Supplement

**Table 1. The NGS analysis of the quality control.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Raw Read | Raw Base | Clean Read | Clean base | Q20 (%) | Q30 (%) | GC content (%) |
| Control | 52507748 | 7.9 G | 47230360 | 6.9 G | 98.75 | 95.22 | 51.875 |
| C\_10ug | 50871132 | 7.6 G | 45522748 | 6.7 G | 98.65 | 94.935 | 51.68 |
| C\_20ug | 58785584 | 8.8 G | 52546180 | 7.7 G | 98.71 | 95.1 | 52.015 |
| C\_30ug | 51634468 | 7.7 G | 45635416 | 6.7 G | 98.67 | 94.975 | 51.125 |

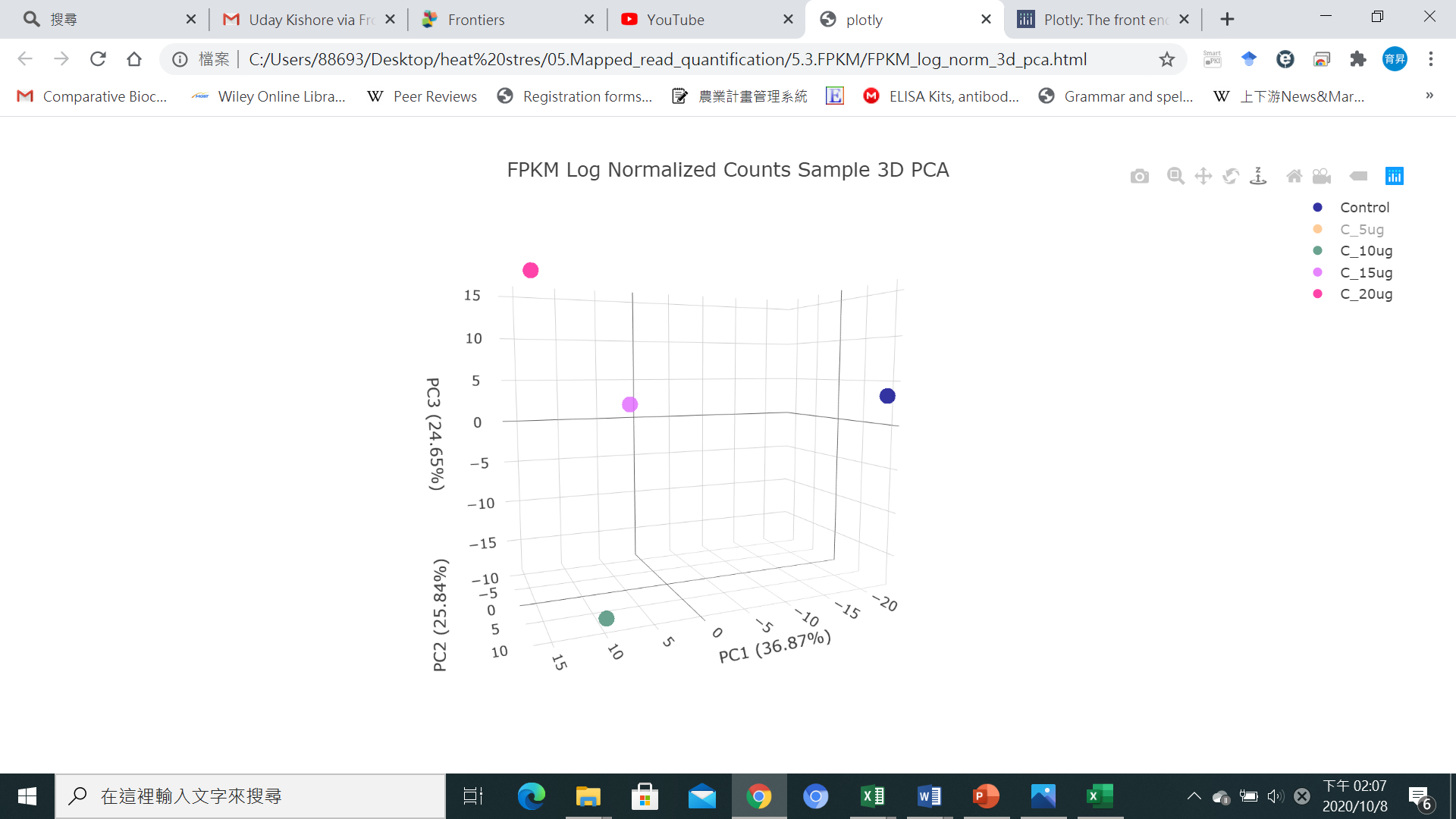
**Table 2. The NGS analysis of the DEGseq Processlog**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Set.Name | Trt | Ctrl | Raw.  Gene  Count | Prefilter.  Gene  Count | DEGseq.  outlier | DEGseq.  Outlier.  remove.  Gene  Count | Filter.  Gene  Count | Filter.  Gene  Count.  Up | Filter.  Gene  Count.  Down | Filter. Criteria |
| group 10ug vs Control | C\_10ug | Control | 55536 | 11187 | 5 | 11182 | 279 | 177 | 102 | fc.threshold = 2 ; l2fc.threshold = 1 ; p.threshold = 0.005 ; ptype = adjust |
| group 20ug vs Control | C\_20ug | Control | 55536 | 11187 | 5 | 11182 | 176 | 83 | 93 | fc.threshold = 2 ; l2fc.threshold = 1 ; p.threshold = 0.005 ; ptype = adjust |
| group 30ug vs Control | C\_30ug | Control | 55536 | 11187 | 7 | 11180 | 360 | 228 | 132 | fc.threshold = 2 ; l2fc.threshold = 1 ; p.threshold = 0.005 ; ptype = adjust |

