

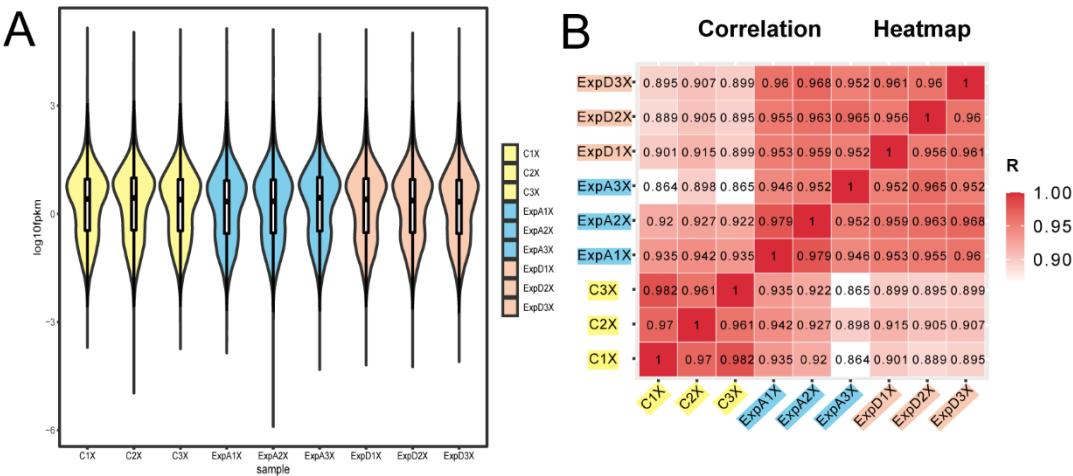
## Supplementary Material

### 1. Supplementary Table

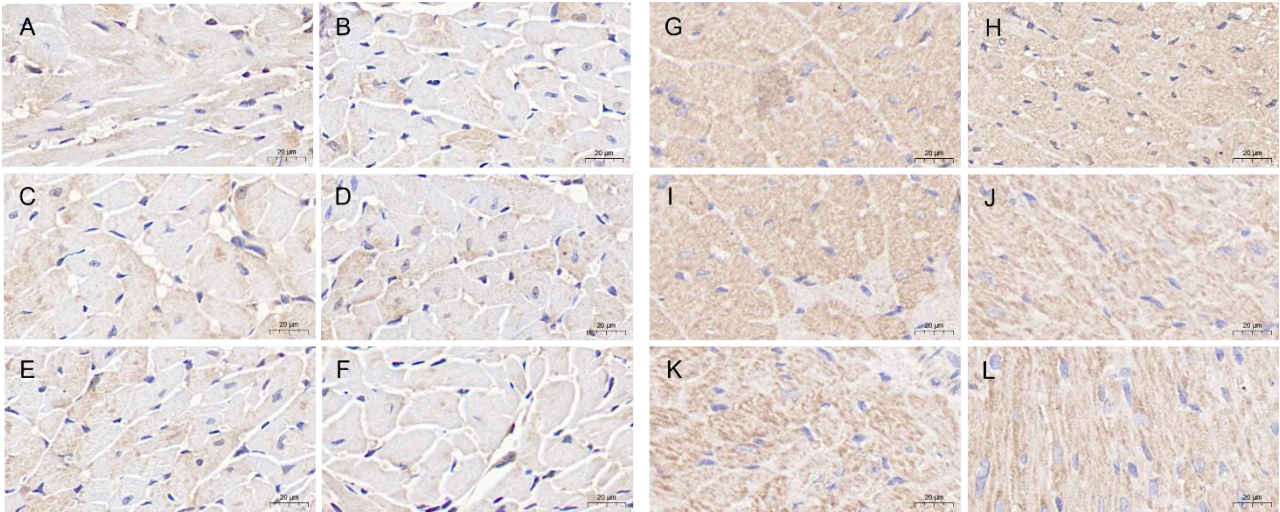
**Supplementary Table S1.** Primers used for validation of RNA-seq data.

Gene name	Primer sequence (5' -3' )	Amplicon length (bp)
<i>Nfkbia</i>	F: GCCAGTGTAGCAGTCTTGAC R: CAGGTAGCCGTGGATAGAGG	117
<i>Junb</i>	F: CAGCCTTTCTATCACGACGAC R: GGTGGGTTTCAGGAGTTTGTAG	96
<i>Gadd45g</i>	F: TCTACGAGTCCGCCAAAGTC R: CACAGCAGAACGCCTGAATC	132
<i>Iigp1</i>	F: CAAATGAAGCAGATGGCAAACC R: TTGTTAGAGAGCAGGAAGATTGG	130
<i>C3</i>	F: ACTTCTTCATTGACCTGCGGC R: CGAGGACTTGGGAGGGATTT	197
<i>Myd88</i>	F: AAGCAGCAGAACCAGGAGTC R: GCAGTAGCAGATAAAGGCATCG	150
<i>Tbk1</i>	F: ATCAAGAAGGCACGCATCCA R: GGCTCATTGCTTTTGTGGCA	186
<i>Stat1</i>	F: GCCTCTCATTGTCACCGAAGAAC R: TGGCTGACGTTGGAGATCACCA	123
<i>Il4ra</i>	F: GCTTGAAGAAGAACTCTAGTGTT R: GATGTGGACTTGGACTCATTC	109
<i>Cd14</i>	F: TCGCTCAATCTGTCTTTCA R: CTATCCAGCCTGTTGTAACT	95
<i>β-actin</i>	F: CCTCTATGCCAACACAGT R: TAGGAGCCAGAGCAGTAA	92

2. Supplementary Figure



**Supplementary Figure S1.** The quality of sequencing data. (A) The abundance of gene transcript. (B) Correlation heatmap of samples. The gradient color barcode at the right indicates the minimum value in white and the maximum in red. If one sample is highly similar to another one, the correlation value between them is very close to 1.



**Supplementary Figure S2.** The IHC of MYD88. (A-F) The control group, (G-L) the Pm HN02 group. The quantification of staining intensity was analyzed using these fields.