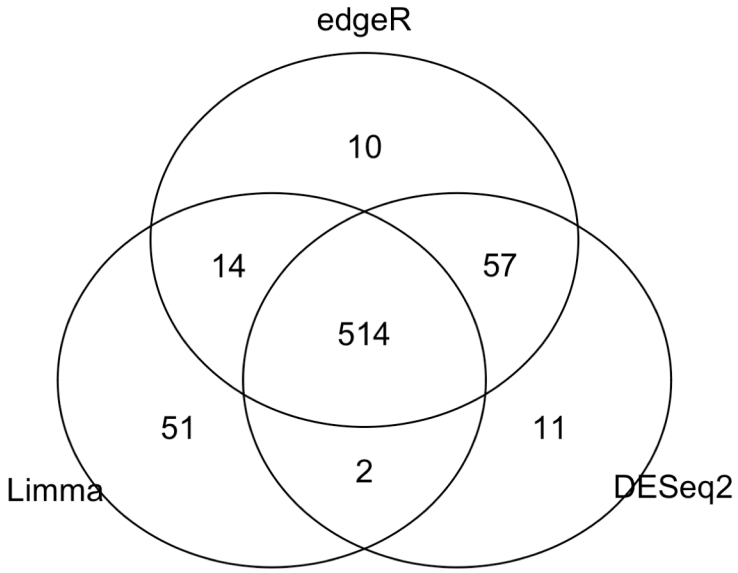
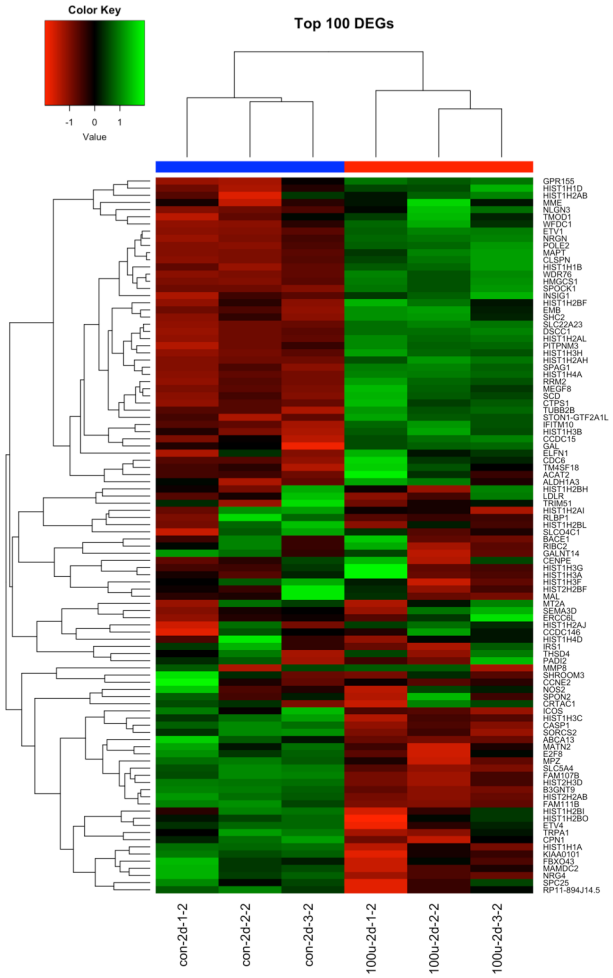
Supplementary Figure-1



