

Appendix

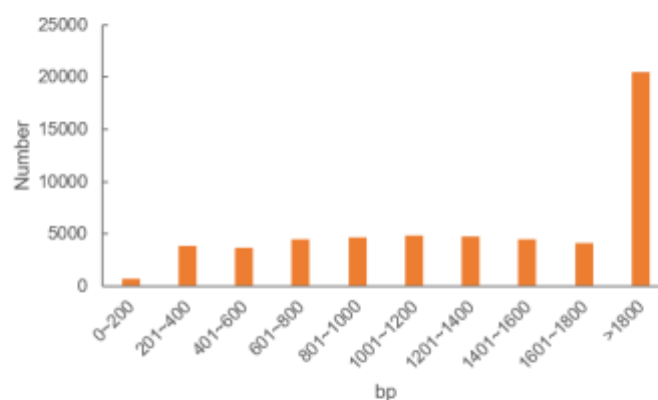
Appendix A. Summary of the sequence assembly after Illumina sequencing of sweet cherry roots inoculated (S16) and non-inoculated (CK) with dark separate strain S16.

A1. A de novo assembled blueberry seedlings transcriptome was generated. **A2.** The total transcripts generated by Trinity software. **A3.** Transcripts with significant similarity to sequences in the GO, KEGG, COG, NR, Swissprot and Pfam.

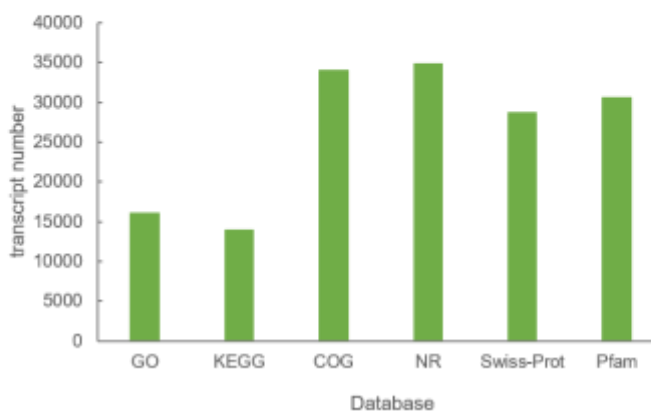
A1

Sample	Raw reads	Raw bases	Clean reads	Clean bases	Error rate(%)	Q20(%)	Q30(%)	GC content(%)
S16	46825678	7.07E+09	46158884	6.86E+09	0.0265	97.49	92.69	47.53
CK	49936760	7.54E+09	49386040	7.33E+09	0.0254	97.94	93.73	46.36

A2

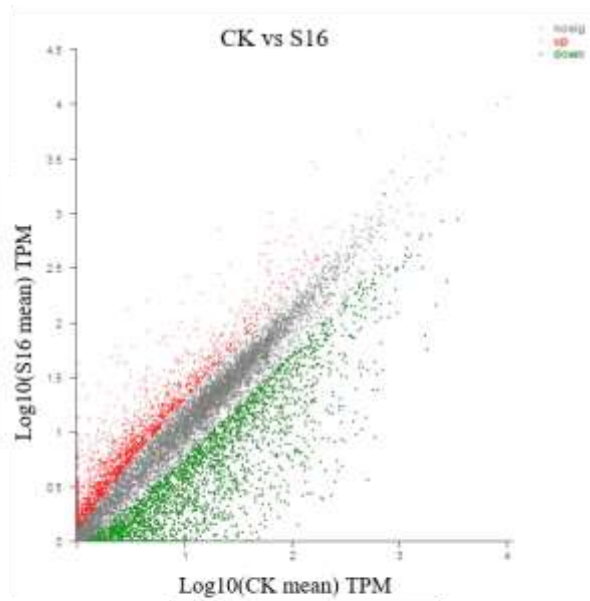


A3



Appendix B. FPKM distribution of differentially expressed genes (DEGs) from roots of sweet cherry inoculated and non-inoculated with S16. B1. The up-regulated DEGs were showed in red, while the down-regulated DEGs were in green, and genes that were not differentially expressed in grey. **B2.** The numbers of up-regulated DEGs and down-regulated DEGs.

B1



B2

