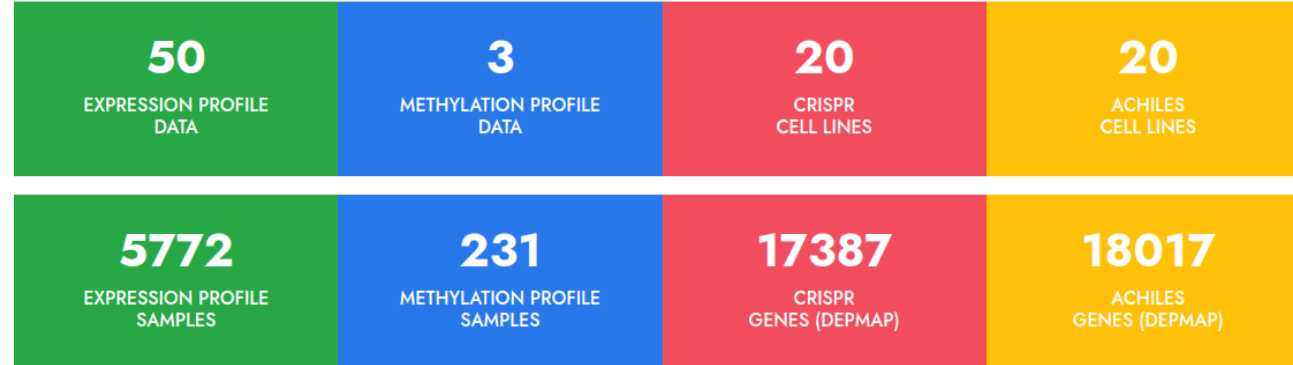


MyeloDB (Multiple Myeloma Database)

MyeloDB is aimed to maintain gene expression, methylation, CRISPR and Achilles datasets from public repositories. Myeloma is a blood cancer of cells found in the bone marrow, specifically the so-called "plasma cells." Plasma cells produce antibodies that help the body fight infection. Myeloma begins when healthy plasma cells change and grow out of control. This may result in multiple bone lesions that increase the risk of bone fractures. That is where the phrase "multiple myeloma" comes from.

Stats of MyeloDB are shown below:



WHAT WE PROVIDE?

Dataset section

MyeloDB: Multiple Myeloma Database

Home Datasets Analysis Biomarker Downloads Help Team

HELP SECTION!

- GEO Data:**
 - Browse on
 - Profiling Technique
- CRISPR-Cas9 Screens:**
 - DepMap
 - Achilles
- GDSC Data:**
 - Browse by Drug

Datasets has following options to choose from

Information about multiple myeloma. This manual is intended to help users navigate the webpage and utilize its various features. For more information, please refer the MyeloDB manual

- About MyeloDB
- Navigating the Webpage
- User manual
- Glossary
- Contact us

USER MANUAL



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BROWSE ON

Browse on page provides information of all the data of expression and methylation collected from GEO portal. In this page user can search the gene expression datasets uploaded in this database. User needs to fill the query submission form then select the type of query to be searched followed by typing his query to get the required results. In case of difficulty reach out to the [Help](#) section!

Query submission form

Search the GSE ID/PubMed ID/Profiling Technique/processing package/Type of data/Sample source here..



Example Search:

GSE ID:
PubMed ID:
Profiling Technique:

Processing package:

Type of data:

Sample source:

User can search by typing his query here and then click on search icon to view result

Here are some example search which user can try



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Click here to export your result as a csv

Dataset section

Click here to download the specific GSE ID

MyeloDB: Multiple Myeloma Database

Home Datasets Analysis Biomarker Downloads Help Team

Your search result for Profiling Technique Affymetrix:

Export Table to CSV



GSE ID	No of Samples	Profiling Technique	Pubmed ID	Platform	Values of matrix	No of Probes	No of genes	Package for data preprocessing	Source of sample	Type of Data	Download
GSE164706	240	Affymetrix	35357885	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Bone marrow	Expression profile	
GSE164701	109	Affymetrix	35357885	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Bone marrow	Expression profile	
GSE201846	12	Affymetrix	NA	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Human Aortic Endothelial Cells	Expression profile	
GSE146649	41	Affymetrix	NA	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Mesenchymal stromal cell	Expression profile	
GSE87900	180	Affymetrix	33351127	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Bone marrow	Expression profile	
GSE70515	7	Affymetrix	NA	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Bone marrow	Expression profile	
GSE109651	14	Affymetrix	31406992	[HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	RMA (Robust Multi Array)	45782	25849	Affy	Bone marrow	Expression profile	

