

## Supplementary Materials

Table S1. Summary of primers used in this study.

Gene	Forward(5'-3')	Reverse(5'-3')
<b>For RT-qPCR</b>		
<i>FiHDA2</i>	ACCGGATTCTGTCGAGCAAG	TGCGTCCCCATTTTGAGGAA
<i>FiHDA5</i>	TCCCTTCGAGTCAACATGGC	CAGAATCAGAGCTCGGGCAT
<i>FiHDA6-1</i>	TTCTCTCCCCTGTCGGGAAT	CCTGCAGAAGCCTGACAGAA
<i>FiHDA6-2</i>	TGGAGATCAACCGCCCTTTC	CGCGAATGAGAGTGATCGGA
<i>FiHDA8-1</i>	AGGCTTTCTTGACGTCCTCG	ATTCGGAGAGTGAAGCTGGC
<i>FiHDA8-2</i>	TGGCGGAAAGGAACTGTGTT	GTATGTGCTTCATGGCTGCG
<i>FiHDA9</i>	GAGAACCTGACAAACGCCT	AGCGTCGTCCATGTTGTGAT
<i>FiHDA14</i>	ATGCAGCGTCTTTTGTGCTG	ATGACCAGAGGCAGGAGCTA
<i>FiHDA19</i>	GTTCACTCGGGGGATCTGTG	CACGTACAAGACTCGCCCAT
<i>FiSRT1</i>	AAGGACAGATTGCGGGACAG	AAGCTTCCCGCCATTACGAA
<i>FiSRT2</i>	ATGATGCAACGGTCTACGCA	AACGCTTACCGGTTGTTCTT
<i>FiHDT1</i>	TGACTGGAACATGGGAGCG	GCTTTTGTTCAGCTACCCC
<i>FiHDT2</i>	GAGCCAAGTAGTCCACCTTTCAC	CAGACAGAATCCCAATCACCAAT
<i>FiHDT3</i>	TCATGTGGCAACCCCATACC	CAAGAGCTGCAGGTAACGGA
<i>FiH3</i>	GAAATTCGCAAGTACCAGAAGAG	CCAACAAGGTATGCCTCAGC
<i>FiACTIN7</i>	CCGCCACTCAACACAATGTTATTAT	GAGTTATGAGCTTCCTGATGGACAA

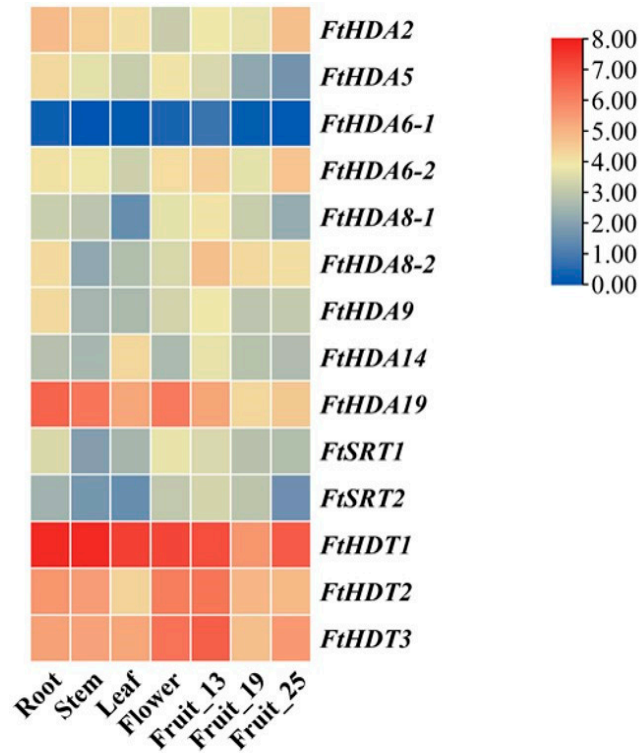


Figure S1. Expression patterns of 14 HDAC genes in diverse tissues of *F. tataricum*. RNA-seq data were downloaded from Tartary Buckwheat Database using gene IDs of 14 FtHDACs. The RPKM (Reads Per Kilobase of exon model per Million mapped reads) values were transformed to  $\log_2$  (value + 1) and used for heatmap. The expression in diverse *F. tataricum* tissues was demonstrated, including root, stem, leaf, flower, fruit\_13, fruit\_19 and fruit\_25.

