|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Treatment T1** | **Treatment T2** | **Treatment T3** |
| **Repl\_1** | **Repl\_2** | **Repl\_3** | **Repl\_1** | **Repl\_2** | **Repl\_3** | **Repl\_1** | **Repl\_2** | **Repl\_3** |
| CcRNM1 | 1081.0  | 1003.0  | 810.0  | 810.0  | 1007.0  | 866.0  | 1103.0  | 860.0  | 1146.0  |
| CcSPAC6B12.04c | 594.0  | 623.0  | 410.0  | 423.0  | 526.0  | 498.0  | 604.0  | 478.0  | 539.0  |
| CcHpcob | 2730.0  | 3197.0  | 3151.0  | 2051.0  | 3236.0  | 3359.0  | 3613.0  | 2800.0  | 2850.0  |
| Ccnew1 | 274.0  | 230.0  | 157.0  | 209.0  | 253.0  | 222.0  | 312.0  | 247.0  | 311.0  |
| CcHplo | 1356.0  | 1252.0  | 841.0  | 961.0  | 1230.0  | 1083.0  | 1228.0  | 1001.0  | 1210.0  |
| CcfaeB-2 | 64.0  | 77.0  | 38.0  | 49.0  | 64.0  | 46.0  | 56.0  | 42.0  | 77.0  |
| CcWDR83 | 279.0  | 273.0  | 230.0  | 217.0  | 280.2  | 209.0  | 249.0  | 177.0  | 301.0  |
| Cchp11 | 190.0  | 208.0  | 127.0  | 114.0  | 174.0  | 185.0  | 195.0  | 168.0  | 157.0  |
| CcRNF5 | 528.0  | 568.0  | 451.0  | 394.0  | 565.0  | 422.0  | 540.0  | 452.0  | 525.0  |
| CcYER010C | 68.0  | 69.0  | 56.0  | 23.0  | 90.0  | 83.0  | 73.0  | 62.0  | 61.0  |
| CcUP18 | 20.0  | 32.0  | 34.0  | 25.0  | 33.0  | 22.0  | 38.0  | 18.0  | 32.0  |

**Table S1.** The counts of candidate reference genes in *C. camelliae* during interaction with hosts at different time points observed by the RNA sequence.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Reference** **gene** | **Total amino acid** | **MW （kDa）** | **PI** | **Homologous** **Specie** | **Colletotrichum Ortholog** | **Similarity****(%)** |
| CcUP18 | 217 | 26.3 | 11.0 | *C.fructicola* Nara gc5 | ELA35911  | 89.5 |
| CcSPAC6B12.04c | 452 | 50.4 | 6.2 | *C.fructicola* Nara gc5 | ELA24928 | 98.9 |
| CcRNM1 | 194 | 21.6 | 4.3 | *C.gloeosporioides* Cg-14 | EQB58236  | 98.97 |
| CcHpcob | 876 | 100.5 | 5.9 | *C.gloeosporioides* Cg-14 | EQB50494  | 98.4 |
| Ccnew1 | 78 | 8.6 | 10.4 | *C.gloeosporioides* Cg-14 | EQB44976 | 98.7 |
| CcHplo | 404 | 44.8 | 6.9 | *C.gloeosporioides* Cg-14 | EQB45128  | 92.2 |
| CcfaeB-2 | 559 | 60.5 | 4.7 | *C.gloeosporioides* Cg-14 | EQB48532  | 95.0 |
| CcWDR83 | 361 | 38.6 | 7.6 | *C.gloeosporioides* Cg-14 | EQB49172  | 97.0 |
| Cchp11 | 572 | 64.3 | 5.4 | *C.gloeosporioides* Cg-14 | EQB55695 | 96.9 |
| CcRNF5 | 405 | 43.3 | 4.7 | *C.gloeosporioides* Cg-14 | EQB48134  | 82.3 |
| CcYER010C | 218 | 23.6 | 7.2 | *C.gloeosporioides* Cg-14 | EQB57386 | 98.6 |

**Table S2.** Bioinformatics analysis of the candidate reference genes.

A.



B.

C.

D.



F.



G.



H.



I.



J.



K.

**Figure S1.** The alignment of candidate reference genes encoding proteins with their orthologous proteins analyzed by DNAMAN. A-K, The alignment of CcRNM1, CcSPAC6B12.04c, CcHpcob, Ccnew1, CcHplo, CcfaeB-2, CcWDR83, Cchp11, CcRNF5, CcYER010C, and CcUP18 with the orthologous protein, respectively.