dbDEMC 3.0: Functional Exploration of Differentially Expressed miRNAs in Cancers of Human and Model Organisms

Feng Xu[1#], Yifan Wang[2#], Yunchao Ling[2], Chenfen Zhou[2], Haizhou Wang[1], Andrew E. Teschendorff[3], Yi Zhao[4], Haitao Zhao[5], Yungang He[6*], Guoqing Zhang[2*], Zhen Yang[1*]

[1] *Center for Medical Research and Innovation of Pudong Hospital, Fudan University, and the Shanghai Key Laboratory of Medical Epigenetics, the International Co-laboratory of Medical Epigenetics and Metabolism, Ministry of Science and Technology, Institutes of Biomedical Sciences, Fudan University, Shanghai 200032, China*

[2] *Bio-Med Big Data Center, CAS Key Laboratory of Computational Biology, Shanghai Institute of Nutrition and Health, University of Chinese Academy of Sciences, Chinese Academy of Sciences, Shanghai 200031, China*

[3] *CAS Key Lab of Computational Biology, Shanghai Institute for Nutrition and Health, University of Chinese Academy of Sciences, Chinese Academy of Sciences, Shanghai 200031, China*

[4] *Key Laboratory of Intelligent Information Processing, Advanced Computer Research Center, Institute of Computing Technology, Chinese Academy of Sciences, Beijing 100190, China*

[5] *Department of Liver Surgery, Peking Union Medical College Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, 100730, China*

[6] *Shanghai Fifth People's Hospital, and the Shanghai Key Laboratory of Medical Epigenetics, International Co-laboratory of Medical Epigenetics and Metabolism, Ministry of Science and Technology, Institutes of Biomedical Sciences, Fudan University, Shanghai 200032, China*

[#] Equal contribution.

[*] Corresponding authors.

E-mail: zhenyang@fudan.edu.cn (Yang Z), gqzhang@picb.ac.cn (Zhang GQ), heyungang@fudan.edu.cn (He YG)

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Abstract

microRNAs (miRNAs) are important regulators in gene expression. The deregulation of miRNA expression is widely reported in the transformation from physiological to pathological state of cells. A large amount of differentially expressed miRNAs (DEMs) have been identified in various human cancers by using high-throughput technologies, such as microarray and miRNA-seq. Through mining of published researches with high-throughput experiment information, the database of differentially expressed miRNAs in human cancers (dbDEMC) was constructed with the aim of providing a systematic resource for the storage and query of the DEMs. Here we report an update of the dbDEMC to version 3.0, containing two-fold more data entries than the previous version, now including also data from mouse and rat. The dbDEMC 3.0 contains 3,268 unique DEMs in 40 different cancer types. The current datasets for differential expression analysis have expanded to 9 generalized categories. Moreover, the current release integrates functional annotations of DEMs obtained from experimentally validated targets. The annotations can greatly benefit integrative analysis of DEMs. In summary, dbDEMC 3.0 provides a valuable resource for characterizing molecular functions and regulatory mechanisms of DEMs in human cancers. The dbDEMC 3.0 is freely accessible at https://www.biosino.org/dbDEMC.

KEYWORDS: miRNA; Cancer; Differential expression; Model Organisms; Database

Introduction

Since the first discovery of microRNAs (miRNAs) at the beginning of this century, this class of small non-coding RNA has received extensive attention [1]. As an important gene expression regulator acting at the post-transcriptional level, studies have disclosed the critical role of miRNAs in targeting mRNAs for the degradation or translational repression [2]. Till now, a total of 2,654 miRNAs have been identified in the human genome according to the latest version of miRBase database [3]. Significant researches on miRNAs have dramatically expanded our understanding about gene regulatory network and its roles in physiological and pathological conditions, such as in broad spectrums of biological processes including cell cycle, cell proliferation, differentiation, apoptosis and cellular signaling [4, 5]. Owing to the biological significance of miRNAs, alterations of the miRNAs are linked to the development of many diseases including the cancer [6]. Differentially expressed miRNAs (DEMs) are widely reported to hold great value in the diagnosis or prognosis as well as treatment targeting for cancer research [7]. The potential use of circulating miRNAs in serum, plasma and other body fluids as non-invasive cancer biomarkers have also been thoroughly investigated [8].

Given the important functions of miRNA in cancer development, several on-line resources have been built for warehousing information of cancer-related miRNAs, such as the HMDD [9], miRCancer [10], and OncomiRDB [11]. With the development of high-throughput techniques such as microarray and miRNA-seq, large amount of cancer DEMs were identified from miRNA profiling data each year. However, these valuable data were scattered in the vast literatures and it is of great necessity to catalogue them in a favorable way, thus to provide integrative tools for the effective utilization and systematic investigation. With this aim, we developed the initial database of differentially expressed miRNAs in human cancers (dbDEMC) in 2010 [12] and further updated in 2017 [13]. To our knowledge, dbDEMC is the only working repository currently available for storing DEMs from de-novo analysis of high-throughput profiling data in human cancers, characteristic with miRNANome

data in various types of cancer. It greatly facilitates the efforts to excavate cancer associated miRNAs and investigate their roles in pathological processes of cancer. While the database could have been much more useful had there been more high-quality data included.

In recent years, cancer quantitative miRNA profiling data has been increasing at an unprecedented rate, and given the success of dbDEMC 2.0, this motivates an update of this database. Here we introduce dbDEMC 3.0, a significantly expanded version of this database. This update incorporates a substantial amount of new data. Besides the human data, we have also incorporated the miRNA expression profiling data of mouse and rat. A total of 403 datasets of high-throughput miRNA expression encompassing 40 cancer-types, with the results of 807 differential expression analyses, have been included. The present update is nearly doubling the data amount over the previous version. In addition to the expanded data volume, the content of the database has also been enriched. The new database firstly recorded the experimentally validated DEMs targets and also their enrichment analysis on Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. In this way, we provided the functional annotation of DEMs for various cancers. Also, the web interface of the database was refined for a better visualization of the aforementioned data. Taken together, the dbDEMC 3.0 is a comprehensive resource to systematically characterize the function of DEMs in human cancers as well as other model organisms.

Data collection and processing

Data collection

To compile the datasets, we used the keywords ‘cancer’, ‘tumor’, ‘carcinoma’ and ‘neoplasm’, in combination with ‘microRNA’ or ‘miRNA’ to conduct an exhaustive search for the microarray based miRNA expression profiles in Gene Expression Omnibus (GEO) [14] and ArrayExpress [15], and further for miRNA-seq based miRNA expression profiles in Sequence Read Archive (SRA) [16]. While the miRNA

profiles of mouse and rat were rapidly accumulating, we also incorporated the miRNA data of the two model organisms in the current update. In addition, we also appended the new miRNA profiling data from TCGA that was released since the last update of dbDEMC 2.0. All the involved data were published as of June 2021. The data records were manually reviewed and evaluated rigorously to guarantee that only high-quality data sets were included. To ensure analysis reliability, we required at least three biological replicates of samples each condition (for both case and control) as usual.

Data processing

For miRNA profiling data sets based on microarray, we used the same protocol as that of dbDEMC 2.0 to identify the DEMs [13]. Briefly, the expression values were logarithmically transformed (base 2) and quantile normalized. Then the limma (Linear Models for Microarray Data) package was applied to select miRNAs whose mean expression level is significantly different between case and control samples with FDR value < 0.05.

