

Table S1. Sequencing data statistics

Samples	<i>Shiraia</i> sp. Slf14	<i>Shiraia</i> sp. Slf14(w)
Raw reads	4.96×10^7	4.30×10^7
Raw bases	7.49×10^9	6.49×10^9
Clean Reads	4.92×10^7	4.24×10^7
Clean bases	7.37×10^9	6.34×10^9
Error%	0.0248	0.0252
Q20	98.14	97.94
Q30	94.33	93.91
GC content%	51.21	51.83

Table S2. Quantitative Real-time PCR primer

Target gene	Primer name	Primer sequence (5'-3')
<i>GAPDH</i>	GAPDH-F	ACGAGGAGATCAAGGAG
	GAPDH-R	GATGGAAGAGCGAGTGT
<i>PKS</i>	PKS-F	GATGCGTGATGAACTGGAATTAG
	PKS-R	TTGCTTCGGACTCGGTAGG
<i>OmeF</i>	OmeF-F	GACTGGTCGGACAAGTATGC
	OmeF-R	GGCTCTGGCACAATGACTTC
<i>FAD</i>	FAD-F	TGCCGTCTGCTGGTCTTG
	FAD-R	ACACCAACGCCACCTACTC
<i>ztf</i>	ztf-F	CCTGGGCGAACTGAAAGA
	ztf-R	AGCCTGGACATTGTTGGAAG
<i>Hydro</i>	Hydro-F	TCTACACCGATGAAGACTACAATG
	Hydro-R	TCAGCCGAAGTCCAGAGAAC
<i>CAT</i>	CAT-F	CATTGCCGATGGAAGTGT
	CAT-R	TGGATACAAGGTGGACAGC
<i>NOX</i>	NOX2-F	GGGTTTCGCTTATTTGGCTGA
	NOX2-R	GCGTGAAGGGATGGTACTGC
<i>APIL</i>	APIL-F	GAATCTCCCTCCTCCTCA
	APIL-R	ACACACATAACCCTCCGT
<i>GR</i>	GR-F	TGTTGTTTTCTCCCACCCT
	GR-R	CGACGACCTTTTCTTCCTC
<i>APX</i>	APX-F	TGCCCCACTGACATGGAAAT
	APX-R	GCTGAGCGAAAGGAACACC
<i>PDH</i>	PDH-F	TTCGGCGAGAAGCGAGTGATT
	PDH-R	GTGTGTCTTTGCGGCGGAGTT
<i>MDH</i>	MDH-F	GCACCTTCTCGTCGTCT
	MDH-R	GGTAACCTCGCTCTTGG
<i>CS</i>	CS-F	ACAAGGATGGCAAGGTT
	CS-R	GTAGGGCGAGGAGAGAG
<i>HK</i>	HK-F	TGCATTTTTGGTACTGGTTG
	HK-R	GAGGACTTTGTGCTCGTTGT
<i>PFK</i>	PFK-F	AGATTACACCCCAACAGG
	PFK-R	GCATACAAATGACAGGAC

Figure S1. Volcano map of differentially expressed genes. The horizontal coordinate is the differential gene expression multiplicity between the experimental group and the control group, and the vertical coordinate is the FDR (False Discovery Rate), which is obtained by correcting for the significance of the difference p-value (p-value), with a smaller FDR indicating a larger significant difference. Each triangle and circle in the graph corresponds to a gene, with red and yellow indicating up-regulated genes, where yellow points are significant up-regulated genes with $0.01 < \text{FDR} < 0.05$, and red is highly significant up-regulated genes with $\text{FDR} < 0.01$. Dark blue and light blue indicate down-regulated genes, where light blue dots are significant down-regulated genes with $0.01 < \text{FDR} < 0.05$ and red are highly significant down-regulated genes with $\text{FDR} < 0.01$. Black dots are non-significant up- and down-regulated genes.

Figure S2. GO enrichment bubble diagram of differentially expressed genes between *Shiraia* sp. Slf14 and *Shiraia* sp. Slf14(w). X axis represents the name of GO Term; the Y axis represents the enrichment factor. * indicates significant difference $p < 0.05$, ** indicates extremely significant difference $p < 0.01$. *** indicates extremely significant difference $p < 0.001$.

Figure S3. KEGG enrichment bubble diagram of the differentially expressed gene between *Shiraia* sp. Slf14 and *Shiraia* sp. Slf14(w). X axis represents the name of KEGG Pathway; the Y axis represents the enrichment factor. * indicates significant difference $p < 0.05$, ** indicates extremely significant difference $p < 0.01$. *** indicates extremely significant difference $p < 0.001$.

Figure S1.

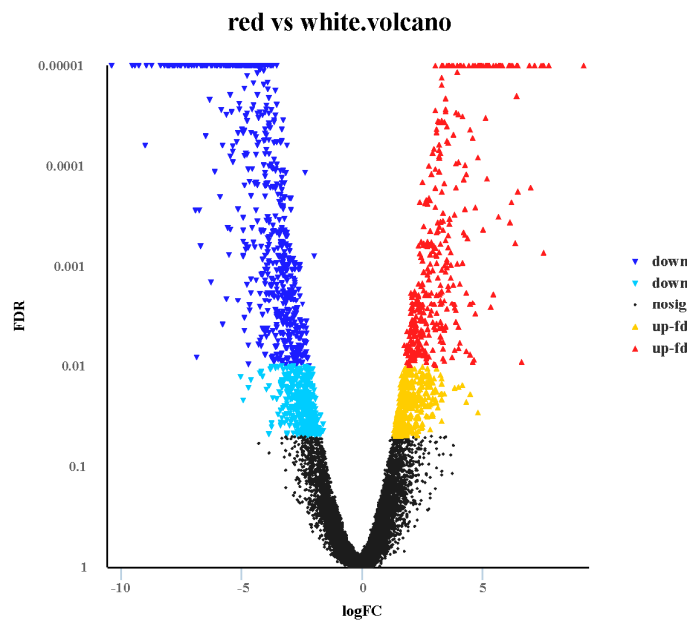


Figure S2.

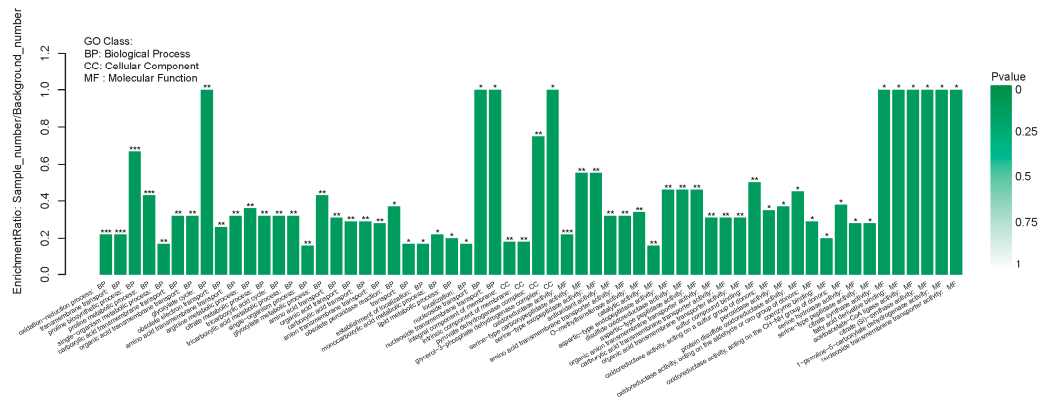


Figure S3.