This link will take you to GEO website to the respective GSE study

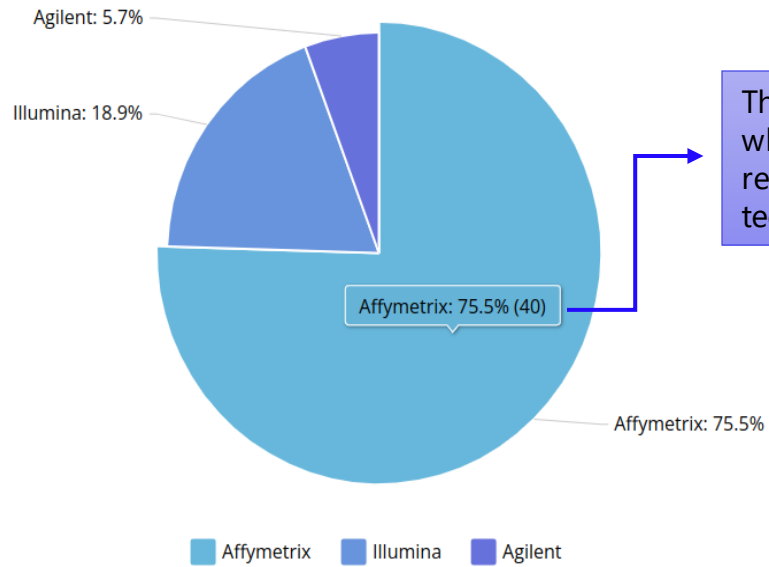
This link will take you to Pubmed

This is how search for profiling technique: Affymetrix looks like

Dataset section

Profiling Technique

Gene expression profiling measures expression of a gene in a cell at any given moment. It measures mRNA levels i.e., pattern of genes expressed by a cell at the transcription level. Similarly Methylation arrays enable quantitative interrogation of selected methylation sites across the genome. Categorization based on profiling techniques are shown below. User can see data according to the total entries based on type of profiling techniques used. Here, data is shown for both expression and methylation data. For detailed assistance visit [Help](#) section!



These are clickable link which takes to the respective profiling technique data



DepMap and Achilles have similar search interface

MyeloDB:Multiple Myeloma Database

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DepMap Search

CRISPR-Cas9 is a unique technology that enables geneticists and medical researchers to edit parts of the genome by removing, adding or altering sections of the genome. Project Achilles data is hosted on the Cancer Dependency Map Portal (DepMap). Here we have data of a 17387 genes and 20 MM cell lines with their dependency scores. For detailed assistance visit [Help](#) section!

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Achilles Search

Project Achilles uses shRNAs or Cas9/sgRNAs to silence or knock-out individual genes and identify those genes that affect cell survival. The overall goal of the project is to identify cancer genetic dependencies and link them to molecular characteristics in order to prioritize targets for therapeutic development. Project Achilles data is hosted on the Cancer Dependency Map Portal (DepMap). Here we have data of a 17387 genes and 20 MM cell lines with their dependency scores. For detailed assistance visit [Help](#) section!

User can search for one gene here or try examples below

Search the gene here..


Example Search:

Genes:

Search the gene here..

