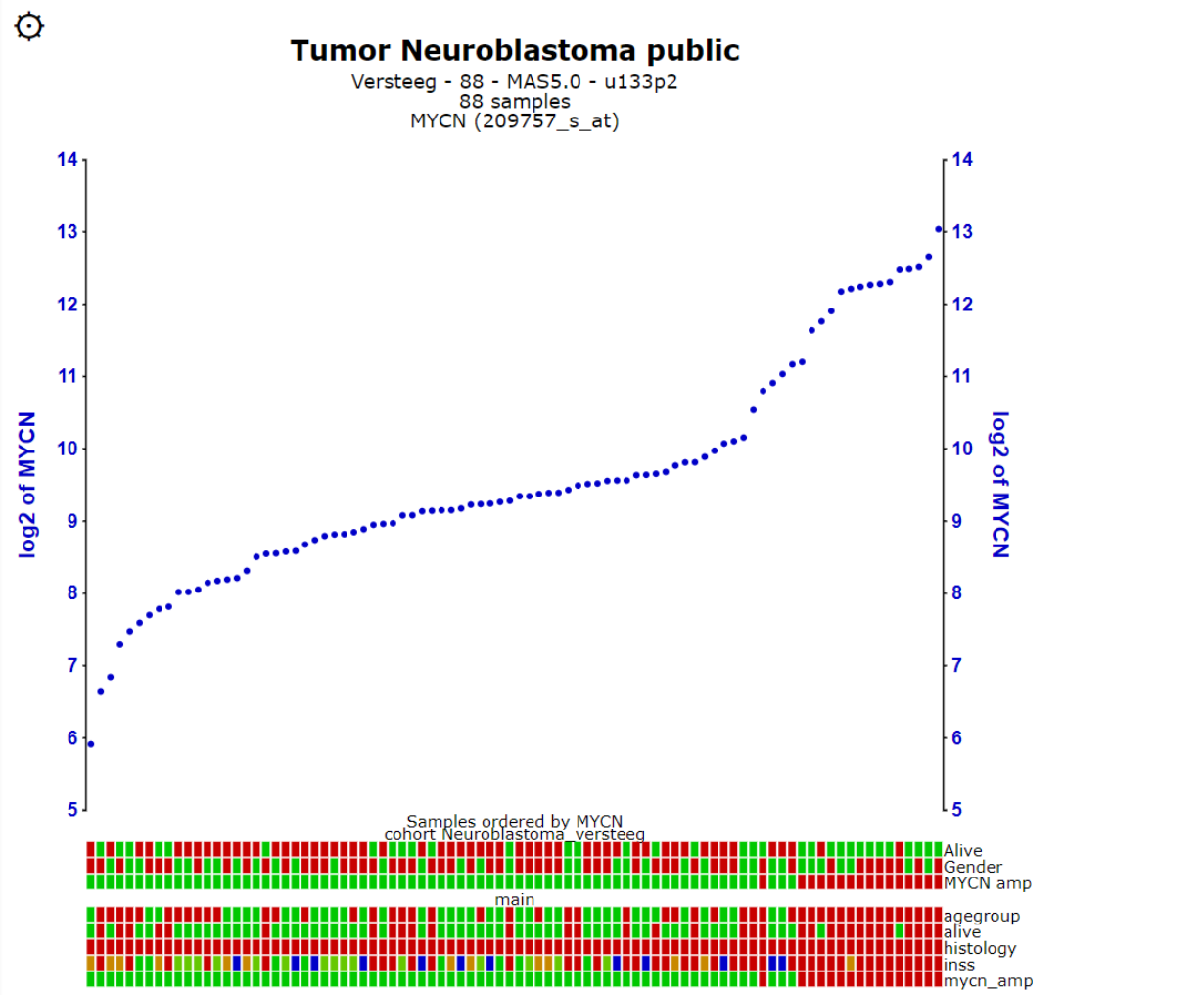
Annot Graph: ⓘ ▾

Draw legend: ⓘ ▾

fontsize_footnote:

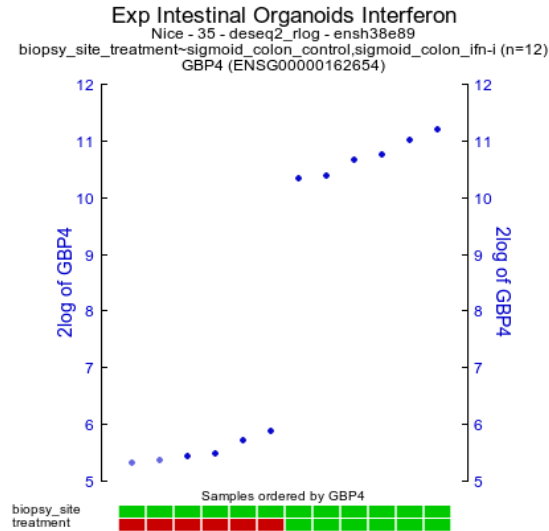
redraw plot

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



Changing analysis type

Exp Intestinal Organoids Interferon - Nice - 35 - deseq2_rlog - ensh38e89 public ⓘ



GeneID	Hugo	Description	R2 gene categories
115361	GBP4	guanylate binding protein 4-	

▶ View additional details

View data table

Adjustable settings

Analysis type: gene vs track ▾

Gene / Reporter: single gene advanced

Values: gene vs gene

Transformation: gene vs track ▾ ⓘ

Sample Filter

Subset track: Number of samples in subset ⚙️ ✖️ ⓘ

n=12

Selected sample subset: biopsy_site_treatment

sigmoid_colon_control

Changing the analysis type will alter the settings of the Adjustable settings box.

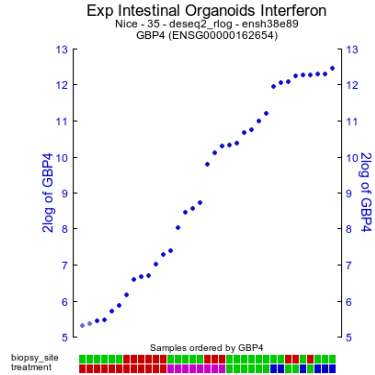
Easy to switch view

- Pubsniffer**
- GBP4
- GeneCards**
- GBP4
- Time Series**
- Check
- CliniSnitch**
- GBP4
- Across datasets**
- Expression in datasets
- Data set**
- Sample overview

Analysis types in x-gene-view (example)

Single gene

Exp Intestinal Organoids Interferon - Nice - 35 - dese2_rlog - ensh38e89



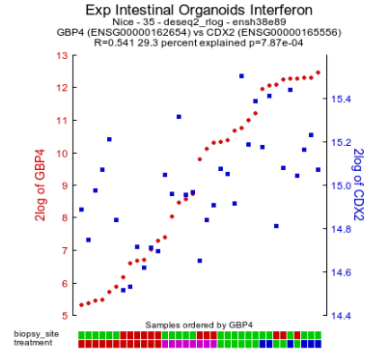
GeneID	Hugo	Description	R2 gene categories
1045	CDX2	caudal type homeobox 2	development, transcription factor, differentiation
115361	GBP4	guanylate binding protein 4	

View additional details

View data table

Gene vs gene

Exp Intestinal Organoids Interferon - Nice - 35 - dese2_rlog - ensh38e89



Significance of correlation:
r-value=0.541 p-value= 7.87e-04 T-value=3.698 degrees of freedom=33

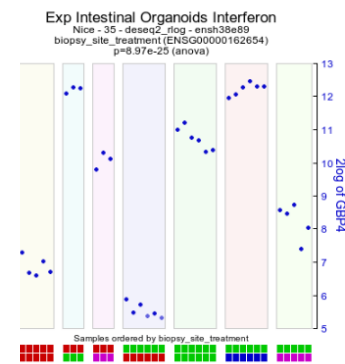
GeneID	Hugo	Description	R2 gene categories
1045	CDX2	caudal type homeobox 2	development, transcription factor, differentiation
115361	GBP4	guanylate binding protein 4	

View additional details

View data table

Gene vs track

Exp Intestinal Organoids Interferon - Nice - 35 - dese2_rlog - ensh38e89



One Way Analysis of variance (ANOVA):
ANOVA sum_square df mean_square F p-value
etweeen 219.396 6 36.566 337.617 8.97e-26
r/ithin 3.033 28.0108

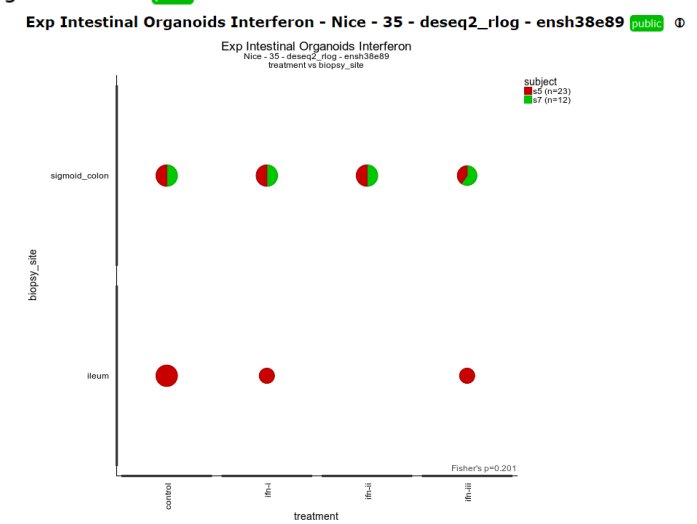
GeneID	Hugo	Description	R2 gene categories
115361	GBP4	guanylate binding protein 4	

View additional details

View data table

Track vs track

Exp Intestinal Organoids Interferon - Nice - 35 - dese2_rlog - ensh38e89



Fisher's p=0.201

Adjustable settings

Analysis type: single gene

Gene / Reporter: GBP4

Values: data

Transformation: Log2

Sample Filter

Subset track:

Selected sample subset: None

Graphics

Graph type: YY plot with annotation

Extra Graph Option: off

Samples to mark: comma separated sample names

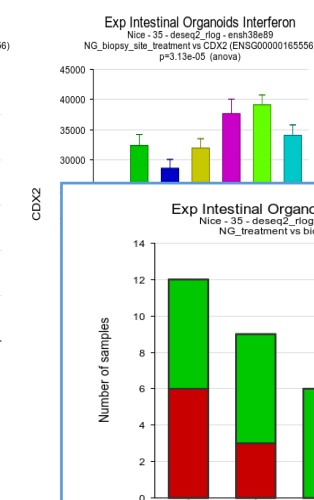
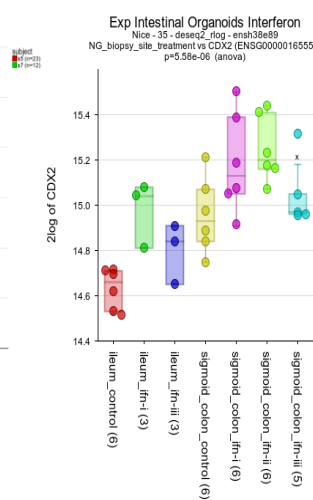
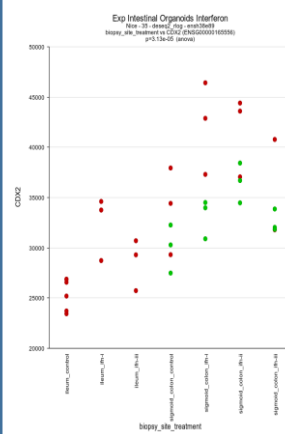
Color mode: Default Color

Track Display Selection

Select tracks

More Settings

Submit



Adjustable settings

gene vs track

GBP4

ENSG00000162654

advanced

biopsy_site_treatment (7 cat)

data

Log2

Sample Filter

Submit

Adjustable settings

Analysis type: track vs track

X track: treatment (4 cat)

Y track: biopsy_site (2 cat)

Sample Filter

Subset track:

Selected sample subset: None

Graphics

XY plot

mark: comma separated sample names

Color by Track

subject (2 cat)

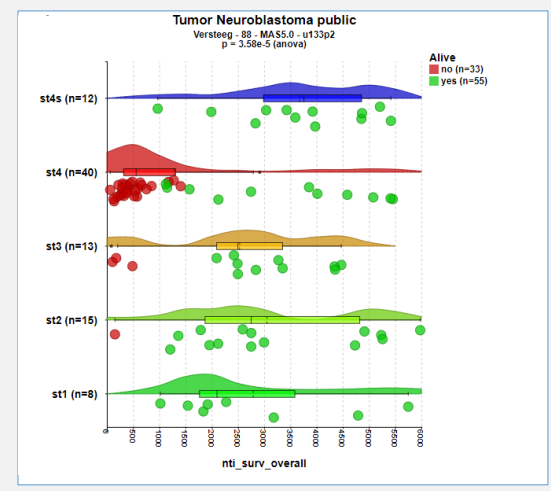
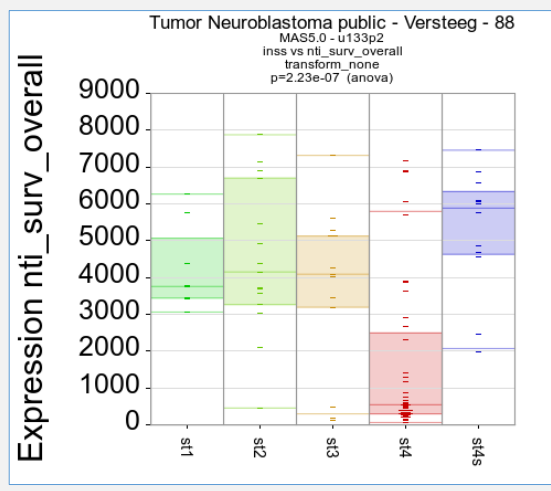
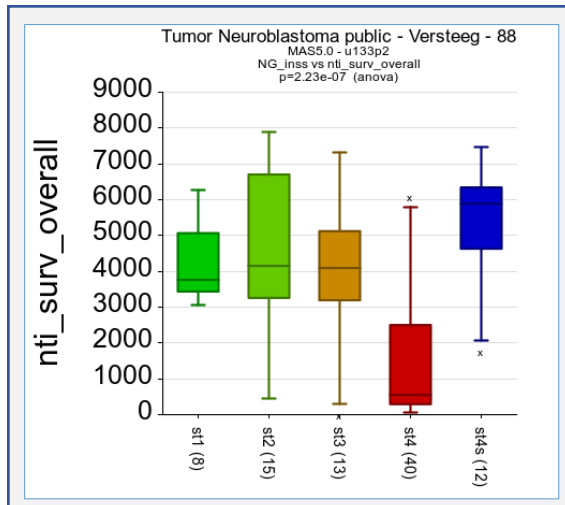
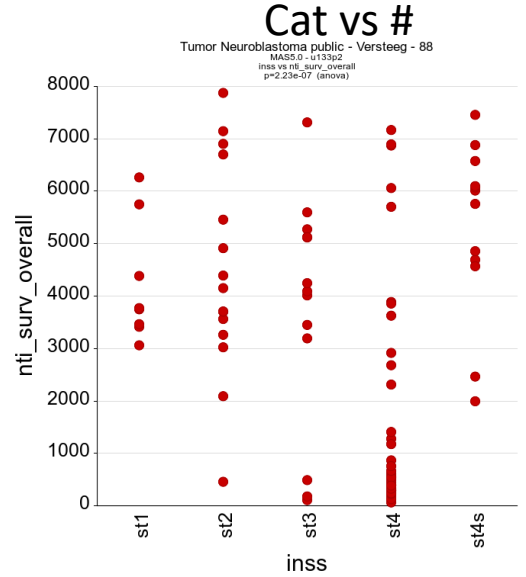
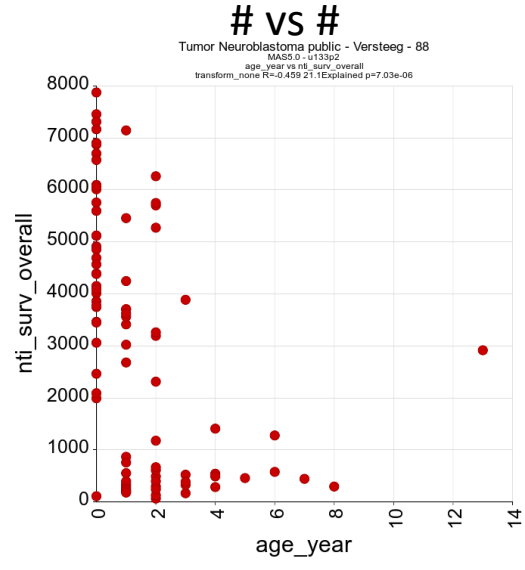
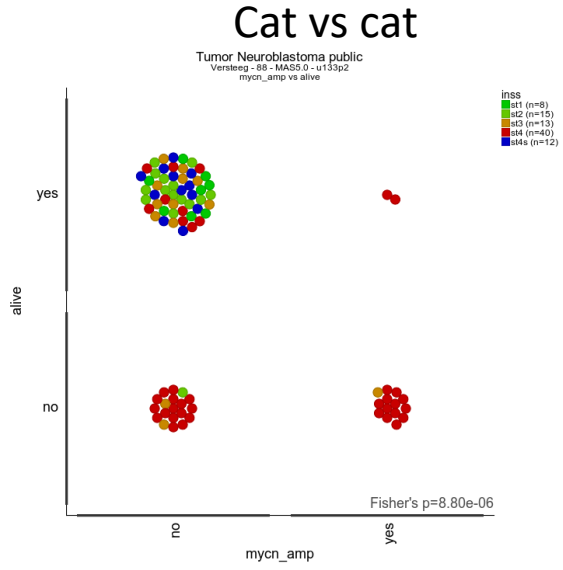
Track Display Selection

Select tracks

More Settings

Submit

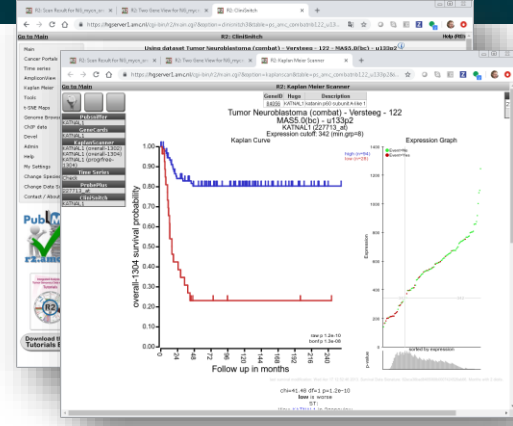
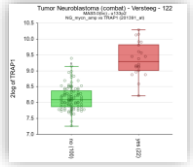
Relate 2 tracks



