



*AMARETTO for network biology and medicine:

linking diseases, drivers, targets and drugs

via graph-based fusion of multi-omics, clinical, imaging and perturbation data

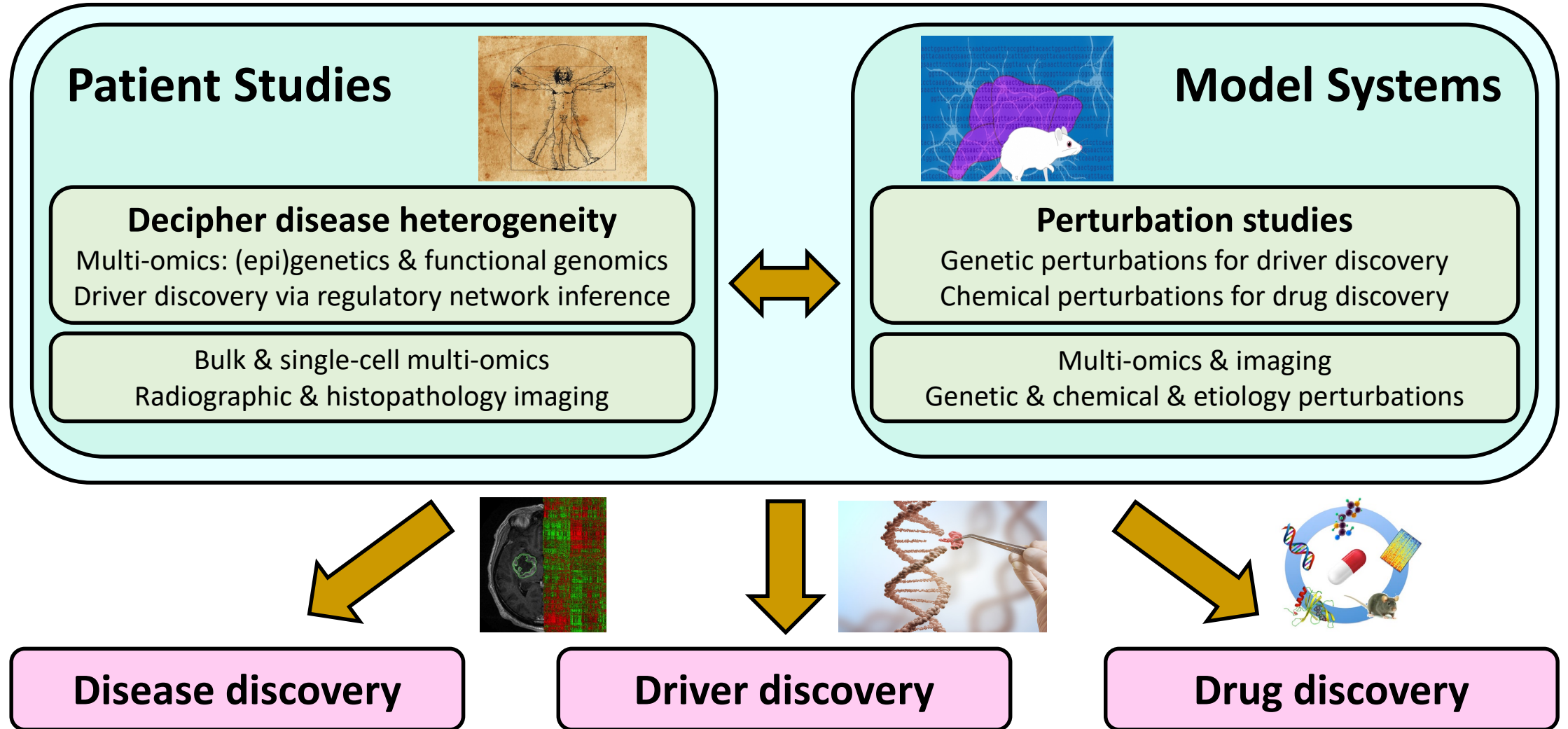
Nathalie Pochet, Ph.D.

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Associate Scientist, Brigham and Women's Hospital
Associate Member, Broad Institute of MIT and Harvard

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<http://portals.broadinstitute.org/pochetlab/amaretto.html>
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Funded by NIH NCI ITCR

Big Data: multi-omics, clinical, imaging, perturbations,... across biological systems



Data-driven hypothesis generators based on multimodal and multiscale big data fusion?

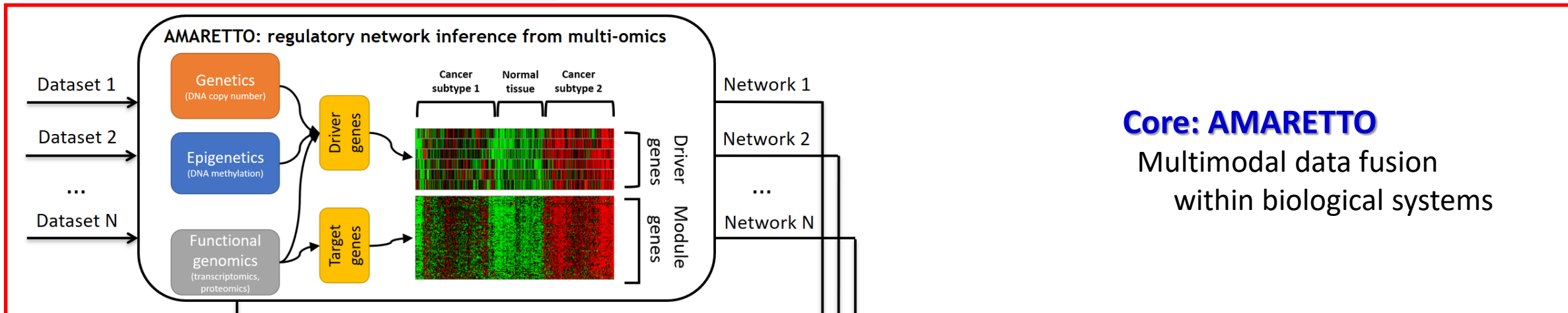
*AMARETTO

links **diseases, drivers, targets** and **drugs**

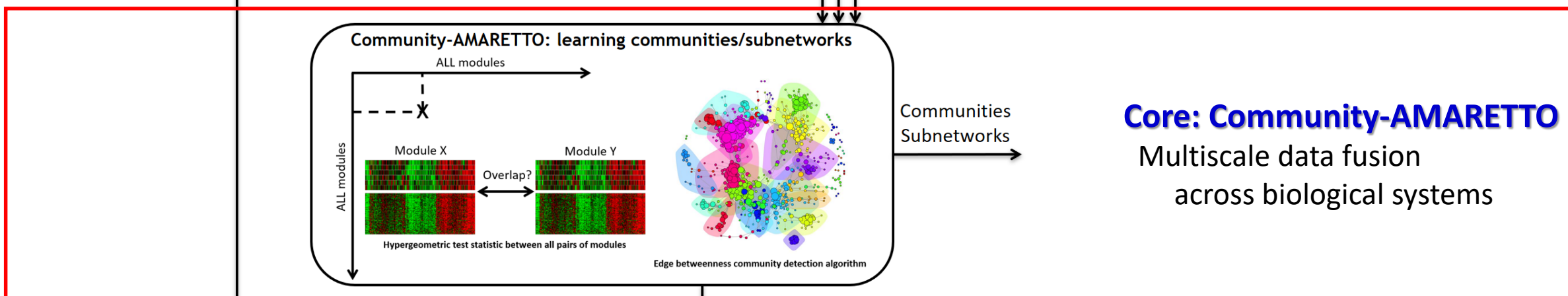
via network graph-based fusion
of **multi-omics, clinical, imaging** and **perturbation** data
across model systems and patient studies of complex disease

software toolbox for **network biology and medicine**
towards developing a **data-driven platform** for **diagnostic,**
prognostic and therapeutic decision-making in complex disease

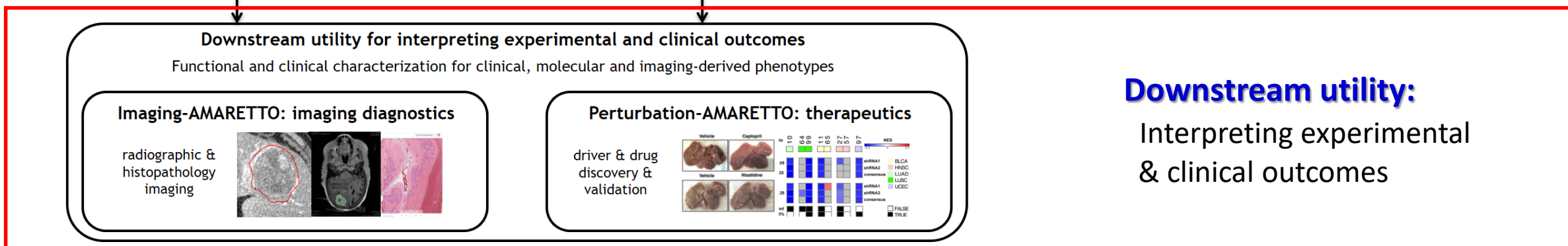
*AMARETTO framework



Core: AMARETTO
Multimodal data fusion
within biological systems



Core: Community-AMARETTO
Multiscale data fusion
across biological systems



Downstream utility:
Interpreting experimental
& clinical outcomes

*AMARETTO discovers **drugs** reversing **drivers** and **targets** in complex **disease**

AMARETTO

- ❑ learns networks of regulatory circuits (modules) - circuits of drivers and target genes
- ❑ infers networks from functional genomics or multi-omics data
- ❑ associates circuits to clinical, molecular and imaging-derived phenotypes
- ❑ learns networks within each biological system (e.g., model systems or patients)

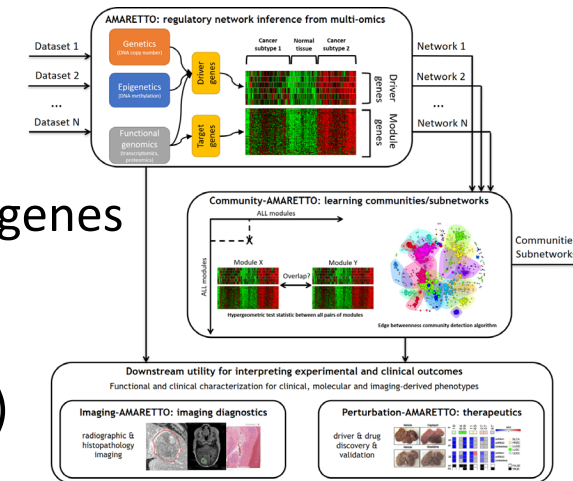
Community-AMARETTO

- ❑ learns subnetworks (communities) of regulatory circuits shared or distinct across multiple networks
- ❑ learns networks across multiple biological systems (e.g., model systems and patients, cohorts and individuals, diseases and etiologies, *in vitro* and *in vivo* systems)

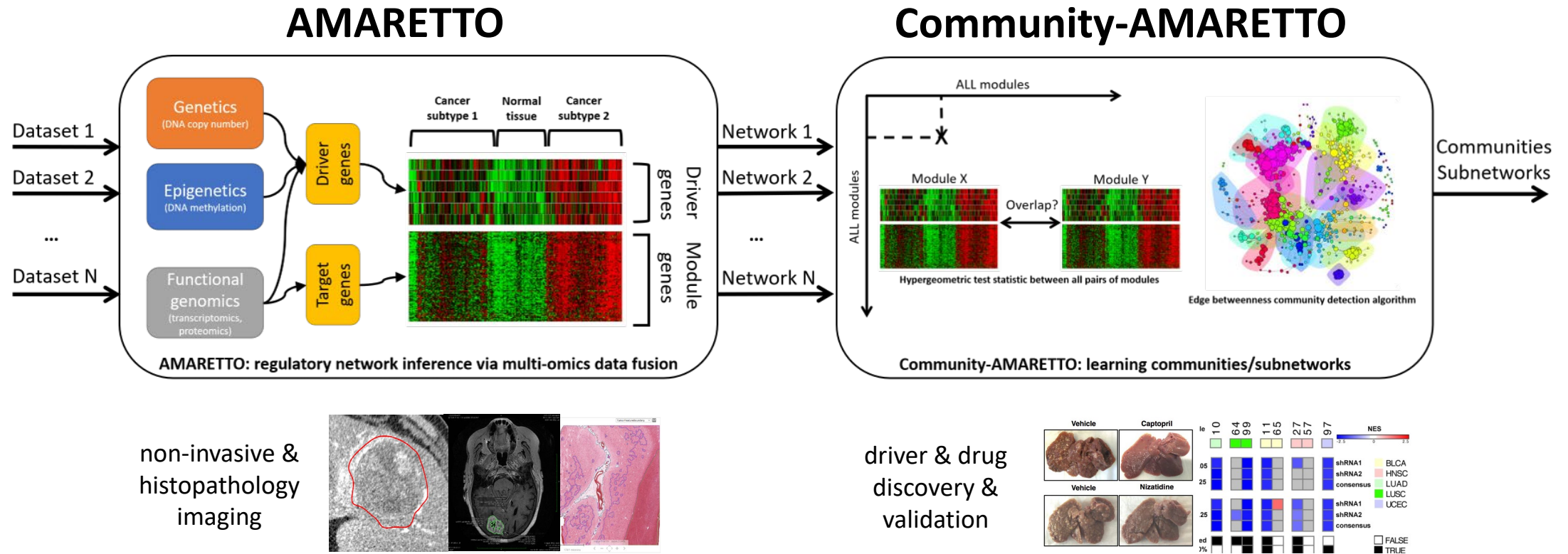
Perturbation-AMARETTO

- ❑ maps driver (genetic) perturbations in model systems onto patient-derived networks
- ❑ maps drug (chemical) perturbations in model systems onto patient-derived networks
- ❑ identifies perturbations reversing disease-associated behavior, not affecting normal behavior
- ❑ prioritizes lead drivers, targets and drugs for follow-up with experimental validation

➤ ***AMARETTO** links **diseases** – **drivers** – **targets** – **drugs**



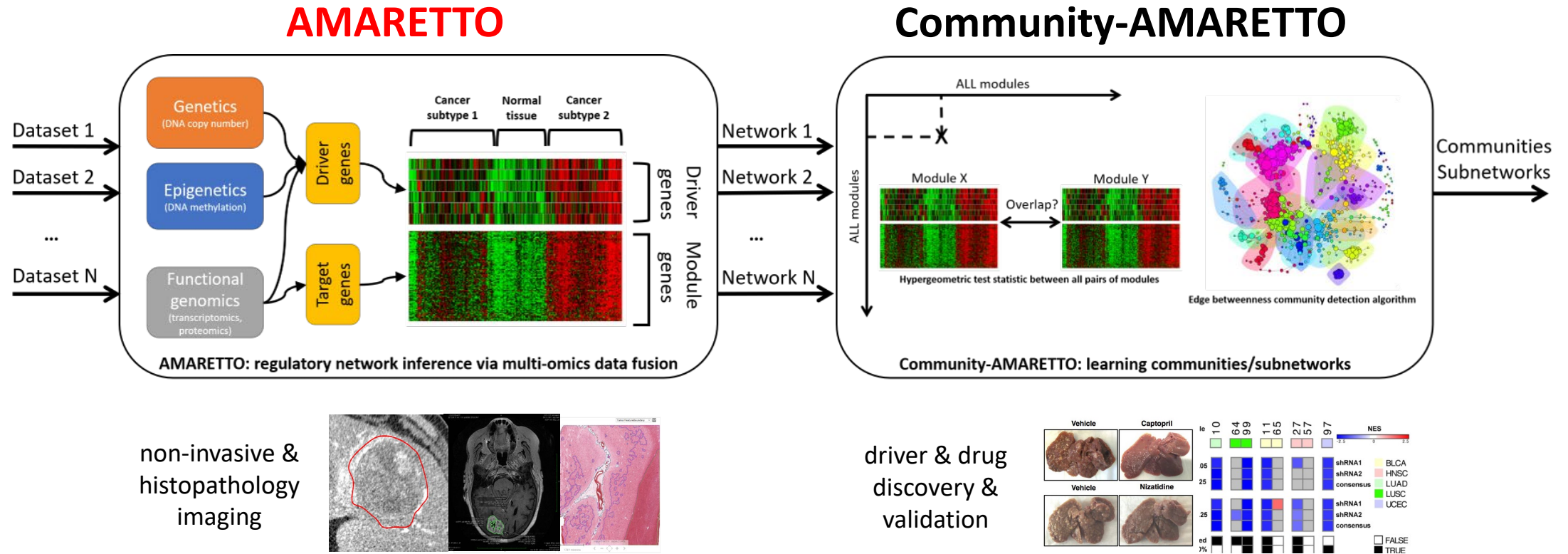
The *AMARETTO framework



The *AMARETTO framework:

1. the **AMARETTO** algorithm for inferring regulatory networks via multi-omics and imaging data fusion
2. the **Community-AMARETTO** algorithm for learning subnetworks shared/distinct across systems and diseases

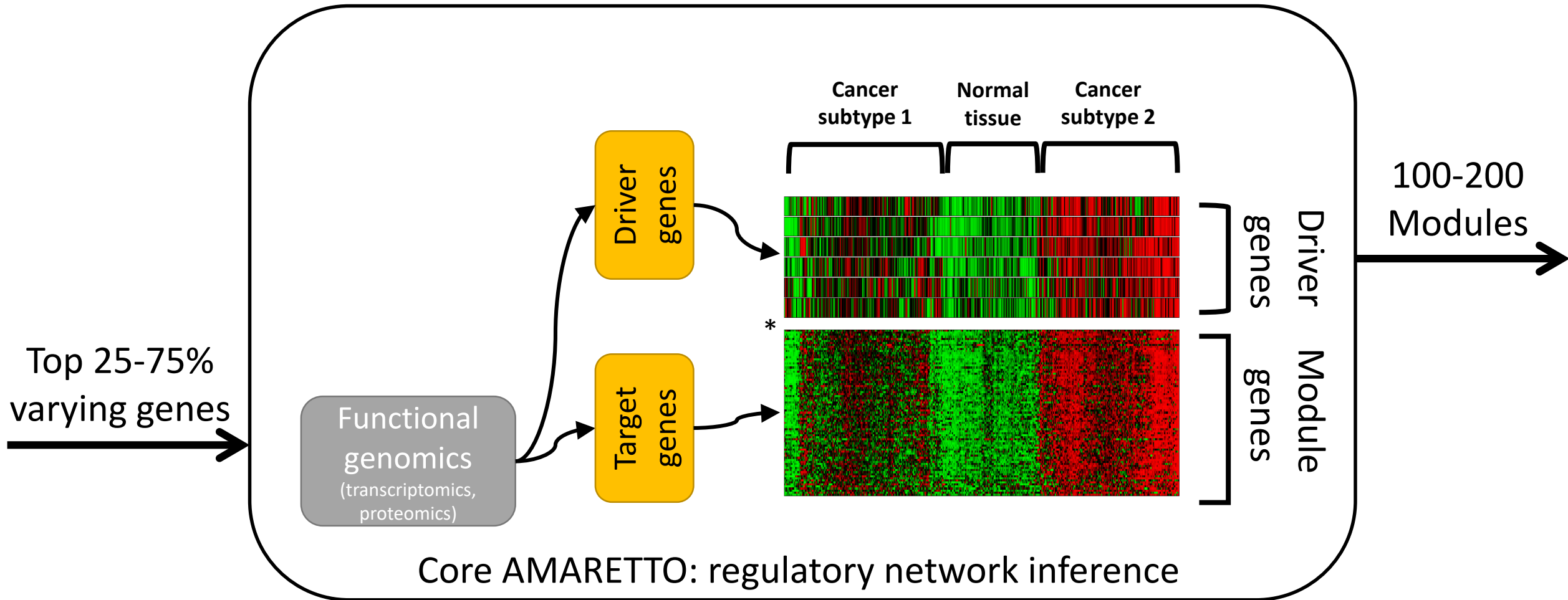
The *AMARETTO framework



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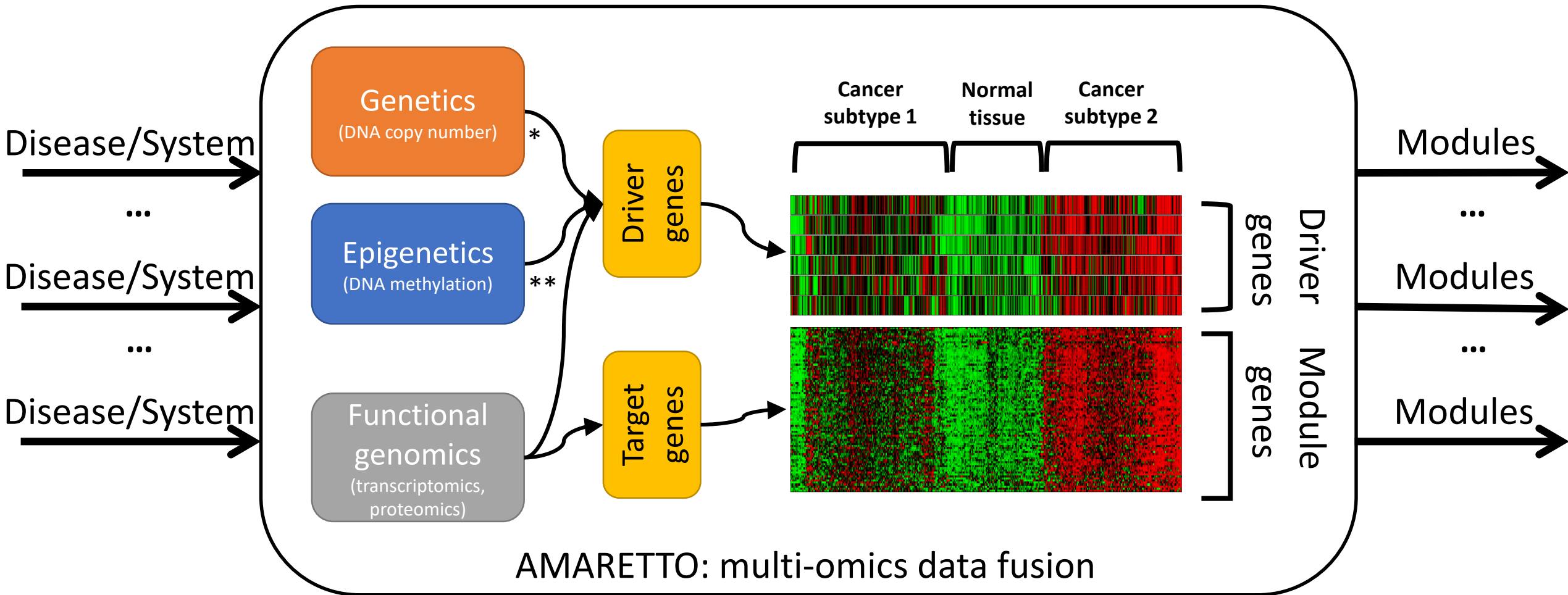
1. the **AMARETTO** algorithm for inferring regulatory networks via multi-omics and imaging data fusion
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*AMARETTO for regulatory network inference within systems and diseases



(*) Regularized regression: Lee *et al.*, PLoS Genetics 2009; Zou and Hastie, J R Stat Soc 2005; Tibshirani, J R Stat Soc 1996

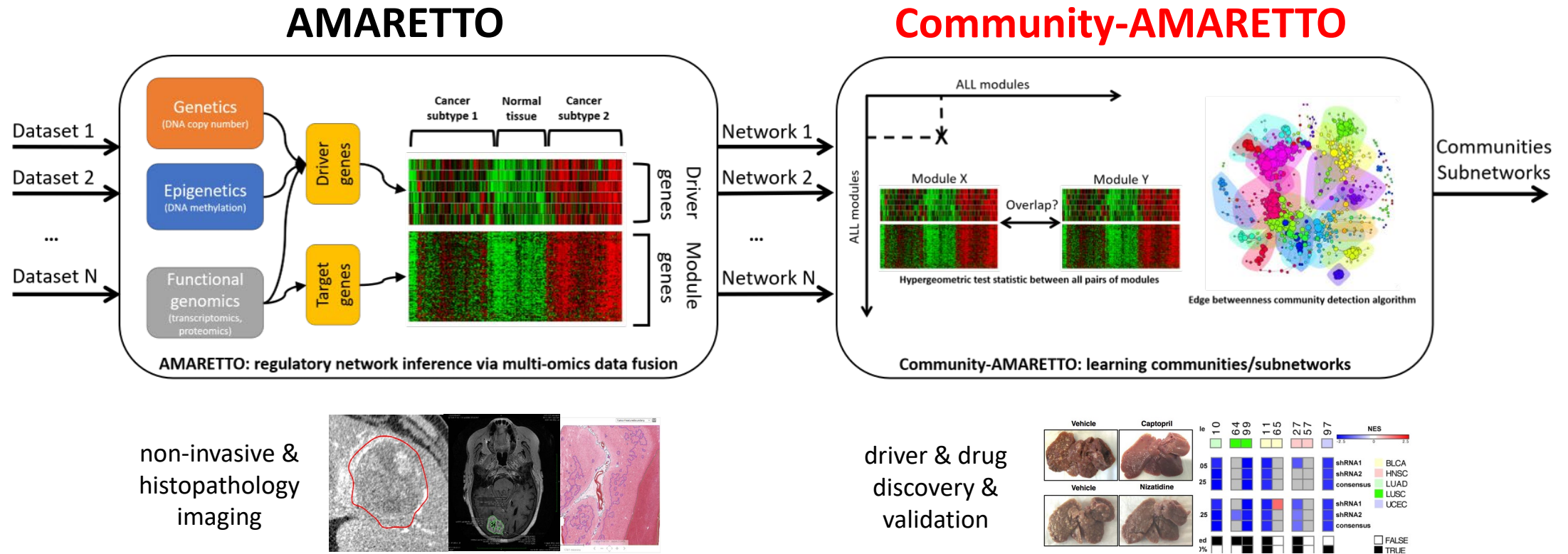
*AMARETTO for multi-omics data fusion in multiple systems and diseases



(*) GISTIC: Mermel *et al.*, Genome Biology 2011; Beroukhim *et al.*, Nature 2010

(**) MethylMix: Gevaert, Bioinformatics 2015; Gevaert *et al.*, Genome Biology 2015; Cedoz *et al.*, Bioinformatics 2018

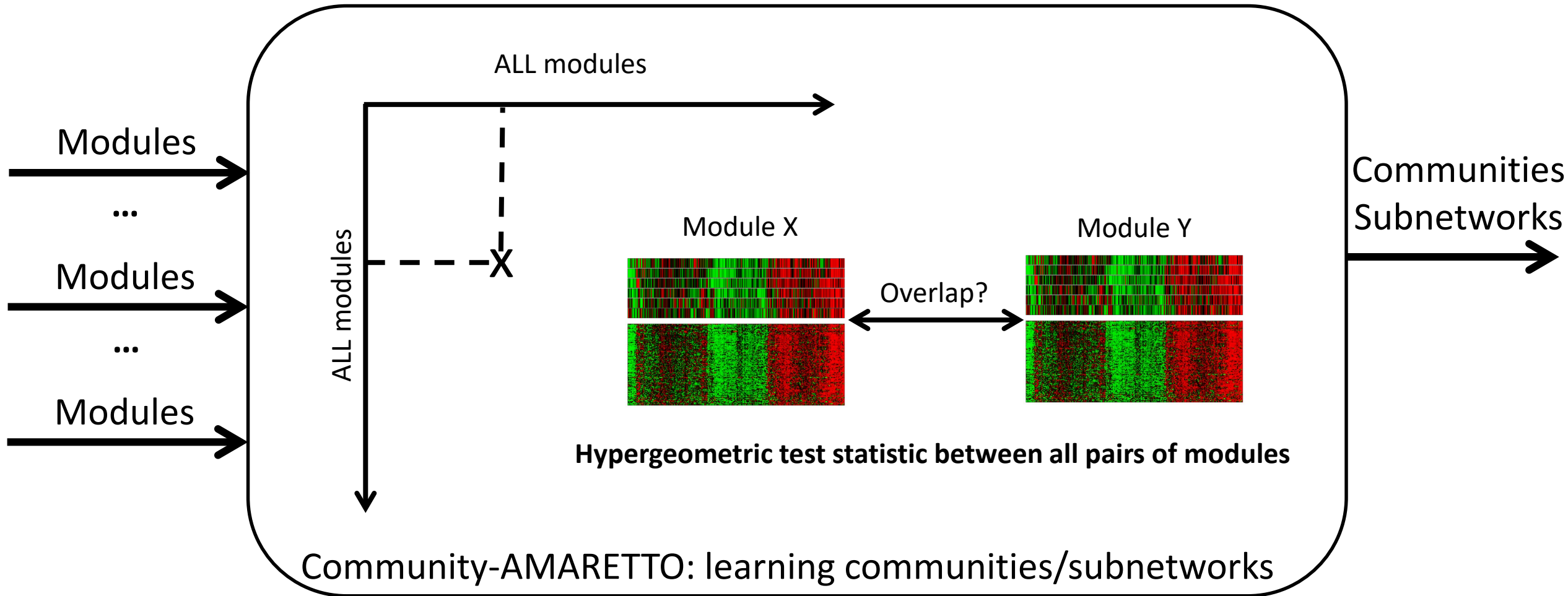
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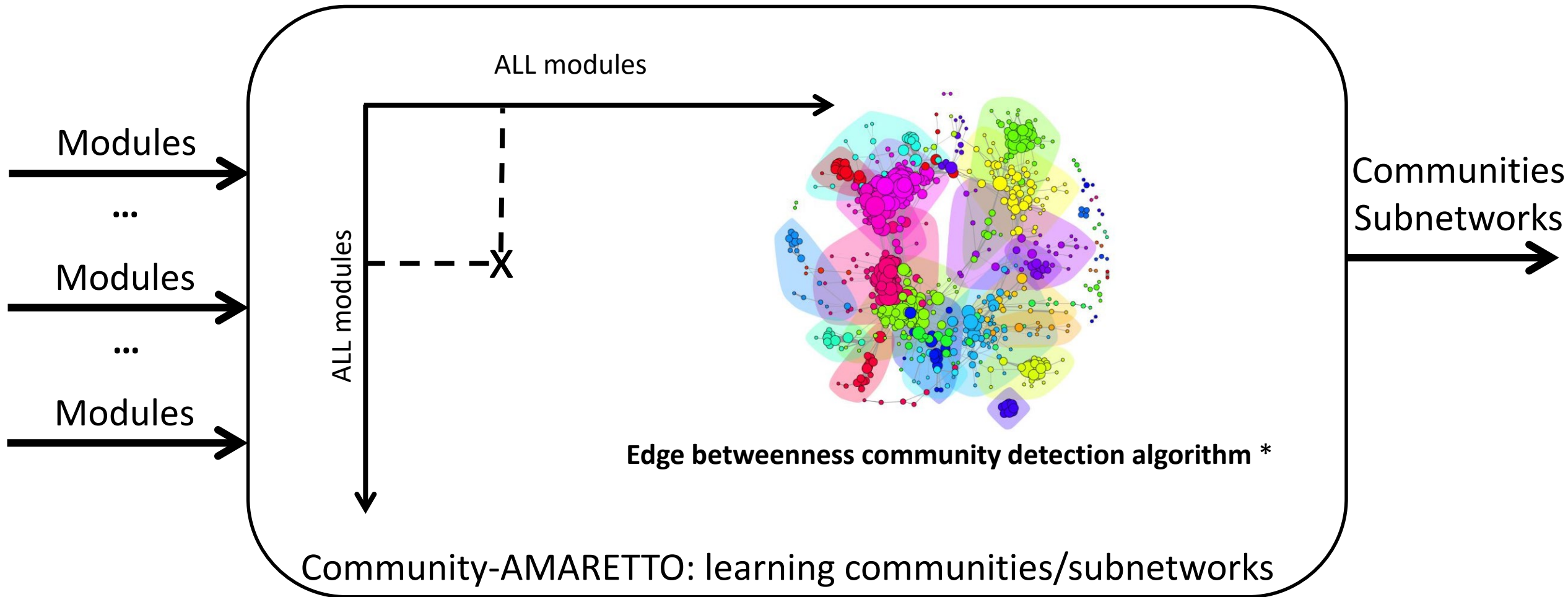
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*AMARETTO for learning subnetworks across systems and diseases



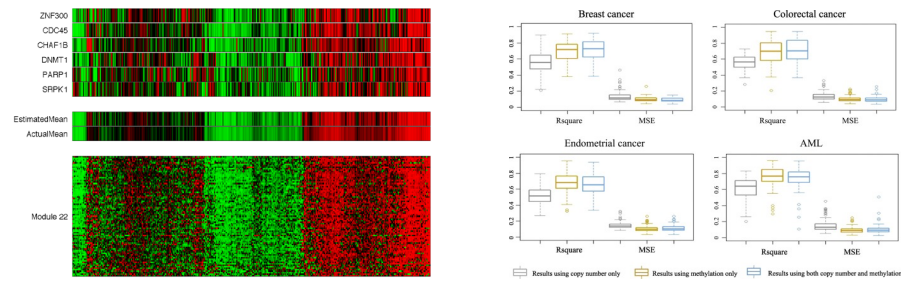
*AMARETTO for learning subnetworks across systems and diseases



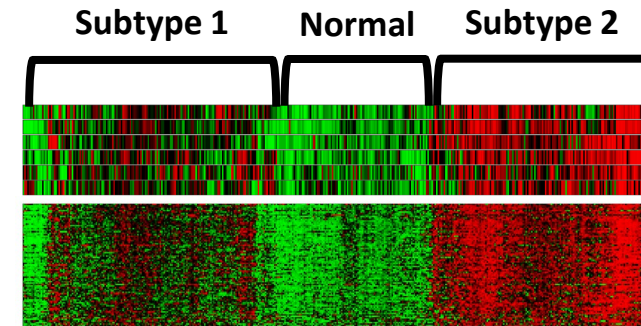
(*) Girvan and Newman, Physical Review E. 2004

Functionalities for optimization and downstream analytics

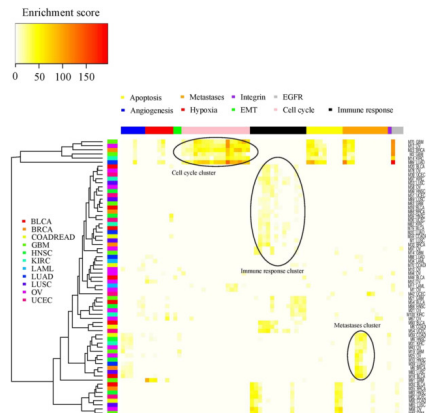
Optimal generalization performance



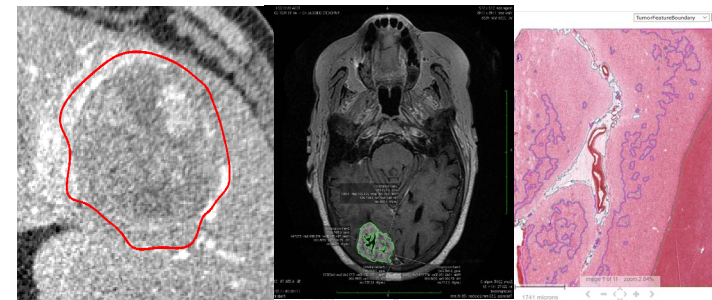
Stratification for disease phenotypes



Annotation of functional categories

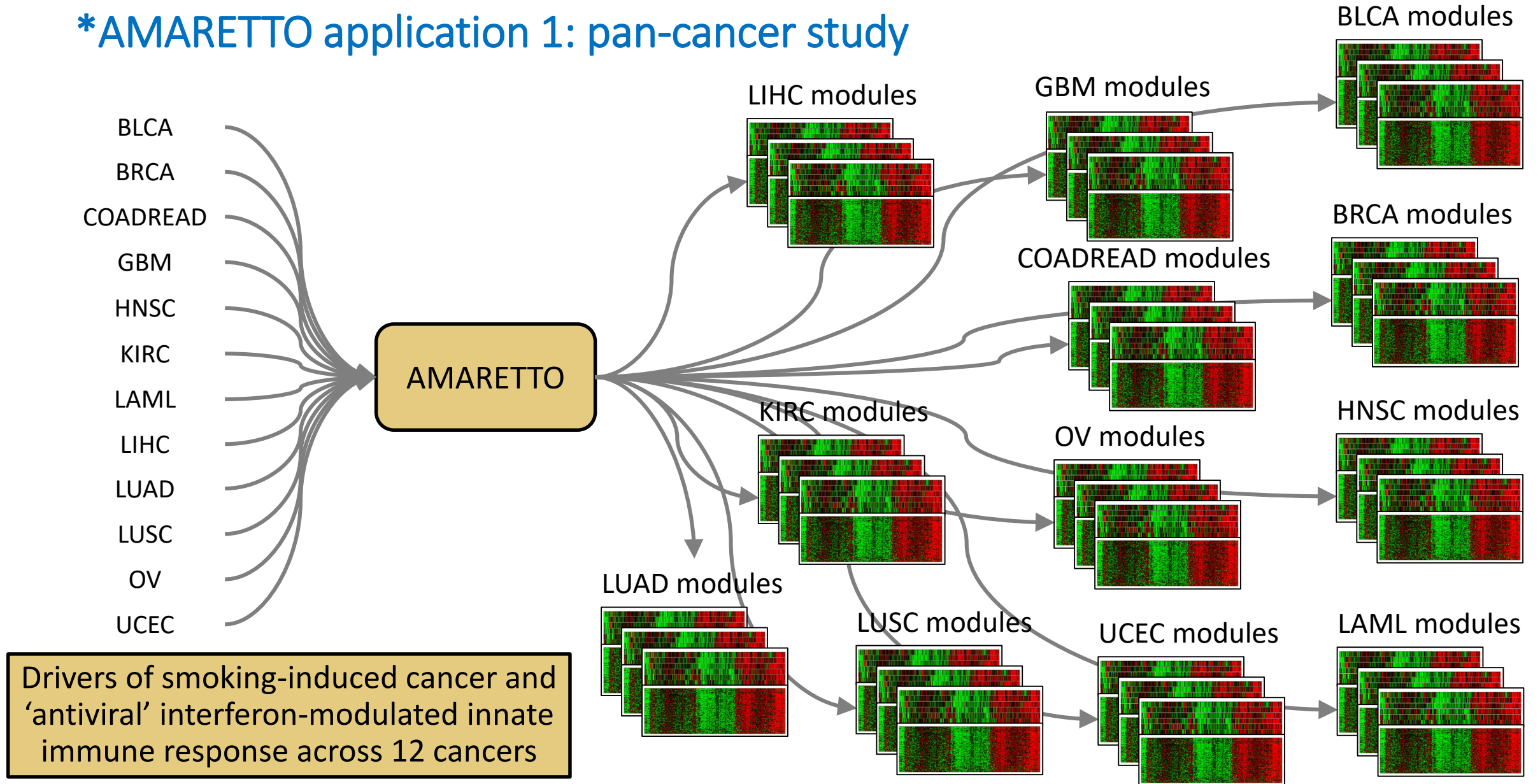


Association with imaging features



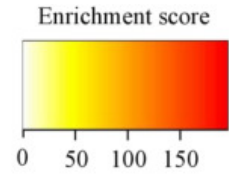
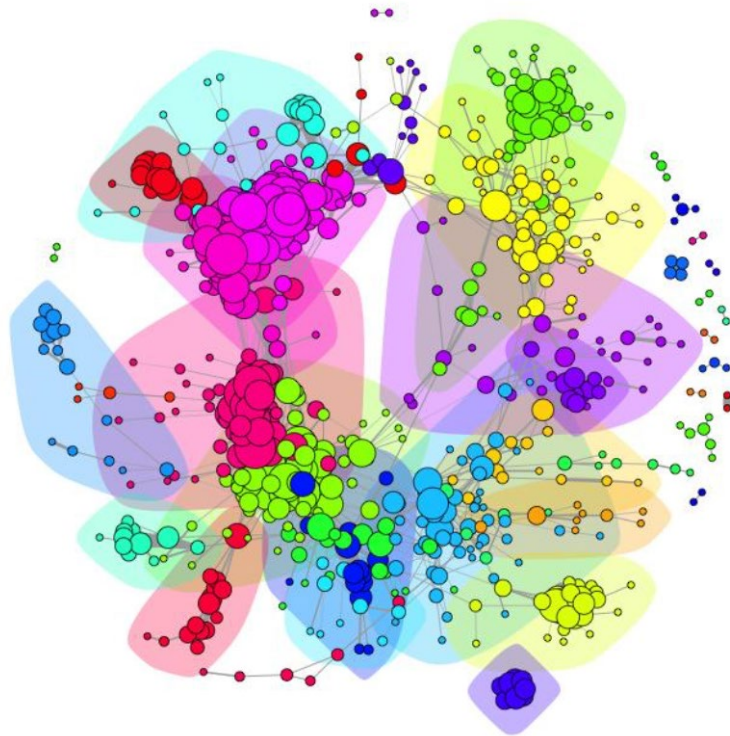
radiographic & histopathology imaging

*AMARETTO application 1: pan-cancer study

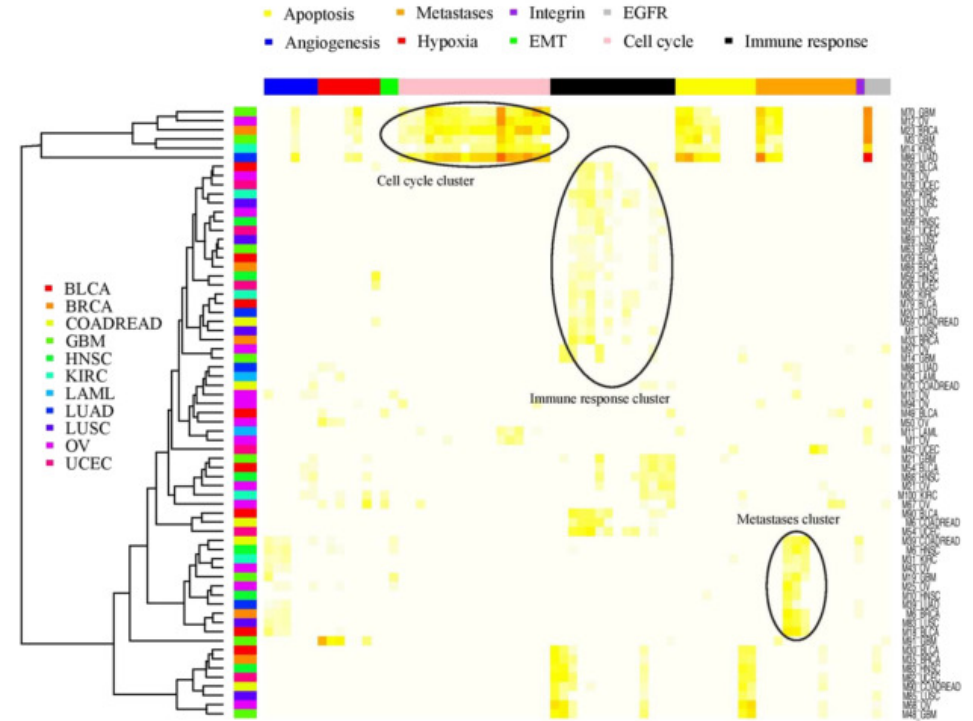


*AMARETTO application 1: pan-cancer study

Pan-cancer communities or subnetworks



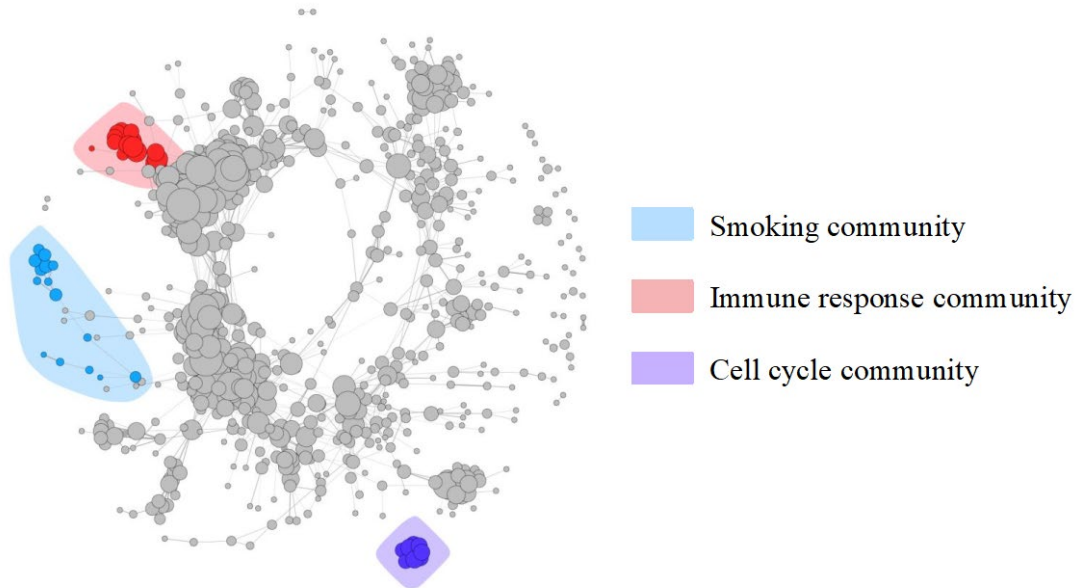
Pan-cancer functional categories



⇒ AMARETTO captures hallmarks of cancer

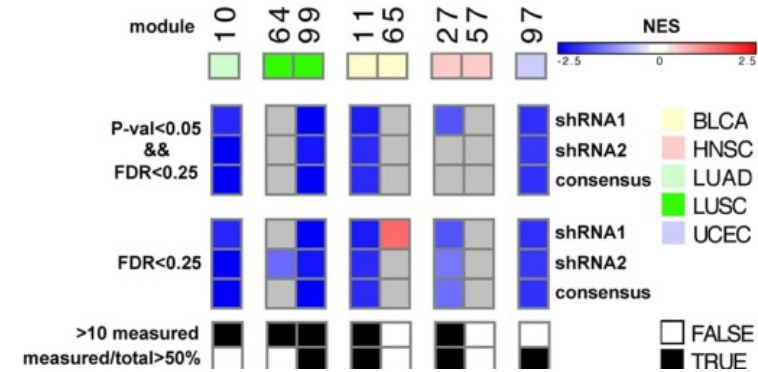
*AMARETTO application 1: pan-cancer study

Driver discovery



- OAS2 pan-cancer driver of ‘antiviral’ interferon-modulated innate immune response
- GPX2 pan-cancer driver of smoking-induced cancer

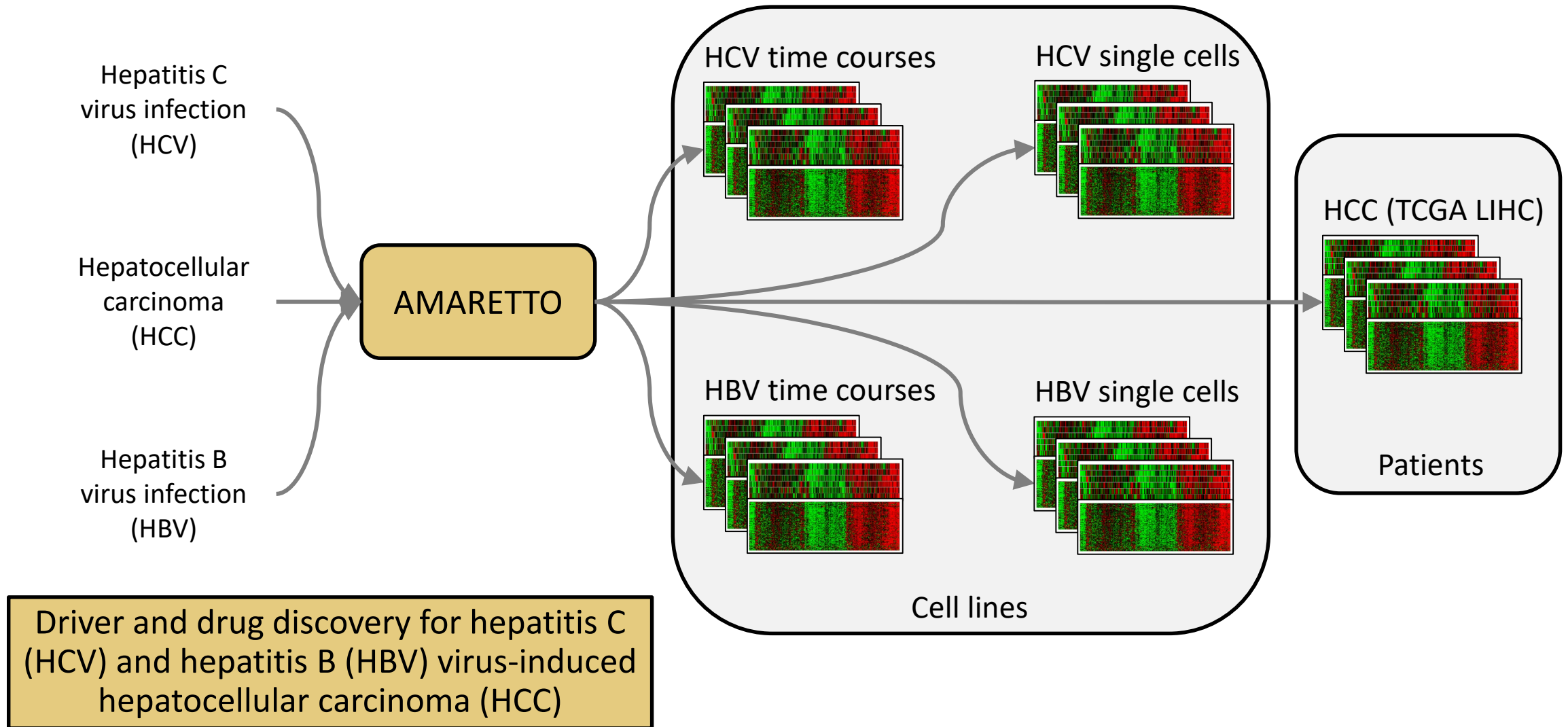
Driver validation



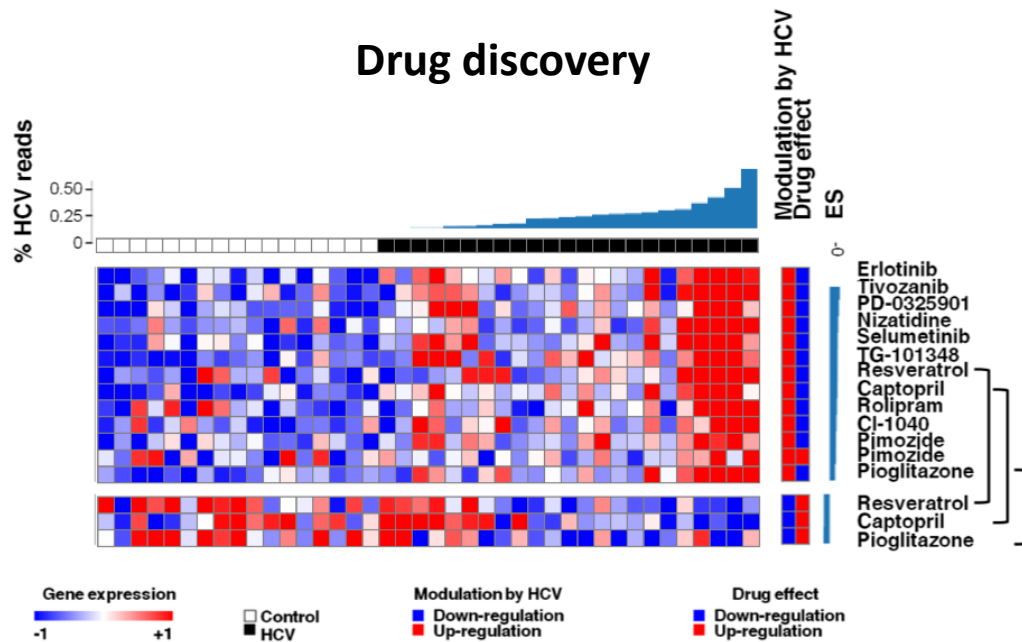
Genetic perturbation of GPX2 in the A549 (LUAD) cell line
 ⇒ Knocking down GPX2 represses target genes in GPX2-regulated modules

⇒ **AMARETTO facilitates identification of known and novel cancer drivers and their targets**

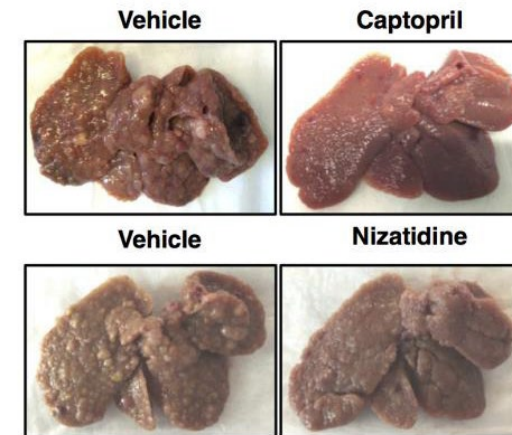
*AMARETTO application 2: virus-induced cancer



*AMARETTO application 2: virus-induced cancer



Drug validation

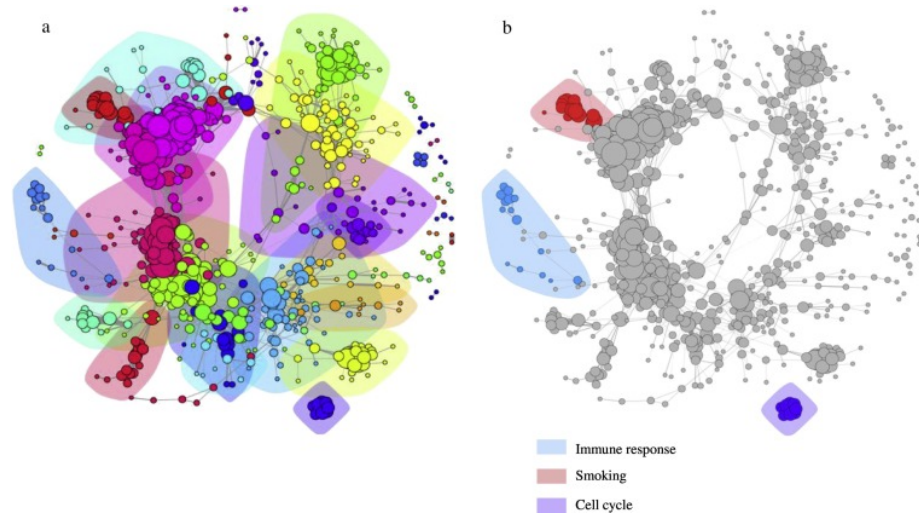
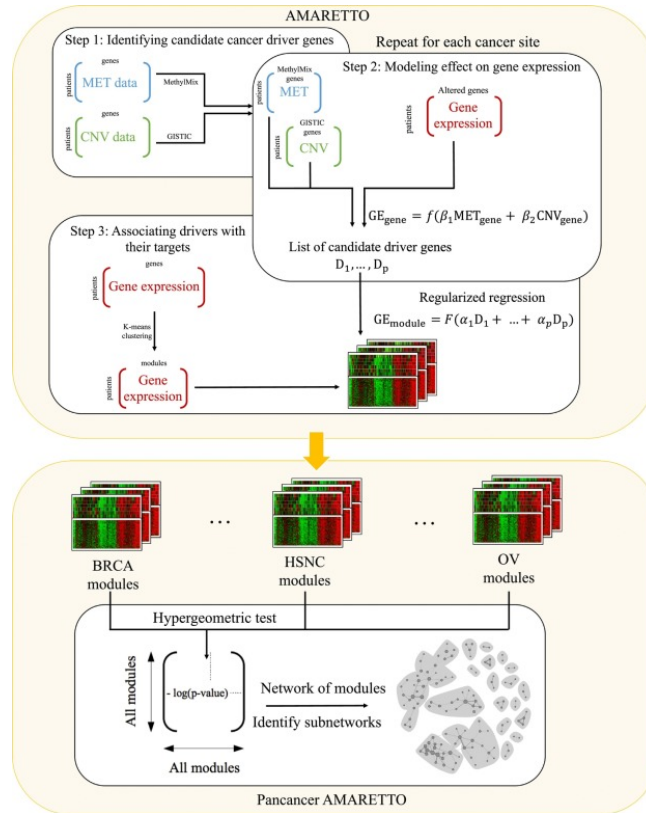


Chemical perturbations in cell lines
 Predict which drugs can reverse disease-associated modules
 Alternative treatments with less severe adverse effects

Experimental validation of drugs in rat models
 ⇒ Two novel compounds attenuate HCC development
 ⇒ Safe and low-cost approach for chemoprevention of HCC?

⇒ **AMARETTO facilitates identification of known and novel drug compounds and how they modulate cancer drivers and their targets**

*AMARETTO



Champion *et al.*, EBioMedicine 2018

*AMARETTO:

1. Captures hallmarks of cancer
2. Facilitates identification of known and novel cancer drivers and their targets
3. Facilitates identification of known and novel drug compounds and how they modulate cancer drivers and their targets

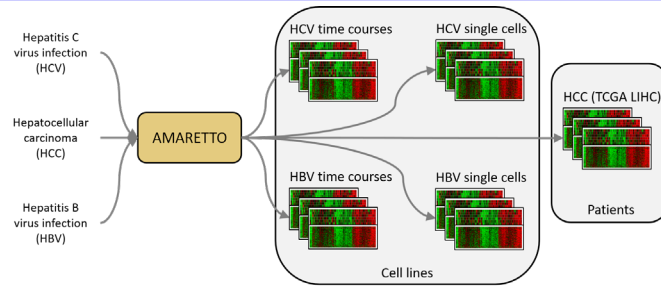
Use Cases: integrating multi-omics, clinical, imaging, and driver and drug perturbation data across model systems and patient studies of cancer

1. A study of hepatitis C and B virus-induced hepatocellular carcinoma (LIHC) with driver and drug discovery for chemoprevention across pan-etiologicals of hepatocellular carcinoma, experimentally validated in rat models

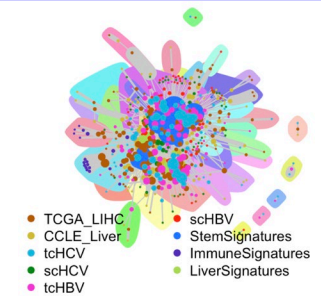
Use Case 1: Studying virus-induced hepatocellular carcinoma

Driver prediction for hepatitis C and B virus-induced hepatocellular carcinoma across subnetworks derived from >6 systems validated in cell lines, and prediction of chemopreventive treatments modulating disease-associated subnetworks using chemical perturbations in cell lines, experimentally validated in rat models

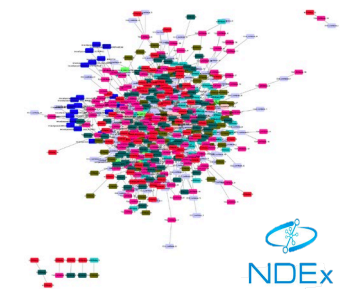
Driver and drug discovery for hepatitis C (HCV) and hepatitis B (HBV) virus-induced hepatocellular carcinoma (HCC)



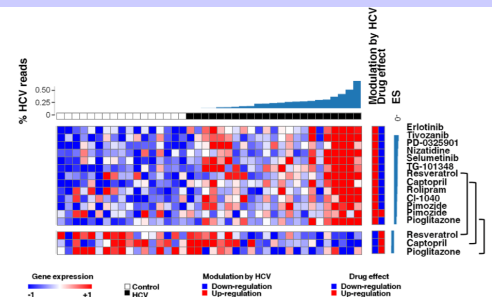
Pan-etiology of cancer communities or subnetworks



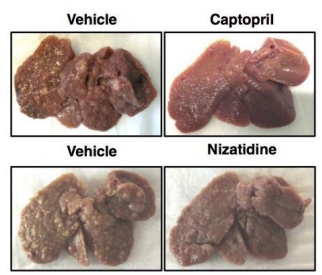
Community-AMARETTO



Drug discovery:
Chemical perturbations in cell lines
Predict which drug compounds can reverse disease-associated circuits
Alternative treatments with less severe adverse effects?



Drug validation:
Experimental validation of drugs in rat models
⇒ Two novel compounds attenuate HCC development
⇒ Safe and low-cost approach for chemoprevention of HCC?