Example Search:

Genes:



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DepMap and Achilles have similar result interface

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Your search result for A1BG :

This page shows DepMap data of A1BG gene against MM cell lines with their gene effect scores

Click here to get more gene information from genecards

To View Plot

Click here

Click here to get a plot of gene effect score vs all 17 cell lines

Export Table to CSV



Click here to export your result as a csv

DepMap_ID	ACH-000024	ACH-000183	ACH-000204	ACH-000363	ACH-000426	ACH-000436	ACH-000512	ACH-000541	ACH-000576	ACH-000588	ACH-000653	ACH-000658	ACH-000714	ACH-000763	A
Cell_line	OPM2	L363	LP1	SKMM2	KMS20	OCIMY7	INA6	KMS34	KMS27	KMS26	JJN3	KMS18	KMS11	MM1S	
Sample collection site	Haematopoietic and lymphoid tissue	Haematopoietic and lymphoid tissue	Haematopoietic and lymphoid tissue	Haematopoietic and lymphoid tissue	Bone Marrow	Haematopoietic and lymphoid tissue	Pleural effusion	Pleural effusion	Haematopoietic and lymphoid tissue	Pleural effusion	Bone marrow	Haematopoietic and lymphoid tissue	Pleural effusion	Haematopoietic and lymphoid tissue	Ha
Primary/Metastasis	Primary	Primary	Primary	Primary	Primary	NA	NA	Primary	Primary	Primary	Primary	Primary	Primary	Primary	
sex	Female	Female	Female	Male	Female	Male	Male	Female	Male	Male	Female	Male	Female	Female	
age	56	36	56	54	65	NA	80	60	52	50	57	60	67	45	
A1BG	-0.041681353	0.053245979	-0.076795183	0.061275249	0.145334198	-0.006208071	-0.305974546	-0.052823006	-0.043200151	0.003307671	0.126440936	-0.095707035	-0.071643887	0.137728322	-0



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CRISPR and Achilles have similar plot interface

Click to print/download image as PNG/JPEG

Your search result:

Here you get a plot for your searched gene within DepMap dataset, with gene dependency score on y-axis and respective multiple myeloma cell lines on x-axis. This score represents how important a gene is for that particular cell line. A lower score indicates a higher likelihood that the gene of interest is essential in a given cell line.

Plot for Gene A1BG



Dependency scores on y axis

Cell lines on x axis

BROWSE BY DRUG

Browse by Drug:

This page allows user to search one drug stored in MyeloDB from the GDSC v2 dataset. A total of 279 drug data is stored in MyeloDB for 17 MM cell lines. For de

Select a drug from the list in dropdown and click on search button

Select a Drug:

- Select--
- 5-azacytidine
- 5-Fluorouracil
- A-366
- ABT737
- Afatinib
- Afuresertib
- AGI-5198
- AGI-6780
- AGK2
- Alisertib
- Alpelisib
- alpha-lipoic acid
- AMG-319
- ascorbate (vitamin C)
- AT13148
- Avagacestat
- Axitinib
- AZ6102
- AZ960

*Drug names are provided in dropdown and In some cases where drug ID was present those IDs are written as CID_drugId. For example: if drugid = 123456 then it is shown in dropdown as CID_123456.

BROWSE BY DRUG

MyeloDB: Multiple Myeloma Database

[Home](#) [Datasets](#) [Analysis](#) [Biomarker](#) [Downloads](#) [Help](#) [Team](#)

Your search result:

This page shows Drug sensitivity data of cell line against drugs stored in MyeloDB. This data is acquired from GDSC portal consisting latest version of data i.e, GDSC v2. For detailed assistance visit [Help](#) section!

To View Plot [Click here](#)

To view plot of logIC50 vs cell line click here

Export Table to CSV



Click here to export table as a csv

Drug Name: **5-Fluorouracil**

Cell Line	AMO-1	ARH-77	EJM	IM-9	JJN-3	KARPAS-620	KMS-11	KMS-12-BM	L-363	LP-1	MM1S	MOLP-8	NCI-H929	OPM-2	RPMI-8226	SK-MM-2	U-266
log IC50	1.9138	1.6747	4.5403	1.4757	4.1613	5.2890	2.4043	3.7541	3.4176	6.1824	3.6889	2.5312	2.3707	3.4542	1.3903	4.7731	4.6769