Supplementary Figure-2

A



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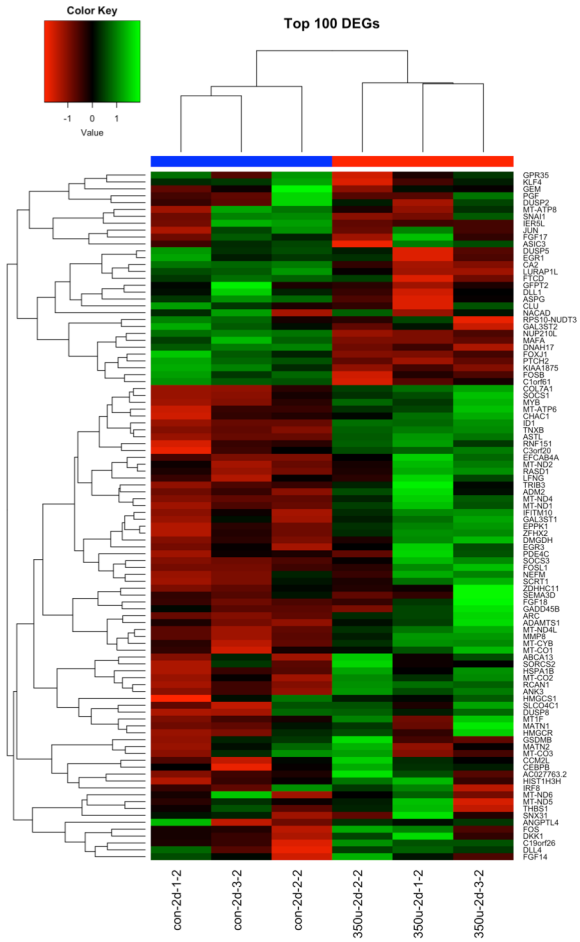
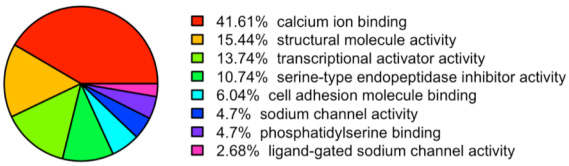


