

The biotroph *Agrobacterium tumefaciens* thrives in tumors by exploiting a wide spectrum of plant host metabolites

Subtitle: Plant host exploitation by the *Agrobacterium* biotroph

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Supplementary files:

- **Figure S1. The *A. tumefaciens* C58 essential genes identified in the Tn5 and *Himar1* transposon libraries.**
- **Figure S2. Classification of essential genes by COG categories.**
- **Figure S3. RT-qPCR and transcriptome comparative gene expression.**
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- **Table S1. Primer list.**
- **Table S2. Plant metabolomics.**
- **Table S3. Tn-seq data.**
- **Table S4. Transcriptomics.**

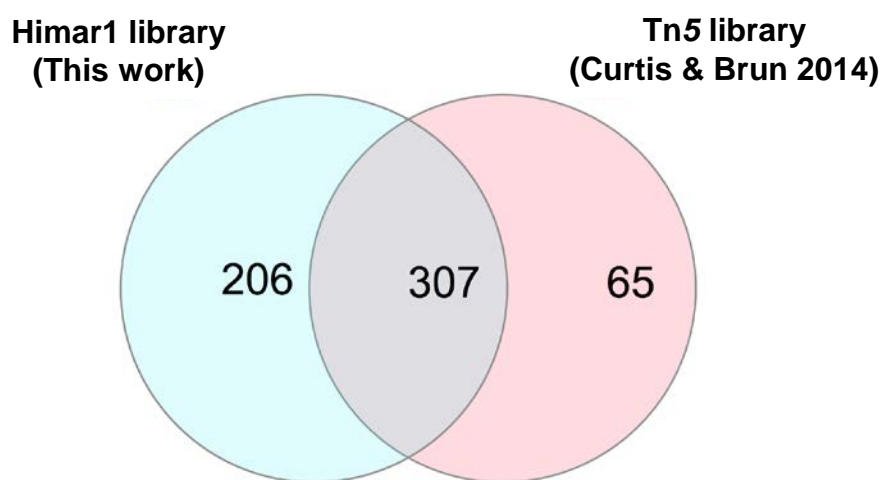


Figure S1. The *A. tumefaciens* C58 essential genes identified in the Tn5 and *Himar1* transposon libraries.

The Venn diagram shows the essential genes obtained by the Tn5 library (Curtis & Brun, 2014) and the Himar1 transposon library (this work). The complete list of the genes is available in Table S3.

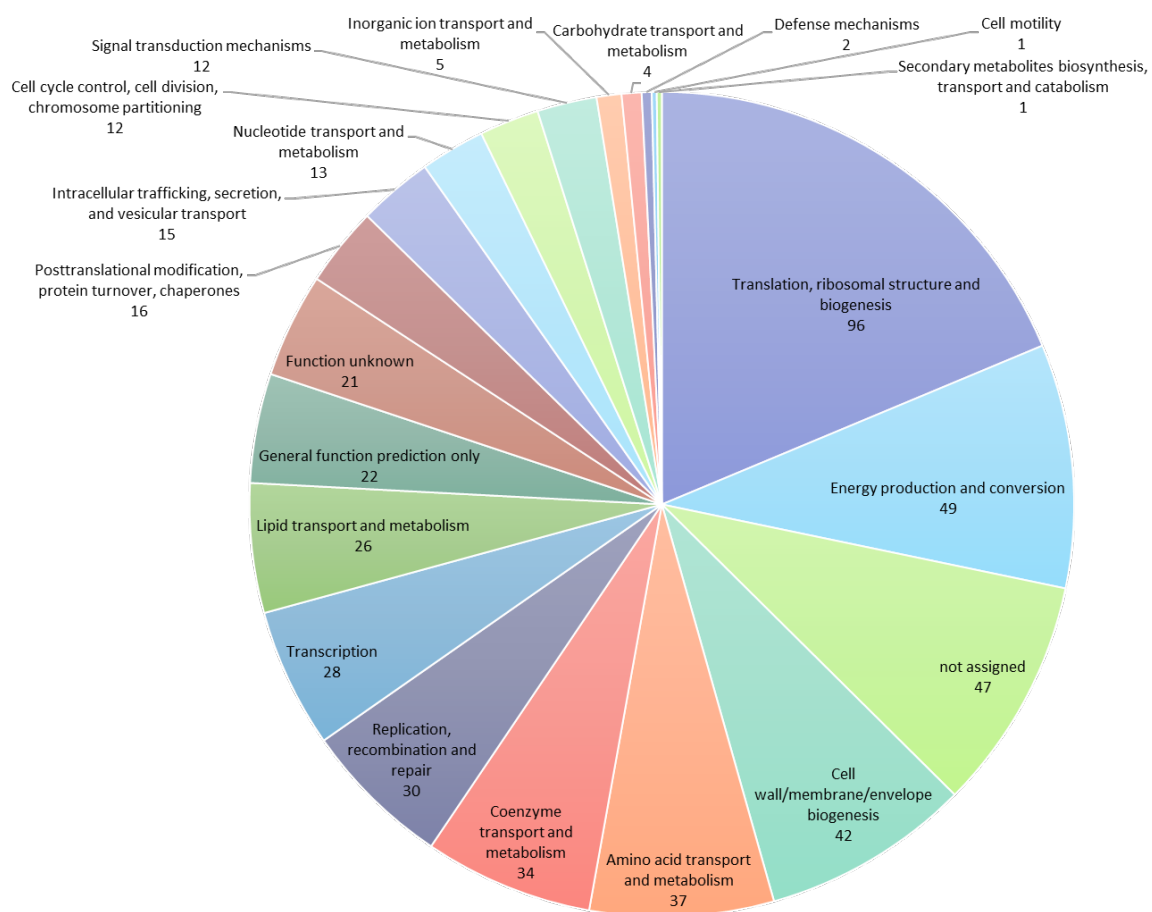


Figure S2. Classification of essential genes by COG categories.