For miRNA-seq based profiling data obtained from SRA database, we downloaded the SRA files of raw sequence reads and converted them into FASTQ format using the fastq-dump of SRA Toolkit. Here we included only the data produced on Illumina systems (Genome Analyzer I, II, IIx, HiSeq 1000, HiSeq 2000, HiSeq 2500, HiSeq 4000, NextSeq, MiSeq). The involving miRNA-seq data was analyzed by using QuickMIRSeq toolkit [17]. This toolkit utilizes the Cutadapt to remove sequence adapters and performs quality control [18]. We collected detailed information of DNA adapters of different miRNA-seq libraries from public resources to guarantee that the adapters can be properly trimmed from the raw reads (Table S1) [19]. The clean reads were then aligned to the reference genome by using Bowtie [20], and miRDeep2 was used to obtain count tables of aligned reads for miRNA quantification [21]. The reads count table was further normalized by using limma-voom [22], and DEMs were then identified. For the datasets obtained from TCGA, we directly used the prepared reads count data for further analysis [23].

Experimental validation of DEMs in low-throughput methods (such as real-time PCR and northern blot, etc.) were manually collected from the original papers. These types of information were carefully formatted and integrated into our update.

Functional annotation

For each obtained DEMs set, we collected the experimentally validated targets by using multiMiR [24], which integrate miRNA target data from TarBase [25] and miRTarBase [26]. Then we performed the enrichment analysis of the DEMs targets on GO terms and KEGG pathways by using clusterProfiler package to facilitate the study of context-dependent miRNA functional mechanisms [27]. Enriched GO terms and KEGG pathways were selected where adjusted P value < 0.05. The data collection and curation procedure for dbDEMC 3.0 is shown in **Figure 1**.

Database construction

All the data in dbDEMC 3.0 was managed by using MongoDB. The dynamic web interface was developed using JSP and JavaScript. Data visualization was achieved through the tools of vue, jquery, and Echarts, Elasticsearch was used for search engine. The database was developed by Spring Boot framework. Apache Tomcat web server was used for the http server. All the information in dbDEMC 3.0 is freely available to the public domain through https://www.biosino.org./dbDEMC.

miRNA cluster annotation

A miRNA cluster is defined as set of miRNAs which located adjacent genomic regions in the same or opposite orientation and not separated by other transcriptional units. miRNAs within a cluster are thought to be regulated by common factors and involved in same signaling pathways. According to Kabekkodu SP et al., among 1881 precursor miRNAs of human origin annotated in miRBase, 468 of which can be attributed to 153 clusters [28]. Here we obtained these data about miRNA clusters and annotated mature miRNAs by using annotation file from miRBase. Finally, a total of 688 (22.8%) mature miRNAs from 143 clusters were annotated in the human genome.

Analysis of homogeneous dysregulation pattern of miRNA clusters in cancer

For systematic study of co-dysregulation pattern of miRNA clusters in human cancers, we considered all miRNAs associated with specific cancer. miRNAs not

187 belonging to any cluster and clusters of which at least half the members are not
188 associated with any cancer were discarded. To avoid potential bias introduced by
189 different expression platforms, here we only use the results obtained from TCGA and
190 checked for experimental design of Cancer vs. Normal for 19 kinds of epithelial
191 cancers. We finally obtained 106 unique clusters for these cancer types. A cluster was
192 designated to be homogeneous if at least half of its members show the same direction
193 of expression pattern (either up- or down-regulated). For each cluster, we computed
194 the homogeneous fraction as that of co-dysregulation throughout all cancer types
195 analyzed. A significant P-value for this fraction was calculated as follow: for each
196 cancer type, the expression of all its associated miRNAs was distributed randomly
197 within these miRNAs for 10,000 times, keeping the distribution of up- and
198 down-regulated miRNAs constant for each step. The homogeneous fraction over all
199 cancers was computed, which yields the P-value as the number of sampled
200 homogeneous fractions exceeding the original homogeneous fractions divided by
201 10,000.
202 In order to check whether clustered miRNAs are more enriched in cancer
203 development compared to single miRNA, we calculated an enrichment score of
204 log-odds (LOD) score for each cancer type:

205 $$\mathrm{LOD} = log2\left(\left(\frac{X_c}{X_c+Y_c}\right)/\left(\frac{X_{all}}{X_{all}+Y_{all}}\right)\right)$$

206 Where X_c and Y_c denote the number of cluster miRNAs and non-cluster
207 miRNAs for each cancer type, and X_{all} denotes the number of the cluster miRNAs
208 and denotes the number of the miRNAs not contained in any cluster. Here we take
209 into account all known human miRNAs annotated in the human genome, thus
210 designate as the 688 clustered miRNAs and 900 non-clustered miRNAs. In this case, a
211 positive LOD score indicates enrichment for cluster miRNAs compared to non-cluster
212 miRNAs in a specific cancer.
213

214 ## Implementation and results

Database content

In the current release of dbDEMC, the data of miRNA transcriptome of total 46,388 samples from 403 studies of human, mouse or rat were collected from public resources (Table S2). These profiles are derived from 149 subtypes of 40 different cancers and many different cell lines (Table S3). We then performed a systematic analysis on each dataset, and yielded a total of 807 experiments for differential expression analysis. dbDEMC 3.0 now hosts a total of 3,268 differentially expressed miRNAs, among them, 2,584 are specific to human. A total of 160,799 miRNA variations related to cancers were deposited in our database. The detailed information about number of miRNAs, cancer types, datasets, and experiments for different species was presented in **Table 1**.

Figure 2A depicts the number of DEMs for each type of human cancer. The breast cancer presents a large number of DEMs that 1,833 up-regulated and 1,988 down-regulated DEMs had been identified. The number of DEMs from mouse and rat can be found in Figure S1. Whereas Figure 2B demonstrates the number of DEMs validated by low-throughput methods across major cancers, the brain cancer, colorectal cancer and breast cancer are top ranked cancer types. Figure 2C shows the percentages of experiments for top ranked cancers. The breast cancer accounted 15% of the total experiments and ranked the first of the list. It was followed by colorectal cancer and lung cancer. Whereas the 9 different comparisons, cancer samples vs. normal controls constitutes about half of the total experiments, and followed by comparisons of high-grade versus low-grade cancer samples (Figure 2D). Overall, the sizes of analysis experiments and related literatures in dbDEMC 3.0 have a two-fold increment by comparing with the previous version (Figure S2).

New features

In the dbDEMC 2.0, we assigned the different experimental designs to 7 different classes: Cancer vs. Normal; High grade vs. Low grade; Metastasis vs. Primary cancer; Subtype1 vs. Subtype2; Poor outcome vs. Good outcome; Blood sample of patients vs. Blood sample of normal controls, and also Treatment vs. Non-treatment. In recent years, many studies disclosed exosomes and microvesicles act as cell communication

agents, where miRNA is the most important molecular in exosomes and microvesicles for regulating cancer progression [29]. In addition, circulating miRNAs were also widely found in body fluids and represent a gold mine of noninvasive biomarkers in cancer [30]. In this update version, we thus added these two classes of experimental design: Exosome sample from patients vs. Exosome sample from control, and Body fluid from patients vs. Body fluid from control. Moreover, for each DEMs set, targets of miRNAs and enrichment information of the target genes in the KEGG pathways and GO terms were deposited in the dbDEMC 3.0, which makes it possible for inspecting functional mechanisms behind a set of miRNAs.