Differential Expression

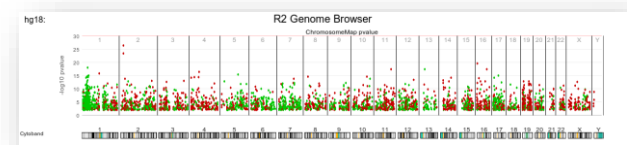
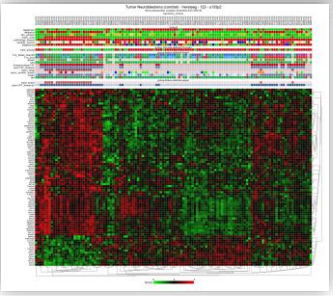
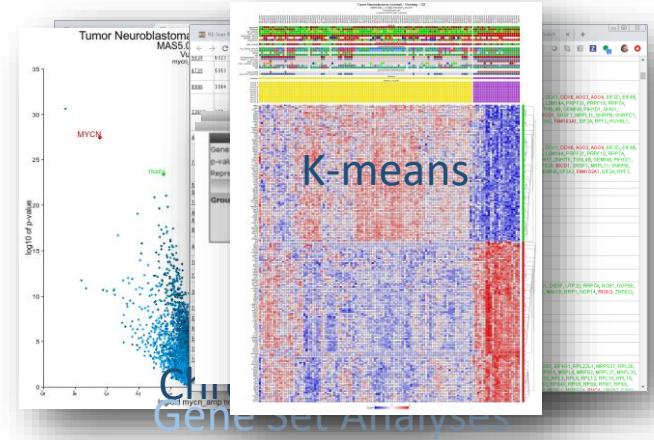


Example: Differential Expression Analysis



122 samples, transform_log, Prescaled=1
14988 combinations did not meet $p < 0.01$ and ≤ 1 minimal # of PresentCalls
3854 combinations meet your criteria (0 / 3854)
p-value correction for multiple testing: False Discovery Rate
Gene Hover Information is only added to the first 250 genes of a table

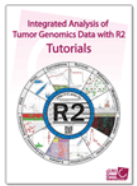
HUGO	FC	Color	padj	FC10P
MEIS1	0.824	red	1.5e-27	21
MEIS1	0.788	red	3.22e-24	122
TRAF3IP1	0.759	red	2.71e-20	122
MEIS1	-0.739	red	5.13e-18	122
CCND3	0.733	red	3.18e-18	122
KATNAL1	-0.726	red	4.65e-18	122
SOX1	0.720	red	4.22e-18	117
SOX1	0.717	red	3.98e-17	122
ENCL1	0.715	red	4.59e-17	122
ENCL1	0.707	red	5.96e-17	122
TRIM8	-0.702	red	3.47e-16	120
SOX1	-0.696	red	3.18e-16	122
KATNAL1	-0.695	red	3.10e-16	102
SOX1	-0.693	red	3.26e-16	122
SOX1	0.689	red	3.25e-15	98
SLUG	-0.689	red	2.99e-15	122
KATNAL1	0.687	red	3.24e-15	122
SOX1	0.684	red	3.51e-15	122
SOX1	-0.683	red	4.01e-15	122
SOX1	0.683	red	4.29e-15	117
DLX4	0.680	red	4.95e-15	49
SOX1	-0.680	red	6.19e-15	121
ENCL1	-0.679	red	6.99e-15	121
DLX4	0.678	red	7.91e-15	116
SOX1	0.678	red	8.02e-14	122
DLX4	0.673	red	1.54e-14	9
DLX4	0.671	red	1.82e-14	112
DLX4	0.670	red	1.94e-14	122
DLX4	0.669	red	3.15e-14	120
SOX1	-0.668	red	4.75e-14	120
SOX1	-0.668	red	5.19e-14	120
SOX1	0.663	red	8.06e-14	122
SOX1	0.660	red	1.24e-13	116



Differential Expression

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

2,191,787 (2,029,846 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
 - 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
- 4

[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](#)



Differential Expression

Go to: [Main](#)

R2: Two-group differential expression

[Online Tutorial](#)

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

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

Select a test

Test: T-test

Group by: mycn_amp (2 cat) ⓘ

Sample Filters

Subset track: ⓘ ⓘ

Submit

Did You Know

By combining 'group' variable with 'sample filters' you can make any intersection of interest.

Nb. You can also make your own private tracks.

Differential Expression settings

Go to: [Main](#)

R2: Two-group differential expression

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

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

Select a test

Test:

Group by:

Sample Filters

Subset track:

Selected sample subset: None

Adjustable settings

Group 1:

Group 2:

Data transformation

Floor value:

Transformation:

Statistics

Corr. multiple testing:

P-value cutoff:

Max number of results:

HugoOnce mode:

Min. # Present calls:

Minimal maximum value:

Minimal range size:

Chromosome:

Gene ontology:

Gene set:

Manual list:

Differential Expression result page

Go to: [Main](#)

R2: Scan result for track mycn_amp

[Online Tutorial](#)

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

88 samples, transform_log2, present >= 1
track mycn_amp

2495 combinations meet your criteria

15410 combinations did not meet **p-value <= 0.01**

Multiple testing correction applied: False Discovery Rate

Results are limited to 1500 rows

View	Gene	P	Difference	Group	Presence
	MYCNOS	3.75e-17	4.55	mycn_amp: no < yes	14/88
	MYCN	7.07e-17	3.14	mycn_amp: no < yes	88/88
	NOB1	1.38e-15	1.58	mycn_amp: no < yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no >= yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no >= yes	73/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no < yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no < yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no >= yes	88/88
	MEAF6	2.46e-12	-1.23	mycn_amp: no >= yes	88/88
	NRCAM	3.49e-12	-1.66	mycn_amp: no >= yes	88/88
	PAICS	3.72e-12	1.35	mycn_amp: no < yes	88/88
	NOA1	9.6e-12	1.08	mycn_amp: no < yes	88/88
	SLC18A2	7.01e-11	-3.76	mycn_amp: no >= yes	80/88
	RAB15	8.88e-11	-1.37	mycn_amp: no >= yes	86/88
	TIMM9	9.18e-11	1.02	mycn_amp: no < yes	88/88
	CDC42	9.47e-11	-2.33	mycn_amp: no >= yes	87/88
	ICA1L	1.71e-10	-1.49	mycn_amp: no >= yes	88/88
	ADGRA3	2.1e-10	1.27	mycn_amp: no < yes	88/88
	PHGDH	2.33e-10	2.01	mycn_amp: no < yes	58/88
	NOP14	2.69e-10	1.1	mycn_amp: no < yes	86/88

Gene: KATNAL1 (4056)
 katanin p60 ATPase-containing subunit A-like 1
Alternative names:
 • KATNAL1
Other designations:
 • katanin p60 ATPase-containing subunit A-like 1
 • p60 katanin-like 1

- Gene set analysis
- Known interactions
- Gene Ontology Analysis
- Enrichr
- DataAdder
- Chromosome Map
- Heatmap(zscore)
- k-means
- Plot all genes (xy, volcano etc)
- Group change bar plot
- Save current selection as TXT file
- Save selection as TXT file (no header)
- Reference for current selection
- Store result as custom gene set

Differential expression

Group	Count
mycn_amp: no < yes	1268
mycn_amp: no >= yes	1227

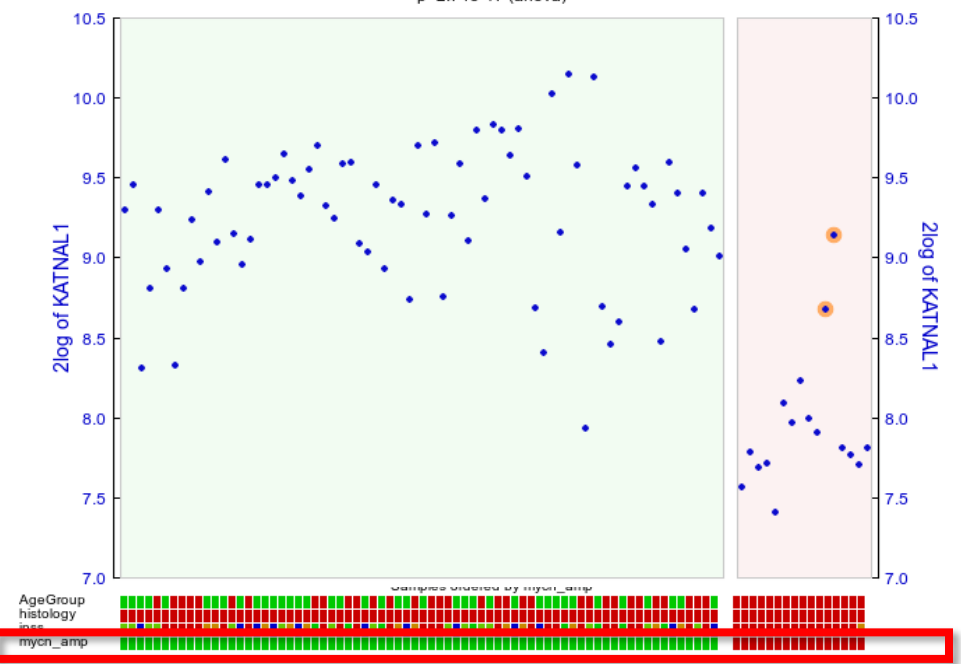
Mini ontology analysis

Category	Cutoff	Total	%	pval
All	2495	17905	13.9%	1.000
DNA repair	39	197	19.8%	0.018
apoptosis	72	577	12.5%	0.312
cell cycle	88	469	14.1%	0.931
development	185	1389	13.3%	0.508
differentiation	72	578	12.5%	0.305
drug target	150	1031	14.5%	0.589
kinase	89	600	14.8%	0.525
membrane	531	3981	13.3%	0.277
signal transduction	338	2385	14.1%	0.829
transcription factor	81	890	11.7%	0.098

One Gene View

NOB1 ← KATNAL1 (227713_at)
pvalue=9.82e-14 → KRT19

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
mycn_amp () vs KATNAL1 (227713_at)
p=2.74e-17 (anova)



One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	22.081	1	22.081	112.442	2.74e-17
Within	16.888	86	0.196	-	-

GeneID	Hugo	Description	R2 gene categories
84956	KATNAL1	katanin p60 subunit A-like 1	-

▶ View additional details

View data table

Adjustable settings

Analysis type:

Gene / Reporter: | |

One Gene View: adjust settings



One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	22.081	1	22.081	112.442	2.74e-17
Within	16.888	86	0.196	-	-

GeneID	Hugo	Description	R2 gene categories
84056	KATNAL1	katanin p60 subunit A-like 1-	-

► View additional details

View data table

Adjustable settings

Analysis type: gene vs track

Gene / Reporter: KATNAL1 227713_at advanced

Track: mycn_amp (2 cat)

Transformation: default

Subset track:

Selected sample subset:

Graph type:

Extra Graph Option:

Samples to mark:

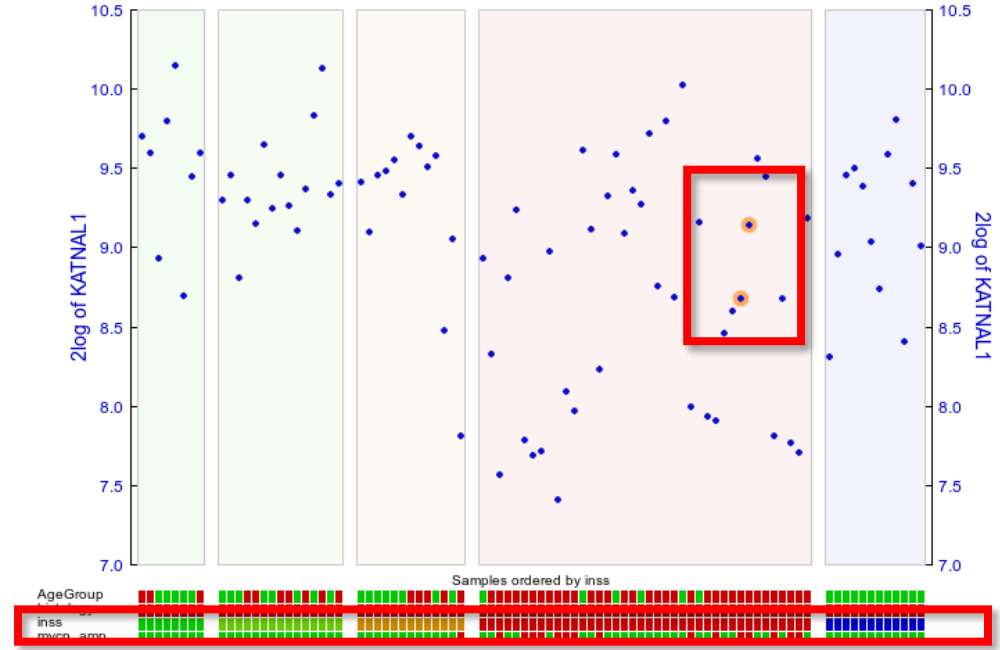
Color mode:

- age_year (#)
- AgeGroup (2 cat)
- Alive (2 cat)
- Death_cause (3 cat)
- gender (2 cat)
- histology (1 cat)
- inss (5 cat)**
- mycn_amp (2 cat)
- NTI_event_overall (2 cat)
- NTI_event_progfree (2 cat)
- nti_surv_overall (#)
- nti_surv_progfree (#)
- r2_label (88 cat)
- recurrence_or_progression (3 cat)
- samplenames (88 cat)
- m-cg_som_1base_corr
- A_C (#)
- A_C (#)

One Gene View

NOB1 ← KATNAL1 (227713_at)
pvalue=9.82e-14 → KRT19

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
inss (227713_at)
p=1.46e-04 (anova)



One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	9.227	4	2.307	6.438	1.46e-04
Within	29.742	83	0.358	-	-

GeneID	Hugo	Description	R2 gene categories
84056	KATNAL1	katanin p60 subunit A-like 1	-

► View additional details

View data table

Adjustable settings

Analysis type: ▼

Gene / Reporter:

X-gene-view



One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	22.081	1	22.081	112.442	2.74e-17
Within	16.888	86	0.196	-	-

GeneID	Hugo	Description	R2 gene categories
84056	KATNAL1	katanin p60 subunit A-like 1-	-

YY plot with annotation
YY plot with annotation (v2)

default

- age_year (#)
- AgeGroup (2 cat)
- Alive (2 cat)
- Death_cause (3 cat)
- gender (2 cat)
- histology (1 cat)
- inss (5 cat)
- mycn_amp (2 cat)**
- NT1_event_overall (2 cat)
- NT1_event_progfree (2 cat)
- nti_surv_overall (#)
- nti_surv_progfree (#)
- r2_label (88 cat)
- recurrence_or_progression (3 cat)
- samplenames (88 cat)
- m-cg_som_1base_corr**
- A_C (#)
- A_G (#)

Color track: mycn_amp (2 cat)

Track Display Selection

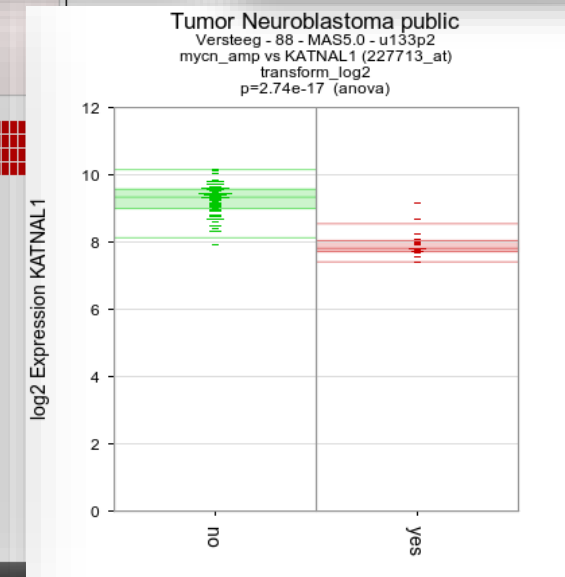
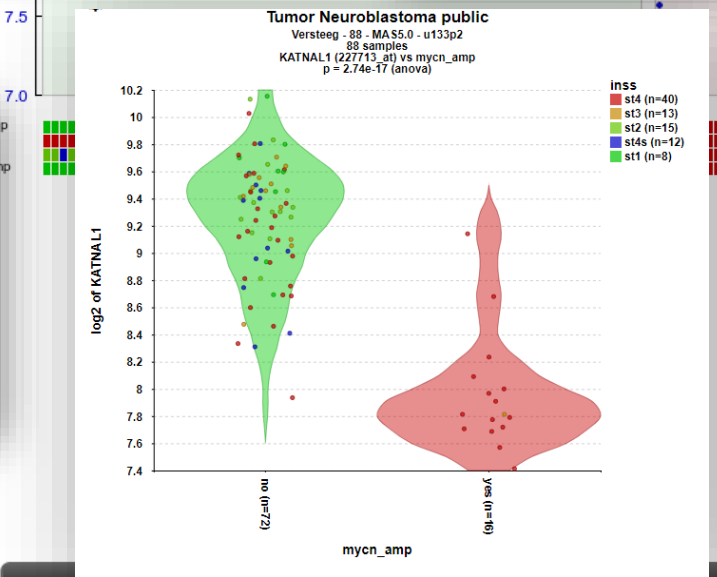
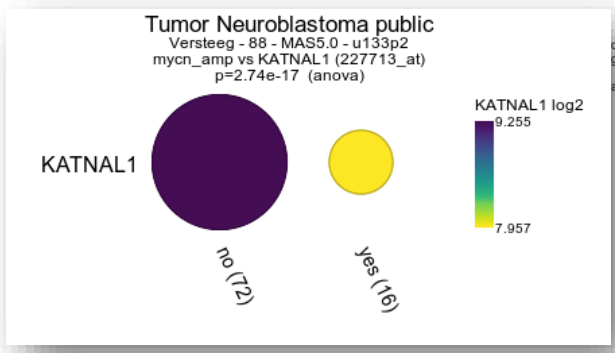
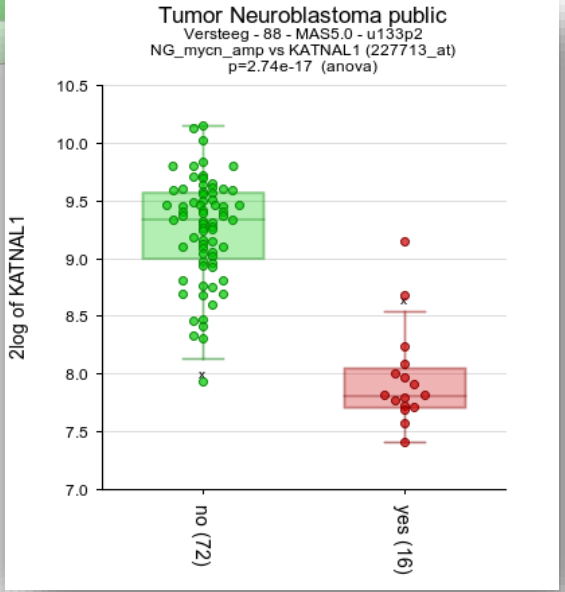
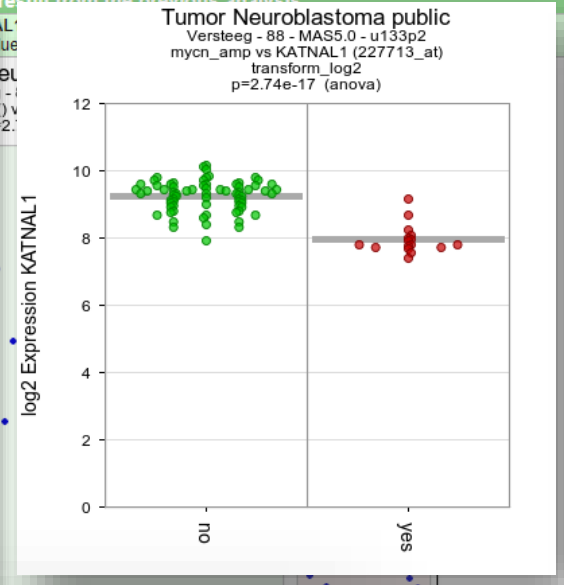
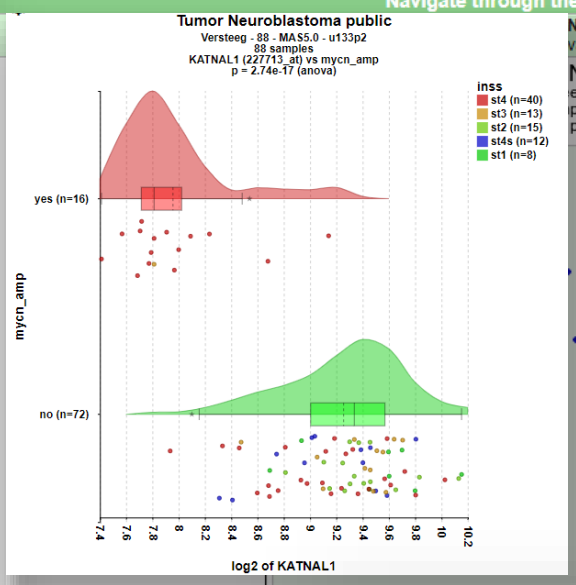
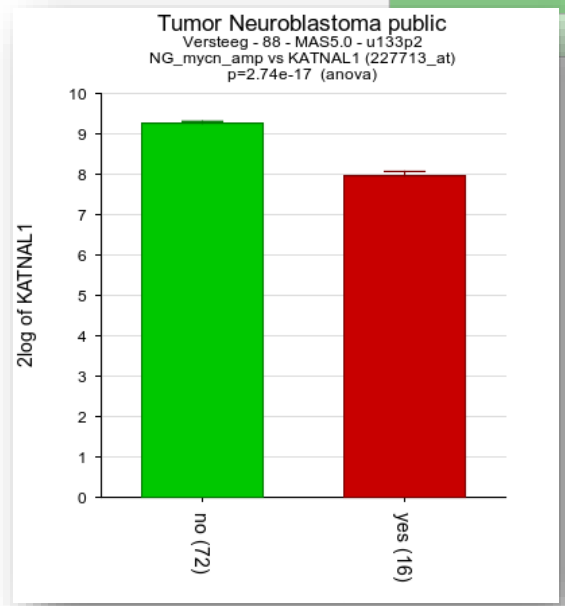
Select tracks

