

Supplementary Materials

Table S1. Summary of primers used in this study.

Gene	Forward(5'-3')	Reverse(5'-3')
For RT-qPCR		
<i>FtHDA2</i>	ACCGGATTCTGTCGAGCAAG	TGCGTCCCATTGAGGAA
<i>FtHDA5</i>	TCCCTTCGAGTCAACATGGC	CAGAATCAGAGCTCGGGCAT
<i>FtHDA6-1</i>	TTCTCTCCCCTGTCGGGAAT	CCTGCAGAAGCCTGACAGAA
<i>FtHDA6-2</i>	TGGAGATCAACCGCCCTTTC	CGCGAATGAGAGTGATCGGA
<i>FtHDA8-1</i>	AGGCTTTCTTGACGTCCTCG	ATTCGGAGAGTGAAGCTGGC
<i>FtHDA8-2</i>	TGGCGGAAAGGAACTGTGTT	GTATGTGCTTCATGGCTGCG
<i>FtHDA9</i>	GAGAACCTGACAAACGCCT	AGCGTCGTCCATGTTGTGAT
<i>FtHDA14</i>	ATGCAGCGTCTTTTGTGCTG	ATGACCAGAGGCAGGAGCTA
<i>FtHDA19</i>	GTTCACTCGGGGATCTGTG	CACGTACAAGACTCGCCCAT
<i>FtSRT1</i>	AAGGACAGATTGCGGGACAG	AAGCTTCCCGCCATTACGAA
<i>FtSRT2</i>	ATGATGCAACGGTCTACGCA	AACGCTTACCGGTTGTTCTT
<i>FtHDT1</i>	TGACTGGAAACATGGGAGCG	GCTTTTGTTCAGCTACCCC
<i>FtHDT2</i>	GAGCCAAGTAGTCCACCTTTCAC	CAGACAGAATCCCAATCACCAAT
<i>FtHDT3</i>	TCATGTGGCAACCCATACC	CAAGAGCTGCAGGTAACGGA
<i>FtH3</i>	GAAATTCGCAAGTACCAGAAGAG	CCAACAAGGTATGCCTCAGC
<i>FtACTIN7</i>	CCGCCACTCAACACAATGTTATTAT	GAGTTATGAGCTTCTGATGGACAA

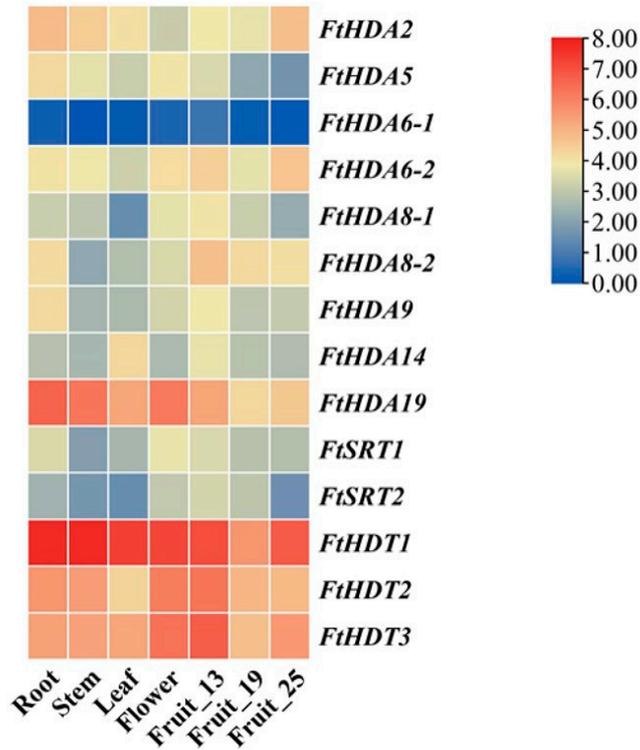


Figure S1. Expression patterns of 14 HDAC genes in diverse tissues of *F. tataricum*. RNA-seq data were downloaded from Tartary Buckwheat Database using gene IDs of 14 FtHDACs. The RPKM (Reads Per Kilobase of exon model per Million mapped reads) values were transformed to \log_2 (value + 1) and used for heatmap. The expression in diverse *F. tataricum* tissues was demonstrated, including root, stem, leaf, flower, fruit_13, fruit_19 and fruit_25.