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BROWSE BY DRUG

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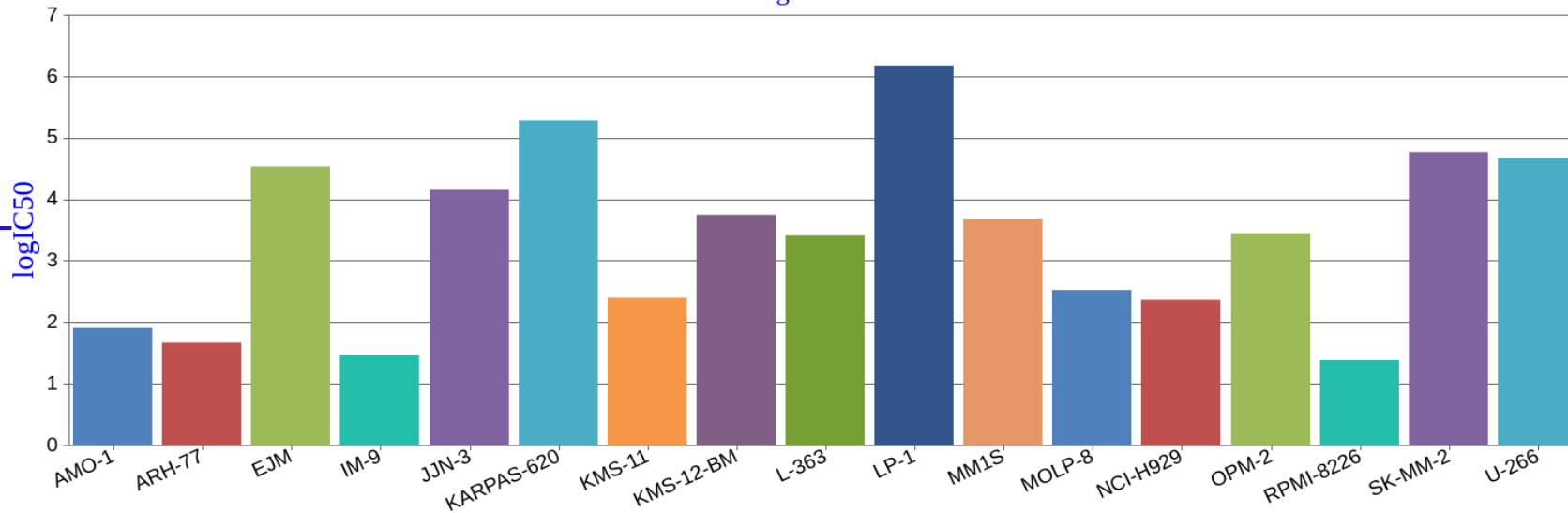
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Your search result for drug: 5-Fluorouracil

Here you get a plot for your searched drug against 17 MM cell lines present in CRISPR dataset and GDSC dataset, with logIC50 on y-axis and respective multiple myeloma cell lines on x-axis. logIC50 is the concentration of drug required to inhibit 50% of cell lines. The lower the logIC50 value, the more potent the drug is in inhibiting the cell line. For detailed assistance visit Help section!

Plot for Drug 5-Fluorouracil



LogIC50 on y axis

Cell lines

Cell lines on x axis

Get In Touch

Mutational analysis

MyeloDB: Multiple Myeloma Database

[Home](#) [Datasets](#) [Analysis](#) [Biomarker](#) [Downloads](#) [Help](#) [Team](#)

Mutational analysis:

This page allows user to search and analyze one gene-drug combinations integrated from COSMIC and GDSC v2 which are stored in MyeloDB. There are a total of [17 MM cell lines](#) and [23 genes](#) data stored with significant drugs only. User will be able to get the mutated and wildtype cell lines for the gene searched. Further, [logIC50 value](#) is also provided to make data more informative. For detailed assistance visit [Help](#) section!

Select a Gene:

Select a Drug:



Select a gene and then respective drug from dropdown then search



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Mutational analysis

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Your search result:

This page shows Drug sensitivity and Mutation data of searched gene **CCDC80** and drug **Entinostat** against the MM cell lines. The table shows median logIC50 value of mutated and wildtype cell lines across cell mutated and wildtype cell lines. **p value ≤ 0.05** is considered statistically significant. For detailed assistance visit [Help](#) section!