Newly designed web interface

The web interface of dbDEMC 3.0 has been significantly refined and improved, allowing better use of the data. The Search page permits users to perform a quick search and extract summarized information of a DEM list across cancer types. Users can also specify the cancer type, experimental design or platform to select the interested experiments (**Figure 3**A–C). After filtering the experimental results, users can select interested experiments. Detailed information of DEM related experiment, which includes description with the up-regulated and down-regulated miRNAs, can be accessed. In the functional chart section, heatmap of the DMEs expression, miRNA-target regulatory network for top ranked DEMs, as well as the bubble chart for miRNA targets enriched KEGG and GO terms were presented (Figure 3D). Using a single miRNA query, summary information of the interested miRNA can be retrieved, including the general description of the interested miRNA and differential expression summary heatmap which decided by number of experiments shows up expression or down expression. In addition, summary statistics tables for both high-throughput data analysis and low-throughput validation data were also displayed (Figure 3E).

Analysis tools

miRBase is the central reference database for miRNA annotation by assigning names and unique gene IDs for novel miRNAs. During its development, some miRNA definition and annotation may have been changed. This leads to the inconsistence of

the miRNA IDs from different data sets, which derived from different miRBase versions and making it difficult for comparing research results for integrative analysis. To solve this problem, we provide a "ID convertor" in our database, by which users could convert miRBase old version IDs to the latest version (v22.0) for the three species of human, mouse, and rat. In addition, other analyzing tools including BLAST and meta-profiling, which are used for sequence similarity search of unknown miRNAs and identify the confident cancer related miRNAs in pan-cancer wide, are also available in dbDEMC v3.0. For the meta-profiling study, the vote-counting approach was used to calculate the consistent score of differential expression for meta-analysis [31]. Common miRNAs identified in multiple cancer types with similar differential expression pattern may suggest they could have similar regulatory mechanisms and play important roles in cancer development.

miRNA clusters are significantly overrepresented in cancers

A large proportion of miRNAs localized as conserved clusters in the genome and present similar expression pattern across tissues. It is critical to understand whether miRNA clusters present similar differential expression across cancers and correlate with the similar pathobiology. Here we obtained human miRNA cluster annotation from public resources, which includes 22.8% (688/2588) of mature miRNAs appear as 143 clusters of at least two members within (Table S4). We systematically analyzed the homogeneity of expression patterns within miRNA clusters. We excluded those clusters having less than half of all miRNAs annotated from the results of TCGA, which leads to 106 remaining clusters. The clusters are denoted as exhibiting a homogeneous expression pattern if annotated miRNA members are either up- or down-regulated (see Data processing). In total, cancer-associated clusters revealed homogeneous expression patterns for 74% of all annotated cancer, which confirms the hypothesis of co-regulation pattern of miRNA clusters in cancer. For example, the cluster of miR-142-5p, miR-142-3p, miR-4736 presents a consistent differential expression pattern in 91% (11/12) of the cancers analyzed (Table S5). A null model by randomly linking miRNA expression patterns (permutation 10,000 times within each cancer) indicated 52 clusters (49%, P-value < 0.05) showed a

significantly higher homogeneity pattern in all 19 kinds of cancer compared to that expected by chance (Table S5). These clusters exhibit a homogeneous expression pattern in at least 78.5% of all these types of cancer.

To further investigate the association of miRNA clusters with different kinds of cancer, we estimated the enrichment of miRNA clusters in cancer-associated miRNAs by using a LOD score. We found enrichment for all 19 kinds of cancer (**Figure 4**). Within these 19 kinds of cancer, miRNAs located in clusters are, on average, 1.56 times (LOD = 0.65) enriched compared to random. In summary, our analyses show a significant enrichment of clustered miRNAs in cancers compare to the single miRNA members, which demonstrated that the different miRNAs within cluster act synergistically in cancer development.

Discussion

Over the last decade, a large amount of miRNA transcriptome profiles of various cancers have been generated. Many studies have performed miRNA transcriptome analysis to explore the underlying molecular mechanisms of miRNA genes in cancer development [32, 33]. This progress motivated a novel release of dbDEMC to keep track of the latest published data. Along with this, we curate these data and provide a platform to facilitate the study of miRNA-cancer associations. For dbDEMC 3.0, it not only contains more miRNA-cancer associations, we also extended our database to the species of mouse and rat, which benefits those studies characterizing the miRNA functional machinery in cancer using the model organisms. Beyond the rapid increase of data amount, our database now offers many new features and powerful tools for the downstream analysis of DEMs, such as the integrated target identification and functional enrichment analysis for miRNA-regulated biological processes.

One of the key questions of differential expression analysis of miRNAs is which cancer types are regulated by a particular miRNA (miRNA-centric view), or conversely, which miRNAs may involve in a given type of cancer (cancer-centric view). Our databases support both miRNA- and cancer-centric investigations, users

334 are able to search miRNAs to determine the spectrum of cancer types that it involved,
335 or to find candidate miRNA list based on reference of the miRBase which link to
336 individual type of cancer. Although studies have indicated false positive and negative
337 records may exist in miRBase, researchers need to be cautious about resources based
338 on references from miRBase [34, 35]. Overall, we expect that dbDEMC 3.0 could
339 serve as a valuable resource with comprehensive data amount and data analysis tools
340 to facilitate the study of DEMs in cancers. In the future, we will continue to make
341 improvements to the functional characterizations as well as integrate more
342 heterogeneous data for the flexible analysis of miRNA functions in various cancers.
343 We believe that the development of dbDEMC database can help accelerate the
344 integration between miRNANome and cancer studies.
345
346

Data availability

dbDEMC v3.0 is freely accessible at https://www.biosino.org/dbDEMC/.

CRediT author statement

Feng Xu: Data curation, Formal analysis. **Yifan Wang:** Methodology, Validation. **Yunchao Ling:** Visualization. **Chenfen Zhou:** Data curation. **Haizhou Wang:** Data curation. **Andrew E. Teschendorff:** Methodology, Software. **Yi Zhao:** Investigation, Software. **Haitao Zhao:** Validation. **Yungang He:** Supervision, Investigation. **Guoqing Zhang:** Methodology, Supervision. **Zhen Yang:** Conceptualization, Supervision, Writing- Original draft. All authors read and approved the final manuscript.

Competing interest

The authors declare that they have no competing interests.