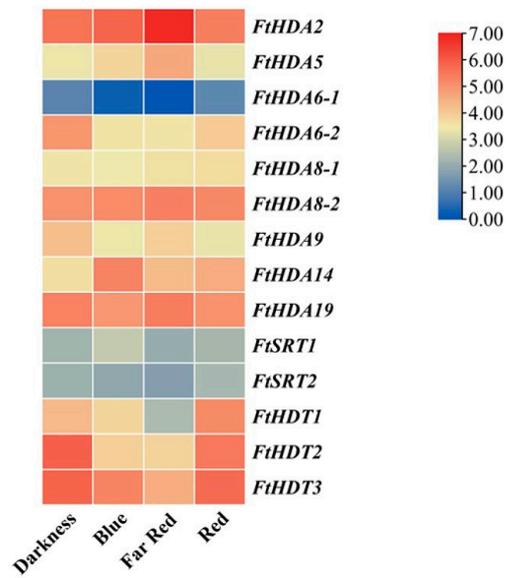


Figure S2. Expression profiles of 14 *FtHDAC* genes under different light wavelengths. The transcript profiles of *FtHDAC* genes in seedlings of *F. tataricum* under different light wavelengths (red light (670 nm), blue light (470 nm), and far-red light (735 nm)) were extracted from Zhang et al.[37]. The RPKM (Reads Per Kilobase of exon model per Million mapped reads) values were transformed to $\log_2(\text{value} + 1)$ and used for heatmap.

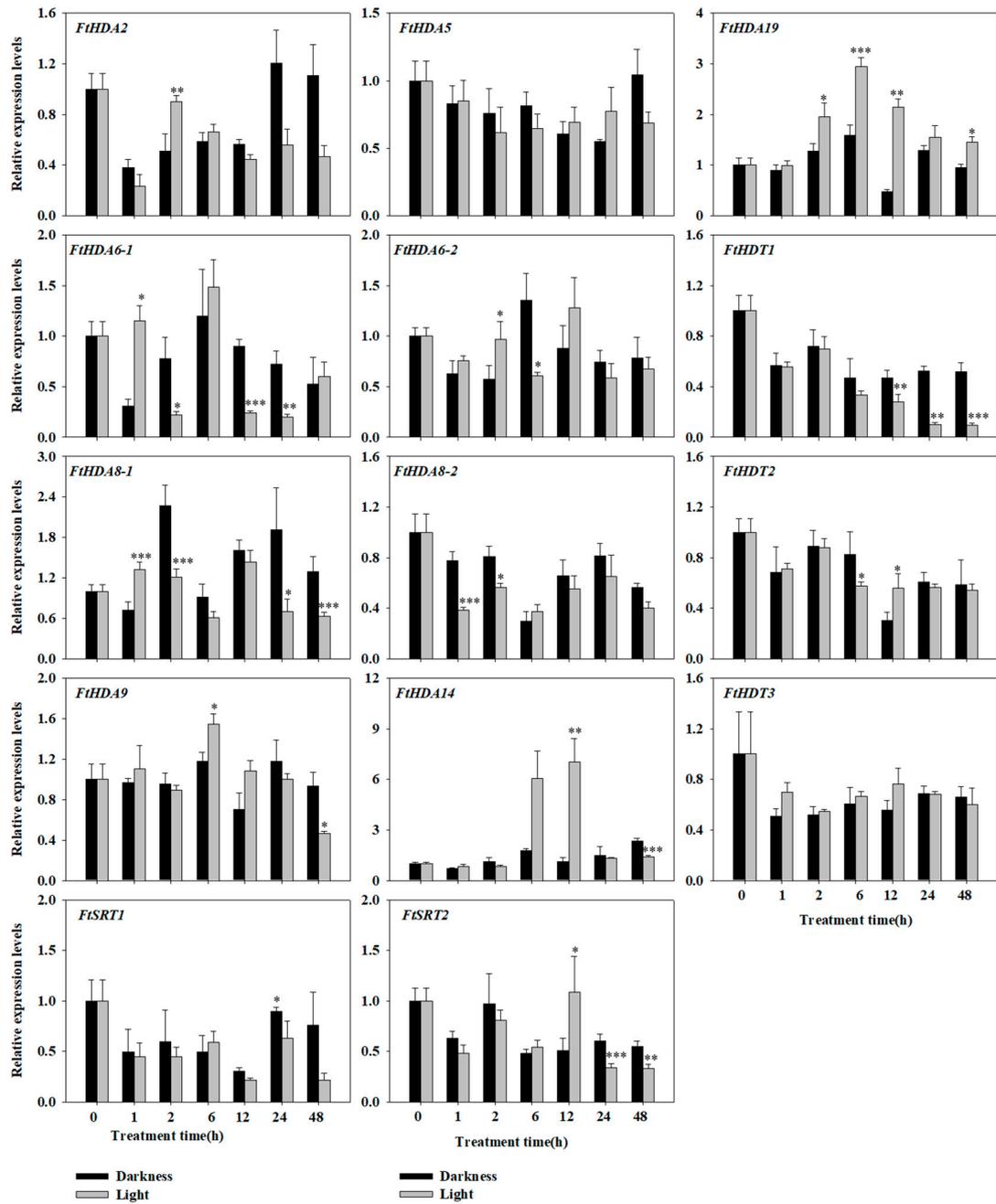


Figure S3. Expression profiles of 14 *FtHDAC* genes in response to light. *FtACTIN7* was used as reference gene. Expression levels of each gene were expressed as a ratio relative to that of untreated seedlings (Darkness 0 h), which was set as 1. Each data point represents a mean \pm standard error ($n=3$). Asterisks above the bars indicate significant differences ($p < 0.05$) among the treatments.