To View Plot

[Click here](#)

To view plot of log IC50 vs cell line click here

Export Table to CSV



Click here to export table as a csv

Gene Name	Drug Name	Mutated Cell Lines	Wildtype Cell Lines	Median log IC50(MUT Cell Lines)	Median log IC50(WT Cell Lines)	p_value
CCDC80	Entinostat	KMS-11, KMS-12-BM, MM1S, MOLP-8, RPMI-8226	AMO-1, ARH-77, EJM, IM-9, JJN-3, KARPAS-620, L-363, LP-1, NCI-H929, OPM-2, SK-MM-2, U-266	-0.015905	0.632466	0.000018



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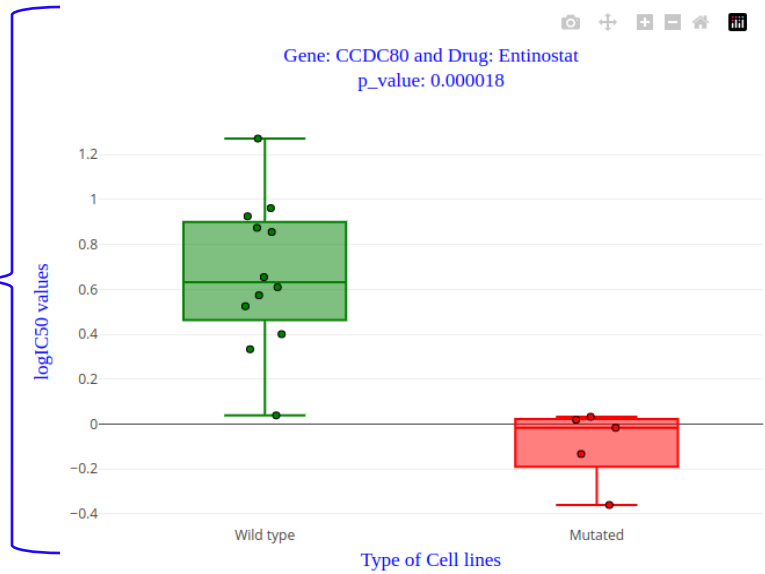
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Mutational analysis

Your search result:

This page shows the logIC50 values of drugs on mutated and wild type cell Lines for your searched gene and drug combination. Box-whisker plots are used as representation of logIC50 values of drugs on cell lines. In plot, Wt represents Wild Type cell lines and Mut represents Mutated cell lines. $p\text{ value} \leq 0.05$ is considered statistically significant. To download hover over the plot. For detailed assistance visit [Help](#) section!

Box plot result displayed with significant p value between wildtype and mutant cell lines



Expression and Methylation analysis have similar search user interface

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Gene search (Expression profiling)

Here user can search genes expression data stored in MyeloDB. A total of 10763 genes data can be found for different techniques. Gene data here is from Affymetrix, Agilent and Illumina. For detailed assistance visit Help section!

MyeloDB: Multiple Myeloma Database

Home Datasets Analysis Biomarker Downloads Help Team

Gene Search (Methylation profiling)

Here user can search genes methylation data (beta values) stored in MyeloDB. A total of 11627 genes data can be found for 3 different datasets. Gene data here was made available only when beta values were present in all 3 datasets. For detailed assistance visit Help section!

User can search for one gene here or try examples below

Example Search:

Genes: **A2M** **IDH1** **KITLG**

Example Search:
Genes: **A2M** **IDH1** **KITLG**



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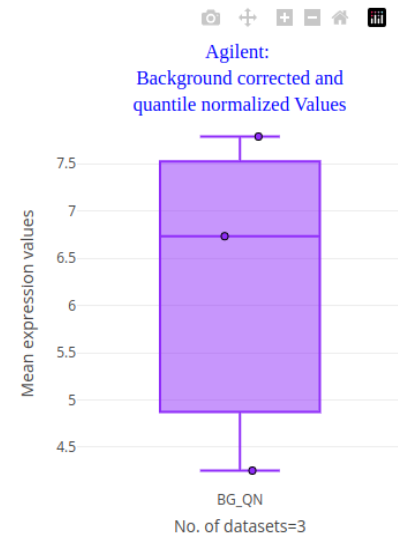
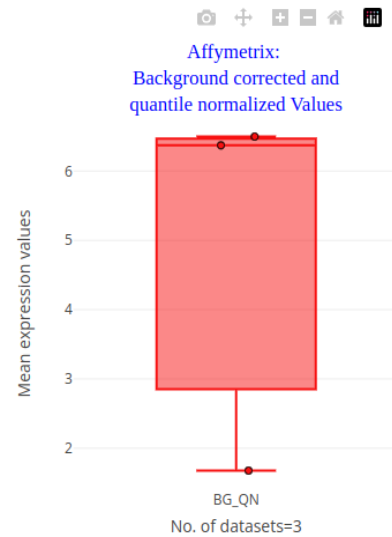
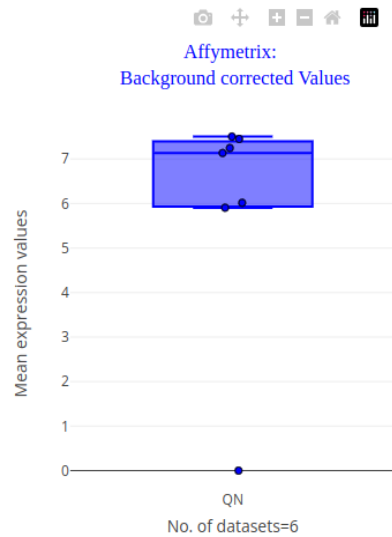
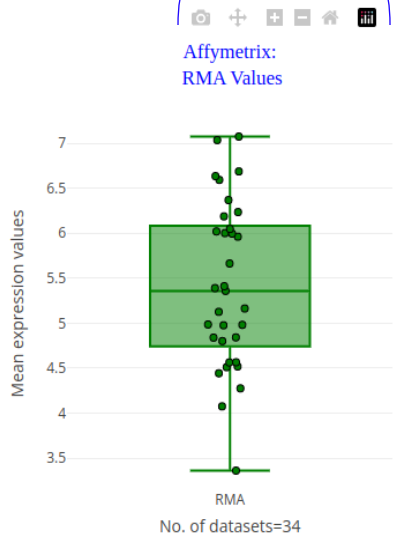
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Expression analysis result page

Your search result for A2M

This page shows the mean expression value across different technique for your searched gene. Box-whisker plots are used as representation of searched gene for mean values across all datasets stored in MyeloDB. For detailed assistance visit Help section!

Explore options to download/zoom in/out etc



RMA: Robust Multi Array normalized values
BG: Background corrected values
BG_QN: Background corrected and quantile normalized values

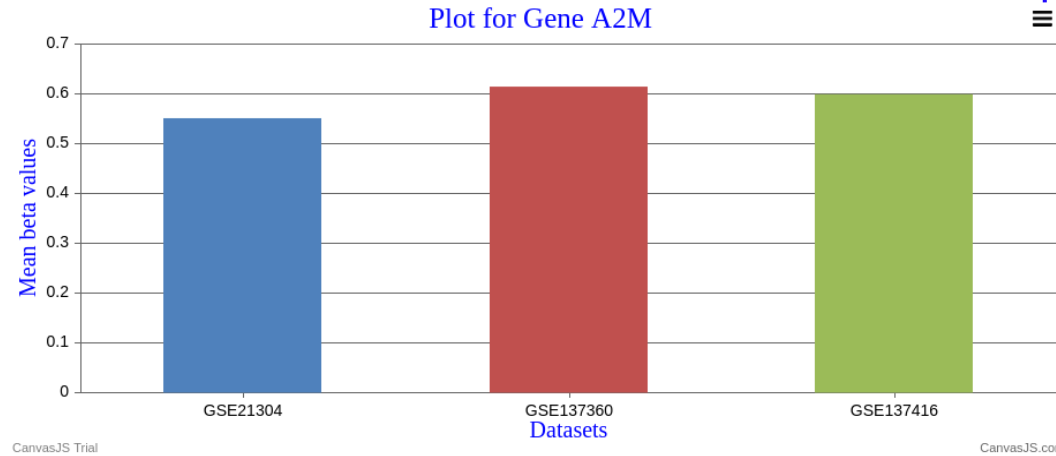
As a result, box plot will show mean expression values in different techniques

Methylation analysis result page

Click to print/download image as PNG/JPEG

Your search result for A2M

This page shows the mean beta values across different datasets for your searched gene. Column chart are used as representation of searched gene for mean values across all datasets stored in MyeloDB. For detailed assistance visit Help section!



