**Table S1 Single Sequence Repeat (SSR) linkage markers used in this study**

| Linkage Marker | *vic* | Forward primer | Reverse primer | Scaffold map positions* |
|---|---|---|---|---|
| CpSI002 | *vic2* | TTGGATAGACCCAGGTGTCC | GAGGTCTTCGAGGGCGTAG | 7:1522713-1523193 |
| Co16_1800 | *vic2* | TGGCGGGATATGAAATAT | TGTTGGAGCGCCTTGCGGA | 7:1762655-1763779 |
| CpSI116 | *vic4* | TGTCAAAGTTGACCACCACC | ATCAGCGTGTCCATACCACA | 4:345343-345591 |
| CPG3 | *vic4* | CGTAAGGCAGAGGCAGAGAC | TCCCTATGCCCAAGACACTC | 4:1897980-1898174 |
| CpSI135 | *vic6* | TACTCTTCGTGTCCCTTCGG | GGCAGAACAGTGACCGAAAT | 3:5015099-5015384 |
| CpSI136 | *vic6* | AAGCTGTACAGTCAACGCGA | ACCTGGAATGGAGACACAGG | 3:5033364-5033641 |
| CpSI006 | *vic7* | ATGTCGAGTTTACCCGATGG | GAGATGTGTGGAATGCAACG | 6:2553319-2553459 |

* The map positions define the fragment containing the SSR region that would be amplified from *C. parasitica* genomic DNA. (Kubisiak T. L., C. Dutech and M. G. Milgroom, 2007 Fifty-three polymorphic microsatellite loci in the chestnut blight fungus, *Cryphonectria parasitica*. Mol. Ecol. Notes **7**: 428-432)