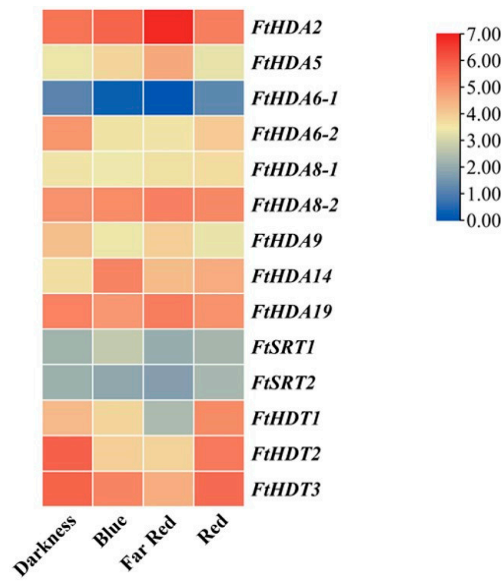


Figure S2. Expression profiles of 14 *FtHDAC* genes under different light wavelengths. The transcript profiles of *FtHDAC* genes in seedlings of *F. tataricum* under different light wavelengths (red light (670 nm), blue light (470 nm), and far-red light (735 nm)) were extracted from Zhang et al.[37]. 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.

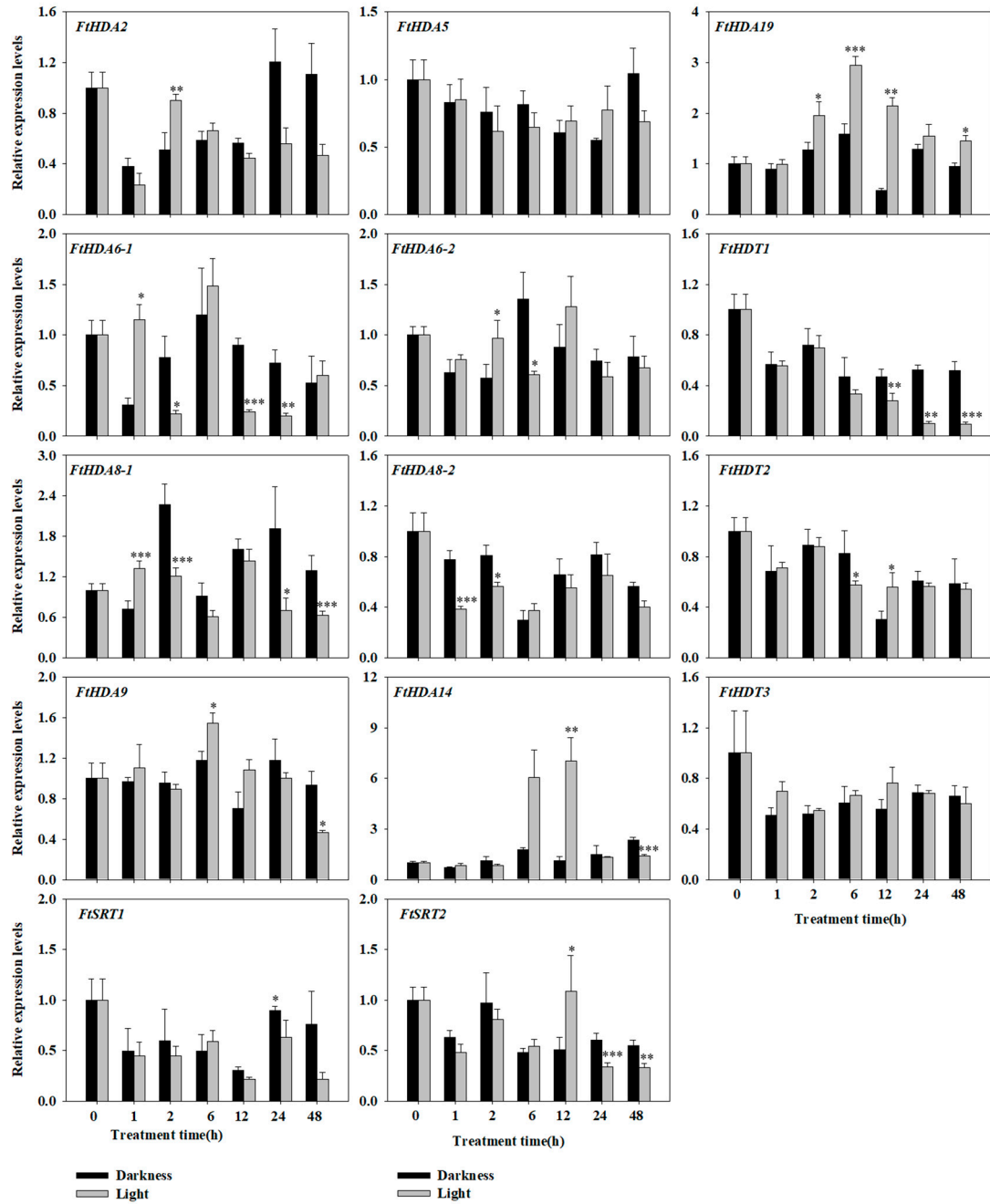


Figure S3. Expression profiles of 14 *FtHDAC* genes in response to light. *FtACTIN7* was used as reference gene. Expression levels of each gene were expressed as a ratio relative to that of untreated seedlings (Darkness 0 h), which was set as 1. Each data point represents a mean  $\pm$  standard error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