As a result, bar plot will show mean methylation values of different GSE study

Biomarker section

MyeloDB: Multiple Myeloma Database

[Home](#) [Datasets](#) [Analysis](#) [Biomarker](#) [Downloads](#) [Help](#) [Team](#)

Your search result:

This page gives you biomarkers data for MM reported in different studies.
For detailed assistance visit [Help](#) section!

Export Table to CSV



[Click here to export table as a csv](#)

Biomarker	Biomolecule	Subject	Regulation	Type	Experiment	Significance	Source	Cohort	Pubmed ID	Methods used	Tools used
miR-134-5p	miRNA	human	downregulated	Diagnostic	MM patients vs healthy controls (HC)	P < 0.05	urine	For miRNAs microarray, 4 MM and 4 HC samples were used. In qRT-PCR validated, 27 MM and 12 HC samples were used.	33068078	microarray analysis, qRT-PCR, ROC curve analysis, Correlation analysis, Kaplan-Meier, Spearman bivariate t test	Agilent Human (Release 21), miRWalk 3.0 and miRDB 6.0 databases
miR-6500-5p	miRNA	human	downregulated	Diagnostic	MM patients vs healthy controls (HC)	P < 0.06	urine	For miRNAs microarray, 4 MM and 4 HC samples were used. In qRT-PCR validated, 27 MM and 12 HC samples were used.	33068078	microarray analysis, qRT-PCR, ROC curve analysis, Correlation analysis, Kaplan-Meier, Spearman bivariate t test	Agilent Human (Release 21), miRWalk 3.0 and miRDB 6.0 databases
								For miRNAs microarray, 4 MM		microarray analysis.	

[Click here to explore each biomarker](#)

Download section

MyeloDB:Multiple Myeloma Database

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List of Expression, Methylation, CRISPR and Achilles data maintained in MyeloDB

Profiling Data:



Click here to explore profiling data study and to download them

CRISPR-cas9 Data:



Click here to explore CRISPR-cas9 study and to download them



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Download section for profiling data

MyeloDB:Multiple Myeloma Database

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Total profiling data maintained in MyeloDB

In this page user can download profiling data including both expression profiles and methylation profiles maintained on MyeloDB individually in form of matrix file. The data available here has already been normalized. The downloaded file contains expression/methylation values along with gene symbol, entrez gene ID, patient: sex/age, source of sample and other characteristics.

GSE ID	No of Samples	Type of Data	Value of Data	Download
GSE164706	240	Expression profile	RMA (Robust Multi Array)	
GSE164701	109	Expression profile	RMA (Robust Multi Array)	
GSE201846	12	Expression profile	RMA (Robust Multi Array)	
GSE146649	41	Expression profile	RMA (Robust Multi Array)	
GSE87900	180	Expression profile	RMA (Robust Multi Array)	
GSE70515	7	Expression profile	RMA (Robust Multi Array)	
GSE109651	14	Expression profile	RMA (Robust Multi Array)	
GSE133346	24	Expression profile	RMA (Robust Multi Array)	
GSE13591	158	Expression profile	RMA (Robust Multi Array)	
GSE7116	26	Expression profile	RMA (Robust Multi Array)	
GSE6401	102	Expression profile	RMA (Robust Multi Array)	

This link will take you to GEO website to the respective GSE study

Click to download each GSE study





Download section for CRISPR-cas9 data

MyeloDB: Multiple Myeloma Database

Home Datasets ▾ Analysis ▾ Biomarker Downloads Help Team

DepMap and Achilles project data maintained in MyeloDB

In this page user can download CRISPR-cas9 screens from DepMap and Achilles project maintained on MyeloDB individually in form of csv file. This data was downloaded from DepMap portal and further filtered only for the disease subtype multiple myeloma. The downloaded file contains dependency scores along with cell lines, Patient sample collection site, sex and age.

Data type	No of Cell lines	No of genes	Gene effect	Gene dependency
DepMap	20	17387		
Achilles project	20	18017		

Click to download file according to your need



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