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Scope: **Self** Format: **HTML** Amount: **Quick** GEO accession: **GSM5179454** **GO**

**Sample GSM5179454**[Query DataSets for GSM5179454](#)

Status	Public on Mar 19, 2021
Title	Optn-KD 1
Sample type	SRA
Source name	BV2 cells
Organism	<a href="#">Mus musculus</a>
Characteristics	cell type: cell line treatment: Optn-siRNA
Treatment protocol	The Optn-KD group was treated with siRNA for 24 hours.
Growth protocol	Cells were cultured with Dulbecco's Modified Eagle Media (DMEM), supplemented with 10% fetal bovine serum (FBS), and incubated at 37 °C in a humidified incubator containing 5% CO <sub>2</sub> .
Extracted molecule	total RNA
Extraction protocol	We isolated the exosomes using the Umibio® exosome isolation kit (UR52121, Umibio, China). MiRNA was harvested using Trizol reagent for library construction. Total RNA of each sample was used to prepare the miRNA sequencing library, which included the following steps: 1) 3'-adaptor ligation; 2) 5'-adaptor ligation; 3) cDNA synthesis; 4) PCR amplification; 5) Size selection of ~150 bp PCR amplicons (corresponding to ~22nt miRNAs)
Library strategy	miRNA-Seq
Library source	transcriptomic
Library selection	size fractionation
Instrument model	Illumina HiSeq 4000
Description	exosomal miRNA

**Data processing** Data were generated after sequencing, image analysis, base calling and quality filtering on Illumina sequencer.  
The adaptor sequences were trimmed and the adaptor-trimmed-reads ( $\geq 15$ nt) were left by cutadapt software (v1.9.3).  
MiRDeep2 software (v2.0.0.5) was used to predict novel miRNAs  
The trimmed reads were aligned to the merged pre-miRNA databases (known pre-miRNA from miRBase plus the newly predicted pre-miRNAs) using Novoalign software (v3.02.12) with at most one mismatch.  
The numbers of mature miRNA mapped tags were defined as the raw expression levels of that miRNA. The read counts were normalized by TPM (tag counts per million aligned miRNAs) approach.  
Differentially expressed miRNAs between two samples were filtered through Fold change. Differentially expressed miRNA between two groups were filtered by Fold Change and P-value based on volcano plot.  
Genome\_build: miRBase (v22)  
Supplementary\_files\_format\_and\_content: The miRNA\_expression.xlsx file includes the miRNA information and tag counts.  
Supplementary\_files\_format\_and\_content: xlsx

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**Platform ID** [GPL21103](#)  
**Series (1)** [GSE169175](#) Exosomal-miRNA sequencing of optineurin gene knockdown BV2 cells and wild type BV2 cells

### Relations

**BioSample** [SAMN18350780](#)  
**SRA** [SRX10378828](#)

### Supplementary data files not provided

[SRA Run Selector](#) 

*Raw data are available in SRA*

*Processed data are available on Series record*



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