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ORCID

0000-0001-5185-2164 (Feng Xu)

0000-0003-4256-2696 (Yifan Wang)

0000-0002-5438-0753 (Yunchao Ling)

0000-0002-0294-7308 (Chenfen Zhou)

0000-0002-3376-386X (Haizhou Wang)

0000-0001-7410-6527 (Andrew E. Teschendorff)

375 0000-0001-6046-8420 (Yi Zhao)

376 0000-0002-3444-8044 (Haitao Zhao)

377 0000-0002-2931-2871 (Yungang He)

378 0000-0001-8827-7546 (Guoqing Zhang)

379 0000-0002-5647-9976 (Zhen Yang)

380

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Figure legends

Figure 1 Schematic illustration of the data collection and architecture of the dbDEMC 3.0

Figure 2 Statistics of data content in dbDEMC 3.0 for humans

A. Number of DEMs from each cancer types identified by high-throughput methods. **B.** Number of DEMs from major cancer types identified by low-throughput methods. **C.** The percentage of experiments for major cancer types. **D.** The percentage of experiments in seven types of experimental design.

Figure 3 Web interface of dbDEMC 3.0

A. Search page. miRNAs can be searched via miRBase IDs, or filter experiments with interested conditions. **B.** Filtering result page of experiments. **C.** Search result page with example miRNAs. **D.** Experiment page. The page summarizes the description of the experiments and associated differentially expressed miRNA list, functional chart for expression heatmap, regularly network and miRNA targets enriched KEGG pathways and GO terms are also depicted. **E.** miRNA page. This page mainly consists of four sections: miRNA Summary, Expression Profile and Expression Detail and Validation.

Figure 4 miRNA cluster enrichment for 19 kinds of cancer

For each cancer type, the log-odds (LOD) score is plotted. There is an enrichment of miRNA cluster members for all 19 kinds of cancer (100%, P-value < 1e-4). Within these 19 types of cancer, miRNAs located in clusters are, on average, 1.56 times (LOD = 0.65) enriched compared to random.

Tables

Table 1 Summary of the data content of the current release of dbDEMC

Supplementary material

Figure S1 Number of differentially expressed miRNAs identified by high-throughput methods for each cancer type. A. Number of DEMs for mouse; **B.** Number of DEMs for rat.

Figure S2 Increasing number of experiments for each cancer type. The number of experiments for each cancer type in dbDEMC v3.0 and v2.0 are depicted.

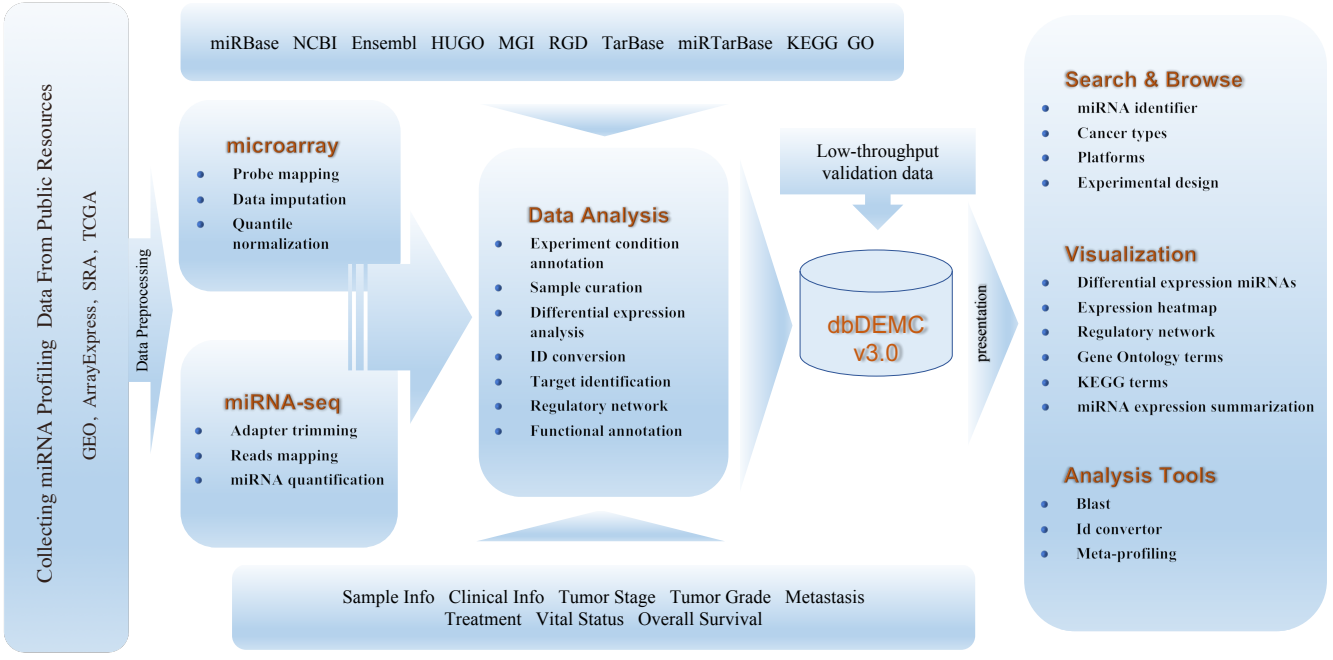
Table S1 Adapters for miRNA-seq kits for the Illumina platform.

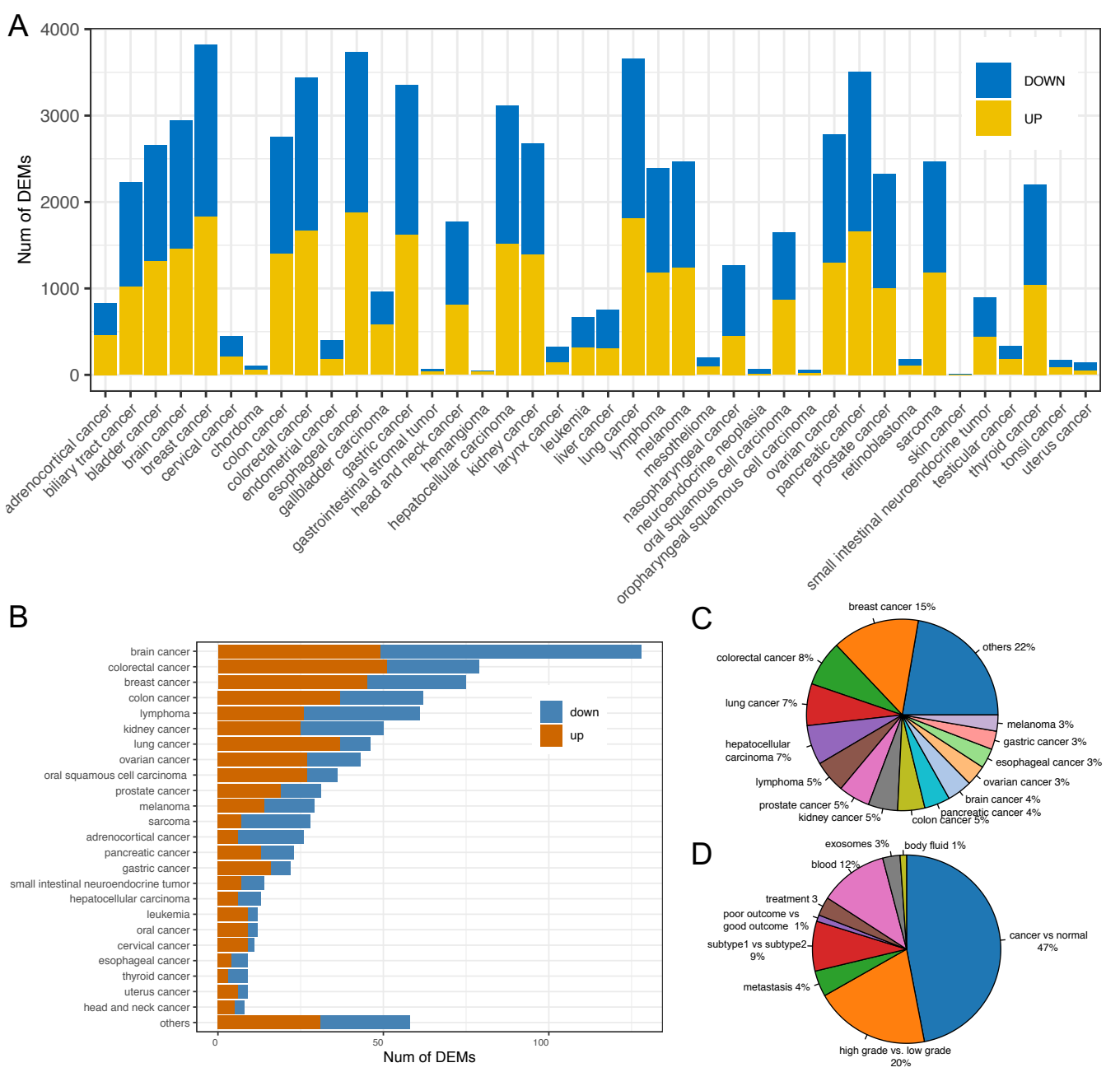
Table S2 The table below lists datasets collected from public resources, including the GEO, ArrayExpress, SRA and TCGA. The Source Data ID, PubMed ID, Species, Cancer Type, platform ID and the total number of samples for each dataset were listed.