More Settings +

Submit

X-gene-view

Navigate through the result from the previous analysis



X-gene-view

Navigate through the result from the previous analysis

Gene / Reporter: KATNAL1 227713_at advanced

Track: inss (5 cat)

Transformation: Log2

Sample Filter

Subset track:

Selected sample subset: None

Graphics

Graph type: Violin plot (dots)

Order Groups By: group name

Samples to mark: itcc0198,itcc0219

Sample paths:

Color mode (groups): Color by Track

Color mode: Color by a Track

Color track: inss (5 cat)

Track Display Selection

Select tracks

More Settings

Min (X):

Max (X):

Color (X):

Min (Y):

Max (Y):

Color (Y):

Mark method: dot

Vector (SVG) output: false

Draw height: 400

Dot size: 2pt

fontsize_x: 14

rotate_x: 90

fontsize_y: 14

fontsize_ruler: 12

fontsize_t1: 17

fontsize_tsub: 12

fontsize_legend: 12

fontsize_legend_header: 14

axis_width: 1

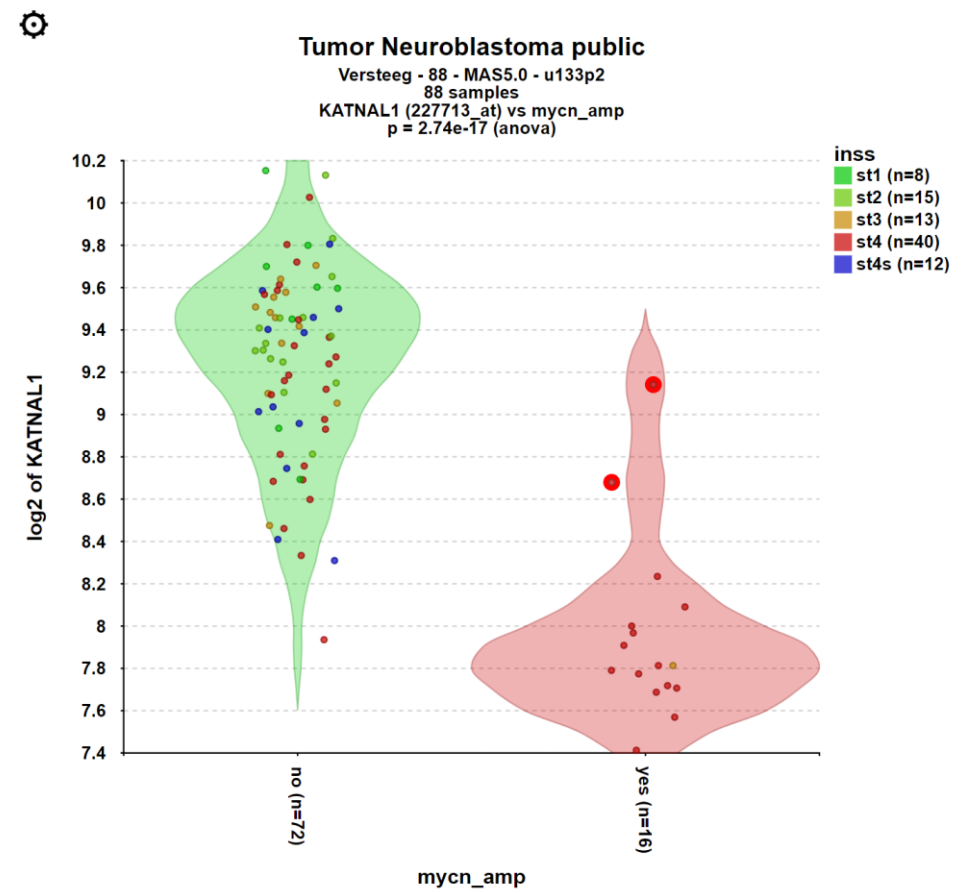
Box plot opacity: 30

Data point opacity: 70

Circle type: semi

KATNAL1 (227713_at)
pvalue=9.82e-14

⇒ KRT19



One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	9.227	4	2.307	6.438	1.46e-04
Within	29.742	83	0.358	-	-

GeneID	Hugo	Description	R2 gene categories
84056	KATNAL1	katanin p60 subunit A-like 1	-

X-gene-view

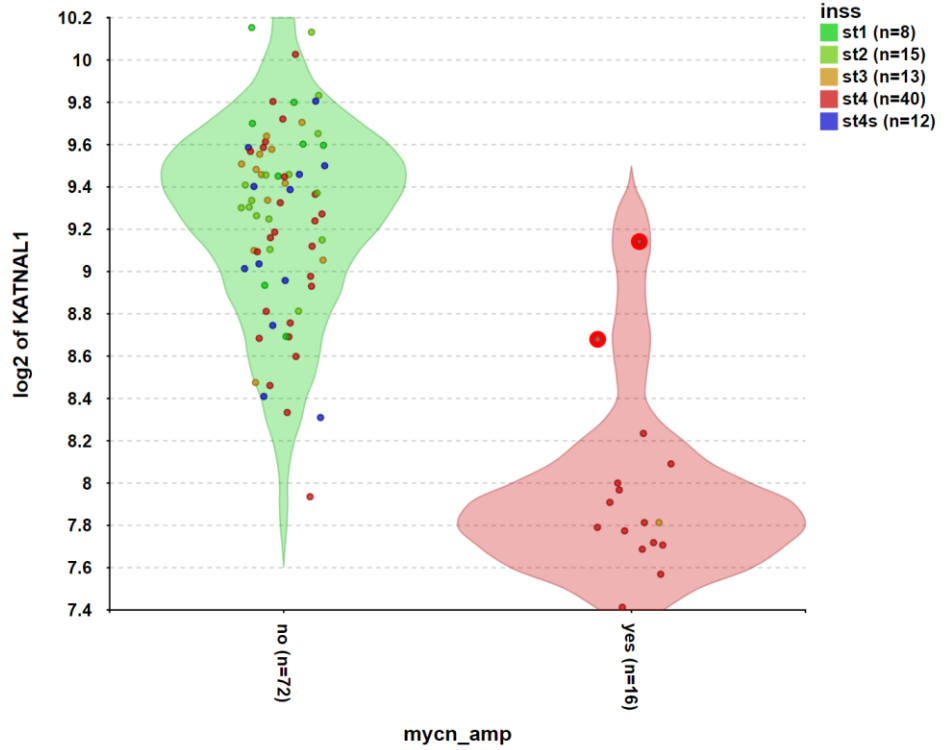
Navigate through the result from the previous analysis

NOB1 ← KATNAL1 (227713_at)
pvalue=9.82e-14 ⇒ KRT19



Tumor Neuroblastoma public

Versteeg - 88 - MAS5.0 - u133p2
88 samples
KATNAL1 (227713_at) vs mycn_amp
p = 2.74e-17 (anova)



One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	9.227	4	2.307	6.438	1.46e-04
Within	29.742	83	0.358	-	-

GeneID	Hugo	Description	R2 gene categories
84056	KATNAL1	katanin p60 subunit A-like 1	-

Differential Expression result page

Go to: [Main](#)

R2: Scan result for track mycn_amp

[Online Tutorial](#)

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

88 samples, transform_log2, present >= 1
track mycn_amp

2495 combinations meet your criteria

15410 combinations did not meet p-value <= 0.01

Multiple testing correction applied: False Discovery Rate

Results are limited to 1500 rows

View	Gene	P	Difference	Group	Presence
	MYCNOS	3.75e-17	4.55	mycn_amp: no < yes	14/88
	MYCN	7.07e-17	3.14	mycn_amp: no < yes	88/88
	NOB1	1.38e-15	1.58	mycn_amp: no < yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no >= yes	88/88
	KRT19	1.17e-13	-5.9	mycn_amp: no >= yes	73/88
	DDX10	2.37e-13	1.19	mycn_amp: no < yes	88/88
	TRAP1	3.85e-13	1.22	mycn_amp: no < yes	88/88
	SCFD2	8.1e-13	1.04	mycn_amp: no < yes	88/88
	TRIM36	2.15e-12	-1.9	mycn_amp: no >= yes	88/88
	MEAF6	2.46e-12	-1.23	mycn_amp: no >= yes	88/88
	NRCAM	3.49e-12	-1.66	mycn_amp: no >= yes	88/88
	PAICS	3.72e-12	1.35	mycn_amp: no < yes	88/88
	NOA1	9.6e-12	1.08	mycn_amp: no < yes	88/88
	SLC18A2	7.01e-11	-3.76	mycn_amp: no >= yes	80/88
	RAB15	8.88e-11	-1.37	mycn_amp: no >= yes	86/88
	TIMM9	9.18e-11	1.02	mycn_amp: no < yes	88/88
	CDC42	9.47e-11	-2.33	mycn_amp: no >= yes	87/88
	ICA1L	1.71e-10	-1.49	mycn_amp: no >= yes	88/88
	ADGRA3	2.1e-10	1.27	mycn_amp: no < yes	88/88
	PHGDH	2.33e-10	2.01	mycn_amp: no < yes	58/88
	NOP14	2.69e-10	1.1	mycn_amp: no < yes	86/88



- Gene set analysis
- Known interactions
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- Save current selection as TXT file
- Save selection as TXT file (no header)
- Reference for current selection
- Store result as custom gene set

Differential expression

Group	Count
mycn_amp: no < yes	1288
mycn_amp: no >= yes	1227

Mini ontology analysis

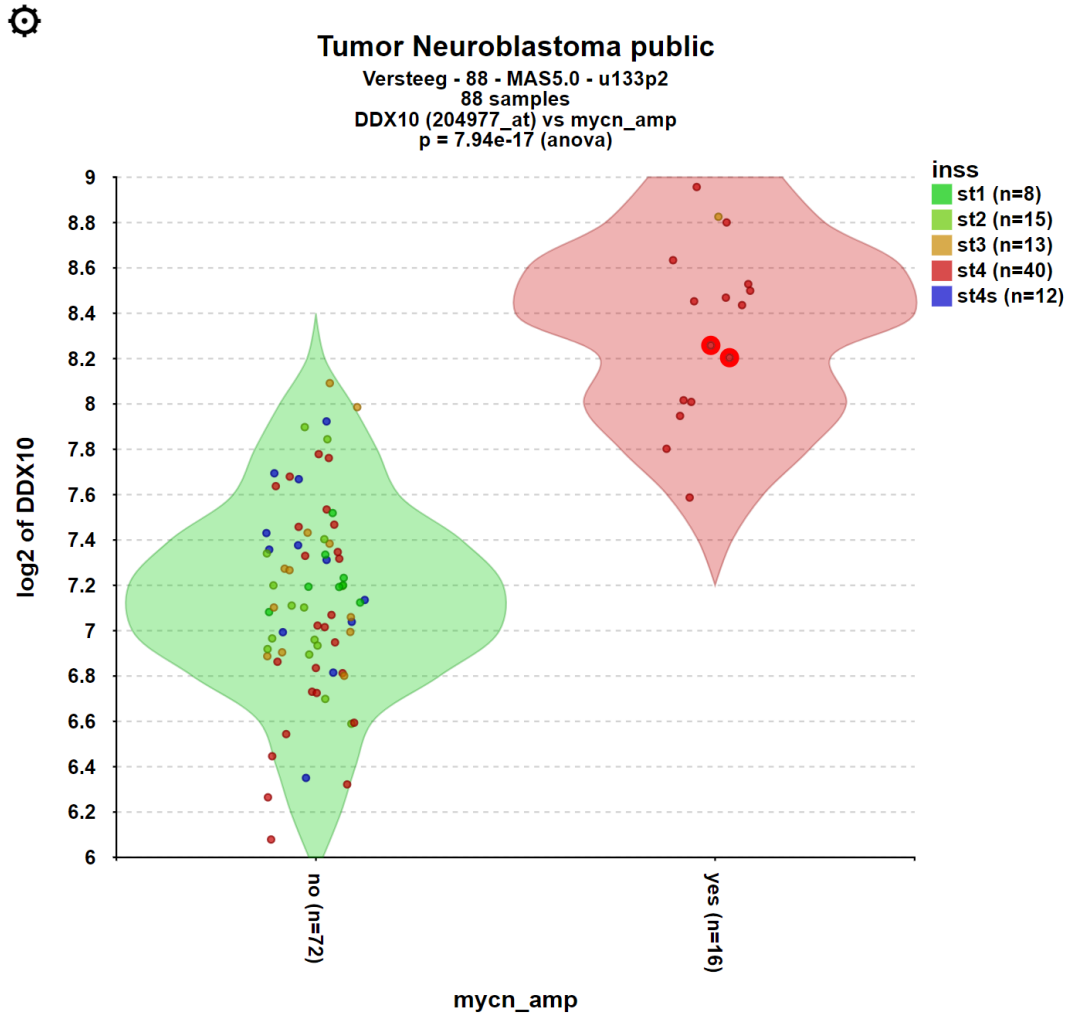
Category	Cutoff	Total	%	pval
All	2495	17905	13.9%	1.000
DNA repair	39	197	19.8%	0.018
apoptosis	72	577	12.5%	0.312
cell cycle	66	469	14.1%	0.931
development	185	1389	13.3%	0.508
differentiation	72	578	12.5%	0.305
drug target	150	1031	14.5%	0.569
kinase	89	600	14.8%	0.525
membrane	531	3681	13.3%	0.277
signal transduction	338	2385	14.1%	0.829
transcription factor	81	690	11.7%	0.068

X-gene-view

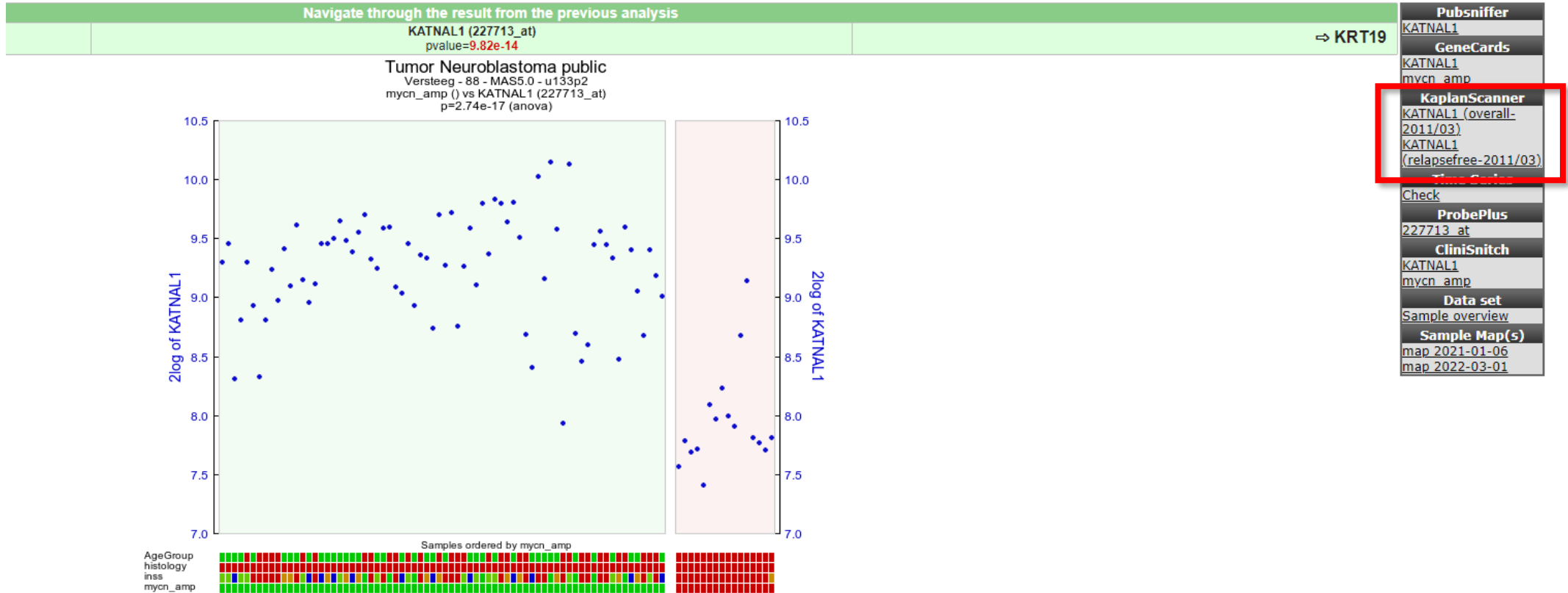
Navigate through the result from the previous analysis

