

Step 1, visit UMARS via <http://musk.ibms.sinica.edu.tw/UMARS/>



UMARS

Un-Mappable Reads Solution

miRNA Series

- VirMir
- ZooMir
- UMARS
- UMARS:EEJ
- UMARS:Vir

Links

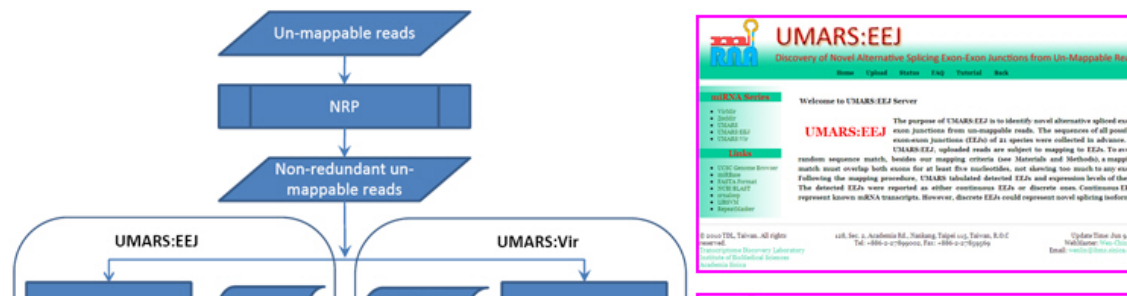
- UCSC Genome Browser
- miRBase
- FASTA Format
- NCBI BLAST
- srnaloop
- LIBSVM
- RepeatMasker

Welcome to UMARS Server

UMARS Recently, next generation sequencing (NGS) technology, including Roche 454, Illumina GA and ABI SOLiD platforms etc, emerged as a powerful tool for generating high-throughput sequencing data. In a typical analysis pipeline, the generated NGS sequence reads were first subject to adaptor trimming and mapping back to reference sequences, including genomes, scaffolds or transcripts. However, a fraction of sequence reads can not be mapped back to the reference sequences. These un-mappable reads were usually discarded without further consideration. It is of our interest to examine the possible biological relevance of un-mappable reads. Therefore, we have developed Un-Mappable Reads Solution (UMARS) pipeline to solve such problem. UMARS focuses on the scanning of viral genome (UMARS:Vir) or novel splicing junction (UMARS:EEJ) from un-mappable reads.

The first step of UMARS is to deal with the redundancy problem of NGS reads. For convenience and efficiency, we developed an in-house tool, called Non-redundant Reads Producer (NRP), to solve such a problem. **The reads uploaded to UMARS must be processed by NRP in advance or be presented as the format of NRP output.** Then, the un-redundant reads can be processed by either UMARS:Vir or UMARS:EEJ.

UMARS Flowchart & Services



Step 2, visit UMARS:EEJ by clicking UMARS:EEJ



UMARS

Un-Mappable Reads Solution

miRNA Series

- VirMir
- ZooMir
- UMARS
- UMARS:EEJ
- UMARS:Vir

Links

- UCSC Genome Browser
- miRBase
- FASTA Format
- NCBI BLAST
- srnaloop
- LIBSVM
- RepeatMasker