Table S3 Cancer types and associated subtypes and cell line names covered in dbDEMC 3.0.

Table S4 All miRNA clusters and associated miRNA IDs identified. A total of 143 miRNA clusters and associated 688 human mature miRNAs were obtained in the human genome.

Table S5 miRNA clusters showing a homogenous expression pattern in all 19 kinds of cancer. T: number of cancers for which each cluster showing a homogeneous expression pattern; **F:** number of diseases for which each cluster shows no homogeneous expression pattern; **Homogeneous-fraction:** number of diseases for which each cluster shows a homogeneous expression pattern for each miRNA cluster as defined; **P-value:** estimate by randomly linking miRNA-expression patterns 10,000 times within each cancer.


Collecting miRNA Profiling Data From Public Resources
GEO, ArrayExpress, SRA, TCGA
Data Preprocessing
miRBase NCBI Ensembl HUGO MGI RGD TarBase miRTarBase KEGG GO
microarray
Probe mapping
Data imputation
Quantile normalization
miRNA-seq
Adapter trimming
Reads mapping
miRNA quantification
Data Analysis
Experiment condition annotation
Sample curation
Differential expression analysis
ID conversion
Target identification
Regulatory network
Functional annotation
Low-throughput validation data
dbDEMC v3.0
presentation
Search & Browse
miRNA identifier
Cancer types
Platforms
Experimental design
Visualization
Differential expression miRNAs
Expression heatmap
Regulatory network
Gene Ontology terms
KEGG terms
miRNA expression summarization
Analysis Tools
Blast
Id convertor
Meta-profiling
Sample Info Clinical Info Tumor Stage Tumor Grade Metastasis
Treatment Vital Status Overall Survival


A
Num of DEMs
4000
3000
2000
1000
0
DOWN
UP
adrenocortical cancer
biliary tract cancer
bladder cancer
brain cancer
breast cancer
cervical cancer
chordoma
colon cancer
colorectal cancer
endometrial cancer
esophageal cancer
gallbladder carcinoma
gastric cancer
gastrointestinal stromal tumor
head and neck cancer
hemangioma
hepatocellular carcinoma
kidney cancer
larynx cancer
leukemia
liver cancer
lung cancer
lymphoma
melanoma
mesothelioma
nasopharyngeal cancer
neuroendocrine neoplasia
oral squamous cell carcinoma
oropharyngeal squamous cell carcinoma
ovarian cancer
pancreatic cancer
prostate cancer
retinoblastoma
sarcoma
skin cancer
small intestinal neuroendocrine tumor
testicular cancer
thyroid cancer
tonsil cancer
uterus cancer
B
brain cancer
colorectal cancer
breast cancer
colon cancer
lymphoma
kidney cancer
lung cancer
ovarian cancer
oral squamous cell carcinoma
prostate cancer
melanoma
sarcoma
adrenocortical cancer
pancreatic cancer
gastric cancer
small intestinal neuroendocrine tumor
hepatocellular carcinoma
leukemia
oral cancer
cervical cancer
esophageal cancer
thyroid cancer
uterus cancer
head and neck cancer
others
down
up
0
50
100
Num of DEMs
C
breast cancer 15%
others 22%
colorectal cancer 8%
lung cancer 7%
hepatocellular carcinoma 7%
lymphoma 5%
prostate cancer 5%
kidney cancer 5%
colon cancer 5%
pancreatic cancer 4%
brain cancer 4%
ovarian cancer 3%
esophageal cancer 3%
gastric cancer 3%
melanoma 3%
D
exosomes 3%
body fluid 1%
blood 12%
treatment 3
poor outcome vs good outcome 1%
subtype1 vs subtype2 9%
metastasis 4%
high grade vs. low grade 20%
cancer vs normal 47%

User Interface

dbDEMC 3.0 | Home | Search | Browse | Blast | ID Convertor | Meta-profiling | Statistics | Download | Help

A

Search miRNA ID

hsa-miR-122a
hsa-miR-133a

(please type in one miRNA ID per line.)

Submit Reset

Search experiment

Cancer Type: all | Platform: all
Experimental Design: all | Sample Size: all

Submit Reset

B

Experiment List

Please select conditions to filter the experiment results.

Cancer Type: all | Platform: all | Experimental Design: all | Submit

Experiment ID	Cancer Type	Cancer Subtype	Design	Sample Case	Sample Control	Up	Down	Download
EXP00001	lymphoma	B cell lymphoma	cancer vs normal	OCI-Ly4	Normal B cell	55	41	
EXP00002	lymphoma	B cell lymphoma	cancer vs normal	OCI-Ly7	Normal B cell	46	41	
EXP00003	lymphoma	B cell lymphoma	cancer vs normal	OCI-Ly8	Normal B cell	38	36	
EXP00004	lymphoma	Burkitt's lymphoma	cancer vs normal	Namalwa	Normal B cell	55	47	
EXP00005	lymphoma	Burkitt's lymphoma	cancer vs normal	Raji	Normal B cell	46	45	
EXP00006	lymphoma	Splenic lymphoma	cancer vs normal	Karpas-1718	Normal B cell	51	45	
EXP00007	lymphoma	Gastric lymphoma	cancer vs normal	Manca	Normal B cell	54	47	
EXP00008	lymphoma	Lymphoblastoid	cancer vs normal	HG-1125	Normal B cell	47	42	
EXP00009	leukemia	T cell leukemia	cancer vs normal	Jurkat	Normal B cell	42	35	
EXP00010	lymphoma	B cell lymphoma	subtype1 vs subtype2	OCI-Ly4	OCI-Ly7	20	14	
EXP00011	lymphoma	B cell lymphoma	subtype1 vs subtype2	OCI-Ly4	OCI-Ly8	18	20	
EXP00012	lymphoma	B cell lymphoma	subtype1 vs subtype2	OCI-Ly7	OCI-Ly8	6	16	
EXP00013	lymphoma	Splenic lymphoma	subtype1 vs subtype2	Karpas-1718	OCI-Ly4	12	15	
EXP00014	lymphoma	Splenic lymphoma	subtype1 vs subtype2	Karpas-1718	Manca	14	16	
EXP00015	lymphoma	Gastric lymphoma	subtype1 vs subtype2	Manca	OCI-Ly4	7	13	