KRT19 ⇐ DDX10 (204977_at) pvalue=**2.37e-13** ⇒ TRAP1

- Pubsniffer**
DDX10
- GeneCards**
DDX10
mycn_amp
- KaplanScanner**
DDX10 (overall-2011/03)
DDX10 (relapsefree-2011/03)
- Time Series**
Check
- ProbePlus**
204977 at
- CliniSnitch**
DDX10
mycn_amp
- Data set**
Sample overview
- Sample Map(s)**
map 2021-01-06
map 2022-03-01



KaplanScanner



- PubsNiffer**
- KATNAL1
- GeneCards**
- KATNAL1
- mycn_amp
- KaplanScanner**
- KATNAL1 (overall-2011/03)
- KATNAL1 (relapsefree-2011/03)
- Time Series
- Check
- ProbePlus**
- 227713_at
- CliniSnitch**
- KATNAL1
- mycn_amp
- Data set**
- Sample overview
- Sample Map(s)**
- map 2021-01-06
- map 2022-03-01

One Way Analysis of variance (ANOVA):

ANOVA	sum_square	df	mean_square	F	p-value
Between	22.081	1	22.081	112.442	2.74e-17
Within	16.888	86	0.196	-	-

GeneID	Hugo	Description	R2 gene categories
84056	KATNAL1	katanin p60 subunit A-like 1-	-

► View additional details

View data table

KaplanScanner

Go to: [Main](#) Kaplan start

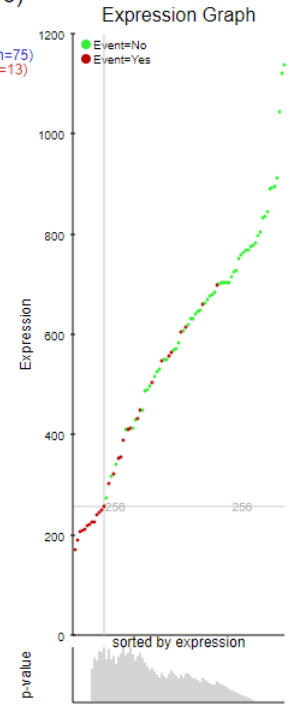
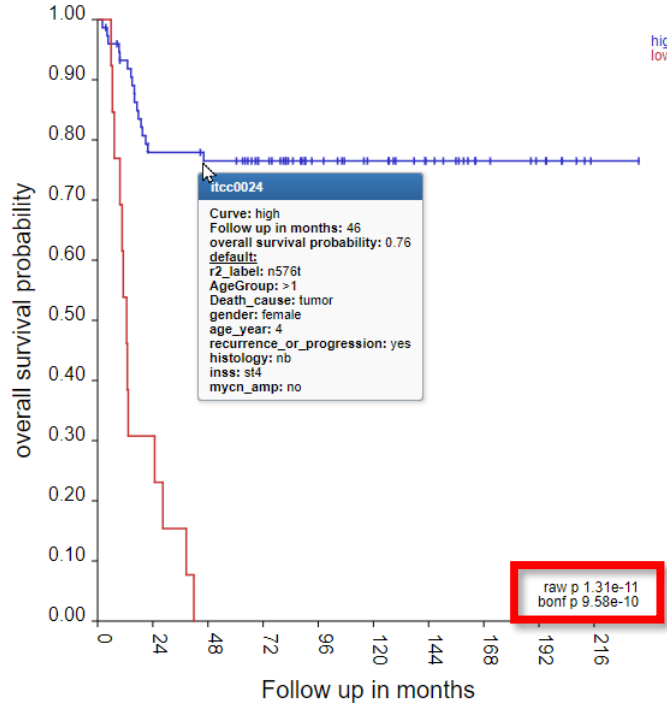
R2: Kaplan Meier Scanner

[Online Tutorial](#)

- [PubsNiffer](#)
- [GeneCards](#)
- [KaplanScanner](#)
- [Time Series](#)
- [Check](#)
- [ProbePlus](#)
- [CliniSnitch](#)
- [Across datasets](#)
- [Expression in datasets](#)
- [Data set](#)
- [Sample overview](#)
- [Sample Map\(s\)](#)
- [map 2021-01-06](#)
- [map 2022-03-01](#)

GeneID	Hugo	Description
84056	KATNAL1	katanin p60 subunit A-like 1

Tumor Neuroblastoma public
Versteeg - 88 - MAS5.0 - u133p2
KATNAL1 (227713_at)
Expression cutoff: 256.0 (min.grp=8)



chi=45.80 df=1 p=1.31e-11
View [KATNAL1](#) in 2geneview

TrackSaver

store as track

Store Preset

Store Settings as Preset

Reset Stored Settings to Default

Adjustable settings

Gene / Reporter:	KATNAL1	227713_at	advanced
------------------	---------	-----------	----------

Adjustable settings

Gene / Reporter:

Cutoff mode:

Cutoff:

Subset track:

Selected sample subset:

Only draw up to: months

Minimal groupsize:

Line width:

Expression Graph:

Color for low group:

Color for high group:

fontsize_ruler:

fontsize_y:

fontsize_t1:

fontsize_tsub:

fontsize_inline:

axis_width:

Plot all genes

R2: Scan result for track mycn_amp

Online Tutorial

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

88 samples, transform_log2, present>=1
track mycn_amp

2495 combinations meet your criteria

15410 combinations did not meet **p-value<=0.01**

Multiple testing correction applied: False Discovery Rate

Results are limited to 1500 rows

View	Gene	P	Difference	Group	Presence
	MYCNOS	3.75e-17	4.55	mycn_amp: no < yes	14/88
	MYCN	7.07e-17	3.14	mycn_amp: no < yes	88/88
	NOB1	1.38e-15	1.58	mycn_amp: no < yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no >= yes	88/88
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	SCFD2	8.1e-13	1.04	mycn_amp: no < yes	88/88
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	PAICS	3.72e-12	1.35	mycn_amp: no < yes	88/88
	NOA1	9.6e-12	1.08	mycn_amp: no < yes	88/88

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- Reference for current selection
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Differential expression	
Group	Count
mycn_amp: no < yes	1268
mycn_amp: no >= yes	1227

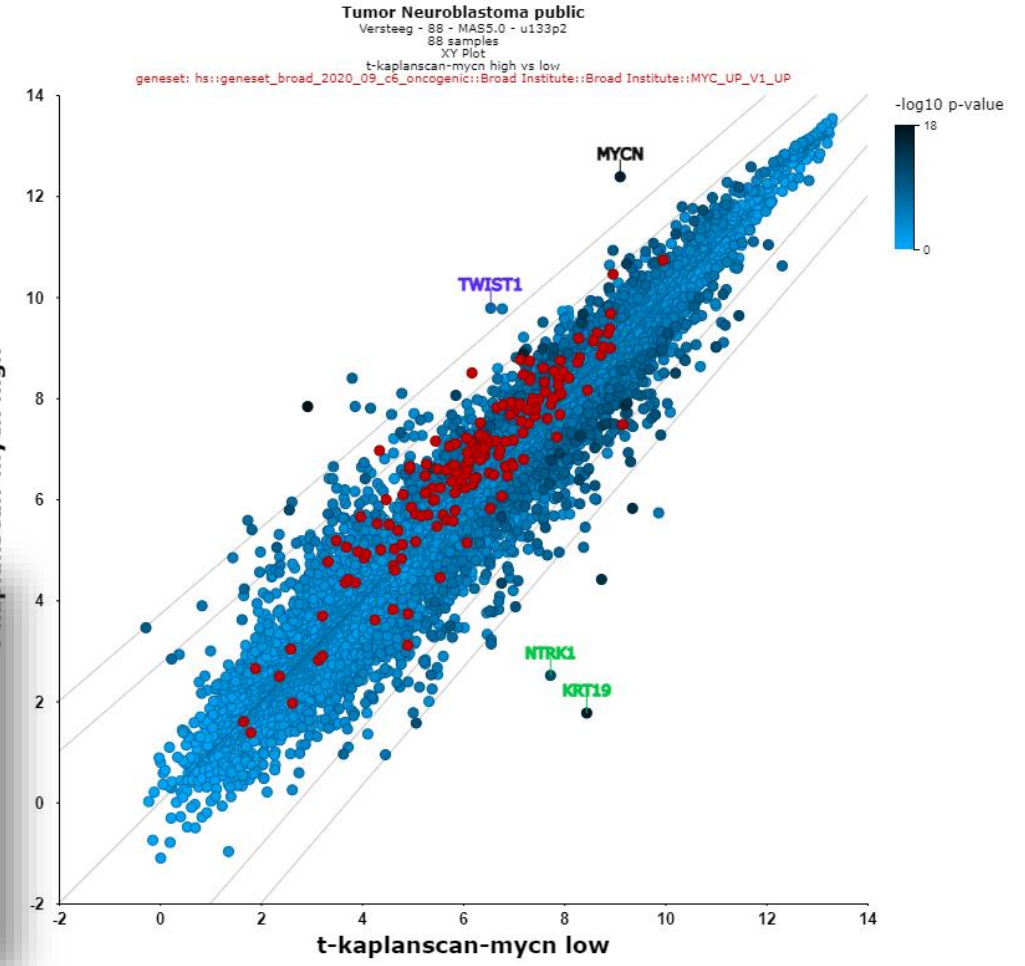
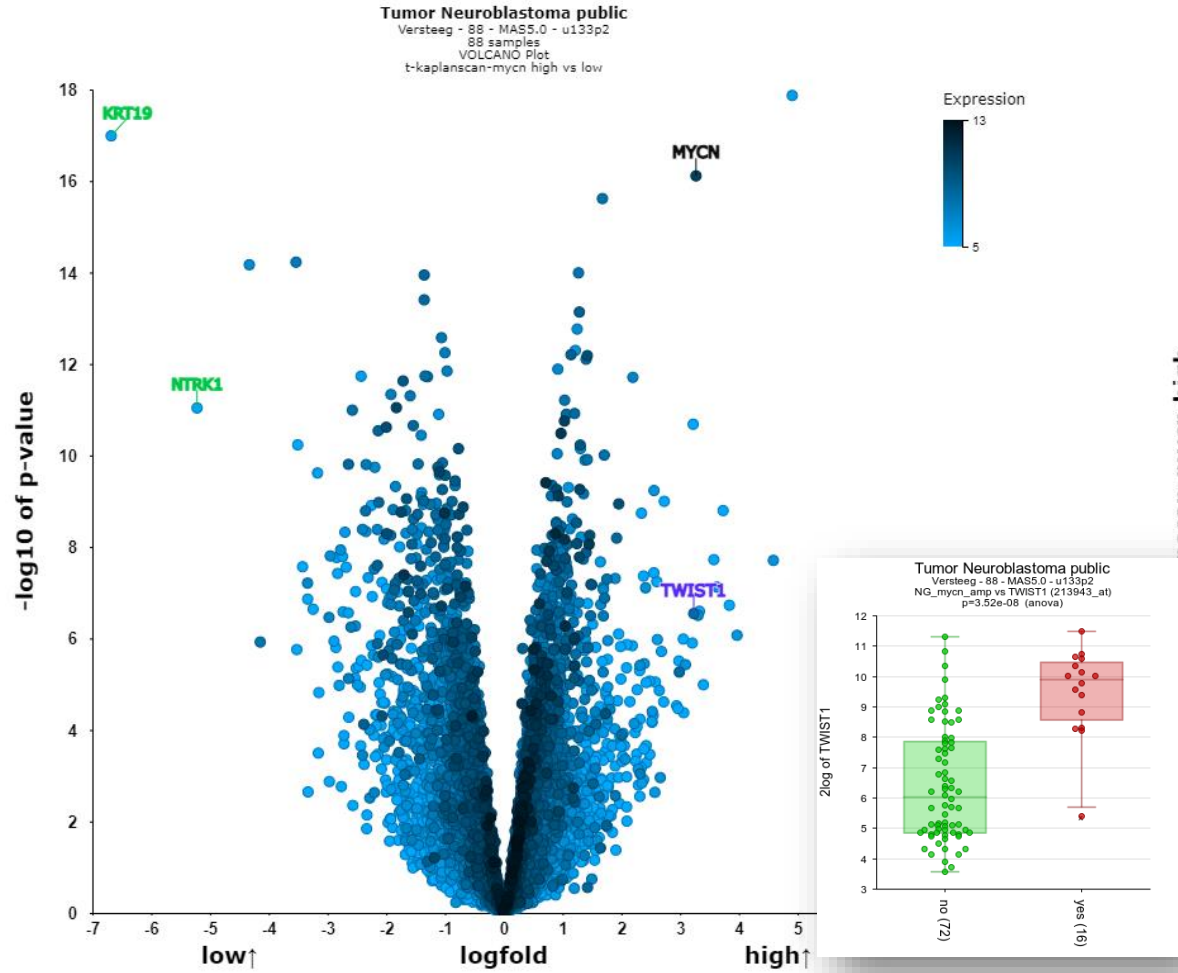
Plot all genes

Go to: [Main](#)

R2:

[Online Tutorial](#)

- 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



(KRT19,NTRK1):S=15:C=0,170,0,
MYCN:S=16:C=0,0,0;
(TWIST1):S=10:C=0,0,200

color by highest expression

[Export data from plot](#)

[Adjustable settings](#)

Plot type:	Vulcano plot ▼
p-values:	fdr-p-value ▼

Plot all genes

Search gene-set.
x

drug target (1174)

Name

Q

Name	Count
▶ <input type="checkbox"/> Personal gene sets	6154
▶ <input type="checkbox"/> Community gene sets	83365
▼ <input checked="" type="checkbox"/> Categories	18553
<input type="checkbox"/> apoptosis	677
<input type="checkbox"/> cancer_gene_census	738
<input type="checkbox"/> cell cycle	537
<input type="checkbox"/> development	1696
<input type="checkbox"/> differentiation	718
<input type="checkbox"/> DNA repair	247
<input type="checkbox"/> drugged_kinase	74
<input checked="" type="checkbox"/> drug target	1174
<input type="checkbox"/> kinase	700
<input type="checkbox"/> membrane	5599
<input type="checkbox"/> Oncogenesis	449
<input type="checkbox"/> signal transduction	3385
<input type="checkbox"/> transcription factor	945
<input type="checkbox"/> transcription regulator activation	1412
<input type="checkbox"/> transcription repressor activation	202
▶ <input type="checkbox"/> r2 curated gene sets	7664
▶ <input type="checkbox"/> r2 provided gene lists	1168
▶ <input type="checkbox"/> amc genes	22409
▶ <input type="checkbox"/> amc genome	36510
▶ <input type="checkbox"/> amc test	7433
▶ <input type="checkbox"/> Bindea immune signatures	503
▶ <input type="checkbox"/> Broad 2019 archived	76860

Clear selection

Confirm selection

Gene ontology analysis

R2: Scan result for track mycn_amp

Online Tutorial

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

88 samples, transform_log2, present>=1
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Differential expression	
Group	Count
mycn_amp: no < yes	1268
mycn_amp: no >= yes	1227

Gene ontology analysis

Go to: [Main](#)

R2: Gene Ontology Analysis

[Online Tutorial](#)



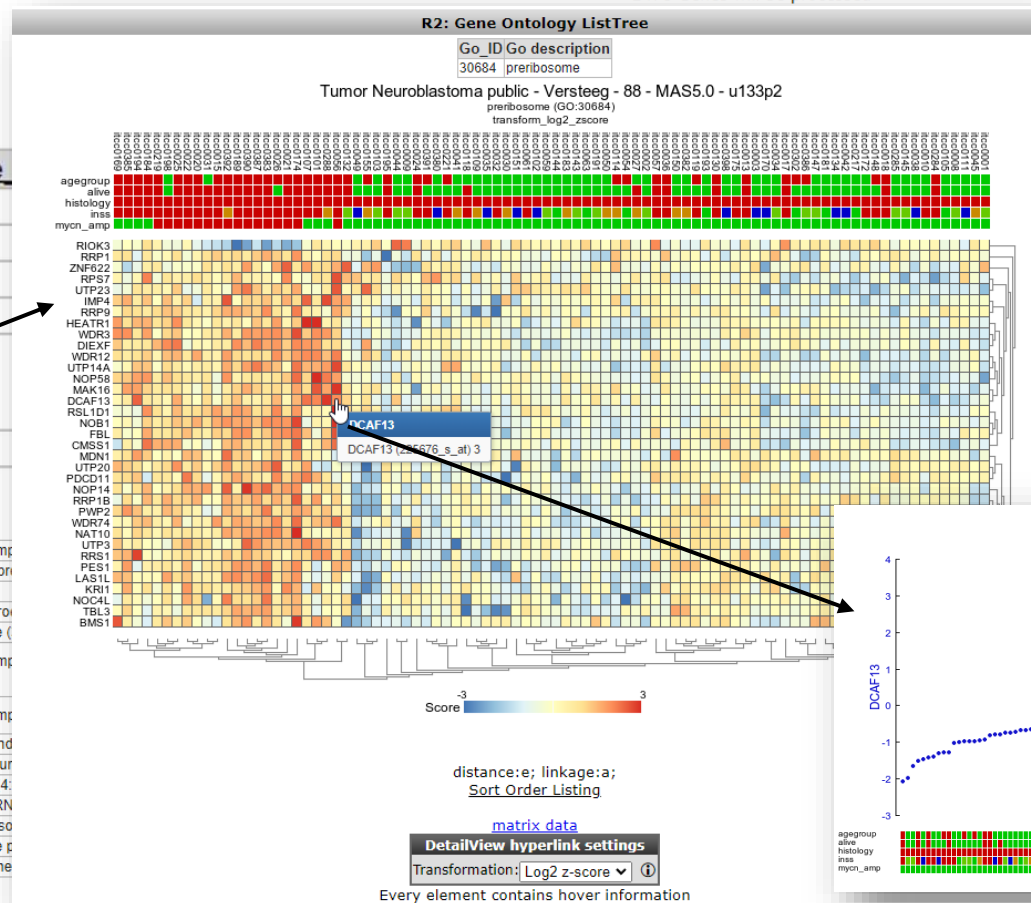
Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2 public

Input=symbol
Deepestpath=9
Show:5 <= #symbols <= 100
Using: All ontologies
▶ my file

Detected reference set: ps_avgpres_nbadam88_u133p2; 1
Test Set:

2 Symbols could not be translated back to GeneID, but could be translated to current HUGO annotation.
17 Symbols could not be translated back to GeneID.
2478 Genes will be processed