Nathalie Pochet and Thomas Baumert, submitted

Driver and drug discovery for chemoprevention of hepatitis C (HCV) and hepatitis B (HBV) virus-induced hepatocellular carcinoma (HCC)
⇒ **AMARETTO facilitates identification of known and novel drug compounds and how they modulate cancer drivers and their targets**

Community	CCLE_Liver	scHBV	scHCV	TCGA_LIHC	tcHBV	tcHCV	ImmuneSignatures	LiverSignatures	StemSignatures
Community 1	Module 13, Module 15, Module 23, Module 31, Module 33, Module 35, Module 37, Module 102, Module 115, Module 118, Module 119, Module 121, Module 147	Module 21, Module 41, Module 59	Module 22, Module 33, Module 100	Module 1, Module 2, Module 3, Module 4, Module 5, Module 6, Module 7, Module 8, Module 9, Module 10, Module 11, Module 12, Module 13, Module 14, Module 15, Module 16, Module 17, Module 18, Module 19, Module 20, Module 21, Module 22, Module 23, Module 24, Module 25, Module 26, Module 27, Module 28, Module 29, Module 30, Module 31, Module 32, Module 33, Module 34, Module 35, Module 36, Module 37, Module 38, Module 39, Module 40, Module 41, Module 42, Module 43, Module 44, Module 45, Module 46, Module 47, Module 48, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145	Module 14, Module 15, Module 16, Module 17, Module 18, Module 19, Module 20, Module 21, Module 22, Module 23, Module 24, Module 25, Module 26, Module 27, Module 28, Module 29, Module 30, Module 31, Module 32, Module 33, Module 34, Module 35, Module 36, Module 37, Module 38, Module 39, Module 40, Module 41, Module 42, Module 43, Module 44, Module 45, Module 46, Module 47, Module 48, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145	Module 35, Module 42, Module 43, Module 115, Module 118, Module 140	OBERSOFT_MAST_CELL_RESTING	HOSHIDA_LIVER_CANCER_SUBCLASS_39, HOSHIDA_LIVER_CANCER_SURVIVAL_39	BENFORNTH_EED_TARGETS, BENFORNTH_EE_WITH_LIGANDS, BENFORNTH_PRC2_TARGETS, BENFORNTH_SUZ12_TARGETS
	<ul style="list-style-type: none"> Genes from 'subtype S1' signature of hepatocellular carcinoma (HCC): aberrant activation of the WNT signaling pathway Survival signature genes defined in adjacent liver tissue: genes correlated with poor survival of hepatocellular carcinoma (HCC) patients Polycarb Reppression Complex 2 (PRC) targets; identified by ChIP on chip on human embryonic stem cells as genes that: possess the trimethylated H3K27 mark in their promoters and are bound by SUZ12 and EED Polycarb proteins IL8 pan-etiology driver of HCV and HBV virus-induced HCC associated with HCV and HBV viral load and HCC survival 								
Community 3	Module 4, Module 5, Module 10, Module 12, Module 20, Module 21, Module 23, Module 32, Module 33, Module 41, Module 47, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 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Module 30, Module 35, Module 40, Module 45, Module 50, Module 55, Module 60, Module 65, Module 70, Module 75, Module 80, Module 85, Module 90, Module 95, Module 100, Module 105, Module 110, Module 115, Module 120, Module 125, Module 130, Module 135, Module 140	HOSHIDA_LIVER_CANCER_SUBCLASS_32	BENFORNTH_MYC_MAX_TARGETS, BENFORNTH_MYC_TARGETS_WITH_EBOX, BENFORNTH_NANOG_TARGETS, BENFORNTH_OCT4_TARGETS, BENFORNTH_SOX2_TARGETS		
	<ul style="list-style-type: none"> Genes from 'subtype S2' signature of hepatocellular carcinoma (HCC): proliferation, MYC and AKT1 activation MYC targets; targets of c-Myc and Max identified by ChIP on chip in a Burkitt's lymphoma cell line; overlap set; and in cultured cell lines, focusing on E-box-containing genes; high affinity bound subset CORE stemness genes upregulated and identified by ChIP on chip as NOS (Nanog, OCT4, SOX2) transcription factor targets in human embryonic stem cells STX7 pan-etiology driver of HCV and HBV virus-induced HCC 								
Community 5	Module 6, Module 8, Module 10, Module 11, Module 12, Module 13, Module 14, Module 15, Module 16, Module 17, Module 18, Module 19, Module 20, Module 21, Module 22, Module 23, Module 24, Module 25, Module 26, Module 27, Module 28, Module 29, Module 30, Module 31, Module 32, Module 33, Module 34, Module 35, Module 36, Module 37, Module 38, Module 39, Module 40, Module 41, Module 42, Module 43, Module 44, Module 45, Module 46, Module 47, Module 48, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145	Module 21, Module 28, Module 33, Module 71, Module 81, Module 82	Module 8, Module 24, Module 41, Module 83, Module 97	Module 12, Module 22, Module 24, Module 35, Module 42, Module 43, Module 53, Module 63, Module 64, Module 70, Module 75, Module 84, Module 92, Module 102, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140	Module 14, Module 45, Module 46, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140	Module 5, Module 7, Module 10, Module 15, Module 20, Module 25, Module 30, Module 35, Module 40, Module 45, Module 50, Module 55, Module 60, Module 65, Module 70, Module 75, Module 80, Module 85, Module 90, Module 95, Module 100, Module 105, Module 110, Module 115, Module 120, Module 125, Module 130, Module 135, Module 140	HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_CN, HOSHIDA_LIVER_CANCER_SUBCLASS_38, HOSHIDA_LIVER_CANCER_SURVIVAL_38		
	<ul style="list-style-type: none"> Genes from 'subtype S3' signature of hepatocellular carcinoma (HCC): hepatocyte differentiation Survival signature genes defined in adjacent liver tissue: genes correlated with good survival of hepatocellular carcinoma (HCC) patients Liver specific genes from Human Gene Expression Index, the HUGe Index, http://www.hugeindex.org APOC3 pan-etiology driver of HCV and HBV virus-induced HCC validated in all 6 data sources using genetic perturbations of APOC3 in the HepG2 liver cancer cell line 								

Community-AMARETTO report: http://portals.broadinstitute.org/pochettab/demo/cAMARETTO_Liver_6DS/index.html
NDEX network visualization: <http://www.ndexbio.org/#/network/f50b3ecb-7b47-11e9-848d-0ac135e8bacf>

Use Case 1: Studying virus-induced hepatocellular carcinoma

Driver prediction for hepatitis C and B virus-induced hepatocellular carcinoma across subnetworks derived from >6 systems validated in cell lines, and prediction of chemopreventive treatments modulating disease-associated subnetworks using chemical perturbations in cell lines, experimentally validated in rat models

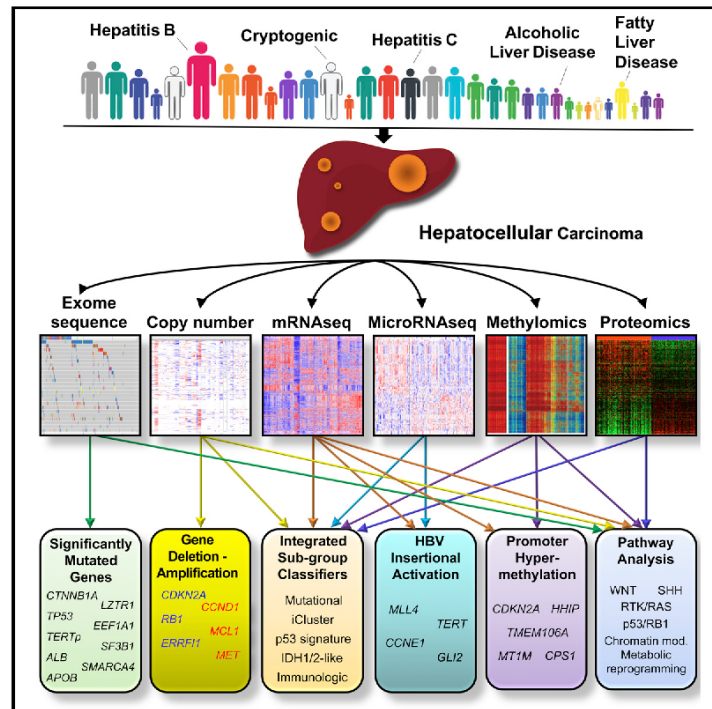
Resource

Cell

Cell

Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma

Graphical Abstract



Authors

The Cancer Genome Atlas Research Network

Correspondence

wheeler@bcm.edu (David A. Wheeler), roberts.lewis@mayo.edu (Lewis R. Roberts)

In Brief

Multiplex molecular profiling of human hepatocellular carcinoma patients provides insight into subtype characteristics and points toward key pathways to target therapeutically.

Highlights

- Analysis of hepatocellular carcinomas integrates data of

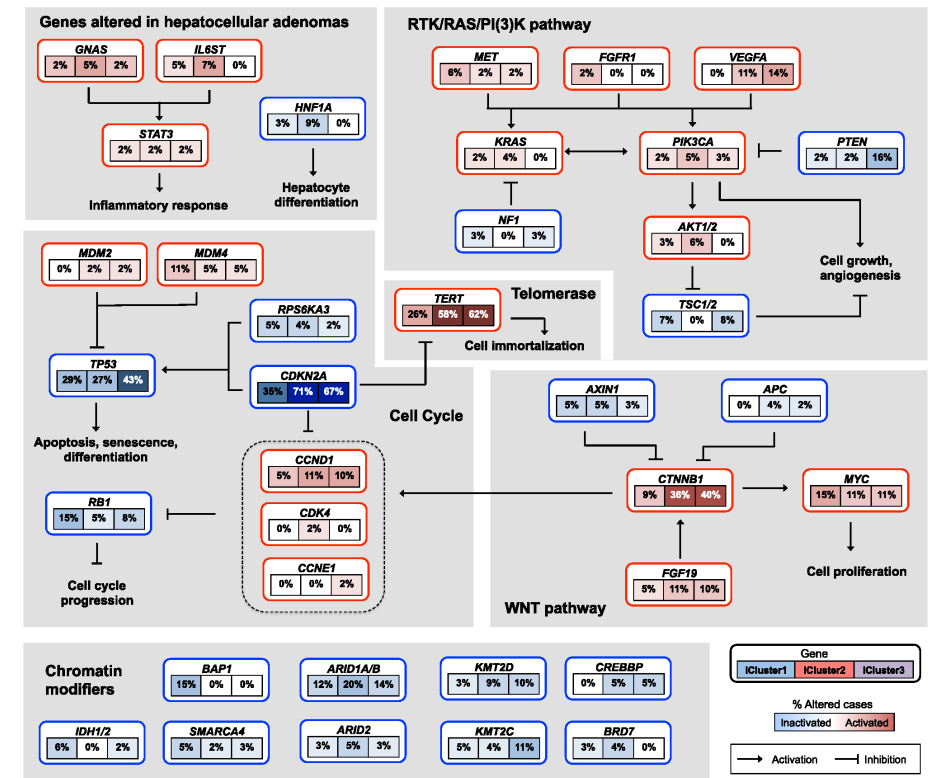


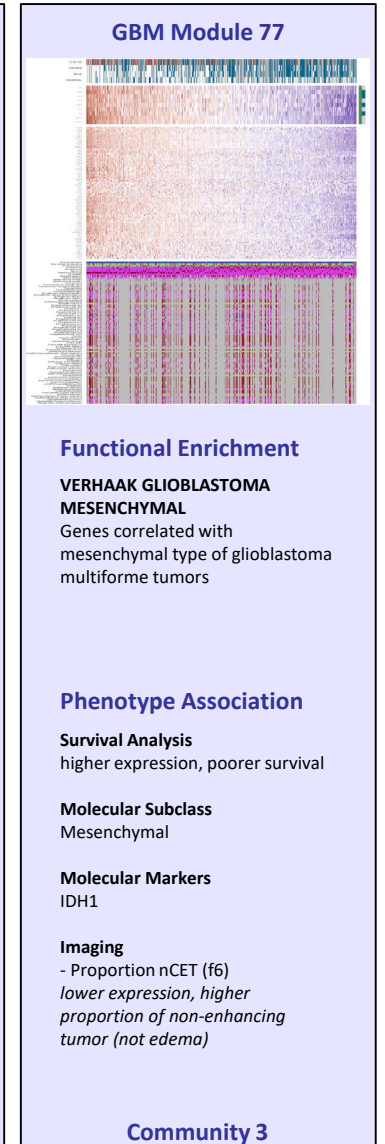
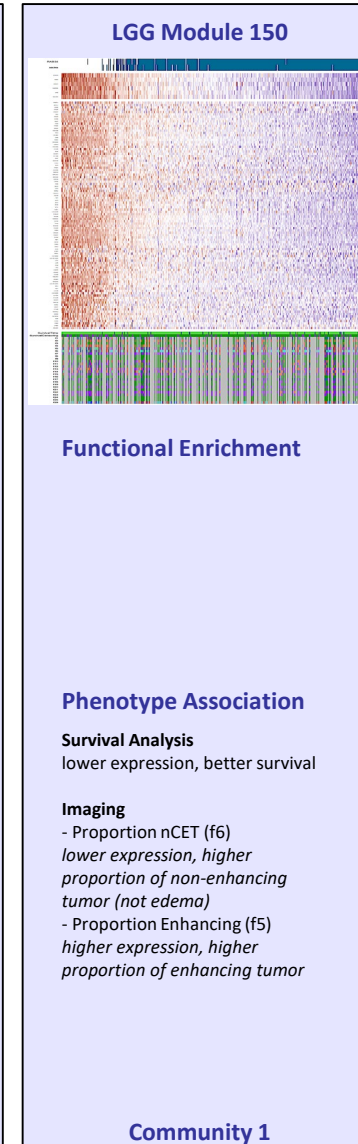
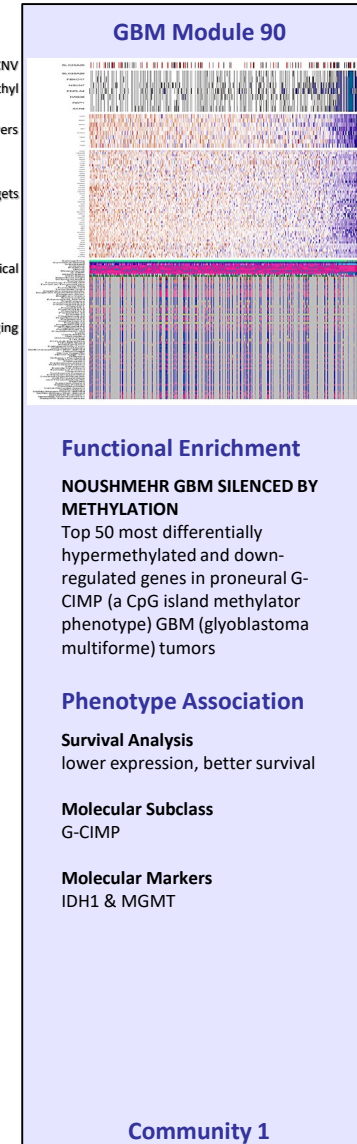
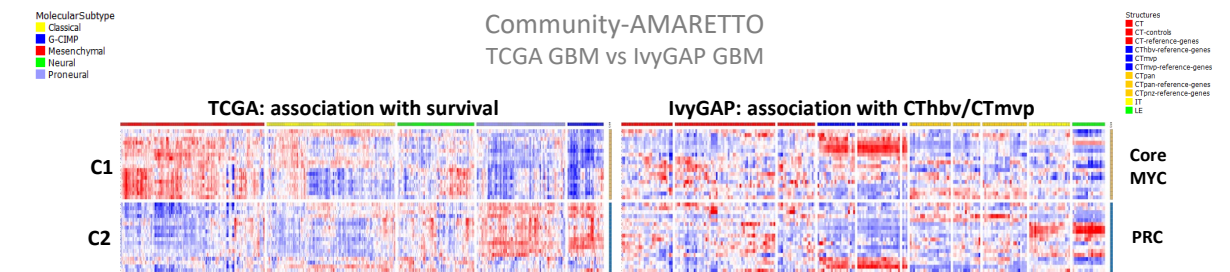
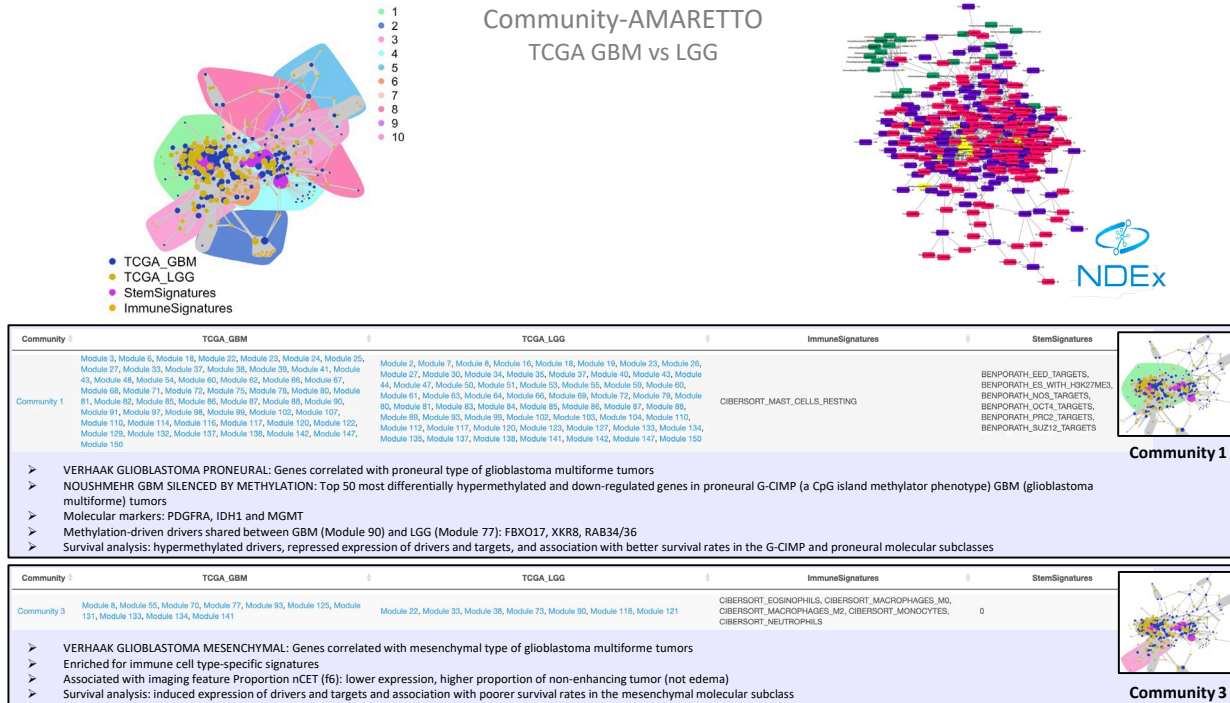
Figure 6. Integrated Molecular Comparison of Somatic Alterations in Signaling Pathways across iCluster Groups. Each gene box includes three percentages representing the frequency of activation or inactivation in iClusters 1, 2, and 3 based on the core 196 sample HCC dataset. All somatic changes are tallied together in calculating the percentages of altered cases within each of the iCluster sample groups. Somatic alterations include mutations and copy-number changes (homozygous deletion and high-level amplifications), as well as epigenetic silencing of CDKN2A. Missense mutations are only counted if they have known oncogenic function, have been reported in COSMIC, or occur at known mutational hotspots. Genes are grouped by signaling pathways, with edges showing pairwise molecular interactions. See also Figure S6.

Use Cases: integrating multi-omics, clinical, imaging, and driver and drug perturbation data across model systems and patient studies of cancer

1. A study of hepatitis C and B virus-induced hepatocellular carcinoma (LIHC) with driver and drug discovery for chemoprevention across pan-etiologicals of hepatocellular carcinoma, experimentally validated in rat models
2. A study of glioblastoma multiforme (GBM) and low-grade glioma (LGG) with driver discovery for diagnostic and prognostic molecular subclasses associated with imaging-derived features for non-invasive imaging diagnostics

Use Case 2: Studying multi-omics and imaging of gliomas

Driver prediction for multi-omics subnetworks associated with imaging-derived features representing prognostic molecular subclasses of gliomas and glioblastoma multiforme



Community-AMARETTO report: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Brain_2DS/index.html
 NDEx network visualization: <http://www.ndexbio.org/#/network/c1f0fccf-80b6-11e9-848d-0ac135e8bacf>

Use Case 2: Studying multi-omics and imaging of gliomas

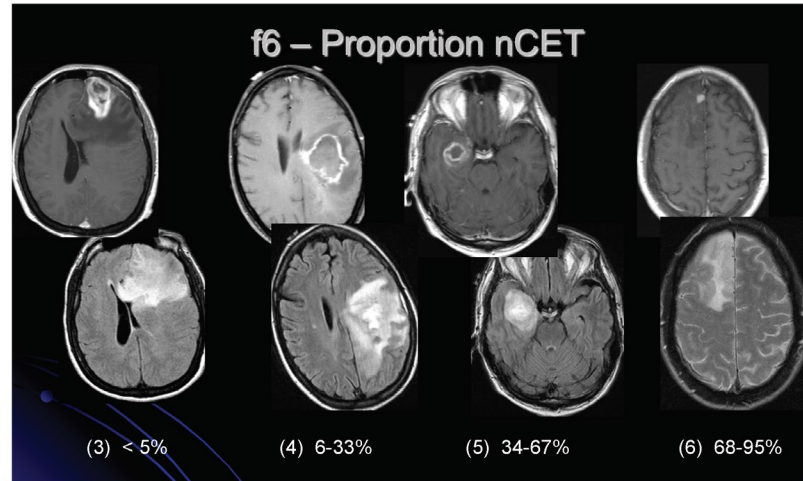
Driver prediction for multi-omics subnetworks associated with imaging-derived features representing prognostic molecular subclasses of gliomas and glioblastoma multiforme

Vasari MRI Visual Feature Guide

Sample images derived from the Rembrandt MRI examinations contributed by Thomas Jefferson University Hospital



Rev 1.1



Visually, when scanning through the entire tumor volume, what proportion of the entire tumor is estimated to represent non-enhancing tumor (not edema)? Non-enhancing tumor is defined as regions of T2W hyperintensity (less than the intensity of cerebrospinal fluid, with corresponding T1W hypointensity) that are associated with mass effect and architectural distortion, including blurring of the gray-white interface. (Assuming that the the entire abnormality may be comprised of: (1) an enhancing component, (2) a non-enhancing component, (3) a necrotic component and (4) a edema component.)

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ESTABLISHED IN 1812 JUN E 25, 2015 VOL. 372 NO. 26

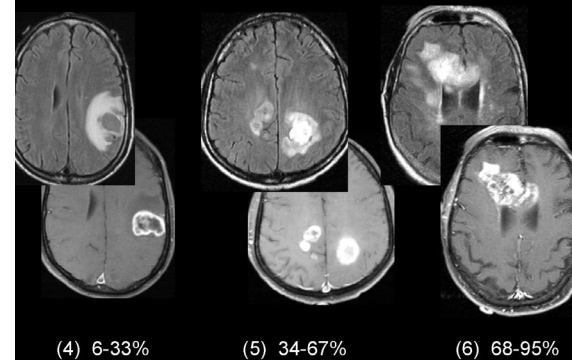
Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas

The Cancer Genome Atlas Research Network*

ABSTRACT

BACKGROUND

f5 - Proportion Enhancing

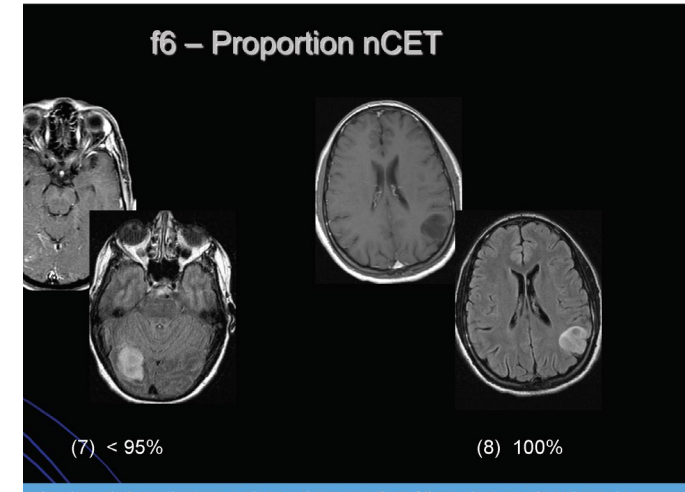


through the entire tumor volume, what proportion of the entire tumor is estimated to represent enhancing tumor (not edema)? Enhancing tumor is defined as regions of T1W hyperintensity (greater than the intensity of cerebrospinal fluid, with corresponding T2W hypointensity) that are associated with mass effect and architectural distortion, including blurring of the gray-white interface. (Assuming that the the entire abnormality may be comprised of: (1) an enhancing component, (2) a non-enhancing component, (3) a necrotic component and (4) a edema component.)

Comprehensive genomic defines human glioblastoma core pathways

Research Network*

harbour multiple chromosomal aberrations and harbor multiple chromosomal aberrant transformation. The Cancer Genome Atlas Research Network* Here we report the interim integrative analysis of 206 glioblastomas—the most common type of brain cancer. This analysis



When scanning through the entire tumor volume, what proportion of the entire tumor is estimated to represent non-enhancing tumor (not edema)? Non-enhancing tumor is defined as regions of T2W hyperintensity (less than the intensity of cerebrospinal fluid, with corresponding T1W hypointensity) that are associated with mass effect and architectural distortion, including blurring of the gray-white interface. (Assuming that the the entire abnormality may be comprised of: (1) an enhancing component, (2) a non-enhancing component, (3) a necrotic component and (4) a edema component.)

Cell

Resource

The Somatic Genomic Landscape of Glioblastoma

Cameron W. Brennan,^{1,2,45,*} Roel G.W. Verhaak,^{3,11,40} Aaron McKenna,^{4,40} Benito Campos,^{5,6} Houtan Noushmehr,^{7,8} Sofie R. Salama,⁹ Siyuan Zheng,⁹ Debbyani Chakravarty,¹ J. Zachary Sanborn,⁹ Samuel H. Bernier,¹⁰ Rameen Beroukhi,^{4,2} Brady Bernard,¹⁰ Chang-Jun Wu,¹¹ Giannicola Genovesi,¹¹ Ilya Shmulevich,¹⁰ Jill Barnholtz-Sloan,¹² Linus Zou,⁴ Rajulshimam Vegeeta,³ Sachet A. Shukla,³ Giovanni Cirillo,¹³ W.K. Yung,¹⁴ Wei Zhang,¹⁵ Carrie Sougnez,¹⁶ Tom Mikkelson,¹⁶ Kenneth Aldape,¹⁵ Darrell D. Bigner,¹⁷ Erwin G. Van Meir,¹⁸ Michael Prados,¹⁹ Andrew Sloan,²⁰ Keith L. Black,²¹ Jennifer Eschbacher,²² Gaetano Finocchiaro,²³ William Friedman,²⁴ David W. Andrews,²⁵ Abhijit Guha,²⁶ Mary Iacocca,²⁷ Brian P. O'Neill,²⁸ Greg Foltz,²⁹ Jerome Myers,²⁹ Daniel J. Weisenberger,³⁰ Robert Perry,³¹ Raju Kuchersappalli,³² Charles M. Perou,³³ D. Neil Hayes,³⁴ Richard Gibbs,³⁴ Marco Marra,³⁵ Gordon B. Mills,³⁵ Eric Lander,⁴ Paul Spellman,³⁷ Richard Wilson,³⁸ Chris Sander,¹⁰ John Weinstein,³ Matthew Meyerson,^{3,5} Stacey Gabriel,⁴ Peter W. Laird,⁷ David Haussler,^{3,39} Gad Getz,⁴ Lynda Chin,^{4,11,*} and TCGA Research Network

*Human Oncology and Pathogenesis Program, Brain Tumor Center, Memorial Sloan-Kettering Cancer Center, New York, NY 10065, USA
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⁴Cancer Program, The Broad Institute of Harvard and MIT, Cambridge, MA 02142, USA
⁵Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA 02115, USA
⁶Division of Experimental Neurosurgery, Department of Neurosurgery, Heidelberg University Hospital, 69120 Heidelberg, Germany
⁷University of Southern California, Engineering Center, University of Southern California, Keck School of Medicine, Los Angeles, CA 90033, USA
⁸Department of Genetics, Center for Integrative System Biology, Faculty of Medicine at Riberião Preto, University of São Paulo, 14049-900 Riberião Preto, São Paulo, Brazil

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2H 44106, USA

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A

School of Medicine, Emory University,

Cincinnati, OH 45229, USA

10,

30, USA

239, USA



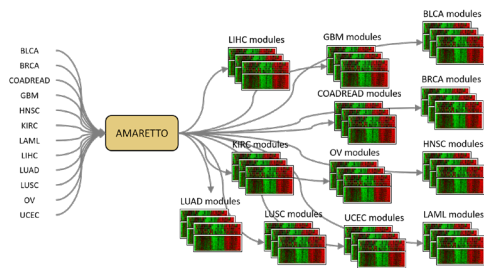
Use Cases: integrating multi-omics, clinical, imaging, and driver and drug perturbation data across model systems and patient studies of cancer

1. A study of hepatitis C and B virus-induced hepatocellular carcinoma (LIHC) with driver and drug discovery for chemoprevention across pan-etiologicals of hepatocellular carcinoma, experimentally validated in rat models
2. A study of glioblastoma multiforme (GBM) and low-grade glioma (LGG) with driver discovery for diagnostic and prognostic molecular subclasses associated with imaging-derived features for non-invasive imaging diagnostics
3. A pan-cancer study across twelve cancer sites with driver discovery of pan-cancer drivers of smoking-induced and 'antiviral' interferon-modulated innate immune response cancer

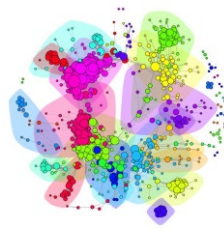
Use Case 3a: Pan-cancer driver discovery

Driver prediction for pan-cancer multi-omics subnetworks across 12 cancer (sub)types validated using genetic perturbations in cell lines

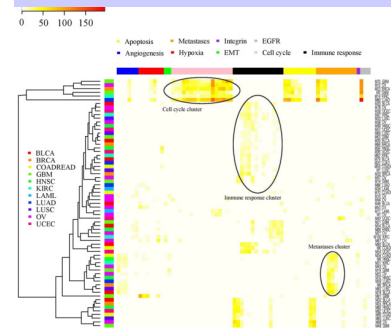
Drivers of smoking-induced cancer and 'antiviral' interferon-modulated innate immune response across 12 cancer (sub)types



Pan-cancer communities or subnetworks

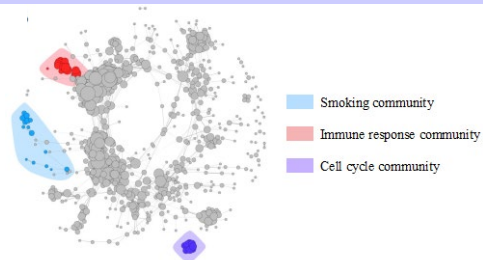


Pan-cancer functional categories ⇒ AMARETTO captures hallmarks of cancer



Driver discovery:

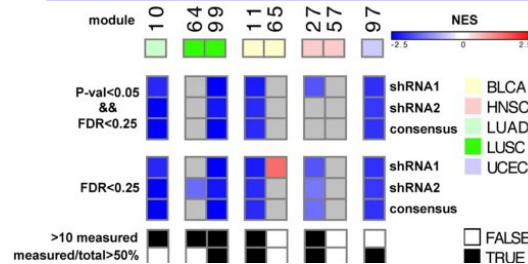
- OAS2 pan-cancer driver of 'antiviral' interferon-modulated innate immune response
- GPX2 pan-cancer driver of smoking-induced cancer



Nathalie Pochet and Olivier Gevaert, *EBioMedicine* 2018

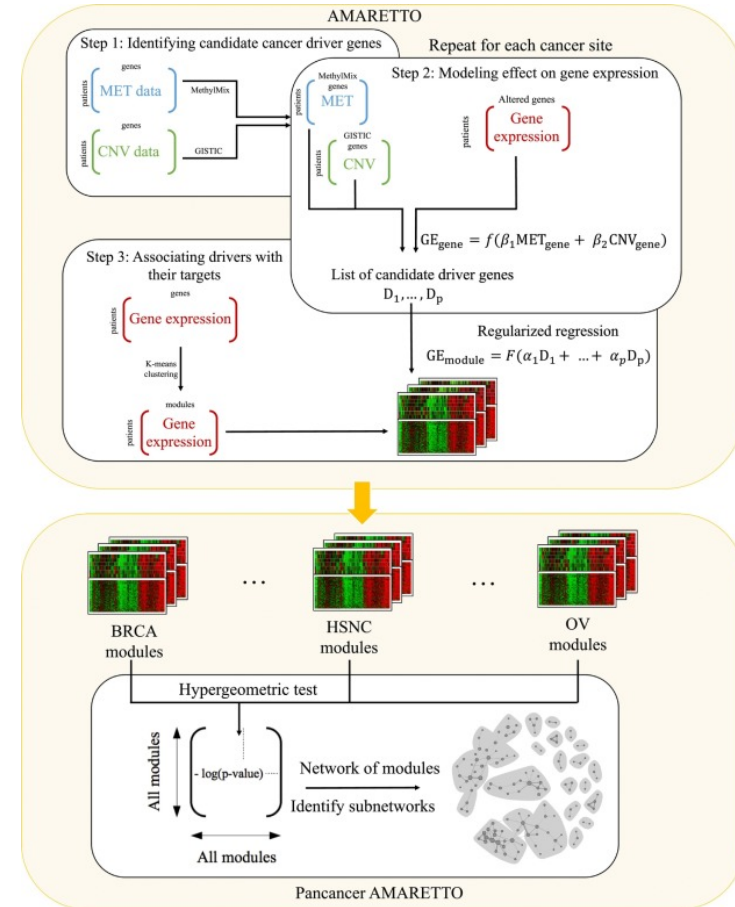
Driver validation:

Genetic perturbations of GPX2 in the A549 (LUAD) cell line ⇒ Knocking down GPX2 represses target genes in GPX2-regulated circuits



Drivers of smoking-induced cancer and 'antiviral' interferon-modulated innate immune response across 12 cancer (sub)types (GBM, LIHC)

⇒ **AMARETTO facilitates identification of known and novel cancer drivers and their targets**



Workflow of *AMARETTO:

First, AMARETTO infers regulatory networks within each biological system via multi-omics data fusion. Specifically, AMARETTO identifies potential cancer drivers by identifying genes whose genetic and epigenetic cancer aberrations have a direct functional impact on their own transcriptomic or proteomic expression. AMARETTO then connects these drivers with modules of co-expressed target genes that they putatively control, defined as regulatory circuits, using a penalized regulatory program. Second, Community-AMARETTO learns communities or subnetworks by connecting the regulatory circuits inferred from different systems to identify drivers across diseases or biological systems.

Use Cases: integrating multi-omics, clinical, imaging, and driver and drug perturbation data across model systems and patient studies of cancer

1. A study of hepatitis C and B virus-induced hepatocellular carcinoma (LIHC) with driver and drug discovery for chemoprevention across pan-etiologicals of hepatocellular carcinoma, experimentally validated in rat models
2. A study of glioblastoma multiforme (GBM) and low-grade glioma (LGG) with driver discovery for diagnostic and prognostic molecular subclasses associated with imaging-derived features for non-invasive imaging diagnostics
3. A pan-cancer study across twelve cancer sites with driver discovery of pan-cancer drivers of smoking-induced and 'antiviral' interferon-modulated innate immune response cancer
3. A pan-cancer study of squamous cell carcinoma (SCC) across five SCC cancer sites, in particular, lung (LUSC), head and neck (HNSC), esophageal (ESCA), cervical (CESC) and bladder (BLCA)

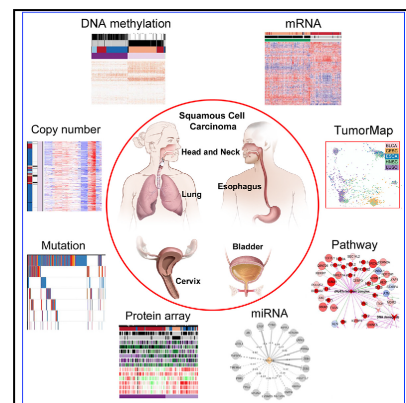
Use Case 3b: Pan-squamous cell carcinoma driver discovery

Driver prediction for pan-squamous cell carcinoma multi-omics subnetworks across 5 cancer sites, i.e., in lung (LUSC), head and neck (HNSC), esophageal (ESCA), cervical (CESC) and bladder (BLCA), validated using genetic perturbations in cell lines

Cell Reports

Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas

Graphical Abstract



Highlights

- SCCs show chromosome or methylation alterations affecting multiple related genes
- These regulate squamous stemness, differentiation, growth, survival, and inflammation
- Copy-quiet SCCs have hypermethylated (*FANCF*, *TET1*) or mutated (*CASP8*, *MAPK-RAS*) genes
- Potential targets include Δ Np63, WEE1, IAPs, PI3K-mTOR/MAPK, and immune responses

Resource



Authors

Joshua D. Campbell, Christina Yau, Reanne Bowlby, ..., Curtis R. Pickering, Zhong Chen, Carter Van Waes

Correspondence

chenz@nidcd.nih.gov (Z.C.), vanwaesc@nidcd.nih.gov (C.V.W.)

In Brief

Campbell et al. reveal that squamous cell cancers from different tissue sites may be distinguished from other cancers and subclassified molecularly by recurrent alterations in chromosomes, DNA methylation, messenger and microRNA expression, or by mutations. These affect squamous cell pathways and programs that provide candidates for therapy.

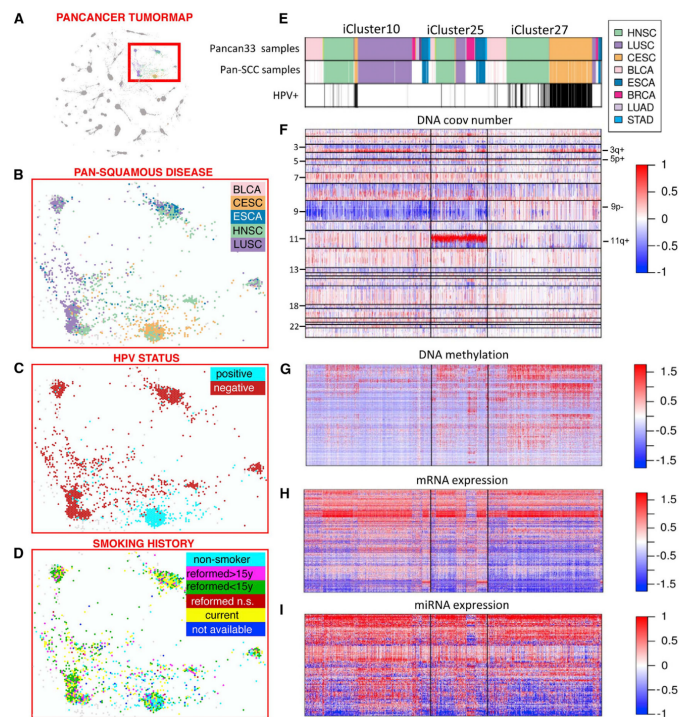
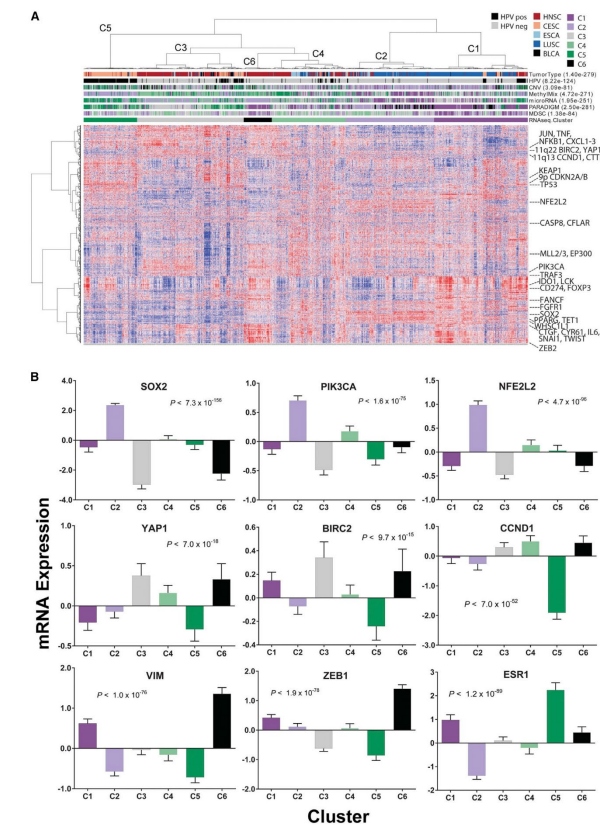


Figure 1. TumorMap and iCluster of Squamous Cancers from PanCancer-33 Analysis

(A) TumorMap analysis visualizing close mapping of LUSC, HNSC, ESCA, CESC, and BLCA among 28 PanCancer-33 islands. (B) Higher resolution view of TM islands and distribution of SCC from 5 sites. (C) HPV status showing the majority of HPV(+) CESC and HNSC map around a distinct island. (D) Smoking history of SCC. Each spot in the map represents a sample. The colors of the sample spots represent attributes as described for each panel. (E–I) Summary of Cluster analysis (E), DNA copy-number (F), methylation (G), mRNA (H), and miRNA (I) expression. PanCancer-33 SCC and other tumors and Pan-SCC from 5 sites identified by histopathologic diagnosis cluster within C10, C25, and C27. Annotation bars show cancer type and HPV status, and keys show an increase (red) or decrease (blue) in features as indicated: DNA copy number, copy-number log ratio (tumor versus normal); DNA methylation, normalized beta values; mRNA expression, normalized log expression counts; miRNA expression, normalized log expression counts.



(legend on next page)

AMARETTO reports for case studies

Case Study 1 (virus-induced LIHC):

- TCGA LIHC: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/TCGA_LIHC/AMARETTOhtmls/index.html
- CCLE liver: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/CCLE_Liver/AMARETTOhtmls/index.html
- Time-course HCV: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/tcHCV/AMARETTOhtmls/index.html
- Single-cell HCV: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/scHCV/AMARETTOhtmls/index.html
- Time-course HBV: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/tcHBV/AMARETTOhtmls/index.html
- Single-cell HBV: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/scHBV/AMARETTOhtmls/index.html

Case Study 2 (gliomas GBM and LGG):

- TCGA GBM: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Brain_2DS/TCGA_GBM/AMARETTOhtmls/index.html
- TCGA LGG: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Brain_2DS/TCGA_LGG/AMARETTOhtmls/index.html

Case Study 3 (pan-squamous BLCA, CESC, ESCA, HNSC, LUSC):

- TCGA BLCA: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_PanCancer_5DS/TCGA_BLCA/AMARETTOhtmls/index.html
- TCGA CESC: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_PanCancer_5DS/TCGA_CESC/AMARETTOhtmls/index.html
- TCGA ESCA: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_PanCancer_5DS/TCGA_ESCA/AMARETTOhtmls/index.html
- TCGA HNSC: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_PanCancer_5DS/TCGA_HNSC/AMARETTOhtmls/index.html
- TCGA LUSC: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_PanCancer_5DS/TCGA_LUSC/AMARETTOhtmls/index.html

Community-AMARETTO reports for case studies

Case Study 1 (virus-induced LIHC):

- TCGA LIHC & CCLE liver & Time-course HCV & Single-cell HCV & Time-course HBV & Single-cell HBV: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/index.html

Case Study 2 (gliomas GBM and LGG):

- TCGA GBM & LGG: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Brain_2DS/index.html

Case Study 3 (pan-squamous BLCA, CESC, ESCA, HNSC, LUSC):

- TCGA BLCA & CESC & ESCA & HNSC & LUSC: http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_PanCancer_5DS/index.html

Perturbation-AMARETTO reports for case studies

Case Study 1 (virus-induced LIHC):

- Driver discovery: [https://pochetlab.shinyapps.io/pAMARETTO Liver 6DS Drivers](https://pochetlab.shinyapps.io/pAMARETTO_Liver_6DS_Drivers)
- Drug discovery: [https://pochetlab.shinyapps.io/pAMARETTO Liver 6DS Drugs Diseases](https://pochetlab.shinyapps.io/pAMARETTO_Liver_6DS_Drugs_Diseases)

Case Study 2 (gliomas GBM and LGG):

- Driver discovery: [https://pochetlab.shinyapps.io/pAMARETTO Brain 2DS Drivers](https://pochetlab.shinyapps.io/pAMARETTO_Brain_2DS_Drivers)

Case Study 3 (pan-squamous BLCA, CESC, ESCA, HNSC, LUSC):

- Driver discovery:
[https://pochetlab.shinyapps.io/pAMARETTO AMARETTO PanCancer 5DS Drivers](https://pochetlab.shinyapps.io/pAMARETTO_AMARETTO_PanCancer_5DS_Drivers)

Case Study 1

Hepatitis C and B virus-induced
Hepatocellular Carcinoma (LIHC)

AMARETTO Report Run Information

Number of Samples in Gene Expression Data = 367
Number of Samples in DNA Copy Number Data = 360
Number of Samples in DNA Methylation Data = 373
Number of 75% most variable Genes = 11180
Number of Regulatory Modules = 150

Overview of Regulatory Modules

CSV Excel PDF Print Column visibility Show entries Search:

Module	# Target Genes	# Driver Genes	# Gene Sets
<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>
Module 1	37	9	105
Module 2	35	7	196
Module 3	124	9	228
Module 4	15	7	84
Module 5	142	6	247
Module 6	74	8	185
Module 7	60	7	265
Module 8	104	6	229
Module 9	42	8	57
Module 10	58	7	207

AMARETTO Report

Run Information

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Overview of Regulatory Modules

CSV Excel PDF Print Column visibility Show entries Search:

Module	# Target Genes	# Driver Genes	# Gene Sets
<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>
Module 1	37	9	105
Module 2	35	7	196
Module 3	124	9	228
Module 4	15	7	84
Module 5	142	6	247
Module 6	74	8	185
Module 7	60	7	265
Module 8	104	6	229
Module 9	42	8	57
Module 10	58	7	207

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Overview of Regulatory Modules

- Assignments of Genes to Regulatory Modules
- Enrichments of Functional Categories in Regulatory Modules
- Enrichments of Driver Perturbations in Regulatory Modules
- Enrichments of Drug Perturbations in Regulatory Modules
- Associations of Phenotypes to Regulatory Modules

AMARETTO Report Run Information

Number of Samples in Gene Expression Data = 367
Number of Samples in DNA Copy Number Data = 360
Number of Samples in DNA Methylation Data = 373
Number of 75% most variable Genes = 11180
Number of Regulatory Modules = 150

Overview of Regulatory Modules

CSV Excel PDF Print Column visibility Show 10 entries Search:

Module	# Target Genes	# Driver Genes	# Gene Sets
<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value="All"/>
Module 1	37	9	105
Module 2	35	7	196
Module 3	124	9	228
Module 4	15	7	84
Module 5	142	6	247
Module 6	74	8	185
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Overview of Regulatory Modules

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AMARETTO Report Overview of Regulatory Modules

CSV Excel PDF Print Column visibility Show 200 entries Search:

Module	# Target Genes	# Driver Genes	# Gene Sets
All	All	All	All
Module 1	37	9	105
Module 2	35	7	196
Module 3	124	9	228
Module 4	15	7	84
Module 5	142	6	247
Module 6	74	8	185
Module 7	60	7	265
Module 8	104	6	229
Module 9	42	8	57
Module 10	58	7	207
Module 11	61	7	170
Module 12	83	6	200
Module 13	82	8	227
Module 14	117	10	66
Module 15	75	7	404
Module 16	25	9	106
...			
Module 147	73	6	198
Module 148	49	6	62
Module 149	103	7	300
Module 150	107	5	255

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Overview of Regulatory Modules

All tables: functionalities for querying, saving and viewing results

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Module	# Target Genes	# Driver Genes	# Gene Sets
Module 1	37	9	105
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Module 11	61	7	170
Module 12	83	6	200
Module 13	82	8	227
Module 14	117	10	66
Module 15	75	7	404
Module 16	25	9	106
...			
Module 147	73	6	198
Module 148	49	6	62
Module 149	103	7	300
Module 150	107	5	255

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Assignments of Genes to Regulatory Modules

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Assignments of Genes to Regulatory Modules

CSV Excel PDF Print Column visibility Show 100 entries Search:

Gene	Module	Gene Type
All	All	All
A1BG	Module 53	Target
A1CF	Module 64	Target
A2LD1	Module 64	Target
A2M	Module 81	Target
A4GALT	Module 123	Target
AACS	Module 104	Target
AADAC	Module 22	Target
AADAT	Module 70	Target
AAK1	Module 89	Target
AARS	Module 145	Target
AARSD1	Module 94	Target
AASS	Module 85	Target
AASS	Module 85	Driver
AATK	Module 59	Target
ABAT	Module 70	Target
ABCA1	Module 101	Target
...
ZXDB	Module 55	Target
ZYG11A	Module 47	Target
ZYG11B	Module 70	Target
ZYX	Module 93	Target
ZZEF1	Module 134	Target
ZZEF1	Module 134	Driver

Showing 12,101 to 12,183 of 12,183 entries

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Enrichments of Functional Categories in Regulatory Modules

➤ Functional characterization

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Enrichments of Functional Categories in Regulatory Modules

CSV Table PDF Heat Column visibility Show 20 entries Search: hepatocellular

Module	Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
Module 50	YAMASHITA LIVER CANCER WITH EPCAM UP	Up-regulated genes distinguishing hepatocellular carcinoma (HCC) samples positive for EPCAM [GeneID=4072] from the negative ones.	53	14	EP30, HNR1A1, RPL13A, RPL11, RPL23A, RPL25, RPL31, RPL33, RPL8, RPL9, RPL10, RPL53, RPS24	0.25	1.3e-27	3.5e-24
Module 52	LEE LIVER CANCER SURVIVAL UP	Genes highly expressed in hepatocellular carcinoma with good survival.	185	13	AM1, APOC3, ASB1, F15, H10, M511, M1551, HGN, SALL1, SERP1N1, SERP1F1, SLC22A2, SLC22A7	0.070	8.5e-17	6.4e-14
Module 123	BOYAUULT LIVER CANCER SUBCLASS G3 UP	Up-regulated genes in hepatocellular carcinoma (HCC) subclass G3, defined by unsupervised clustering.	188	14	ACACA, ADL5, CUX3, GDL, KIF81, MED1, MEO24, NME1, NSP, PMS, PMS3, P1302, HBBN4, U11F15	0.074	1.2e-16	9.1e-14
Module 46	VILLANUEVA LIVER CANCER KRT19 UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).	174	12	BUB1, CD320, CD3A, CLM10, GOLGA3, KIF20A, KIF4A, MKR7, SGOL2, S1L, TPX2, T1K	0.069	7.1e-16	5.0e-13
Module 50	ANDERSEN LIVER CANCER KRT19 UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma.	35	8	RPL10A, RPL13A, RPL27A, RPL3, RPL9, RPL17, RPL15, RPS3A	0.23	1.2e-15	8.1e-13
Module 52	KIM LIVER CANCER POOR SURVIVAL DN	Genes under-expressed in hepatocellular carcinoma (HCC) with poor survival.	43	8	APOC3, F15, M511, M1551, HGN, SERP1N10, SERP1F2, SLC22A2	0.19	2.6e-14	1.4e-11
Module 130	CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	Top 200 marker genes up-regulated in the 'proliferation' subclass of hepatocellular carcinoma (HCC), characterized by increased proliferation, high levels of serum AFP [GeneID=174], and chromosomal instability.	178	11	EP3, FANCI, FOXM1, G2T1, HMG22, LMNB1, MDR3, RNF212, RNF224, RNF2, NAD21A11	0.062	6.1e-14	3.0e-11
Module 50	LEE LIVER CANCER SURVIVAL DN	Genes highly expressed in hepatocellular carcinoma with poor survival.	175	10	HNR1A1, RPL12, RPL11, RPL31, RPL15, RPL8, RPL15, RPS3, RPS24, RPS28	0.057	5.7e-13	2.4e-10
Module 46	CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	Top 200 marker genes up-regulated in the 'proliferation' subclass of hepatocellular carcinoma (HCC), characterized by increased proliferation, high levels of serum AFP [GeneID=174], and chromosomal instability.	178	10	CD320, KIF14, KIF20A, KIF4A, MKR7, RACGAP1, SGOL2, SKA1, TPX2, T1K	0.056	1.6e-12	6.2e-10
Module 52	CERVERA SDHB TARGETS 2	Genes present but differentially expressed between Hep3B cells (hepatocellular carcinoma, HCC) with RNAi knockdown of SDHB [GeneID=6390] and control cells.	114	8	AP1, APOA1, APOB, GAS2, M511, F1, HBSA, TM SF4, T1K	0.079	1.9e-12	7.1e-10
Module 118	CERVERA SDHB TARGETS 2	Genes present but differentially expressed between Hep3B cells (hepatocellular carcinoma, HCC) with RNAi knockdown of SDHB [GeneID=6390] and control cells.	114	9	CHKB, CYBB, EPNA5, KIF18L, L1BP2, MATN2, NAK1, S1K17A, T1G32	0.079	3.1e-12	1.1e-9
Module 59	HOSHIDA LIVER CANCER SUBCLASS S3	Genes from 'subtype S3' signature of hepatocellular carcinoma (HCC): hepatocyte differentiation.	266	12	ACD1, APOB, BAI1, CA2, CH1, FGB, FGL2, GSK3, PONS, P10S1, SEI11, SERP1NAB	0.045	3.2e-12	1.2e-9
Module 55	LEE LIVER CANCER SURVIVAL UP	Genes highly expressed in hepatocellular carcinoma with good survival.	185	10	ANKK4, CTG112A, CY222, GAB1, HGO, KHK, MLXIP, PCSK6, TCF12, S1ARF10	0.054	1.4e-11	4.2e-9
Module 43	HOSHIDA LIVER CANCER SUBCLASS S1	Genes from 'subtype S1' signature of hepatocellular carcinoma (HCC): aberrant activation of the WNT signaling pathway.	237	10	CU151, COL4A1, COL6A1, EFEMP1, GNS, HP1A, MSN, SLC39A6, SNAI2, TM1F2	0.042	1.7e-11	5.2e-9
Module 8	LEE LIVER CANCER SURVIVAL UP	Genes highly expressed in hepatocellular carcinoma with good survival.	185	8	C2, CASP9, FBXO1, HVAL1, MASH2, P10X, RPL5, SLC39A3	0.043	4.5e-11	1.3e-8
Module 130	VILLANUEVA LIVER CANCER KRT19 UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).	174	9	BUX, CD3A3, UNAZ, FANCI, GNS1, KIAA1936, LMNB1, TMEM194A, T1GAP1	0.052	6.4e-11	1.7e-8
Module 139	ACEVEDO LIVER CANCER UP	Genes up-regulated in hepatocellular carcinoma (HCC) compared to normal liver samples.	973	16	CAU3, CD92, DRPC2, EHEC1, F10C16, GDM, HYDUT, I11G1, LMAN2, OSIC, P3A6, RING2, SERP1, SSI1, SSI2, TMED10	0.016	1.4e-10	3.5e-8
Module 121	WOO LIVER CANCER RECURRENCE DN	Genes negatively correlated with recurrence free survival in patients with hepatitis B-related (HBV) hepatocellular carcinoma (HCC).	80	7	ACD12, ADPR, DMR1A, CY11F12, CY11F3, F10Z, F0H	0.087	1.6e-10	3.9e-8
Module 52	HOSHIDA LIVER CANCER SUBCLASS S3	Genes from 'subtype S3' signature of hepatocellular carcinoma (HCC): hepatocyte differentiation.	266	10	ABCS4, AM1, APOA1, APOC2, ASB1, F2, H10, HGN, SLC22A2, SLC6A12	0.038	1.7e-10	4.1e-8
Module 52	WOO LIVER CANCER RECURRENCE DN	Genes negatively correlated with recurrence free survival in patients with hepatitis B-related (HBV) hepatocellular carcinoma (HCC).	80	7	APOC3, GCDM, GLUD2, H10, M111, SARAH, SLC2A2	0.087	2.5e-10	6.5e-8

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Links to html descriptions of gene signatures from MSigDB (H+C2)

Enrichments of Functional Categories in Regulatory Modules

➤ Functional characterization

AMARETTO Report
Enrichments of Functional Categories in Regulatory Modules

CSV Excel PDF Heat Columns visibility Show 20 entries Search: hepatocellular

Module	Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
Module 50	YAMASHITA LIVER CANCER WITH EPCAM UP	Up-regulated genes distinguishing hepatocellular carcinoma (HCC) from the negative ones.	10	10		100%		
Module 52	LEE LIVER CANCER SURVIVAL UP	Genes highly expressed in hepatocellular carcinoma with good survival.	10	10		100%		
Module 123	BOYVAULT LIVER CANCER SUBCLASS G3 UP	Up-regulated genes in hepatocellular carcinoma (HCC) subtype unsupervised clustering.	10	10		100%		
Module 46	VILLANUEVA LIVER CANCER KRT19 UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).	10	10		100%		
Module 50	ANDERSEN LIVER CANCER KRT19 UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).	10	10		100%		
Module 52	KIM LIVER CANCER RORR SURVIVAL DN	Genes under-expressed in hepatocellular carcinoma (HCC) with poor survival.	10	10		100%		
Module 130	CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	Top 200 marker genes up-regulated in the 'proliferation' subtype hepatocellular carcinoma (HCC), characterized by increased proliferation, high [GeneID=174], and chromosomal instability.	10	10		100%		
Module 50	LEE LIVER CANCER SURVIVAL DN	Genes highly expressed in hepatocellular carcinoma with poor survival.	10	10		100%		
Module 46	CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	Top 200 marker genes up-regulated in the 'proliferation' subtype hepatocellular carcinoma (HCC), characterized by increased proliferation, high [GeneID=174], and chromosomal instability.	10	10		100%		
Module 52	CERVERA SDHB TARGETS 2	Genes present but differentially expressed between Hep3B cell carcinoma, HCC) with RNAi knockdown of SDHB [GeneID=63].	10	10		100%		
Module 118	CERVERA SDHB TARGETS 2	Genes present but differentially expressed between Hep3B cell carcinoma, HCC) with RNAi knockdown of SDHB [GeneID=63].	10	10		100%		
Module 59	HOSHIDA LIVER CANCER SUBCLASS S3	Genes from 'subtype S3' signature of hepatocellular carcinoma differentiation.	10	10		100%		
Module 55	LEE LIVER CANCER SURVIVAL UP	Genes highly expressed in hepatocellular carcinoma with good survival.	10	10		100%		
Module 43	HOSHIDA LIVER CANCER SUBCLASS S1	Genes from 'subtype S1' signature of hepatocellular carcinoma of the WNT signaling pathway.	10	10		100%		
Module 8	LEE LIVER CANCER SURVIVAL UP	Genes highly expressed in hepatocellular carcinoma with good survival.	10	10		100%		
Module 130	VILLANUEVA LIVER CANCER KRT19 UP	Genes over-expressed in KRT19-positive [GeneID=3880] hepatocellular carcinoma (HCC).	10	10		100%		
Module 139	ACEVEDO LIVER CANCER UP	Genes up-regulated in hepatocellular carcinoma (HCC) comparison samples.	10	10		100%		
Module 121	WOO LIVER CANCER RECURRENCE DN	Genes negatively correlated with recurrence free survival in post-treated (HBV) hepatocellular carcinoma (HCC).	10	10		100%		
Module 52	HOSHIDA LIVER CANCER SUBCLASS S3	Genes from 'subtype S3' signature of hepatocellular carcinoma differentiation.	10	10		100%		
Module 52	WOO LIVER CANCER RECURRENCE DN	Genes negatively correlated with recurrence free survival in post-treated (HBV) hepatocellular carcinoma (HCC).	10	10		100%		

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Gene Set: HALLMARK_MYC_TARGETS_V2

Standard name: HALLMARK_MYC_TARGETS_V2
Systematic name: H5920
Brief description: A subgroup of genes regulated by MYC - version 2 (v2).
Full description or abstract: A subgroup of genes regulated by MYC - version 2 (v2).
Collection: H: hallmark gene sets
Source publication: H: hallmark gene sets
Exact source: H: hallmark gene sets
Related gene sets: (hide 6 founder gene sets for this hallmark gene set)
Download founder gene sets: gmt | gmx | xml

