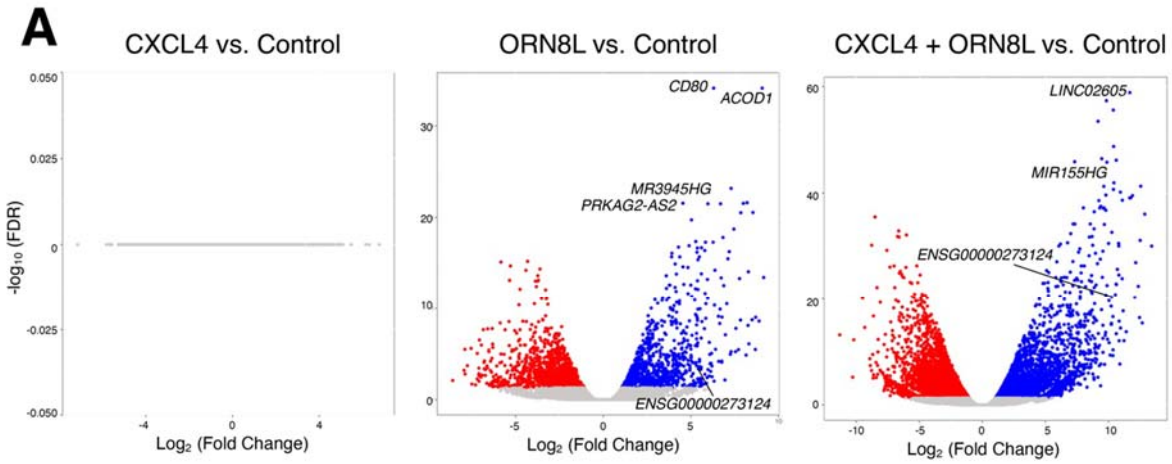
Comment 3 was partially addressed. Now, given the identities of differentially expressed genes upon treatment with CXCL4, ORN8L, or both, it would be ideal to detail the functional attributes of the highlighted molecules in NLRP3 inflammasome complex. Same with, LPS+MSU. Moreover, it would be worth showing the lnc-RNA ENSG00000273124 in the valcono plots for better identification of the rationale for specifically knocking down this lnc-RNA.

Response: The figures were modified as follows to highlight our target lncRNA, ENSG00000273124.



B

Up-regulated	CXCL4 vs. Control	ORN8L vs. Control	CXCL4+ORN8L vs. Control
protein_coding	0	851	2,101
lncRNA	0	146	713
Others	0	51	275
Total	0	1,048	3,089

Down-regulated	CXCL4 vs. Control	ORN8L vs. Control	CXCL4+ORN8L vs. Control
protein_coding	0	1,148	3,122
lncRNA	0	168	459
Others	0	26	96
Total	0	1,342	3,677