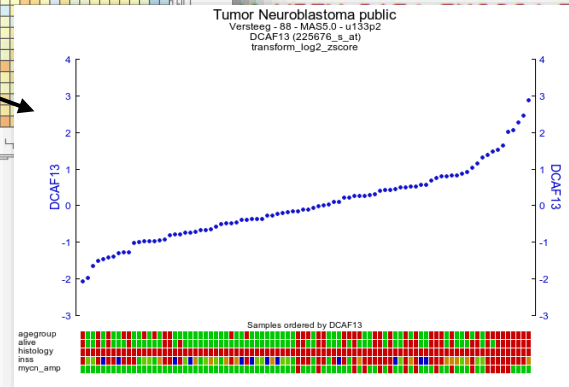
GoPath	R#	#	p_value	
22613	417	143	6.3e-29	
34660	518	164	3.9e-27	
3723	1490	357	1.5e-24	
34470	359	118	1.2e-21	
16072	257	93	1.4e-21	
6396	849	222	7.5e-21	
42254	287	90	1.5e-20	
1990904	672	171	9.3e-15	3: ribonucleoprotein comp
43043	548	145	2.3e-14	1: peptide biosynthetic pr
5622	12455	1992	3.2e-14	3: intracellular (3:4)
43604	662	165	2.8e-13	1: amide biosynthetic pro
43229	10820	1756	5.5e-12	3: intracellular organelle (
71826	197	64	7.5e-12	1: ribonucleoprotein comp (5.5)
22618	187	61	1.9e-11	1: ribonucleoprotein comp
1901363	5150	910	2.1e-11	2: heterocyclic compound
97159	5207	917	3.9e-11	2: organic cyclic compour
3676	3462	639	5.6e-11	2: nucleic acid binding (4:
30490	49	24	8.6e-11	1: maturation of SSU-rRN
32040	31	18	8.8e-11	3: small-subunit process
44446	8013	1341	9.2e-11	3: intracellular organelle p
43231	9415	1546	1.2e-10	3: intracellular membrane
5737	9930	1618	2.4e-10	3: cytoplasm (4:6)



using 2x2 contingency table analysis (chi-square) with contin
mycn_amp: no < yes, mycn_amp: no >= yes,

WDR3, SPIN1, C7ORF60, FBL, XRN2, PDCD11, EXOSC7, RRP1B, WDR43, MDN1
0, YBEY, GAR1, EXOSC4, DDX49, TEX10, TRMT61B, NOL8, HEATR1, SHQ1, NA
MRPS9, KRI1, BYSL, UBA52, C19ORF43, NOC4L, METTL16, LAS1L, WDR75, RF

PL10, RPL10L, C7ORF60, FBL, XRN2, FASTKD2, PDCD11, EXOSC7, RRP1B, WI
DX49, WDR74, ZNHIT6, TEX10, TRMT61B, NOL8, I



4A, MCTS1, HSP90AB1, KLC1, MAPT, NPM1, PELO, ZNHIT6, GEMIN8,
M103A1, EIF2A, RPF2, RUVBL1, EIF3A, EIF3D, LIMD1, TICRR, SART1,

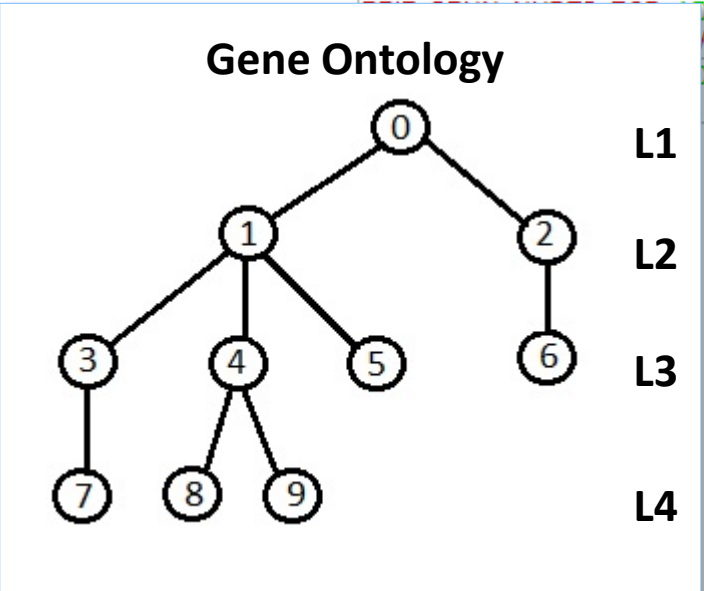
4A, MCTS1, HSP90AB1, MAPT, NPM1, ZNHIT6, GEMIN8, SHQ1, CELF4,
A, RPF2, RUVBL1, EIF3A, EIF3D, LIMD1, TICRR, SART1, PRPF3, NAF1

MS1

Gene ontology analysis

imoyladosine metabolic	TRIT1, TRMT61B, TRMT5, OSGEPL1, PUS1
(5:5)	over 100 entries (57, 69,)
assembly checkpoint (6:15)	CENPF, APC, GEN1, MAD2L1, PSMG2, BUB1B, XRCC3, CDT1, TRIP13
checkpoint (5:9)	CENPF, APC, GEN1, MAD2L1, PSMG2, BUB1B, XRCC3, CDT1, TRIP13
checkpoint (5:14)	CENPF, APC, GEN1, MAD2L1, PSMG2, BUB1B, XRCC3, CDT1, TRIP13
along microtubule (5:8)	LRPPRC, KIF3A, KIFAP3, KIF1B, HIF1A, MAPT, PAFAH1B1, BLOC1S4, SYBU, PRKCZ, ARHGAP21, BICD1, TRAK2, UXT, FEZ1, CDC42
to membrane (6:6)	OPTN, FLOT1, GPHN, RAMP2, RAMP3, SORBS1, RER1, ATG4A, FCHO2, RAB3IP, MIEF2, CHMP4B, ZFAND2B, DYNLL2, CSNK2A1, AP2B1, CNST, DLG2, DPP6, FLNA, ICMT, MA TIMM22, HSPA4, GOLGA7B, MYO5A, OXA1L, SH3GLB1, PDZK1, RAB8B, NUP54, WNT4, SCN3B, PRKCZ, GPR158, PTN, RAP2A, RPL12, RPL18, RPL29, RPS3, RPS4X, RPS5, R SNAP25, BRAF, SSR2, SSR3, STAC, STX1A, TP53, TUB, UBA52, WRB, YWHAH, CACNB3, KCNIP4, EFCAB7, LIN7A, KALRN, IFT20, RPL14, MAP7, VAMP3, PEX16, CRIPT, STX8,
it (6:9)	MRE11A, RAD51D, BLM, WRN, XRCC2, XRCC3, BRIP1, EXO1
enzyme activity (6:6)	PRMT3, PRMT5, CARM1, METTL21A, FBL, EZH1, DIMT1, PRMT2, PRMT1, HEMK1, TRMT1, SMYD3, METTL16, WDR77, METTL22, SUV39H2, SETD7, FAM103A1, SETDB2, EED
some transport (5:7)	CACNG2, LYST, ADRB2, VPS41, HOOK1, SNX16, AKTIP, VPS33A, TRAK2, TGFBRAP1, STX8, VPS4B
me biogenesis (4:6)	WDR43, DIMT1, HEATR1, SHQ1, WDR75
:10)	ERCC1, BLM, WRN, XRCC3, EXO1
nce via telomere trimming (7:9)	ERCC1, BLM, WRN, XRCC3, EXO1

...CYAP1, NUP35, COX15, NUP205, NUP160, NUP188, NUP62, AK5, GPI, PGM2L1, OLA1, HIF1A, STOML2, HK2, IMPDH2, LDHA, NDUFA5, NDUFA10
...1B1, ATP6V1B2, PKM, NUP54, ATP5O, NDUFB11, PRKAG1, RAN, BID, NMNAT1, PINK1, SNCA, STAT3, TSPO, UQCRC2, CAD, NUP37, DCTPP1, SL
...CYAP1, NUP35, COX15, NUP205, NUP160, NUP188, NUP62, AK5, GPI, PGM2L1, OLA1, HIF1A, STOML2, HK2, IMPDH2, LDHA, NDUFA5, NDUFA10
...PKM, NUP54, ATP5O, NDUFB11, PRKAG1, RAN, BID, NMNAT1, PINK1, SNCA, STAT3, TSPO, UQCRC2, NUP37, SLC25A23, SEH1L, COX5A, ATPIF



[Download Go result](#)

Show the result as a network
this job took me 4 seconds
Redo the analysis:

Adjustable settings

Ontology: All ontologies

Start level: 3

End level: 9

mycn_amp: no < yes

mycn_amp: no >= yes

Redo analysis

Gene ontology analysis

Go to: [Main](#)

R2: Gene Ontology Analysis

[Online Tutorial](#)



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

Input=symbol
Deepestpath=9
Show:5 <= #symbols <= 100
Using: All ontologies
► my file
Detected reference set: ps_avgpres_nbadam88_u133p2; 1
Test Set:
10 Symbols could not be translated back to GeneID.
1217 Genes will be processed
1091 are mentioned in GO 126 However are not
uid=14d3175e92efe7046c881d779ba45632
Reference set:
15257 are mentioned in GO 2511 However are not
ExpectedRatio=0.0715081601887658
Using 2X2 contingency table analysis (chi-square) with continuity correction
mycn_amp: no < yes, mycn_amp: no >= yes,

GoPath	R#	#	p_value	GoId-Desc	GeneSymbols
97458	1274	159	1.9e-14	3: neuron part (3:4)	over 100 entries (159,)
120025	1650	187	4.2e-12	3: plasma membrane bounded cell projection (4:5)	over 100 entries (187,)
98588	1807	200	8.2e-12	3: bounding membrane of organelle (4:5)	over 100 entries (200,)
42995	1718	191	1.8e-11	3: cell projection (3:4)	over 100 entries (191,)
98805	1464	165	1.8e-10	3: whole membrane (3:3)	over 100 entries (165,)
5768	801	103	1.9e-10	3: endosome (4:9)	over 100 entries (103,)
3924	251	44	2.8e-10	2: GTPase activity (8:8)	RAB3C, ARL8A, RAB18, RAB21, RAB26, DNM3, GCH1, TUBG2, GNA12, GNAI1, GNAZ, GNB1, GNG3, GNL1, RAB15, ARL4D, ARF5, KRAS, RND3, NRAS, SAR1B, RAB14, RAB6B, RAB8B, SEPT4, GPN2, RAB22A, RAB2A, RAB3B, RAB5B, RAB5C, RALA, RAP1B, RAP2A, RIT2, RIT1, RRAGC, TUBB2A, RSG1, RND2, TUBA1C, RAB2B, MFN2, CDC42
44456	629	85	4.2e-10	3: synapse part (2:3)	ACTR2, CACNG2, SLC9A6, CAP2, UNC13B, CHRNA3, CHRN81, FCHO2, RAB3C, ADCYAP1, AP1S1, CNR1, TPRG1L, SYT2, SYNPR, STXB5, DDC, DLG2, STX2, CPEB3, RIMS1, SYT11, ZDHHC17, RUSC1, GABBR1, RAB26, GAP43, DNM3, SLC17A5, AMPH, GNG3, APBA1, KCNC4, KCND2, ASIC2, MAP4, MAPT, ACHE, NSF, SYT17, RAB8B, ATP6V1G2, CAMK2N1, PRKAR2B, TBC1D24, MIB1, SYT13, HCN3, PTPRN2, RAB3B, RAB5B, RAB5C, LIN7B, SLC8A1, SLC18A1, SLC18A2, BMPR2, SNAP25, SNCA, STRN, STX1A, VAMP1, SYT5, LRRTM4, CPEB4, SRCIN1, RAB2B, PPFIA4, STON2, CADPS, NPFF, LIN7A, SYNJ1, KALRN, SYT7, NEURL1, ZNF804A, CRIPT, SNPH, LZTS3, RIMS3, DNAJC6, PJA2, SV2B, CDC42
120038	1149	135	4.6e-10	3: plasma membrane bounded cell projection part (4:6)	over 100 entries (135,)
44463	1149	135	4.6e-10	3: cell projection part (3:5)	over 100 entries (135,)
31410	2010	211	5.5e-10	3: cytoplasmic vesicle (5:8)	over 100 entries (211,)
98793	323	52	5.7e-10	3: presynapse (3:5)	SLC9A6, UNC13B, FCHO2, RAB3C, ADCYAP1, AP1S1, CNR1, TPRG1L, SYT2, SYNPR, STXB5, DDC, STX2, RIMS1, SYT11, ZDHHC17, GABBR1, RAB26, SLC17A5, AMPH, APBA1, KCNC4, SYT17, RAB8B, ATP6V1G2, TBC1D24, SYT13, HCN3, PTPRN2, RAB3B, RAB5B, RAB5C, LIN7B, SLC18A1, SLC18A2, SNAP25, SNCA, STX1A, VAMP1, SYT5, RAB2B, PPFIA4, STON2, CADPS, NPFF, LIN7A, SYNJ1, SYT7, ZNF804A, SNPH, RIMS3, SV2B
97708	2012	211	6.1e-10	3: intracellular vesicle (4:7)	over 100 entries (211,)
10975	402	60	1.6e-09	1: regulation of neuron projection development (7:12)	ACTR2, PLXNC1, STMN2, CHRNA3, ADCYAP1, CNR1, CNTN1, SYT2, DPYSL3, EFN2, EPHB3, FKBP1B, CPEB3, ZNF365, RIMS1, RAB21, SETX, RAP1GAP2, MACF1, NEGR1, SS18L1, DNM3, NRG1, IFRD1, MAPT, NRCAM, NTRK1, PAFAH1B1, PAK3, TRPV2, SYT17, PMP22, TMEM106B, PPP2R5B, CCDC88A, TMEM30A, KIDINS220, PTN, PTPRF, RAP2A, RIT2, NDRG4, BMPR2, TRAK2, SNAP25, BRAF, TNF, YWHAH, MUL1, SRCIN1, RND2, KNDC1, KALRN, NEURL1, PLXNA4, ZNF804A, RAPGEF2, ULK2, LZTS3, KIAA0319, SEPT7, CDC42
31344	574	77	4.8e-09	1: regulation of cell projection organization (5:6)	ACTR2, PLXNC1, STMN2, CHRNA3, ADCYAP1, CNR1, CNTN1, SYT2, TBC1D20, CYLD, DPYSL3, EFN2, EPHB3, FER, FKBP1B, CPEB3, ZNF365, RIMS1, RAB21, SETX, RAP1GAP2, ATMIN, MACF1, NEGR1, GAP43, SS18L1, DNM3, NRG1, APC, IFRD1, MAP4, MAPT, NRCAM, NTRK1, PAFAH1B1, PAK3, TRPV2, SYT17, RAB8B, PMP22, TMEM106B, EPS8L1, PPP2R5B, CCDC88A, TMEM30A, TBC1D24, KIDINS220, PTN, PTPRF, RALA, RAP2A, RIT2, NDRG4, BMPR2, TRAK2, SNAP25, BRAF, KLF5, TNF, YWHAH, MUL1, SRCIN1, RND2, KNDC1, NAV3, KALRN, IFT20, NEURL1, PLXNA4, ZNF804A, CD44, RAPGEF2, ULK2, LZTS3, KIAA0319, SEPT7, CDC42
120035	565	76	5.2e-09	1: regulation of plasma membrane bounded cell projection organization (6:7)	ACTR2, PLXNC1, STMN2, CHRNA3, ADCYAP1, CNR1, CNTN1, SYT2, TBC1D20, CYLD, DPYSL3, EFN2, EPHB3, FER, FKBP1B, CPEB3, ZNF365, RIMS1, RAB21, SETX, RAP1GAP2, ATMIN, MACF1, NEGR1, GAP43, SS18L1, DNM3, NRG1, APC, IFRD1, MAP4, MAPT, NRCAM, NTRK1, PAFAH1B1, PAK3, TRPV2, SYT17, PMP22, TMEM106B, EPS8L1, PPP2R5B, CCDC88A, TMEM30A, TBC1D24, KIDINS220, PTN, PTPRF, RALA, RAP2A, RIT2, NDRG4, BMPR2, TRAK2, SNAP25, BRAF, KLF5, TNF, YWHAH, MUL1, SRCIN1, RND2, KNDC1, NAV3, KALRN, IFT20, NEURL1, PLXNA4, ZNF804A, CD44, RAPGEF2, ULK2, LZTS3, KIAA0319, SEPT7, CDC42
43005	1000	118	5.3e-09	3: neuron projection (4:6)	over 100 entries (118,)
70382	157	30	1.3e-08	3: exocytic vesicle (5:10)	RAB3C, TPRG1L, SYT2, SYNPR, STXB5, DDC, DPYSL3, UNC13D, STX2, SYT11, RAB26, SLC17A5, AMPH, APBA1, RAB8B, ATP6V1G2, PTPRN2, RAB3B, RAB5B, RAB5C, SLC18A1, SLC18A2, SNAP25, SNCA, STX1A, VAMP1, SYT5, STON2, SYT7, SV2B
51641	2413	239	1.4e-08	1: cellular localization (3:3)	over 100 entries (239,)
31175	833	101	1.5e-08	1: neuron projection development (6:11)	over 100 entries (101,)
8021	143	28	1.8e-08	3: synaptic vesicle (3:11)	RAB3C, TPRG1L, SYT2, SYNPR, STXB5, DDC, STX2, SYT11, RAB26, SLC17A5, AMPH, APBA1, RAB8B, ATP6V1G2, PTPRN2, RAB3B, RAB5B, RAB5C, SLC18A1, SLC18A2, SNAP25, SNCA, STX1A, VAMP1, SYT5, STON2, SYT7, SV2B
149	114	24	2.1e-08	2: SNARE binding (4:4)	YKT6, GABARAPL2, SYT2, STXB5, TXLNA, STX2, SYT11, STX12, NSF, VPS54, SYT17, SYBU, SYT13, NAPB, SNAP25, STX1A, VAMP1, SYT5, STX16, SYT7, VAMP3, STX8, STXB5L, SNPH
120036	1302	143	2.8e-08	1: plasma membrane bounded cell projection organization (5:5)	over 100 entries (143,)
1904925	11	6	3.4e-08	1: positive regulation of autophagy of mitochondrion in response to mitochondrial depolarization (7:10)	OPTN, VPS13C, PINK1, MUL1, ATP1F1, MFN2

Gene set analysis

R2: Scan result for track mycn_amp

Online Tutorial

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

88 samples, transform_log2, present >= 1
track mycn_amp

2495 combinations meet your criteria

15410 combinations did not meet **p-value <= 0.01**

Multiple testing correction applied: False Discovery Rate

Results are limited to 1500 rows

View	Gene	P	Difference	Gr
	MYCNOS	3.75e-17	4.55	mycn_amp:
	MYCN	7.07e-17	3.14	mycn_amp:
	NOB1	1.38e-15	1.58	mycn_amp:
	KATNAL1	9.82e-14	-1.3	mycn_amp:
	KRT19	1.17e-13	-5.9	mycn_amp:
	DDX10	2.37e-13	1.19	mycn_amp:
	TRAP1	3.85e-13	1.22	mycn_amp:
	SCFD2	8.1e-13	1.04	mycn_amp:
	TRIM36	2.15e-12	-1.9	mycn_amp:
	MEAF6	2.46e-12	-1.23	mycn_amp:
	NRCAM	3.49e-12	-1.66	mycn_amp:
	PAICS	3.72e-12	1.35	mycn_amp:
	NOA1	9.6e-12	1.08	mycn_amp:

R2: Scavenger

Adjustable settings

Gene set Collection: Select a collection

p-value cutoff:

Representation:

Groups of genes (selected = all)

