



Sarcoma miRNA Expression Database for Cancer Treatment

Sarcoma miRNA Expression Database For Cancer Diagnosis and Cancer Treatment

The Sarcoma miRNA Expression Database (S-MED) provides comprehensive information about microRNA expression patterns in sarcomas and other relevant cancer tissue types, helping the diagnosis, classification, prognosis, and treatment of malignant tumors. MicroRNAs (miRNAs), a class of small RNAs regulating expressed genes in human sarcomas, can assist in the development of cancer treatments. However, miRNA expression patterns in sarcomas are poorly understood and no central information resource exists. The Sarcoma miRNA Expression Database addresses this gap by systematically providing comprehensive sarcoma miRNA expression profiles. The database is the first of its kind and not available anywhere else in the world. The database is web-accessible and provides both basic and advanced search options.

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Technology ID

20090011

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Comprehensive Information in the Sarcoma miRNA Expression Database

The Sarcoma miRNA Expression Database contains the miRNA expression patterns for 310 tissue samples representing 22 sarcoma types. The database replaces frozen tumor tissue samples, the availability of which is a major challenge in studying sarcoma miRNA or gene expression patterns. The database also includes experimentally validated unique miRNA expression levels in angiosarcoma and other uncommon sarcomas. In addition, the database includes miRNA expression data from normal tissues such as bone, smooth muscle, and skeletal muscle, and from benign tumors such as neurofibroma and leiomyoma for comparative studies with their malignant counterparts. To make the information easy to understand, the database uses heat maps to visualize information and color codes to represent data in absolute and relative formats. Each miRNA is linked to the database so that users can easily track its basic information. Statistical details are provided, such as fold changes and P-values for differentially expressed miRNAs in each sarcoma type and corresponding normal tissues.

Application of the Sarcoma miRNA Expression Database in Cancer Treatment

DNA microarray studies have identified differentially expressed genes in various sarcomas. Many of these genes are regulated by miRNAs. miRNAs are non-coding regulatory small RNAs that display tissue and stage specific expression. By accelerating the understanding and identification of miRNAs in sarcomas, the Sarcoma miRNA Expression Database facilitates the development of miRNA-based cancer biomarkers for different sarcoma subtypes. These miRNAs can also be used to differentiate the stages of the tumors (i.e., primary or metastatic) and the origin of the metastatic tumors. The database facilitates the diagnosis, prognosis and treatment of different types of sarcomas, for which very few diagnostic markers currently exist.

THE SARCOMA MIRNA EXPRESSION DATABASE SERVES AS AN IMPORTANT RESOURCE TO:

- understand sarcoma biology,
- develop miRNA-based cancer biomarkers and
- provide improved medical treatment of rare and diagnostically challenging diseases.

Sarcoma miRNA Expression Database Advantages

MiRNAs were discovered relatively recently and their functions are still being studied. Our lab is the first to study miRNAs in sarcomas using cutting edge ultra high throughput detection procedures. The data in this Sarcoma miRNA Expression Database is not available through any other researchers or organizations across the globe. It would be extremely difficult for researchers to independently assemble the tumors in this dataset due to their rarity. The Sarcoma MiRNA Expression Database allows users to define the miRNA types or relationships they are interested in studying, instead of being limited by previously analyzed data. This is the first database that allows users across the globe to search and view microRNA expression levels in different sarcomas through a web interface.

SARCOMA MIRNA EXPRESSION DATABASE FEATURES

- Comprehensive database of sarcoma microRNA expression patterns for 310 tissue samples representing 22 sarcoma types
- Contains miRNA expression profiles from normal tissues and benign tumors for comparative studies
- Includes statistical details such as fold changes and P-values for differentially expressed miRNAs in each sarcoma type and corresponding normal tissue
- Heat maps and color codes assist the user in visualizing the information
- Browser-based access with basic and advanced search options
- The first to study microRNAs in sarcomas using ultra-high throughput detection procedures.

Phase of Development The database is complete and available for licensing.

Snap-frozen patient tumor tissue samples were collected through the tissue procurement facility and from collaborators at the Masonic Cancer Center, University of Minnesota, and stored at -80° C until used. Institutional review board approved this study.

Sarcoma tumors and normal tissue in MiRNA database

Phase	Sarcoma/tissue type	Number of cases/samples
I	Fibromatosis	16
	Gastrointestinal stromal tumor	13
	Malignant fibrous histiocytoma	30
	Osteosarcoma	15
	Synovial sarcoma	15
II	Ewing's sarcoma	7
	Leiomyosarcoma	25
	Malignant peripheral nerve sheath tumor	25
	Neurofibroma	14
	Schwannoma	16
	Solitary fibrous tumor	5
III	Angiosarcoma	5
	Embryonal rhabdomyosarcoma	22
	Alveolar rhabdomyosarcoma	19
	Liposarcoma well differentiated	10
	Liposarcoma dedifferentiated	12
	Skeletal muscle (normal)	7
	Smooth muscle (normal)	10
IV	Chondrosarcoma	5
	Epithelioid sarcoma	5
	Fibrosarcoma	8
	Histiocytoma	9
	Leiomyoma	8
	Bone tissue (normal)	6
	Spindle cell sarcoma	3
	Total	310

Researchers

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[External Link](http://www.surg.umn.edu) (www.surg.umn.edu)

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