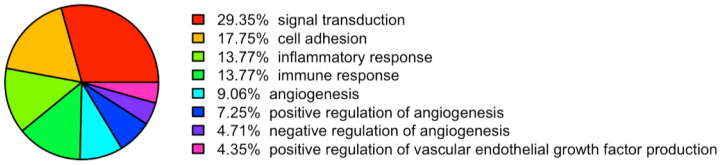
Supplementary Figure-3

Con vs 100 µM- 48 h

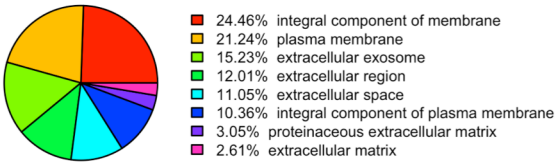
Molecular Function



Biological Process

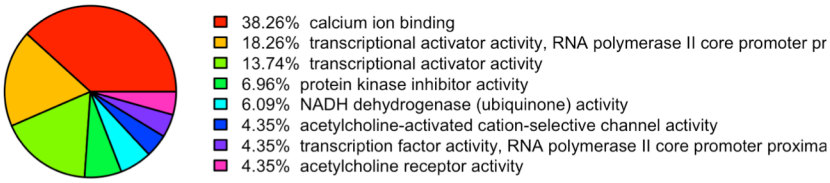


Cellular Component

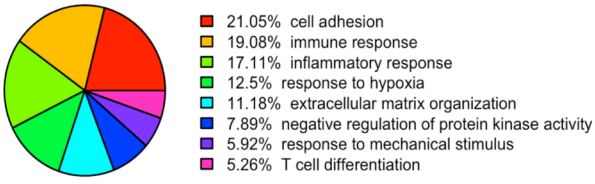


Con vs 350 µM-48 h

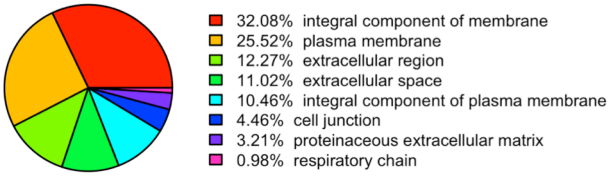
Molecular Function



Biological Process

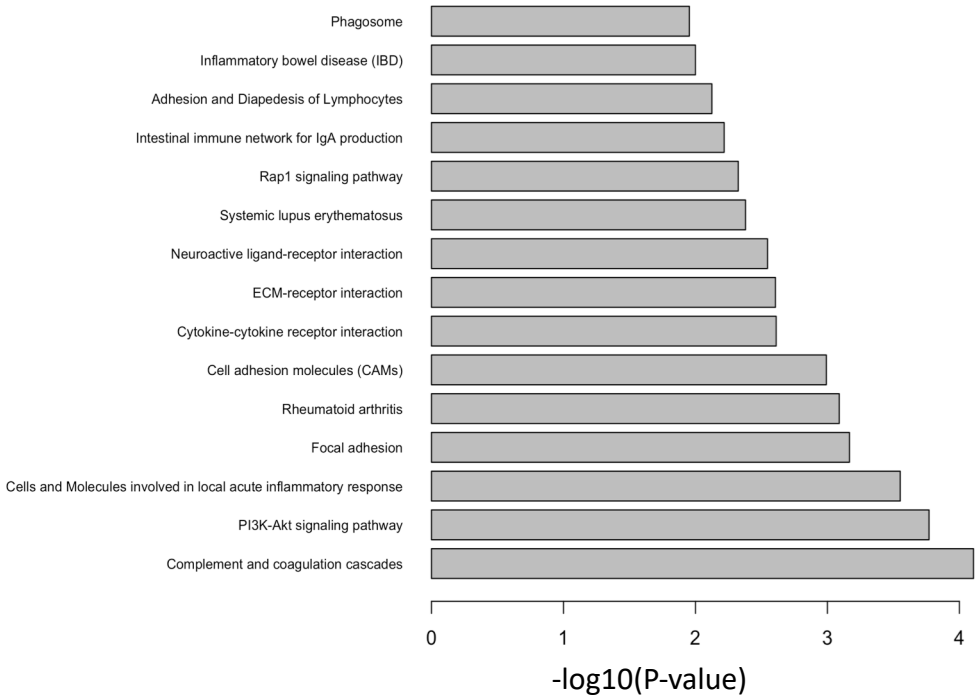


Cellular Component

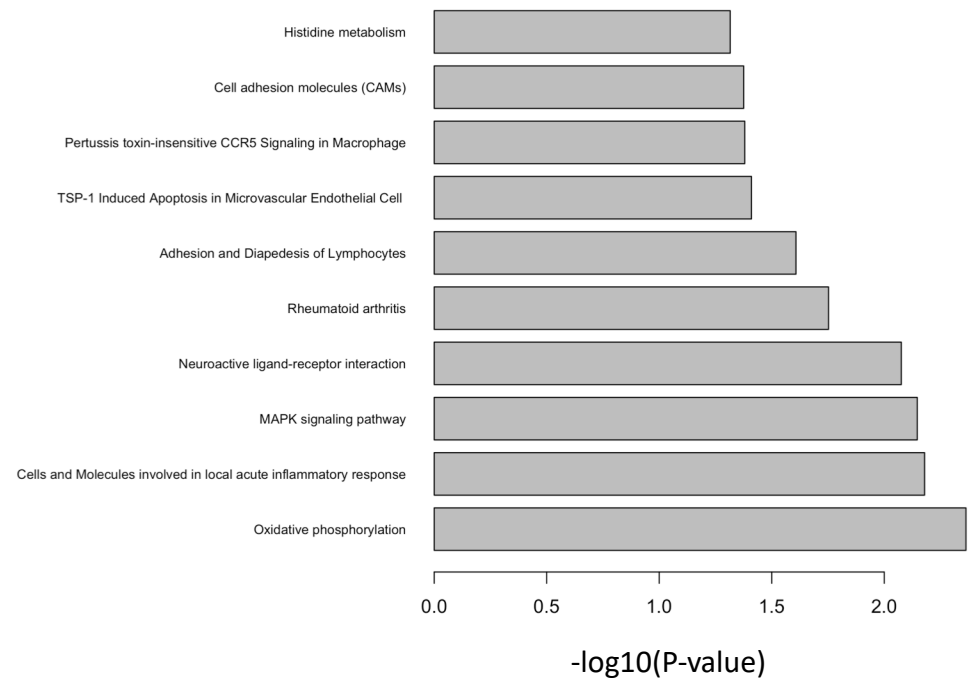


Supplementary Figure-4

Con vs 100 µM- 48 h

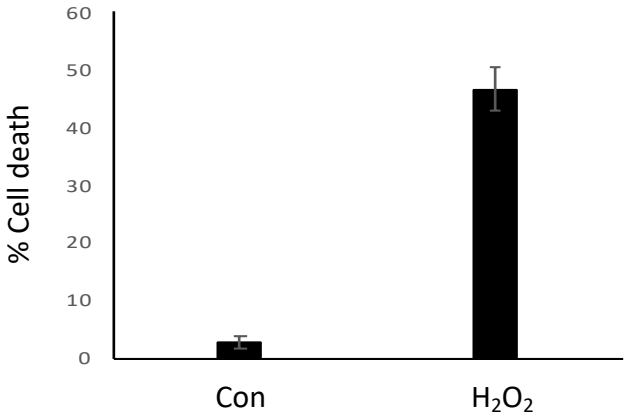


Con vs 350 µM-48 h



Supplementary Figure-5

A



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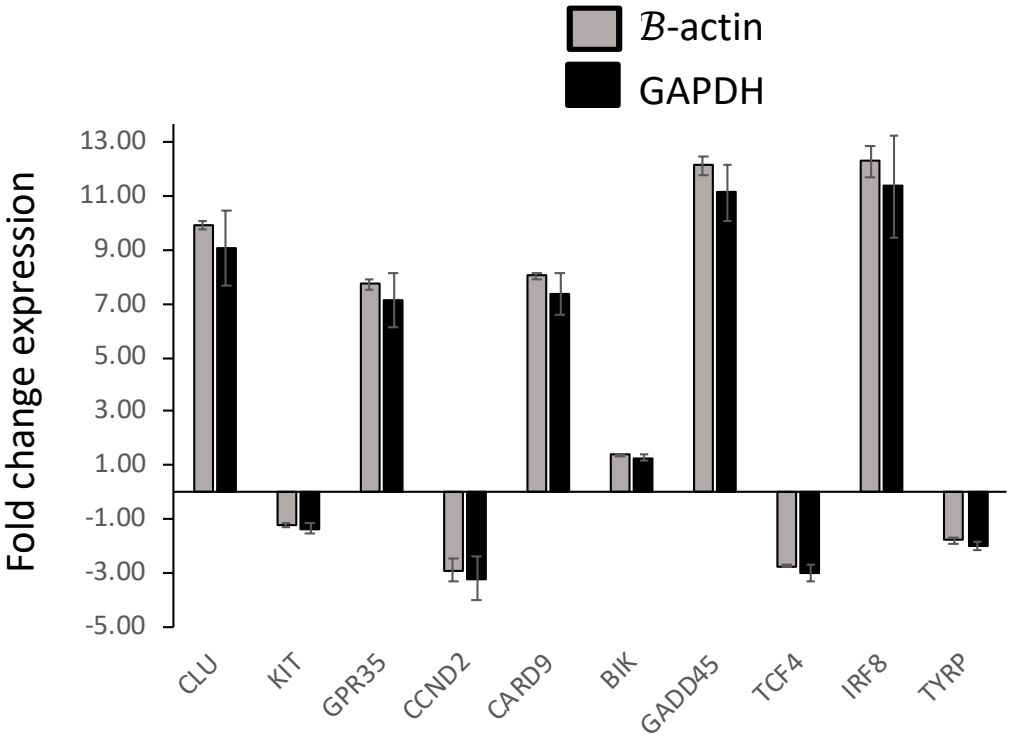

SUPPLEMENTARY INFORMATION:

Supplementary Figure-1: Comparison of the DEGs detected by three methods: Venn diagram of DEGs detected by the edgeR, DESeq and Limma.

Supplementary Figure-2: The hierarchical clustering of top 100 differentially expressed genes **(A):** Control vs 100 µM H_2O_2 **(B):** Control vs 350 µM H_2O_2 at 48 h treatment and control. Red color is the upregulated and Green color is the downregulated genes.