- Broad 2019 archived
- Broad 2019 c1 position
- Broad 2019 c2 curated
- Broad 2019 c3 motif
- Broad 2019 c4 computational
- Broad 2019 c5 gene ontology
- Broad 2019 c6 oncogenic
- Broad 2019 c7 immunologic
- Broad 2019 h hallmark
- Broad 2020 09 archived
- Broad 2020 09 c cell type
- Broad 2020 09 c1 position
- Broad 2020 09 c2 curated
- Broad 2020 09 c3 motif
- Broad 2020 09 c4 computational
- Broad 2020 09 c5 gene ontology
- Broad 2020 09 c6 oncogenic
- Broad 2020 09 c7 immunologic
- Broad 2020 09 h hallmark
- Dorothea_regulons
- EMTmeta

Gene set analysis

Known interactions

Gene Ontology Analysis

Enrichr

DataAdder

Chromosome Map

Heatmap(zscore)

k-means

Plot all genes (xy, volcano etc)

Group change bar plot

Save current selection as TXT file

Save selection as TXT file (no header)

Reference for current selection

Store result as custom gene set

Differential expression	
Group	Count
mycn_amp: no <= yes	1268
mycn_amp: no >= yes	1227

Gene set analysis

Go to: [Main](#)

R2: Scavenger

From your input (n=2495), 2402 genes were also present in the current geneset collection (db:geneset_broad_2020_09_c2_curated).
 Within the dataset ps_avgpres_nbadam88_u133p2, 16150 genes were detected in the current geneset selection (hugoonce=yes and minimal present call=1)
 The table below lists genesets where the number of genes from your list are present more than expected ($p < .05$ from 2X2 contingency table analysis with continuity correction)
 mycn_amp: no < yes, mycn_amp: no >= yes,

set	R#	#	p_value	Genelist
over-representation HMSigDB Team:LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN	771	262	2.3e-52	, mycn_amp: no < yes (n=85), mycn_amp: no >= yes (n=177)
over-representation HMSigDB Team:CAIRO_HEPATOBlastoma_CLASSES_UP	578	208	1.9e-47	, mycn_amp: no < yes (n=193), mycn_amp: no >= yes (n=15)
over-representation HMSigDB Team:KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN	959	273	5.6e-34	, mycn_amp: no < yes (n=239), mycn_amp: no >= yes (n=34)
over-representation HMSigDB Team:KRIGE_I	874	234	4.6e-24	, mycn_amp: no < yes (n=194), mycn_amp: no >= yes (n=40)
over-representation HMSigDB Team:DODD_N	1340	325	1.0e-23	, mycn_amp: no < yes (n=275), mycn_amp: no >= yes (n=50)
over-representation Broad Institute: SCHUH	75	42	5.6e-23	, ABCE1, AHCY, AIMP2, AKAP1, AUH, CAD, CEBPZ, DANCR, DDX10, DDX21, DHO, IMPDH2, LDHA, MRPL3, MTHFD1, MYC, NME1, ODC1, PAICS, PNO1, POLD2, POLR3K, RRP9, SLC16A1, SLC20A1, SRM, TBL3, TMEM97, TRAP1, VARS, ZNF239
over-representation HMSigDB Team:MANALC	279	97	1.0e-20	, ABCF2, AIMP2, AKAP1, ARMC6, ATIC, BYSL, C20ORF27, CAD, CD3EAP, CHAF1A, FAM136A, FASN, FBXO42, FERMT1, GART, GEMIN6, GRWD1, GTPBP4, H2AFX, HLMNB2, MAD2L1, MAZ, MCM10, MCM2, MCM4, MCM5, MCM6, METTL2B, MFN2, MNDUF4F4, NME1, NOP16, NUP160, NUP188, NUP205, ODC1, ORC6, PA2G4, PDS, POLR3K, PPAT, PPIF, PRMT5, PSMG1, PUS1, PWP2, RGS4, RRP1, RRP1B, RRP9, SLC5A6, SLCO4A1, SNRPA1, SNRPD1, SNRPD3, SRM, TRIP13, UBE2S, URB1, UTRN, WDR77
over-representation HMSigDB Team:BILD_M	184	72	3.7e-20	, AIMP2, ALG3, ALS2CL, ANAPC1, ARNTL, ATIC, ATP2B4, BID, C10ORF2, C12ORF6, DDX18, DHODH, DHRS1, DIEXF, DUSP22, EPS8L1, ERBB3, ERCC1, EXOSC5, FANCD1, HSPD1, IMP4, IPO4, METTL1, MYC, NCL, NCR3LG1, NEU3, NOP16, NPM1, PA2G4, PMM2, PNPT1, PTRH2, RABEPK, RRP9, SCFD2, SFXN4, SLC12A8, SLC6A15, SLC16A1, SLC20A1, SLC20A2, SLC20A3, SLC20A4, SLC20A5, SLC20A6, SLC20A7, SLC20A8, SLC20A9, SLC20A10, SLC20A11, SLC20A12, SLC20A13, SLC20A14, SLC20A15, SLC20A16, SLC20A17, SLC20A18, SLC20A19, SLC20A20, SLC20A21, SLC20A22, SLC20A23, SLC20A24, SLC20A25, SLC20A26, SLC20A27, SLC20A28, SLC20A29, SLC20A30, SLC20A31, SLC20A32, SLC20A33, SLC20A34, SLC20A35, SLC20A36, SLC20A37, SLC20A38, SLC20A39, SLC20A40, SLC20A41, SLC20A42, SLC20A43, SLC20A44, SLC20A45, SLC20A46, SLC20A47, SLC20A48, SLC20A49, SLC20A50, SLC20A51, SLC20A52, SLC20A53, SLC20A54, SLC20A55, SLC20A56, SLC20A57, SLC20A58, SLC20A59, SLC20A60, SLC20A61, SLC20A62, SLC20A63, SLC20A64, SLC20A65, 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Tumor Neuro

View	Gene
	MYCNOS
	MYCN
	NOB1
	KATNAL1
	KRT19
	DDX10
	TRAP1
	SCFD2
	TRIM36
	MEAF6
	NRCAM
	PAICS
	NOA1

maayanlab.cloud/Enrichr/enrich

Enrichr Login | Register

Transcription Pathways Ontologies Diseases/Drugs Cell Types Misc Legacy Crowd

Description R2 gene list (2495 genes)

ChEA 2022

CREM 20920259 ChIP-Seq GC1-SPG Mouse

MYC 28411283 ChIP-Seq MDA231-LM2-4175

MYC 22102868 ChIP-Seq CA46 Human Bloo

MYCN 28898695 ChIP-Seq NB1643 Human T

MYC 19030024 ChIP-ChIP MESC

ENCODE and ChEA Consensus TFs from

MAX ENCODE

MYC ENCODE

E2F6 ENCODE

MYC CHEA

BRCA1 ENCODE

ARCHS4 TFs Coexp

SF3A3 human tf ARCHS4 coexpression

PRMT3 human tf ARCHS4 coexpression

FARSA human tf ARCHS4 coexpression

NOC3L human tf ARCHS4 coexpression

TP53 human tf ARCHS4 coexpression

TF Perturbations Followed by Expression

MYC KD HUMAN GSE22139 CREEDSID GENE

MYC OE MOUSE GSE38304 CREEDSID GENE

TCF4 KD HUMAN GSE18560 CREEDSID GENE

RELA KD HUMAN GSE1676 CREEDSID GENE

HSF1 KO MOUSE GSE41005 CREEDSID GENE

TRRUST Transcription Factors 2019

MYCN human

EZH2 human

ASCL1 mouse

NEUROG2 mouse

TCF4 human

FANTOM6 lncRNA KD DEGs

RP11-458D21.1-ASO_G0233396_07-DEGs Do

RP11-38L15.3-ASO_G0231187_02-DEGs Dow

AC124789.1-ASO_G0260833_06-DEGs Down

CTD-2587H24.5-ASO_G0267577_01-DEGs Do

RP11-417E7.1-ASO_G0223485_AD_04-DEGs I

lncHUB lncRNA Co-Expression

LINC01357

ELOA-AS1

WDR7-OT1

IGBP1-AS2

LINC00641

Enrichr Submissions TF-Gene Cooccurrence

TRMT1

NOC4L

FARSA

NOC3L

DUS3L

TRANSFAC and JASPAR PWMs

NRF1 (human)

ATF4 (human)

E2F1 (human)

NRF1 (mouse)

PLAU (human)

Epigenomics Roadmap HM ChIP-seq

H3K27ac CD4 Naive Primary Cells

H3K4me3 CD4+ CD25- CD45RA+ Naive Prim.

TargetScan microRNA 2017

mmu-miR-496

mmu-miR-1191

miRTarBase 2017

hsa-miR-16-5p

hsa-miR-193b-3p

Online Tutorial

- Gene set analysis
- Known interactions
- Gene Ontology Analysis
- Enrichr**
- DataAdder
- Chromosome Map
- Heatmap(zscore)
- k-means
- Plot all genes (xy, volcano etc)
- Group change bar plot
- Save current selection as TXT file
- Save selection as TXT file (no header)
- Reference for current selection
- Store result as custom gene set

Differential expression

Group	Count
mycn_amp: no <= yes	1268
mycn_amp: no >= yes	1227

Chromosome map

R2: Scan result for track mycn_amp

Online Tutorial

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

88 samples, transform_log2, present >= 1
track mycn_amp

2495 combinations meet your criteria

15410 combinations did not meet **p-value <= 0.01**

Multiple testing correction applied: False Discovery Rate

Results are limited to 1500 rows

View	Gene	P	Difference	Group	Presence
	MYCNOS	3.75e-17	4.55	mycn_amp: no < yes	14/88
	MYCN	7.07e-17	3.14	mycn_amp: no < yes	88/88
	NOB1	1.38e-15	1.58	mycn_amp: no < yes	88/88
	KATNAL1	9.82e-14	-1.3	mycn_amp: no >= yes	88/88
	KRT19	1.17e-13	-5.9	mycn_amp: no >= yes	73/88
	DDX10	2.37e-13	1.19	mycn_amp: no < yes	88/88
	TRAP1	3.85e-13	1.22	mycn_amp: no < yes	88/88
	SCFD2	8.1e-13	1.04	mycn_amp: no < yes	88/88
	TRIM36	2.15e-12	-1.9	mycn_amp: no >= yes	88/88
	MEAF6	2.46e-12	-1.23	mycn_amp: no >= yes	88/88
	NRCAM	3.49e-12	-1.66	mycn_amp: no >= yes	88/88
	PAICS	3.72e-12	1.35	mycn_amp: no < yes	88/88
	NOA1	9.6e-12	1.08	mycn_amp: no < yes	88/88

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Differential expression	
Group	Count
mycn_amp: no < yes	1268
mycn_amp: no >= yes	1227

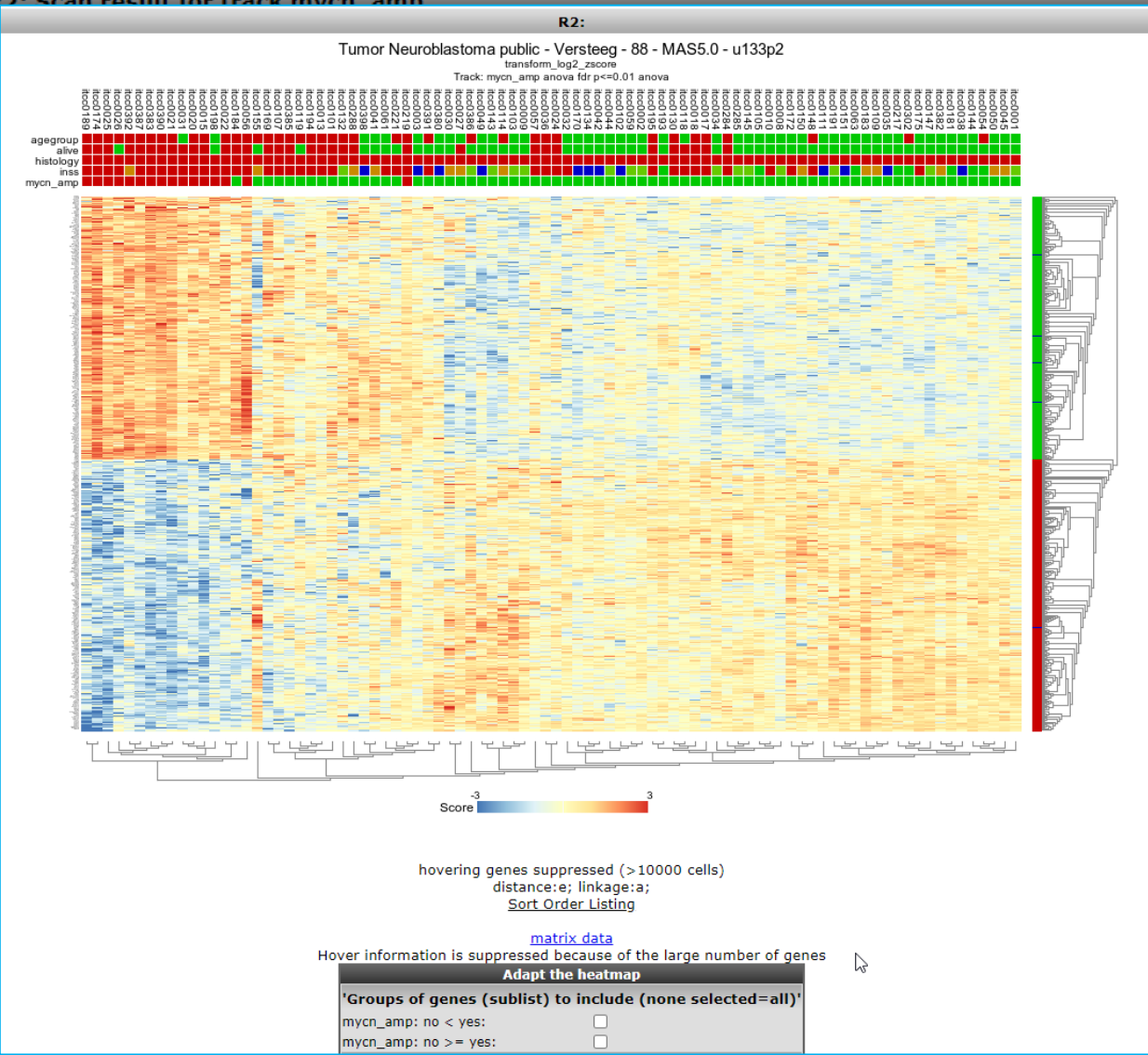
Heatmap

Tumor Neuroblastoma p

R2: Scan result for track mycn_amp

15410
Multiple t

View	Gene	P	D
	MYCNOS	3.75e-17	
	MYCN	7.07e-17	
	NOB1	1.38e-15	
	KATNAL1	9.82e-14	
	KRT19	1.17e-13	
	DDX10	2.37e-13	
	TRAP1	3.85e-13	
	SCFD2	8.1e-13	
	TRIM36	2.15e-12	
	MEAF6	2.46e-12	
	NRCAM	3.49e-12	
	PAICS	3.72e-12	
	NOA1	9.6e-12	



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- Reference for current selection
- Store result as custom gene set

Differential expression

Group	Count
mycn_amp: no < yes	1268
mycn_amp: no >= yes	1227

Present the result as top 100 change bars

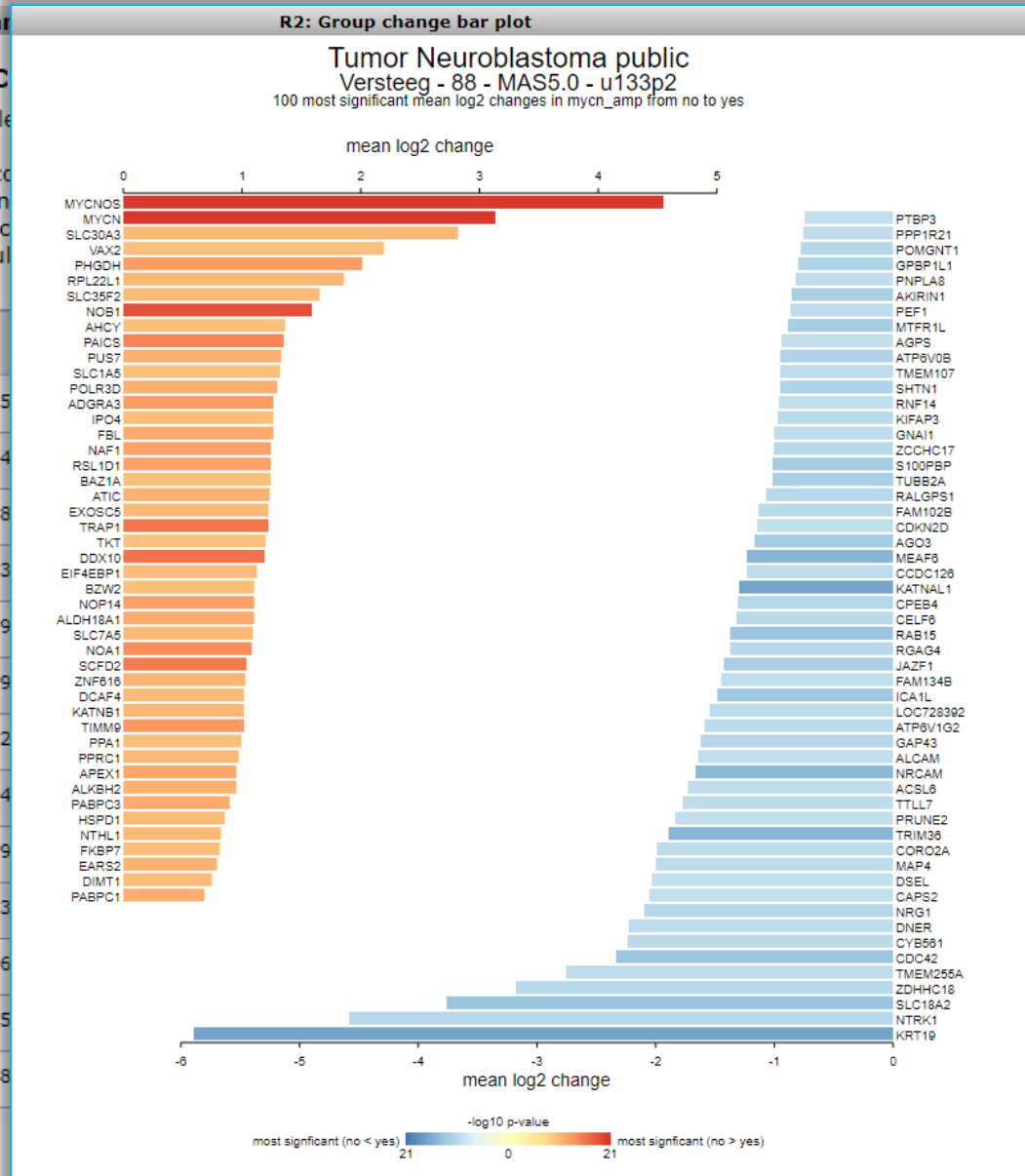
Online Tutorial

Tumor Neuroblastoma public

88 samples

2495 comparisons
15410 combinations
Multiple testing correction
Result

View	Gene	P	Difference
	MYCNOS	3.75e-17	4.55
	MYCN	7.07e-17	3.14
	NOB1	1.38e-15	1.58
	KATNAL1	9.82e-14	-1.3
	KRT19	1.17e-13	-5.9
	DDX10	2.37e-13	1.19
	TRAP1	3.85e-13	1.22
	SCFD2	8.1e-13	1.04
	TRIM36	2.15e-12	-1.9
	MEAF6	2.46e-12	-1.23
	NRCAM	3.49e-12	-1.66
	PAICS	3.72e-12	1.35
	NOA1	9.6e-12	1.08