**Table 3. DEG seq prediction demonstrating *S. suieae* acetyl-xylogalactan facilitated the regulation of the apoptotic relative factors. Predicted expressed genes included *Nfkbia*, *Hyou1*, *Ddit3*, *Gadd45a*, *Akt3*, and *Cflar*.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Ensembl\_gene\_id | Symbol | Treatment | log2 FoldChange | P value | padj |
| ENSMUSG00000021025 | *Nfkbia* | 10ug | - | - | - |
| 20ug | 1.347814544 | 7.4173E-18 | 8.3778E-16 |
| 30ug | 1.380527451 | 3.36846E-19 | 3.6211E-17 |
| ENSMUSG00000032115 | *Hyou1* | 10ug | 0.962404421 | 2.51659E-39 | 5.51776E-37 |
| 20ug | 1.190381588 | 1.27077E-67 | 5.68391E-65 |
| 30ug | 1.045345064 | 3.17948E-52 | 9.11451E-50 |
| ENSMUSG00000025408 | *Ddit3* | 10ug | 2.425985578 | 6.59176E-15 | 4.23615E-13 |
| 20ug | 2.831432378 | 4.85266E-23 | 7.4332E-21 |
| 30ug | 2.497456474 | 9.87924E-17 | 9.28151E-15 |
| ENSMUSG00000036390 | *Gadd45a* | 10ug | 2.191850959 | 3.91206E-05 | 0.00068458 |
| 20ug | 2.747488401 | 9.0039E-09 | 4.55573E-07 |
| 30ug | 2.727069935 | 1.06739E-08 | 3.8998E-07 |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Ensembl\_gene\_id | Symbol | Treatment | Log2 FoldChange | P value | padj |
| ENSMUSG00000019699 | *Akt3* | 10ug | - | - | - |
| 20ug | - | - | - |
| 30ug | 1.006068089 | 2.29643E-05 | 0.000423665 |
| ENSMUSG00000026031 | *Cflar* | 10ug | 1.16575601 | 1.65751E-08 | 5.43527E-07 |
| 20ug | 0.663139925 | 0.001510975 | 0.022348842 |
| 30ug | 1.244150052 | 1.81719E-10 | 8.87169E-09 |



