

# 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

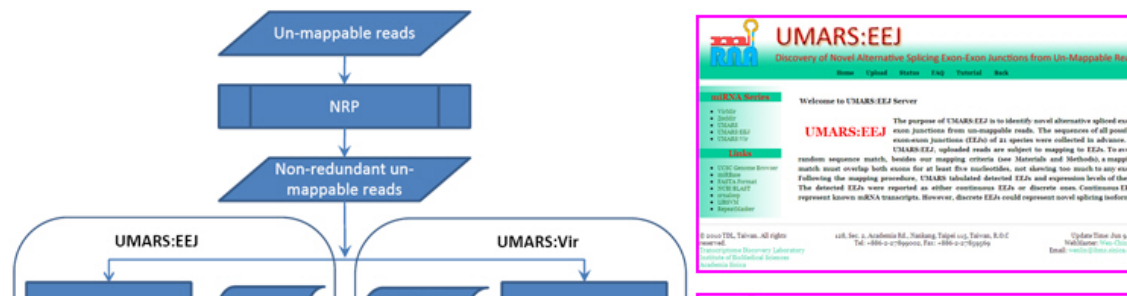
- UCSC Genome Browser
- miRBase
- FASTA Format
- NCBI BLAST
- sRNAloop
- LIBSVM
- RepeatMasker

### 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:Vir by clicking UMARS:Vir



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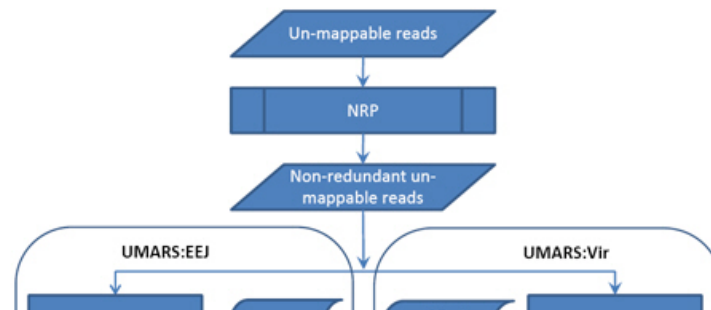
### Welcome to UMARS Server

## UMARS

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### UMARS Flowchart & Services



UMARS:EEJ  
Discovery of Novel Alternative Splicing Exon-Exon Junctions from Un-Mappable Reads

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miRNA Series

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Welcome to UMARS:EEJ Server

The purpose of UMARS:EEJ is to identify novel alternative spliced exon-exon junctions (EEJs) from un-mappable reads. The sequences of all possible exon-exon junctions (EEJs) of all species were collected in advance. In UMARS:EEJ, uploaded reads are subject to mapping to EEJs. To avoid random sequence match, besides our mapping criteria (see Materials and Methods), a mapping match must overlap both exons for at least five nucleotides, not sharing too much to any exon. Following the mapping procedure, UMARS tabulated detected EEJs and expression levels of them. The detected EEJs were reported as either continuous EEJs or discrete ones. Continuous EEJs represent known mRNA transcripts. However, discrete EEJs could represent novel splicing isoforms.

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# Step 3, visit UMARS:Vir upload page

**Space separated**

## UMARS:Vir

Discovery of Virus Genomic Regions from Un-Mappable Reads

**Step 4: key in your e-mail address**

Your E-mail:

**Step 5: click test for demonstration**

Use [right click to save our test data: virTest.fna](#) or Click  to test

Please give an UNIQUE name for each query sequence!!

Enter sequence(s) in FASTA format

```
>NR17 47941
GACTCTTAGCGGTGGATCGCCTTGG
>NR18 43825
ACGCGACCTCAGATCAGACGTGGCG
>NR19 42247
CGCCTTGGCCGTACAGCAGGGGGAA
>NR21 4888
GGTAGCGTGGCCGAG
```

**Step 5: OR paste your query seq.**

**Step 5: OR upload your query seg.**

Or, upload FASTA file with its max size less than 10 MB

Choose Host Category of Virus:

Parameter Criteria:

Would you like to use miRNA gene prediction model to predict miRNA genes?

**Step 6: select the host category of virus**

**Step 7: select parameter criteria, Standard or Loose. This is an empirical criterion**

**Step 8: select whether miRNA prediction done**

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