Fig. S2 Genome-wide comparison of pathogenic Lam and nonpathogenic Leu.
A). Genome alignment of *C.* Liberibacter americanus (Lam, isolate Sao Paolo) and
nonpathogenic *C.* Liberibacter europeaus (Leu, isolate ASNZ1). Linear chromosomal
maps were build using AliTV visualization software, based on whole-genome
alignments with Lastz aligner. Both panels depict pair-wise comparisons, expressed
as percentage of nucleotide similarity, that connect different homologous genomic
regions. Genomes are pictured in blue. Lam is a completely finished genome while
Leu is not (note breaks in the blue genome depiction). **B).** The presence of different
putative virulence genes in *C.* Liberibacter species. LPS = Lipopolysaccharide, SDE =
Sec-dependent effectors, SEC = Sec Translocon, Type I= Type I secretion system.