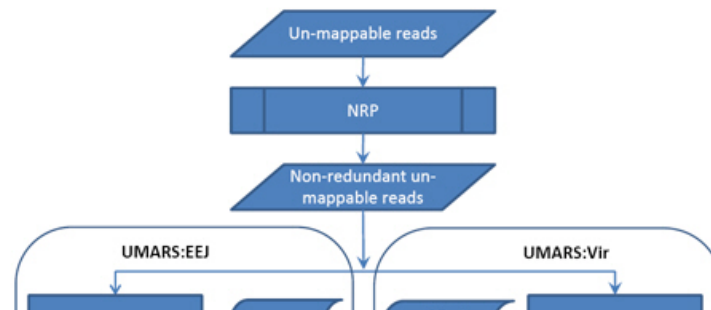
Welcome to UMARS Server

UMARS

Recently, next generation sequencing (NGS) technology, including Roche 454, Illumina GA and ABI SOLiD platforms etc, emerged as a powerful tool for generating high-throughput sequencing data. In a typical analysis pipeline, the generated NGS sequence reads were first subject to adaptor trimming and mapping back to reference sequences, including genomes, scaffolds or transcripts. However, a fraction of sequence reads can not be mapped back to the reference sequences. These un-mappable reads were usually discarded without further consideration. It is of our interest to examine the possible biological relevance of un-mappable reads. Therefore, we have developed Un-Mappable Reads Solution (UMARS) pipeline to solve such problem. UMARS focuses on the scanning of viral genome (UMARS:Vir) or novel splicing junction (UMARS:EEJ) from un-mappable reads.

The first step of UMARS is to deal with the redundancy problem of NGS reads. For convenience and efficiency, we developed an in-house tool, called Non-redundant Reads Producer (NRP), to solve such a problem. **The reads uploaded to UMARS must be processed by NRP in advance or be presented as the format of NRP output.** Then, the un-redundant reads can be processed by either UMARS:Vir or UMARS:EEJ.

UMARS Flowchart & Services



The screenshot shows the UMARS:EEJ website. The header includes the logo and the title "UMARS:EEJ Discovery of Novel Alternative Splicing Exon-Exon Junctions from Un-Mappable Reads". Below the header, there is a navigation menu with links for Home, Tutorials, Methods, FAQs, and Contact Us. The main content area features a "miRNA Series" list with a red arrow pointing to "UMARS:EEJ", and a "Links" section with various bioinformatics tools. A "Welcome to UMARS:EEJ Server" message is displayed, followed by a detailed description of the tool's purpose and usage. The footer contains contact information for the research group at Academia Sinia, including the address, phone number, and email.

Step 3, visit UMARS:EEJ upload page

The screenshot shows the UMARS:EEJ upload page. The page title is "UMARS:EEJ" and the subtitle is "Discovery of Novel Alternative Splicing Exon-Exon Junctions from Un-Mappable Reads". The page is divided into several sections:

- miRNA Series:** VirMir, ZooMir, UMARS, UMARS:EEJ, UMARS:Vir
- Links:** UCSC Genome Browser, miRBase, FASTA Format, NCBI BLAST, srnaloop, LIBSVM, RepeatMasker

The main content area contains the following form fields and buttons:

- your E-mail:** XXXXX@AAA.BBB.CCC
- Buttons:** Back, test
- Text:** You might click to save our test data: [eejTest.fna](#) or Click **test** to test
- Text:** Please give an UNIQUE name for each query sequence!!
- Text:** Enter sequence(s) in FASTA format
- FASTA Sequence:**

```
>NR1 2663238
CGCCTTGGCCGTACAGCAGGGGCTT
>NR2 452461
CGCGACCTCAGATCAGACGTGGCGA
>NR3 292066
GCCCGGCTAGCTCAGTCGGTAGAGC
>NR4 216559
CGACTCTTAGCGGTGGATCGCCTTG
>NR5 154402
CGCGACCTCAGATCGCCTTGGCCGT
```
- Text:** Or, upload FASTA file with its max. size less than 10 MB
- Text:** Please choose the target species:
- Buttons:** submit, Clear

Instructional callouts are provided for several steps:

- Step 3:** Space separated (pointing to the FASTA sequence)
- Step 4:** key in your e-mail address (pointing to the email field)
- Step 5:** click test for demonstration (pointing to the test button)
- Step 5:** OR paste your query seq. (pointing to the FASTA sequence)
- Step 5:** OR upload your query seq. (pointing to the file upload field)
- Step 6:** Select the species whose EEJ collection is going to be mapped (pointing to the species dropdown)