Supplementary Figure-3: GO enrichment analysis of DEGs **(A):** 100 µM H_2O_2 and control samples at 48 h; **(B):** 350 µM H_2O_2 and control samples at 48 h, according to DAVID Bioinformatics tool.

Supplementary Figure-4: Biological pathway enrichment analysis of DEGs **(A):** 100 µM H_2O_2 and control for 48 h; **(B):** 350 µM H_2O_2 and control for 48 h using DAVID bioinformatics tool.

Supplementary Figure-5: PIG1 cells were treated with 250 µM H_2O_2 for 48 h and cell viability was measured by trypan blue dye exclusion assay (A). Relative gene expression of indicated genes was measured using quantitative RT-PCR (B). GAPDH and beta-actin were used as internal controls separately.

Supplementary Table-1: List of differentially regulated selected apoptotic proteins after 24 h of treatment with H_2O_2

Putative Function	**Genes**	**Log2 Fold Change**
Apoptosis	TNFRSF9	+3.4
	TNFRSF8	+3.8
	TNFRSF1B	+1.5
	TNFRSF10A	+1.2
	TNFRSF11B	+2.5
	TNFRSF12A	+3.2
	TNFRSF13C	+1.2
	CARD9	+2.6
	CARD11	+3.1
	NALP3/NLRP3	+5.0