External links: Hemo sapiens
Organism: HUMAN_GENE_SYMBOL
Contributed by: Arthur Liberzon (Broad Institute)
Source platform: HUMAN_GENE_SYMBOL
Dataset references: (hide 3 hallmark refinement datasets)

Dataset Identifier	Description
GSE37276	MYC WT vs KD (RNAi) (Bae 1 Raj)
GSE23239	promalignant (th Myc) vs wt B lymphocytes (to Myc)
GSE37792	Enna-Myc vs WT bone marrow B220+ cells
GSE4356	MYC OE 2-8h vs Oh 1 day 21 day pancreatic beta cells
GSE3962	MYC WT vs MYC KD (RNAi)
(hide 3 hallmark refinement datasets)	

Download gene set: format: gmt | heat | gmt | gmx | xml
Compute overlap: (show collections to investigate for overlap with this gene set)
Compendia expression profiles: (Human tissue compendium (Novartis) HCC cell lines (National Cancer Institute) Further investigate these 59 genes)
Advanced query: Categorize these 58 genes by gene family (hide 58 members mapped to 58 genes)

Original Member	Entrez Gene Id	Gene Symbol	Gene Description
AIMP2	7565	AIMP2	aminocyclitol RNA synthetase complex inter...
BYSL	7055	BYSL	lysine-like
CBX3	11335	CBX3	chromobox homolog 3
CDK4	1019	CDK4	cyclin-dependent kinase 4
DCTP1	79077	DCTP1	dCTP pyrophosphatase 1
DDB1B	8886	DDB1B	DDB1 (Rsp-100-Aa-Aaa) box polypeptide 1B
DUSP2	1844	DUSP2	dual specificity phosphatase 2
EXOSC5	56915	EXOSC5	exosome component 5
FARSA	2193	FARSA	phenylalanyl-tRNA synthetase, alpha sub...
GNL3	26254	GNL3	guanine nucleotide binding protein-like...
GRWD1	83743	GRWD1	glutamate-rich WD repeat containing 1
HK2	3099	HK2	hexokinase 2

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Associations of Phenotypes to Regulatory Modules

- Clinical characterization for clinical, molecular and imaging-derived phenotypes

AMARETTO Report Associations of Phenotypes to Regulatory Modules

CSV Excel FDR Plot Column visibility Show 50 entries Search:

Module	Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
105	All	All	All	All	All
Module 105	mRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	4.4e-11	1.2e-10	Statistic: 54.4
Module 105	mRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	3.1e-8	1.2e-7	Statistic: 49.7
Module 105	DNA_Copy_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	8.4e-9	1.3e-7	Statistic: 49.5
Module 105	CTNNB1_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0000023	0.000018	Estimate: 0.47, 95% CI: [0.291, 0.658], Statistics: 4730
Module 105	Hoshida_Cluster_S3_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000032	0.000070	Estimate: -0.351, 95% CI: [-0.511, -0.18], Statistics: 2730
Module 105	Hoshida_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00017	0.00029	Statistic: 17.3
Module 105	CDKN2A_Silencing (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000034	0.0010	Estimate: 0.357, 95% CI: [0.19, 0.518], Statistics: 5750
Module 105	Hypomethylation_Cluster (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00025	0.0011	Statistic: 16.6
Module 105	Hoshida_Cluster_S2_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00011	0.0019	Estimate: 0.28, 95% CI: [0.108, 0.455], Statistics: 5510
Module 105	TERT_Promoter_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00018	0.0051	Estimate: 0.329, 95% CI: [0.156, 0.486], Statistics: 5580
Module 105	TP53_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0002	0.014	Estimate: 0.276, 95% CI: [0.0981, 0.462], Statistics: 4610
Module 105	IDH_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00039	0.021	Estimate: -0.714, 95% CI: [-1.3, -0.274], Statistics: 56
Module 105	Consensus_Clinical_and_RNA_Seq_Heatitis_B_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0066	0.052	Estimate: 0.281, 95% CI: [0.0788, 0.476], Statistics: 4000
Module 105	Hypermethylation_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.044	0.061	Statistic: 6.08
Module 105	SurvivalTime (COXPORPHAZARDTIMEEVENT), SurvivalCensoring (COXPORPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0019	0.14	Beta: 0.62117, Hazard Ratio: 1.8611, 95% CI: [1.2581, 2.7532], Wald Statistic: 9.67
Module 105	iCluster_Clusters_3_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.074	0.16	Estimate: 0.15, 95% CI: [-0.044, 0.318], Statistics: 4500
Module 105	iCluster_Clusters_1_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.20	0.26	Estimate: -0.113, 95% CI: [-0.286, 0.0552], Statistics: 3460
Module 105	iCluster_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.21	0.27	Statistic: 3.1
Module 105	Hoshida_Cluster_S1_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.23	0.34	Estimate: 0.134, 95% CI: [-0.0877, 0.356], Statistics: 2480
Module 105	Paradigm_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.38	0.40	Statistic: 3.08
Module 105	Clinical_Alcoholic_Liver_Disease (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0063	0.41	Estimate: 0.263, 95% CI: [0.0723, 0.441], Statistics: 4480
Module 105	Consensus_Clinical_and_RNA_Seq_Heatitis_C_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.033	0.58	Estimate: 0.237, 95% CI: [0.0233, 0.433], Statistics: 3140
Module 105	Clinical_Heatitis_C_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.043	0.73	Estimate: 0.227, 95% CI: [0.00842, 0.426], Statistics: 2910
Module 105	iCluster_Clusters_2_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.85	0.90	Estimate: 0.0214, 95% CI: [-0.163, 0.23], Statistics: 3570
Module 105	RPPA_Clusters (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.87	0.90	Estimate: -0.0114, 95% CI: [-0.185, 0.167], Statistics: 2520
Module 105	Clinical_NAFLD (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.26	0.93	Estimate: -0.184, 95% CI: [-0.521, 0.151], Statistics: 734
Module 105	Clinical_Heatitis_B_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.37	0.98	Estimate: 0.115, 95% CI: [-0.14, 0.366], Statistics: 1980

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- Assignments of Genes to Regulatory Modules
- Enrichments of Functional Categories in Regulatory Modules
- Enrichments of Driver Perturbations in Regulatory Modules
- Enrichments of Drug Perturbations in Regulatory Modules
- Associations of Phenotypes to Regulatory Modules

Clinical, molecular & imaging-derived phenotypes from TCGA/TCIA

AMARETTO Report Associations of Phenotypes to Regulatory Modules

Columns: Module, Phenotype, Statistics Test, P-value, FDR Q-value, Descriptive Statistics

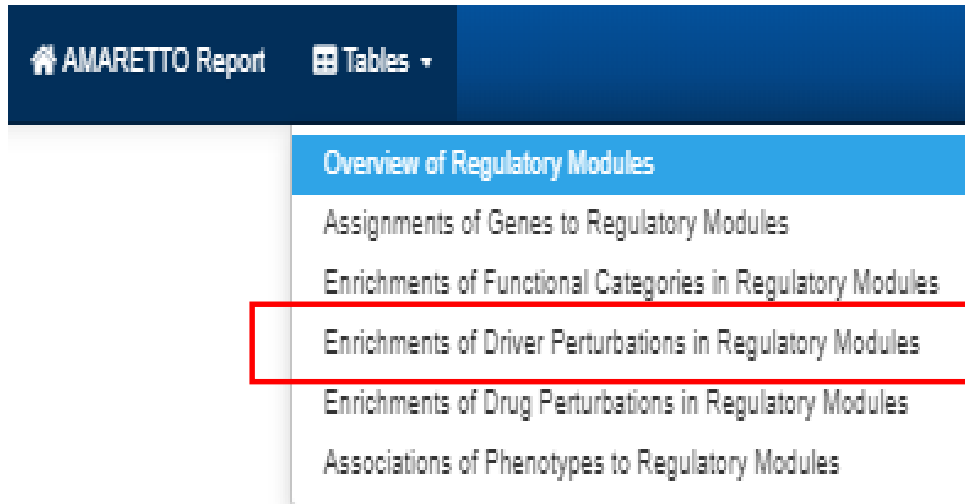
Module	Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
Module 105	miRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	4.4e-11	1.2e-10	Statistic: 54.4
Module 105	miRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	3.1e-8	1.2e-7	Statistic: 49.7
Module 105	DNA_Copy_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	8.4e-9	1.3e-7	Statistic: 40.5
Module 105	CTNNB1_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0000023	0.000018	Estimate: 0.47, 95% CI: [0.291, 0.658], Statistics: 4730
Module 105	Hoshida_Cluster_S3_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000032	0.000070	Estimate: -0.351, 95% CI: [-0.511, -0.18], Statistics: 2730
Module 105	Hoshida_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00017	0.00029	Statistic: 17.3
Module 105	CDKN2A_Silencing (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000034	0.0010	Estimate: 0.357, 95% CI: [0.19, 0.518], Statistics: 5750
Module 105	Hypomethylation_Cluster (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00025	0.0011	Statistic: 16.6
Module 105	Hoshida_Cluster_S2_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0011	0.0019	Estimate: 0.28, 95% CI: [0.108, 0.455], Statistics: 5510
Module 105	TERT_Promoter_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00018	0.0051	Estimate: 0.329, 95% CI: [0.156, 0.486], Statistics: 5580
Module 105	TP53_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0032	0.014	Estimate: 0.276, 95% CI: [0.0981, 0.462], Statistics: 4610
Module 105	IDH_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0039	0.021	Estimate: -0.714, 95% CI: [-1.3, -0.274], Statistics: 56
Module 105	Consensus_Clinical_and_RNA_Seq_Heatitis_B_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0066	0.052	Estimate: 0.281, 95% CI: [0.0788, 0.476], Statistics: 4000
Module 105	Hypermethylation_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.044	0.061	Statistic: 6.08
Module 105	SurvivalTime (COXPROPHAZARDTIMEEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0019	0.14	Beta: 0.62117, Hazard Ratio: 1.8611, 95% CI: [1.2581, 2.7532], Wald Statistic: 9.67
Module 105	iCluster_Clusters_3_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.074	0.16	Estimate: 0.15, 95% CI: [-0.044, 0.358], Statistics: 4500
Module 105	iCluster_Clusters_1_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.20	0.26	Estimate: -0.113, 95% CI: [-0.286, 0.0592], Statistics: 3460
Module 105	iCluster_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.21	0.27	Statistic: 3.1
Module 105	Hoshida_Cluster_S1_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.23	0.34	Estimate: 0.134, 95% CI: [-0.0877, 0.356], Statistics: 2480
Module 105	Paradigm_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.38	0.40	Statistic: 3.08
Module 105	Clinical_Alcoholic_Liver_Disease (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0063	0.41	Estimate: 0.263, 95% CI: [0.0723, 0.441], Statistics: 4480
Module 105	Consensus_Clinical_and_RNA_Seq_Heatitis_C_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.033	0.58	Estimate: 0.237, 95% CI: [0.0233, 0.433], Statistics: 3140
Module 105	Clinical_Heatitis_C_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.043	0.73	Estimate: 0.227, 95% CI: [0.00842, 0.426], Statistics: 2910
Module 105	iCluster_Clusters_2_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.85	0.90	Estimate: 0.0214, 95% CI: [-0.163, 0.23], Statistics: 3570
Module 105	RPPA_Clusters (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.87	0.90	Estimate: -0.014, 95% CI: [-0.185, 0.167], Statistics: 2520
Module 105	Clinical_NAFLD (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.26	0.93	Estimate: -0.184, 95% CI: [-0.521, 0.151], Statistics: 734
Module 105	Clinical_Heatitis_B_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.37	0.98	Estimate: 0.115, 95% CI: [-0.14, 0.366], Statistics: 1980

Showing 1 to 27 of 27 entries (filtered from 4,050 total entries)

Associations of Phenotypes to Regulatory Modules

- Clinical characterization for clinical, molecular and imaging-derived phenotypes

AMARETTO report LIHC



Enrichments of Driver Perturbations in Regulatory Modules

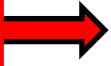
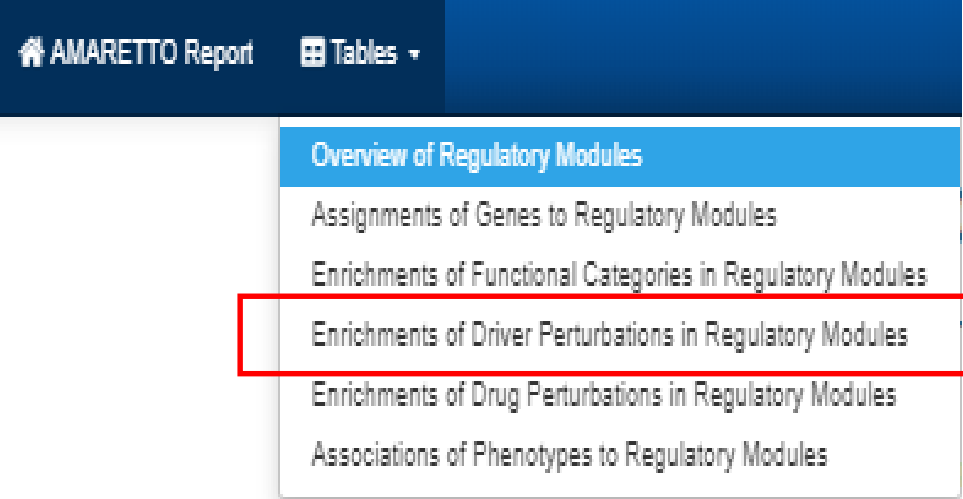
- Perturbation-AMARETTO v1 for driver discovery using genetic perturbations in model systems

AMARETTO Report
Enrichments of Driver Perturbations in Regulatory Modules

CSV Excel PDF HTML Column visibility Show 150 entries Search:

Module	Gene Set Name	Gene Set Description	# Genes In Gene Set	# Genes In Overlap	Genes In Overlap	% Genes In Overlap	P-value	FDR Q-value
All	All	All			All			
Module 50	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_HT29_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_HT29_DN	300	17	RP121, RP117, RP141, RP122, RP120, RP123, RP124, RP125, RP126, RP127, RP128, RP129, RP130, RP131, RP132, RP133, RP134, RP135, RP136, RP137, RP138, RP139, RP140, RP141, RP142, RP143, RP144, RP145, RP146, RP147, RP148, RP149, RP150, RP151, RP152, RP153, RP154, RP155, RP156, RP157, RP158, RP159, RP160, RP161, RP162, RP163, RP164, RP165, RP166, RP167, RP168, RP169, RP170, RP171, RP172, RP173, RP174, RP175, RP176, RP177, RP178, RP179, RP180, RP181, RP182, RP183, RP184, RP185, RP186, RP187, RP188, RP189, RP190, RP191, RP192, RP193, RP194, RP195, RP196, RP197, RP198, RP199, RP200, RP201, RP202, RP203, RP204, RP205, RP206, RP207, RP208, RP209, RP210, RP211, RP212, RP213, RP214, RP215, RP216, RP217, RP218, RP219, RP220, RP221, RP222, RP223, RP224, RP225, RP226, RP227, RP228, RP229, RP230, RP231, RP232, RP233, RP234, RP235, RP236, RP237, RP238, RP239, RP240, RP241, RP242, RP243, RP244, RP245, RP246, RP247, RP248, RP249, RP250, RP251, RP252, RP253, RP254, RP255, RP256, RP257, RP258, RP259, RP260, RP261, RP262, RP263, RP264, RP265, RP266, RP267, RP268, RP269, RP270, RP271, RP272, RP273, RP274, RP275, RP276, RP277, RP278, RP279, RP280, RP281, RP282, RP283, RP284, RP285, RP286, RP287, RP288, RP289, RP290, RP291, RP292, RP293, RP294, RP295, RP296, RP297, RP298, RP299, RP300	0.057	2.5e-21	2.1e-17
Module 50	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	300	16	RP121, RP141, RP122, RP123, RP124, RP125, RP126, RP127, RP128, RP129, RP130, RP131, RP132, RP133, RP134, RP135, RP136, RP137, RP138, RP139, RP140, RP141, RP142, RP143, RP144, RP145, RP146, RP147, RP148, RP149, RP150, RP151, RP152, RP153, RP154, RP155, RP156, RP157, RP158, RP159, RP160, RP161, RP162, RP163, RP164, RP165, RP166, RP167, RP168, RP169, RP170, RP171, RP172, RP173, RP174, RP175, RP176, RP177, RP178, RP179, RP180, RP181, RP182, RP183, RP184, RP185, RP186, RP187, RP188, RP189, RP190, RP191, RP192, RP193, RP194, RP195, RP196, RP197, RP198, RP199, RP200, RP201, RP202, RP203, RP204, RP205, RP206, RP207, RP208, RP209, RP210, RP211, RP212, RP213, RP214, RP215, RP216, RP217, RP218, RP219, RP220, RP221, RP222, RP223, RP224, RP225, RP226, RP227, RP228, RP229, RP230, RP231, RP232, RP233, RP234, RP235, RP236, RP237, RP238, RP239, RP240, RP241, RP242, RP243, RP244, RP245, RP246, RP247, RP248, RP249, RP250, RP251, RP252, RP253, RP254, RP255, RP256, RP257, RP258, RP259, RP260, RP261, RP262, RP263, RP264, RP265, RP266, RP267, RP268, RP269, RP270, RP271, RP272, RP273, RP274, RP275, RP276, RP277, RP278, RP279, RP280, RP281, RP282, RP283, RP284, RP285, RP286, RP287, RP288, RP289, RP290, RP291, RP292, RP293, RP294, RP295, RP296, RP297, RP298, RP299, RP300	0.053	1.1e-19	7.0e-16
Module 140	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	300	13	UGCH10, G13E1, XPODE, NDA192, CDKN1B, PRICK3, SP1AT, HNRJ, PEST, HNF1A, GNG1, POLR2B, POLR2P	0.043	1.9e-16	6.4e-13
Module 15	Encode_RAD21_H4L4-S3_hg19	Encode_RAD21_H4L4-S3_hg19	2000	25	NEAT1, EGF1K, SP142L, TNFRSF1A, MYO1E, ZNF504, SH3BP1, PPIA, FCH1, ZSCAN1B, MYO18A, RPL10, LOC101918, PPIH2, PPIH1, LOC101918, ROR2, STOM2, CUG1, LOC101918, STOM2L1, STOM2L2, AHR, SP100, INH3	0.013	7.5e-15	1.8e-12
Module 15	CHEA_MTF_21258399_Chip-Seq_MELANOMA_Human	CHEA_MTF_21258399_Chip-Seq_MELANOMA_Human	5578	36	BA3, NCAT1, HNR9B, CARD10, TNFAIP2, LAMP1, UBE1, GAS5, RPL13, GPR103D, MET, SH2D4A, LGALS3BP1, ZNF12, NCF1, HNF1, EGF1K, MYO1E, NUCDC3, PPIA, CAB1, MYO18A, RAB3C, LAMA3, CDK3, HNF1V, HNF1B, TM6SF1, PPIH1B, STOM2, AHR, EPH3, SPK3, INH3, ARHGAP18, PRKDC1	0.0065	1.1e-12	2.3e-10
Module 50	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_MCFT_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_MCFT_DN	300	12	RP141, RP122, RP123, RP124, RP125, RP126, RP127, RP128, RP129, RP130, RP131, RP132, RP133, RP134, RP135, RP136, RP137, RP138, RP139, RP140, RP141, RP142, RP143, RP144, RP145, RP146, RP147, RP148, RP149, RP150, RP151, RP152, RP153, RP154, RP155, RP156, RP157, RP158, RP159, RP160, RP161, RP162, RP163, RP164, RP165, RP166, RP167, RP168, RP169, RP170, RP171, RP172, RP173, RP174, RP175, RP176, RP177, RP178, RP179, RP180, RP181, RP182, RP183, RP184, RP185, RP186, RP187, RP188, RP189, RP190, RP191, RP192, RP193, RP194, RP195, RP196, RP197, RP198, RP199, RP200, RP201, RP202, RP203, RP204, RP205, RP206, RP207, RP208, RP209, RP210, RP211, RP212, RP213, RP214, RP215, RP216, RP217, RP218, RP219, RP220, RP221, RP222, RP223, RP224, RP225, RP226, RP227, RP228, RP229, RP230, RP231, RP232, RP233, RP234, RP235, RP236, RP237, RP238, RP239, RP240, RP241, RP242, RP243, RP244, RP245, RP246, RP247, RP248, RP249, RP250, RP251, RP252, RP253, RP254, RP255, RP256, RP257, RP258, RP259, RP260, RP261, RP262, RP263, RP264, RP265, RP266, RP267, RP268, RP269, RP270, RP271, RP272, RP273, RP274, RP275, RP276, RP277, RP278, RP279, RP280, RP281, RP282, RP283, RP284, RP285, RP286, RP287, RP288, RP289, RP290, RP291, RP292, RP293, RP294, RP295, RP296, RP297, RP298, RP299, RP300	0.040	1.7e-13	3.2e-10
Module 15	Encode_POLR2A_HapQ2_hg19	Encode_POLR2A_HapQ2_hg19	6264	36	SHR, LAMP1, ZSCAN12, ZSCAN1B, GAS5, UCL3, LGALS3BP1, CDKN1, ZNF504, RAB3C, HNF1V, GPR103D, ENAH1, TM6SF1, STOM2, HNF1B, AHR, ARHGAP18, HNF1B, FIC3, MAP3K3, ZNF134, ZNF135, NCF1, HNF1, CAB1, EGF1K, SP142L, MYO1E, HNF1A, MYO18A, LAMA3, CDK3, CAB1, AHR, SP100	0.0057	3.4e-11	2.6e-9
Module 15	Encode_NRC1_A549_hg19	Encode_NRC1_A549_hg19	1855	19	NCAT1, EGF1K, TNFRSF1A, HNF1A, SH3BP1, LAMP1, UCL3, LAMA3, CDK3, STOM2, MET, SCHL1, TNFR1, CDKN1, STOM2L1, GSDMC1, NCF1, INH3, HNF1	0.010	6.5e-10	3.2e-8
Module 15	CHEA_SMAD2_18955504_Chip-Seq_HaCt_Human	CHEA_SMAD2_18955504_Chip-Seq_HaCt_Human	1936	19	EGFR, TNFRSF1A, HNF1B, HNF1A, NDC103, SH3BP1, CAB1, RPL13, CDK3, HNF1V, GPR103D, FOSL1, ENAH1, MET, SH2D4A, SCHL1, TM6SF1, STOM2L1, AHR	0.0098	1.3e-9	1.1e-7
Module 15	CHEA_SMAD3_18955504_Chip-Seq_HaCt_Human	CHEA_SMAD3_18955504_Chip-Seq_HaCt_Human	1936	19	EGFR, TNFRSF1A, HNF1B, HNF1A, NDC103, SH3BP1, CAB1, RPL13, CDK3, HNF1V, GPR103D, FOSL1, ENAH1, MET, SH2D4A, SCHL1, TM6SF1, STOM2L1, AHR	0.0098	1.3e-9	1.1e-7
Module 15	Encode_SMARCC1_H4L4-S3_hg19	Encode_SMARCC1_H4L4-S3_hg19	2000	18	C22orf1, EGF1K, FIC3, FCH1, HNF1A, RPL13, MAP3K3, LAMA3, ROR2, ENAH1, MET, SCHL1, CDKN1, HNF1B, STOM2L1, GSDMC1, AHR, NCF1	0.0090	1.5e-8	4.3e-7
Module 15	CHEA_TP03_22573176_Chip-Seq_HFK3_Human	CHEA_TP03_22573176_Chip-Seq_HFK3_Human	4229	26	TNFRSF1A, HNF1B, CARD10, TNFAIP2, RPL13, UBE1, GAS5, MET, LGALS3BP1, SPK3, PRKDC1, CAB1, CAB1, EGF1K, NUCDC3, PPIA, MYO18A, RAB3C, HNF1B, ENAH1, CDKN1, STOM2L1, STOM2L2, STOM2L1, COL4, HNF1B, SP142L	0.0062	1.4e-8	8.0e-7
Module 15	CHEA_BRD4_25478310_Chip-Seq_HGPS_Human	CHEA_BRD4_25478310_Chip-Seq_HGPS_Human	2326	19	EGFR, SH3BP1, FIC3, GAS5, RPL13, LAMA3, ROR2, STOM2, MET, SH2D4A, SCHL1, TM6SF1, CDKN1, STOM2L1, STOM2L1	0.0082	2.5e-8	0.0000013

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Enrichments of Driver Perturbations in Regulatory Modules

➤ Perturbation-AMARETTO v1 for driver discovery using genetic perturbations in model systems

Genetic perturbations from Encode, ChEA, LINCS/CMAP

AMARETTO Report
Enrichments of Driver Perturbations in Regulatory Modules

CSV Excel PDF HTML Column visibility Show 50 entries Search:

Module	Gene Set Name	Gene Set Description	# Genes In Gene Set	# Genes In Overlap	Genes In Overlap	% Genes In overlap	P-value	FDR Q-value
Module 50	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_H729_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_H729_DN	300	17	RP121, RP117, RP141, RP152, RP153, RP154, RP155, RP156, RP157, RP158, RP159, RP160, RP161, RP162, RP163, RP164, RP165, RP166, RP167, RP168, RP169, RP170, RP171, RP172, RP173, RP174, RP175, RP176, RP177, RP178, RP179, RP180, RP181, RP182, RP183, RP184, RP185, RP186, RP187, RP188, RP189, RP190, RP191, RP192, RP193, RP194, RP195, RP196, RP197, RP198, RP199, RP200, RP201, RP202, RP203, RP204, RP205, RP206, RP207, RP208, RP209, RP210, RP211, RP212, RP213, RP214, RP215, RP216, RP217, RP218, RP219, RP220, RP221, RP222, RP223, RP224, RP225, RP226, RP227, RP228, RP229, RP230, RP231, RP232, RP233, RP234, RP235, RP236, RP237, RP238, RP239, RP240, RP241, RP242, RP243, RP244, RP245, RP246, RP247, RP248, RP249, RP250, RP251, RP252, RP253, RP254, RP255, RP256, RP257, RP258, RP259, RP260, RP261, RP262, RP263, RP264, RP265, RP266, RP267, RP268, RP269, RP270, RP271, RP272, RP273, RP274, RP275, RP276, RP277, RP278, RP279, RP280, RP281, RP282, RP283, RP284, RP285, RP286, RP287, RP288, RP289, RP290, RP291, RP292, RP293, RP294, RP295, RP296, RP297, RP298, RP299, RP300	0.057	2.5e-21	2.1e-17
Module 50	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	300	16	RP121, RP141, RP152, RP153, RP154, RP155, RP156, RP157, RP158, RP159, RP160, RP161, RP162, RP163, RP164, RP165, RP166, RP167, RP168, RP169, RP170, RP171, RP172, RP173, RP174, RP175, RP176, RP177, RP178, RP179, RP180, RP181, RP182, RP183, RP184, RP185, RP186, RP187, RP188, RP189, RP190, RP191, RP192, RP193, RP194, RP195, RP196, RP197, RP198, RP199, RP200, RP201, RP202, RP203, RP204, RP205, RP206, RP207, RP208, RP209, RP210, RP211, RP212, RP213, RP214, RP215, RP216, RP217, RP218, RP219, RP220, RP221, RP222, RP223, RP224, RP225, RP226, RP227, RP228, RP229, RP230, RP231, RP232, RP233, RP234, RP235, RP236, RP237, RP238, RP239, RP240, RP241, RP242, RP243, RP244, RP245, RP246, RP247, RP248, RP249, RP250, RP251, RP252, RP253, RP254, RP255, RP256, RP257, RP258, RP259, RP260, RP261, RP262, RP263, RP264, RP265, RP266, RP267, RP268, RP269, RP270, RP271, RP272, RP273, RP274, RP275, RP276, RP277, RP278, RP279, RP280, RP281, RP282, RP283, RP284, RP285, RP286, RP287, RP288, RP289, RP290, RP291, RP292, RP293, RP294, RP295, RP296, RP297, RP298, RP299, RP300	0.053	1.1e-19	7.0e-16
Module 140	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_A549_DN	300	13	UGT1H, G13E1, XPODE, NDU4B, CDMR1, FMO3, SP1AT, UHRF1, PEST, HNF1A, QSOX1, POLR2B, POLR2F	0.043	1.9e-16	6.4e-13
Module 15	Encode_RAD21_H4L-S3_hg19	Encode_RAD21_H4L-S3_hg19	2000	25	NEAT1, EGFR, SP14G1, TFP15P1A, MYO1E, ZNF384, SH3BP1, PPA, FCH1, ZSCAN1B, MYO18A, RP123, TCF12, P115G1, RFX1, GATC2, ROR1, S100A8, CUG1, LOC101931, S100A18, S100A16, AHR, SP153, TNSI3	0.013	7.5e-15	1.8e-12
Module 15	ChEA_MTF_21258399_Chip-Seq_MELANOMA_Human	ChEA_MTF_21258399_Chip-Seq_MELANOMA_Human	5578	36	BA3, NEAT1, TNSI3, CARD10, TNPAP2, LAM11, LIG1, GAS2, RP123, GATC2, MLI1, SH2D4A, LOC101931, ZNF12, NCF1, TFRP1, EGFR, MYO1E, NUCDC3, PPA, CAB1, MYO18A, RAB3C, LAMA, CBX3, H2AFV, HES6, TM6SF1, PPI1T3B, S100B, ATRX1, EPH2, SPIN3L, TNSI, AHRMGP18, HKDC1	0.0065	1.1e-12	2.3e-10
Module 50	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_MCFT7_DN	LINCSCMAP_GeneticPerturbation_EGFR_knockdown_96h_MCFT7_DN	300	12	RP121, RP152, RP154, RP155, RP156, RP157, RP158, RP159, RP160, RP161, RP162, RP163, RP164, RP165, RP166, RP167, RP168, RP169, RP170, RP171, RP172, RP173, RP174, RP175, RP176, RP177, RP178, RP179, RP180, RP181, RP182, RP183, RP184, RP185, RP186, RP187, RP188, RP189, RP190, RP191, RP192, RP193, RP194, RP195, RP196, RP197, RP198, RP199, RP200, RP201, RP202, RP203, RP204, RP205, RP206, RP207, RP208, RP209, RP210, RP211, RP212, RP213, RP214, RP215, RP216, RP217, RP218, RP219, RP220, RP221, RP222, RP223, RP224, RP225, RP226, RP227, RP228, RP229, RP230, RP231, RP232, RP233, RP234, RP235, RP236, RP237, RP238, RP239, RP240, RP241, RP242, RP243, RP244, RP245, RP246, RP247, RP248, RP249, RP250, RP251, RP252, RP253, RP254, RP255, RP256, RP257, RP258, RP259, RP260, RP261, RP262, RP263, RP264, RP265, RP266, RP267, RP268, RP269, RP270, RP271, RP272, RP273, RP274, RP275, RP276, RP277, RP278, RP279, RP280, RP281, RP282, RP283, RP284, RP285, RP286, RP287, RP288, RP289, RP290, RP291, RP292, RP293, RP294, RP295, RP296, RP297, RP298, RP299, RP300	0.040	1.7e-13	3.2e-10
Module 15	Encode_POLR2A_HapQ2_hg19	Encode_POLR2A_HapQ2_hg19	6264	36	SRR, LAM11, ZSCAN12, ZSCAN1B, GAS2, SCL3, LOC101931, C22orf247, ZNF384, RAB3C, H2AFV, GATC2, LNAH1, TM6SF1, S100A10, HES6, ATRX1, AHRMGP18, HES6, TTC37, NAF1K13, ZNF154, ZNF152, NCF1, HNF1A, CAB1, EGFR, S100B, MYO18A, LAMA, CBX3, CASP1, AHR, SP153	0.0057	3.4e-11	2.6e-9
Module 15	Encode_NR3C1_A549_hg19	Encode_NR3C1_A549_hg19	1855	19	NEAT1, EGFR, TFP15P1A, TNSI3, LAMA, SH3BP1, LAM11, SCL3, LAMA, CBX3, S100A8, MLI1, SGNL1, TNSI3, CDMR1, S100A10, GOSU1, NCF1, TNSI, HNF1A	0.010	6.5e-10	3.2e-8
Module 15	ChEA_SMAD2_18955504_Chip-Seq_HaCat_Human	ChEA_SMAD2_18955504_Chip-Seq_HaCat_Human	1936	19	EGFR, TFP15P1A, TNSI3, HNF1A, NDU4, NDC103, SH3BP1, CAB1, RP123, CBX3, H2AFV, GATC2, FMO3, UHRF1, MLI1, SH2D4A, SGNL1, TM6SF1, S100A10, AHR	0.0098	1.3e-9	1.1e-7
Module 15	ChEA_SMAD3_18955504_Chip-Seq_HaCat_Human	ChEA_SMAD3_18955504_Chip-Seq_HaCat_Human	1936	19	EGFR, TFP15P1A, TNSI3, HNF1A, NDU4, NDC103, SH3BP1, CAB1, RP123, CBX3, H2AFV, GATC2, FMO3, UHRF1, MLI1, SH2D4A, SGNL1, TM6SF1, S100A10, AHR	0.0098	1.3e-9	1.1e-7
Module 15	Encode_SMARCC1_H4L-S3_hg19	Encode_SMARCC1_H4L-S3_hg19	2000	18	C22orf247, EGFR, TTC37, TCF11, HNF1A, RP123, NAF1K13, LAMA, ROR1, SH3BP1, MLI1, SGNL1, CDMR1, PPI1T3B, S100A10, GOSU1, AHR, NCF1	0.0090	1.5e-8	4.3e-7
Module 15	ChEA_TP03_22573176_Chip-Seq_HFK3_Human	ChEA_TP03_22573176_Chip-Seq_HFK3_Human	4229	26	TFP15P1A, TNSI3, CARD10, TNPAP2, LAM11, LIG1, GAS2, MLI1, LOC101931, SH2D4A, JARID2, CAB1, EGFR, NUCDC3, PPA, MYO18A, RAB3C, HNF1A, NCF1, CDMR1, S100A8, S100A10, S100A16, AHR, NCF1, SP14G1	0.0062	1.4e-8	8.0e-7
Module 15	ChEA_BRD4_25478319_Chip-Seq_HGPS_Human	ChEA_BRD4_25478319_Chip-Seq_HGPS_Human	2326	19	EGFR, SH3BP1, TTC37, GAS2, RP123, LAMA, ROR1, S100A8, MLI1, SH2D4A, SGNL1, TM6SF1, CDMR1, S100A10, S100A11	0.0082	2.5e-8	0.0000013

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Enrichments of Chemical Perturbations in Regulatory Modules

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Module	Gene Set Name	Gene Set Description	# Genes In Gene Set	# Genes In Overlap	Genes In Overlap	% Genes in overlap	P-value	FDR q-value
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-MCF7_UP	LINCSCMAP_ChemicalPerturbation_IFNA-MCF7_UP	143	35	SP110, SAP1, SAP1, PSMB9, HSD17B, SARDU, USBL2L, ANCL8, GBP1, PLAC, PLAA, PLAS, PLAF, FANF12, FANF11A, PSMB2, PSMB1, F1D3, F1F2, F1F3, B1NDA3, F1F1, NMI, B1NDA3, F1F1, F1F1, CAS3, CASY1, F1M3R, F1M3S, UH3R3, F1M3Z1, F1M3Z2	0.24	1.2e-71	1.3e-65
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-SKBR3_UP	LINCSCMAP_ChemicalPerturbation_IFNA-SKBR3_UP	138	31	SP110, SAP1, SAP1, PSMB9, SARDU, USBL2L, PSMB2, PSMB1, F1D3, F1F2, F1F3, PLAS, PLAF, FANF12, PSMB1, F1D3, F1F2, F1F3, B1NDA3, F1F1, NMI, B1NDA3, F1F1, CAS3, CASY1, F1M3R, CUX1A, PSMB8, F1M3Z1, F1M3Z2	0.23	9.9e-62	5.7e-56
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-SKBR3_UP	LINCSCMAP_ChemicalPerturbation_IFNG-SKBR3_UP	135	30	SP110, SAP1, SAP1, USBL2L, PSMB10, ANCL8, GBP1, ANCL2, PLAC, PLAA, PLAS, PLAF, FANF12, PSMB2, PSMB1, F1D3, F1F2, F1F3, B1NDA3, F1F1, NMI, B1NDA3, F1F1, CAS3, CASY1, F1M3R, F1M3Z1, F1M3Z2	0.22	1.7e-59	6.6e-54
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-MCF7_UP	LINCSCMAP_ChemicalPerturbation_IFNG-MCF7_UP	132	27	SP110, SAP1, PSMB9, USBL2L, PSMB10, ANCL8, GBP1, ANCL2, PLAC, PLAA, PLAS, PLAF, FANF12, PSMB2, PSMB1, F1D3, F1F2, F1F3, B1NDA3, F1F1, NMI, B1NDA3, F1F1, CAS3, CASY1, F1M3R, F1M3Z1, F1M3Z2	0.20	3.1e-52	8.8e-47
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-MCF10A_UP	LINCSCMAP_ChemicalPerturbation_IFNG-MCF10A_UP	138	27	SP110, SAP1, PSMB9, SARDU, USBL2L, PSMB10, ANCL8, GBP1, PLAC, PLAA, PLAS, PLAF, FANF12, PSMB2, PSMB1, F1D3, F1F2, F1F3, B1NDA3, B1NDA1, NMI, B1NDA3, F1F1, CAS3, CASY1, PSMB8, F1M3Z1, F1M3Z2	0.20	1.2e-51	2.7e-46
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-BT20_UP	LINCSCMAP_ChemicalPerturbation_IFNA-BT20_UP	137	26	SP110, SAP1, PSMB9, SARDU, USBL2L, ANCL8, GBP1, PLAC, PLAA, PLAS, PLAF, FANF12, F1D3, F1F2, F1F3, B1NDA3, F1F1, NMI, B1NDA3, F1F1, CAS3, CASY1, PSMB8, UH3R3, F1M3Z1, F1M3Z2	0.19	2.6e-49	5.0e-44
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-BT20_UP	LINCSCMAP_ChemicalPerturbation_IFNG-BT20_UP	136	25	SP110, SAP1, PSMB9, USBL2L, PSMB10, ANCL8, GBP1, ANCL2, PLAC, PLAA, PLAS, PLAF, FANF12, F1D3, F1F2, F1F3, B1NDA3, B1NDA1, NMI, B1NDA3, F1F1, CAS3, CASY1, PSMB8, F1M3Z1, F1M3Z2	0.18	5.5e-47	9.1e-42
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-MDM2B21_UP	LINCSCMAP_ChemicalPerturbation_IFNG-MDM2B21_UP	131	23	SP110, SAP1, PSMB9, USBL2L, PSMB10, ANCL8, GBP1, ANCL2, PLAC, PLAA, PLAS, PLAF, FANF12, F1D3, F1F2, F1F3, B1NDA3, B1NDA1, NMI, B1NDA3, F1F1, CAS3, CASY1, PSMB8, F1M3Z1, F1M3Z2	0.18	1.2e-42	1.7e-37
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-MDM2B21_UP	LINCSCMAP_ChemicalPerturbation_IFNA-MDM2B21_UP	148	23	SP110, SAP1, PSMB9, SARDU, USBL2L, ANCL8, GBP1, ANCL2, PLAC, PLAA, PLAS, PLAF, FANF12, F1D3, F1F2, F1F3, F1F1, NMI, B1NDA3, CAS3, F1M3R, F1M3S, F1M3Z1, F1M3Z2	0.15	2.5e-41	3.2e-36
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-HS578T_UP	LINCSCMAP_ChemicalPerturbation_IFNA-HS578T_UP	149	22	SP110, SAP1, PSMB9, SARDU, USBL2L, ANCL8, GBP1, PLAC, PLAA, PLAS, PLAF, FANF12, F1D3, F1F2, F1F3, B1NDA3, F1F1, NMI, B1NDA3, F1F1, CAS3, CASY1, PSMB8, UH3R3, F1M3Z1, F1M3Z2	0.15	5.5e-39	6.4e-34
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-HS578T_UP	LINCSCMAP_ChemicalPerturbation_IFNG-HS578T_UP	138	21	SP110, SAP1, PSMB9, HSD17B, USBL2L, GBP1, PLAC, PLAA, PLAS, PLAF, FANF12, PSMB2, PSMB1, F1D3, F1F2, F1F3, NMI, B1NDA3, F1F1, CAS3, CASY1, PSMB8, F1M3Z1, F1M3Z2	0.15	1.7e-37	1.8e-32
Module 130	LINCSCMAP_ChemicalPerturbation_LIP006_PC3_24H-NVP-TA6884-10_DN	LINCSCMAP_ChemicalPerturbation_LIP006_PC3_24H-NVP-TA6884-10_DN	186	21	GN51, GUC1, E2F8, FANF2, CDCA3, BLM, FOXM1, FANF1, RCT1, ESR1, CDCA, MCM7, MCM2, MCM3, LMNB1, HMG2, RAD21A1, SNAI2, FNCT1, F1M3L5S, F1C1U1	0.11	1.8e-31	1.7e-26
Module 130	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-palboodib-10_DN	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-palboodib-10_DN	215	21	F1M3M94A, UNAZ, E2F8, CDCA3, TMPO, RCT1, RAD21A1, F1M3L5S, GN51, FANF2, FNDA1, BLM, FOXM1, ESR1, MCM7, MCM2, MCM3, LMNB1, HMG2, SNAI2, FNCT1	0.098	4.3e-30	3.8e-25
Module 130	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-NVP-BE2235-1.11_DN	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-NVP-BE2235-1.11_DN	199	20	F1M3M94A, UNAZ, E2F8, CDCA3, TMPO, RAD21A1, FANF1, F1M3L5S, UNZ, GN51, FANF2, FNDA1, BLM, FOXM1, ESR1, MCM7, LMNB1, HMG2, SNAI2, FNCT1	0.10	6.2e-29	5.1e-24
Module 46	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-palboodib-10_DN	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-palboodib-10_DN	215	20	CDCA3, RFX2B, RAD21A1, E2F8, CDCA3, F1M3A, SKA1, RFX14, RFX1, CDCA3, MCM7, CDCA3, RFX4A, USP1, HMG2, HMG2, FNCT1, TTK, SUG1	0.093	1.4e-28	1.1e-23
Module 130	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dox91b-10_DN	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dox91b-10_DN	215	20	UNAZ, E2F8, CDCA3, TMPO, RAD21A1, F1M3L5S, GN51, FANF2, FNDA1, BLM, FOXM1, ESR1, MCM7, MCM2, MCM3, LMNB1, HMG2, SNAI2, FNCT1, PCLE	0.093	3.1e-28	2.2e-23
Module 130	LINCSCMAP_ChemicalPerturbation_LIP006_HS578T_24H-palboodib-0.04_DN	LINCSCMAP_ChemicalPerturbation_LIP006_HS578T_24H-palboodib-0.04_DN	108	17	F1M3M94A, GN51, FANF2, NRG2, CDCA3, FOXM1, FANF1, RCT1, ESR1, MCM2, MCM3, LMNB1, HMG2, RAD21A1, FNCT1, FANF1, F1M3L5S	0.16	3.6e-28	2.4e-23
Module 46	LINCSCMAP_ChemicalPerturbation_LIP006_BT20_24H-PHA-793887-3.33_DN	LINCSCMAP_ChemicalPerturbation_LIP006_BT20_24H-PHA-793887-3.33_DN	184	19	CDCA3, RFX2B, RAD21A1, E2F8, FNDA1, ESR1, HMG2, E2F8, CDCA3, F1M3A, RFX14, RFX1, RFX2, CDCA3, MCM7, F1A, CDCA3, SUG1	0.10	4.7e-28	3.0e-23
Module 46	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dox91b-10_DN	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dox91b-10_DN	199	19	F1M3M94A, GN51, UNAZ, E2F8, FANF2, CDCA3, BLM, FOXM1, TMPO, ESR1, MCM7, MCM2, MCM3	0.11	5.7e-28	5.2e-23

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Enrichments of Chemical Perturbations in Regulatory Modules

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Module	Gene Set Name	Gene Set Description	# Genes In Gene Set	# Genes In Overlap	Genes In Overlap	% Genes In Overlap	P-value	FDR Q-value
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-MCF7_UP	LINCSCMAP_ChemicalPerturbation_IFNA-MCF7_UP	143	35	SP110, SAP1, SAP1, PSMB9, HSD17C, SANDU, UBE2L6, APOB, GBP1, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, FAM171A, PSMB2, PSMT1, FOS, IFI2, IFI3, BTNGA2, PPI1, NMI, BTNGA3, TAPB1, PP1, CAS3, CASY1, FHM3B, PSMB5, UH43B, FHMZ1, FHMZ2	0.24	1.2e-71	1.3e-65
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-SKBR3_UP	LINCSCMAP_ChemicalPerturbation_IFNA-SKBR3_UP	138	31	SP110, SAP1, SAP1, PSMB9, SANDU, UBE2L6, PSMB2, PSMT1, FOS, IFI2, IFI3, BTNGA2, PPI1, NMI, BTNGA3, TAPB1, PP1, CAS3, CASY1, FHM3B, CUX1A, PSMB5, FHMZ1, FHMZ2	0.23	9.9e-62	5.7e-56
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-SKBR3_UP	LINCSCMAP_ChemicalPerturbation_IFNG-SKBR3_UP	135	30	SP110, SAP1, SAP1, UBE2L6, PSMB10, APOB, GBP1, APOB, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, PSMB2, PSMT1, FOS, IFI2, IFI3, BTNGA2, PPI1, NMI, BTNGA3, TAPB1, PP1, CAS3, CASY1, PSMB9, FHMZ1, FHMZ2	0.22	1.7e-59	6.6e-54
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-MCF7_UP	LINCSCMAP_ChemicalPerturbation_IFNG-MCF7_UP	132	27	SP110, SAP1, PSMB9, UBE2L6, PSMT10, APOB, GBP1, APOB, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, PSMT1, FOS, IFI2, IFI3, BTNGA2, PPI1, NMI, BTNGA3, TAPB1, PP1, CAS3, CASY1, FHMZ2	0.20	3.1e-52	8.9e-47
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-MCF10A_UP	LINCSCMAP_ChemicalPerturbation_IFNG-MCF10A_UP	138	27	SP110, SAP1, PSMB9, SANDU, UBE2L6, PSMT10, APOB, GBP1, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, PSMB2, PSMT1, FOS, IFI2, IFI3, BTNGA2, BTNGA1, NMI, BTNGA3, PPI1, CAS3, CASY1, PSMB9, FHMZ2	0.20	1.2e-51	2.7e-46
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-BT20_UP	LINCSCMAP_ChemicalPerturbation_IFNA-BT20_UP	137	26	SP110, SAP1, PSMB9, SANDU, UBE2L6, APOB, GBP1, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, FOS, IFI2, IFI3, BTNGA2, PPI1, NMI, BTNGA3, PPI1, CAS3, CASY1, PSMB9, UH43B, FHMZ1, FHMZ2	0.19	2.6e-49	5.0e-44
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-BT20_UP	LINCSCMAP_ChemicalPerturbation_IFNG-BT20_UP	136	25	SP110, SAP1, SAP1, PSMB9, UBE2L6, PSMT10, APOB, GBP1, APOB, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, FOS, IFI2, IFI3, BTNGA2, BTNGA1, NMI, BTNGA3, PPI1, CAS3, CASY1, PSMB9, FHMZ2	0.18	5.5e-47	9.1e-42
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-MDA-MB231_UP	LINCSCMAP_ChemicalPerturbation_IFNG-MDA-MB231_UP	131	23	SP110, SAP1, PSMB9, UBE2L6, PSMT10, APOB, GBP1, APOB, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, FOS, IFI2, IFI3, BTNGA2, PPI1, NMI, BTNGA3, TAPB1, PP1, CAS3, CASY1, PSMB9, FHMZ2	0.18	1.2e-42	1.7e-37
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-MDA-MB231_UP	LINCSCMAP_ChemicalPerturbation_IFNA-MDA-MB231_UP	148	23	SP110, SAP1, PSMB9, SANDU, UBE2L6, APOB, GBP1, APOB, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, FOS, IFI2, IFI3, PPI1, NMI, BTNGA3, CAS3, FHM3B, PSMB9, FHMZ1, FHMZ2	0.15	2.5e-41	3.2e-36
Module 103	LINCSCMAP_ChemicalPerturbation_IFNA-HS578T_UP	LINCSCMAP_ChemicalPerturbation_IFNA-HS578T_UP	149	22	SP110, SAP1, PSMB9, SANDU, UBE2L6, APOB, GBP1, HLAC, PLAA, PLAA, HLAC, PLAF, PRN12, FOS, IFI2, IFI3, PPI1, NMI, BTNGA3, CAS3, FHM3B, UH43B, FHMZ1, FHMZ2	0.15	5.5e-39	6.4e-34
Module 103	LINCSCMAP_ChemicalPerturbation_IFNG-HS578T_UP	LINCSCMAP_ChemicalPerturbation_IFNG-HS578T_UP	138	21	SP110, SAP1, SAP1, PSMB9, HSD17C, UBE2L6, GBP1, HLAC, PLAA, PLAA, PLAA, HLAC, PLAF, PRN12, PSMB2, PSMT1, FOS, IFI2, IFI3, NMI, BTNGA3, PPI1, CAS3, CASY1, PSMB9, FHMZ2	0.15	1.7e-37	1.8e-32
Module 130	LINCSCMAP_ChemicalPerturbation_LIP006_PC3_24H-NVP-T6684-10_DN	LINCSCMAP_ChemicalPerturbation_LIP006_PC3_24H-NVP-T6684-10_DN	186	21	GN51, QSOX1, E2F8, FANCD1, CDC43, BLM, FOXM1, TRIP1, RCT1, ESP1, CDKN1, MCMY, MCM2, MCM3, LMNB1, HMG2, RAD21, SNAI2, FNCT1, FIML1, FOL11	0.11	1.8e-31	1.7e-26
Module 130	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-pab00db-10_DN	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-pab00db-10_DN	215	21	FHM194A, UNAZ, E2F8, CDC43, TMPO, RCT1, RAD21, FIML1, FIML1, FIML1, GINS1, FANCD1, HDMY, BLM, FOXM1, MCMY, MCM2, MCM3, LMNB1, HMG2, SNAI2, FNCT1	0.098	4.3e-30	3.8e-25
Module 130	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-NVP-BE2235-1_11_DN	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-NVP-BE2235-1_11_DN	199	20	FHM194A, UNAZ, E2F8, CDC43, TMPO, RAD21, FAPB1, FIML1, FIML1, GINS1, FANCD1, HDMY, BLM, FOXM1, MCMY, MCM2, LMNB1, HMG2, SNAI2, FNCT1	0.10	6.2e-29	5.1e-24
Module 46	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-pab00db-10_DN	LINCSCMAP_ChemicalPerturbation_LIP006_HME1_24H-pab00db-10_DN	215	20	CDC32, NIF2A, RAG3A, IFI2, CDC43, FHM3A, SKA1, RP14, TKT1, C1, SPC25, MRFB, CENPA, KFNA, USP1, HMG2, HMG2, FNCT1, TTK, BUB1	0.093	1.4e-28	1.1e-23
Module 130	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dov9nb-10_DN	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dov9nb-10_DN	215	20	UNAZ, E2F8, CDC43, TMPO, RAD21, FIML1, FIML1, GINS1, FANCD1, HDMY, BLM, FOXM1, MCMY, MCM2, MCM3, LMNB1, HMG2, SNAI2, FNCT1, FOL11, FOL11	0.093	3.1e-28	2.2e-23
Module 130	LINCSCMAP_ChemicalPerturbation_LIP006_H578T_24H-pab00db-0.04_DN	LINCSCMAP_ChemicalPerturbation_LIP006_H578T_24H-pab00db-0.04_DN	108	17	FHM194A, GINS1, FANCD1, NRG2, CDC43, FOXM1, MCMY, RCT1, ESP1, MCM2, MCM3, LMNB1, HMG2, RAD21, FNCT1, FANCD1, FIML1	0.16	3.6e-28	2.4e-23
Module 46	LINCSCMAP_ChemicalPerturbation_LIP006_BT20_24H-PHA-793887-3_33_DN	LINCSCMAP_ChemicalPerturbation_LIP006_BT20_24H-PHA-793887-3_33_DN	184	19	CDC32, NIF2A, RAG3A, RAG3A, USP1, HMG2, IFI2, CDC43, FHM3A, SKA1, RP14, TKT1, C1, SPC25, MRFB, CENPA, KFNA, USP1, HMG2, HMG2, FNCT1, TTK, BUB1	0.10	4.7e-28	3.0e-23
Module 46	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dov9nb-10_DN	LINCSCMAP_ChemicalPerturbation_LIP005_A549_24H-dov9nb-10_DN	186	18	FHM194A, GINS1, UNAZ, E2F8, FANCD1, CDC43, BLM, FOXM1, TMPO, ESP1, MCMY, MCM2, MCM3	0.11	5.7e-28	5.2e-23

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Assignments of Genes to Regulatory Modules

CSV Excel PDF Print Column visibility Show 100 entries Search: MYC

Gene Module Gene Type

MYC All All

Gene	Module	Gene Type
MYC	Module 112	Target
MYC	Module 112	Driver
MYCBP	Module 7	Target
MYCBP2	Module 30	Target
MYCL1	Module 70	Target
MYCN	Module 35	Target
MYCT1	Module 48	Target

Showing 1 to 7 of 7 entries (filtered from 12,183 total entries) Previous 1 Next

Search for module(s) regulated by MYC

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Assignments of Genes to Regulatory Modules

CSV Excel PDF Print Column visibility Show 100 entries Search: MYC

Gene Module Gene Type

MYC All All

MYC	Module 112	Target
MYC	Module 112	Driver
MYCBP	Module 7	Target
MYCBP2	Module 30	Target
MYCL1	Module 70	Target
MYCN	Module 35	Target
MYCT1	Module 48	Target

Showing 1 to 7 of 7 entries (filtered from 12,183 total entries) Previous 1 Next

Search for module(s) regulated by MYC

⇒ Module 112 is regulated by MYC

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Assignments of Genes to Regulatory Modules

Gene	Module	Gene Type
MYC	Module 112	Target
MYC	Module 112	Driver
MYCBP	Module 7	Target
MYCBP2	Module 30	Target
MYCL1	Module 70	Target
MYCN	Module 35	Target
MYCT1	Module 48	Target

Showing 1 to 7 of 7 entries (filtered from 12,183 total entries) Previous 1 Next

Search for module(s) regulated by MYC

⇒ Module 112 is regulated by MYC

Link to GeneCards description of MYC

Link to Module 112 report page

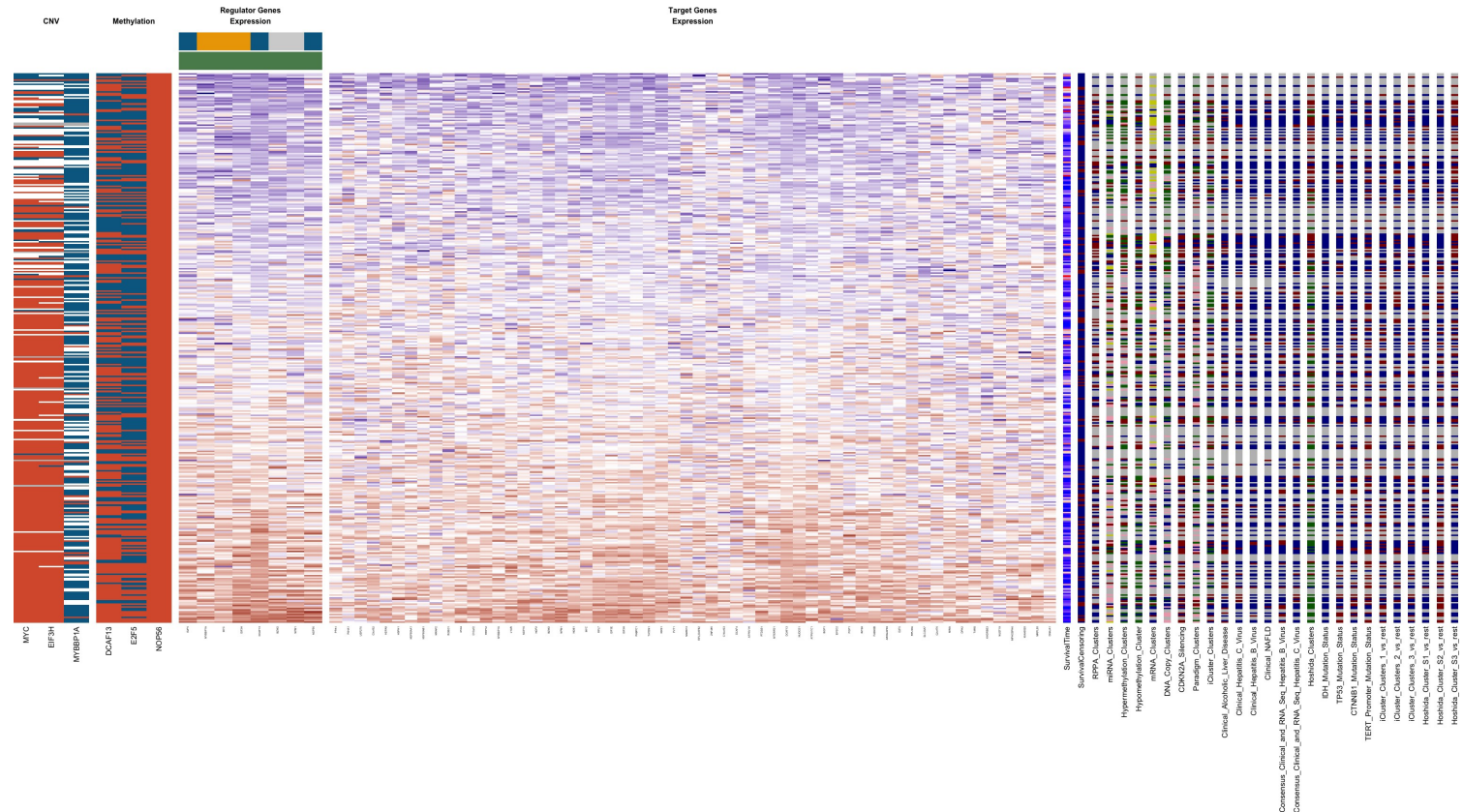
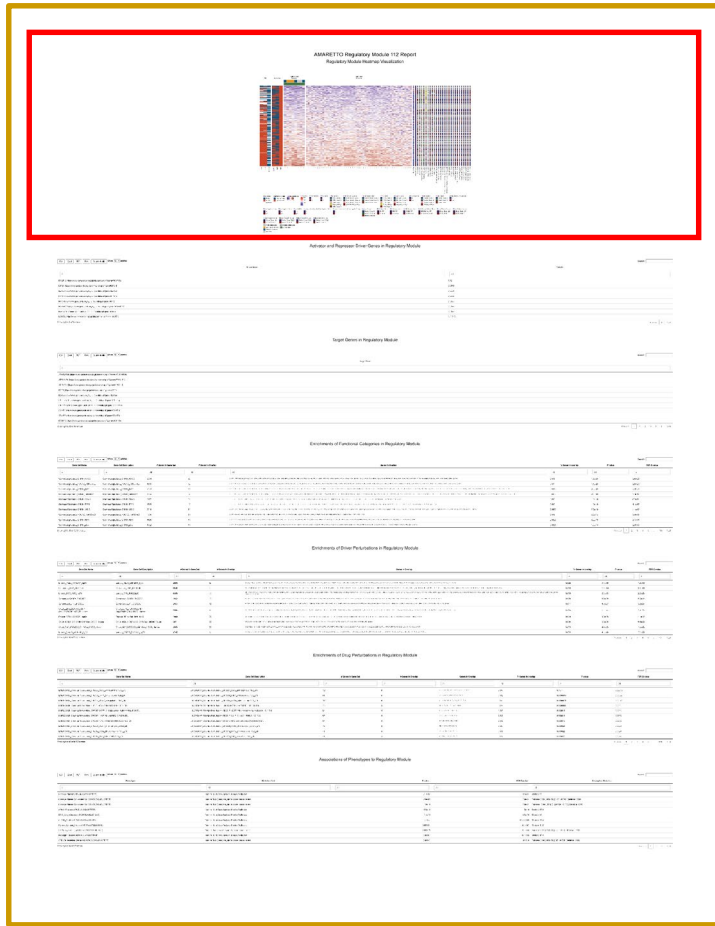
GeneCards

