Due to the lengthy comments, I have also attached my comments in PDF form.

The two reviewers have provided some very insightful comments that I ask you to address. In general, the reviewers' suggestions are centered on three main themes:
1) data that reveal insights into the proposed polar nature of the insertion mutants, e.g. qRT-PCR of neighboring genes, and data showing the complementing clone was sufficiently expressed, e.g., qRT-PCR or western of a tagged protein.
2) significant improvements in data presentation/analysis and greater transparency in experimental design (conclusions should recognize limitations of the experiments). In particular, I agree with the reviewers that it is difficult to draw conclusions regarding in planta behavior in the absence of key information. Please also recognize that there is a potential for the temperature (and perhaps fluctuations, in environments that are not as controlled as a growth chamber) in which plants were grown and inoculated, to have affected the phenotypes (and their less than optimal repeatibility) of the various bacterial mutants.
3) Improve the stated justification of the work. The justification for the described work is framed around the enrichment of SNPs in MCPs of T1 strains and the potential that chemotaxis may have contributed to the expansion of the T1 lineage. One of the reviewers asked about evidence regarding selection. Moreover, counterintuitively, the manuscript focuses primarily on DC3000 (with T1 playing second fiddle in supplementary data), a lineage that T1 replaced. In addition to addressing the reviewer's comment, I suggest the justification be reworded to better reflect the focus of the work. It may also behoove the authors to consider how similarities/differences in phenotypes of DC3000 and T1 mutants address the hypothesis that polymorphisms in chemotaxis-associated genes are associated with the success of T1 in tomato.

I also noticed that a data point for the wild type strain is missing in agar concentration 0.9% in figure 4.