- Gene set analysis
- Known interactions
- Gene Ontology Analysis
- Enrichr
- DataAdder
- Chromosome Map
- Heatmap(zscore)
- k-means
- Plot all genes (xy, volcano etc)
- Group change bar plot**
- Save current selection as TXT file
- Save selection as TXT file (no header)
- Reference for current selection
- Store result as custom gene set

Differential expression	
Group	Count
mycn_amp: no <= yes	1268
mycn_amp: no >= yes	1227

Store the result as a personal gene set

R2: Scan result for track mycn_amp

Online Tutorial

Tumor Neuroblastoma publ

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Multiple testin

Re

View	Gene	P	Differen
	MYCNOS	3.75e-17	4
	MYCN	7.07e-17	3
	NOB1	1.38e-15	1
	KATNAL1	9.82e-14	
	KRT19	1.17e-13	
	DDX10	2.37e-13	1
	TRAP1	3.85e-13	1
	SCFD2	8.1e-13	1
	TRIM36	2.15e-12	
	MEAF6	2.46e-12	
	NRCAM	3.49e-12	
	PAICS	3.72e-12	1
	NOA1	9.6e-12	1

Custom gene set editor

Name (must be unique):

Species:

Comparison: groups
 Data transformation: transform_log2
 Dataset: ps_avgpres_nbadam88_u133p2
 Date: Mon May 22 13:51:05 2023
 Group: mycn_amp -> no mycn_amp -> yes

Description:

Gene symbols (1 per line):

ABCA5
 ABCC4
 ABCE1
 ABCF2
 ABLIM3
 ACBD6
 ACSL6
 ADCK3
 ADGRA3
 AGO3
 AGO4
 AGPS
 AHCY
 AHI1
 AKIRIN1

Storage options

Save mode:

Community:

Temporary: ⓘ

Collection:

-
-
-
-
-
-
-
-
-
-
-
-
-
-

Did You Know

Personal / Group gene sets can be found in the 'gene set' selection pop up window

Differential expression	
Group	Count
mycn_amp: no <= yes	1268
mycn_amp: no >= yes	1227

Save the analysis result as text file

R2: Scan result for track mycn_amp

Tumor Neuroblastom

View	Gene	P
	MYCNOS	3.75e-1
	MYCN	7.07e-1
	NOB1	1.38e-1
	KATNAL1	9.82e-1
	KRT19	1.17e-1
	DDX10	2.37e-1
	TRAP1	3.85e-1
	SCFD2	8.1e-1
	TRIM36	2.15e-1
	MEAF6	2.46e-1
	NRCAM	3.49e-1
	PAICS	3.72e-1
	NOA1	9.6e-1

```
#Program: R2: Genomics analysis and visualization platform
#Website: http://r2.amc.nl
#Lead Contact: Jan Koster (jankoster@amsterdamumc.nl)
#Support: r2-support@amsterdamumc.nl
#Date: Mon May 22 13:51:05 2023
#Dataset: ps_avgpres_nbadam88_u133p2
#Pretty_dataset: Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 - u133p2
#Data transformation: transform_log2
#Values field:
#Comparison: groups
#Track: mycn_amp
#Group: mycn_amp -> no
#Group: mycn_amp -> yes
#Test: anova
#Output: anova fdr p<=0.01
#Minimal presentcalls: 1
#Number of lines: 500
#r2filetype: datasetresult
#H:probeset      hugo      corrected-pvalue      Difference      sublist
207028_at        MYCNOS  3.74853223995156e-17  4.54811668730662  mycn_amp: no < yes
209757_s_at      MYCN    7.0727633888616e-17  3.1378143641975  mycn_amp: no < yes
223018_at        NOB1    1.38109476704544e-15  1.58373748822094  mycn_amp: no < yes
227713_at        KATNAL1 9.82447670728964e-14  -1.29873269120862  mycn_amp: no >= yes
201650_at        KRT19   1.17370381131875e-13  -5.89504261732814  mycn_amp: no >= yes
204977_at        DDX10   2.37036280406065e-13  1.1891909332795  mycn_amp: no < yes
201391_at        TRAP1   3.85201852262052e-13  1.22400817616631  mycn_amp: no < yes
226923_at        SCFD2   8.10314443370423e-13  1.03927144755694  mycn_amp: no < yes
219736_at        TRIM36  2.14967392034356e-12  -1.8963886423243  mycn_amp: no >= yes
218165_at        MEAF6   2.4641224971919e-12  -1.23212276822419  mycn_amp: no >= yes
204105_s_at      NRCAM   3.48839919103934e-12  -1.66362289013188  mycn_amp: no >= yes
201013_s_at      PAICS   3.71853745289075e-12  1.35256400812253  mycn_amp: no < yes
223157_at        NOA1    9.59503859621163e-12  1.07653106339411  mycn_amp: no < yes
205857_at        SLC18A2 7.01293650614807e-11  -3.75832367478995  mycn_amp: no >= yes
59697_at         RAB15   8.87839826797986e-11  -1.36739628948066  mycn_amp: no >= yes
218316_at        TIMM9   9.17914764738803e-11  1.0176842366833  mycn_amp: no < yes
214230_at        CDC42   9.46578947029879e-11  -2.33494854621019  mycn_amp: no >= yes
230454_at        ICA1L   1.71349116176549e-10  -1.48589773506536  mycn_amp: no >= yes
210473_s_at      ADGRA3  2.10485841342648e-10  1.26738001660787  mycn_amp: no < yes
201397_at        PHGDH   2.33279064679616e-10  2.0098385741988  mycn_amp: no < yes
```

- Gene set analysis
- Known interactions
- Gene Ontology Analysis
- Enrichr
- DataAdder
- Chromosome Map
- Heatmap(zscore)
- k-means
- Plot all genes (xy, volcano etc)
- Group change bar plot
- Save current selection as TXT file**
- Save selection as TXT file (no header)
- Reference for current selection
- Store result as custom gene set

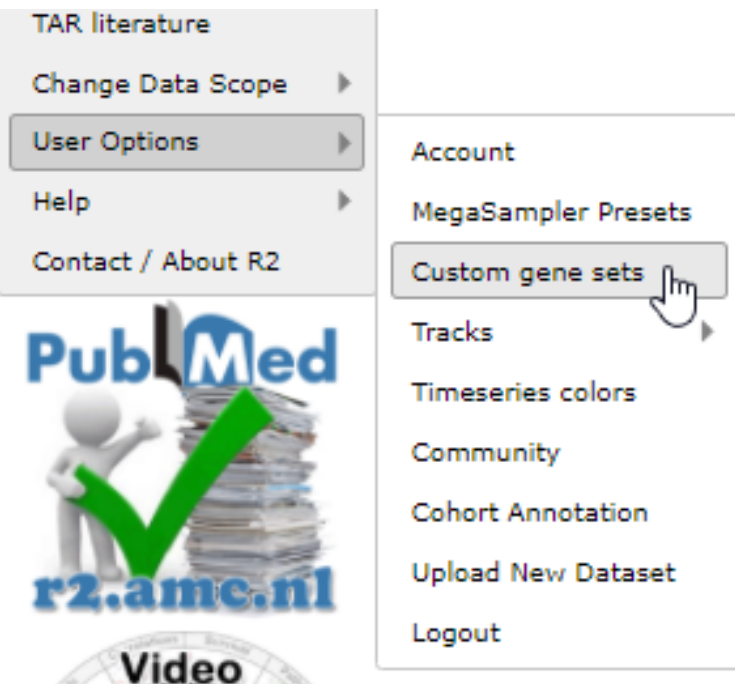
Differential expression	
Group	Count
mycn_amp: no < yes	1268
mycn_amp: no >= yes	1227

Adapting R2



Custom gene sets

- R2 can store 'lists of genes' for later usage
 - Official gene symbols are being stored
- List of genes
 - Of many analyses, the result can be stored via the button 'Store result as Gene Set' (example in Diff. Express)
 - Via 'User options' -> Custom gene sets you can create gene sets manually as well and save them for analyses
 - copy/paste gene symbols in editor
 - Or edit earlier saved gene sets



Custom gene sets (created by you)

Custom gene set overview (private)

- All
 - main +
 - alive_yes_no ↘

Operation: Select an operation ▼

Custom gene set editor

Custom gene set editor

Name (must be unique):

Species:

Description:

Gene symbols (1 per line):

Storage options

Save mode:
Community:
Temporary: ⓘ
Collection:

Custom gene set overview (private)

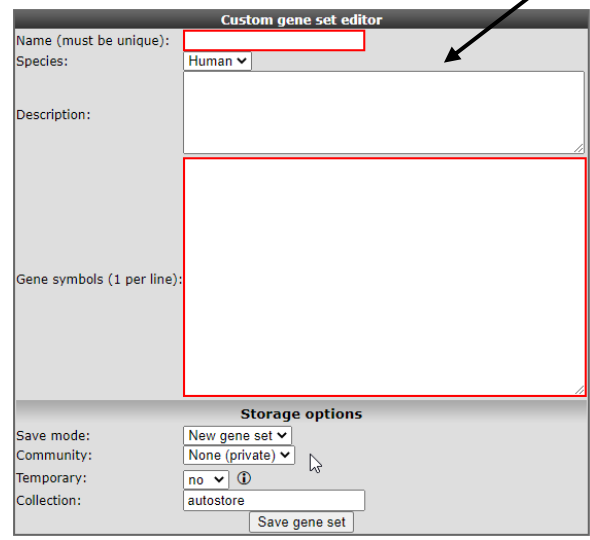
Custom gene set overview (private)

- All
 - main +
 - alive_yes_no ↘
 - my_gene_list ↘

Operation: Select an operation ▼

Custom gene set editor

Custom gene sets (created by you) collections



Custom gene set editor

Name (must be unique):

Species:

Description:

Gene symbols (1 per line):

Storage options

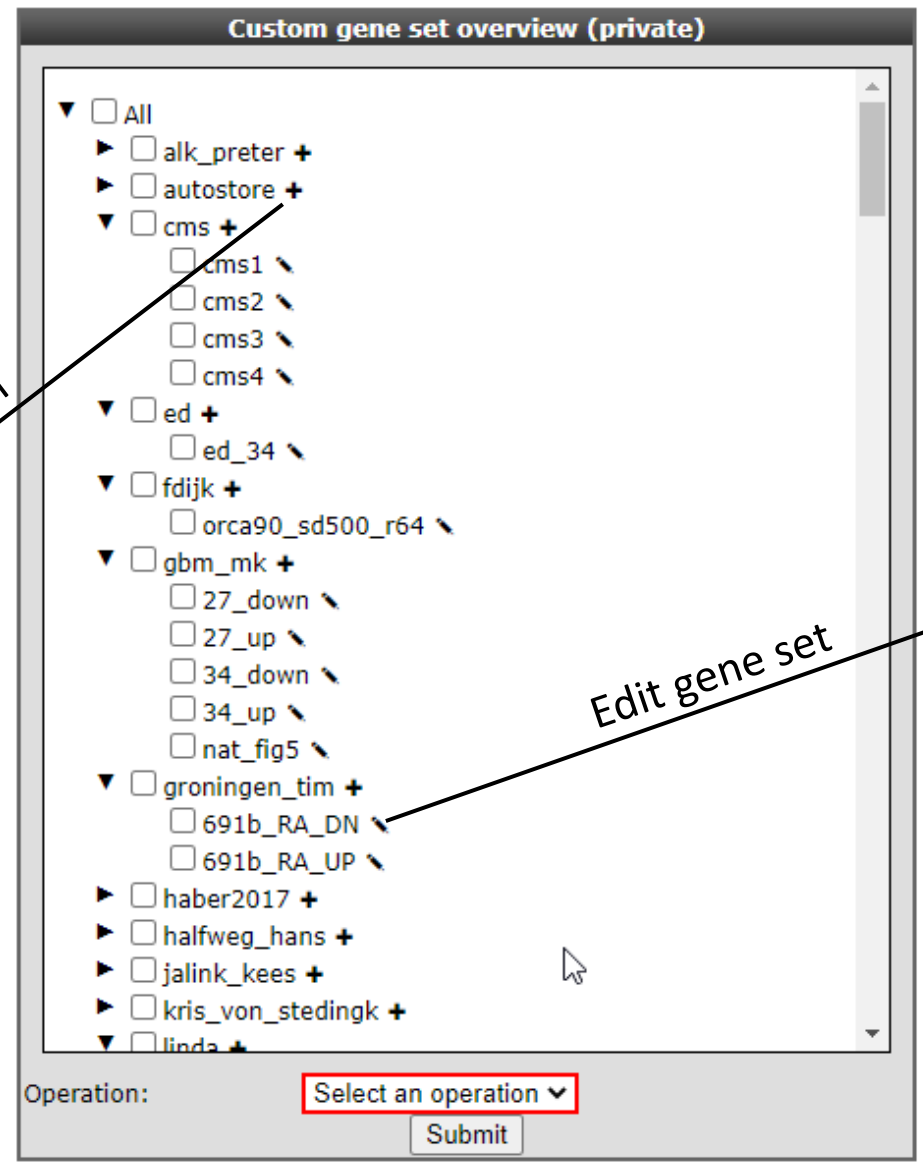
Save mode:

Community:

Temporary:

Collection:

add gene set to collection

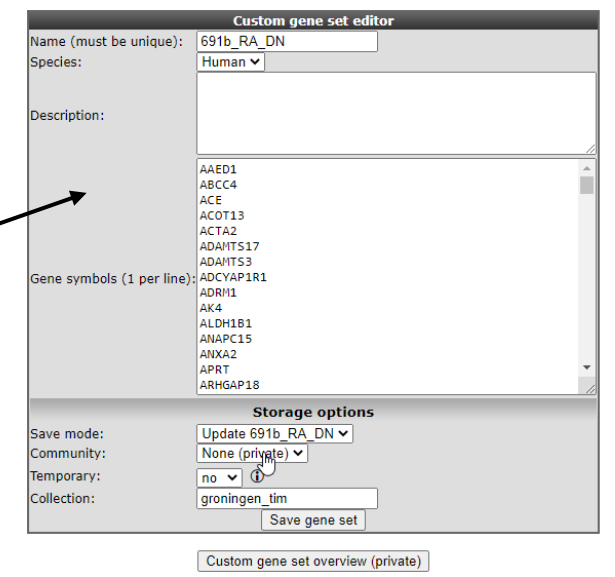


Custom gene set overview (private)

- All
 - alk_preter +
 - autostore +
 - cms +
 - cms1 ↘
 - cms2 ↘
 - cms3 ↘
 - cms4 ↘
 - ed +
 - ed_34 ↘
 - fdijk +
 - orca90_sd500_r64 ↘
 - gbm_mk +
 - 27_down ↘
 - 27_up ↘
 - 34_down ↘
 - 34_up ↘
 - nat_fig5 ↘
 - groningen_tim +
 - 691b_RA_DN ↘
 - 691b_RA_UP ↘
 - haber2017 +
 - halfweg_hans +
 - jalink_kees +
 - kris_von_stedingk +
 - linda +

Operation:

Edit gene set



Custom gene set editor

Name (must be unique):

Species:

Description:

Gene symbols (1 per line):
AAED1
ABCC4
ACE
ACOT13
ACTA2
ADAHTS17
ADAHTS3
ADCYAP1R1
ADR11
AK4
ALDH1B1
ANAPC15
ANXA2
APRT
ARHGAP18

Storage options

Save mode:

Community:

Temporary:

Collection:

Custom gene set overview (private)

Custom gene sets (stored via R2)

Go to: [Main](#)

R2: Scan result for track mycn_amp

[Online Tutorial](#)



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

88 samples, transform_log2, present >= 1
track mycn_amp

2495 combinations meet your criteria

15410 combinations did not meet **p-value <= 0.01**

Multiple testing correction applied: False Discovery Rate

Results are limited to 1500 rows

View	Gene	P	Difference	Group	Presence
------	------	---	------------	-------	----------

R2: Custom gene set editor

Custom gene set editor

Name (must be unique):

Species:

Description:

Gene symbols:

Included groups (none=all):
 mycn_amp: no < yes
 mycn_amp: no >= yes

Storage options

Save mode:

Community:

Temporary:

Collection:

-
-
-
-
-
-
-
-
-
-
-
-
-
-

Differential expression

Group	Count
mycn_amp: no < yes	1288
mycn_amp: no >= yes	1227

Mini ontology analysis

Category	Cutoff	Total	%	pval
All	2495	17005	13.9%	1.00
DNA repair	39	197	19.8%	0.02
apoptosis	72	577	12.5%	0.31
cell cycle	66	469	14.1%	0.03
development	185	1389	13.3%	0.51
differentiation	72	578	12.5%	0.30
drug target	150	1031	14.5%	0.57
kinase	89	600	14.8%	0.53
membrane	531	3981	13.3%	0.28
signal transduction	338	2385	14.1%	0.83
transcription factor	81	660	11.7%	0.10

Personal / Group gene sets can be found in the Adjustable settings panel. In the gene set section: **GS** button

Gene plot options

Using your gene sets as gene filter (e.g. diff expression)

Go to: [Main](#) R2: Differential expression between groups [Online Tutorial](#)

Search gene-set.

Name	Count
<input type="checkbox"/> Personal gene sets	6154
<input type="checkbox"/> main	3798
<input type="checkbox"/> _TEMPORARY	2356
<input type="checkbox"/> kaplanscan_mycn100	100
<input type="checkbox"/> kaplanscan_mycn_deg	2256
<input type="checkbox"/> Community gene sets	83365
<input type="checkbox"/> r2	83365
<input type="checkbox"/> ensembl	20525
<input type="checkbox"/> gencodev40	60324
<input type="checkbox"/> illumina	523
<input type="checkbox"/> itccp4	74
<input type="checkbox"/> ither_trial_genes_v1	36
<input type="checkbox"/> langenberg_ither_ppr_v1	200
<input type="checkbox"/> main	998
<input type="checkbox"/> manuscript	200
<input type="checkbox"/> pedcan	86
<input type="checkbox"/> ppr	399
<input type="checkbox"/> Categories	18553
<input type="checkbox"/> r2 curated gene sets	7664
<input type="checkbox"/> r2 provided gene lists	1168

Using gene sets in Venn diagrams

Go to: [M](#), Go to: [Main](#)
Online Tutorial [ne Tutorial](#)

- Main
- ITCC-P4 (ITCC-P4 (IMI2) ▶)
- Cancer Po Cancer Portals
- Time serie Time series
- Amplicon\ AmpliconView
- Kaplan-Me Kaplan-Meier
- Sample m Sample maps
- Small Too Small Tools
- DataGrab Genome Browser
- Genome E ChIP data
- ChIP data TAR literature
- TAR litera Change Data Scope ▶
- Change D User Options ▶
- User Opti Administrator ▶
- Administ Help ▶
- Help Contact / About R2
- Contact /

R2: Gene Category Venn Diagram

Adjustable settings

Gene set A: Search GS

Gene set B: Search GS

Gene set C: Search GS

Type of Venn: next Reset

Type of Venn: next Reset

Intersection	Size
a only	449
b only	537
c only	700
a & b	68
a & c	49
b & c	43
a & b & c	9

Gene Category Venn Diagram

Region	Size
A only	361
B only	429
C only	593
A & B	40
A & C	39
B & C	59
A & B & C	9

red=A, blue=B, green=C

Type of Venn: next Reset

Region	Size
a only	449
b only	537
c only	700
a & b	39
a & c	40
b & c	59
a & b & c	9

Venn Diagrams

Select 2 or 3 gene categories (lists of gene names) from the dropdown lists and R2 will determine their overlaps and plot this as a Venn diagram.