Detailed report of MYC-driven Module 112

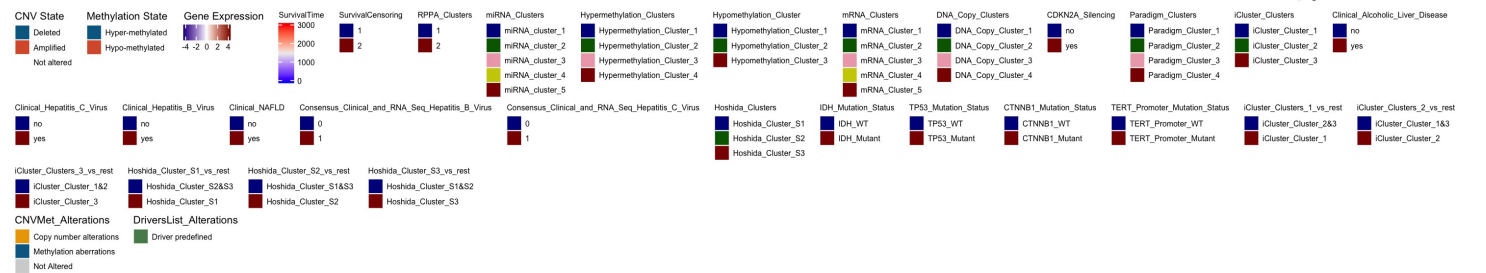
[http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO Liver 6DS/TCGA LIHC/AMARETTOhtmls/modules/module112.html](http://portals.broadinstitute.org/pochetlab/demo/cAMARETTO_Liver_6DS/TCGA_LIHC/AMARETTOhtmls/modules/module112.html)

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AMARETTO Regulatory Module 112 Report Regulatory Module Heatmap Visualization

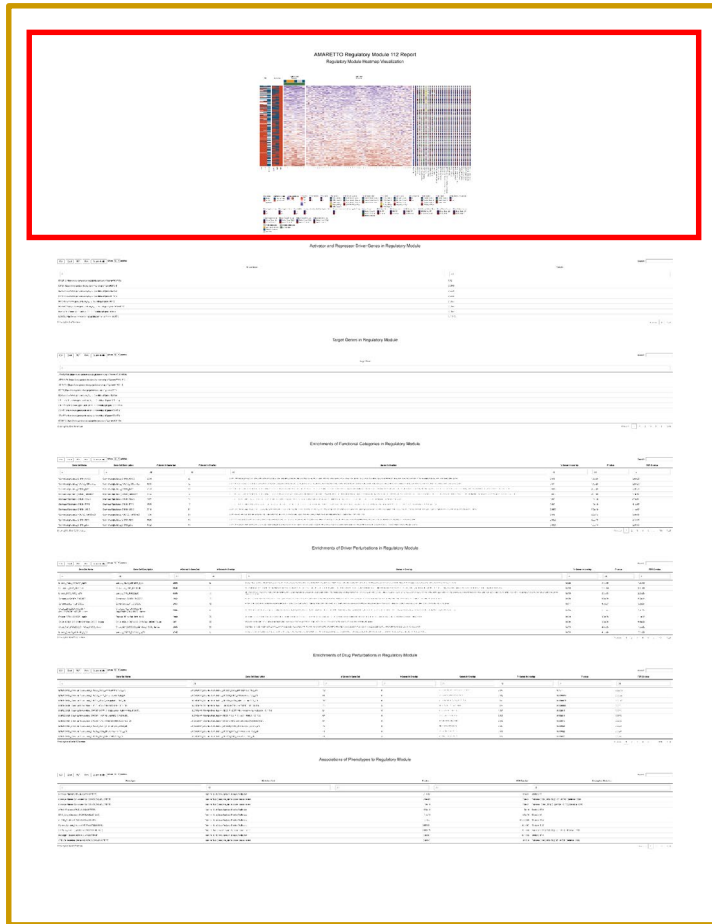


Detailed report of MYC-driven Module 112: heatmap visualization

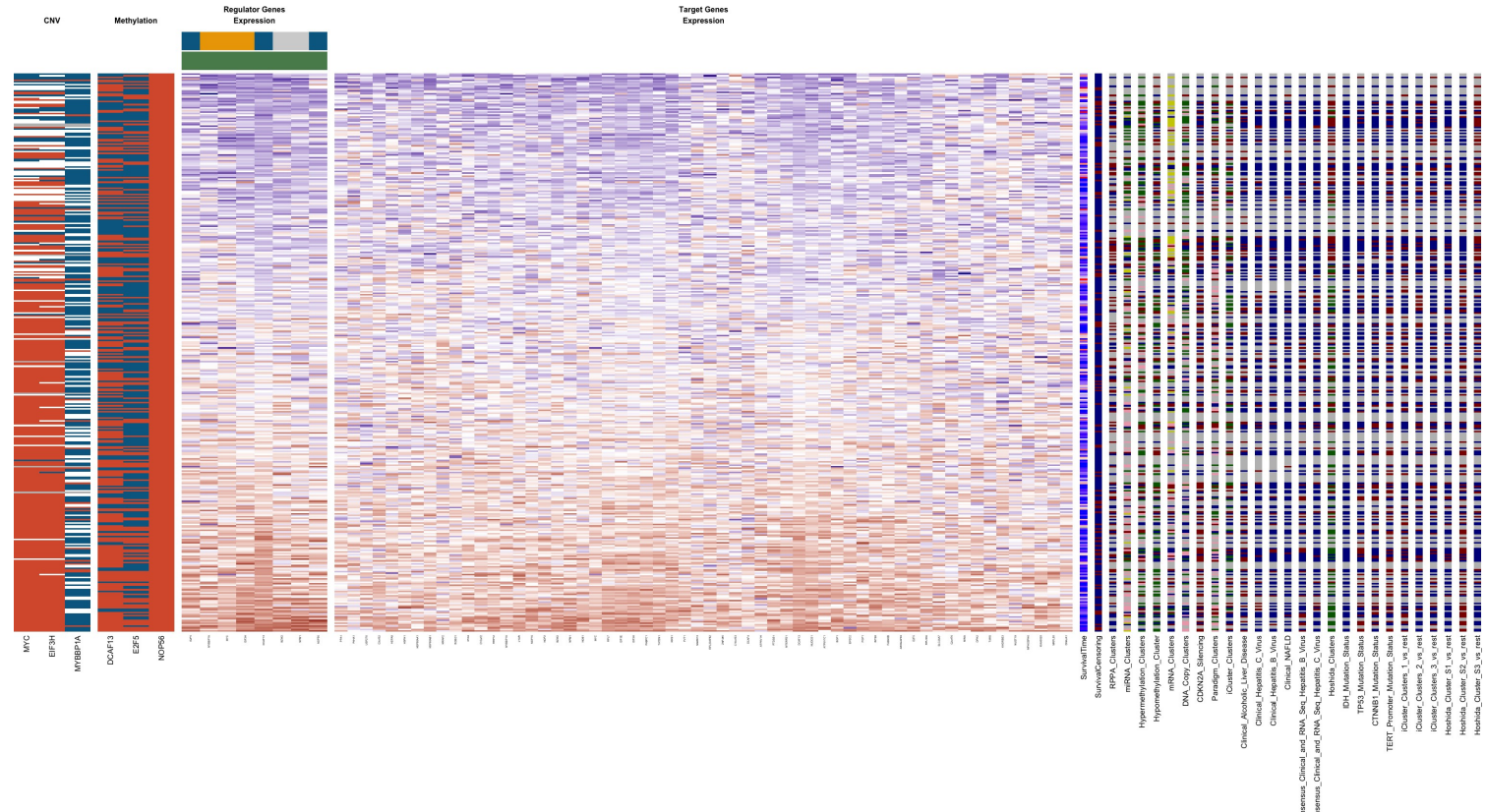


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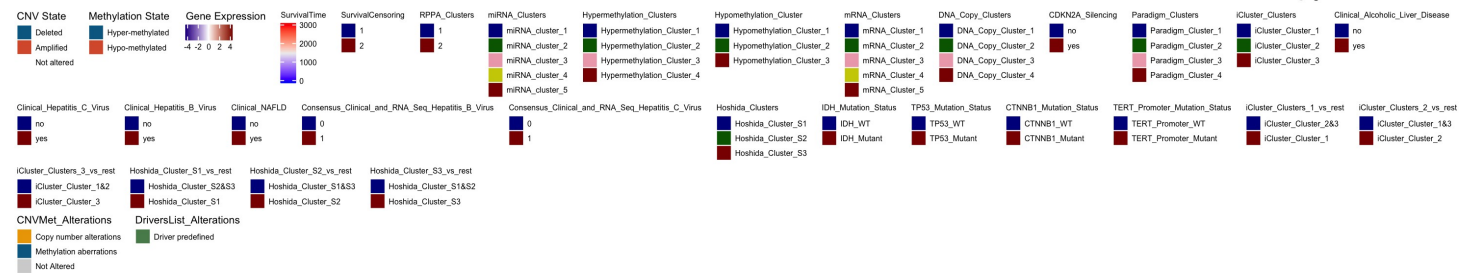
AMARETTO Regulatory Module 112 Report Regulatory Module Heatmap Visualization



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Tumor
Samples

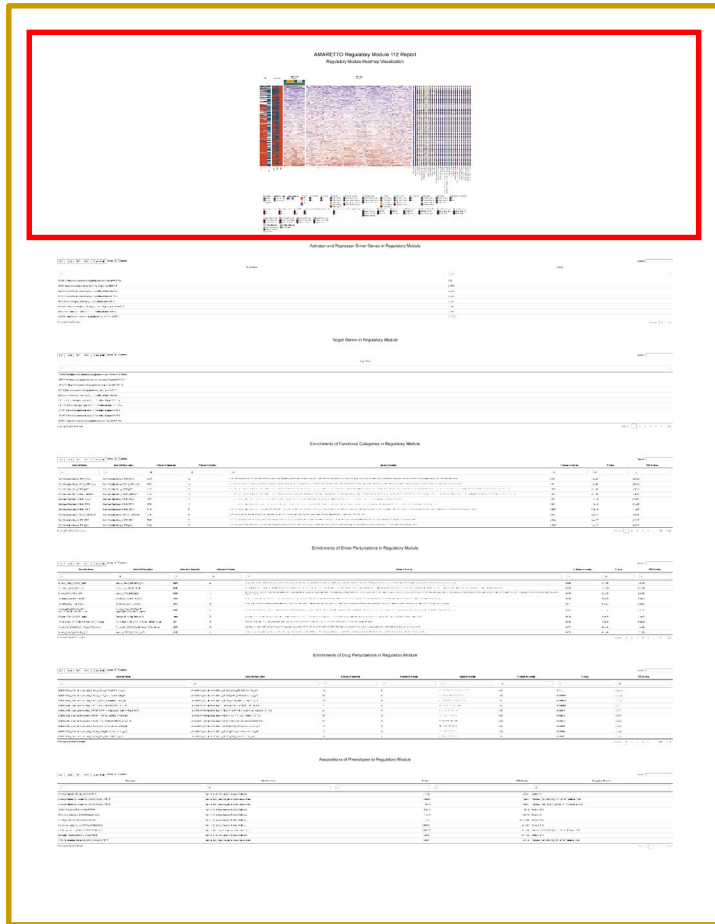


Detailed report of MYC-driven Module 112: heatmap visualization

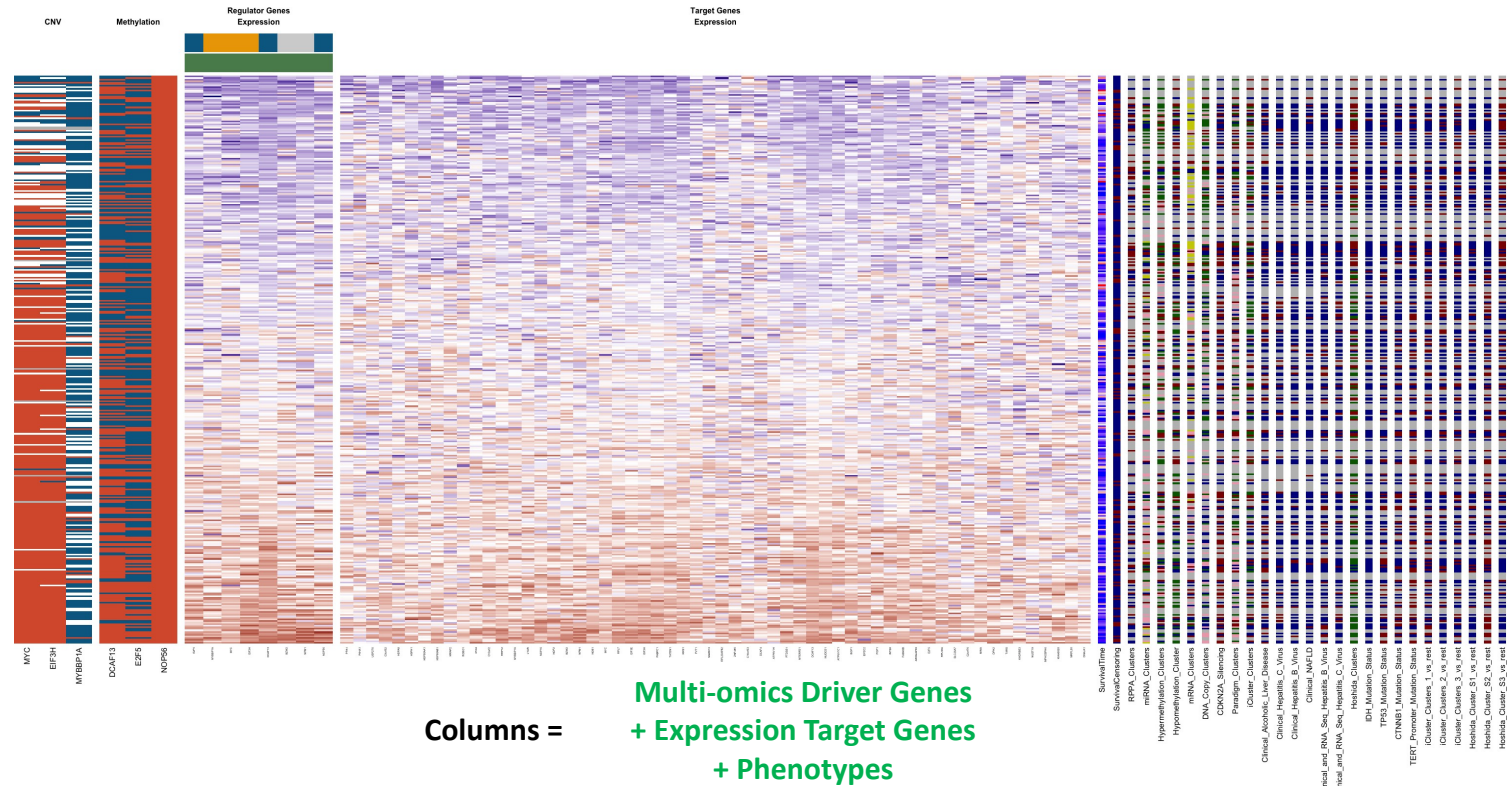


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AMARETTO Regulatory Module 112 Report Regulatory Module Heatmap Visualization

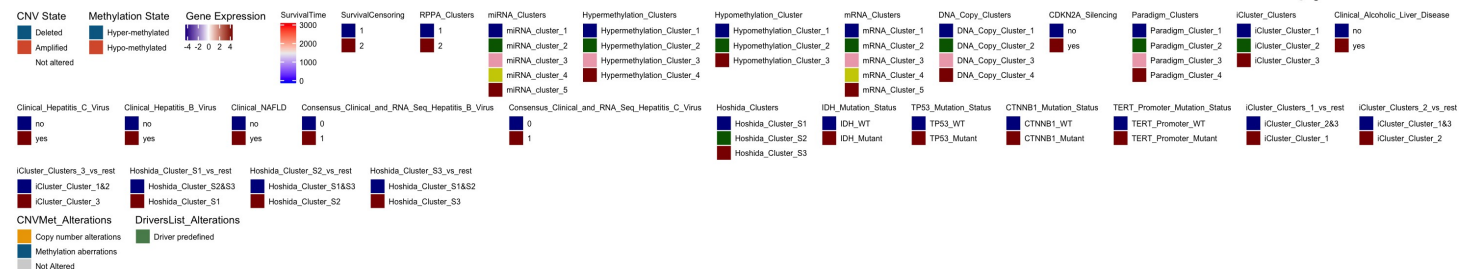


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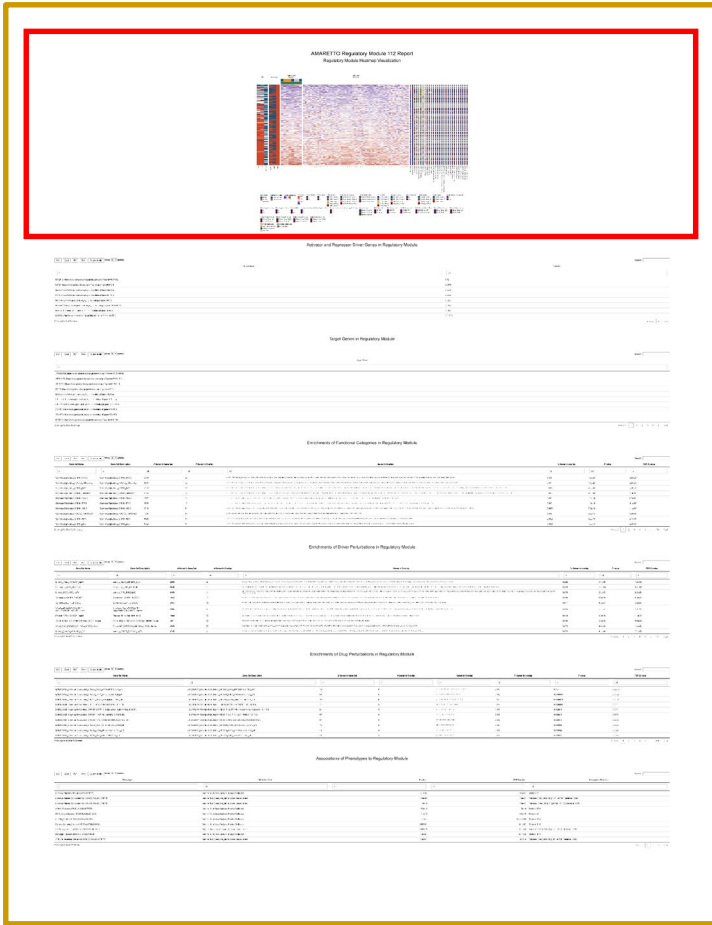
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+ Expression Target Genes
+ Phenotypes

Detailed report of MYC-driven
Module 112:
heatmap visualization

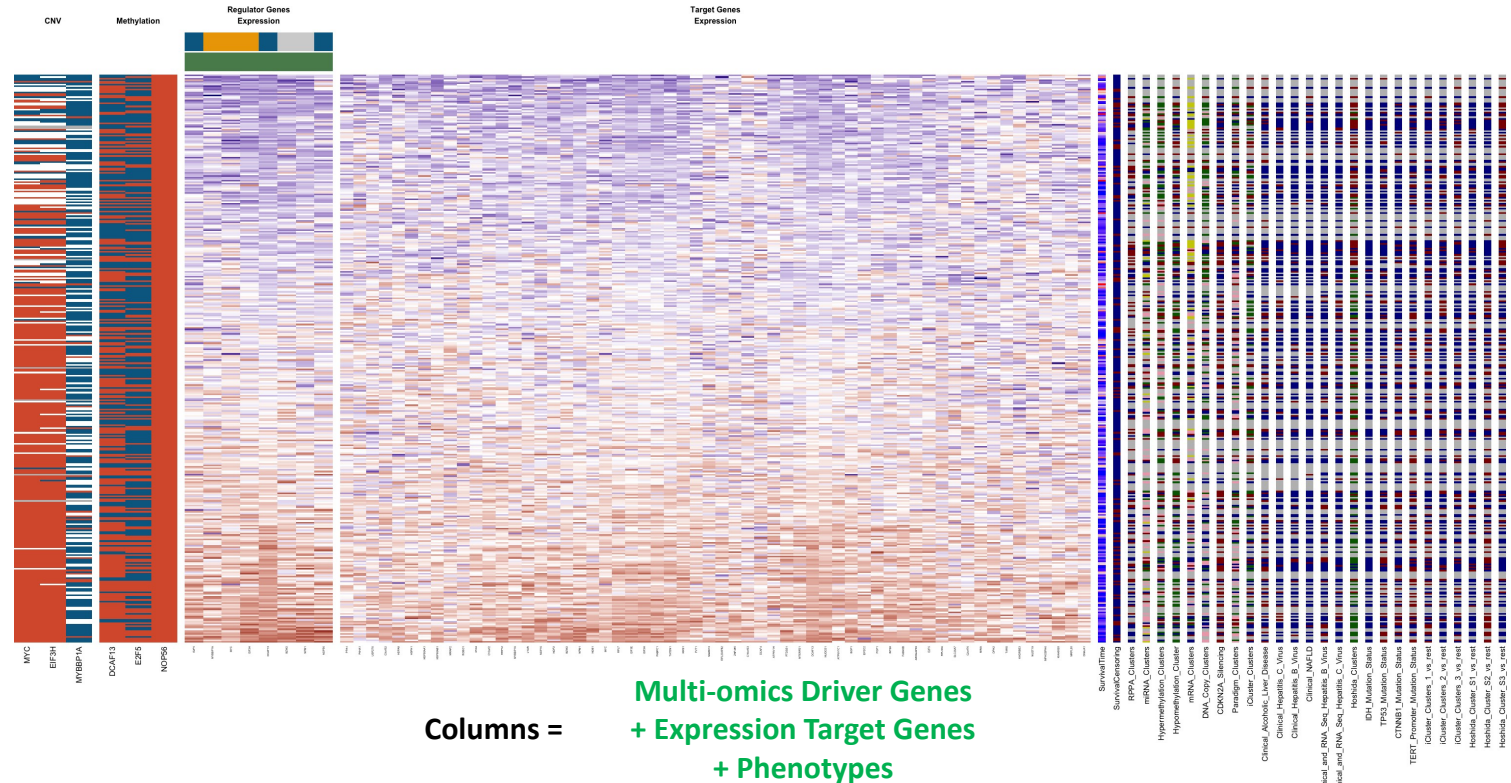


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AMARETTO Regulatory Module 112 Report Regulatory Module Heatmap Visualization

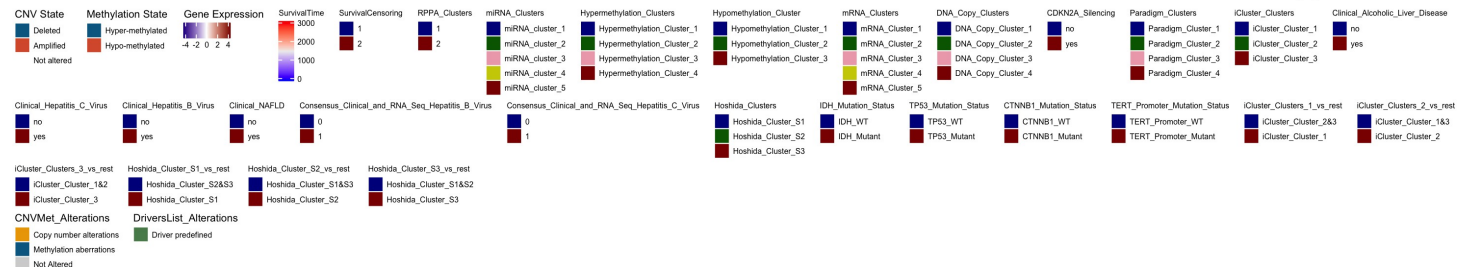


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Tumor
Samples



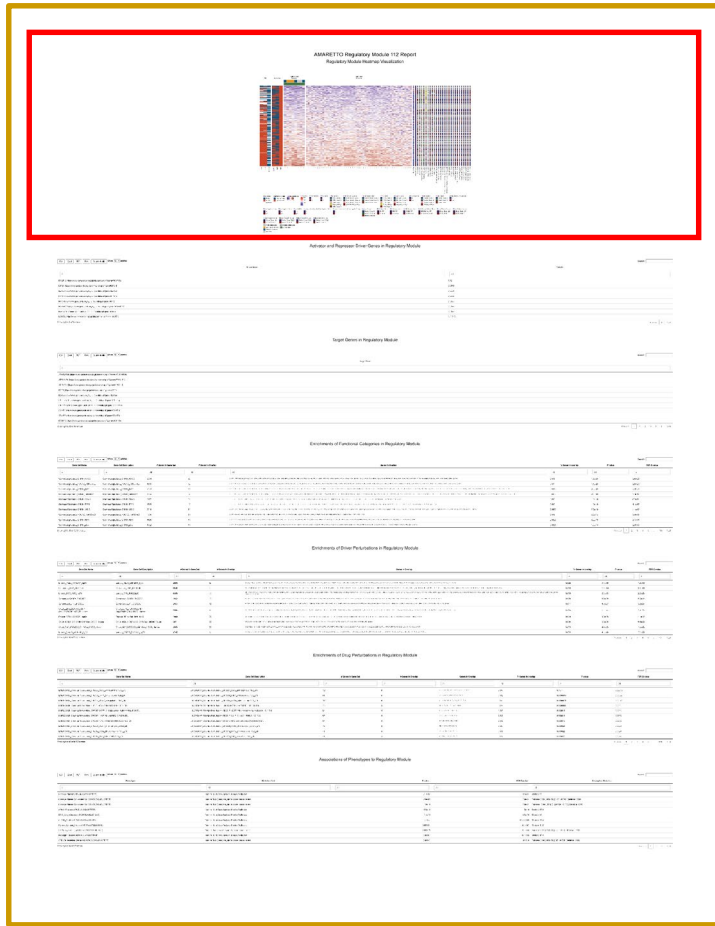
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Multi-omics Driver Genes
+ Expression Target Genes
+ Phenotypes

Detailed report of MYC-driven Module 112: heatmap visualization

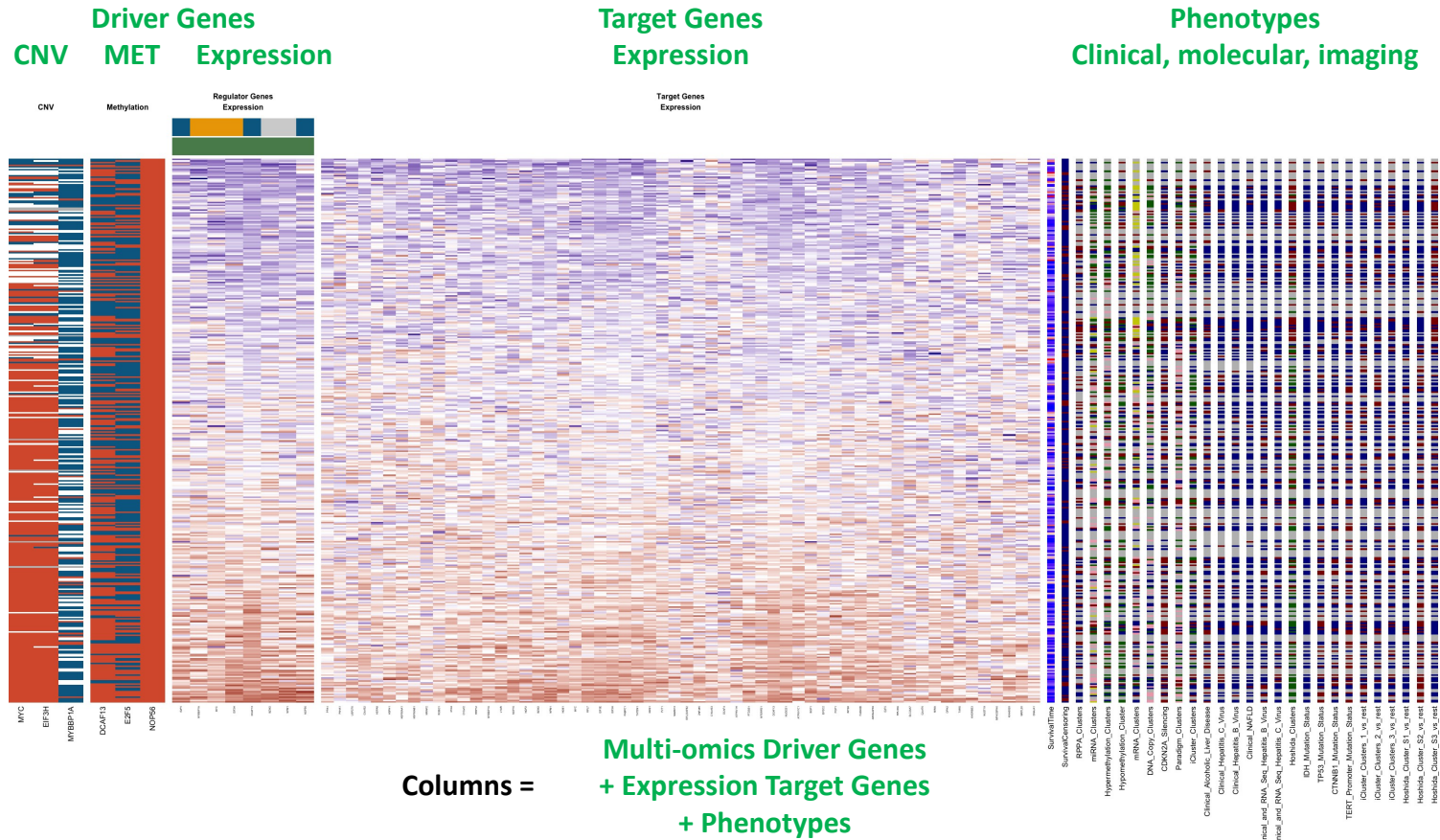


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AMARETTO Regulatory Module 112 Report Regulatory Module Heatmap Visualization

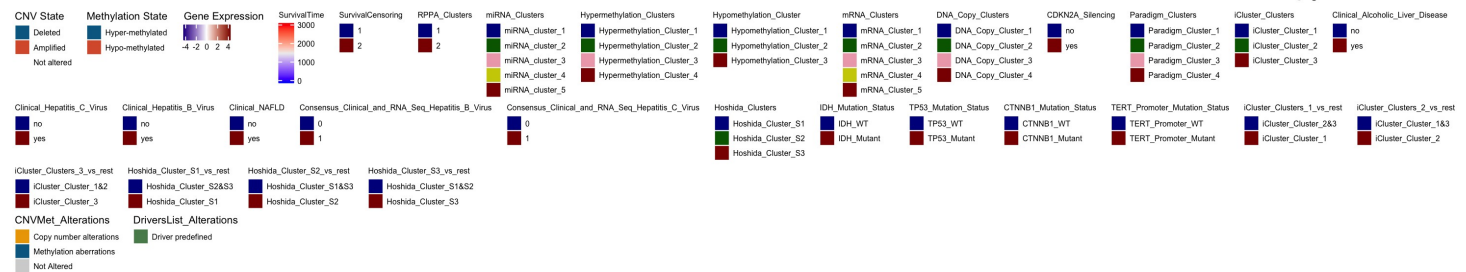


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Tumor
Samples



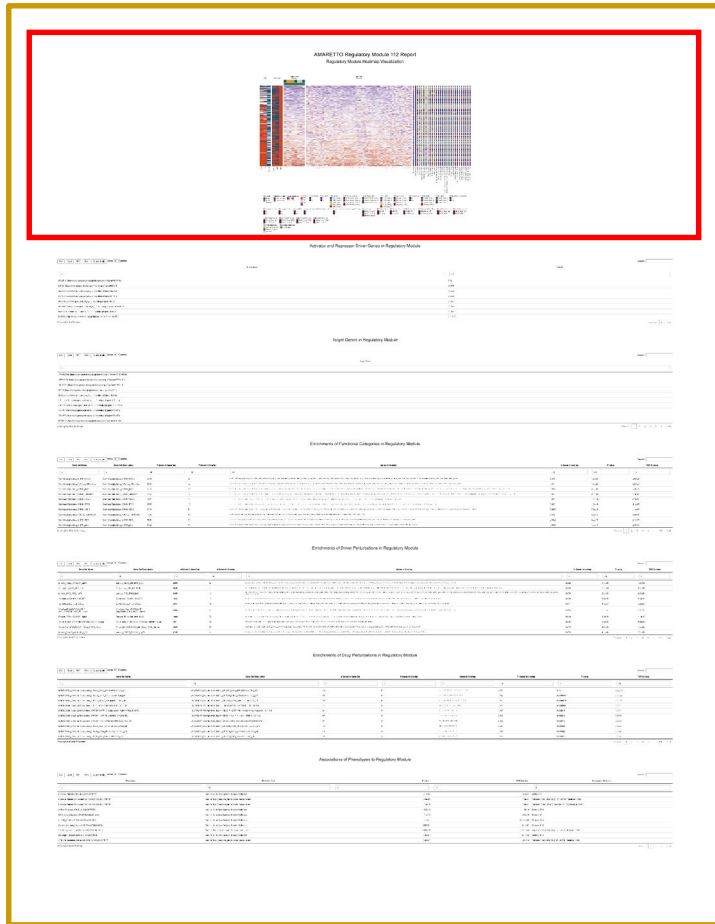
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Multi-omics Driver Genes
+ Expression Target Genes
+ Phenotypes

Detailed report of MYC-driven
Module 112:
heatmap visualization

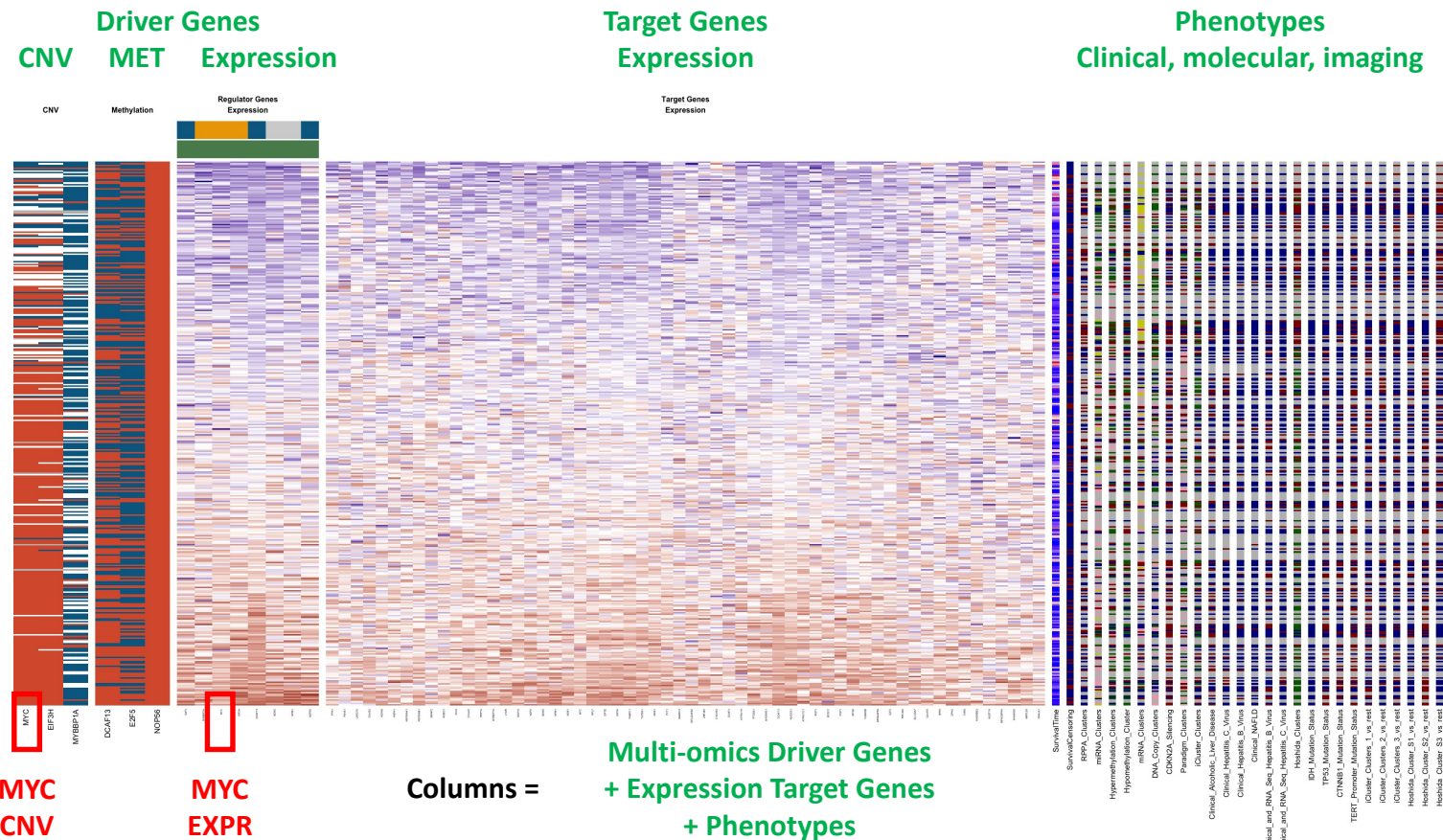


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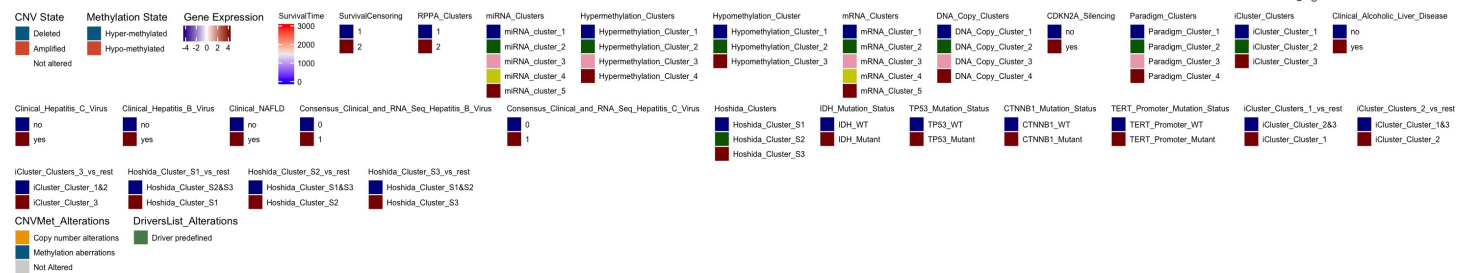
AMARETTO Regulatory Module 112 Report Regulatory Module Heatmap Visualization



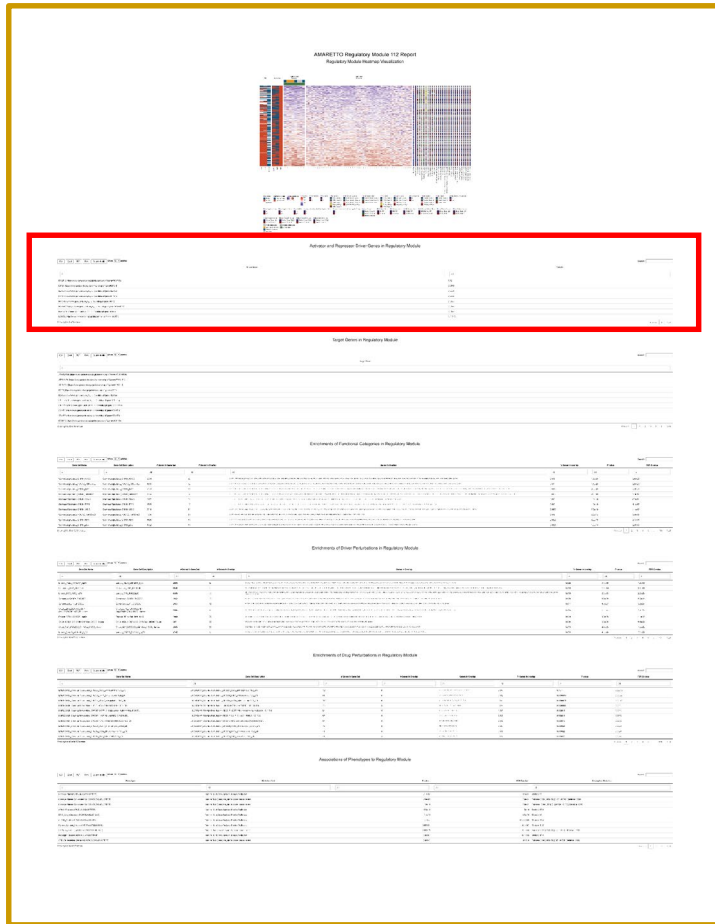
Rows =
Patient
Tumor
Samples



Detailed report of MYC-driven
Module 112:
heatmap visualization



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Detailed report of MYC-driven
Module 112:
activator and repressor
driver genes

Activator and Repressor Driver Genes in Regulatory Module

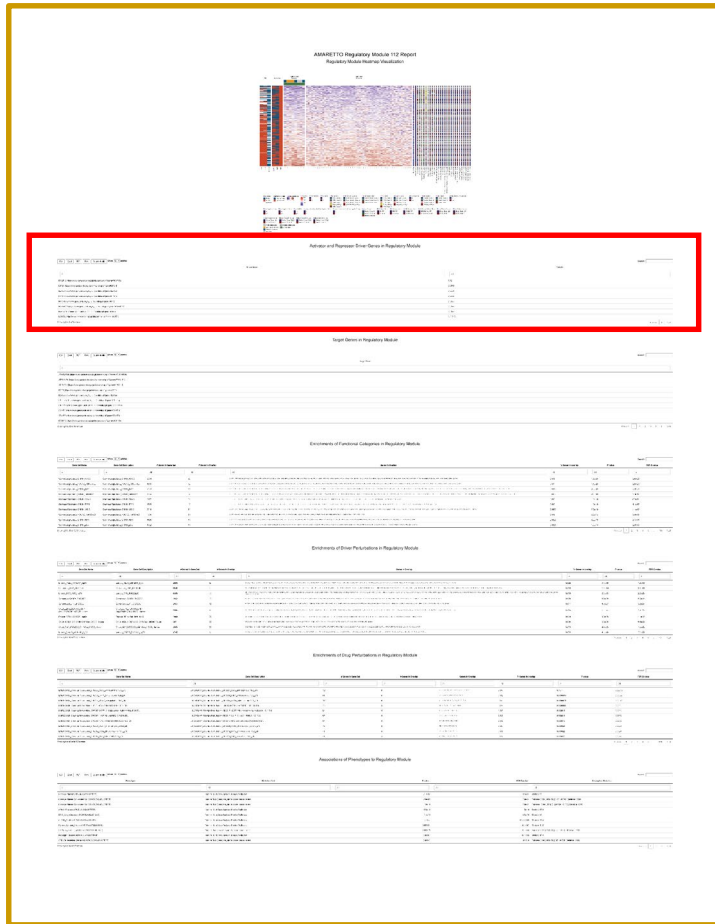
[CSV](#)
[Excel](#)
[PDF](#)
[Print](#)
[Column visibility](#)
 Show entries
 Search:

Driver Gene	Weight
All	All
DCAF13	0.29
EIF3H	0.0348
BZW2	0.0206
NPM1	0.0205
MYC	0.0179
MYBBP1A	0.0148
E2F5	0.0129
NOP56	0.00215

Showing 1 to 8 of 8 entries

Previous Next

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Detailed report of MYC-driven
Module 112:
activator and repressor
driver genes

Activator and Repressor Driver Genes in Regulatory Module

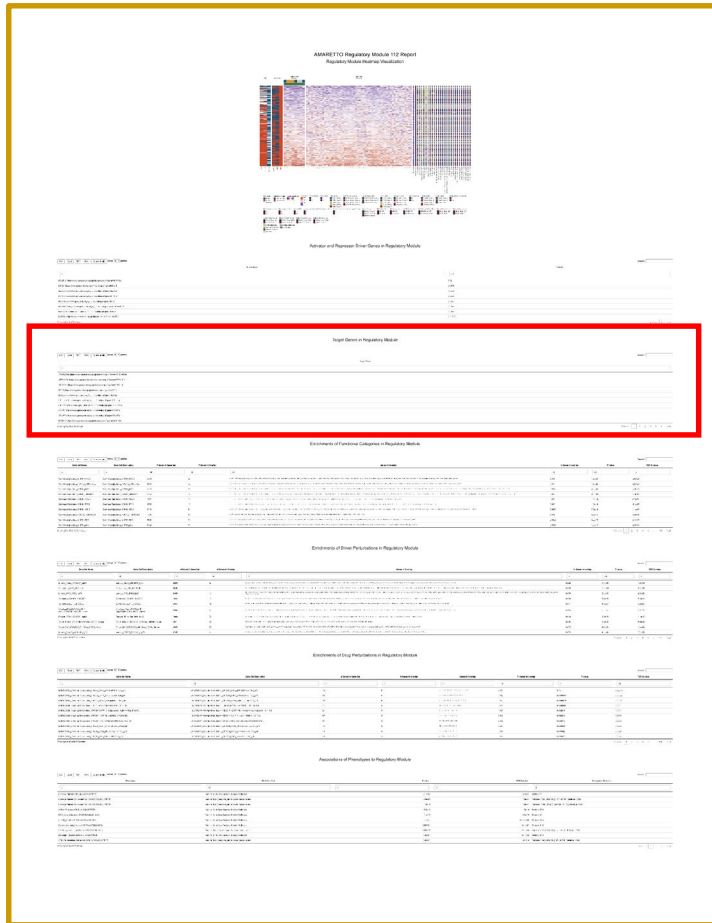
[CSV](#)
[Excel](#)
[PDF](#)
[Print](#)
[Column visibility](#)
 Show entries
 Search:

Driver Gene	Weight
All	All
DCAF13	0.29
EIF3H	0.0348
BZW2	0.0206
NPM1	0.0205
MYC	0.0179
MYBBP1A	0.0148
E2F5	0.0129
NOP56	0.00215

Showing 1 to 8 of 8 entries Previous Next

Activator Driver Genes (weight > 0)
Repressor Driver Genes (weight < 0)

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Target Genes in Regulatory Module

CSV Excel PDF Print Column visibility Show 10 entries Search:

Target Gene

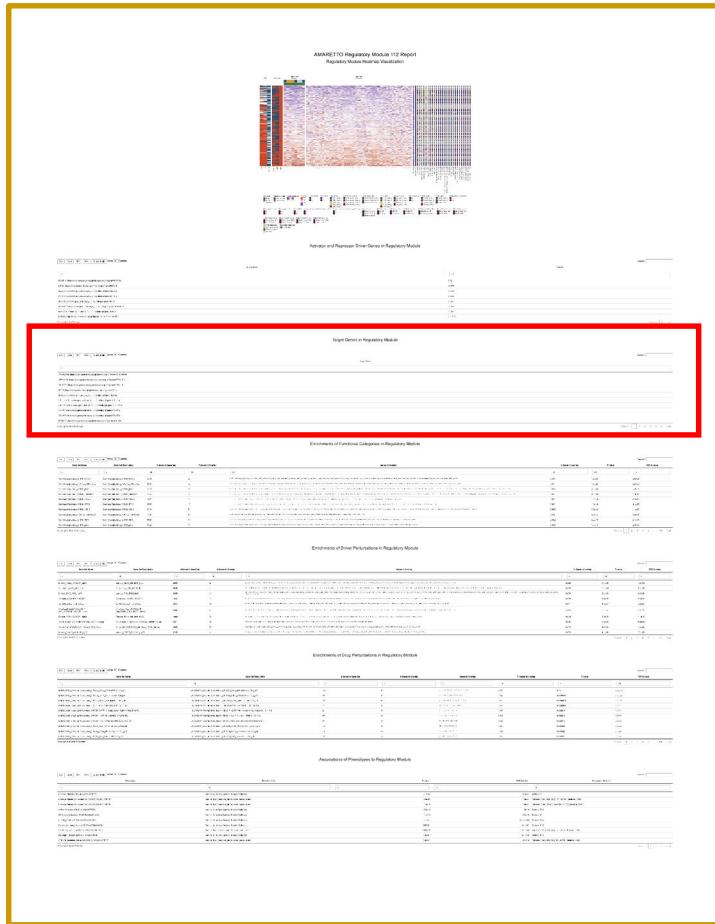
All

- [ARHGAP39](#)
- [ATP6V1C1](#)
- [ATP6V1H](#)
- [BOP1](#)
- [BZW2](#)
- [C10orf2](#)
- [C14orf33](#)
- [C2orf76](#)
- [C3orf32](#)
- [DCAF13](#)

Showing 1 to 10 of 58 entries Previous 1 2 3 4 5 6 Next

Detailed report of MYC-driven
Module 112:
target genes

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Detailed report of MYC-driven
Module 112:
target genes

Target Genes in Regulatory Module

CSV Excel PDF Print Column visibility Show 10 entries Search:

Target Gene

All

- [ARHGAP39](#)
- [ATP6V1C1](#)
- [ATP6V1H](#)
- [BOP1](#)
- [BZW2](#)
- [C10orf2](#)
- [C14orf33](#)
- [C2orf76](#)
- [C3orf32](#)
- [DCAF13](#)

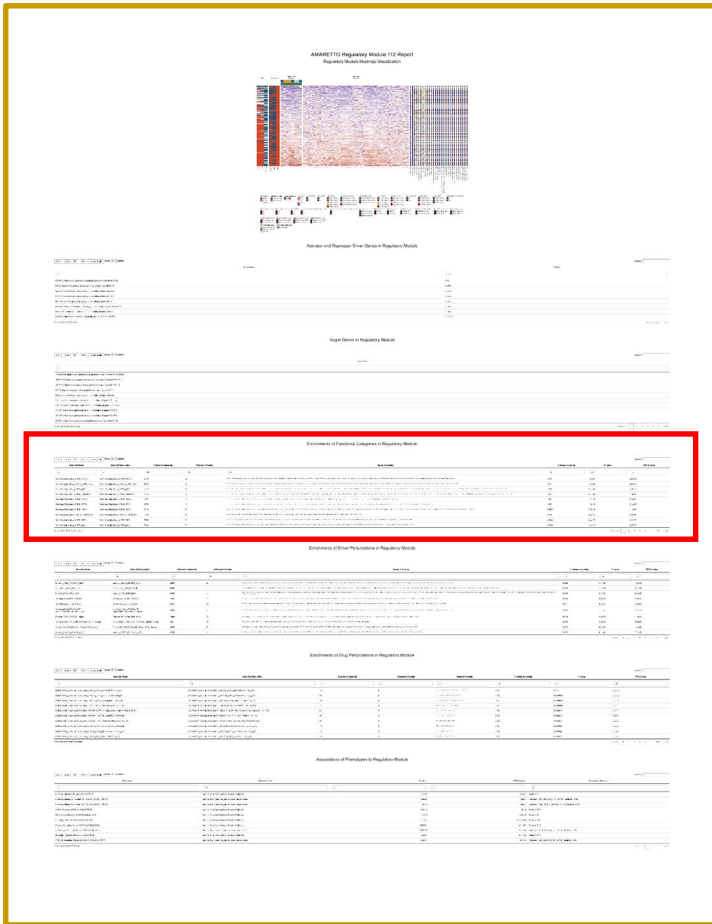
Showing 1 to 10 of 58 entries Previous 1 2 3 4 5 6 Next

58 Target Genes in Module 112:

ARHGAP39, ATP6V1C1, ATP6V1H, BOP1, BZW2, C10orf2, C14orf33, C2orf76, C3orf32, DCAF13, DCAF4, DNAJA1, DPH2, E2F5, EIF2C2, EIF3E, EIF3H, FAM49B, HSP90AA1, HSP90AB1, HSPA8, HSPH1, INTS8, IPO4, KHDRBS3, KIAA0020, LYAR, MINA, MPHOSPH6, MRAP2, MRPL50, MTERFD1, MYBBP1A, MYC, NOB1, NOP16, NOP2, NPM1, NUDCD1, NUDT19, P4HA1, PABPC1, POP1, PPA1, PTDSS1, PVT1, ROBO1, RPL23AP82, RPL36A, RPL7, RRP12, RRS1, SAMD13, SLC26A7, TARS, TATDN1, USP27X, ZNF485

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Enrichments of Functional Categories in Regulatory Module



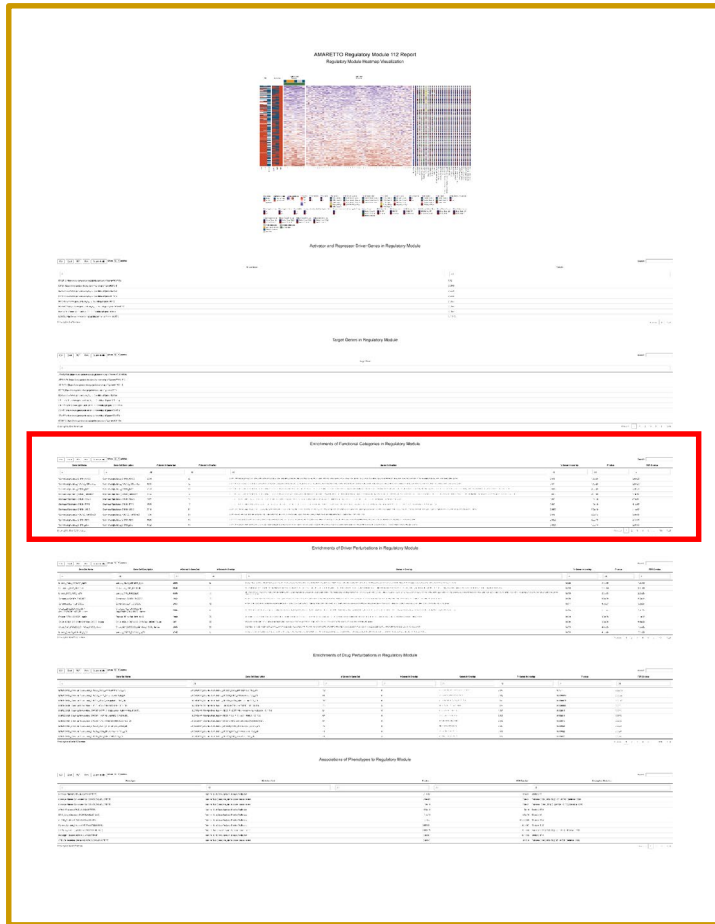
Detailed report of MYC-driven
Module 112:
functional characterization

CSV Excel PDF Print Column visibility Show 10 entries Search: MYC

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
MYC	All						
StemnessSignatures_ORKIN_MYC	StemnessSignatures_ORKIN_MYC	355	9	COX8A, DBP1, GTF3C4, INCE1P, IPO7, MRPL49, PRPF19, XPOS, ZNHIT2	0.025	1.4e-7	0.000012
WEI MYCN TARGETS WITH E BOX	Genes whose promoters contain E-box motifs and whose expression changed in MYCN-3 cells (neuroblastoma) upon induction of MYCN [GeneID=4613].	795	11	AHCTF1, C11orf83, CDC45, GTF3C4, MTC2, NSL2, PRMT3, QSER1, RNF219, SAAL1, TMM10	0.014	0.000022	0.00014
StemnessSignatures_WEINBERG_MYC_MAX_TARGETS	StemnessSignatures_WEINBERG_MYC_MAX_TARGETS	775	8	DBP1, SNX15, GTF3C4, BAZ1B, UBXN1, HNRNPL, ARFIP2, CSTF3	0.010	0.00042	0.0015
DANG BOUND BY MYC	Genes whose promoters are bound by MYC [GeneID=4609], according to MYC Target Gene Database.	1103	11	ARFGAP2, ARFIP2, BAZ1B, CLP1, CSTF3, DBP1, GTF3C4, MEN1, NAT10, TMM10, UBXN1	0.010	0.000046	0.0015
SCHLOSSER SERUM RESPONSE AUGMENTED BY MYC	Cluster 2: genes up-regulated in B493-6 cells (B lymphocytes) by serum alone or in combination with MYC [GeneID=4609] but not by MYC alone.	108	4	KAT5, OTUB1, PRPF19, TAF6L	0.037	0.00011	0.0030
BENPORATH MYC MAX TARGETS	Set 'Myc targets2': targets of c-Myc [GeneID=4609] and Max [GeneID=4149] identified by ChIP on chip in a Burkitt's lymphoma cell line; overlap set.	775	8	ARFIP2, BAZ1B, CSTF3, DBP1, GTF3C4, HNRNPL, SNX15, UBXN1	0.010	0.00042	0.0075
BILD MYC ONCOGENIC SIGNATURE	Genes selected in supervised analyses to discriminate cells expressing c-Myc [GeneID=4609] from control cells expressing GFP.	206	4	C11orf88, SHHG1, WDR74, XPOS	0.019	0.0013	0.016
HALLMARK MYC TARGETS V2	A subgroup of genes regulated by MYC - version 2 (v2).	58	2	PRMT3, WDR74	0.035	0.0079	0.050

Showing 1 to 8 of 8 entries (filtered from 1,137 total entries) Previous 1 Next

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Detailed report of MYC-driven Module 112: functional characterization

Enrichments of Functional Categories in Regulatory Module

CSV Excel PDF Print Column visibility Show 10 entries Search: MYC

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
MYC	All						
StemnessSignatures_ORKIN_MYC	StemnessSignatures_ORKIN_MYC	355	9	COX8A, DOB1, GTF3C4, INCE1P, IPO7, MRPL49, PRPF19, XPOS, ZNHIT2	0.025	1.4e-7	0.0000012
WEI MYCN TARGETS WITH E BOX	Genes whose promoters contain E-box motifs and whose expression changed in MYCN-3 cells (neuroblastoma) upon induction of MYCN [GeneID=4613].	795	11	AHCTF1, C11orf83, CDC45, GTF3C4, MTC2, NSL2, PRMT3, QSER1, RNF219, SAAL1, TMM10	0.014	0.0000022	0.00014
StemnessSignatures_WEINBERG_MYC_MAX_TARGETS	StemnessSignatures_WEINBERG_MYC_MAX_TARGETS	775	8	DOB1, SNX15, GTF3C4, BAZ1B, UBXN1, HNRNP1, ARFP2, CSTF3	0.010	0.00042	0.0015
DANG BOUND BY MYC	Genes whose promoters are bound by MYC [GeneID=4609], according to MYC Target Gene Database.	1103	11	ARFGAP2, ARFP2, BAZ1B, CLP1, CSTF3, DOB1, GTF3C4, MEN1, NAT10, TMM10, UBXN1	0.010	0.000046	0.0015
SCHLOSSER SERUM RESPONSE AUGMENTED BY MYC	Cluster 2: genes up-regulated in B493-6 cells (B lymphocytes) by serum alone or in combination with MYC [GeneID=4609] but not by MYC alone.	108	4	KAT5, OTUB1, PRPF19, TAF6L	0.037	0.00011	0.0030
BENPORATH MYC MAX TARGETS	Set 'Myc targets2': targets of c-Myc [GeneID=4609] and Max [GeneID=4149] identified by ChIP on chip in a Burkitt's lymphoma cell line; overlap set.	775	8	ARFP2, BAZ1B, CSTF3, DOB1, GTF3C4, HNRNP1, SNX15, UBXN1	0.010	0.00042	0.0075
BILD MYC ONCOGENIC SIGNATURE	Genes selected in supervised analyses to discriminate cells expressing c-Myc [GeneID=4609] from control cells expressing GFP.	206	4	C11orf83, SHHG1, WDR74, XPOS	0.019	0.0013	0.016
HALLMARK MYC TARGETS V2	A subgroup of genes regulated by MYC - version 2 (v2).	58	2	PRMT3, WDR74	0.035	0.0079	0.050

Showing 1 to 8 of 8 entries (filtered from 1,137 total entries) Previous 1 Next

Filter for significant results & Search for MYC gene signatures

Link to MSigDB description of Hallmark MYC targets:

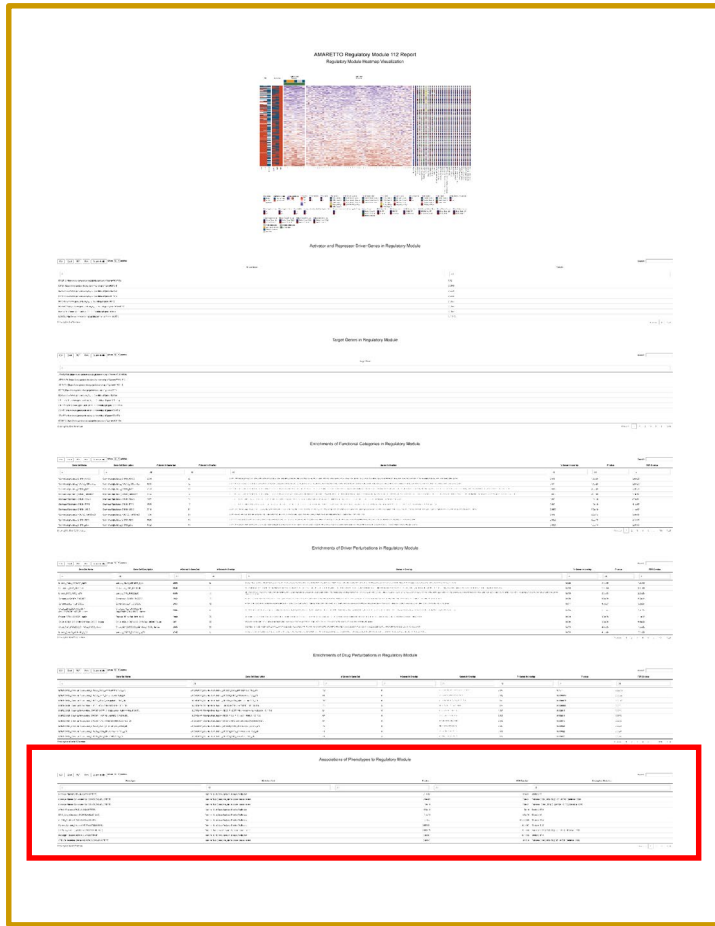
GSEA Molecular Signatures Database

Gene Set: HALLMARK_MYC_TARGETS_V2

Standard name	HALLMARK_MYC_TARGETS_V2
Systematic name	R5928
Brief description	A subgroup of genes regulated by MYC - version 2 (v2).
Full description or abstract	
Collection	H: hallmark gene sets
Source publication	
Exact source	
Related gene sets	(this is founder gene sets for this hallmark gene set) BILD_MYC_ONCOGENIC_SIGNATURE E2F3_UP_V1_OH MYC_UP_V1_OH MYC_UP_V1_LP SRC_UP_V1_LP

Download founder gene sets as: [gmt](#) | [LomV](#) | [LymL](#)

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Detailed report of MYC-driven
Module 112:
clinical characterization

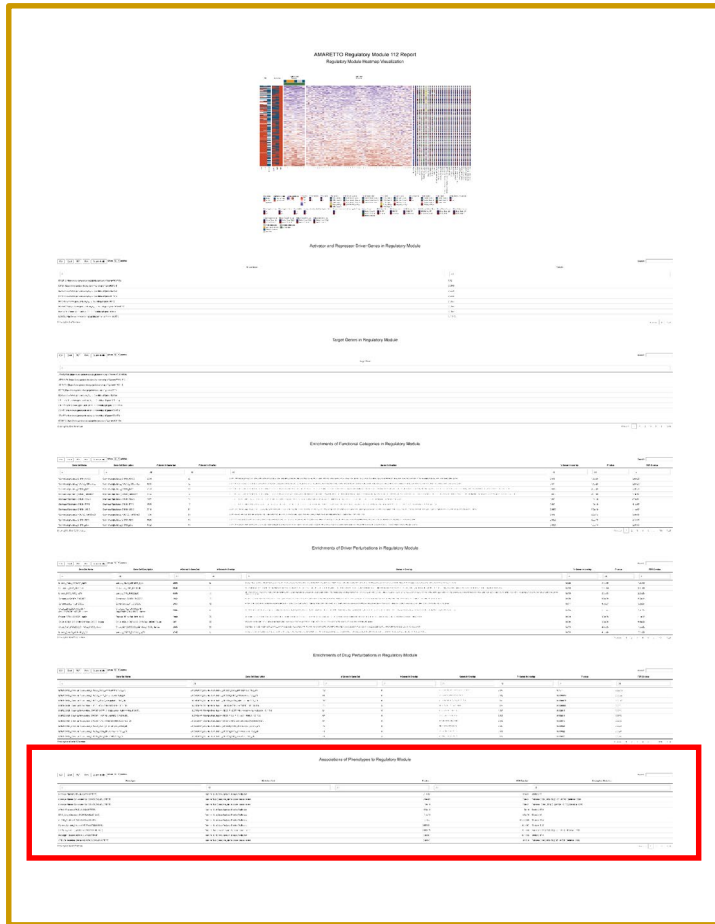
Associations of Phenotypes to Regulatory Module

CSV Excel PDF Print Column visibility Show 20 entries Search:

Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
All	All	0.000000	All	All
Hoshida_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	3.1e-12	1.1e-11	Statistic:53
Hoshida_Cluster_S2_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	6.9e-12	3.0e-11	Estimate: 0.581, 95% CI: [0.423 , 0.726], Statistics: 6820
Hoshida_Cluster_S3_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	1.5e-11	6.5e-11	Estimate: -0.564, 95% CI: [-0.709 , -0.407], Statistics: 1790
mRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	6.8e-11	1.8e-10	Statistic: 53.5
DNA_Copy_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	1.1e-11	5.6e-10	Statistic: 54
miRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	9.7e-7	0.0000028	Statistic:33.4
Hypomethylation_Cluster (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.000069	0.00041	Statistic: 19.2
CDKN2A_Silencing (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000021	0.00078	Estimate: 0.374, 95% CI: [0.207 , 0.54], Statistics: 5800
Paradigm_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00060	0.00085	Statistic: 17.4
CTNNB1_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00040	0.0016	Estimate: 0.362, 95% CI: [0.17 , 0.554], Statistics: 4360
TERT_Promoter_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00011	0.0041	Estimate: 0.33, 95% CI: [0.169 , 0.502], Statistics: 5620
TP53_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0028	0.013	Estimate: 0.3, 95% CI: [0.0977 , 0.496], Statistics: 4620
Consensus_Clinical_and_RNA_Seq_Hepatitis_B_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0014	0.019	Estimate: 0.323, 95% CI: [0.129 , 0.517], Statistics: 4150
iCluster_Clusters_1_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.027	0.046	Estimate: 0.213, 95% CI: [0.0224 , 0.386], Statistics: 4680
RPPA_Clusters (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.031	0.054	Estimate: -0.208, 95% CI: [-0.402 , -0.0173], Statistics: 2370
SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013	0.14	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34

Showing 1 to 16 of 16 entries (filtered from 27 total entries)

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Associations of Phenotypes to Regulatory Module

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Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
All	All	0.000000	All	All
Hoshida_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	3.1e-12	1.1e-11	Statistic:53
Hoshida_Cluster_S2_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	6.9e-12	3.0e-11	Estimate: 0.581, 95% CI: [0.423, 0.726], Statistics: 6820
Hoshida_Cluster_S3_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
mRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test			
DNA_Copy_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test			
miRNA_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test			
Hypomethylation_Cluster (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test			
CDKN2A_Silencing (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
Paradigm_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test			
CTNNB1_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
TERT_Promoter_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
TP53_Mutation_Status (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
Consensus_Clinical_and_RNA_Seq_Hepatitis_B_Virus (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
iCluster_Clusters_1_vs_rest (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
RPPA_Clusters (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test			
SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald)			

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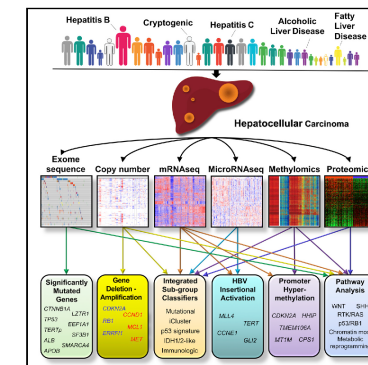
Detailed report of MYC-driven Module 112: clinical characterization

Clinical and molecular phenotypes from TCGA

Cell

Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma

Graphical Abstract



Highlights

- Analysis of hepatocellular carcinomas integrates data of multiple genomic platforms
- Mutated genes reveal oncogenic processes altering hepatocyte energy balance
- Multiplex analyses suggest a key role for Sonic hedgehog signaling in HCC
- IDH mutations point to a HCC subgroup molecularly similar to cholangiocarcinoma

Resource

Authors

The Cancer Genome Atlas Research Network

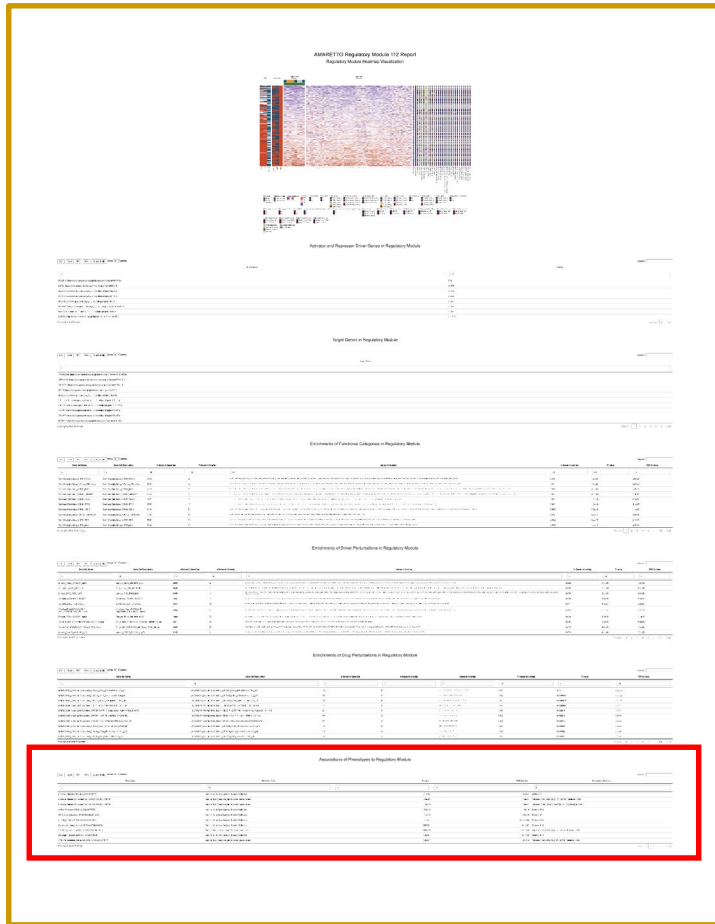
Correspondence

wheeler@bcm.edu (David A. Wheeler), roberts.lewis@mayo.edu (Lewis R. Roberts)

In Brief

Multiplex molecular profiling of human hepatocellular carcinoma patients provides insight into subtype characteristics and points toward key pathways to target therapeutically.

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Detailed report of MYC-driven Module 112: clinical characterization

Associations of Phenotypes to Regulatory Module

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Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
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Hoshida_Clusters (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	3.1e-12	1.1e-11	Statistic:53
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AMARETTO Regulatory Module 112 Report
Regulatory Module (cluster visualization)

Heatmap visualization of gene expression data.

Annotations and Phenotype Data Series in Regulatory Module

Sign Genes in Regulatory Module

Enrichment of Functional Categories in Regulatory Module

Enrichment of Drug Perturbations in Regulatory Module

Enrichment of Drug Perturbations in Regulatory Module

Associations of Phenotypes to Regulatory Module

Detailed report of MYC-driven
Module 112:
clinical characterization

Associations of Phenotypes to Regulatory Module

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Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
All	All	0.000000	All	All
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DNA_Copy_Clusters (KRUSKALWALLISTEST)				
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Hypomethylation_Cluster (KRUSKALWALLISTEST)				
CDKN2A_Silencing (WILCOXONRANKSUMTEST)				
Paradigm_Clusters (KRUSKALWALLISTEST)				
CTNNB1_Mutation_Status (WILCOXONRANKSUMTEST)				
TERT_Promoter_Mutation_Status (WILCOXONRANKSUMTEST)				
TP53_Mutation_Status (WILCOXONRANKSUMTEST)				
Consensus_Clinical_and_RNA_Seq_Hepatitis (WILCOXONRANKSUMTEST)				
iCluster_Clusters_1_vs_rest (WILCOXONRANKSUMTEST)				
RPPA_Clusters (WILCOXONRANKSUMTEST)				
SurvivalTime (COXPROPHAZARDTIMETOEVENT) SurvivalCensoring (COXPROPHAZARDRISK)				

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GSEA Gene Set Enrichment Analysis

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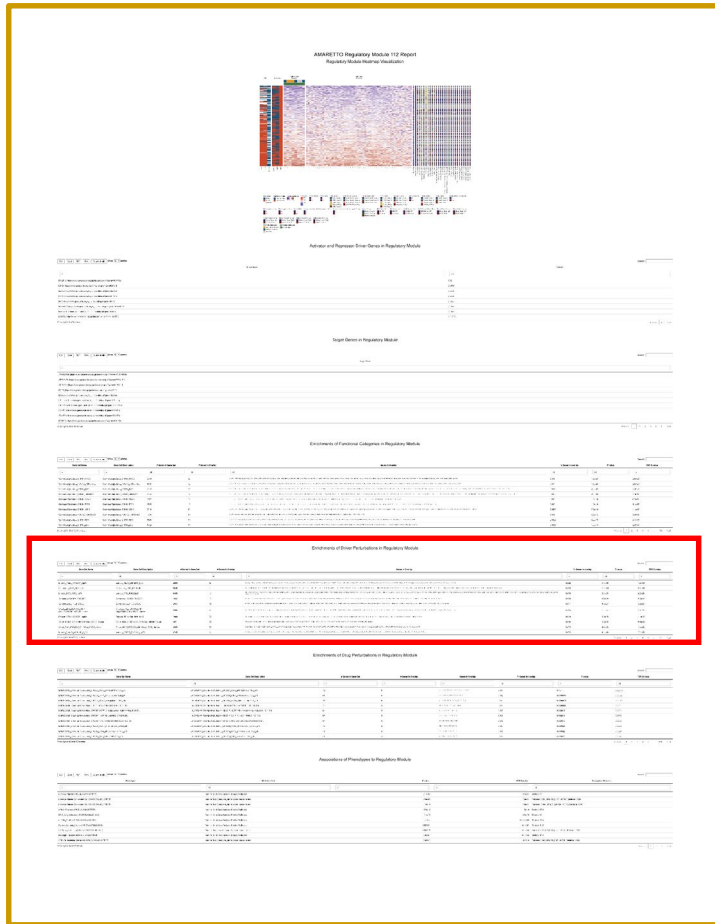
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Gene Set: HOSHIDA_LIVER_CANCER_SUBCLASS_S2

Standard name	HOSHIDA_LIVER_CANCER_SUBCLASS_S2
Systematic name	M7995
Brief description	Genes from 'subtype S2' signature of hepatocellular carcinoma (HCC): proliferation, MYC and AKT1 [GeneID=4609;207] activation.
Full description or abstract	Hepatocellular carcinoma (HCC) is a highly heterogeneous disease, and prior attempts to develop genomic-based classification for HCC have yielded highly divergent results, indicating difficulty in identifying unified molecular anatomy. We performed a meta-analysis of gene expression profiles in data sets from eight independent patient cohorts across the world. In addition, aiming to establish the real world applicability of a classification system, we profiled 118 formalin-fixed, paraffin-embedded tissues from an additional patient cohort. A total of 603 patients were analyzed, representing the major etiologies of HCC (hepatitis B and C) collected from Western and Eastern countries. We observed three robust HCC subclasses (termed S1, S2, and S3), each correlated with clinical parameters such as tumor size, extent of cellular differentiation, and serum alpha-fetoprotein levels. An analysis of the components of the signatures indicated that S1 reflected aberrant activation of the WNT signaling pathway, S2 was characterized by proliferation as well as MYC and AKT activation, and S3 was associated with hepatocyte differentiation. Functional studies indicated that the WNT pathway activation signature characteristic of S1 tumors was not simply the result of beta-catenin mutation but rather was the result of transforming growth factor-beta activation, thus representing a new mechanism of WNT pathway activation in HCC. These experiments establish the first consensus classification framework for HCC based on gene expression profiles and highlight the power of integrating multiple data sets to define a robust molecular taxonomy of the disease. [Cancer Res 2009;69(18):7385-92].
Collection	C2: curated gene sets CGP: chemical and genetic perturbations
Source publication	Pubmed 19723656 Authors: Hoshida Y, Nijman SM, Kobayashi M, Chan JA, Brunet JP, Chiang DY, Villanueva A, Newell P, Ikeda K, Hashimoto M, Watanabe G, Gabriel S, Friedman SL, Kumada H, Llovet JM, Golub TR
Exact source	Table 35: Subtype=S2
Related gene sets	(show 2 additional gene sets from the source publication) (show 300 gene sets from the same authors)
External links	
Organism	Homo sapiens
Contributed by	Jessica Robertson (Broad Institute)
Source platform	EntrezGeneIds
Dataset references	
Download gene set	format: grp txt gmt gmx xml
Compute overlaps	(show collections to investigate for overlap with this gene set)
Compendia expression profiles	Human tissue compendium (Novartis)

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Enrichments of Driver Perturbations in Regulatory Module

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Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
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Encode_MYC_K562_hg19	Encode_MYC_K562_hg19	6800	70	SF1, MTC2, CWF19L2, MRPS17, RRP8, CPSF7, VPS37C, BANF1, EIF4G2, ZFP91, MAPK2, PRMT3, FAU, DNAC24, HNRNPA1L2, CDCA5, EIF1AD, EIF3M, ATF7IP, SSRP1, TAF6L, KAT5, FTSJ2, GTF3C4, TMEM41B, CLP1, MAD2L1BP, METTL12, CLPTMIL, FEN1, MARK2, TRIM11, COX8A, NUP188, POLA2, WDR74, POM121C, IPO7, TDKH, CSTF3, AHCTF1, NSUN2, UTP3, MGA, INTS5, ZDHHC5, SAAL1, SNHG1, PRPF19, BAZ1B, RNF219, INCENP, DDB1, NAT10, HNRNPL, ZNHIT2, KBTBD4, XPO5, CAPRN1, KDM9B, PSMC3, TUT1, MRPL49, HNRNPUL2, PDSS5B, PDSSA, NDUFS3, TIMM10, CKAP5, ZNF195	0.010	2.2e-33	2.2e-29
Encode_MYC_HeLa-S3_hg19	Encode_MYC_HeLa-S3_hg19	3080	43	MTC2, MRPS17, RRP8, IPO7, ARFIP2, CSTF3, UBXN1, NSUN2, UTP3, MGA, INTS5, ZDHHC5, EIF3M, NAT10, USSER1, ATF7IP, SSRP1, ZNF112, KAT5, XPO5, KDM9B, PSMC3, TUT1, MRPL49, GTF3C4, HNRNPUL2, PDSSA, TMEM41B, CLP1, ARFGAP2, FEN1, ZNF195	0.014	2.3e-23	4.6e-20
Encode_MYC_MCF-7_hg19	Encode_MYC_MCF-7_hg19	5003	50	SF1, SDHAF2, TRIM11, COX8A, MRPS17, NUP188, POLA2, RRP8, POM121C, IPO7, ARFIP2, CPSF7, VPS37C, UTP3, MGA, INTS5, ZDHHC5, SAAL1, PRPF19, FAU, DNAC24, BAZ1B, HNRNPA1L2, CDCA5, DDB1, ZNF431, EIF1AD, TBC1D14, ATF7IP, SSRP1, ZNHIT2, KAT5, KBTBD4, KDM9B, TMEM33, TUT1, MRPL49, FTSJ2, GANAB, HNRNPUL2, PDSS5B, PDSSA, PSMC3, SF3B2, TIMM10, ZNF107, METTL12, ARFGAP2, CKAP5, ZNF195	0.010	3.4e-21	4.2e-18
Encode_MYC_GM12878_hg19	Encode_MYC_GM12878_hg19	2000	31	BAZ1B, HNRNPA1L2, RNF219, DDB1, EIF1AD, COX8A, MRPS17, NUP188, OTUB1, RRP8, ARFIP2, KAT5, KBTBD4, KDM9B, TUT1, UTP3, MRPL49, FTSJ2, MGA, INTS5, HNRNPUL2, PDSSA, NDUFS3, CLP1, SF3B2, TIMM10, SAAL1, FEN1, FAU, DNAC24, ZNF195	0.015	8.7e-18	5.0e-15
ChEA_MYC_18358816_ChIP-ChIP_MESCs_Mouse	ChEA_MYC_18358816_ChIP-ChIP_MESCs_Mouse	3413	38	COX8A, NUP188, POLA2, WDR74, MTA2, IPO7, CSTF3, AHCTF1, DDAH1, NSUN2, MGA, INTS5, BANF1, TGFBRAP1, PCNX3, MEN1, PRPF19, MAP4K2, FAU, FIZ1, CDCA5, INCENP, DDB1, NAT10, ATF7IP, OTUB1, ZNHIT2, XPO5, PSMC3, TMEM33, TUT1, MRPL49, GTF3C4, GANAB, TMEM41B, MAD2L1BP, TIMM10, FEN1	0.011	4.0e-17	2.0e-14
ChEA_MYC_19030024_ChIP-ChIP_MESCs_Mouse	ChEA_MYC_19030024_ChIP-ChIP_MESCs_Mouse	3868	40	MTC2, COX8A, CWF19L2, NUP188, POLA2, WDR74, IPO7, ARFIP2, CSTF3, AHCTF1, DDAH1, NSUN2, MGA, ZDHHC5, BANF1, EIF4G2, ZFP91, PRPF19, PRMT3, FAU, FIZ1, BAZ1B, CDCA5, INCENP, DDB1, NAT10, ATF7IP, SSRP1, OTUB1, TAF6L, XPO5, CAPRN1, TMEM33, GTF3C4, NDUFS3, TMEM41B, MAD2L1BP, TIMM10, CLPTMIL, FEN1	0.010	5.5e-17	2.7e-14
Consensus_MYC_ENCODE	Consensus_MYC_ENCODE	1515	24	BAZ1B, NSUN2, TUT1, UTP3, DDB1, EIF1AD, GTF3C4, EIF3M, MGA, NAT10, MRPS17, HNRNPUL2, BANF1, WDR74, HNRNPL, CLP1, RRP8, IPO7, ZFP91, SNHG1, CSTF3, PRMT3, XPO5, CAPRN1	0.016	5.3e-14	5.9e-12
ChEA_MYC_18555785_ChIP-Seq_MESCs_Mouse	ChEA_MYC_18555785_ChIP-Seq_MESCs_Mouse	1200	20	SF1, CDCA5, INCENP, DDB1, MTC2, COX8A, NAT10, BANF1, NDUFS3, TGFBRAP1, WDR74, SF3B2, TAF6L, EIF4G2, CSTF3, PRPF19, PRMT3, XPO5, FAU, FIZ1	0.017	3.6e-12	6.3e-10
ChEA_MYCN_18555785_ChIP-Seq_MESCs_Mouse	ChEA_MYCN_18555785_ChIP-Seq_MESCs_Mouse	2261	25	DDB1, MTC2, CWF19L2, NUP188, POLA2, SSRP1, OTUB1, IPO7, KBTBD4, XPO5, DDAH1, NSUN2, MRPL49, FTSJ2, GTF3C4, GANAB, ZDHHC5, TMEM41B, TIMM10, DGKZ, EIF4G2, CLPTMIL, FEN1, FIZ1, MARK2	0.011	3.7e-11	5.0e-9
Encode_MYC_MCF 10A_hg19	Encode_MYC_MCF 10A_hg19	3382	29	SDHAF2, MTC2, MRPS17, POM121C, ARFIP2, CPSF7, VPS37C, INTS5, SAAL1, EIF4G2, PRPF19, FIZ1, HNRNPA1L2, CDCA5, RNF219, EIF3M, TMEM223, SNRNP35, KAT5, KBTBD4, TUT1, FTSJ2, GTF3C4, GANAB, PDSS5B, NDUFS3, TMEM41B, ZNF107, METTL12	0.0086	3.1e-10	1.7e-8

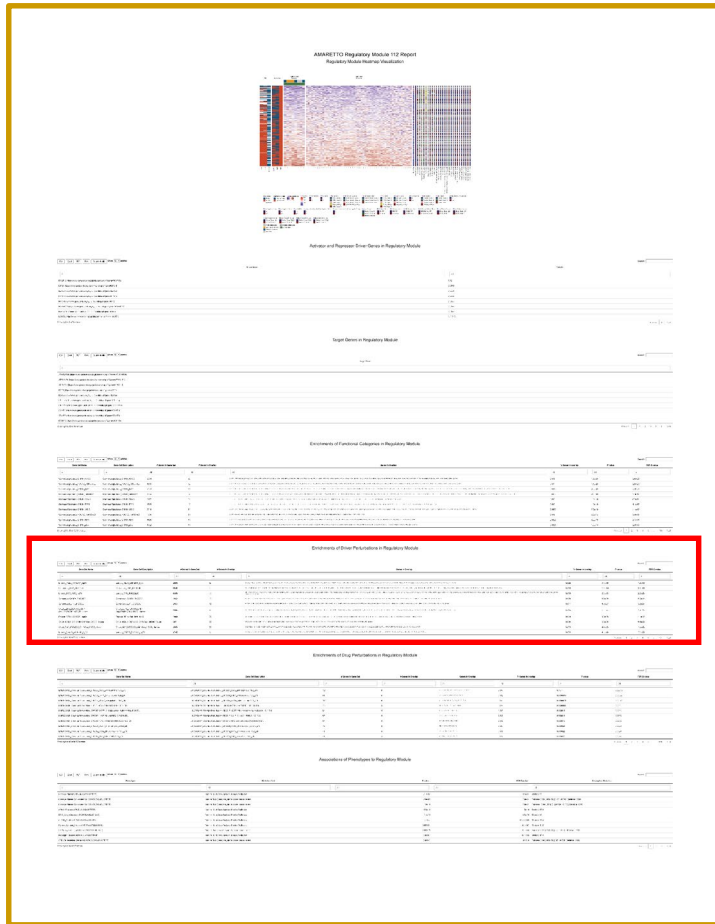
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Detailed report of MYC-driven
 Module 112:
 driver validation & discovery
 ➤ Perturbation-AMARETTO v1

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Enrichments of Driver Perturbations in Regulatory Module

CSV Excel PDF Print Column visibility Show 10 entries Search: MYC

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
Encode_MYC_K562_hg19	Encode_MYC_K562_hg19	6800	70	SF1, MTC2, CWF19L2, MRPS17, RRP8, CPSF7, VPS37C, BANF1, EIF4G2, ZFP91, MAPK2, PRMT3, FAU, DNAC24, HNRNPA1L2, CDCA5, EIF1AD, EIF3M, ATF7IP, SSRP1, TAF6L, KAT5, FTSJ2, GTF3C4, TMEM41B, CLP1, MAD2L1BP, METTL12, CLPTMIL, FEN1, MARK2, TRIM11, COX8A, NUP188, POLA2, WDR74, POM121C, IPO7, TDKX, CSTF3, AHCTF1, NSUN2, UTP3, MGA, INTS5, ZDHHC5, SAAL1, SNHG1, PRPF19, BAZ1B, RNF219, INCENP, DDB1, NAT10, HNRNPL, ZNHIT2, KBTBD4, XPO5, CAPRN1, KDM9B, PSMC3, TUT1, MRPL49, HNRNPUL2, PDSS5B, PDSSA, NDUFS3, TIMM10, CKAP5, ZNF195	0.010	2.2e-33	2.2e-29
Encode_MYC_HeLa-S3_hg19	Encode_MYC_HeLa-S3_hg19	3080	43	MTC2, MRPS17, RRP8, IPO7, ARFIP2, CSTF3, UBXN1, NSUN2, UTP3, MGA, INTS5, ZDHHC5, EIF3M, NAT10, DSSRT1, ATF7IP, SSRP1, ZNF112, KAT5, XPO5, KDM9B, PSMC3, TUT1, MRPL49, GTF3C4, HNRNPUL2, PDSSA, TMEM41B, CLP1, ARFGAP2, FEN1, ZNF195	0.014	2.3e-23	4.6e-20
Encode_MYC_MCF-7_hg19	Encode_MYC_MCF-7_hg19	5003	50	SF1, SDHAF2, TRIM11, COX8A, MRPS17, NUP188, POLA2, RRP8, POM121C, IPO7, ARFIP2, CPSF7, VPS37C, UTP3, MGA, INTS5, ZDHHC5, SAAL1, PRPF19, FAU, DNAC24, BAZ1B, HNRNPA1L2, CDCA5, DDB1, ZNF431, EIF1AD, TBC1D14, ATF7IP, SSRP1, ZNHIT2, KAT5, KBTBD4, KDM9B, TMEM33, TUT1, MRPL49, FTSJ2, GANAB, HNRNPUL2, PDSS5B, PDSSA, NDUFS3, SF3B2, TIMM10, ZNF107, METTL12, ARFGAP2, CKAP5, ZNF195	0.010	3.4e-21	4.2e-18
Encode_MYC_GM12878_hg19	Encode_MYC_GM12878_hg19	2000	31	BAZ1B, HNRNPA1L2, RNF219, DDB1, EIF1AD, COX8A, MRPS17, NUP188, OTUB1, RRP8, ARFIP2, KAT5, KBTBD4, KDM9B, TUT1, UTP3, MRPL49, FTSJ2, MGA, INTS5, HNRNPUL2, PDSSA, NDUFS3, CLP1, SF3B2, TIMM10, SAAL1, FEN1, FAU, DNAC24, ZNF195	0.015	8.7e-18	5.0e-15
ChEA_MYC_18358816_ChIP-ChIP_MESCs_Mouse	ChEA_MYC_18358816_ChIP-ChIP_MESCs_Mouse	3413	38	COX8A, NUP188, POLA2, WDR74, MTA2, IPO7, CSTF3, AHCTF1, DDAH1, NSUN2, MGA, INTS5, BANF1, TGFBRAP1, PCNXL3, MEN1, PRPF19, MAPK4, FAU, FIZ1, CDCA5, INCENP, DDB1, NAT10, ATF7IP, OTUB1, ZNHIT2, XPO5, PSMC3, TMEM33, TUT1, MRPL49, GTF3C4, GANAB, TMEM41B, MAD2L1BP, TIMM10, FEN1	0.011	4.0e-17	2.0e-14
ChEA_MYC_19030024_ChIP-ChIP_MESCs_Mouse	ChEA_MYC_19030024_ChIP-ChIP_MESCs_Mouse	3868	40	MTC2, COX8A, CWF19L2, NUP188, POLA2, WDR74, IPO7, ARFIP2, CSTF3, AHCTF1, DDAH1, NSUN2, MGA, ZDHHC5, BANF1, EIF4G2, ZFP91, PRPF19, PRMT3, FAU, FIZ1, BAZ1B, CDCA5, INCENP, DDB1, NAT10, ATF7IP, SSRP1, OTUB1, TAF6L, XPO5, CAPRN1, TMEM33, GTF3C4, NDUFS3, TMEM41B, MAD2L1BP, TIMM10, CLPTMIL, FEN1	0.010	5.5e-17	2.7e-14
Consensus_MYC_ENCODE	Consensus_MYC_ENCODE	1515	24	BAZ1B, NSUN2, TUT1, UTP3, DDB1, EIF1AD, GTF3C4, EIF3M, MGA, NAT10, MRPS17, HNRNPUL2, BANF1, WDR74, HNRNPL, CLP1, RRP8, IPO7, ZFP91, SNHG1, CSTF3, PRMT3, XPO5, CAPRN1	0.016	5.3e-14	5.9e-12
ChEA_MYC_18555785_ChIP-Seq_MESCs_Mouse	ChEA_MYC_18555785_ChIP-Seq_MESCs_Mouse	1200	20	SF1, CDCA5, INCENP, DDB1, MTC2, COX8A, NAT10, BANF1, NDUFS3, TGFBRAP1, WDR74, SF3B2, TAF6L, EIF4G2, CSTF3, PRPF19, PRMT3, XPO5, FAU, FIZ1	0.017	3.6e-12	6.3e-10
ChEA_MYCN_18555785_ChIP-Seq_MESCs_Mouse	ChEA_MYCN_18555785_ChIP-Seq_MESCs_Mouse	2261	25	DDB1, MTC2, CWF19L2, NUP188, POLA2, SSRP1, OTUB1, IPO7, KBTBD4, XPO5, DDAH1, NSUN2, MRPL49, FTSJ2, GTF3C4, GANAB, ZDHHC5, TMEM41B, TIMM10, DGKZ, EIF4G2, CLPTMIL, FEN1, FIZ1, MARK2	0.011	3.7e-11	5.0e-9
Encode_MYC_MCF 10A_hg19	Encode_MYC_MCF 10A_hg19	3382	29	SDHAF2, MTC2, MRPS17, POM121C, ARFIP2, CPSF7, VPS37C, INTS5, SAAL1, EIF4G2, PRPF19, FIZ1, HNRNPA1L2, CDCA5, RNF219, EIF3M, TMEM223, SNRNP35, KAT5, KBTBD4, TUT1, FTSJ2, GTF3C4, GANAB, PDSS5B, NDUFS3, TMEM41B, ZNF107, METTL12	0.0086	3.1e-10	1.7e-8

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Detailed report of MYC-driven Module 112: driver validation & discovery
 ➤ Perturbation-AMARETTO v1

Experiments validating MYC and MYC-regulated genes in Module 112: Encode and ChEA ChIP-Seq experiments

Perturbation-AMARETTO report LIHC

Perturbation-AMARETTO v2: driver validation & discovery using genetic perturbations from LINCS/CMAP

Case Study 1: virus-induced hepatocellular carcinoma

Driver discovery across 6 data sets

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Search:

PerturbationID	Cell_Line	GeneSymbol	EntrezID	PerturbationType	Type	LIHC
All	All	["MYC","BZW2","E2F5","EI	All	All	All	escore-pval-padj
CGS001_A375_96H.BZW2:1	A375	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_A375_96H.MYC:1	A375	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_A375_96H.NPM1:1	A375	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
OEB005_A375_96H.BRDN0000408975:-666	A375	NPM1	4869	trt_oe	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_A375_96H.EIF3H:1	A375	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj
CGS001_A549_96H.EIF3H:1	A549	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_A549_96H.MYC:1	A549	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_A549_96H.E2F5:1	A549	E2F5	1875	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0129) , escore-pval-padj
CGS001_HA1E_96H.MYC:1.5	HA1E	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HA1E_96H.EIF3H:1.5	HA1E	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_HA1E_96H.BZW2:1.5	HA1E	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_HCC515_96H.MYC:2	HCC515	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HEPG2_96H.MYC:1.5	HEPG2	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HEPG2_96H.BZW2:1.5	HEPG2	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
OEB005_HEPG2_96H.BRDN0000408975:-666	HEPG2	NPM1	4869	trt_oe	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj
CGS001_HT29_96H.BZW2:1	HT29	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_HT29_96H.MYC:1	HT29	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_HT29_96H.E2F5:1	HT29	E2F5	1875	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0129) , escore-pval-padj-zscore
CGS001_MCF7_144H.BZW2:2	MCF7	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_MCF7_144H.MYC:2	MCF7	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_MCF7_96H.BZW2:2	MCF7	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_MCF7_96H.MYC:2	MCF7	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_MCF7_144H.NPM1:2	MCF7	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_MCF7_96H.NPM1:2	MCF7	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj
CGS001_MCF7_96H.EIF3H:2	MCF7	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_NPC_96H.BZW2:1.5	NPC	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_NPC_96H.MYC:1.5	NPC	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_PC3_96H.MYC:2	PC3	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
OEB003_PC3_96H.BRDN0000405602:-666	PC3	BZW2	28969	trt_oe	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_PC3_96H.EIF3H:2	PC3	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj
CGS001_VCAP_120H.NPM1:5	VCAP	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_VCAP_120H.MYC:5	VCAP	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_VCAP_120H.EIF3H:5	VCAP	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore

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Perturbation-AMARETTO report LIHC

Perturbation-AMARETTO v2: driver validation & discovery using genetic perturbations from LINCS/CMAP

Case Study 1: virus-induced hepatocellular carcinoma

Driver discovery across 6 data sets

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Search:

PerturbationID	Cell_Line	GeneSymbol	EntrezID	PerturbationType	Type	LIHC
All	All	["MYC","BZW2","E2F5","EI	All	All	All	escore-pval-padj
CGS001_A375_96H.BZW2:1	A375	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_A375_96H.MYC:1	A375	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_A375_96H.NPM1:1	A375	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
OEB005_A375_96H.BRDN0000408975:-666	A375	NPM1	4869	trt_oe	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_A375_96H.EIF3H:1	A375	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj
CGS001_A549_96H.EIF3H:1	A549	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_A549_96H.MYC:1	A549	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_A549_96H.E2F5:1	A549	E2F5	1875	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0129) , escore-pval-padj
CGS001_HA1E_96H.MYC:1.5	HA1E	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HA1E_96H.EIF3H:1.5	HA1E	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_HA1E_96H.BZW2:1.5	HA1E	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_HCC515_96H.MYC:2	HCC515	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HEPG2_96H.MYC:1.5	HEPG2	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HEPG2_96H.BZW2:1.5	HEPG2	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
OEB005_HEPG2_96H.BRDN0000408975:-666	HEPG2	NPM1	4869	trt_oe	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj
CGS001_HT29_96H.BZW2:1	HT29	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_HT29_96H.MYC:1	HT29	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_HT29_96H.E2F5:1	HT29	E2F5	1875	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0129) , escore-pval-padj-zscore
CGS001_MCF7_144H.BZW2:2	MCF7	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_MCF7_144H.MYC:2	MCF7	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_MCF7_96H.BZW2:2	MCF7	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_MCF7_96H.MYC:2	MCF7	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_MCF7_144H.NPM1:2	MCF7	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_MCF7_96H.NPM1:2	MCF7	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj
CGS001_MCF7_96H.EIF3H:2	MCF7	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_NPC_96H.BZW2:1.5	NPC	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_NPC_96H.MYC:1.5	NPC	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_PC3_96H.MYC:2	PC3	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
OEB003_PC3_96H.BRDN0000405602:-666	PC3	BZW2	28969	trt_oe	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_PC3_96H.EIF3H:2	PC3	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj
CGS001_VCAP_120H.NPM1:5	VCAP	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_VCAP_120H.MYC:5	VCAP	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_VCAP_120H.EIF3H:5	VCAP	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore

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Experiment

Cell line

Gene perturbed

KO or OE

Validation status in LIHC

Perturbation-AMARETTO report LIHC

Perturbation-AMARETTO v2: driver validation & discovery using genetic perturbations from LINCS/CMAP

Case Study 1: virus-induced hepatocellular carcinoma

Driver discovery across 6 data sets

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PerturbationID	Cell_Line	GeneSymbol	EntrezID	PerturbationType	Type	LIHC
All	All	["MYC","BZW2","E2F5","EIF3H"]	All	All	All	escore-pval-padj
CGS001_A375_96H.BZW2:1	A375	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_A375_96H.MYC:1	A375	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_A375_96H.NPM1:1	A375	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
OEB005_A375_96H.BRDN0000408975:-666	A375	NPM1	4869	trt_oe	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_A375_96H.EIF3H:1	A375	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj
CGS001_A549_96H.EIF3H:1	A549	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_A549_96H.MYC:1	A549	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_A549_96H.E2F5:1	A549	E2F5	1875	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0129) , escore-pval-padj
CGS001_HA1E_96H.MYC:1.5	HA1E	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HA1E_96H.EIF3H:1.5	HA1E	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_HA1E_96H.BZW2:1.5	HA1E	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_HCC515_96H.MYC:2	HCC515	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HEPG2_96H.MYC:1.5	HEPG2	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_HEPG2_96H.BZW2:1.5	HEPG2	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
OEB005_HEPG2_96H.BRDN0000408975:-666	HEPG2	NPM1	4869	trt_oe	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj
CGS001_HT29_96H.BZW2:1	HT29	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_HT29_96H.MYC:1	HT29	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_HT29_96H.E2F5:1	HT29	E2F5	1875	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0129) , escore-pval-padj-zscore
CGS001_MCF7_144H.BZW2:2	MCF7	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_MCF7_144H.MYC:2	MCF7	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_MCF7_96H.BZW2:2	MCF7	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_MCF7_96H.MYC:2	MCF7	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_MCF7_144H.NPM1:2	MCF7	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_MCF7_96H.NPM1:2	MCF7	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj
CGS001_MCF7_96H.EIF3H:2	MCF7	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore
CGS001_NPC_96H.BZW2:1.5	NPC	BZW2	28969	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_NPC_96H.MYC:1.5	NPC	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
CGS001_PC3_96H.MYC:2	PC3	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj-zscore
OEB003_PC3_96H.BRDN0000405602:-666	PC3	BZW2	28969	trt_oe	landmark	Module 112 : A_D (w = 0.0206) , escore-pval-padj-zscore
CGS001_PC3_96H.EIF3H:2	PC3	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj
CGS001_VCAP_120H.NPM1:5	VCAP	NPM1	4869	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0205) , escore-pval-padj-zscore
CGS001_VCAP_120H.MYC:5	VCAP	MYC	4609	trt_sh.cgs	landmark	Module 112 : A_D (w = 0.0179) , escore-pval-padj
CGS001_VCAP_120H.EIF3H:5	VCAP	EIF3H	8667	trt_sh.cgs	best inferred	Module 112 : A_D (w = 0.0348) , escore-pval-padj-zscore

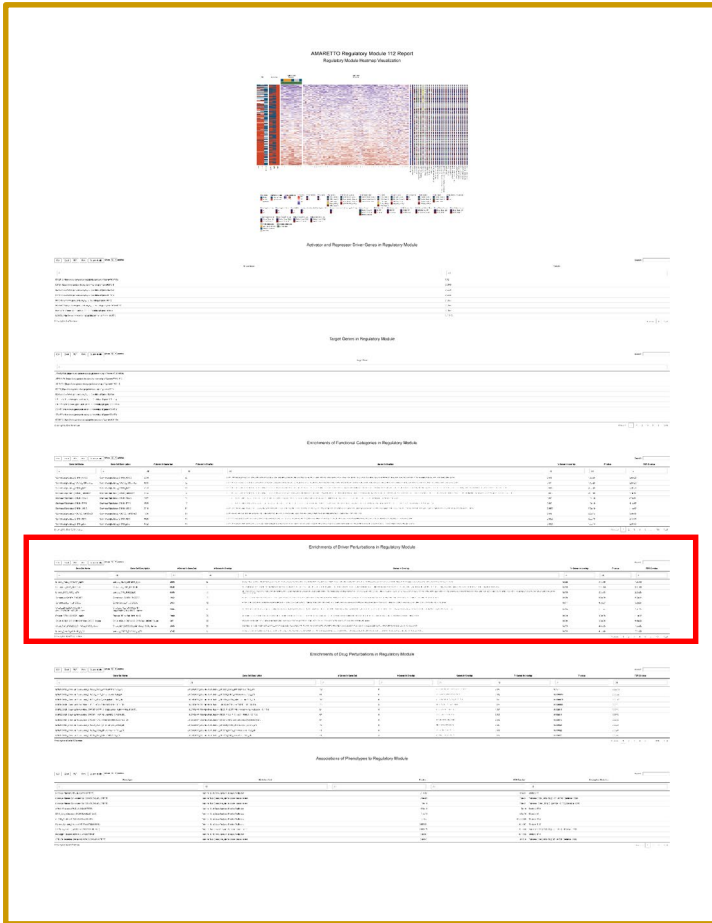
Showing 1 to 33 of 33 entries (filtered from 55,753 total entries)

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Search for drivers of Module 112 validated using genetic perturbations from LINCS/CMAP: MYC, BZW2, E2F5, EIF3H, NPM1

https://pochetlab.shinyapps.io/pAMARETTO_Liver_6DS_Drivers/

AMARETTO report LHC



Enrichments of Drug Perturbations in Regulatory Module

[CSV](#)
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[Column visibility](#)
 Show entries
 Search:

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
<input type="text" value="All"/>	<input type="text" value="All"/>					<input type="checkbox"/>	<input type="checkbox"/>
LINCSCMAP_ChemicalPerturbation_CPC007_A375_24H-t5247673-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC007_A375_24H-t5247673-10.0_DN	127	6	CPSF7, HNRNPL, BAZ1B, CAPRN1, ZNHIT2, NDUFS3	0.047	5.1e-7	0.00013
LINCSCMAP_ChemicalPerturbation_CPC006_THP1_6H-teniposide-1.25_DN	LINCSCMAP_ChemicalPerturbation_CPC006_THP1_6H-teniposide-1.25_DN	81	5	ATF7IP, BAZ1B, CAPRN1, PDSSB, ZNHIT2	0.062	0.0000013	0.00027
LINCSCMAP_ChemicalPerturbation_CPC006_VCAP_24H-piplartine-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC006_VCAP_24H-piplartine-10.0_DN	162	6	CPSF7, HNRNPL, FTSJ2, RRP8, ZNHIT2, KDM3B	0.037	0.0000021	0.00041
LINCSCMAP_ChemicalPerturbation_LJP005_HT29_24H-XMD16-144-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP005_HT29_24H-XMD16-144-3.33_DN	114	5	PDHX, WDR74, PRPF19, NAT10, FEN1	0.044	0.0000068	0.0010
LINCSCMAP_ChemicalPerturbation_CPC017_MCF7_24H-	LINCSCMAP_ChemicalPerturbation_CPC017_MCF7_24H-	64	4	DNAJC24, ATF7IP,	0.063	0.000015	0.0018
LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-vu0418946-2-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-vu0418946-2-10.0_DN	67	4	ATF7IP, CAPRN1,	0.060	0.000018	0.0020
LINCSCMAP_ChemicalPerturbation_CPC013_NPC_24H-	LINCSCMAP_ChemicalPerturbation_CPC013_NPC_24H-	67	4	HNRNPL, ATF7IP,	0.060	0.000018	0.0020
LINCSCMAP_ChemicalPerturbation_CPC004_VCAP_6H-mitomycin_c-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC004_VCAP_6H-mitomycin_c-10.0_DN	70	4	ATF7IP, CAPRN1,	0.057	0.000021	0.0023
LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-	LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-	71	4	ATF7IP, CAPRN1,	0.056	0.000022	0.0024
LINCSCMAP_ChemicalPerturbation_CPC014_ASC_24H-a-1065-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC014_ASC_24H-a-1065-10.0_DN	71	4	HNRNPL, ATF7IP,	0.056	0.000022	0.0024

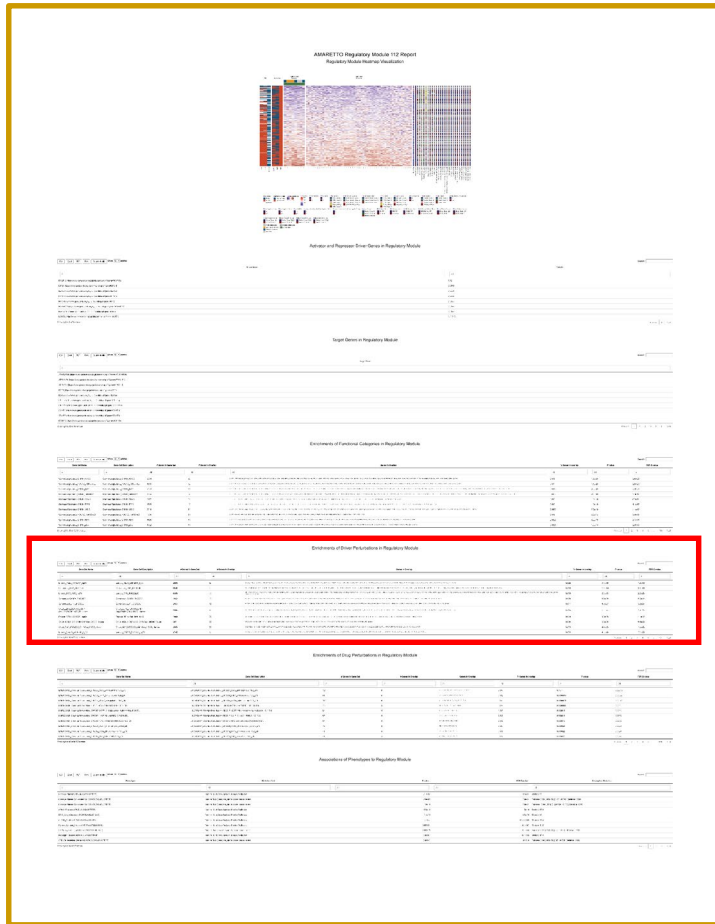
Showing 1 to 10 of 2,167 entries (filtered from 9,505 total entries)

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Detailed report of MYC-driven
Module 112:
drug discovery

➤ Perturbation-AMARETTO v1

AMARETTO report LHC



Enrichments of Drug Perturbations in Regulatory Module

Show entries
 Search:

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
<input type="text" value="All"/>	<input type="text" value="All"/>					<input type="checkbox"/>	<input type="checkbox"/>
LINCSCMAP_ChemicalPerturbation_CPC007_A375_24H-15247673-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC007_A375_24H-15247673-10.0_DN	127	6	CPSF7, HNRNPL, BAZ1B, CAPRN1, ZNHIT2, NDUFS3	0.047	5.1e-7	0.00013
LINCSCMAP_ChemicalPerturbation_CPC006_THP1_6H-teniposide-1.25_DN	LINCSCMAP_ChemicalPerturbation_CPC006_THP1_6H-teniposide-1.25_DN	81	5	ATF7IP, BAZ1B, CAPRN1, PDSSB, ZNHIT2	0.062	0.0000013	0.00027
LINCSCMAP_ChemicalPerturbation_CPC006_VCAP_24H-piplartine-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC006_VCAP_24H-piplartine-10.0_DN	162	6	CPSF7, HNRNPL, FTSJ2, RRP8, ZNHIT2, KDM3B	0.037	0.0000021	0.00041
LINCSCMAP_ChemicalPerturbation_LJP005_HT29_24H-XMD16-144-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP005_HT29_24H-XMD16-144-3.33_DN	114	5	PDHX, WDR74, PRPF19, NAT10, FEN1	0.044	0.0000068	0.0010
LINCSCMAP_ChemicalPerturbation_CPC017_MCF7_24H-	LINCSCMAP_ChemicalPerturbation_CPC017_MCF7_24H-	64	4	DNAJC24, ATF7IP,	0.063	0.000015	0.0018
LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-vu0418946-2-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-vu0418946-2-10.0_DN	67	4	ATF7IP, CAPRN1,	0.060	0.000018	0.0020
LINCSCMAP_ChemicalPerturbation_CPC013_NPC_24H-	LINCSCMAP_ChemicalPerturbation_CPC013_NPC_24H-	67	4	HNRNPL, ATF7IP,	0.060	0.000018	0.0020
LINCSCMAP_ChemicalPerturbation_CPC004_VCAP_6H-mitomycin_c-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC004_VCAP_6H-mitomycin_c-10.0_DN	70	4	ATF7IP, ZNF72,	0.057	0.000021	0.0023
LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-	LINCSCMAP_ChemicalPerturbation_CPC012_HA1E_6H-	71	4	ATF7IP, CAPRN1,	0.056	0.000022	0.0024
LINCSCMAP_ChemicalPerturbation_CPC014_ASC_24H-a-1065-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC014_ASC_24H-a-1065-10.0_DN	71	4	HNRNPL, ATF7IP,	0.056	0.000022	0.0024

Showing 1 to 10 of 2,167 entries (filtered from 9,505 total entries)

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Search for current LHC treatments Sorafenib and Regorafenib:

Show entries
 Search:

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
<input type="text" value="All"/>	<input type="text" value="All"/>					<input type="checkbox"/>	<input type="checkbox"/>
LINCSCMAP_ChemicalPerturbation_LJP006_HEPG2_24H-sorafenib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HEPG2_24H-sorafenib-10_DN	91	2	DDAH1, FEN1	0.022	0.019	0.11
LINCSCMAP_ChemicalPerturbation_LJP009_MCF7_24H-regorafenib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP009_MCF7_24H-regorafenib-10_DN	98	2	BANF1, FEN1	0.020	0.021	0.11

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Detailed report of MYC-driven
Module 112:
drug discovery

➤ Perturbation-AMARETTO v1

Perturbation-AMARETTO report LHC

Perturbation-AMARETTO v2: drug discovery using chemical perturbations from LINCS/CMAP

Case Study 1: virus-induced hepatocellular carcinoma

Drug discovery across 6 data sets

CSV Excel PDF Print Column Visibility Show 8 entries Search:

Dataset	Module	sig_id	Cell_Line	pert_name	pert_type	pval_perturbation	qval_perturbation	ES	NES	nMoreExtreme	size	Phenotypes	Statistical_Test	pval_phenotype	qval_phenotype	Descriptive_Statistics	Chemical_Phenotype_Direction
LHC	Module-112	CPC013_HEPG2_6H:BRD-K49810818-001-01-0:10	HEPG2	sorafenib	trt_cp	0.0114	0.0446	-0.4431	-1.8227	1	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC015_HEPG2_6H:BRD-K73589491-001-05-4:10	HEPG2	nizatidine	trt_cp	0.0017	0.0341	-0.5687	-1.9697	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC018_HEPG2_6H:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0038	0.0341	-0.4938	-2.0441	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC013_MCF7_24H:BRD-K49810818-001-01-0:10	MCF7	sorafenib	trt_cp	0.0203	0.0702	-0.4375	-1.6111	6	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC013_MCF7_6H:BRD-K49810818-001-01-0:10	MCF7	sorafenib	trt_cp	0.0054	0.0341	-0.5196	-1.9476	1	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPD002_MCF7_6H:BRD-K70401846-001-03-3:10	MCF7	erlotinib	trt_cp	0.0039	0.0341	-0.5105	-2.007	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	LJP002_MCF7_24H:BRD-K70401846-001-04-1:10	MCF7	erlotinib	trt_cp	0.0206	0.0702	-0.3627	-1.5352	3	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC018_PHH_24H:BRD-K46652470-001-02-6:10	PHH	nizatidine	trt_cp	0.0039	0.0341	-0.5339	-2.1747	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed

Showing 1 to 8 of 8 entries (filtered from 329,000 total entries)

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Perturbation-AMARETTO report LHC

Perturbation-AMARETTO v2: drug discovery using chemical perturbations from LINCS/CMAP

Case Study 1: virus-induced hepatocellular carcinoma

Drug discovery across 6 data sets

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Dataset	Module	sig_id	Cell_Line	pert_name	pert_type	pval_perturbation	qval_perturbation	ES	NES	nMoreExtreme	size	Phenotypes	Statistical_Test	pval_phenotype	qval_phenotype	Descriptive_Statistics	Chemical_Phenoype_Direction
LHC	Module-112	CPC013_HEPG2_6H:BRD-K49810818-001-01-0:10	HEPG2	sorafenib	trt_cp	0.0114	0.0446	-0.4431	-1.8227	1	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC015_HEPG2_6H:BRD-K73589491-001-05-4:10	HEPG2	nizatidine	trt_cp	0.0017	0.0341	-0.5687	-1.9697	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC018_HEPG2_6H:BRD-K48652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0038	0.0341	-0.4938	-2.0441	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC013_MCF7_24H:BRD-K49810818-001-01-0:10	MCF7	sorafenib	trt_cp	0.0203	0.0702	-0.4375	-1.6111	6	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC013_MCF7_6H:BRD-K49810818-001-01-0:10	MCF7	sorafenib	trt_cp	0.0054	0.0341	-0.5196	-1.9476	1	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPD002_MCF7_6H:BRD-K70401846-001-03-3:10	MCF7	erlotinib	trt_cp	0.0039	0.0341	-0.5105	-2.007	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	LJP002_MCF7_24H:BRD-K70401846-001-04-1:10	MCF7	erlotinib	trt_cp	0.0206	0.0702	-0.3627	-1.5352	3	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC018_PHH_24H:BRD-K48652470-001-02-6:10	PHH	nizatidine	trt_cp	0.0039	0.0341	-0.5339	-2.1747	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed

Showing 1 to 8 of 8 entries (filtered from 329,000 total entries) Previous 1 Next

Data set, Module Experiment, Cell line, Compound, Statistics

Phenotype: Survival Statistics

Reversed?

<https://pochetlab.shinyapps.io/pAMARETTO> Liver 6DS Drugs Diseases/ (under development)

Perturbation-AMARETTO report LHC

Perturbation-AMARETTO v2: drug discovery using chemical perturbations from LINCS/CMAP

Case Study 1: virus-induced hepatocellular carcinoma

Drug discovery across 6 data sets

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Dataset	Module	sig_id	Cell_Line	pert_name	pert_type	pval_perturbation	qval_perturbation	ES	NES	nMoreExtreme	size	Phenotypes	Statistical_Test	pval_phenotype	qval_phenotype	Descriptive_Statistics	Chemical_Phenoype_Direction
LHC	Module-112	CPC013_HEPG2_6H:BRD-K49810818-001-01-0:10	HEPG2	sorafenib	trt_cp	0.0114	0.0446	-0.4431	-1.8227	1	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC015_HEPG2_6H:BRD-K73589491-001-05-4:10	HEPG2	nizatidine	trt_cp	0.0017	0.0341	-0.5687	-1.9697	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC018_HEPG2_6H:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0038	0.0341	-0.4938	-2.0441	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC013_MCF7_24H:BRD-K49810818-001-01-0:10	MCF7	sorafenib	trt_cp	0.0203	0.0702	-0.4375	-1.6111	6	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC013_MCF7_6H:BRD-K49810818-001-01-0:10	MCF7	sorafenib	trt_cp	0.0054	0.0341	-0.5196	-1.9476	1	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPD002_MCF7_6H:BRD-K70401846-001-03-3:10	MCF7	erlotinib	trt_cp	0.0039	0.0341	-0.5105	-2.007	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	LJP002_MCF7_24H:BRD-K70401846-001-04-1:10	MCF7	erlotinib	trt_cp	0.0206	0.0702	-0.3627	-1.5352	3	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed
LHC	Module-112	CPC018_PHH_24H:BRD-K46652470-001-02-6:10	PHH	nizatidine	trt_cp	0.0039	0.0341	-0.5339	-2.1747	0	38	SurvivalTime (COXPROPHAZARDTIMETOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140746	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877, 2.8352], Wald Statistic: 10.34	reversed

Showing 1 to 8 of 8 entries (filtered from 329,000 total entries)

Previous 1 Next

Search drug treatments reversing survival-associated Module 112 using chemical perturbations from LINCS/CMAP, Query: Sorafenib, Erlotinib, Nizatidine

https://pochetlab.shinyapps.io/pAMARETTO_Liver_6DS_Drugs_Diseases/ (under development)

AMARETTO report LHC

MYC-driven Module 112

Summary of MYC-regulated Module 112:

MYC CNV amplification, associated with induced MYC expression, and MYC is activator of its target genes

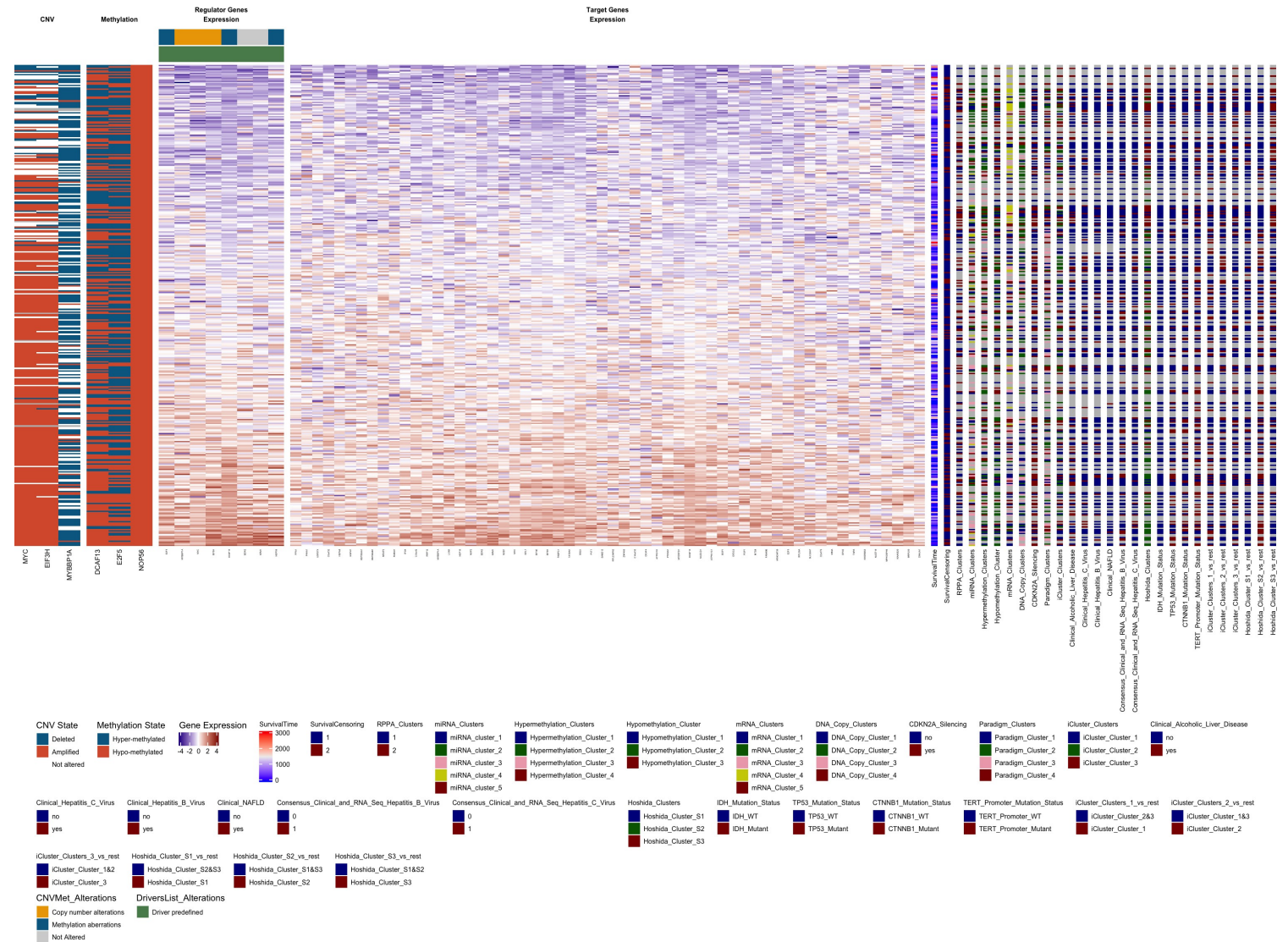
Associated with survival: higher expression, poorer survival

Enriched for gene signature
HOSHIDA_LIVER_CANCER_SUBCLASS_S2 (Genes from 'subtype S2' signature of hepatocellular carcinoma (HCC): proliferation, MYC and AKT1 activation.)