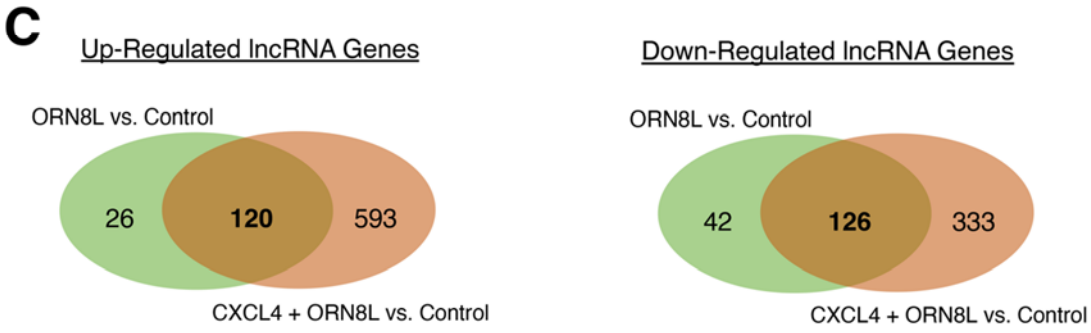
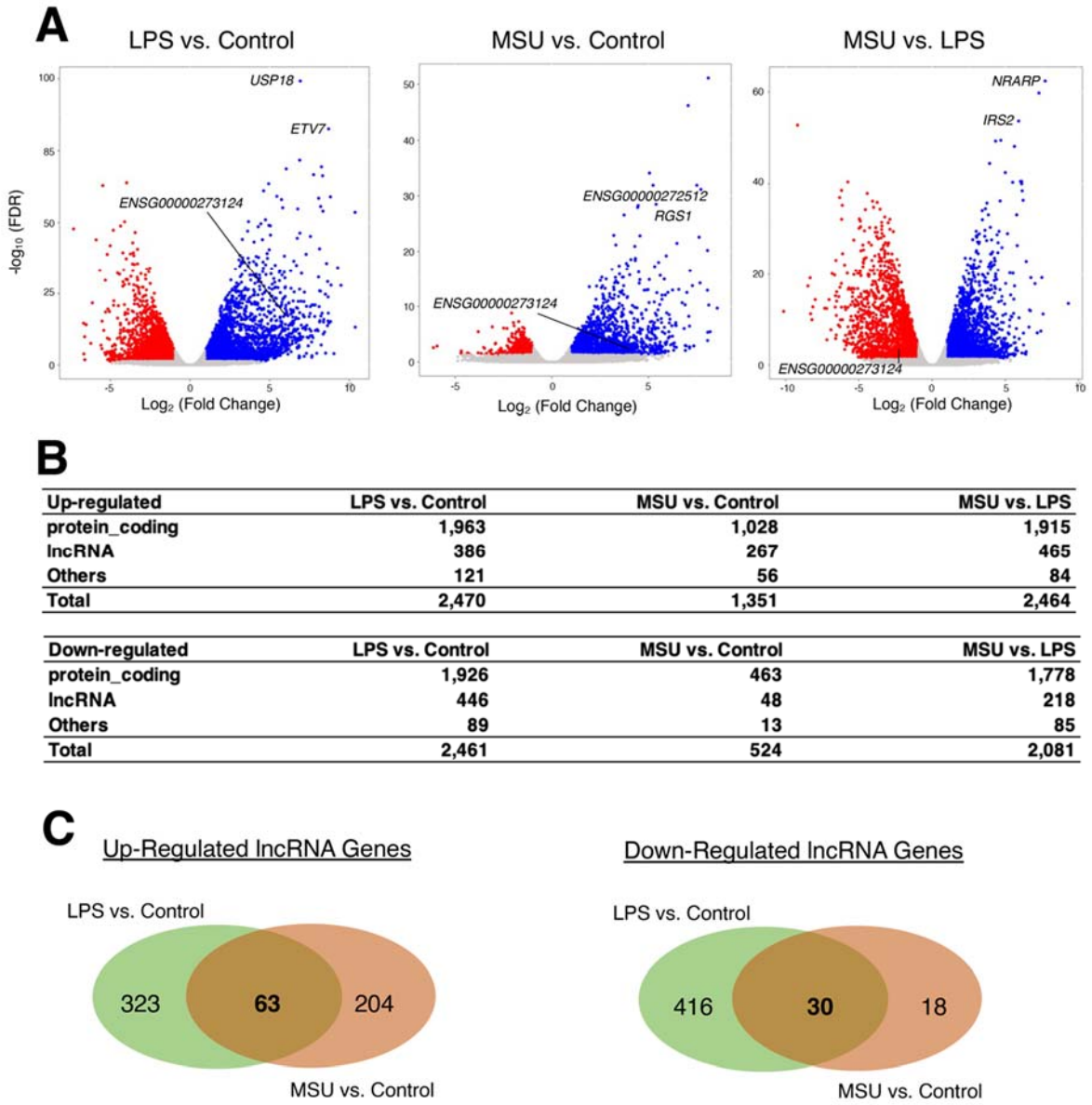


Figure 1



Up-regulated	LPS vs. Control	MSU vs. Control	MSU vs. LPS
protein_coding	1,963	1,028	1,915
lncRNA	386	267	465
Others	121	56	84
Total	2,470	1,351	2,464

Down-regulated	LPS vs. Control	MSU vs. Control	MSU vs. LPS
protein_coding	1,926	463	1,778
lncRNA	446	48	218
Others	89	13	85
Total	2,461	524	2,081

Figure 2

Comment 4 is partially addressed by working on the figure legend. However, it is quite difficult to visualize the figure for better understanding. Though the idea is to provide a overview of the InflammasomeDB, it would worth providing the same with a readable clarity.

Response: The corresponding part was modified as follows:

"The database is structured into four primary pages: Explore, Download, lncRNAs, and Documentation. In the Explore section, users can effortlessly examine expression changes of protein-coding and lncRNA genes across various conditions shown in the previous subsections. Results are neatly displayed in a "Result Table" on the left side of the page (Figure 6B), and the users can customize this dynamic page using fold change (log2FC) and FDR values to control the number of differentially expressed genes (DEGs) identified.

Further investigation into the DEGs is possible through a volcano plot and heat map (Figure 6B), with the volcano plot being directly connected to the "Result Table". The users can highlight a specific gene from the table on the plot to quickly identify the gene of interest on the volcano plot. In addition, DEGs can be examined for enriched gene ontology (GO) terms (Figure 6C) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (Figure 6D), with clear distinctions between up- and down-regulated genes. These functions allow to further examine the biological processes and signaling pathways, respectively, in each condition. Furthermore, the "Comparisons Intersection" window on the Explore page offers a visual representation of shared DEGs across different compar-isons using a Venn diagram, with a text output listing these shared DEGs (Figure 6D). These shared DEGs can be further explored using their Ensembl Gene IDs."