**Discovery of three loci increasing resistance to charcoal rot caused by *Macrophomina* *phaseolina* in octoploid strawberry**

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**Raw genotype/marker information**

**Data File S1**: This file has information for discovery population 16-17. There are 3 sheets in this workbook. First worksheet, “SNP data”, contains SNP data; second worksheet called “Pedigree and Phenotypic data”, contains pedigree structure of the experimental population and associated phenotypic data of seedlings; and the third worksheet has the genetic map used for QTL analysis.

**Data File S2**: This file has information for discovery population 17-18. There are 3 sheets in this workbook. First worksheet, “SNP data”, contains SNP data; second worksheet called “Pedigree and Phenotypic data”, contains pedigree structure of the experimental population and associated phenotypic data of seedlings; and the third worksheet has the genetic map used for QTL analysis.

**Data File S3**: This file has genotypic and phenotypic data used for GWAS analysis. There are 3 sheets in this workbook. First worksheet, “SNP data” has SNP data; second worksheet has associated phenotypic data; and the third worksheet has the physical map used for GWAS.

**Data File S4**: This file has genotypic and phenotypic data used for the validation population 2017-18. There are two worksheets in this workbook. First worksheet, “SNP data” has genotypic data and second worksheet has associated phenotypic data. **Note**: QTL analysis was not performed for the validation populations but only SNP associated with QTL were used for quantitative analysis. Table 4 holds information on SNPs highly associated with the two QTL.

**Data File S5**: This file has genotypic and phenotypic data used for the validation population 2018-19. There are two worksheets in this workbook. First worksheet, “SNP data” has genotypic data and second worksheet has associated phenotypic data. **Note**: QTL analysis was not performed for the validation populations but only SNP associated with QTL were used for quantitative analysis. Table 4 holds information on SNPs highly associated with the two QTL.