Drivers validated:

- MYC: ENCODE and ChEA ChIP-Seq, bound to its target genes
- MYC, BZW2, E2F5, EIF3H, NPM1: LINCS/CMAP genetic perturbations, modulating drivers modulates its target genes

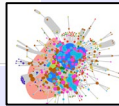
Drugs: Sorafenib, Regorafenib, Erlotinib, Nizatidine,...
reverse survival-associated behavior of driver and target genes of Module 112



Community-AMARETTO report virus-induced LIHC

Community	CCLE_Liver	scHBV	scHCV	TCGA_LIHC	scHBV	scHCV	ImmuneSignatures	LiverSignatures	StemSignatures
Community 1	Module 13, Module 16, Module 23, Module 24, Module 25, Module 70, Module 82, Module 87, Module 102, Module 110, Module 116, Module 142, Module 151, Module 147	Module 31, Module 41, Module 50	Module 22, Module 93, Module 100	Module 3, Module 7, Module 10, Module 13, Module 14, Module 26, Module 30, Module 33, Module 37, Module 40, Module 43, Module 55, Module 76, Module 80, Module 81, Module 85, Module 89, Module 97, Module 110, Module 115, Module 118, Module 121, Module 124, Module 127, Module 128, Module 141, Module 145	Module 14, Module 15, Module 16, Module 19, Module 21, Module 25, Module 28, Module 38, Module 41, Module 45, Module 46, Module 47, Module 48, Module 50, Module 51, Module 52, Module 53, Module 54, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145, Module 146, Module 147, Module 148, Module 149, Module 150, Module 151, Module 152, Module 153, Module 154, Module 155, Module 156, Module 157, Module 158, Module 159, Module 160, Module 161, Module 162, Module 163, Module 164, Module 165, Module 166, Module 167, Module 168, Module 169, Module 170, Module 171, Module 172, Module 173, Module 174, Module 175, Module 176, Module 177, Module 178, Module 179, Module 180, Module 181, Module 182, Module 183, Module 184, Module 185, Module 186, Module 187, Module 188, Module 189, Module 190, Module 191, Module 192, Module 193, Module 194, Module 195, Module 196, Module 197, Module 198, Module 199, Module 200	Module 11, Module 35, Module 42, Module 43, Module 44, Module 45, Module 46, Module 47, Module 48, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145, Module 146, Module 147, Module 148, Module 149, Module 150, Module 151, Module 152, Module 153, Module 154, Module 155, Module 156, Module 157, Module 158, Module 159, Module 160, Module 161, Module 162, Module 163, Module 164, Module 165, Module 166, Module 167, Module 168, Module 169, Module 170, Module 171, Module 172, Module 173, Module 174, Module 175, Module 176, Module 177, Module 178, Module 179, Module 180, Module 181, Module 182, Module 183, Module 184, Module 185, Module 186, Module 187, Module 188, Module 189, Module 190, Module 191, Module 192, Module 193, Module 194, Module 195, Module 196, Module 197, Module 198, Module 199, Module 200	OBERSORT_MMP_CELL_RESTING	HOSHDA_LIVER_CANCER_SURVIVAL_LP	BENFORAH_EED_TARGETS, BENFORAH_ES_WITH_HOBTMETS, BENFORAH_PRC2_TARGETS, BENFORAH_SUZ12_TARGETS

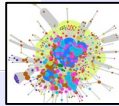
> Genes from 'subtype S1' signature of hepatocellular carcinoma (HCC): aberrant activation of the WNT signaling pathway
 > Survival signature genes defined in adjacent liver tissue: genes correlated with poor survival of hepatocellular carcinoma (HCC) patients
 > Polycomb Repression Complex 2 (PRC) targets; identified by ChIP on chip on human embryonic stem cells as genes that possess the trimethylated H3K27 mark in their promoters and are bound by SUZ12 and EED Polycomb proteins
 > IL8 pan-etiology driver of HCV and HBV virus-induced HCC associated with HCV and HBV viral load and HCC survival



Community 1

Community	CCLE_Liver	scHBV	scHCV	TCGA_LIHC	scHBV	scHCV	ImmuneSignatures	LiverSignatures	StemSignatures
Community 3	Module 4, Module 5, Module 10, Module 12, Module 20, Module 21, Module 27, Module 32, Module 33, Module 41, Module 47, Module 50, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145, Module 146, Module 147, Module 148, Module 149, Module 150, Module 151, Module 152, Module 153, Module 154, Module 155, Module 156, Module 157, Module 158, Module 159, Module 160, Module 161, Module 162, Module 163, Module 164, Module 165, Module 166, Module 167, Module 168, Module 169, Module 170, Module 171, Module 172, Module 173, Module 174, Module 175, Module 176, Module 177, Module 178, Module 179, Module 180, Module 181, Module 182, Module 183, Module 184, Module 185, Module 186, Module 187, Module 188, Module 189, Module 190, Module 191, Module 192, Module 193, Module 194, Module 195, Module 196, Module 197, Module 198, Module 199, Module 200	Module 1, Module 2, Module 3, Module 4, Module 5, Module 6, Module 7, Module 8, Module 9, Module 10, Module 11, Module 12, Module 13, Module 14, Module 15, Module 16, Module 17, Module 18, Module 19, Module 20, Module 21, Module 22, Module 23, Module 24, Module 25, Module 26, Module 27, Module 28, Module 29, Module 30, Module 31, Module 32, Module 33, Module 34, Module 35, Module 36, Module 37, Module 38, Module 39, Module 40, Module 41, Module 42, Module 43, Module 44, Module 45, Module 46, Module 47, Module 48, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 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Module 191, Module 192, Module 193, Module 194, Module 195, Module 196, Module 197, Module 198, Module 199, Module 200	Module 1, Module 25, Module 28, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145, Module 146, Module 147, Module 148, Module 149, Module 150, Module 151, Module 152, Module 153, Module 154, Module 155, Module 156, Module 157, Module 158, Module 159, Module 160, Module 161, Module 162, Module 163, Module 164, Module 165, Module 166, Module 167, Module 168, Module 169, Module 170, Module 171, Module 172, Module 173, Module 174, Module 175, Module 176, Module 177, Module 178, Module 179, Module 180, Module 181, Module 182, Module 183, Module 184, Module 185, Module 186, Module 187, Module 188, Module 189, Module 190, Module 191, Module 192, Module 193, Module 194, Module 195, Module 196, Module 197, Module 198, Module 199, Module 200	HOSHDA_LIVER_CANCER_SUBCLASS_B2	BENFORAH_MYC_MAX_TARGETS, BENFORAH_MYC_TARGETS_WITH_EBOX, BENFORAH_NANOG_TARGETS, BENFORAH_SCCT_TARGETS, BENFORAH_SOC1_TARGETS, BENFORAH_SOC2_TARGETS				

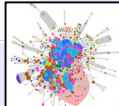
> Genes from 'subtype S2' signature of hepatocellular carcinoma (HCC): proliferation, MYC and AKT1 activation
 > MYC targets; targets of c-Myc and Max identified by ChIP on chip in a Burkitt's lymphoma cell line; overlap set; and in cultured cell lines, focusing on E-box-containing genes; high affinity bound subset
 > CORE stemness genes upregulated and identified by ChIP on chip as NOS (Nanog, OCT4, SOX2) transcription factor targets in human embryonic stem cells
 > STX7 pan-etiology driver of HCV and HBV virus-induced HCC



Community 3

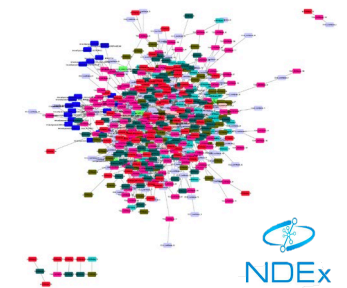
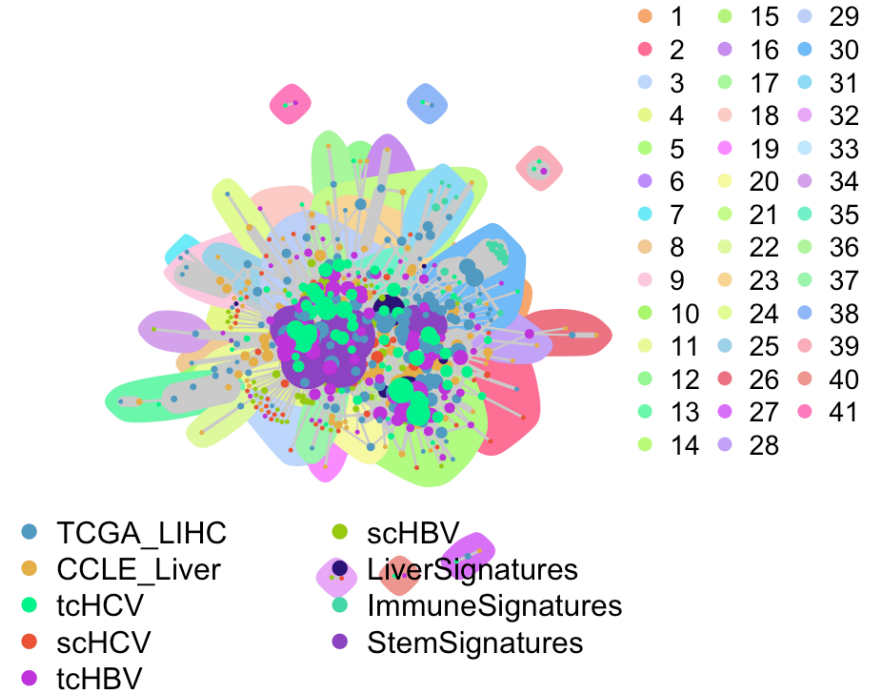
Community	CCLE_Liver	scHBV	scHCV	TCGA_LIHC	scHBV	scHCV	ImmuneSignatures	LiverSignatures	StemSignatures
Community 5	Module 6, Module 05, Module 10, Module 07, Module 11, Module 12, Module 17, Module 11, Module 03, Module 04, Module 10	Module 23, Module 28, Module 31, Module 71, Module 81, Module 82	Module 6, Module 24, Module 41, Module 83, Module 85, Module 89	Module 12, Module 22, Module 24, Module 30, Module 32, Module 34, Module 35, Module 36, Module 37, Module 38, Module 39, Module 40, Module 41, Module 42, Module 43, Module 44, Module 45, Module 46, Module 47, Module 48, Module 49, Module 50, Module 51, Module 52, Module 53, Module 54, Module 55, Module 56, Module 57, Module 58, Module 59, Module 60, Module 61, Module 62, Module 63, Module 64, Module 65, Module 66, Module 67, Module 68, Module 69, Module 70, Module 71, Module 72, Module 73, Module 74, Module 75, Module 76, Module 77, Module 78, Module 79, Module 80, Module 81, Module 82, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 91, Module 92, Module 93, Module 94, Module 95, Module 96, Module 97, Module 98, Module 99, Module 100, Module 101, Module 102, Module 103, Module 104, Module 105, Module 106, Module 107, Module 108, Module 109, Module 110, Module 111, Module 112, Module 113, Module 114, Module 115, Module 116, Module 117, Module 118, Module 119, Module 120, Module 121, Module 122, Module 123, Module 124, Module 125, Module 126, Module 127, Module 128, Module 129, Module 130, Module 131, Module 132, Module 133, Module 134, Module 135, Module 136, Module 137, Module 138, Module 139, Module 140, Module 141, Module 142, Module 143, Module 144, Module 145, Module 146, Module 147, Module 148, Module 149, Module 150, Module 151, Module 152, Module 153, Module 154, Module 155, Module 156, Module 157, Module 158, Module 159, Module 160, Module 161, Module 162, Module 163, Module 164, Module 165, Module 166, Module 167, Module 168, Module 169, Module 170, Module 171, Module 172, Module 173, Module 174, Module 175, Module 176, Module 177, Module 178, Module 179, Module 180, Module 181, Module 182, Module 183, Module 184, Module 185, Module 186, Module 187, Module 188, Module 189, Module 190, Module 191, Module 192, Module 193, Module 194, Module 195, Module 196, Module 197, Module 198, Module 199, Module 200	HOSHDA_LIVER_CANCER_LATE_RECURRENCE_ON, HOSHDA_LIVER_CANCER_SUBCLASS_B3, HOSHDA_LIVER_CANCER_SURVIVAL_ON				

> Genes from 'subtype S3' signature of hepatocellular carcinoma (HCC): hepatocyte differentiation
 > Survival signature genes defined in adjacent liver tissue: genes correlated with good survival of hepatocellular carcinoma (HCC) patients
 > Liver specific genes from Human Gene Expression Index, the HuGE Index, <http://www.hugeindex.org>
 > APOC3 pan-etiology driver of HCV and HBV virus-induced HCC validated in all 6 data sources using genetic perturbations of APOC3 in the HepG2 liver cancer cell line



Community 5

Community Network Visualization



Perturbation-AMARETTO report virus-induced LIHC:

Driver validation & discovery: across modules in tcHCV, scHCV, tcHBV, scHBV, CCLE and LIHC

Case Study 1: virus-induced hepatocellular carcinoma

Driver discovery across 6 data sets

PerturbationID	Cell_Line	GeneSymbol	EntrezID	PerturbationType	Type	DataSetFrequency	CCLE	TCGA	scHBV	scHCV	tcHBV	tcHCV
							CCLE	LIHC	scHBV	scHCV	tcHBV	tcHCV
CGS001_HEPG2_96HAQT.1.5	HEPG2	AOT	183	trt_sh.cgs	best inferred	6	Module 59 : T_CD (w = 0), escore-pval-padj-zscore	Module 63 : T_CD (w = 0), escore-pval-padj-zscore	Module 71 : A_D (w = 0.3526), escore-pval-padj-zscore	Module 22 : R_D (w = -0.0062), pval-padj-zscore; Module 53 : T_CD (w = 0), escore-pval-padj-zscore	Module 83 : A_D (w = 0.116), escore-pval-padj-zscore	Module 96 : T_CD (w = 0), escore-pval-padj-zscore
CGS001_HEPG2_96HAPOC3.1.5	HEPG2	APOC3	345	trt_sh.cgs	inferred	6	Module 92 : T_CD (w = 0), escore-pval-padj-zscore	Module 53 : A_D (w = 0.0681), escore-pval-padj-zscore	Module 23 : A_D (w = 0.0448), escore-pval-padj-zscore	Module 8 : A_D (w = 3e-04), escore-pval-padj-zscore	Module 97 : A_D (w = 0.1519), escore-pval-padj-zscore	Module 79 : A_D (w = 0.1892), escore-pval-padj-zscore
CGS001_PC3_96H.CBR1.2	PC3	CBR1	873	trt_sh.cgs	landmark	6	Module 73 : T_CD (w = 0), escore-pval-padj-zscore	Module 75 : T_CD (w = 0), escore-pval-padj-zscore	Module 20 : T_CD (w = 0), escore-pval-padj-zscore	Module 83 : A_D (w = 0.0269), escore-pval-padj-zscore	Module 89 : R_D (w = -0.2644), escore-pval-padj-zscore; Module 114 : T_CD (w = 0), escore-pval-padj-zscore	Module 54 : T_CD (w = 0), escore-pval-padj-zscore
OEC001_PC3_72H.CCSBBROAD304_03269-666	PC3	CD320	51293	trt_oe	landmark	6	Module 147 : T_CD (w = 0), escore-pval-padj-zscore	Module 76 : T_CD (w = 0), escore-pval-padj-zscore	Module 80 : A_D (w = 0.3247), escore-pval-padj-zscore; Module 91 : A_D (w = 0.0021), escore-pval-padj-zscore	Module 48 : T_CD (w = 0), escore-pval-padj-zscore	Module 60 : T_CD (w = 0), escore-pval-padj-zscore	Module 142 : T_CD (w = 0), escore-pval-padj-zscore
CGS001_MCF7_96H.IIL8.2	MCF7	CXCL8	3576	trt_sh.cgs	best inferred	6	Module 83 : T_CD (w = 0), escore-pval-padj-zscore	Module 115 : A_D (w = 0.0079), escore-pval-padj-zscore	Module 16 : A_D (w = 0.0266), escore-pval-padj-zscore; Module 41 : T_CD (w = 0), escore-pval-padj-zscore	Module 93 : A_D (w = 0.0609), escore-pval-padj-zscore	Module 36 : A_D (w = 0.2325), escore-pval-padj-zscore	Module 130 : A_D (w = 4e-04), escore-pval-padj-zscore
CGS001_PC3_96H.DRAP1.2	PC3	DRAP1	10599	trt_sh.cgs	landmark	6	Module 78 : A_D (w = 0.4877), escore-pval-padj-zscore; Module 121 : R_D (w = -0.0039), pval-padj-zscore	Module 94 : T_CD (w = 0), escore-pval-padj-zscore	Module 15 : A_D (w = 0.001), escore-pval-padj-zscore; Module 73 : A_D (w = 0.0907), escore-pval-padj-zscore	Module 79 : T_CD (w = 0), escore-pval-padj-zscore	Module 67 : T_CD (w = 0), escore-pval-padj-zscore	Module 36 : T_CD (w = 0), escore-pval-padj-zscore
CGS001_A549_96H.FAH.1	A549	FANCA	2175	trt_sh.cgs	best inferred	6	Module 80 : T (w = 0), escore-pval-padj-zscore; Module 94 : T (w = 0), escore-pval-padj-zscore	Module 75 : T (w = 0), escore-pval-padj-zscore; Module 90 : T (w = 0), escore-pval-padj-zscore	Module 82 : T (w = 0), escore-pval-padj-zscore	Module 35 : T (w = 0), escore-pval-padj-zscore; Module 51 : T (w = 0), zscore	Module 19 : T (w = 0), escore-pval-padj-zscore; Module 80 : T (w = 0), escore-pval-padj-zscore	Module 52 : T (w = 0), escore-pval-padj-zscore; Module 131 : T (w = 0), escore-pval-padj-zscore
OEB005_HT29_96H.BRDN0000410732-666	HT29	GABPB1	2553	trt_oe	landmark	6	Module 94 : T_CD (w = 0), escore-pval-padj-zscore	Module 69 : T_CD (w = 0), escore-pval-padj-zscore	Module 89 : A_D (w = 0.0039), escore-pval-padj-zscore	Module 55 : A_D (w = 0.1145), escore-pval-padj-zscore	Module 65 : T_CD (w = 0), escore-pval-padj-zscore	Module 30 : T_CD (w = 0), escore-pval-padj-zscore
OEC001_A375_96H.CCSBBROAD304_03340-666	A375	LSR	51599	trt_oe	landmark	6	Module 71 : T (w = 0), escore-pval-padj-zscore	Module 42 : T (w = 0), escore-pval-padj-zscore	Module 12 : T (w = 0), escore-pval-padj-zscore	Module 65 : T (w = 0), escore-pval-padj-zscore	Module 109 : T (w = 0), escore-pval-padj-zscore	Module 66 : T (w = 0), escore-pval-padj-zscore
OEB006_A549_96H.BRDN0000462006-666	A549	LSR	51599	trt_oe	landmark	6	Module 71 : T (w = 0), escore-pval-padj-zscore	Module 42 : T (w = 0), escore-pval-padj-zscore	Module 12 : T (w = 0), escore-pval-padj-zscore	Module 65 : T (w = 0), escore-pval-padj-zscore	Module 109 : T (w = 0), escore-pval-padj-zscore	Module 66 : T (w = 0), escore-pval-padj-zscore
CGS001_HCC515_96H.MRPL12.2	HCC515	MRPL12	6182	trt_sh.cgs	landmark	6	Module 123 : T (w = 0), escore-pval-padj-zscore	Module 120 : T (w = 0), escore-pval-padj-zscore	Module 28 : T (w = 0), escore-pval-padj-zscore	Module 30 : T (w = 0), escore-pval-padj-zscore	Module 93 : T (w = 0), escore-pval-padj-zscore	Module 44 : T (w = 0), escore-pval-padj-zscore
CGS001_PC3_144H.MRPL12.2	PC3	MRPL12	6182	trt_sh.cgs	landmark	6	Module 123 : T (w = 0), escore-pval-padj-zscore	Module 120 : T (w = 0), escore-pval-padj-zscore	Module 28 : T (w = 0), escore-pval-padj-zscore	Module 30 : T (w = 0), escore-pval-padj-zscore	Module 93 : T (w = 0), escore-pval-padj-zscore	Module 44 : T (w = 0), escore-pval-padj-zscore
CGS001_MCF7_144H.MTHFD2.2	MCF7	MTHFD2	10797	trt_sh.cgs	landmark	6	Module 79 : T_CD (w = 0), escore-pval-padj-zscore	Module 3 : T_CD (w = 0), escore-pval-padj-zscore	Module 71 : T_CD (w = 0), escore-pval-padj-zscore	Module 87 : T_CD (w = 0), escore-pval-padj-zscore	Module 74 : T_CD (w = 0), escore-pval-padj-zscore	Module 148 : A_D (w = 0.0083), escore-pval-padj-zscore
OEC001_A375_96H.CCSBBROAD304_01093-666	A375	NFKBIA	4792	trt_oe	landmark	6	Module 60 : T_CD (w = 0), escore-pval-padj-zscore	Module 85 : T_CD (w = 0), escore-pval-padj-zscore	Module 39 : T_CD (w = 0), escore-pval-padj-zscore	Module 80 : T_CD (w = 0), escore-pval-padj-zscore	Module 112 : T_CD (w = 0), escore-pval-padj-zscore	Module 114 : T_CD (w = 0), escore-pval-padj-zscore
OEB001_HA1E_96H.BRDN0000398867-666	HA1E	NFKBIA	4792	trt_oe	landmark	6	Module 60 : T_CD (w = 0), escore-pval-padj-zscore	Module 85 : T_CD (w = 0), escore-pval-padj-zscore	Module 39 : T_CD (w = 0), escore-pval-padj-zscore	Module 80 : T_CD (w = 0), escore-pval-padj-zscore	Module 112 : T_CD (w = 0), escore-pval-padj-zscore	Module 114 : T_CD (w = 0), escore-pval-padj-zscore
OEB001_HCC515_96H.BRDN0000398867-666	HCC515	NFKBIA	4792	trt_oe	landmark	6	Module 60 : T_CD (w = 0), escore-pval-padj-zscore	Module 85 : T_CD (w = 0), escore-pval-padj-zscore	Module 39 : T_CD (w = 0), escore-pval-padj-zscore	Module 80 : T_CD (w = 0), escore-pval-padj-zscore	Module 112 : T_CD (w = 0), escore-pval-padj-zscore	Module 114 : T_CD (w = 0), escore-pval-padj-zscore
CGS001_HA1E_96H.PCNA.1.5	HA1E	PCNA	5111	trt_sh.cgs	landmark	6	Module 95 : T (w = 0), escore-pval-padj-zscore	Module 149 : T (w = 0), escore-pval-padj-zscore	Module 44 : T (w = 0), escore-pval-padj-zscore	Module 35 : T (w = 0), escore-pval-padj-zscore	Module 60 : T (w = 0), escore-pval-padj-zscore	Module 85 : T (w = 0), escore-pval-padj-zscore
OEB005_MCF7_96H.BRDN0000409395-666	MCF7	PCNA	5111	trt_oe	landmark	6	Module 95 : T (w = 0), escore-pval-padj-zscore	Module 149 : T (w = 0), escore-pval-padj-zscore	Module 44 : T (w = 0), escore-pval-padj-zscore	Module 35 : T (w = 0), escore-pval-padj-zscore	Module 60 : T (w = 0), escore-pval-padj-zscore	Module 85 : T (w = 0), escore-pval-padj-zscore

Experiment, Cell line, Gene perturbed, KO or OE

Validation status in 6 liver disease data sets

Perturbation-AMARETTO report virus-induced LIHC:

Drug discovery: Nizatidine reverses disease-associated modules in scHCV & scHBV (viral load), and LIHC (survival)

Case Study 1: virus-induced hepatocellular carcinoma

Drug discovery across 6 data sets

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Dataset	Module	sig_id	Cell_Line	pert_name	pert_type	pval_perturbation	qual_perturbation	ES	NES	nMoreExtreme	size	Phenotypes	Statistical_Test	pval_phenotype	qual_phenotype	Descriptive_Statistics	Chemical_Phenoype_Direction
LIHC	Module-105	CP C015_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0038	0.0535	-0.5305	-2.1799	0	36	SurvivalTime (COXPROPHAZARDTIMEOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0018766	0.140745	Beta: 0.62117, Hazard Ratio: 1.8611, 95% CI: [1.2581,2.7532], Wald Statistic: 9.67	reversed
LIHC	Module-112	CP C015_HEPG2_SH:BRD-K73589491-001-05-4:10	HEPG2	nizatidine	trt_cp	0.0017	0.0341	-0.5687	-1.9697	0	38	SurvivalTime (COXPROPHAZARDTIMEOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140745	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877,2.8352], Wald Statistic: 10.34	reversed
LIHC	Module-112	CP C018_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0038	0.0341	-0.4938	-2.0441	0	38	SurvivalTime (COXPROPHAZARDTIMEOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0013013	0.140745	Beta: 0.64749, Hazard Ratio: 1.9107, 95% CI: [1.2877,2.8352], Wald Statistic: 10.34	reversed
LIHC	Module-129	CP C018_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0025	0.0155	0.3926	1.5686	1	78	SurvivalTime (COXPROPHAZARDTIMEOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.049614	0.617988461538462	Beta: -0.30619, Hazard Ratio: 0.73625, 95% CI: [0.54234,0.99948], Wald Statistic: 3.85	reversed
LIHC	Module-145	CP C018_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0114	0.0909	-0.3827	-1.5842	2	38	SurvivalTime (COXPROPHAZARDTIMEOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0044566	0.22283	Beta: 0.60976, Hazard Ratio: 1.84, 95% CI: [1.2087,2.8011], Wald Statistic: 8.09	reversed
scHCV	Module-8	CP C015_HEPG2_SH:BRD-K73589491-001-05-4:10	HEPG2	nizatidine	trt_cp	0.0386	0.1512	0.3664	1.4524	13	53	ViralLoad (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000086042	0.000215105	Correlation: -0.64, Statistic: 17500	reversed
scHCV	Module-48	CP C018_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0034	0.1901	-0.4854	-1.9181	0	30	ViralLoad (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	3.5371e-7	0.0000176855	Correlation: 0.706, Statistic: 3130	reversed
scHCV	Module-57	CP C018_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0082	0.1919	-0.3861	-1.6928	1	44	ViralLoad (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.011602	0.0483416866666667	Correlation: 0.395, Statistic: 6450	reversed
scHBV	Module-25	CP C018_HEPG2_SH:BRD-K46652470-001-02-6:10	HEPG2	nizatidine	trt_cp	0.0042	0.1899	-0.3878	-1.7613	0	51	ViralLoad (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.040756	0.5576	Correlation: 0.265, Statistic: 26500	reversed
scHBV	Module-47	CP C015_HEPG2_SH:BRD-K73589491-001-05-4:10	HEPG2	nizatidine	trt_cp	0.0179	0.2449	0.4806	1.6566	6	27	ViralLoad (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.034134	0.5576	Correlation: -0.274, Statistic: 45900	reversed

Showing 1 to 10 of 10 entries (filtered from 329,000 total entries)

Previous 1 Next

Case Study 2

Glioblastoma Multiforme (GBM)
& Low-grade Glioma (LGG)

Community-AMARETTO report GBM/LGG

Community-AMARETTO Report Association of Phenotypes to Communities

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Community	Data Set	Module	Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
All	All	All	All	All	All	0.00000000	All
Community 1	TCGA_LGG	Module 102	IDH.1p19q.Subtype (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	1.5052e-32	1.61271428571429e-31	Statistic: 147
Community 1	TCGA_LGG	Module 102	IDHmut.non.codel (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	1.8077e-27	3.87364285714286e-26	Estimate: -0.798, 95% CI: [-0.907, -0.688], Statistics: 2840
Community 1	TCGA_LGG	Module 102	IDHwt (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	1.4215e-22	3.04607142857143e-21	Estimate: 0.917, 95% CI: [0.774, 1.08], Statistics: 12300
Community 1	TCGA_GBM	Module 102	Subclasses (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	2.7601e-15	4.54961538461538e-15	Statistic: 74.3
Community 1	TCGA_GBM	Module 102	Mesenchymal (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	4.0314e-12	1.23410204081633e-11	Estimate: 0.413, 95% CI: [0.301, 0.525], Statistics: 36400
Community 1	TCGA_GBM	Module 102	G-CIMP (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	8.7648e-9	3.67758333333333e-8	Estimate: -0.58, 95% CI: [-0.74, -0.38], Statistics: 3710
Community 1	TCGA_LGG	Module 102	f29 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.000001022	0.000075915	Correlation: -0.357, Statistic: 1280000
Community 1	TCGA_GBM	Module 102	IDH1status (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00018009	0.000621443181818182	Statistic: 19.9
Community 1	TCGA_LGG	Module 102	IDHmut.codel (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00041739	0.000686047872340425	Estimate: 0.324, 95% CI: [0.147, 0.477], Statistics: 11200
Community 1	TCGA_LGG	Module 102	SurvivalTime (COXPROPHAZARDTIMEOEVENT), SurvivalCensoring (COXPROPHAZARDRIGHTCENSORING)	Survival Analysis: Cox proportional hazards regression (Wald test)	0.0020501	0.00465931818181818	Beta: 0.80074, Hazard Ratio: 1.8235, 95% CI: [1.2448, 2.6716], Wald Statistic: 9.5
Community 1	TCGA_GBM	Module 102	Neural (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0091392	0.0147406451612603	Estimate: -0.189, 95% CI: [-0.335, -0.0433], Statistics: 13600
Community 1	TCGA_GBM	Module 102	Classical (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.031982	0.0487893973469388	Estimate: -0.129, 95% CI: [-0.251, -0.011], Statistics: 21300
Community 1	TCGA_LGG	Module 103	IDHmut.codel (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	2.6111e-24	2.79760714285714e-23	Estimate: -1.1, 95% CI: [-1.28, -0.927], Statistics: 2140
Community 1	TCGA_LGG	Module 103	IDH.1p19q.Subtype (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	8.2739e-24	4.0035e-23	Statistic: 106

Clinical, molecular and imaging-derived phenotypes from TCGA

Community-AMARETTO Report Association of Phenotypes to Communities

CSV Excel PDF Print Column visibility Show [20] entries Search:

Community	Data Set	Module	Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
All	All	All	SPEARMANC	All	All	0.00000000	All
Community 1	TCGA_LGG	Module 102	f29 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.000001022	0.000075915	Correlation: -0.357, Statistic: 1280000
Community 1	TCGA_LGG	Module 104	f5 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000055876	0.0000493023529411785	Correlation: 0.332, Statistic: 638000
Community 1	TCGA_LGG	Module 104	f6 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000062173	0.00007771625	Correlation: -0.331, Statistic: 1270000
Community 1	TCGA_LGG	Module 104	f4 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.00071127	0.00377513763103448	Correlation: 0.251, Statistic: 716000
Community 1	TCGA_GBM	Module 107	PropnCET (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000094704	0.0142058	Correlation: 0.415, Statistic: 116000
Community 1	TCGA_LGG	Module 110	f5 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.00082768	0.002758933333333333	Correlation: -0.248, Statistic: 1190000
Community 1	TCGA_LGG	Module 110	f4 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.010409	0.032526125	Correlation: -0.191, Statistic: 1140000
Community 1	TCGA_LGG	Module 112	f8 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0045288	0.0141525	Correlation: 0.211, Statistic: 754000
Community 1	TCGA_LGG	Module 112	f5 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0057104	0.0145179861018949	Correlation: -0.208, Statistic: 1150000
Community 1	TCGA_LGG	Module 123	f5 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0008606	0.00230441860485116	Correlation: -0.252, Statistic: 1200000
Community 1	TCGA_LGG	Module 123	f6 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.00055167	0.00245779411764706	Correlation: 0.268, Statistic: 711000
Community 1	TCGA_LGG	Module 123	f4 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0045943	0.0164082142857143	Correlation: -0.211, Statistic: 1160000
Community 1	TCGA_LGG	Module 127	f6 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0051505	0.0151485294117647	Correlation: 0.268, Statistic: 757000
Community 1	TCGA_LGG	Module 127	f5 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.012831	0.0287068181818182	Correlation: -0.188, Statistic:

Imaging-derived phenotypes from TCGA/TCIA VASARI/Rembrandt

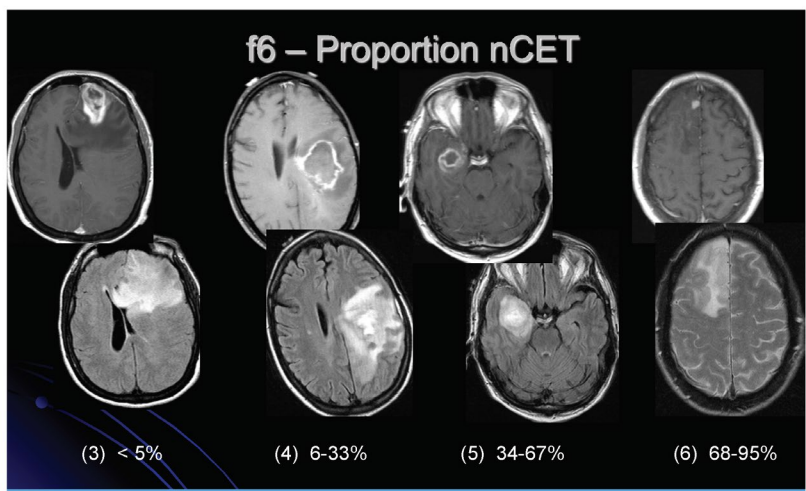
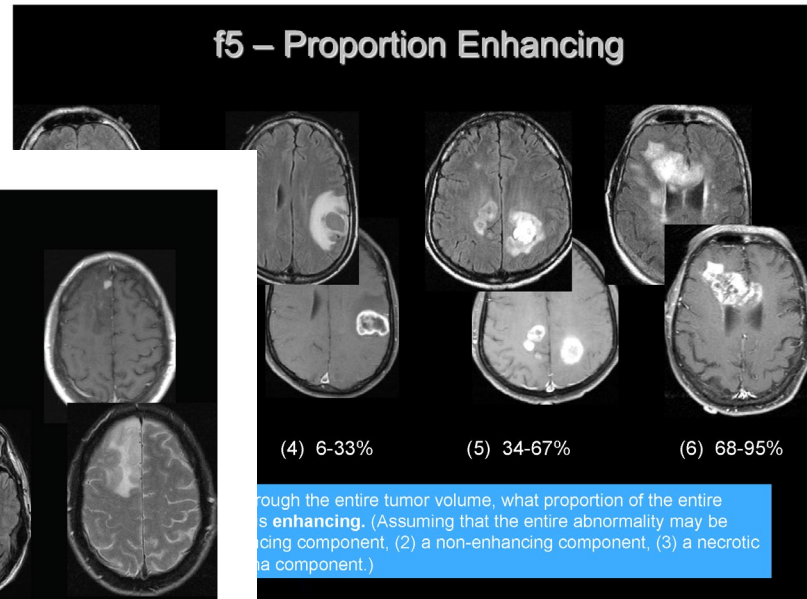
Community-AMARETTO report GBM/LGG

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Vasari MRI Visual Feature Guide

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Search:



Visually, when scanning through the entire tumor volume, what proportion of the entire tumor is estimated to represent non-enhancing tumor (not edema)? Non-enhancing tumor is defined as regions of T2W hyperintensity (less than the intensity of cerebrospinal fluid, with corresponding T1W hypointensity) that are associated with mass effect and architectural distortion, including blurring of the gray-white interface. (Assuming that the entire abnormality may be comprised of: (1) an enhancing component, (2) a non-enhancing component, (3) a necrotic component and (4) a edema component.)

Phenotype	Statistics Test	P-value	FDR Q-value	Descriptive Statistics
129 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000010122	0.000075915	Correlation: -0.337, Statistic: 1280000
15 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000055876	0.0000493023529411785	Correlation: 0.332, Statistic: 638000
16 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000062173	0.00007771625	Correlation: -0.331, Statistic: 1270000
14 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.00071127	0.00377513763103448	Correlation: 0.251, Statistic: 716000
PropnCET (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0000094704	0.00142058	Correlation: 0.415, Statistic: 116000
15 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.00082708	0.0027589333333333333	Correlation: -0.248, Statistic: 1190000
14 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.010409	0.032528125	Correlation: -0.191, Statistic: 1140000
16 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0045288	0.0141525	Correlation: 0.211, Statistic: 754000
15 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0057104	0.0145179861018949	Correlation: -0.208, Statistic: 1150000
15 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0008606	0.002304411860485116	Correlation: -0.252, Statistic: 1200000
16 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.00055167	0.0024577941184706	Correlation: 0.208, Statistic: 711000
14 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0045943	0.0164082142857143	Correlation: -0.211, Statistic: 1160000
16 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.0051505	0.0151485294117847	Correlation: 0.208, Statistic: 757000
15 (SPEARMANCORRTEST)	Continuous or Ordinal Analysis: Spearman rank correlation analysis	0.012831	0.0287068181818182	Correlation: -0.188, Statistic: ...

Estimate: -0.129, 95% CI: -0.251, -0.011, Statistics: 21300

Estimate: -1.1, 95% CI: -1.28, -0.927, Statistics: 140

Statistic: 106

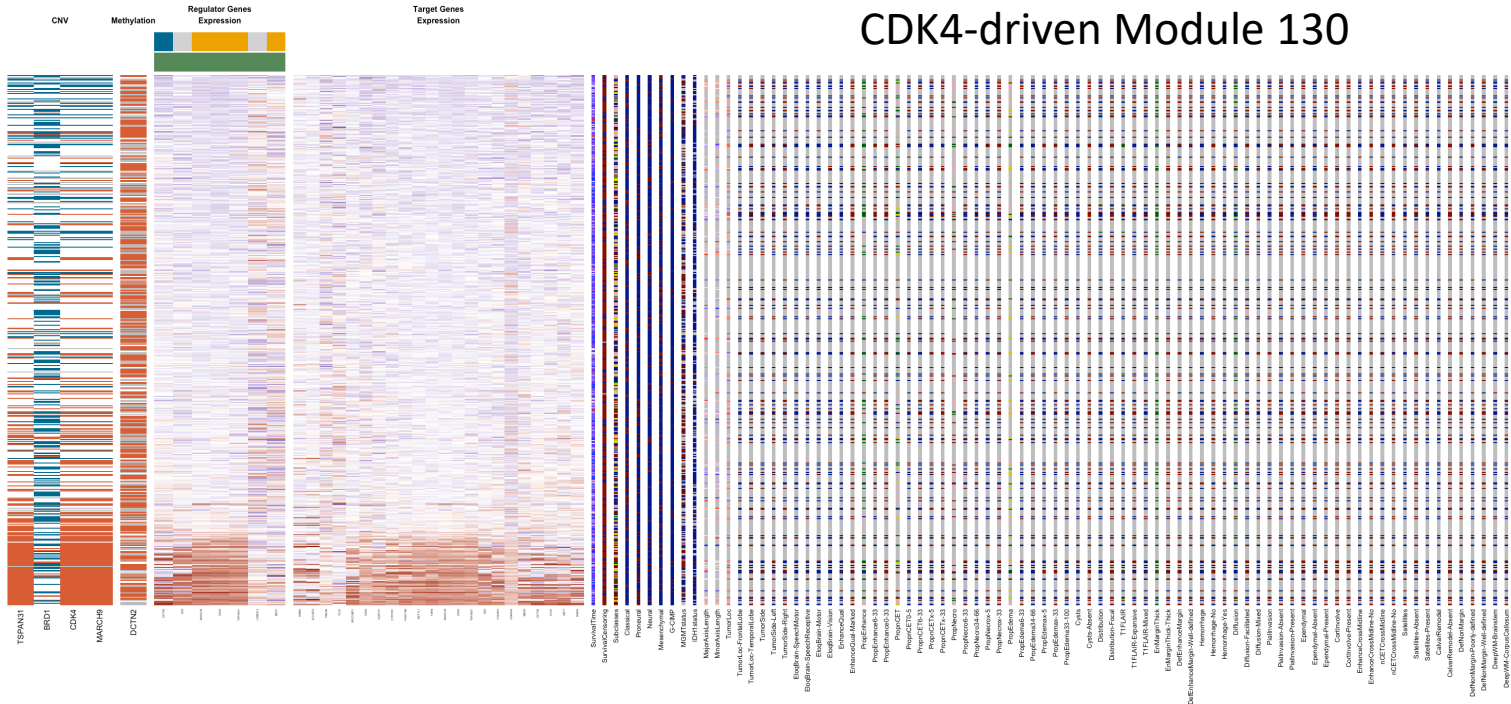
Community 1	TCGA_LGG	Module 123	14 (SPEARMANCORRTEST)	0.0045943	0.0164082142857143	Correlation: -0.211, Statistic: 1160000
Community 1	TCGA_LGG	Module 127	16 (SPEARMANCORRTEST)	0.0051505	0.0151485294117847	Correlation: 0.208, Statistic: 757000
Community 1	TCGA_LGG	Module 127	15 (SPEARMANCORRTEST)	0.012831	0.0287068181818182	Correlation: -0.188, Statistic: ...

Clinical, molecular and imaging-derived phenotypes from TCGA

Imaging-derived phenotypes from TCGA/TCIA VASARI/Rembrandt

AMARETTO report GBM

CDK4-driven Module 130



Module 130 regulated by CDK4

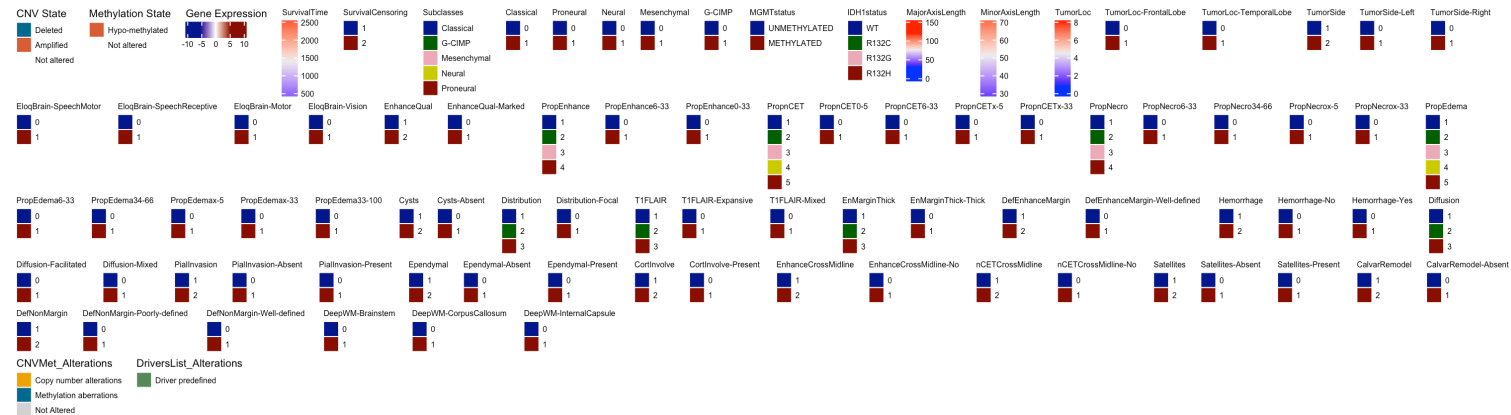
CDK4 amplifications/deletions, associated with induced/repressed CDK4 expression levels

CDK4 is activator of its target genes
Target genes CDKN2A and MDM2

Represents proneural molecular subclass of GBM (higher expression)

Enriched for functional categories:

- TCGA GLIOBLASTOMA COPY NUMBER UP (Genes up-regulated and displaying increased copy number in glioblastoma samples)
- KEGG GLIOMA (Glioma)
- PID RB 1 PATHWAY (Regulation of retinoblastoma protein)
- KEGG P53 SIGNALING PATHWAY (p53 signaling pathway)



Drivers validated (across GBM and related LGG modules): CDK4, CDKN2A, MDM2: LINCS/CMAP

Perturbation-AMARETTO report GBM/LGG

Perturbation-AMARETTO v2: drug discovery using chemical perturbations from LINCS/CMAP

Case Study 2: glioblastoma multiforme and low-grade glioma

Driver discovery across 2 data sets

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Search:

PerturbationID	Cell_Line	GeneSymbol	EntrezID	PerturbationType	Type	DataSetFrequency	GBM	LGG
All	All	["CDK4","C	All	All	All	["2","1"]	Module 130 :	All
CGS001_A375_96H:CDK4:1	A375	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_A549_96H:CDK4:1	A549	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_HA1E_96H:CDK4:1.5	HA1E	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_HCC515_96H:CDK4:2	HCC515	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_HT29_96H:CDK4:1	HT29	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_MCF7_96H:CDK4:2	MCF7	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_PC3_96H:CDK4:2	PC3	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_VCAP_120H:CDK4:5	VCAP	CDK4	1019	trt_sh.cgs	landmark	2	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_HT29_96H:CDKN2A:1	HT29	CDKN2A	1029	trt_sh.cgs	landmark	2	Module 130 : T_CD (w = 0) , escore-pval-padj-zscore	Module 53 : T_CD (w = 0) , escore-pval-padj-zscore
OEB005_HCC515_96H:BRDN0000410000:-666	HCC515	CDK4	1019	trt_oe	landmark	1	Module 130 : A_D (w = 0.198) , zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
CGS001_HEPG2_96H:CDK4:1.5	HEPG2	CDK4	1019	trt_sh.cgs	landmark	1	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , escore-padj-zscore
OEB005_HEPG2_96H:BRDN0000410000:-666	HEPG2	CDK4	1019	trt_oe	landmark	1	Module 130 : A_D (w = 0.198) , padj-zscore	Module 76 : T_CD (w = 0) , escore-pval-padj-zscore
OEB005_MCF7_96H:BRDN0000410000:-666	MCF7	CDK4	1019	trt_oe	landmark	1	Module 130 : A_D (w = 0.198) , escore-pval-padj-zscore	Module 76 : T_CD (w = 0) , pval-padj-zscore
CGS001_HA1E_96H:CDKN2A:1.5	HA1E	CDKN2A	1029	trt_sh.cgs	landmark	1	Module 130 : T_CD (w = 0) , escore-pval-padj-zscore	Module 53 : T_CD (w = 0) , escore-zscore
CGS001_HCC515_96H:CDKN2A:2	HCC515	CDKN2A	1029	trt_sh.cgs	landmark	1	Module 130 : T_CD (w = 0) , escore-pval-padj-zscore	Module 53 : T_CD (w = 0) , zscore
CGS001_MCF7_144H:CDKN2A:2	MCF7	CDKN2A	1029	trt_sh.cgs	landmark	1	Module 130 : T_CD (w = 0) , escore-pval-padj	Module 53 : T_CD (w = 0) , none
CGS001_HT29_96H:MDM2:1	HT29	MDM2	4193	trt_sh.cgs	best inferred	1	Module 130 : T_CD (w = 0) , escore-pval-padj-zscore	Not_in_AMARETTO

Showing 1 to 17 of 17 entries (filtered from 55,753 total entries)

Previous 1 Next

AMARETTO report GBM

Summary of methylation-driven GBM Module 90:

Drivers: methylation-driven RBP1, PNPLA4, NSUN7, SLC25A20, FBXO17, XKR8, RAB36

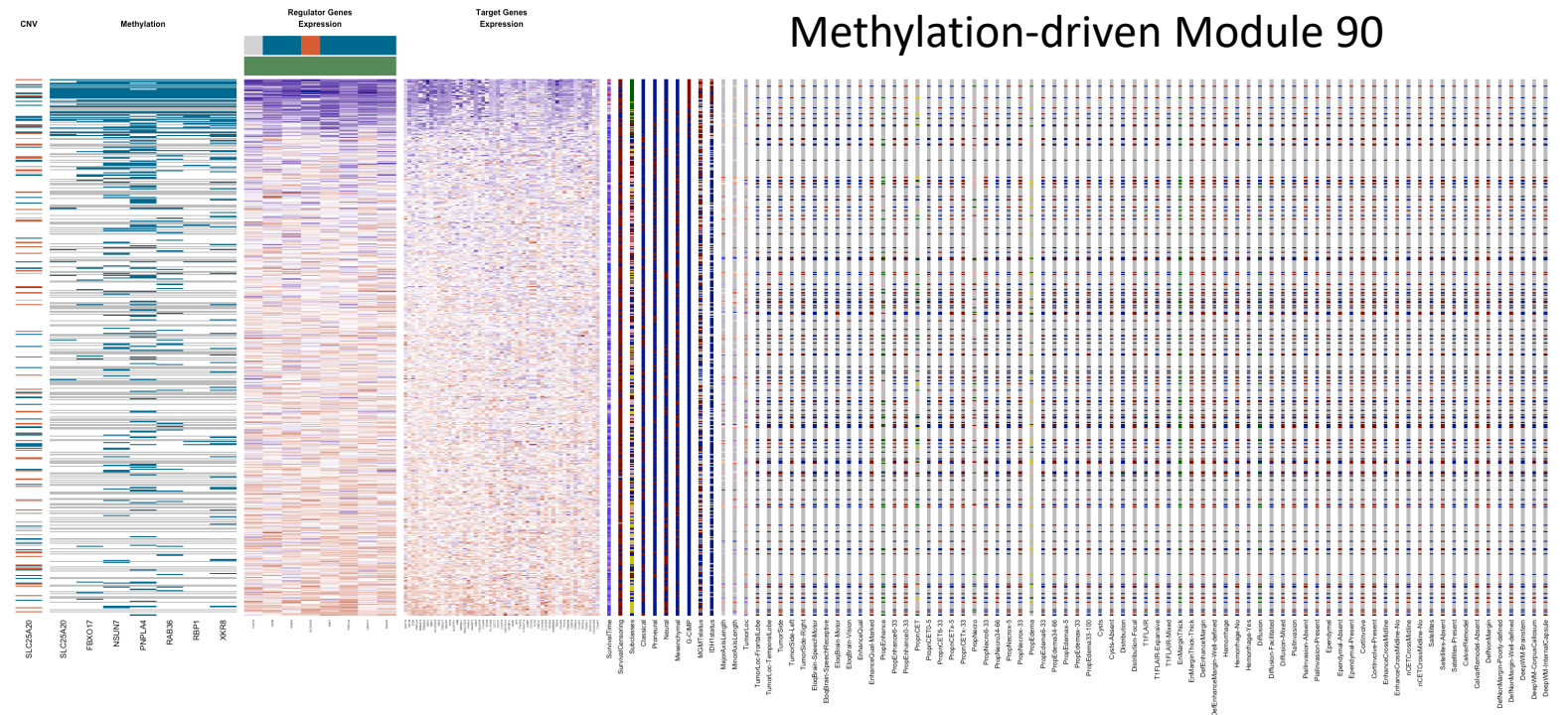
Hypermethylation of drivers, associated with their repressed gene expression levels

Drivers are activators of their targets

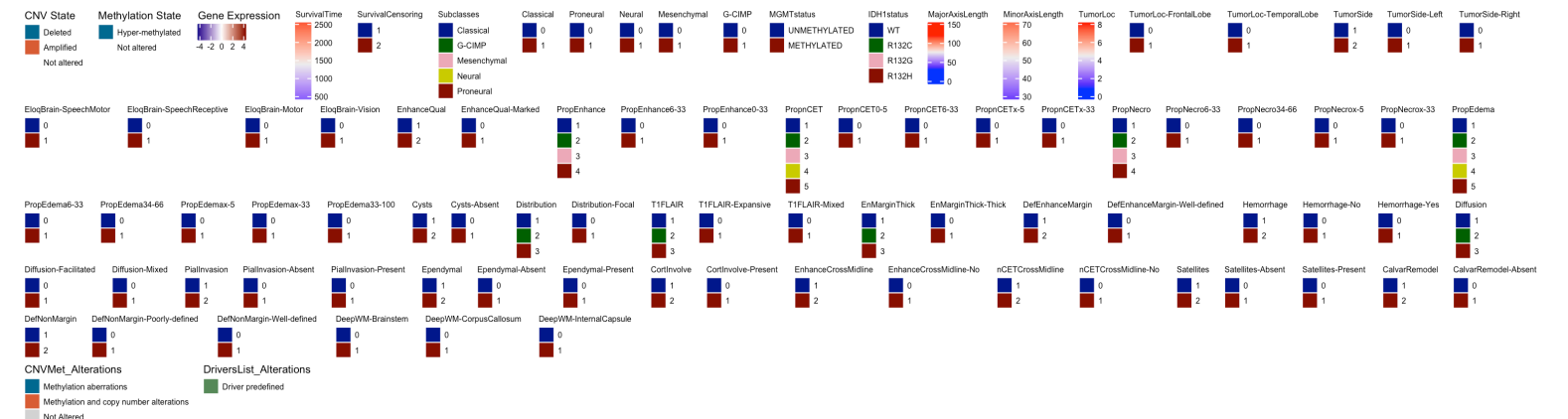
Associated with:

- Survival (lower expression, better survival)
- Molecular subclass G-CIMP (lower expression)
- Molecular markers IDH1 and MGMT

Enriched for NOUSHMEHR GBM SILENCED BY METHYLATION (Top 50 most differentially hypermethylated and down-regulated genes in proneural G-CIMP (a CpG island methylator phenotype) GBM (glioblastoma multiforme) tumors)



Methylation-driven Module 90



AMARETTO report LGG

Summary of methylation-driven LGG Module 150:

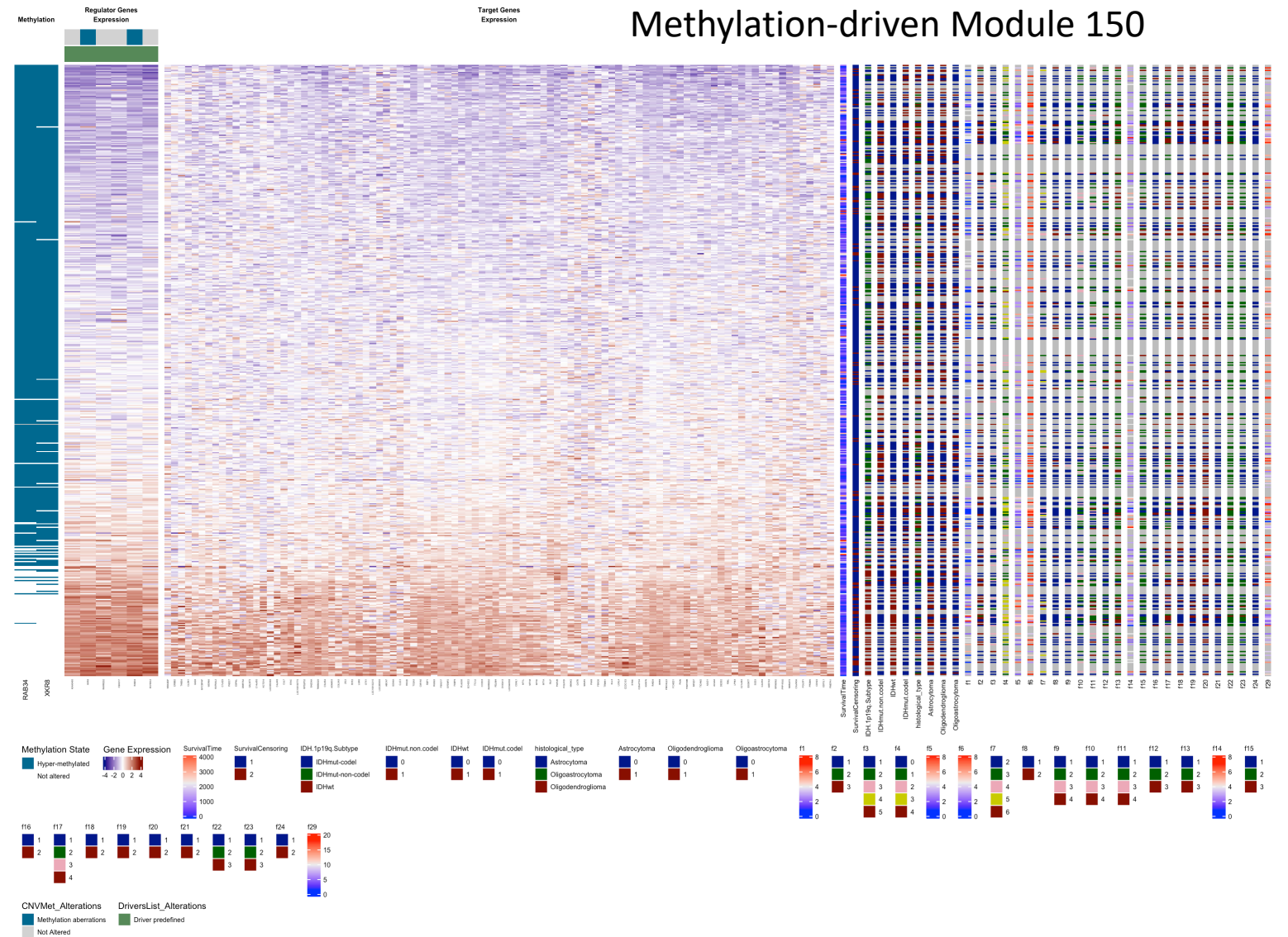
Drivers: methylation-driven, shared drivers with GBM module 90 (Community 1)

Hypermethylation of drivers, associated with their repressed gene expression levels

Drivers are activators of their targets

Associated with:

- Survival (lower expression, better survival)
- Imaging:
 - Proportion nCET (f6): lower expression, higher proportion of non-enhancing tumor (not edema)
 - Proportion Enhancing (f5): higher expression, higher proportion of enhancing tumor



Methylation-driven Module 150

AMARETTO report LGG

Summary of methylation-driven LGG Module 150:

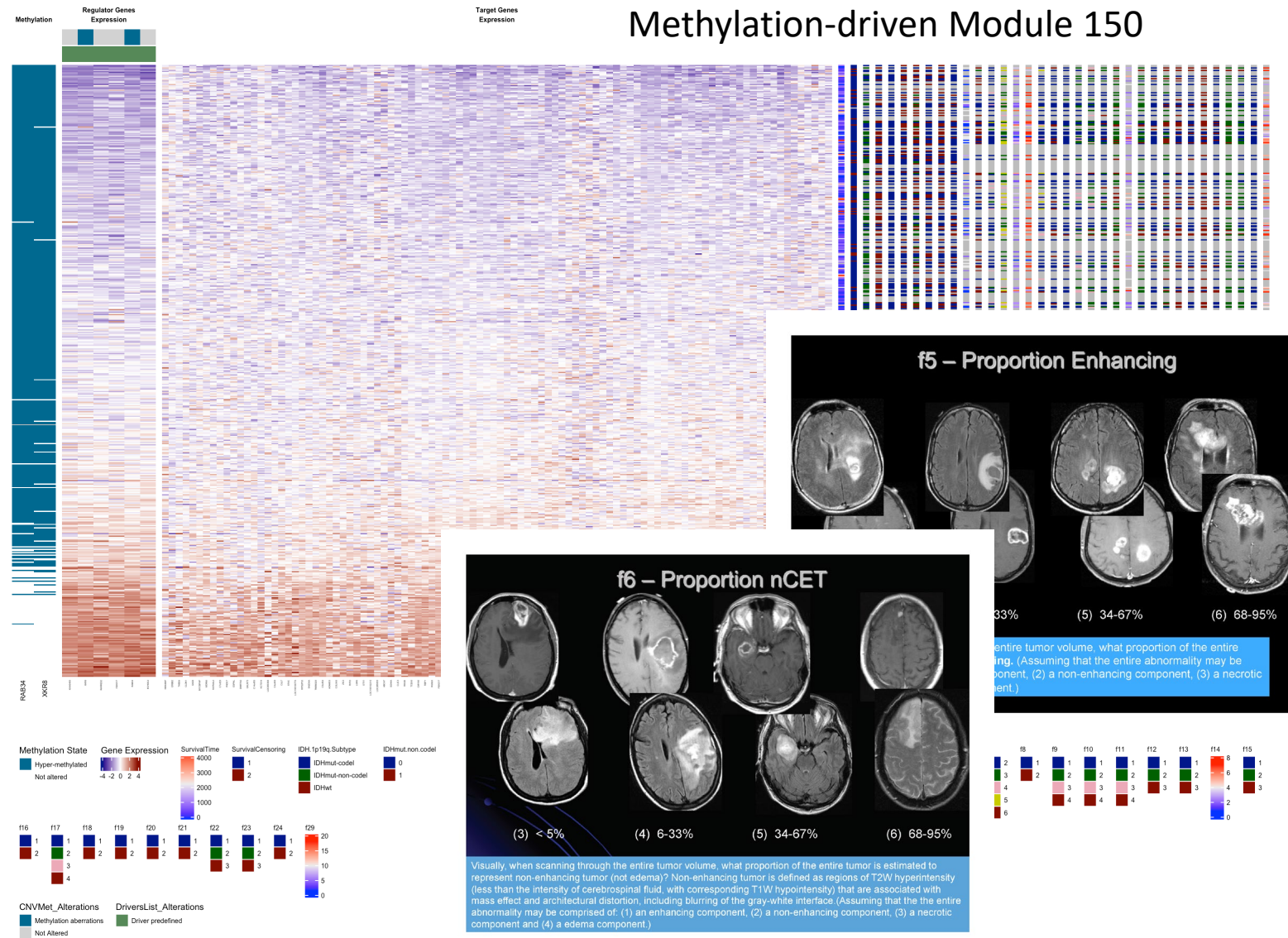
Drivers: methylation-driven, shared drivers with GBM module 90 (Community 1)

Hypermethylation of drivers, associated with their repressed gene expression levels

Drivers are activators of their targets

Associated with:

- Survival (lower expression, better survival)
- Imaging:
 - Proportion nCET (f6): lower expression, higher proportion of non-enhancing tumor (not edema)
 - Proportion Enhancing (f5): higher expression, higher proportion of enhancing tumor



AMARETTO report GBM

Summary of methylation-driven GBM Module 77:

Drivers: methylation-driven

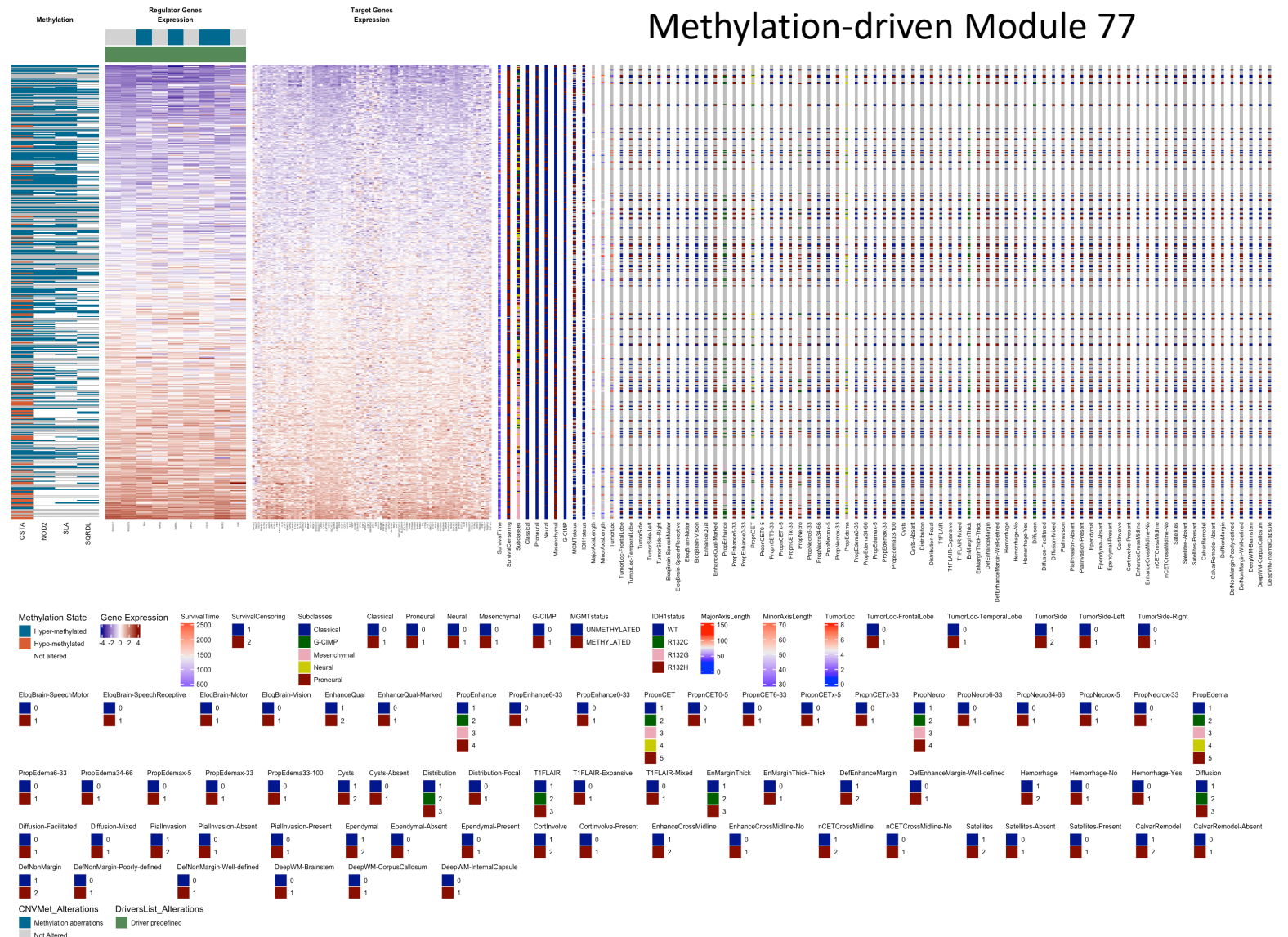
Hypermethylation of drivers, associated with their repressed gene expression levels

Drivers are activators of their targets

Associated with:

- Survival (higher expression, poorer survival)
- Molecular subclass Mesenchymal (higher expression)
- Molecular marker IDH1
- Imaging:
 - Proportion nCET (f6): lower expression, higher proportion of non-enhancing tumor (not edema)

Enriched for VERHAAK GLIOBLASTOMA MESENCHYMAL (Genes correlated with mesenchymal type of glioblastoma multiforme tumors)



Methylation-driven Module 77

AMARETTO report GBM

Summary of methylation-driven GBM Module 77:

Drivers: methylation-driven

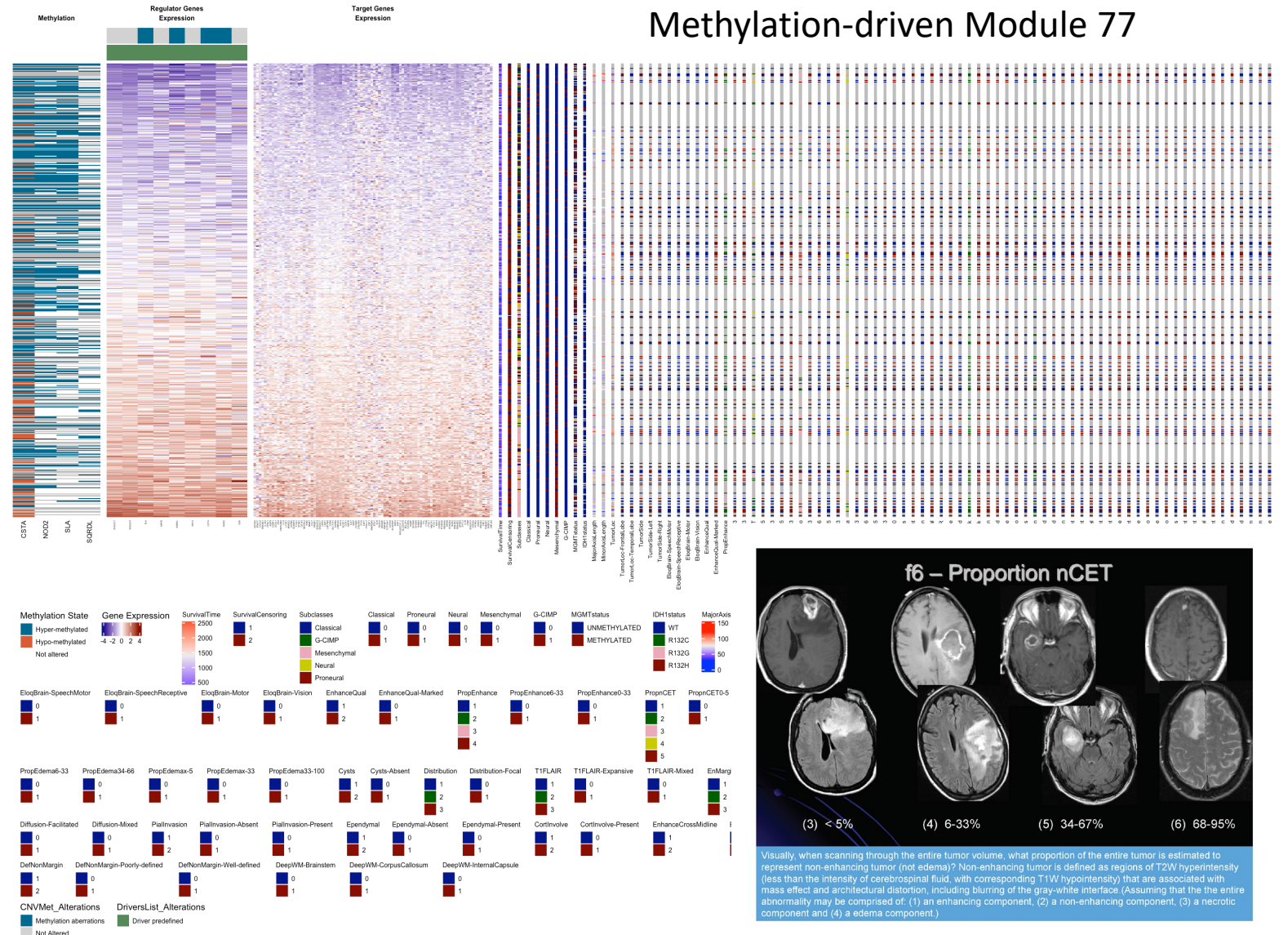
Hypermethylation of drivers, associated with their repressed gene expression levels

Drivers are activators of their targets


Associated with:


- Survival (higher expression, poorer survival)
- Molecular subclass Mesenchymal (higher expression)
- Molecular marker IDH1
- Imaging:
 - Proportion nCET (f6): lower expression, higher proportion of non-enhancing tumor (not edema)

Enriched for VERHAAK GLIOBLASTOMA MESENCHYMAL (Genes correlated with mesenchymal type of glioblastoma multiforme tumors)

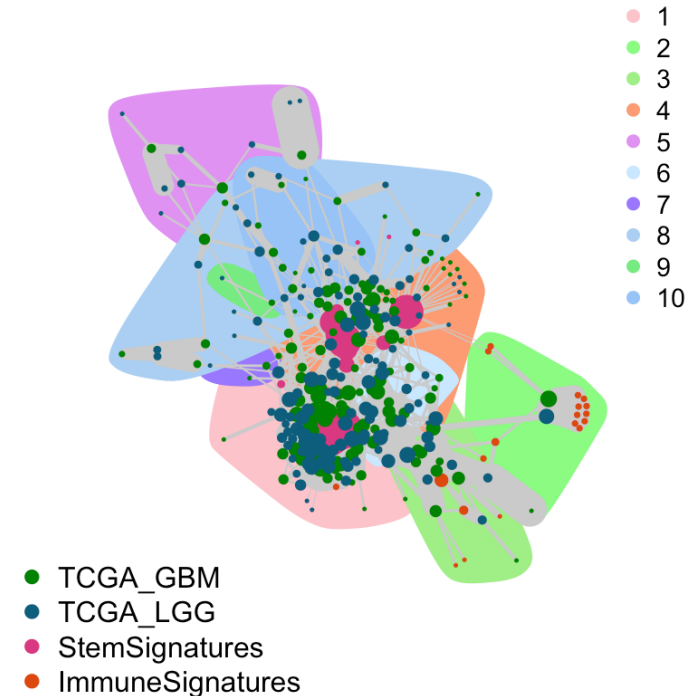


Community-AMARETTO report GBM/LGG

Community	TCGA_GBM	TCGA_LGG	ImmuneSignatures	StemSignatures	
Community 1	Module 3, Module 5, Module 18, Module 22, Module 23, Module 24, Module 25, Module 27, Module 33, Module 37, Module 38, Module 39, Module 41, Module 43, Module 48, Module 54, Module 60, Module 62, Module 66, Module 67, Module 68, Module 71, Module 72, Module 75, Module 78, Module 80, Module 81, Module 82, Module 85, Module 86, Module 87, Module 88, Module 90, Module 91, Module 97, Module 98, Module 99, Module 102, Module 107, Module 110, Module 114, Module 116, Module 117, Module 120, Module 125, Module 129, Module 132, Module 137, Module 138, Module 142, Module 147, Module 150	Module 2, Module 7, Module 8, Module 16, Module 18, Module 19, Module 23, Module 26, Module 27, Module 30, Module 34, Module 35, Module 37, Module 40, Module 43, Module 44, Module 47, Module 50, Module 51, Module 53, Module 56, Module 59, Module 60, Module 61, Module 63, Module 64, Module 66, Module 69, Module 72, Module 79, Module 80, Module 81, Module 83, Module 84, Module 85, Module 86, Module 87, Module 88, Module 89, Module 90, Module 98, Module 102, Module 103, Module 104, Module 110, Module 112, Module 117, Module 120, Module 123, Module 127, Module 133, Module 134, Module 135, Module 137, Module 138, Module 141, Module 142, Module 147, Module 150	CIBERSORT_MAST_CELLS_RESTING	BENPORATH_EED_TARGETS, BENPORATH_ES_WITH_HK27ME3, BENPORATH_LNC8_TARGETS, BENPORATH_OCT4_TARGETS, BENPORATH_P192_TARGETS, BENPORATH_SUZ12_TARGETS	
	<ul style="list-style-type: none"> > VERHAAK GLIOBLASTOMA PRONEURAL: Genes correlated with proneural type of glioblastoma multiforme tumors > NOUSHIMEHR GBM SILENCED BY METHYLATION: Top 50 most differentially hypermethylated and down-regulated genes in proneural G-CIMP (a CpG island methylator phenotype) GBM (glioblastoma multiforme) tumors > Molecular markers: PDGFRA, IDH1 and MGMT > Methylation-driven drivers shared between GBM (Module 90) and LGG (Module 77): FBXO17, XKR8, RAB34/36 > Survival analysis: hypermethylated drivers, repressed expression of drivers and targets, and association with better survival rates in the G-CIMP and proneural molecular subclasses 				Community 1

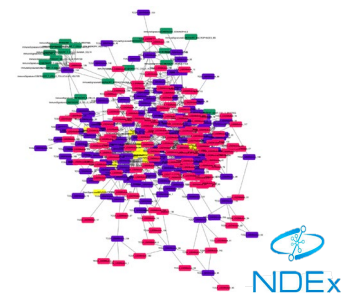
Community	TCGA_GBM	TCGA_LGG	ImmuneSignatures	StemSignatures	
Community 3	Module 8, Module 55, Module 70, Module 77, Module 93, Module 125, Module 131, Module 133, Module 134, Module 141	Module 22, Module 33, Module 38, Module 73, Module 90, Module 118, Module 121	CIBERSORT_ESINOPHILS, CIBERSORT_MACROPHAGES_M0, CIBERSORT_MACROPHAGES_M2, CIBERSORT_MONOCYTES, CIBERSORT_NEUTROPHILS	0	
	<ul style="list-style-type: none"> > VERHAAK GLIOBLASTOMA MESENCHYMAL: Genes correlated with mesenchymal type of glioblastoma multiforme tumors > Enriched for immune cell type-specific signatures > Associated with imaging feature Proportion nCET (f6): lower expression, higher proportion of non-enhancing tumor (not edema) > Survival analysis: induced expression of drivers and targets and association with poorer survival rates in the mesenchymal molecular subclass 				Community 3

Community Network Visualization



Perturbation-AMARETTO (under development):

- driver validation & discovery: https://pochetlab.shinyapps.io/pAMARETTO_Brain_2DS_Drivers/
- drug discovery: https://pochetlab.shinyapps.io/pAMARETTO_Brain_2DS_Drivers



Case Study 3

Pan-squamous cell carcinoma (SCC)

across 5 SCC cancer sites: lung (LUSC), head and neck (HNSC),
esophageal (ESCA), cervical (CESC) and bladder (BLCA)

Community-AMARETTO report SCC

Community-AMARETTO Report

Run Information

CSV Excel PDF Print Column visibility Show 10 entries Search:

AMARETTO Report

All

TCGA_BLCA

TCGA_CESC

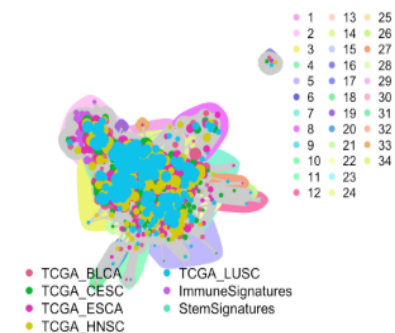
TCGA_ESCA

TCGA_HNSC

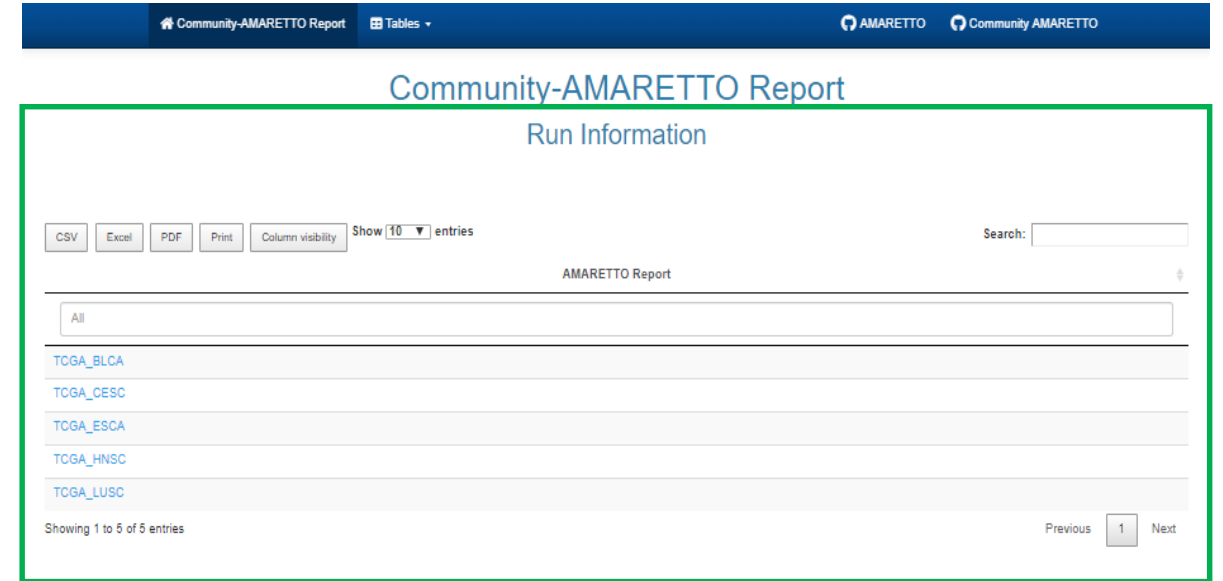
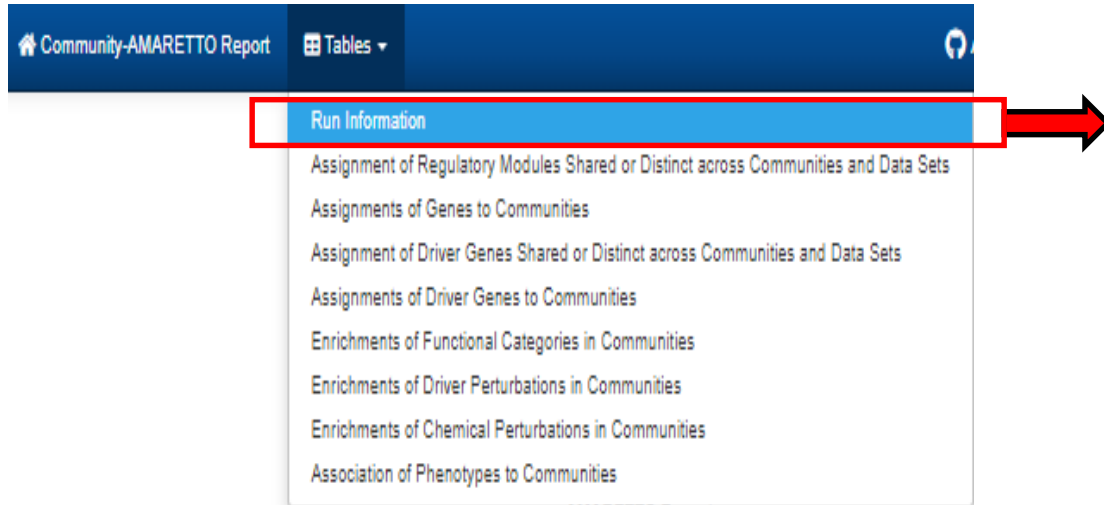
TCGA_LUSC

Showing 1 to 5 of 5 entries Previous 1 Next

Community Network Visualization



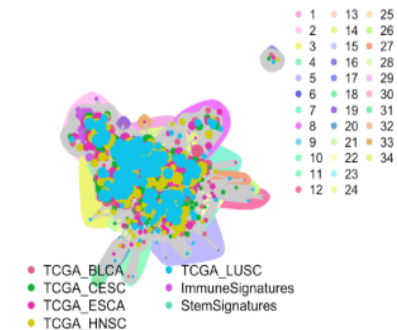
Community-AMARETTO report SCC



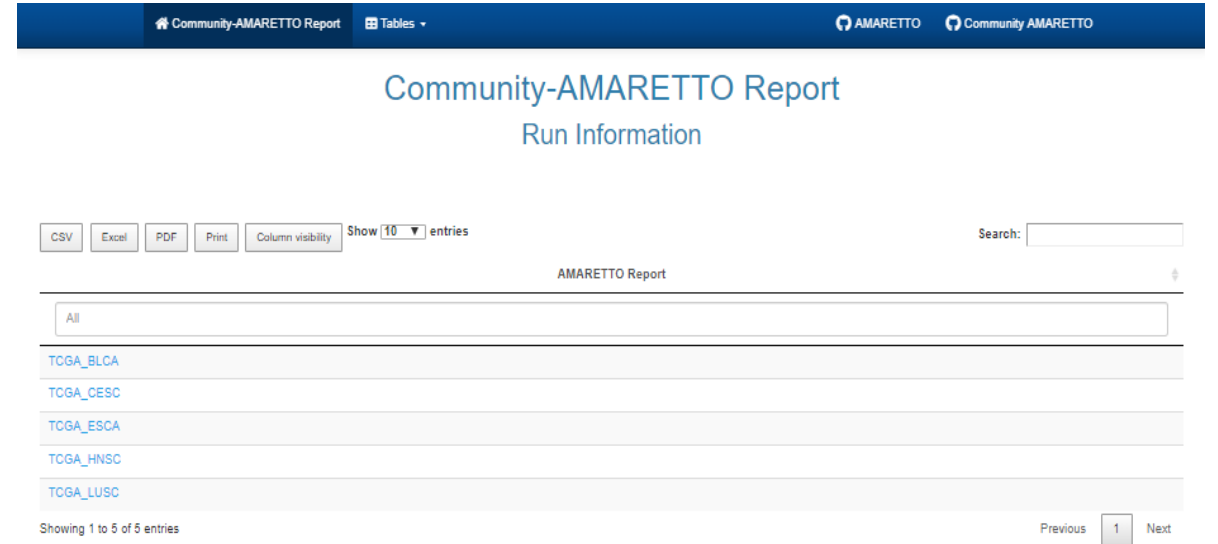
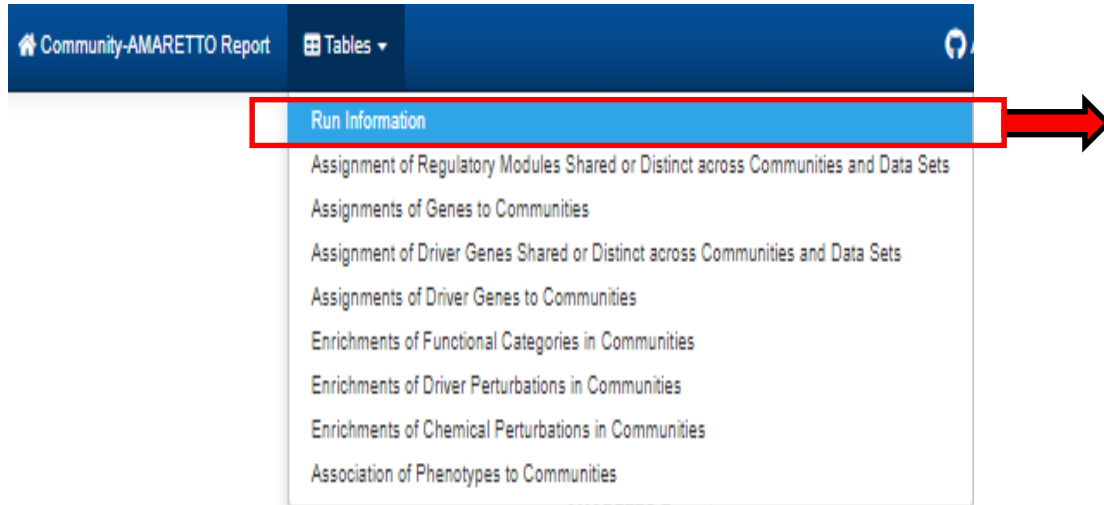
Run Information: links to AMARETTO reports combined in Community-AMARETTO report

Community Network Visualization

Community Network Visualization

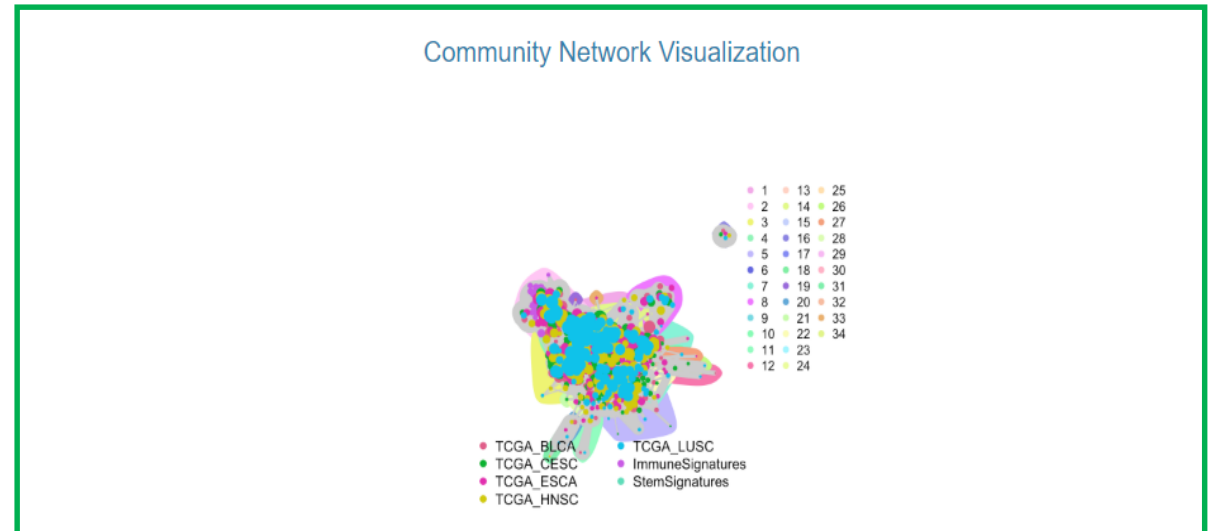


Community-AMARETTO report SCC



Run Information: links to AMARETTO reports combined in Community-AMARETTO report

Community Network Visualization



Community-AMARETTO report SCC



Assignments of Genes to Communities

The screenshot shows the 'Community-AMARETTO Report Assignments of Genes to Communities' page. It features a table with columns for Gene, Community, and Gene Type. The table is filtered to show 20 entries. The data is as follows:

Gene	Community	Gene Type
A1BG	Community 1	Target
A1BG	Community 5	Target
A1BG	Community 5	Driver
A2LD1	Community 2	Target
A2LD1	Community 3	Target
A2LD1	Community 5	Target
A2LD1	Community 12	Target
A2M	Community 1	Target
A2ML1	Community 3	Target
A2ML1	Community 3	Driver
A4GALT	Community 1	Target
A4GALT	Community 3	Target
A4GALT	Community 9	Target
A4GALT	Community 10	Target
AACS	Community 1	Target
AACS	Community 3	Target
AACS	Community 5	Target
AADAC	Community 1	Target
AADAC	Community 1	Driver
AADAC	Community 3	Target

Showing 1 to 20 of 30,312 entries

Community-AMARETTO report SCC

Community-AMARETTO Report Tables

- Run Information
- Assignment of Regulatory Modules Shared or Distinct across Communities and Data Sets
- Assignments of Genes to Communities
- Assignment of Driver Genes Shared or Distinct across Communities and Data Sets
- Assignments of Driver Genes to Communities
- Enrichments of Functional Categories in Communities**
- Enrichments of Driver Perturbations in Communities
- Enrichments of Chemical Perturbations in Communities
- Association of Phenotypes to Communities

Enrichments of Functional Categories in Communities

Community-AMARETTO Report
Enrichments of Functional Categories in Communities

CSV Excel PDF Print Column visibility Show 10 entries Search:

Community	Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
All	All	All					
Community 1	BENPORATH EED TARGETS	Set 'Eed targets': genes identified by ChIP on chip as targets of the Polycomb protein EED [GeneID=8726] in human embryonic stem cells.	1082	1082	1.0	0.0	0.0
Community 1	BENPORATH ES WITH H3K27ME3	Set 'H3K27 bound': genes possessing the trimethylated H3K27 (H3K27me3) mark in their promoters in human embryonic stem cells, as identified by ChIP on chip.	1118	1118	1.0	0.0	0.0
Community 1	BENPORATH NANOG TARGETS	Set 'Nanog targets': genes upregulated and identified by ChIP on chip as Nanog [GeneID=79923] transcription factor targets in human embryonic stem cells.	988	987	1.0	0.0	0.0
Community 1	BENPORATH PRC2 TARGETS	Set 'PRC2 targets': Polycomb Repression Complex 2 (PRC) targets; identified by ChIP on chip on human embryonic stem cells as genes that possess the trimethylated H3K27 mark in their promoters and are bound by SUZ12 [GeneID=23512] and EED [GeneID=8726] Polycomb proteins.	852	852	1.0	0.0	0.0
Community 1	BENPORATH SOX2 TARGETS	Set 'Sox2 targets': genes upregulated and identified by ChIP on chip as SOX2 [GeneID=6867] transcription factor targets in human embryonic stem cells.	734	734	1.0	0.0	0.0
Community 1	BENPORATH SUZ12 TARGETS	Set 'Suz12 targets': genes identified by ChIP on chip as targets of the Polycomb protein SUZ12 [GeneID=23512] in human embryonic stem cells.	1038	1038	1.0	0.0	0.0
Community 1	MEISSNER BRAIN HCP WITH H3K4ME3 AND H3K27ME3	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	1099	857	0.80	0.0	0.0
Community 1	StromalSignatures_EC-sinusoidal_c0	StromalSignatures_EC-sinusoidal_c0	1776	1100	0.62	0.0	0.0
Community 1	StromalSignatures_EC-arteriolar_c6	StromalSignatures_EC-arteriolar_c6	1526	1019	0.67	0.0	0.0
Community 1	StemnessSignatures_WEINBERG_NANOG_TARGETS	StemnessSignatures_WEINBERG_NANOG_TARGETS	988	932	0.94	0.0	0.0

Showing 1 to 10 of 38,703 entries Previous 1 2 3 4 5 ... 3871 Next

Community-AMARETTO report SCC

Community-AMARETTO Report Tables

- Run Information
- Assignment of Regulatory Modules Shared or Distinct across Communities and Data Sets
- Assignments of Genes to Communities
- Assignment of Driver Genes Shared or Distinct across Communities and Data Sets
- Assignments of Driver Genes to Communities
- Enrichments of Functional Categories in Communities
- Enrichments of Driver Perturbations in Communities
- Enrichments of Chemical Perturbations in Communities
- Association of Phenotypes to Communities**

Association of Phenotypes to Communities

Community-AMARETTO Report
Association of Phenotypes to Communities

CSV Excel PDF Print Column visibility Show 20 entries Search:

Community	Data Set	Module	Phenotype	Statistics Test	P-value	FDR Q-value
All	CESC	88	All	All	0.0000000	0.000000000
Community 1	TCGA_CESC	Module 88	SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	1.387e-19	1.80038461538482e-18
Community 1	TCGA_CESC	Module 88	mRNA.clusters.SCC (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	1.7102e-11	5.700868686868687e-11
Community 1	TCGA_CESC	Module 88	mRNA.clusters.5.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0000024124	0.00000952263157894737
Community 1	TCGA_CESC	Module 88	mRNA.clusters.1.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0000029041	0.000010890375
Community 1	TCGA_CESC	Module 88	mRNA.clusters.3.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000007854	0.000022283018887925
Community 1	TCGA_CESC	Module 88	Major.HPV.type.HPV_18.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0000028287	0.00003535875
Community 1	TCGA_CESC	Module 88	Major.HPV.type.SCC (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.000011218	0.0000801285714285714
Community 1	TCGA_CESC	Module 88	Major.HPV.type.HPV_45.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000018035	0.00010821
Community 1	TCGA_CESC	Module 88	PARADIGM.clusters.1.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.000020329	0.000138806818181818
Community 1	TCGA_CESC	Module 88	PARADIGM.clusters.SCC (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.00010917	0.00017808064516129
Community 1	TCGA_CESC	Module 88	patient.stage_event.clinical_stage.stage_ib1 (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00024741	0.00530164285714288
Community 1	TCGA_CESC	Module 88	Major.HPV.type.HPV_18.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0019494	0.01539
Community 1	TCGA_CESC	Module 88	mRNA.clusters.2.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.0043672	0.0158567857142857
Community 1	TCGA_CESC	Module 88	CNV.clusters.SCC (KRUSKALWALLISTEST)	Nominal Multi-Class Analysis: Kruskal-Wallis test	0.0087699	0.0285719230769231
Community 1	TCGA_CESC	Module 88	HPV.status.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.010042	0.032746652173913
Community 1	TCGA_CESC	Module 88	PARADIGM.clusters.5.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.013275	0.038875
Community 1	TCGA_CESC	Module 88	Smoking.Lifelong_Non_smoker.SCC (WILCOXONRANKSUMTEST)	Nominal Two-Class Analysis: Wilcoxon rank sum test	0.00058773	0.04407975

Showing 1 to 17 of 17 entries (filtered from 63,000 total entries) Previous 1 Next

Community-AMARETTO report SCC

Community-AMARETTO Report Tables

- Run Information
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- Assignment of Driver Genes Shared or Distinct across Communities and Data Sets
- Assignments of Driver Genes to Communities
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- Enrichments of Driver Perturbations in Communities**
- Enrichments of Chemical Perturbations in Communities
- Association of Phenotypes to Communities



Enrichments of Driver Perturbations in Communities

Community-AMARETTO Report
Enrichments of Driver Perturbations in Communities


CSV Excel PDF Print Column visibility Show 20 entries Search:

Community	Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
Community 1	CHEA_JARID2_20064375_Chip-Seq_MESCs_Mouse	CHEA_JARID2_20064375_Chip-Seq_MESCs_Mouse	1117	859	0.77	0.0	0.0
Community 1	CHEA_JARID2_20075857_Chip-Seq_MESCs_Mouse	CHEA_JARID2_20075857_Chip-Seq_MESCs_Mouse	1258	948	0.75	0.0	0.0
Community 1	CHEA_RNF2_18974828_Chip-Seq_MESCs_Mouse	CHEA_RNF2_18974828_Chip-Seq_MESCs_Mouse	1302	959	0.74	0.0	0.0
Community 1	CHEA_EZH2_18974828_Chip-Seq_MESCs_Mouse	CHEA_EZH2_18974828_Chip-Seq_MESCs_Mouse	1302	959	0.74	0.0	0.0
Community 1	CHEA_RNF2_27304074_Chip-Seq_ESCs_Mouse	CHEA_RNF2_27304074_Chip-Seq_ESCs_Mouse	1487	1018	0.69	0.0	0.0
Community 1	CHEA_SUZ12_18892474_Chip-Seq_MESCs_Mouse	CHEA_SUZ12_18892474_Chip-Seq_MESCs_Mouse	1909	1380	0.72	0.0	0.0
Community 1	CHEA_SUZ12_18974828_Chip-Seq_MESCs_Mouse	CHEA_SUZ12_18974828_Chip-Seq_MESCs_Mouse	1934	1388	0.72	0.0	0.0
Community 1	CHEA_KDM2B_26808549_Chip-Seq_K562_Human	CHEA_KDM2B_26808549_Chip-Seq_K562_Human	2000	1188	0.59	0.0	0.0
Community 1	CHEA_SUZ12_27294783_Chip-Seq_ESCs_Mouse	CHEA_SUZ12_27294783_Chip-Seq_ESCs_Mouse	2000	1338	0.67	0.0	0.0
Community 1	CHEA_EZH2_27294783_Chip-Seq_ESCs_Mouse	CHEA_EZH2_27294783_Chip-Seq_ESCs_Mouse	2000	1327	0.66	0.0	0.0
Community 1	CHEA_RING1B_27294783_Chip-Seq_ESCs_Mouse	CHEA_RING1B_27294783_Chip-Seq_ESCs_Mouse	2000	1280	0.64	0.0	0.0
Community 1	CHEA_RING1B_27294783_Chip-Seq_NPCs_Mouse	CHEA_RING1B_27294783_Chip-Seq_NPCs_Mouse	2000	1256	0.63	0.0	0.0
Community 1	CHEA_SMAD4_21799915_Chip-Seq_A2780_Human	CHEA_SMAD4_21799915_Chip-Seq_A2780_Human	2484	1429	0.58	0.0	0.0
Community 1	CHEA_FOXA2_19822575_Chip-Seq_HepG2_Human	CHEA_FOXA2_19822575_Chip-Seq_HepG2_Human	2668	1646	0.55	0.0	0.0
Community 1	CHEA_MTF2_20144788_Chip-Seq_MESCs_Mouse	CHEA_MTF2_20144788_Chip-Seq_MESCs_Mouse	2981	2053	0.69	0.0	0.0
Community 1	CHEA_STAT3_23295773_Chip-Seq_U87_Human	CHEA_STAT3_23295773_Chip-Seq_U87_Human	3165	1888	0.53	0.0	0.0
Community 1	CHEA_SOX2_21211035_Chip-Seq_LN229_Gbrn	CHEA_SOX2_21211035_Chip-Seq_LN229_Gbrn	3420	1775	0.52	0.0	0.0
Community 1	CHEA_RUNX2_22187159_Chip-Seq_PCA_Human	CHEA_RUNX2_22187159_Chip-Seq_PCA_Human	3423	1760	0.51	0.0	0.0
Community 1	CHEA_PPARD_21283829_Chip-Seq_MYOFIBROBLAST_Human	CHEA_PPARD_21283829_Chip-Seq_MYOFIBROBLAST_Human	3447	1788	0.52	0.0	0.0

Community-AMARETTO report SCC

Community-AMARETTO Report Tables

- Run Information
- Assignment of Regulatory Modules Shared or Distinct across Communities and Data Sets
- Assignments of Genes to Communities
- Assignment of Driver Genes Shared or Distinct across Communities and Data Sets
- Assignments of Driver Genes to Communities
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- Enrichments of Driver Perturbations in Communities
- Enrichments of Chemical Perturbations in Communities**
- Association of Phenotypes to Communities



Enrichments of Drug Perturbations in Communities

Community-AMARETTO Report
Enrichments of Chemical Perturbations in Communities

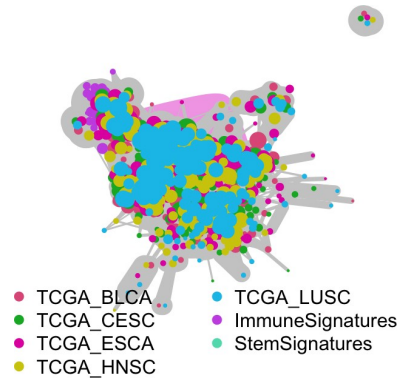
CSV Excel PDF Print Column visibility Show 20 entries Search:

Community	Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_HME1_24H-palbociclib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HME1_24H-palbociclib-10_DN	215	185	0.86	4.8e-191	1.6e-188
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_HME1_24H-palbociclib-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HME1_24H-palbociclib-3.33_DN	183	169	0.92	5.5e-187	9.0e-183
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_PC3_24H-NVP-TAE884-10_DN	LINCSCMAP_ChemicalPerturbation_LJP006_PC3_24H-NVP-TAE884-10_DN	186	164	0.88	3.2e-173	3.5e-169
Community 4	LINCSCMAP_ChemicalPerturbation_LJP005_A549_24H-dovitinib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A549_24H-dovitinib-10_DN	215	175	0.81	7.2e-172	5.8e-168
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_LNCAp_24H-GDC-0941-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP006_LNCAp_24H-GDC-0941-3.33_DN	185	161	0.87	6.0e-168	3.9e-164
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_LNCAp_24H-mitoxantrone-0.37_DN	LINCSCMAP_ChemicalPerturbation_LJP006_LNCAp_24H-mitoxantrone-0.37_DN	195	165	0.85	1.0e-167	5.5e-164
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_A375_24H-mitoxantrone-0.12_DN	LINCSCMAP_ChemicalPerturbation_LJP006_A375_24H-mitoxantrone-0.12_DN	222	175	0.79	3.6e-167	1.7e-163
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_HCC515_24H-PHA-793887-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HCC515_24H-PHA-793887-3.33_DN	186	160	0.86	4.2e-165	1.7e-161
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_BT20_24H-PHA-793887-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP006_BT20_24H-PHA-793887-3.33_DN	184	157	0.85	8.5e-161	3.1e-157
Community 4	LINCSCMAP_ChemicalPerturbation_LJP005_MCF10A_24H-mitoxantrone-0.37_DN	LINCSCMAP_ChemicalPerturbation_LJP005_MCF10A_24H-mitoxantrone-0.37_DN	192	158	0.82	1.2e-156	4.0e-153
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_A375_24H-palbociclib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP006_A375_24H-palbociclib-10_DN	154	141	0.92	1.5e-154	4.3e-151
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_HT29_24H-palbociclib-0.37_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HT29_24H-palbociclib-0.37_DN	195	158	0.81	1.6e-154	4.3e-151
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_MCF10A_24H-mitoxantrone-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP006_MCF10A_24H-mitoxantrone-3.33_DN	181	152	0.84	1.9e-153	4.9e-150
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_HS578T_24H-palbociclib-1.11_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HS578T_24H-palbociclib-1.11_DN	156	141	0.90	1.5e-152	3.5e-149
Community 4	LINCSCMAP_ChemicalPerturbation_LJP005_A549_24H-torin-2-0.12_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A549_24H-torin-2-0.12_DN	180	151	0.84	2.8e-152	6.0e-149
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_BT20_24H-palbociclib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP006_BT20_24H-palbociclib-10_DN	168	146	0.87	4.4e-152	8.9e-149
Community 4	LINCSCMAP_ChemicalPerturbation_LJP005_A549_24H-NVP-BE2235-0.37_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A549_24H-NVP-BE2235-0.37_DN	207	161	0.78	5.1e-152	9.8e-149
Community 4	LINCSCMAP_ChemicalPerturbation_LJP006_HS578T_24H-palbociclib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP006_HS578T_24H-palbociclib-10_DN	152	137	0.90	8.2e-148	1.5e-144

Community-AMARETTO report SCC: Module(s) regulated by SOX2?

Community-AMARETTO report SCC: Module(s) regulated by SOX2?

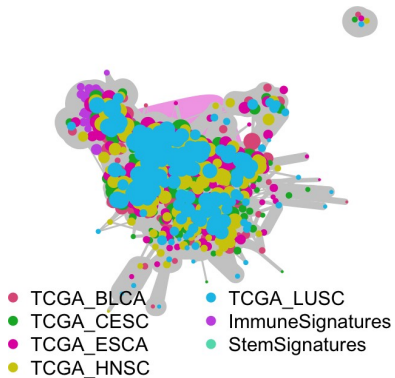
Community-AMARETTO Community 1



Data Set	Module	Gene	Gene Type
TCGA_BLCA	Module 8	SOX2	Target
TCGA_CESC	Module 14	SOX2	Target
TCGA_CESC	Module 14	SOX2	Driver
TCGA_ESCA	Module 83	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Driver
TCGA_HNSC	Module 106	SOX2	Driver
TCGA_LUSC	Module 18	SOX2	Target
TCGA_LUSC	Module 18	SOX2	Driver
TCGA_LUSC	Module 37	SOX2	Driver
TCGA_LUSC	Module 41	SOX2	Driver
TCGA_LUSC	Module 61	SOX2	Driver
TCGA_LUSC	Module 94	SOX2	Driver

Community-AMARETTO report SCC: Module(s) regulated by SOX2?

Community-AMARETTO Community 1



Enrichments of Functional Categories in Community

Show 5 entries

Search: SOX2

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
TARGETS	Polycarb protein EED [GeneID=9726] in human embryonic stem cells.					
BENPORATH_NANOG_TARGETS	Set 'Nanog targets': genes upregulated and identified by ChIP on chip as Nanog [GeneID=79923] transcription factor targets in human embryonic stem cells.	988	987	1.0	0.0	0.0
BENPORATH_SOX2_TARGETS	Set 'Sox2 targets': genes upregulated and identified by ChIP on chip as SOX2 [GeneID=6657] transcription factor targets in human embryonic stem cells.	734	734	1.0	0.0	0.0
BENPORATH_SUZ12_TARGETS	Set 'Suz12 targets': genes identified by ChIP on chip as targets of the Polycarb protein SUZ12 [GeneID=23512] in human embryonic stem cells.	1038	1038	1.0	0.0	0.0
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	1069	857	0.80	0.0	0.0

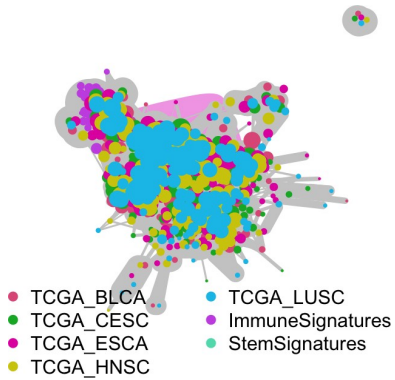
Showing 1 to 5 of 115 entries (filtered from 4,907 total entries)

Previous 1 2 3 4 5 ... 23 Next

Data Set	Module	Gene	Gene Type
TCGA_BLCA	Module 8	SOX2	Target
TCGA_CESC	Module 14	SOX2	Target
TCGA_CESC	Module 14	SOX2	Driver
TCGA_ESCA	Module 83	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Driver
TCGA_HNSC	Module 106	SOX2	Driver
TCGA_LUSC	Module 18	SOX2	Target
TCGA_LUSC	Module 18	SOX2	Driver
TCGA_LUSC	Module 37	SOX2	Driver
TCGA_LUSC	Module 41	SOX2	Driver
TCGA_LUSC	Module 61	SOX2	Driver
TCGA_LUSC	Module 94	SOX2	Driver

Community-AMARETTO report SCC: Module(s) regulated by SOX2?

Community-AMARETTO Community 1



Enrichments of Functional Categories in Community

Show 5 entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value
TARGETS	Polycomb protein EED [GeneID=9726] in human embryonic stem cells.				
BENPORATH NANOG TARGETS	Set 'Nanog targets': genes upregulated and identified by ChIP on chip as Nanog [GeneID=79923] transcription factor targets in human embryonic stem cells.	988	987	1.0	0.0
BENPORATH SOX2 TARGETS	Set 'Sox2 targets': genes upregulated and identified by ChIP on chip as SOX2 [GeneID=6657] transcription factor targets in human embryonic stem cells.	734	734	1.0	0.0
BENPORATH SUZ12 TARGETS	Set 'Suz12 targets': genes identified by ChIP on chip as targets of the Polycomb protein SUZ12 [GeneID=23512] in human embryonic stem cells.	1038	1038	1.0	0.0
MEISSNER BRAIN HCP WITH H3K4ME3 AND H3K27ME3	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	1069	857	0.80	0.0

Showing 1 to 5 of 115 entries (filtered from 4,907 total entries)

Data Set	Module	Gene	Gene Type
TCGA_BLCA	Module 8	SOX2	Target
TCGA_CESC	Module 14	SOX2	Target
TCGA_CESC	Module 14	SOX2	Driver
TCGA_ESCA	Module 83	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Driver
TCGA_HNSC	Module 106	SOX2	Driver
TCGA_LUSC	Module 18	SOX2	Target
TCGA_LUSC	Module 18	SOX2	Driver
TCGA_LUSC	Module 37	SOX2	Driver
TCGA_LUSC	Module 41	SOX2	Driver
TCGA_LUSC	Module 61	SOX2	Driver
TCGA_LUSC	Module 94	SOX2	Driver

Enrichments of Driver Perturbations in Community

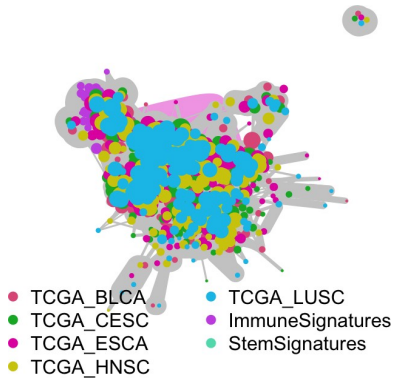
CSV Excel PDF Print Column visibility Show 10 entries Search:

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
SOX2	All	All	All	All	All	All
ChEA_SOX2_21211035_ChIP	ChEA_SOX2_21211035_ChIP	3420	1775	0.52	0.0	0.0
ChEA_SOX2_20726797_ChIP-Seq_SW620_Human	ChEA_SOX2_20726797_ChIP-Seq_SW620_Human	2564	1343	0.52	3.0e-292	5.3e-291
Consensus_SOX2_CHEA	Consensus_SOX2_CHEA	775	556	0.72	5.8e-208	3.0e-206
ChEA_SOX2_16153702_ChIP-ChIP_HESCs_Human	ChEA_SOX2_16153702_ChIP-ChIP_HESCs_Human	1278	755	0.59	4.7e-202	3.6e-201
ChEA_SOX2_18692474_ChIP	ChEA_SOX2_18692474_ChIP	3319	1408	0.42	2.5e-190	1.5e-189
ChEA_SOX2_19829295_ChIP-Seq_ESCs_Human	ChEA_SOX2_19829295_ChIP-Seq_ESCs_Human	2000	940	0.47	6.8e-159	2.6e-158
ChEA_SOX2_18692474_ChIP	ChEA_SOX2_18692474_ChIP	1991	937	0.47	7.7e-159	2.9e-158
ChEA_SOX2_27498859_ChIP-Seq_STOMACH_Mouse	ChEA_SOX2_27498859_ChIP-Seq_STOMACH_Mouse	2000	922	0.46	6.2e-149	1.9e-148
ChEA_SOX2_18555785_ChIP	ChEA_SOX2_18555785_ChIP	2000	900	0.45	3.5e-137	1.0e-136
ChEA_SOX2_21211035_ChIP-Seq_LN229_Human	ChEA_SOX2_21211035_ChIP-Seq_LN229_Human	2000	875	0.44	2.3e-124	5.2e-124

Showing 1 to 10 of 14 entries (filtered from 9,045 total entries)

Community-AMARETTO report SCC: Module(s) regulated by SOX2?

Community-AMARETTO Community 1



Enrichments of Functional Categories in Community

Search: Show entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value
TARGETS	Polycarb protein EED [GeneID=9726] in human embryonic stem cells.				
BENPORATH NANOG TARGETS	Set 'Nanog targets': genes upregulated and identified by ChIP on chip as Nanog [GeneID=79923] transcription factor targets in human embryonic stem cells.	988	987	1.0	0.0
BENPORATH SOX2 TARGETS	Set 'Sox2 targets': genes upregulated and identified by ChIP on chip as SOX2 [GeneID=6657] transcription factor targets in human embryonic stem cells.	734	734	1.0	0.0
BENPORATH SUZ12 TARGETS	Set 'Suz12 targets': genes identified by ChIP on chip as targets of the Polycomb protein SUZ12 [GeneID=23512] in human embryonic stem cells.	1038	1038	1.0	0.0
MEISSNER BRAIN HCP WITH H3K4ME3 AND H3K27ME3	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	1069	857	0.80	0.0

Showing 1 to 5 of 115 entries (filtered from 4,907 total entries)

Enrichments of Driver Perturbations in Community

Search: Show entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
ChEA_SOX2_21211035_ChIP-	ChEA_SOX2_21211035_ChIP-	3420	1775	0.52	0.0	0.0
ChEA_SOX2_20726797_ChIP-Seq_SW620_Human	ChEA_SOX2_20726797_ChIP-Seq_SW620_Human	2564	1343	0.52	3.0e-292	5.3e-291
Consensus_SOX2_CHEA	Consensus_SOX2_CHEA	775	556	0.72	5.8e-208	3.0e-206
ChEA_SOX2_16153702_ChIP-ChIP_HESCs_Human	ChEA_SOX2_16153702_ChIP-ChIP_HESCs_Human	1278	755	0.59	4.7e-202	3.6e-201
ChEA_SOX2_18692474_ChIP-	ChEA_SOX2_18692474_ChIP-	3319	1408	0.42	2.5e-190	1.5e-189
ChEA_SOX2_19829295_ChIP-Seq_ESCs_Human	ChEA_SOX2_19829295_ChIP-Seq_ESCs_Human	2000	940	0.47	6.8e-159	2.6e-158
ChEA_SOX2_18692474_ChIP-	ChEA_SOX2_18692474_ChIP-	1991	937	0.47	7.7e-159	2.9e-158
ChEA_SOX2_27498859_ChIP-Seq_STOMACH_Mouse	ChEA_SOX2_27498859_ChIP-Seq_STOMACH_Mouse	2000	922	0.46	6.2e-149	1.9e-148
ChEA_SOX2_18555785_ChIP-	ChEA_SOX2_18555785_ChIP-	2000	900	0.45	3.5e-137	1.0e-136
ChEA_SOX2_21211035_ChIP-Seq_LN229_Human	ChEA_SOX2_21211035_ChIP-Seq_LN229_Human	2000	875	0.44	2.3e-124	5.2e-124

Showing 1 to 10 of 14 entries (filtered from 9,045 total entries)

Data Set	Module	Gene	Gene Type
TCGA_BLCA	Module 8	SOX2	Target
TCGA_CESC	Module 14	SOX2	Target
TCGA_CESC	Module 14	SOX2	Driver
TCGA_ESCA	Module 83	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Driver
TCGA_HNSC	Module 106	SOX2	Driver
TCGA_LUSC	Module 18	SOX2	Target
TCGA_LUSC	Module 18	SOX2	Driver
TCGA_LUSC	Module 37	SOX2	Driver
TCGA_LUSC	Module 41	SOX2	Driver
TCGA_LUSC	Module 61	SOX2	Driver
TCGA_LUSC	Module 94	SOX2	Driver

Enrichments of Chemical Perturbations in Community

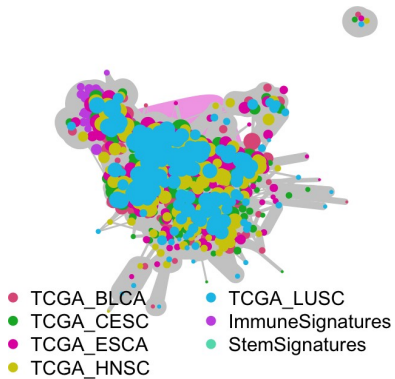
Search: Show entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-buparlisib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-buparlisib-10_DN	147	111	0.75	7.6e-46	4.8e-43
LINCSCMAP_ChemicalPerturbation_IGF1-MCF7_UP	LINCSCMAP_ChemicalPerturbation_IGF1-MCF7_UP	172	122	0.71	2.4e-45	1.3e-42
LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-pelitinib-0.37_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-pelitinib-0.37_DN	73	57	0.78	1.5e-25	4.0e-24
LINCSCMAP_ChemicalPerturbation_LJP005_SKBR3_24H-CGP-80474-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP005_SKBR3_24H-CGP-80474-3.33_DN	114	61	0.54	1.4e-14	7.5e-14
LINCSCMAP_ChemicalPerturbation_CPC009_A549_24H-BRD-A85712510-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC009_A549_24H-BRD-A85712510-10.0_DN	115	52	0.45	3.5e-9	8.8e-9

Showing 1 to 5 of 5 entries (filtered from 33,147 total entries)

Community-AMARETTO report SCC: Module(s) regulated by SOX2?