Note that the dropdown list will update to allow for the selection of deeper levels

You can choose between different types of drawing the Venn diagrams from the dropdown

Below the Venn diagram, a table listing the genes together with their intersection, which allows you to identify the respective genes

Creating tracks (grouping variables)

Go to: [Main](#)
R2: Custom track
[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

Create a Custom Track via R2

Data set:

Build a track based on:

OK

Building Tracks

To build a custom track (grouping of the samples), you should select a dataset and indicate how many groups should be created. Optionally you can use the expression of a gene to determine the group memberships.

Complex tracks with many groups, are likely easier to build as a txt file and uploaded or pasted.

Did you know that you can export an r2 track from your account into a text file via the custom track manager? Those files can be uploaded (by another user) with the upload a track button. Communities are an alternative way to share track with other R2 users

- You can add new grouping variables to R2
 - From an analysis (Example KaplanScan)
 - User defined

Creating Tracks manually

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: customtrack

Custom Track Uploader:

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

How: Input Box

Paste Prescription (tab or ; separated)

ITCC0001	no
ITCC0002	no
ITCC0003	no
ITCC0008	no
ITCC0009	no
ITCC0010	no
ITCC0013	no
ITCC0015	yes
ITCC0017	no
ITCC0018	no
ITCC0020	yes
ITCC0021	yes
ITCC0022	yes
ITCC0024	no
ITCC0025	yes
ITCC0026	yes
ITCC0027	no
ITCC0030	no
ITCC0031	yes
ITCC0032	no
ITCC0034	no
ITCC0035	no
ITCC0036	no
ITCC0038	no
ITCC0041	no
ITCC0042	no
ITCC0044	no
ITCC0045	no
ITCC0049	no
ITCC0050	no

Next

Example of a tab-delimited text file:

```
trackname      testtrackname
group_color    <1      ff00ff
group_color    >=1     00ff00
show_as_track  no
description    this is a test track. description on 1 line
ITCC0001      stage4
ITCC0002      stage4
ITCC0003      stage3
ITCC0004      stage3
ITCC0005      stage4
```

Hex Color Helper:

HexColor: C80000

Online Tutorial

Building Tracks

You can create an R2 track, based on information supplied by yourself. Make sure that you are using the R2 identifiers of the samples as the first column. In the 2nd column, you specify the groupname. Annotation, for the track is provided by special variables (names in the 1st column).

trackname, provides the name to be given to the new track. **show_as_track**, specifies whether you would like the track

- **Manual creation has the most freedom**
 - needs to use the samplenames from R2
 - e.g x-gene-view, datagrabber

Select tracks

More Settings

Alternative Reporter (avgpres signal)	Correlation for combined Reporter 1 (#pc)	Reporter 1 (#pc)
209757_s_at (1389.7)	242026_at (5)	0
209756_s_at (235.5)	234376_at (3)	0

Groups

C:2 / N: / U:

Group 'no':	no	C80000
Group 'yes':	yes	00C800

Track Settings

Track name:

Show as track: no ⓘ

Where: Temporary (24hrs) ▼

Temporary (24hrs)

personal track

Community: student

Community: student_breast

Creating Tracks with expression level thresholds

R2: customtrack

Create a Custom Track via R2

Data Type: Expression data (H. sapiens) [n=1101]

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

Build a track based on: setting expression level thresholds

Provide the gene for thresholding: mycn

Submit Reset

OR

Upload or Paste a Track (txt file)

R2: customtrack

Tumor Neuroblastoma (combat) - Versteeg - 122 - MAS5.0(bc) - u133p2

Gene: mycn

- MYCN (209757_s_at) APS=1394.4(122) Avg=1394.4
- MYCN (209756_s_at) APS=173.6(15) Avg=35.0
- MYCN (211377_x_at) APS=146.2(6) Avg=15.3
- MYCN (234376_at) APS=60.8(4) Avg=10.2
- MYCN (242026_at) APS=26(5) Avg=12.2 ⚠

Define your Categories

bin_1	: less than	100	
bin_2	: at least 100 and less than	1000	Clear
bin_3	: at least 1000 and less than	2000	Clear
bin_4	: at least 2000 and less than	∞	

Next Reset

Custom group labels

Add as many sections as you like. Type in the infinite box

Groups

C:4 / N: / U:

Group 'bin_1':	bin_1	C80000
Group 'bin_2':	bin_2	00C800
Group 'bin_3':	bin_3	0000C8
Group 'bin_4':	bin_4	C8C800

Track Settings

Track name:

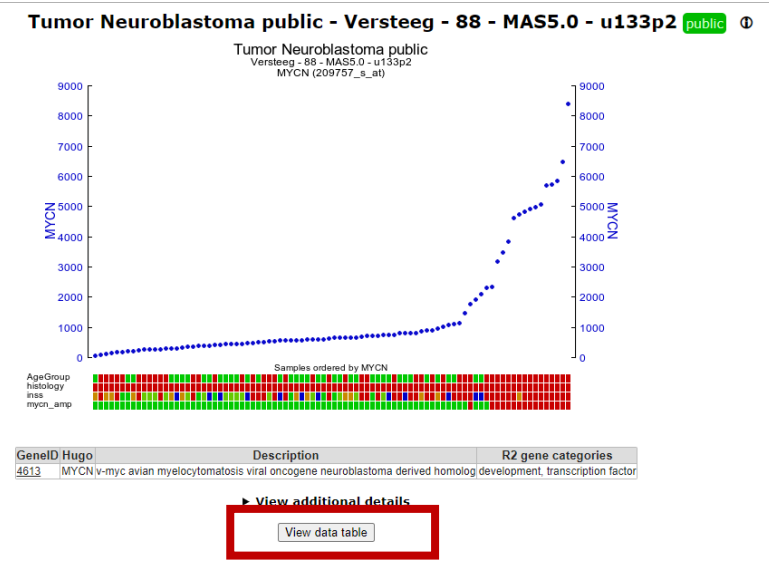
Show as track: no

Where: Temporary (24hrs)

Description (usergroups only):

Creating Tracks directly from dataset table

e.g: Sorting the gene expression level



Data table - current dataset: Tumor Neuroblastoma public - Versteeg - 88 - MAS5.0 -

sample	209757_s_at
ITCC0030	5.91169158187234
ITCC0184	6.63662462054365
ITCC0114	6.84423498775875
ITCC0288	7.28909670241999
ITCC0194	7.47654370621426
ITCC0063	7.59395128394841
ITCC0105	7.70113315484797
ITCC0027	7.78528898070402
ITCC0169	7.81570350334807
ITCC0191	8.01736520529273
ITCC0009	8.01959072835788
ITCC0386	8.05148086534133
ITCC0119	8.14720492494223
ITCC0103	8.17242750864548
ITCC0041	8.19130601891869
ITCC0035	8.21140163741847
ITCC0045	8.31197531446116
ITCC0001	8.50581155391959

Choose column(s) for track annotation

209757_s_at

samplenames

209757_s_at

OK

Groups
C:1 / N: / U:1

Group 'defined': defined C80000

Group 'not_defined': not_defined C6C6C6

Track Settings

Track name: track-from-grid

Show as track: no

Where: Temporary (24hrs)

Description (usergroups only):
this track was created from a grid selection

Build set Reset

Creating tracks via cohort overview

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

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

Tumor Neuroblastoma public
agegroup (n=88)

agegroup

Applied filters.
none

histology

inss

agegroup,alive,histology,ins...

checkbox	default	samplenames	link	sampleid	samplenames	agegroup	alive	histology	inss	mycn_amp	age_year	death_cause	gender	nti_event_overall	nti_event_progfree	nti_surv_overall	nti_surv_progfree	r2_label	recurrence_or_progression	link	
<input checked="" type="checkbox"/>	default	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>			ITCC0001	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd	female	no	no	7876	7876	n062t	nd	
<input checked="" type="checkbox"/>						ITCC0002	_less_than_or_equal_18_months	yes	nb	st2	no	0	nd	male	no	no	4914	4914	n066t	nd	

Choose column(s) for track annotation

agegroup,alive

- sampleid
- samplenames
- agegroup
- alive
- histology
- inss

OK

Groups
C:4 / N: / U:

- Group '_less_than_or_equal_18_months_no': _less_than_or_equal_18_mc C80000
- Group '_less_than_or_equal_18_months_yes': _less_than_or_equal_18_mc 00C800
- Group '_more_than_18_months_no': _more_than_18_months_no 0000C8
- Group '_more_than_18_months_yes': _more_than_18_months_yes C8C800

Track Settings

Track name:

Show as track: ⓘ

Where:

Description (usergroups only):

Build set Reset

Build a track

Managing your tracks

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 >
 - Account
 - MegaSampler Presets
 - Custom gene sets
 - Tracks >
 - Manage Default Tracks
 - Build Custom Track
 - Manage Custom Tracks
 - Manage Temp Tracks
 - Timeseries colors
 - Community
 - Cohort Annotation
 - Upload New Dataset
 - Logout
- Help >
- Contact / About R2

R2: Genomics Analysis and Visualization Platform

967627 (866122 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 Proceed


Online Tutorial

What is R2?



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

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

Financial Supporter of R2



[all news](#)

Using HGserver1(7)

PubMed

r2.amc.nl

Video training

Download the R2 Tutorials Book

Manage R2 default tracks

Manage your tracks
Here you can also export tracks which can be uploaded by others

Export data from R2

Go to: [Main](#)

R2: DataGrabber

[Online Tutorial](#)

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

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

Adjustable settings

Sample Filter

Subset track: mycn_amp (2 cat) ⚙️ ❌ ⓘ

Number of samples in subset
16

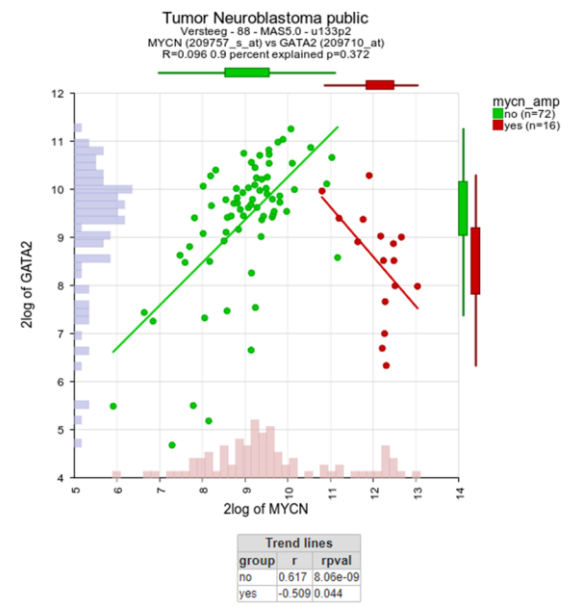
Selected sample subset:
mycn_amp
yes

ps_avgpres_nbadam88_u133p2_box1687227393-datagrabber-.txt - Kladblok

Bestand Bewerken Opmaak Beeld Help

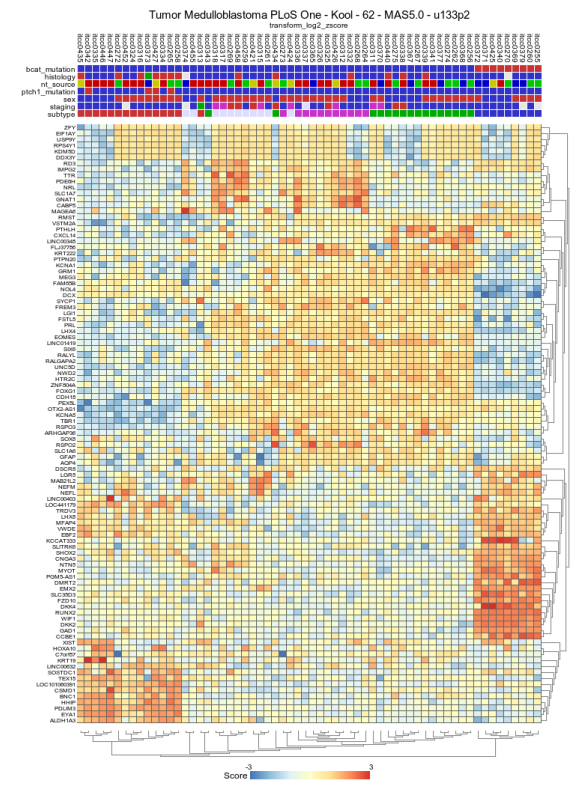
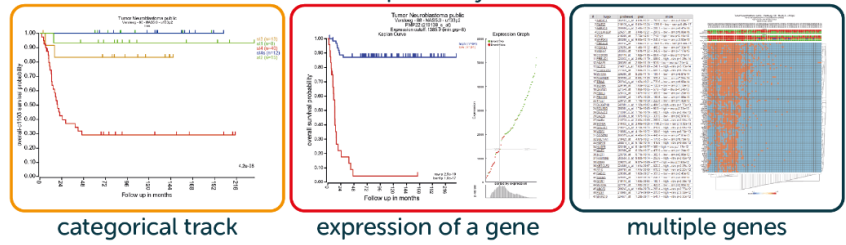
#H:hugo probeset	itcc0015	itcc0020	itcc0021	itcc0022	itcc0025	itcc0026	itcc0031	itcc0056	itcc0174	itcc0189										
#age_year	age_year	6	1	1	13	1	2	2	1	2	3	3	1	1						
#agegroup	agegroup	>1	>1	>1	>1	>1	>1	>1	>1	>1	>1	>1	>1	>1						
#alive	alive	no	no	no	yes	no	no	no	no	yes	no	no	no	no	no	no	no	no	no	no
#death_cause	death_cause	tumor	tumor	tumor	tumor	tumor	nd	tumor	tumor	tumor	tumor	tumor	nd	tumor	tumor	tumor	tumor	tumor	tumor	tumor
#gender	gender	female	male	male	female	male	male	male	female	male	male	female	male	female	female	male	female	female	female	female
#histology	histology	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb	nb
#id	id	7	10	11	12	14	15	18	31	60	65	70	72	80	83	84	86	86	86	86
#inss	inss	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st4	st3	st3	st3
#mycn_amp	mycn_amp	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
#nti_event_overall	nti_event_overall			yes	yes	yes	yes	yes	yes	no	yes	yes	yes	yes	yes	no	yes	yes	yes	yes
#nti_event_progrfree	nti_event_progrfree			yes	yes	yes	yes	yes	yes	no	yes	yes	yes	yes	yes	no	yes	yes	yes	yes
#nti_surv_overall	nti_surv_overall			1277	340	296	394	196	1577	853	63	406	1176	2128	638	325	385	757	178	178
#nti_surv_progrfree	nti_surv_progrfree			549	340	209	394	196	1577	609	45	334	1031	2128	77	315	365	660	174	174
#r2_label	r2_label	n425t	n538t	n540t	n557t	n583t	n593t	n089t	n159t	n194t	n561t	n579t	n604t	n567t	n608t	n619t	n637t	n637t	n637t	n637t
#recurrence_or_progression	recurrence_or_progression			yes	yes	yes	yes	yes	yes	no	yes	yes	yes	yes	yes	no	yes	yes	yes	yes
A1BG	229819_at	52.0	51.8	40.2	26.9	23.1	42.1	46.8	64.9	32.2	33.1	21.8	13.4	52.1	34.0	60.2	49.1			
A2M	217757_at	1605.6	1715.8	1074.8	698.1	454.9	246.8	1564.7	199.8	244.7	263.8	881.7	489.8	1444.7	474.2	511.0	519.5			
A2M-AS1	1564139_at	48.1	26.5	69.6	45.5	100.1	33.3	65.8	75.3	12.6	15.0	31.9	54.4	80.1	119.7	129.0	117.5			
AA06	241552_at	11.7	7.7	15.6	3.3	24.6	30.7	8.8	25.6	10.5	22.7	19.5	16.0	28.0	0.9	28.2	17.1			
AAAS	218075_at	134.5	108.7	121.9	116.9	55.6	87.4	62.2	67.8	148.6	107.7	141.9	82.5	111.1	90.1	110.0	71.2			
AACS	218434_s_at	112.4	350.2	150.7	212.4	226.5	430.1	165.6	209.9	362.6	304.0	297.4	211.2	226.7	242.2	221.3	374.7			
AACSP1	1570020_at	133.9	295.5	525.3	210.1	177.2	599.7	349.3	574.8	462.5	674.5	388.9	512.7	637.3	118.7	374.6	350.3			
AADACL2	240420_at	3.6	3.8	8.5	5.5	1.4	1.0	0.7	0.8	2.0	0.9	0.9	10.9	3.3	2.0	14.5	2.4			
AADAT	223593_at	164.2	101.7	85.6	149.2	173.9	236.5	70.6	185.7	177.1	227.2	165.0	188.3	158.7	149.1	129.4	155.5			
AAED1	227534_at	112.7	84.6	71.1	75.4	35.8	10.5	207.9	89.5	14.9	4.6	100.9	96.4	81.0	48.7	44.4	32.3			
AAGAB	202852_s_at	91.1	155.3	52.2	20.1	107.3	78.5	136.5	126.5	136.9	209.4	129.4	187.4	181.5	127.4	155.7	146.7			
AAK1	205434_s_at	243.5	254.1	338.2	385.3	144.9	132.5	337.2	151.2	151.9	177.9	317.6	275.4	341.0	402.2	316.7	398.3			
AAMDC	221599_at	139.7	134.8	109.2	80.6	94.3	94.2	172.3	83.9	87.0	91.9	161.9	128.3	115.2	71.5	85.0	86.4			
AAMP	201511_at	218.1	280.1	186.0	262.1	122.1	267.8	160.4	162.4	175.1	230.8	281.0	215.0	148.0	172.4	268.7				

Coming up in Basics Part 2



Most common survival analyses in R2

separate by:



Fun things to do:

Email your R2 username to:
r2-support@amsterdamumc.nl

Computer login:
func_user
Welkom01

R2 MSCA-DN Training Courses

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

Do your own research

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

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

The screenshot shows the R2 platform interface. On the left, a navigation menu is visible with 'Help' and 'Training Courses' highlighted. The main content area displays a document titled '1.3. Different expression patterns between subgroups and the underlying biology'. The document includes text about prognostic factors of survival chances and a figure showing a 'Relapse' event over 'Time' with a 'Detection limit' line. A red box highlights the 'Help' menu item, and a red dashed box highlights the 'Training Courses' option. A grey box with the number '4' is overlaid on the right side of the interface.

The screenshot shows the 'Online Tutorial' section of the R2 platform. The heading 'Online Tutorial' is highlighted with a red box. Below it, the text reads: '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,'.

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

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 ... (many more names and counts)

