# **List of Additional Files (file name).** Brief description.

# **Supplemental Table S1 (Supplemental Table S1.docx)**. Summary of raw and length-filtered MinION data used for assembly of taro contigs. Sequencing data were obtained from n=14 MinIONs cells. Each group represents a single cell, or data from a cell that stopped prematurely (n = 3). A total of 12,302,477 reads were generated to produce 63,657,010,728 nucleotides of sequence data. Of those, 6,501,305 were filtered for short length (< 3,500 nt) and 43 for long length (> 150 Kb). The remaining 5,801,129 sequences produced 54,118,492,459 nucleotides of data used for the nanopore genome assembly (~23x coverage @ 1C).

**Supplemental Figure 1 (Figure\_S1.pdf)**. Initial Genetic Linkage map based on 558 SNP markers and 84 individuals of the ‘1025’ mapping population (LOD = 5.97 and maximum recombination frequency = 0.3). Groups 17 and onwards showed a heavy reduction in the number of markers.

**Supplemental Figure 2 (Figure\_S2.pdf)**. Location of QTLs for TLB resistance in various linkage groups. (A) The color red is used to indicate QTLs for isolate S1 and (B) yellow is used to indicate QTLs for S3 isolate.

# **Supplemental Appendix 1 (Supplemental\_Appendix 1.docx).** For the “merged” taro genome assembly, a list of contigs and start and end positions of motifs characteristic of plant disease resistance genes belonging to the nucleotide-binding site leucine-rich repeat gene family. The motifs are based on Jupe et al. 2012 (see text for details).

# **Supplemental Appendix 2 (Supplemental\_Appendix2.docx).** List of linkage groups, marker positions and confidence scores, and locations of QTLs significant for resistance to taro leaf blight.

**10x Genomics linked-read assembly (taro\_10xGenomics.fasta.gz).** A taro genome assembled from linked-read sequences prepared using the 10x Genomics (Pleasanton, California) microfluidic gel bead partitioning Chromium system and sequenced on two lanes of an Illumina HiSeq X short-read platform.

**Taro contigs assembled from Oxford Nanopore Technology MinIon long reads. (Taro\_nanopore\_assembled\_contigs.fasta.gz).**

**“Merged” taro genome assembly (Taro.merged\_for\_aln\_shortcontigID.fasta.gz).** The linked-read taro genome assembly was and gap-filled and scaffolded with contigs assembled from Oxford Nanopore Technology MinIon long reads.

**VCF file used for linkage mapping and QTL analysis, based on the merged genome reference (taro\_imputed\_loci\_vcf.txt.vcf)**

**Phenotypic data for the ‘1025’ mapping population (Phenotypic data for the ‘1025’ mapping population.xls)**

**R script for linkage group formation (R\_script\_onemap.R)**

**Taro *de novo* repeat library from RepeatModeler (consensi.fa.classified.gz)**