total num: 807, page size: 15, skip to page: Skip — Prev 1 2 3 4 5 ... 54 Next

C

miRNA List

Differentially Expressed miRNAs List

miRNA ID	Source ID	Cancer Type	Cancer Subtype	Cell Line	Design	logFC	Expression Status	Experiment ID
hsa-miR-133a	GSE6188	esophageal cancer	esophageal cancer	N/A	cancer vs normal	-2.16	DOWN	EXP00031
hsa-miR-133a	GSE6636	prostate cancer	prostate cancer	N/A	cancer vs normal	-4.09	DOWN	EXP00032
hsa-miR-133a	GSE10259	colorectal cancer	colorectal cancer	N/A	cancer vs normal	-2.41	DOWN	EXP00047
hsa-miR-133a	GSE10259	colorectal cancer	colorectal cancer	N/A	cancer vs normal	-2.18	DOWN	EXP00049
hsa-miR-133a	GSE10259	colorectal cancer	colorectal cancer	N/A	cancer vs normal	-3.12	DOWN	EXP00050
hsa-miR-133a	GSE18392	colon cancer	colon cancer	N/A	cancer vs normal	-1.32	DOWN	EXP00096
hsa-miR-133a	GSE22058	hepatocellular carcinoma	hepatocellular carcinoma	N/A	cancer vs normal	-0.22	DOWN	EXP00100
hsa-miR-133a	GSE21036	prostate cancer	prostate cancer	N/A	cancer vs normal	-1.15	DOWN	EXP00101
hsa-miR-133a	GSE21036	prostate cancer	prostate cancer	N/A	metastasis	-3.12	DOWN	EXP00102
hsa-miR-133a	GSE16456	esophageal cancer	esophageal cancer	N/A	cancer vs normal	1.15	UP	EXP00075
hsa-miR-133a	GSE2564	leukemia	leukemia	N/A	subtype1 vs subtype2	0.37	UP	EXP00026
hsa-miR-133a	GSE4989	breast cancer	breast cancer	N/A	cancer vs normal	-1.27	DOWN	EXP00029
hsa-miR-133a	GSE16025	lung cancer	lung cancer	N/A	cancer vs normal	-0.54	DOWN	EXP00071
hsa-miR-133a	GSE16025	lung cancer	lung cancer	N/A	cancer vs normal	-0.50	DOWN	EXP00072
hsa-miR-133a	GSE16025	lung cancer	lung cancer	N/A	cancer vs normal	-0.62	DOWN	EXP00073

total num: 254, page size: 15, skip to page: Skip — Prev 1 2 3 4 5 ... 17 Next

D

Experiment Description

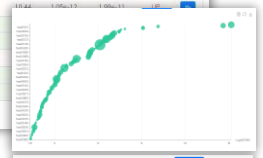
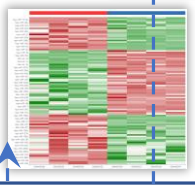
Reference: Title: ... Author: ... Journal: ... Abstract: ... PMID: ...
Expression Profile: Description: ... Organism: ... Source: ... Source ID: ... Platform: ... Number of samples: ... Overall design: ... Instrument: ...
Design and Sample: Cancer Type: ... Cancer SubType: ... Cell Line: ... Experimental Design: ... Case Sample: ... Control Sample: ... Num of Case: ... Num of Control: ... Quantification Sat: ... Num of miRNAs: ...
Identification: Num of Up: ... Num of Down: ...
Time Info: Create Time: ... Update Time: ...

Differentially Expressed miRNA list

miRNA ID	Cancer Type	Design	logFC	AveExpr	T value	P value	adj.P.value	Status	Plot
hsa-miR-106a	lymphoma	cancer vs normal	2.89	5.20	14.56	4.36e-17	4.01e-15	UP	dl
hsa-let-7g	lymphoma	cancer vs normal	-3.58	1.77	-14.49	4.92e-17	4.01e-15	DOWN	dl
hsa-miR-17-5p	lymphoma	cancer vs normal	3.12	4.54	14.38	6.33e-17	4.01e-15	UP	dl
hsa-let-7f	lymphoma	cancer vs normal	-4.01	3.21	-13.61	3.66e-16	1.74e-14	DOWN	dl
hsa-let-7a	lymphoma	cancer vs normal	-2.96	2.59	-13.45	5.27e-16	2.00e-14	DOWN	dl
hsa-miR-150	lymphoma	cancer vs normal	-5.20	0.20	-12.96	1.70e-15	5.37e-14	DOWN	dl
hsa-miR-9	lymphoma	cancer vs normal	3.70	-0.05	12.13	1.28e-14	3.48e-13	UP	dl
hsa-miR-20	lymphoma	cancer vs normal	2.75	4.40	11.82	2.82e-14	6.71e-13	UP	dl
hsa-miR-92	lymphoma	cancer vs normal	2.56	2.32	11.37	8.85e-14	1.87e-12	UP	dl
hsa-miR-19a	lymphoma	cancer vs normal	2.74	2.04	10.44	1.09e-12	1.98e-11	UP	dl
hsa-let-7d	lymphoma	cancer vs normal	-3.09	2.40	-10.43	1.10e-12	1.98e-11	DOWN	dl
hsa-miR-18	lymphoma	cancer vs normal	-2.09	2.02	-10.39	1.14e-12	1.98e-11	DOWN	dl
hsa-miR-368	lymphoma	cancer vs normal	2.39	1.51	10.38	1.15e-12	1.98e-11	UP	dl
hsa-miR-1	lymphoma	cancer vs normal	-3.12	-2.35	-10.37	1.16e-12	1.98e-11	DOWN	dl
			-2.72	-1.77	-10.36	1.17e-12	1.98e-11	DOWN	dl

Total: 98

Functional Charts

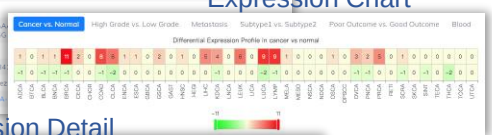



E

miRNA Detail

miRNA ID:	hsa-miR-106a
miRBase ID (latest):	hsa-miR-106a-5p
miRBase Accession:	MIMAT0000103
miRNA Sequence:	AAAAGUGCUUACAGUGCAGGUAG
Precursor miRNA ID:	hsa-mir-106a
Precursor miRNA Accession:	MI0000113
Precursor miRNA sequence:	CCUUGGCCAUGUAAA... UUACAUUACCAUGG...
Organism:	Homo sapiens
Genomic Location:	chrX:134170244-134...
Other Database Links:	HGNC: 31494; Entrez...
Predicted Target:	TargetScan; ... DIANA...