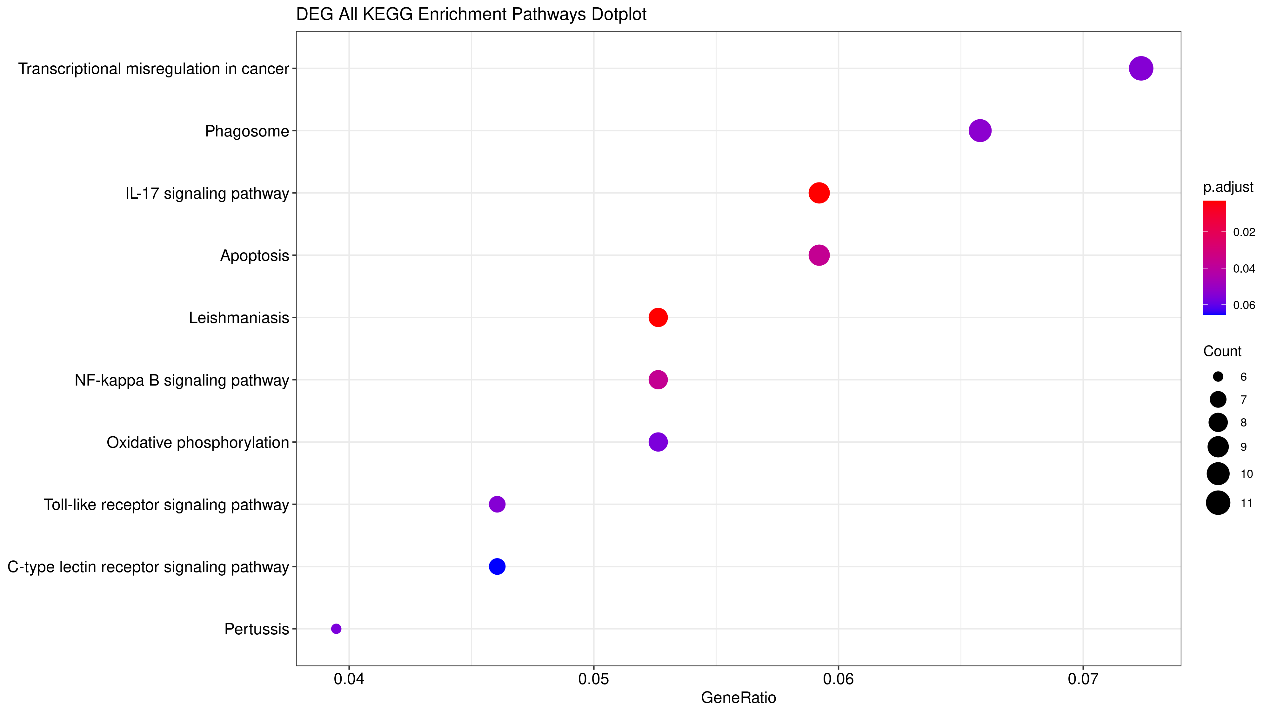
Control

30 μg

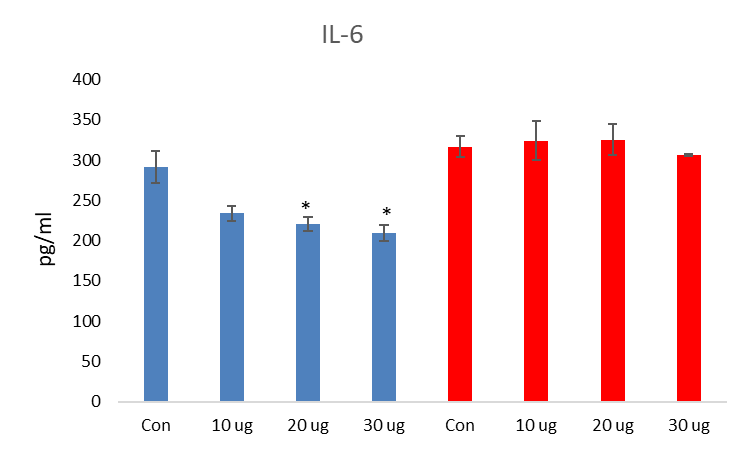
20 μg

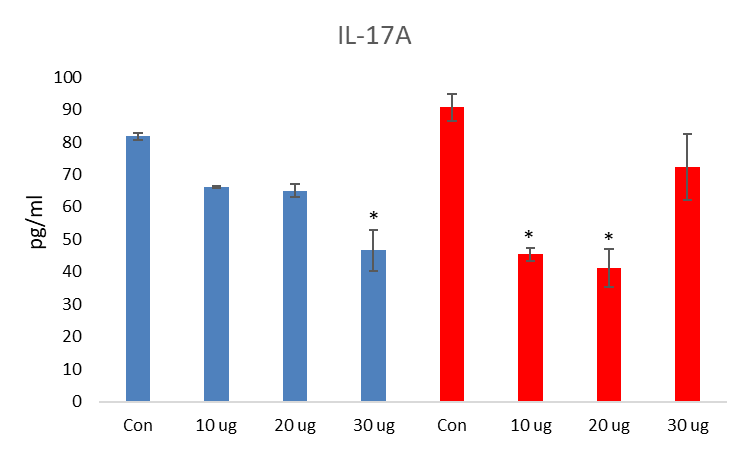
10 μg

**Figure 1. The NGS analysis of the FPKM Log Normalized Counts Sample 3D PCA**



**Figure 2. The NGS analysis of the KEGG pathway.**

**A.**

**B.**

**Figure 3. Effect of the RAW 264.7 macrophage cytokine IL-6 (A) and IL-17A (B) production**