Community-AMARETTO Community 1



Data Set	Module	Gene	Gene Type
TCGA_BLCA	Module 8	SOX2	Target
TCGA_CESC	Module 14	SOX2	Target
TCGA_CESC	Module 14	SOX2	Driver
TCGA_ESCA	Module 83	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Target
TCGA_HNSC	Module 51	SOX2	Driver
TCGA_HNSC	Module 106	SOX2	Driver
TCGA_LUSC	Module 18	SOX2	Target
TCGA_LUSC	Module 18	SOX2	Driver
TCGA_LUSC	Module 37	SOX2	Driver
TCGA_LUSC	Module 41	SOX2	Driver
TCGA_LUSC	Module 61	SOX2	Driver
TCGA_LUSC	Module 94	SOX2	Driver

Enrichments of Functional Categories in Community

Search: Show entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value
TARGETS	Polycarb protein EED [GeneID=9726] in human embryonic stem cells.				
BENPORATH NANOG TARGETS	Set 'Nanog targets': genes upregulated and identified by ChIP on chip as Nanog [GeneID=79923] transcription factor targets in human embryonic stem cells.	988	987	1.0	0.0
BENPORATH SOX2 TARGETS	Set 'Sox2 targets': genes upregulated and identified by ChIP on chip as SOX2 [GeneID=6657] transcription factor targets in human embryonic stem cells.	734	734	1.0	0.0
BENPORATH SUZ12 TARGETS	Set 'Suz12 targets': genes identified by ChIP on chip as targets of the Polycarb protein SUZ12 [GeneID=23512] in human embryonic stem cells.	1038	1038	1.0	0.0
MEISSNER BRAIN HCP WITH H3K4ME3 AND H3K27ME3	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	1069	857	0.80	0.0

Showing 1 to 5 of 115 entries (filtered from 4,907 total entries)

Enrichments of Driver Perturbations in Community

Search: Show entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
ChEA_SOX2_21211035_ChIP-	ChEA_SOX2_21211035_ChIP-	3420	1775	0.52	0.0	0.0
ChEA_SOX2_20726797_ChIP-Seq_SW620_Human	ChEA_SOX2_20726797_ChIP-Seq_SW620_Human	2564	1343	0.52	3.0e-292	5.3e-291
Consensus_SOX2_CHEA	Consensus_SOX2_CHEA	775	556	0.72	5.8e-208	3.0e-206
ChEA_SOX2_16153702_ChIP-ChIP_HESCs_Human	ChEA_SOX2_16153702_ChIP-ChIP_HESCs_Human	1278	755	0.59	4.7e-202	3.6e-201
ChEA_SOX2_18692474_ChIP-	ChEA_SOX2_18692474_ChIP-	3319	1408	0.42	2.5e-190	1.5e-189
ChEA_SOX2_19829295_ChIP-Seq_ESCs_Human	ChEA_SOX2_19829295_ChIP-Seq_ESCs_Human					
ChEA_SOX2_18692474_ChIP-	ChEA_SOX2_18692474_ChIP-					
ChEA_SOX2_27498859_ChIP-Seq_STOMACH_Mouse	ChEA_SOX2_27498859_ChIP-Seq_STOMACH_Mouse					
ChEA_SOX2_18555785_ChIP-	ChEA_SOX2_18555785_ChIP-					
ChEA_SOX2_21211035_ChIP-Seq_LN229_Human	ChEA_SOX2_21211035_ChIP-Seq_LN229_Human					

Showing 1 to 10 of 14 entries (filtered from 9,045 total entries)

Enrichments of Chemical Perturbations in Community

Search: Show entries

Gene Set Name	Gene Set Description	# Genes in Gene Set	# Genes in Overlap	% Genes in overlap	P-value	FDR Q-value
LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-buparlisib-10_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-buparlisib-10_DN	147	111	0.75	7.6e-46	4.8e-43
LINCSCMAP_ChemicalPerturbation_IGF1-MCF7_UP	LINCSCMAP_ChemicalPerturbation_IGF1-MCF7_UP	172	122	0.71	2.4e-45	1.3e-42
LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-pelitinib-0.37_DN	LINCSCMAP_ChemicalPerturbation_LJP005_A375_24H-pelitinib-0.37_DN	73	57	0.78	1.5e-25	4.0e-24
LINCSCMAP_ChemicalPerturbation_LJP005_SKBR3_24H-CGP-80474-3.33_DN	LINCSCMAP_ChemicalPerturbation_LJP005_SKBR3_24H-CGP-80474-3.33_DN	114	61	0.54	1.4e-14	7.5e-14
LINCSCMAP_ChemicalPerturbation_CPC009_A549_24H-BRD-A85712510-10.0_DN	LINCSCMAP_ChemicalPerturbation_CPC009_A549_24H-BRD-A85712510-10.0_DN	115	52	0.45	3.5e-9	8.8e-9

Showing 1 to 5 of 5 entries (filtered from 33,147 total entries)

THE LANCET Oncology

Articles | VOLUME 18, ISSUE 3, P323-335, MARCH 01, 2017

Buparlisib and paclitaxel in patients with platinum-pretreated recurrent or metastatic squamous cell carcinoma of the head and neck (BERIL-1): a randomised, double-blind, placebo-controlled phase 2 trial

Prof Denis Soulières, MD • Prof Sandrine Falvre, MD • Prof Ricardo Mesía, MD • Prof Eva Remenár, MD • Prof Shau-Hsuan Li, MD • Prof Andrey Karpenko, MD • et al. [Show all authors](#)

Published: January 25, 2017 • DOI: [https://doi.org/10.1016/S1470-2045\(17\)30064-5](https://doi.org/10.1016/S1470-2045(17)30064-5) [Check for updates](#)

Summary

Background

Phosphatidylinositol 3-kinase (PI3K) pathway activation in squamous cell carcinoma of the head and neck contributes to treatment resistance and disease progression. Buparlisib, a pan-PI3K inhibitor, has shown preclinical antitumour activity and objective responses in patients with epithelial malignancies. We assessed whether the addition of buparlisib to paclitaxel improves clinical outcomes compared with paclitaxel and placebo in patients with recurrent or metastatic squamous cell carcinoma of the head and neck.

Interpretation

On the basis of the improved clinical efficacy with a manageable safety profile, the results of this randomised phase 2 study suggest that buparlisib in combination with paclitaxel could be an effective second-line treatment for patients with platinum-pretreated recurrent or metastatic squamous cell carcinoma of the head and neck. Further phase 3 studies are warranted to confirm this phase 2 finding.

Funding

Novartis Pharmaceuticals Corporation.

Community-AMARETTO report pan-SCC - AMARETTO report LUSC

Summary of SOX2-regulated LUSC Module 37:

Drivers: SOX2, TP63, PIK3CA

SOX2 CNV amplification, associated with induced SOX2 expression

SOX2, TP63, PIK3CA are activators of their targets

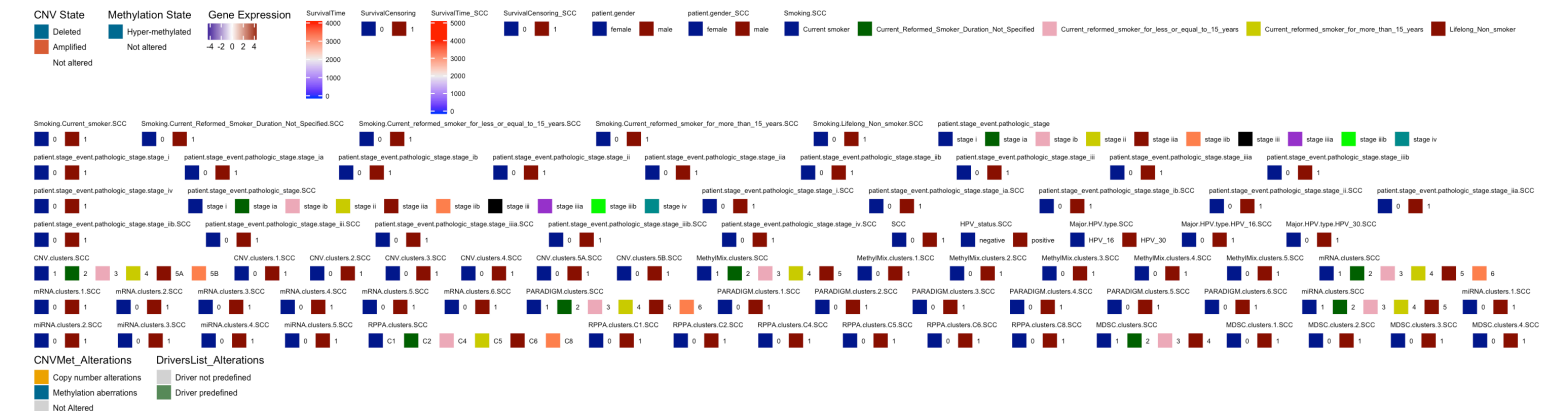
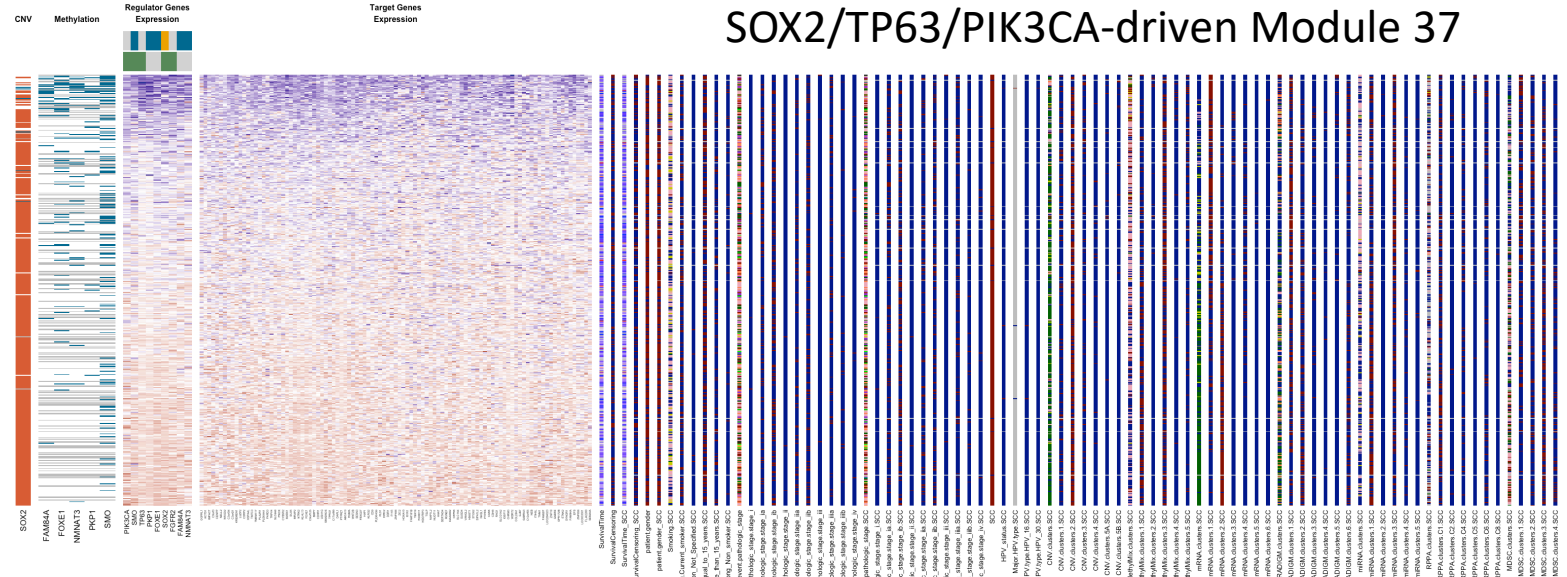
Associated with survival (lower expression, poorer survival) and TCGA multi-omics clusters (CNV)

Enriched for PI3K pathway, stemness and squamous-specific gene signatures

Drivers validated:

- SOX2 and TP63: ENCODE and ChEA ChIP-Seq, bound to its target genes
- SOX2 and PIK3CA: LINCS/CMAP genetic perturbations, modulating drivers modulates its target genes

SOX2/TP63/PIK3CA-driven Module 37



Perturbation-AMARETTO report SCC/LUSC

Perturbation-AMARETTO v2: driver validation & discovery using genetic perturbations from LINCS/CMAP

Case Study 3: squamous cell carcinoma across 5 cancer sites

Driver discovery across 5 data sets

Search:

PerturbationID	Cell_Line	GeneSymbol	EntrezID	PerturbationType	Type	DataSetFrequency	BLCA	CESC	ESCA	HNSC	LUSC
<input type="text" value="All"/>	<input type="text" value="/"/>	<input type="text" value="[*]SC"/>	<input type="text" value=""/>	<input type="text" value="All"/>	<input type="text" value=""/>	<input type="text" value="All"/>	<input type="text" value="All"/>	<input type="text" value=""/>	<input type="text" value=""/>	<input type="text" value="All"/>	<input type="text" value="Module 37:"/>
OEC001_A375_48H:CCSBBRQAD304_01579-666	A375	SOX2	6657	trt_oe	landmark	5	Module 8 : T_CD (w = 0) , escore-pval-padj-zscore	Module 14 : A_D (w = 0.0737) , escore-pval-padj-zscore	Module 83 : T_CD (w = 0) , escore-pval-padj-zscore	Module 51 : A_D (w = 0.1625) , escore-pval-padj-zscore; Module 76 : R_D (w = -0.0149) , escore-pval-padj-zscore; Module 106 : A_D (w = 0.0034) , escore-pval-padj-zscore	Module 18 : A_D (w = 0.2285) , escore-pval-padj-zscore; Module 37 : A_D (w = 0.0975) , escore-pval-padj-zscore; Module 41 : A_D (w = 0.0128) , escore-pval-padj-zscore; Module 61 : A_D (w = 0.0357) , escore-pval-padj-zscore; Module 73 : A_D (w = 0.0547) , escore-pval-padj-zscore; Module 94 : A_D (w = 0.0282) , escore-pval-padj-zscore
OEB002_HT29_96H:BRDN0000401187-666	HT29	SOX2	6657	trt_oe	landmark	5	Module 8 : T_CD (w = 0) , escore-pval-padj-zscore	Module 14 : A_D (w = 0.0737) , escore-pval-padj-zscore	Module 83 : T_CD (w = 0) , escore-pval-padj-zscore	Module 51 : A_D (w = 0.1625) , escore-pval-padj-zscore; Module 76 : R_D (w = -0.0149) , zscore; Module 106 : A_D (w = 0.0034) , escore-pval-padj-zscore	Module 18 : A_D (w = 0.2285) , escore-pval-padj-zscore; Module 37 : A_D (w = 0.0975) , escore-pval-padj-zscore; Module 41 : A_D (w = 0.0128) , escore-pval-padj-zscore; Module 61 : A_D (w = 0.0357) , escore-pval-padj-zscore; Module 73 : A_D (w = 0.0547) , pval-padj-zscore; Module 94 : A_D (w = 0.0282) , escore-pval-padj-zscore
OEB002_MCF7_96H:BRDN0000401187-666	MCF7	SOX2	6657	trt_oe	landmark	5	Module 8 : T_CD (w = 0) , escore-pval-padj-zscore	Module 14 : A_D (w = 0.0737) , escore-pval-padj-zscore	Module 83 : T_CD (w = 0) , escore-pval-padj-zscore	Module 51 : A_D (w = 0.1625) , escore-pval-padj-zscore; Module 76 : R_D (w = -0.0149) , escore-zscore; Module 106 : A_D (w = 0.0034) , escore-pval-padj-zscore	Module 18 : A_D (w = 0.2285) , escore-pval-padj-zscore; Module 37 : A_D (w = 0.0975) , escore-pval-padj-zscore; Module 41 : A_D (w = 0.0128) , escore-pval-padj-zscore; Module 61 : A_D (w = 0.0357) , escore-pval-padj-zscore; Module 73 : A_D (w = 0.0547) , escore-zscore; Module 94 : A_D (w = 0.0282) , escore-pval-padj-zscore
OEB002_PC3_96H:BRDN0000401187-666	PC3	SOX2	6657	trt_oe	landmark	5	Module 8 : T_CD (w = 0) , escore-pval-padj-zscore	Module 14 : A_D (w = 0.0737) , escore-pval-padj-zscore	Module 83 : T_CD (w = 0) , escore-pval-padj-zscore	Module 51 : A_D (w = 0.1625) , escore-pval-padj-zscore; Module 76 : R_D (w = -0.0149) , escore-padj-zscore; Module 106 : A_D (w = 0.0034) , escore-pval-padj-zscore	Module 18 : A_D (w = 0.2285) , escore-pval-padj-zscore; Module 37 : A_D (w = 0.0975) , escore-pval-padj-zscore; Module 41 : A_D (w = 0.0128) , escore-pval-padj-zscore; Module 61 : A_D (w = 0.0357) , escore-pval-padj-zscore; Module 73 : A_D (w = 0.0547) , escore-pval-padj-zscore; Module 94 : A_D (w = 0.0282) , escore-pval-padj-zscore
CGS001_A375_96H:PIK3CA:1	A375	PIK3CA	5290	trt_sh.cgs	landmark	4	Not_in_AMARETTO	Module 94 : A_D (w = 0.1491) , escore-pval-padj-zscore	Module 19 : A_D (w = 0.0365) , escore-pval-padj-zscore	Module 16 : A_D (w = 0.0398) , zscore; Module 98 : A_D (w = 0.0123) , escore-pval-padj-zscore	Module 37 : A_D (w = 0.0034) , escore-pval-padj-zscore; Module 51 : A_D (w = 0.002) , escore-zscore; Module 73 : A_D (w = 0.1852) , escore-pval-padj-zscore
CGS001_HA1E_96H:PIK3CA:1.5	HA1E	PIK3CA	5290	trt_sh.cgs	landmark	4	Not_in_AMARETTO	Module 94 : A_D (w = 0.1491) , escore-pval-padj-zscore	Module 19 : A_D (w = 0.0365) , escore-pval-padj-zscore	Module 16 : A_D (w = 0.0398) , zscore; Module 98 : A_D (w = 0.0123) , escore-pval-padj-zscore	Module 37 : A_D (w = 0.0034) , escore-pval-padj-zscore; Module 51 : A_D (w = 0.002) , escore-pval-padj-zscore; Module 73 : A_D (w = 0.1852) , escore-zscore
CGS001_HT29_96H:PIK3CA:1	HT29	PIK3CA	5290	trt_sh.cgs	landmark	4	Not_in_AMARETTO	Module 94 : A_D (w = 0.1491) , escore-pval-padj-zscore	Module 19 : A_D (w = 0.0365) , escore-pval-padj-zscore	Module 16 : A_D (w = 0.0398) , zscore; Module 98 : A_D (w = 0.0123) , escore-pval-padj-zscore	Module 37 : A_D (w = 0.0034) , escore-zscore; Module 51 : A_D (w = 0.002) , escore-zscore; Module 73 : A_D (w = 0.1852) , escore-pval-padj-zscore
CGS001_MCF7_96H:PIK3CA:2	MCF7	PIK3CA	5290	trt_sh.cgs	landmark	4	Not_in_AMARETTO	Module 94 : A_D (w = 0.1491) , escore-pval-padj-zscore	Module 19 : A_D (w = 0.0365) , escore-pval-padj-zscore	Module 16 : A_D (w = 0.0398) , zscore; Module 98 : A_D (w = 0.0123) , escore-pval-padj-zscore	Module 37 : A_D (w = 0.0034) , pval-padj-zscore; Module 51 : A_D (w = 0.002) , zscore; Module 73 : A_D (w = 0.1852) , escore-pval-padj-zscore

Community-AMARETTO report pan-SCC - AMARETTO report HNSC

Summary of SOX2/GPX2-regulated HNSC Module 51:

SOX2 CNV amplification, associated with induced SOX2 expression

GPX2 hypo/hyper-methylation, associated with induced/repressed GPX2 expression

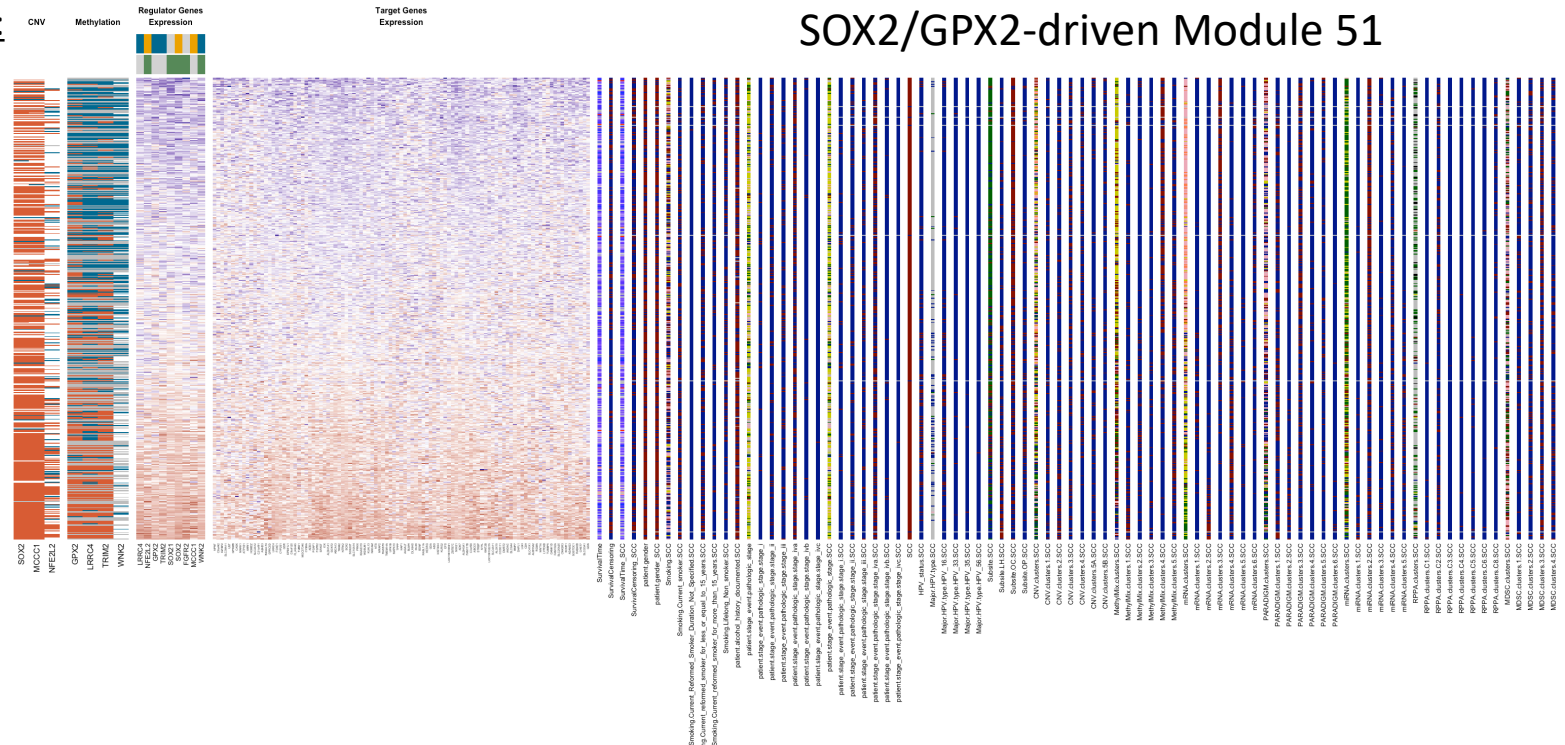
SOX2 and GPX2 are activators of their targets

Associated with smoking and HPV, and TCGA multi-omics clusters (CNV and methylation)

Enriched for HNSC and SCC-specific gene signatures

SOX2 and GPX2 validated for HNSC/LUSC modules

SOX2/GPX2-driven Module 51



Case Study 3: squamous cell carcinoma across 5 cancer sites

Driver discovery across 5 data sets

PathologicID	Cell_Line	QualityScore	EMVID	PathologicType	Type	DUSP4Frequency	BLCA	CESC	ESCA	HNSC	LUSC
C52001_048_Non_GPX2_1	AS49	GPX2	2077	SCC_Orn	rest	2	Module 10: A_D (n = 5920); p-value: 2.00e-160; Module 16: B_D (n = 42780); p-value: 2.00e-160; Module 14: A_D (n = 5784); p-value: 2.00e-160	Module 14: T_CD (n = 75); p-value: 2.00e-160	Module 12: 1 (n = 6); p-value: 2.00e-160	Module 11: A_D (n = 5920); p-value: 2.00e-160; Module 19: A_D (n = 43070); p-value: 2.00e-160; Module 13: A_D (n = 6010); p-value: 2.00e-160	Module 2: B_D (n = 42780); p-value: 2.00e-160; Module 21: A_D (n = 43070); p-value: 2.00e-160; Module 17: A_D (n = 43070); p-value: 2.00e-160

Showing 1 to 1 of 1 entries (filtered from 55,751 total entries)



Community-AMARETTO report pan-SCC - AMARETTO report HNSC

Summary of GPX2-regulated HNSC Module 79:

GPX2 hypo/hyper-methylation, associated with induced/repressed GPX2 expression

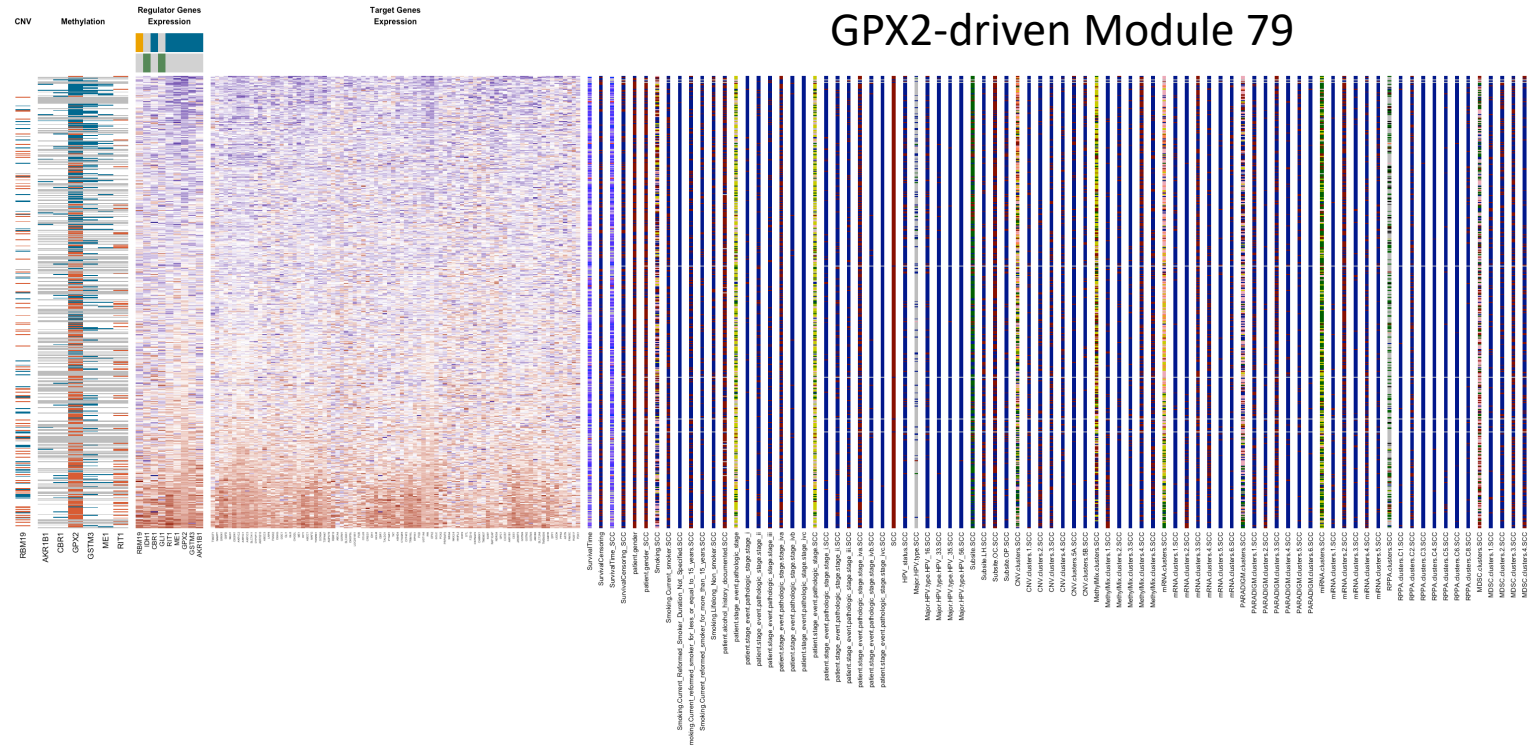
GPX2 is an activator of its target genes

Associated with smoking (lower expression ~non-smoking) and HPV (lower expression ~HPV), and TCGA multi-omics clusters (methylation)

Enriched for HNSC and SCC-specific gene signatures

SOX2 and GPX2 validated using KD experiments in A549 cell line for HNSC/LUSC modules

GPX2-driven Module 79

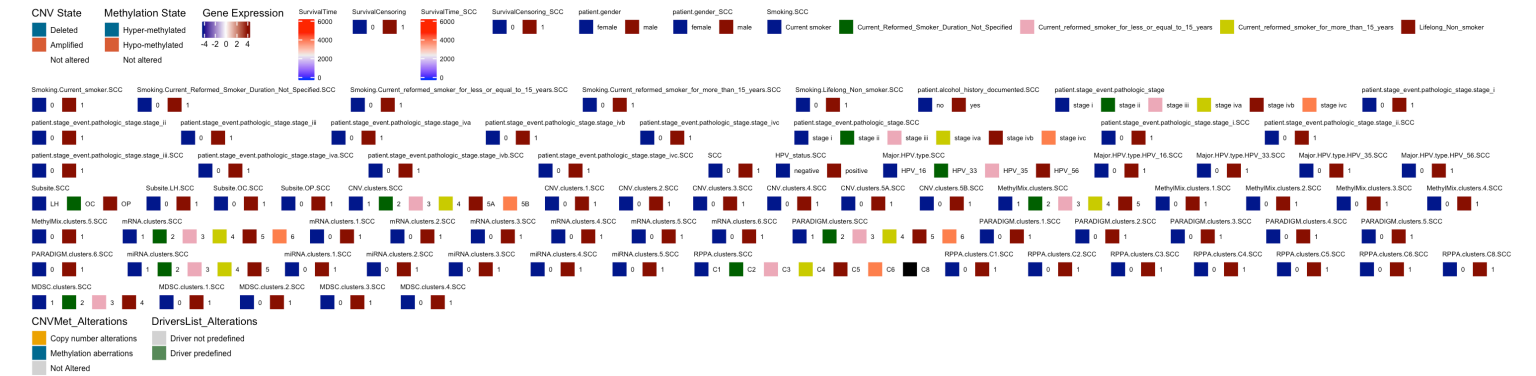


Case Study 3: squamous cell carcinoma across 5 cancer sites

Driver discovery across 5 data sets

PathologicID	Cell_Line	Quantity	EntrezID	PathologicType	Type	DiseaseFrequency	ELCA	C5G3	ESCA	HNSC	LUSC
C52001_GSM_NIN_GPX2_1	A549	GPX2	3077	TCR_inhib	Regulated	2					

Showing 1 to 1 of 1 entries (filtered from 55,751 total entries)



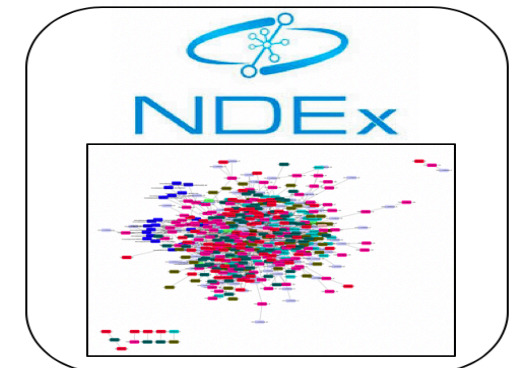
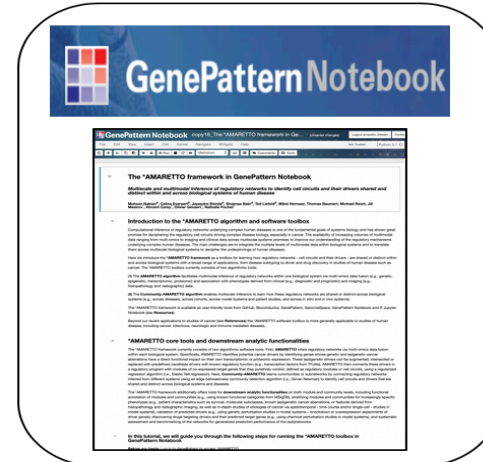
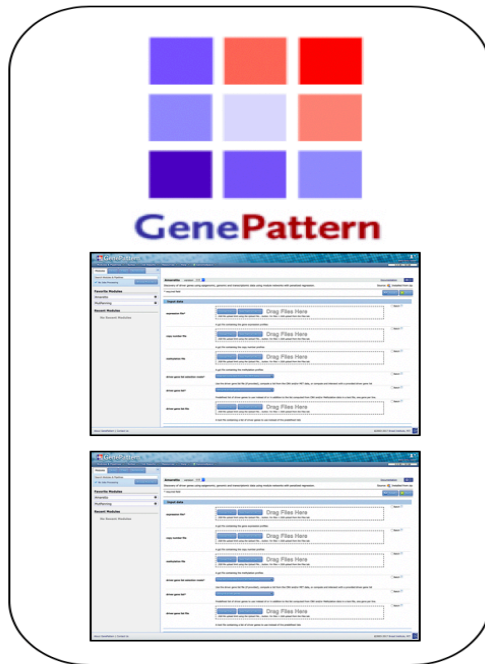
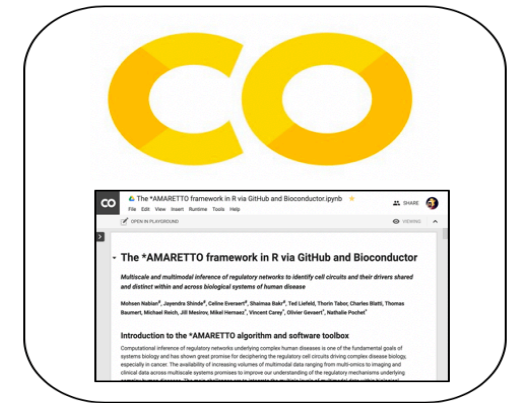
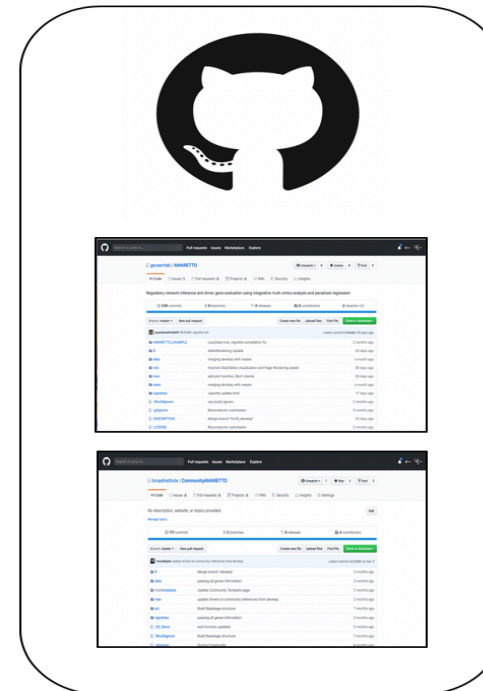
*AMARETTO source code, tools & notebooks

*AMARETTO is available via:

- GitHub
- Bioconductor
- Jupyter Notebook
- GenePattern
- GenomeSpace
- GenePattern Notebook

Tools and resources:

<http://portals.broadinstitute.org/pochetlab/amaretto.html>



*AMARETTO GenePattern Notebook

GenePattern Notebook Login / Register

The *AMARETTO framework in GenePattern Notebook

Multiscale and multimodal inference of regulatory networks to identify cell circuits and their drivers shared/distinct within/across biological systems of human disease, especially cancer

Nabian M, Everaert C, Shinde J, Bakr S, Liefeld T, Hernaez I, Pochet N
 Release amareto-2dteam
 April 11, 2019

Download

The *AMARETTO framework in GenePattern Notebook

Multiscale and multimodal inference of regulatory and distinct within and across biological systems

Mohsen Nabian¹, Celine Everaert¹, Jayendra Shinde¹, Shujaini B. Mehiniv¹, Vincent Carey¹, Olivier Gervart¹, Nathalie Pochet¹

Introduction to the *AMARETTO algorithm

Computational inference of regulatory networks underlying complex human diseases has great promise for deciphering the regulatory cell circuits driving complex multimodal data ranging from multi-omics to imaging and clinical data mechanisms underlying complex human diseases. The main challenge to translate them across multiscale biological systems to decipher the mechanisms underlying complex human diseases.

Here we introduce the ***AMARETTO framework** as a toolbox for learn within and across biological systems with a broad range of application such as cancer. The *AMARETTO toolbox currently consists of two algorithms:

(1) The **AMARETTO algorithm** facilitates multimodal inference of regulatory networks (epigenetic, transcriptomic, proteomic) and association with phenotype (histopathology and radiomics) data.

(2) **TCGA data**: by selecting a cohort from The Cancer Genome Atlas (TCGA) database. In this case, you can control the selection criteria.

Access to processed data from TCGA

The processed genetic, epigenetic and transcriptomic data sources from TCGA are directly accessible via this GenePattern Notebook. These TCGA data files are derived from The Cancer Genome Atlas (TCGA) as available (<https://data.broadinstitute.org/>).

Once you select a cancer site from the drop-down menu, three data files will be loaded: 1) mRNA gene expression and 2) DNA methylation data, and will be available for selection in the drop-down menus in the next steps.

The list of TCGA cancer (subtypes currently available in this *AMARETTO in GenePattern Notebook are:

BLCA	bladder urothelial carcinoma
BRCA	breast invasive carcinoma
CESC	cervical squamous cell carcinoma and endocervical adenocarcinoma
CMLC	colorectal adenocarcinoma
COAD	colon adenocarcinoma
ESCA	esophageal carcinoma
GBM	glioblastoma multiforme
HNSC	head and neck squamous cell carcinoma
KIPAN	kidney renal papillary cell carcinoma
KIPAN	kidney renal papillary cell carcinoma
LIHC	liver hepatocellular carcinoma
LIHC	liver hepatocellular carcinoma
LUSC	lung squamous cell carcinoma
LUSC	lung squamous cell carcinoma
OV	ovarian serous cystadenocarcinoma
PANAD	pancreatic adenocarcinoma
PAAD	pancreatic adenocarcinoma
PLOP	pharynx larynx and hypopharynx carcinoma
READ	rectal adenocarcinoma
SARC	sarcoma
STAD	stomach adenocarcinoma
THCA	thyroid carcinoma
UCEC	uterine corpus endometrial carcinoma
UCEC	uterine corpus endometrial carcinoma

The genetic, epigenetic and transcriptomic data sources for the TCGA cancer (subtypes included in this *AMARETTO Notebook are:

GenePattern gptExampleTCGAFiles { }

cancerType* GBM

Step 2. Running AMARETTO to infer regulatory networks from functional genomics data or via multi-omics data fusion

Running AMARETTO on own and TCGA data

The AMARETTO algorithm that infers regulatory networks within one cohort or biological system can be run in two ways:

(1) **Your own data**: by uploading your own data. In this case, the minimal requirement is to upload a functional genomics (i.e., mRNA or protein gene expression) data file. When available, the user can additionally upload genomic (e.g., DNA copy number variation) and/or epigenetic (e.g., DNA methylation) data files.

(2) **TCGA data**: by selecting the multi-omics (functional genomics: mRNA gene expression, genetic: DNA copy number variation, and epigenetic: DNA methylation) or only the functional genomics (mRNA gene expression) data files from a previously selected cohort from The Cancer Genome Atlas (TCGA) database. See **Step 1**.

For any type of multiomics data (genetic, epigenetic, transcriptomic and proteomic), data files should be formatted as GCT files (rows represent genes, columns represent samples, see GCT format (<https://www.broadinstitute.org/genetics-omics-computational-bioinformatics/gct-format>)).

In both scenarios, the next step involves choosing the candidate driver definitions.

Running AMARETTO with various data and/or candidate driver definitions

Index the URL*

File may not be an acceptable format. This input expects /AMARETTO.html#index.html.

Step 4. Running AMARETTO to infer regulatory networks from multiple data sources (repeat steps 4 & 5) (optional)

Running AMARETTO on one or more additional datasets

For comparative inference of networks shared or distinct across datasets, cohorts, biological systems, or diseases, previous Steps 2 and 3 can be repeated multiple times in Steps 4 and 5.

GenePattern AMARETTO Version 0.5.0

Discovery of driver genes using epigenomic, genomic and transcriptomic data using module networks with penalized regression.

Input data

expression file*
A gct file containing the gene expression profiles

copy number file
A gct file containing the copy number profiles

methylation file
A gct file containing the methylation profiles

driver gene list selection mode*
Use the driver gene list file (if provided), compute a list from the CNV and/or MET data, or compute and intersect with a provided driver gene list

driver gene list
Predefined list of driver genes to use instead of or in addition to the list computed from CNV and/or Methylation data in a text file, one gene per line.

driver gene list file
A text file containing a list of driver genes to use instead of the predefined list

Basic parameters

number of modules*
Number of modules

percent genes*
Percent genes to use

output file*
Base name for output files

Input genomic test

gene sets database*

size (and at least, larger than 2), 3. Ratio between edges inside/outside the community larger than 0.5. The user can choose between filtering according to these criteria, in which case edges in the network that do not satisfy all of these criteria will be filtered out, or whether to not apply these filtering criteria to retain all edges.

Time complexity of Community-AMARETTO

Depending on the number of regulatory networks that are submitted for comparative analysis by Community-AMARETTO, it typically takes ~15 minutes for two networks up to ~45 minutes for more than five networks to run the Community-AMARETTO algorithm and generate the report on the GenePattern Amazon Cloud server. Once the report is generated, it can be accessed for viewing in **Step 7**.

GenePattern Community-AMARETTO Version 0.000000

Compute module overlap between multiple AMARETTO results

amareto result files*

Files containing the zipped AMARETTO results

output file*
Name for the output file

amareto report files

Files containing the zipped AMARETTO reports with name prefixes matching the AMARETTO result files.

gene sets database*

Gene sets database from GSEA website. Upload a gene set if your gene set is not listed as a choice from MSigDB.

p-value*
The network edges with their p-value larger than this value will be filtered out.

min number overlapping genes*
The network edges with their number of overlapping genes less than this value will be filtered out.

filter communities*
If it is set to 0? Yes??. Communities (subnetworks) that do not satisfy all these following conditions will be filtered out: 1- Number of nodes in the community to be larger than 1% of the total number of nodes in the network. 2- Number of represented cancers in the community to be larger than the 10% of the subnetwork size (at least, larger than 3). 3- Ratio between edges inside/outside the community to be larger than 0.5.

Error loading job: 102365

Step 7. Viewing Community-AMARETTO results combining multiple AMARETTO analyses (optional)

Queryable report generated for Community-AMARETTO analysis

The Community-AMARETTO report includes:

Funding

This work was supported by grants from NIH NCI ITCR R21 CA209940 (Pochet), NIH NCI ITCR U01 CA214846 Collaborative Supplement (Carey/Pochet) and NIH NIAID R03 AI131066 (Pochet).

Questions?

For any questions with the *AMARETTO Notebooks, please contact **Nathalie Pochet** (npochet@broadinstitute.org) and **Olivier Gervart** (ogervart@broadinstitute.org).

bladder carcinoma patient data from TCGA, liver hepatocellular carcinoma patient data in HepG2 in a HepG2 model, further augmented with AMARETTO results.

ultraform based on multi-omics and non-RNA-Seq refined for anatomic structures and 5 on single-cell RNA-Seq studies:

- doi: 10.1101/2019.03.29.331175
- is Captures PanCancer Genetically and 56-166. PMID:29331675
- using module network integration of multi-omics. Genome Biology, 16(1), 17.
- 3(11), 1839-41. PMID:25609794
- a structures for transcription factor
- Berges Rivera D, Tabor T, Thornaldsson D, Hs, 4:804
- doi: 10.1101/2019.03.29.331175
- Chang H Y, Mesirov J P (2015), 3(3), 245-247. PMID:26780084
- n genes. Bioinformatics, 2018 Sep 19. PMID:3029298
- in. Genome Biology 2015 Jun 29;16:17. doi: 10.1186/s12864-015-1609-4

*AMARETTO R Jupyter Notebook

▼ The *AMARETTO framework in R via GitHub and Biocond

Multiscale and multimodal inference of regulatory networks to identify cell circuits and their drivers biological systems of human disease

Mohsen Nabian[#], Jayendra Shinde[#], Celine Everaert[#], Shaimaa Bakr[#], Ted Liefeld, Thorin Tabor, Charles Blatti, Th Mikel Hernandez^{*}, Vincent Carey^{*}, Olivier Gevaert^{*}, Nathalie Pochet^{*}

Introduction to the *AMARETTO algorithm and software toolbox

Computational inference of a promise for deciphering the ranging from multi-omics to complex human diseases. The multiscale biological system

Here we introduce the *AMA across biological systems with *AMARETTO toolbox current

(1) The **AMARETTO algorithm** epigenetic, transcriptomic, p radiographic) data.

(2) The **Community-AMARETTO** (e.g., across diseases, across The *AMARETTO framework Notebook (see **Resources**).

Beyond our recent applications including cancer, infectious,

▼ *AMARETTO core

The *AMARETTO framework each biological system. Specific direct functional impact on candidate drivers with known modules of co-expressed target Elastic Net regression). Next an edge betweenness communities systems and diseases.

The *AMARETTO framework of modules and communities (e.g., patient characteristics

For running the Notebook on **preloaded TCGA data** please continue in this **Step 2** | https://datasets.genepattern.org/?prefix=data/module_support_files/Amaretto/ in automatically read from this link and how they are converted to data matrices in R

For running the Notebook on **example data** you can immediately proceed to **Step 3** and also available for download from <https://www.broadinstitute.org/~npochet/Nc> example data are available here: (1) for 150 modules and 75% variation filtering (see <https://www.broadinstitute.org/~npochet/NotebookExample/ExampleResults/res>; <https://www.broadinstitute.org/~npochet/NotebookExample/ExampleResults/res>; <https://www.broadinstitute.org/~npochet/NotebookExample/ExampleResults/res>);

▼ Access to processed data from TCGA

The processed genetic, epigenetic and transcriptomic data sources from TCGA are Notebook. These TCGA data files are derived from The Cancer Genome Atlas (TCG <https://gdac.broadinstitute.org/>).

From https://datasets.genepattern.org/?prefix=data/module_support_files/Amare downloaded: (1) mRNA gene expression data (MA), (2) DNA copy number variation

The list of TCGA cancer (sub)types currently available in this *AMARETTO in R Not

BLCA	bladder urothelial carcinoma
BRCA	breast invasive carcinoma
CESC	cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL	cholangiocarcinoma
COAD	colon adenocarcinoma
ESCA	esophageal carcinoma
GBM	glioblastoma multiforme
HNSC	head and neck squamous cell carcinoma
KIRC	kidney renal clear cell carcinoma
KIRP	kidney renal papillary cell carcinoma
LAML	acute myeloid leukemia
LGG	brain lower grade glioma
LIHC	liver hepatocellular carcinoma
LUAD	lung adenocarcinoma
LUSC	lung squamous cell carcinoma
OV	ovarian serous cystadenocarcinoma
PAAD	pancreatic adenocarcinoma
PCPG	pheochromocytoma and paraganglioma
READ	rectum adenocarcinoma
SARC	sarcoma
STAD	stomach adenocarcinoma
THCA	thyroid carcinoma

Step 3. Running AMARETTO on first example study: infer networks via multi-omics data fusion for TCGA LIHC pati

The AMARETTO algorithm that infers regulatory networks within one cohort or biological system can be run in multi genetic, epigenetic and functional genomics data are available (see example in this **Step 3** for multi-omics data from are available (see example in next **Step 4** for transcriptomic data from CCLE).

When **either genetic** (e.g., DNA copy number variation) or **epigenetic** (e.g., DNA methylation) data or **both** are available transcriptomic or proteomic) data, there are various options for defining candidate drivers for analysis by the AMAR In case **only functional genomics** (i.e., mRNA or protein gene expression) data are available, a predefined list of can AMARETTO algorithm.

The AMARETTO algorithm can take vario

(1) Select **computed lists of candidate driver** data files are uploaded);

(2) Select or upload **predefined lists of candidate driver** data (e.g., <https://bioconductor.org/packages/release/annotation/html/BroadInstitute.html>);

(3) Take the **union or intersection** between

For computed lists of candidate drivers for TCGA data, however, for processing of recurrent DNA copy number aberrations (recurrent DNA methylation aberrations (association for DNA copy number aberra

▼ Step 3.a. Preparing data ar

▼ Loading multi-omics data from TC

▼ Loading Gene Expression (MA) data fro

Step 4. Running AMARETTO on second example networks from RNA-Seq data from CCLE liver

The AMARETTO algorithm that infers regulatory networks within one cohort or biological system genetic, epigenetic and functional genomics data are available (see example in previous **Step 3** data are available (see example in this **Step 4** for transcriptomic data from CCLE). See **Step 3**

▼ Step 4.a. Preparing data and parameter settings for running A

▼ Loading RNA-Seq data from CCLE liver cell lines

▼ Loading Gene Expression (MA) data from CCLE liver cell lines (Required)

```
MA_matrix_CCLE <- readRDS(url("https://www.broadinstitute.org/~npochet/NotebookExample/ProcessedData_CCLE = list(MA_matrix=MA_matrix_CCLE, CNV_matrix=NULL, MET_matrix=NULL)
```

▼ Defining List(s) of Candidate Driver Genes (Required)

In this example, we precompiled a list of candidate driver genes that takes the union of TCGA list of candidate drivers as in **Step 3**)

```
candidate_drivers_CCLE <- readRDS(url("https://www.broadinstitute.org/~npochet/NotebookExample/ProcessedData_CCLE = list(MA_matrix=MA_matrix_CCLE, CNV_matrix=NULL, MET_matrix=NULL)
```

▼ Setting parameters for running AMARETTO (Required)

Core parameters that can be set by the user for running AMARETTO. See **Step 3** for more details

```
nrModules = 150  
VarPercentage = 75
```

▼ Setting parameters for generating HTML results reports (Optional)

Additional parameters that can be set by the user for running AMARETTO. See **Step 3** for more detailed information.

```
genesets_database_reference <- "H_C2_genesets.gmt"  
download.file(url="https://www.broadinstitute.org/~npochet/NotebookExample/ExampleData/H_C2_genesets",  
output_directory_CCLE = ". /AMARETTO_report_CCLE/"  
dir.create(output_directory_CCLE)
```

Step 5. Running Community-AMARETTO to combine both identifying regulatory subnetworks or communities shared TCGA and CCLE cohorts

The Community-AMARETTO algorithm takes as input results from two or more previous AMARETTO analyses to identify cell circuits and their drivers) that are shared and distinct across multiple datasets cohorts biological systems

▼ Step 5.a. Preparing data and parameter settings for running Community-AM

▼ Loading two or more results from AMARETTO, in this example the previous TCGA and CCLE results

Selecting AMARETTO analyses for Community-AMARETTO analysis. The user can submit the .rds files that represent more previous AMARETTO analyses (see above, run in **Steps 3 and 4**).

```
AMARETTOresults_TCGA <- readRDS(file="TCGA_AMARETTOresults.rds")  
AMARETTOresults_CCLE <- readRDS(file="CCLE_AMARETTOresults.rds")  
HTMLAMARETTOlist <- c("TCGA"=output_directory_TCGA, "CCLE"=output_directory_CCLE)
```

▼ Loading additional networks as a set of signatures in .GMT format (Optional)

One or more additional networks can be submitted as signatures files in .GMT format and combined by running the Community-AMARETTO as separate networks. In this example, we submit previously published signatures and/or network CiberSort, stemness signatures from *Ben-Porath et al.*, and diagnostic and prognostic liver cancer signatures from H be analyzed together with the liver cancer networks derived from TCGA in **Step 3** and CCLE in **Step 4**.

If additional networks are submitted, please run following cell code to include them in the analysis.

```
ImmuneSignatures <- "ImmuneSignatures.gmt"  
download.file(url="https://www.broadinstitute.org/~npochet/NotebookExample/ExampleData/ImmuneSignatures",  
StemSignatures <- "StemSignatures.gmt"  
download.file(url="https://www.broadinstitute.org/~npochet/NotebookExample/ExampleData/StemSignatures",  
LiverSignatures <- "LiverSignatures.gmt"  
download.file(url="https://www.broadinstitute.org/~npochet/NotebookExample/ExampleData/LiverSignatures",  
list_additional_networks = list(ImmuneSignatures = "ImmuneSignatures.gmt", StemSignatures = "StemSignatures.gmt",  
LiverSignatures = "LiverSignatures.gmt")  
Otherwise set to NULL.  
list_additional_networks = NULL
```

▼ Setting parameters for generating HTML results reports (Optional)

11. Reich M, Liefeld T, Ocanca M, Jang D, Bistline J, Robinson J, Carr P, Hill B, McLaughlin J, Pochet N, Borge Mesirov J.P. (2013). GenomeSpace: an environment for frictionless bioinformatics. *FT000Posters*, 4:804. <https://doi.org/10.1093/bioinformatics/btt000>

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Questions?

For any questions with the *AMARETTO Notebooks, please contact **Nathalie Pochet** (npochet@broadinstitute.org)

*AMARETTO R Jupyter Notebook Use Case 3

*AMARETTO Use Case 3: pan-cancer study of squamous cell carcinoma

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Preparing...

The following commands are to prepare, install and load AMARETTO and Community AMARETTO packages. These installation process must be done again everytime the notebook is reopened.

```
system("sudo apt-get install libfido-dev", intern = TRUE, ignore.stderr = TRUE) |
devtools::install_all_thru_deps("AMARETTO", ref="for3_develop", dependencies=TRUE)
library("AMARETTO")
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("ComplexHeatmap")
BiocManager::install("Rcpp")
devtools::install_all_thru_deps("CommunityAMARETTO", ref="master", dependencies=TRUE)
library("CommunityAMARETTO")
```

A. AMARETTO for each of the 5 squamous disease data sets

A1. AMARETTO for TCGA-LUSC

Loading Multi-Omics data including Gene Expression (MA), Copy Number Variation (CNV) and DNA Methylation (MT): (Only MA is mandatory)

```
MA_matrix_ESCA <- AMARETTO::read_get(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/TCGA_ESCA_Expression.gct"))
CNV_matrix_ESCA <- AMARETTO::read_get(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/TCGA_ESCA_CNV.gct"))
MT_matrix_ESCA <- AMARETTO::read_get(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/TCGA_ESCA_Methylation.gct"))
```

Defining List(s) of Candidate Driver Genes (Optional):

```
dataDriver_Genes
driver_genes_Driver_ScenesCancer_Scenes_Genes
Running AMARETTO core for regulatory network inference: Number of regulatory modules (NModules), percentage of most varying genes (VnPercentage) are required. Here we specified NModules and VnPercentage to be 150 and 75 respectively. We can optionally specify number of cores (NnCores) for parallel processing. As for the combination method for (1) the computed and (2) the predefined list of drivers, we specified 'union' (as opposed to 'Intersection').
ProcessedData_TCGA_ESCA_LUSC <- AMARETTO::init_initialize(ProcessedData = ProcessedData_TCGA_ESCA_LUSC,
AMARETTO_NModules = 150,
Driver_List = driver_genes,
Method = "union",
NModules = 150,
VnPercentage = 75,
NnCores = 8,
Random_Seed = c(42,42))
AMARETTO_Results_LUSC <- AMARETTO::run(AMARETTO_NModules,
AMARETTO_Results_LUSC)
```

Loading phenotypes and statistical tests data, and performing performing the phenotype association tests:

```
samples_LUSC <- read.csv("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/LUSC_All_phenotypes.csv")
phenotype_tests_LUSC <- read.csv("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/LUSC_All_statistical_tests.csv")
LUSC_phenotype_tests_all <- AMARETTO::init_initialize(AMARETTO_Results_LUSC, AMARETTO_Results_LUSC, samples_LUSC, phenotype_tests_LUSC)
```

Performing GeneSet Enrichment Analysis:

```
functional_genes <- c(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/H_C_genesets.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_LUSC, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

```
functional_genes <- c(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/H_C_genesets.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_LUSC, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

Performing GeneSet Enrichment Analysis for driver perturbations:

```
genetic_genes <- c(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_LUSC, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

Performing GeneSet Enrichment Analysis for drug perturbations:

```
chemical_genes <- c(url("signature/ChemicalPerturbationSignatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_LUSC, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

Creating AMARETTO HTML report:

```
AMARETTO_HTML_report <- AMARETTO::results_MA,
AMARETTO_Results_MA,
ProcessedData_TCGA_ESCA_LUSC,
hyper_geo_reference_chemical_genes,
driver_genes_Driver,
NnCores = 8,
NModules = 150,
VnPercentage = 75,
Random_Seed = c(42,42),
show_row_names=FALSE,
phenotype_association_table = HNSC_phenotype_tests_all)
```

A3. AMARETTO for TCGA-ESCA

Loading Multi-Omics data including Gene Expression (MA), Copy Number Variation (CNV) and DNA Methylation (MT): (Only MA is mandatory)

```
MA_matrix_ESCA <- AMARETTO::read_get(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/TCGA_ESCA_Expression.gct"))
CNV_matrix_ESCA <- AMARETTO::read_get(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/TCGA_ESCA_CNV.gct"))
MT_matrix_ESCA <- AMARETTO::read_get(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/TCGA_ESCA_Methylation.gct"))
ProcessedData_TCGA_ESCA <- AMARETTO::init_initialize(ProcessedData = ProcessedData_TCGA_ESCA,
AMARETTO_NModules = 150,
Driver_List = driver_genes,
Method = "union",
NModules = 150,
VnPercentage = 75,
NnCores = 8,
Random_Seed = c(42,42))
AMARETTO_Results_ESCA <- AMARETTO::run(AMARETTO_NModules,
AMARETTO_Results_ESCA)
```

Defining List(s) of Candidate Driver Genes (Optional):

```
dataDriver_Genes
driver_genes_Cancer_ScenesCancer_Scenes_Genes
Running AMARETTO core for regulatory network inference: Number of regulatory modules (NModules), percentage of most varying genes (VnPercentage) are required. Here we specified NModules and VnPercentage to be 150 and 75 respectively. We can optionally specify number of cores (NnCores) for parallel processing. As for the combination method for (1) the computed and (2) the predefined list of drivers, we specified 'union' (as opposed to 'Intersection').
ProcessedData_TCGA_ESCA <- AMARETTO::init_initialize(ProcessedData = ProcessedData_TCGA_ESCA,
AMARETTO_NModules = 150,
Driver_List = driver_genes,
Method = "union",
NModules = 150,
VnPercentage = 75,
NnCores = 8,
Random_Seed = c(42,42))
AMARETTO_Results_ESCA <- AMARETTO::run(AMARETTO_NModules,
AMARETTO_Results_ESCA)
```

Loading phenotypes and statistical tests data, and performing performing the phenotype association tests:

```
samples_ESCA <- read.csv("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/ESCA_All_phenotypes.csv")
phenotype_tests_ESCA <- read.csv("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/ESCA_All_statistical_tests.csv")
ESCA_phenotype_tests_all <- AMARETTO::init_initialize(AMARETTO_Results_ESCA, AMARETTO_Results_ESCA, samples_ESCA, phenotype_tests_ESCA)
```

GeneSet Enrichment Analysis:

```
functional_genes <- c(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/H_C_genesets.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/DRB88_including_signatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_ESCA, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

GeneSet Enrichment Analysis for driver perturbations:

```
genetic_genes <- c(url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"),
url("http://portals.broadinstitute.org/portals/1406/NotebookExample/ExampleData/GeneticPerturbationSignatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_ESCA, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

GeneSet Enrichment Analysis for drug perturbations:

```
chemical_genes <- c(url("signature/ChemicalPerturbationSignatures.gct"))
hgnetx_tbl <- hyperGeometricTest(AMARETTO_Results_ESCA, hyper_geo_reference_chemical_genes, driver_genes_Driver, NnCores=8)
```

AMARETTO HTML report:

```
AMARETTO_HTML_report <- AMARETTO::results_MA,
AMARETTO_Results_MA,
ProcessedData_TCGA_ESCA,
hyper_geo_reference_chemical_genes,
driver_genes_Driver,
NnCores = 8,
NModules = 150,
VnPercentage = 75,
Random_Seed = c(42,42),
show_row_names=FALSE,
phenotype_association_table = ESCA_phenotype_tests_all)
```

ETTO for TCGA-ESCA

Multi-Omics data including Gene Expression (MA), Copy Number Variation (CNV) and DNA Methylation (MT): (Only MA is mandatory)

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Glass K, Pochet N, Evraert C, Ischy B, Carey V (2019). TIFe: Data structures for transcription factor bioinformatics. <https://github.com/TCR2019/TIFe>.

• Nabian M, Shinde J, Lifshik T, Chavira M, Borger-Rivera D, Pochet N, Robinson T, Durrant D, Jhall T, Ben-Artzi E, Blankenberg L, Nebretskio A, Segal E, Idder T, Reich M, Regier A, Chang H-Y, Mesirov J-F (2016). Integrative genomic analysis by code in GenomSpace. *Nature Methods*. 13(8):245-247. PMID:2678004. PMC:4767623.

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Andrew Gentles

Kevin Brennan

Magali Champion

Mesirov Lab (UCSD/Broad)

Jill Mesirov

Michael Reich

Ted Liefeld

Thorin Tabor

Hernaez Lab (Illinois)

Mikel Hernaez

Baumert Lab (Strasbourg)

Thomas Baumert

Joachim Lupberger

Eloi Verrier

Quintana Lab (BWH/HMS/Broad)

Francisco Quintana

Krichevsky Lab (BWH/HMS)

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