Expression Chart

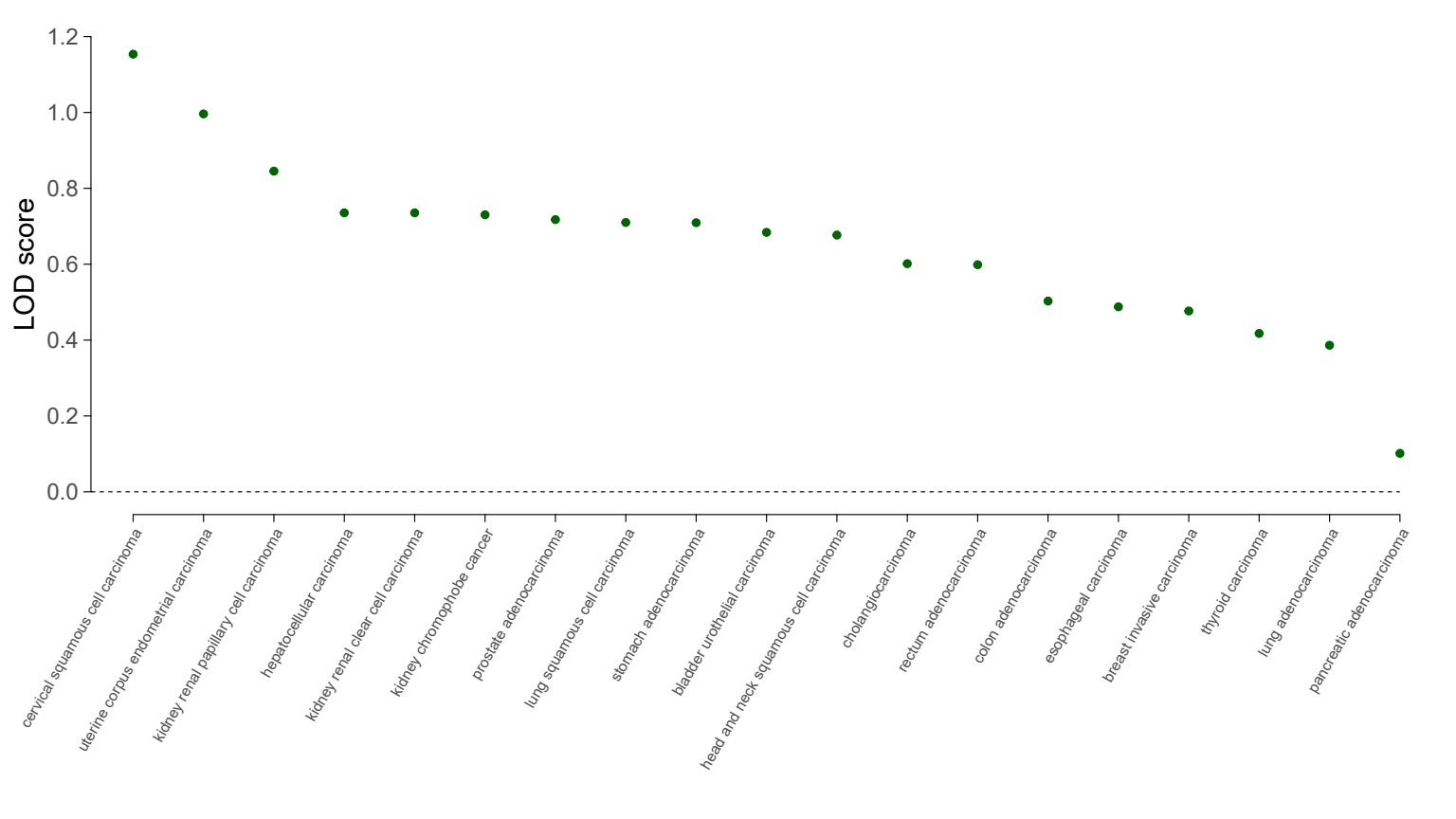


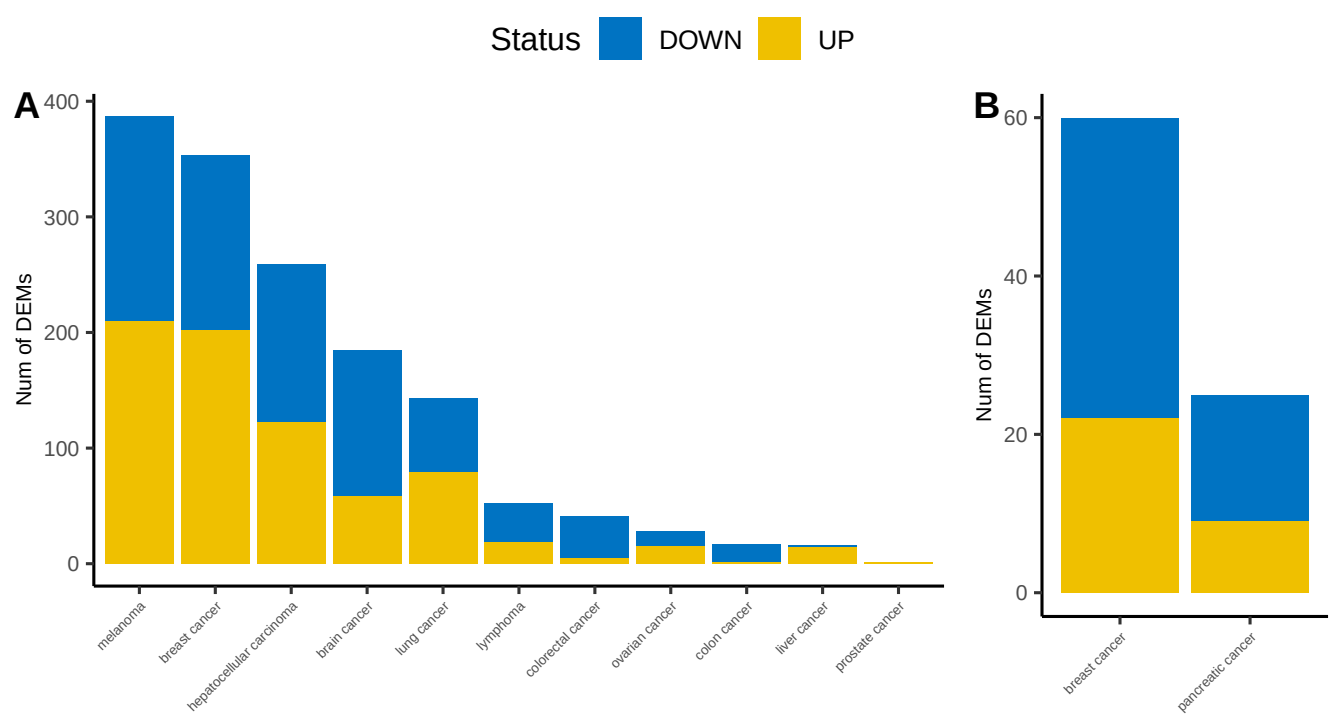
Expression Detail

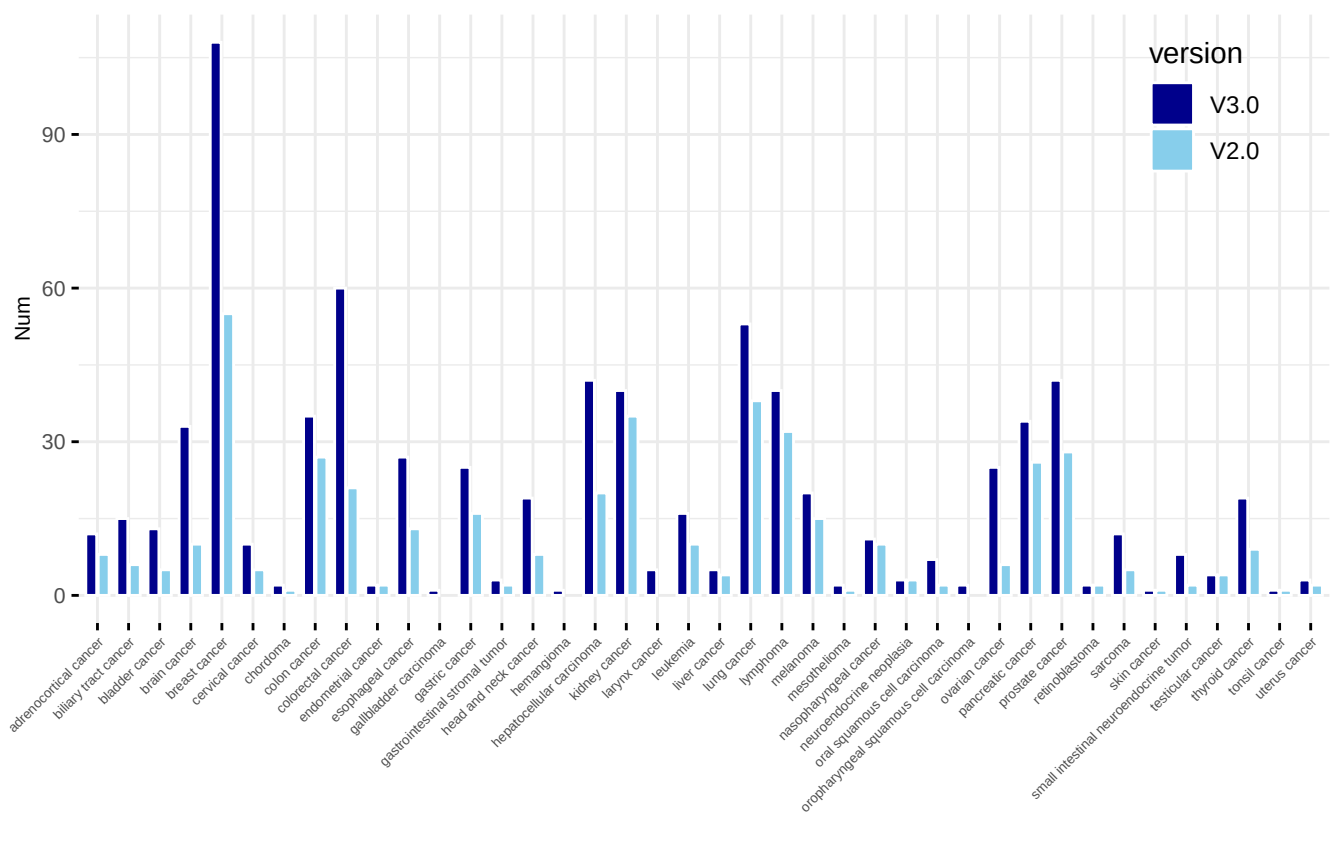
Experiment ID	Cancer Type	Cancer Subtype	Cell Line	Design	logFC	AveExpr	T value	P value
EXP00001	lymphoma	B cell lymphoma	OCI-Ly4	cancer vs normal	2.89	5.20	14.56	4.36e-17
EXP00002	lymphoma	B cell lymphoma	OCI-Ly7	cancer vs normal	3.01	5.20	15.19	1.06e-17
EXP00003	lymphoma	B cell lymphoma	OCI-Ly8	cancer vs normal	3.01	5.20	15.19	1.06e-17
EXP00004	lymphoma	Burkitt's lymphoma	Namalwa	cancer vs normal	2.89	5.20	14.56	4.36e-17
EXP00005	lymphoma	Burkitt's lymphoma	Raji	cancer vs normal	2.76	5.20	13.94	1.70e-16
EXP00006	lymphoma	Splenic lymphoma	Karpas-1718	cancer vs normal	3.01	5.20	15.19	1.06e-17
EXP00007	lymphoma	Gastric lymphoma	Manca	cancer vs normal	3.01	5.20	15.19	1.06e-17

Validation Information

Cancer type	tumor subtype or cell line	Design	platform	status	PubMed ID
colon cancer	N/A	cancer vs normal	QRT-PCR	up	18230780
brain cancer	meningioma	cancer vs normal	QRT-PCR	up	19703993
lung cancer	squamous cell carcinoma	cancer vs normal	QRT-PCR	up	19584273
colon cancer	colon adenocarcinoma tumors/colon adenomas	cancer vs normal	QRT-PCR	up	18230780


LOD score
1.2
1.0
0.8
0.6
0.4
0.2
0.0
cervical squamous cell carcinoma
uterine corpus endometrial carcinoma
kidney renal papillary cell carcinoma
hepatocellular carcinoma
kidney renal clear cell carcinoma
kidney chromophobe cancer
prostate adenocarcinoma
lung squamous cell carcinoma
stomach adenocarcinoma
bladder urothelial carcinoma
head and neck squamous cell carcinoma
cholangiocarcinoma
rectum adenocarcinoma
colon adenocarcinoma
esophageal carcinoma
breast invasive carcinoma
thyroid carcinoma
lung adenocarcinoma
pancreatic adenocarcinoma


Status
DOWN
UP
A
Num of DEMs
400
300
200
100
0
melanoma
breast cancer
hepatocellular carcinoma
brain cancer
lung cancer
lymphoma
colorectal cancer
ovarian cancer
colon cancer
liver cancer
prostate cancer
B
Num of DEMs
60
40
20
0
breast cancer
pancreatic cancer


version
V3.0
V2.0
Num
0
30
60
90
adrenocortical cancer
biliary tract cancer
bladder cancer
brain cancer
breast cancer
cervical cancer
chordoma
colon cancer
colorectal cancer
endometrial cancer
esophageal cancer
gallbladder carcinoma
gastric cancer
gastrointestinal stromal tumor
head and neck cancer
hemangioma
hepatocellular carcinoma
kidney cancer
larynx cancer
leukemia
liver cancer
lung cancer
lymphoma
melanoma
mesothelioma
nasopharyngeal cancer
neuroendocrine neoplasia
oral squamous cell carcinoma
oropharyngeal squamous cell carcinoma
ovarian cancer
pancreatic cancer
prostate cancer
retinoblastoma
sarcoma
skin cancer
small intestinal neuroendocrine tumor
testicular cancer
thyroid cancer
tonsil cancer
uterus cancer