Each number correspond to the total of essential genes of each category in *A. tumefaciens* C58 genome.

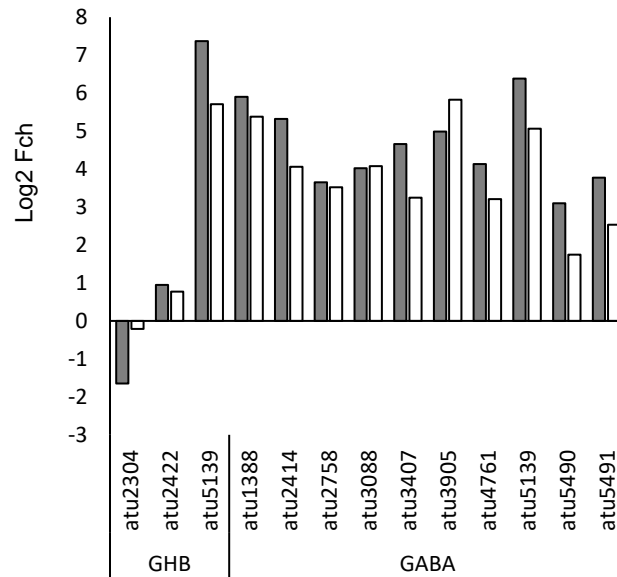


Figure S3. RT-qPCR and transcriptome comparative gene expression.

Comparison of the expression fold change (Log2 Fch) in *A. tumefaciens* C58 cells in GHB-NH₄ vs sucrose-NH₄ and sucrose-GABA vs sucrose-NH₄ growth conditions using quantitative RT-PCR (RT-qPCR in grey) or RNAseq technique (transcriptome in white).

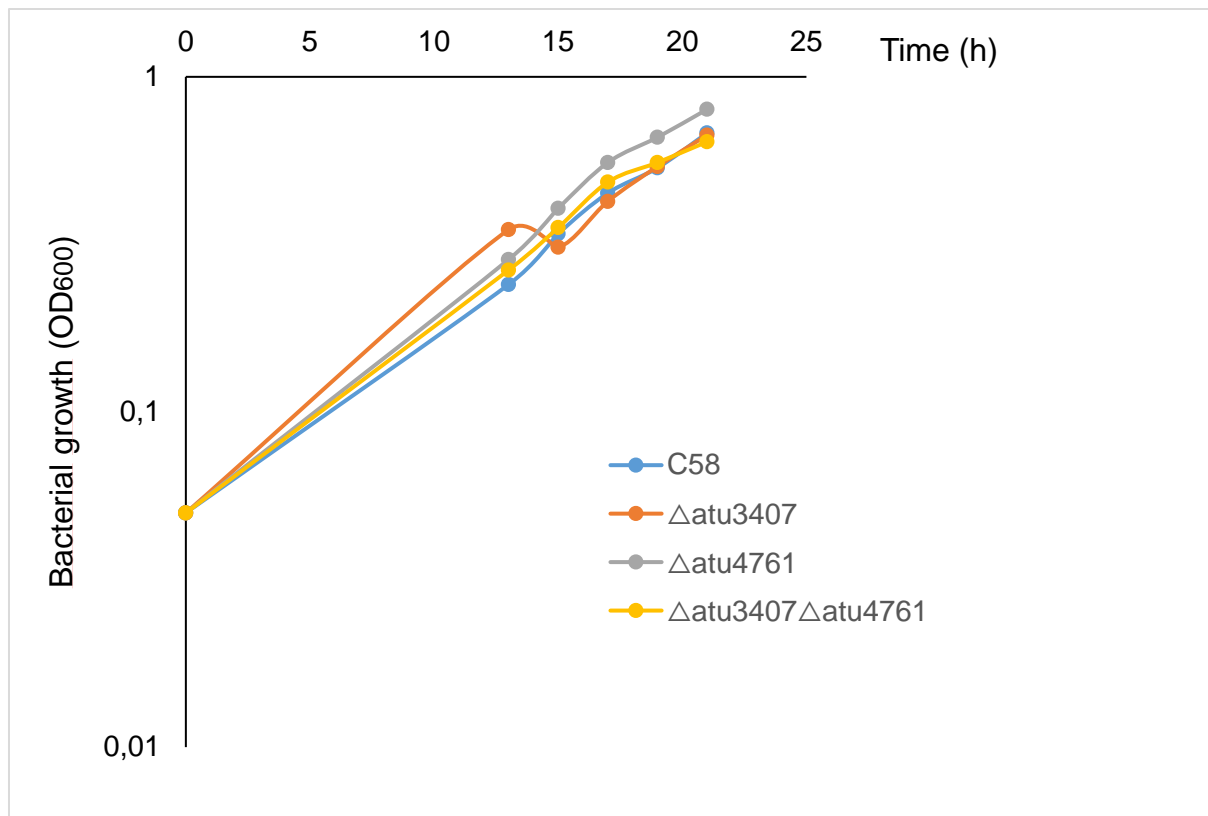


Figure S4. Growth on GABA as a sole nitrogen source.

Growth of the *A. tumefaciens* C58 wild-type and its derivatives (the single KO-mutants Δ atu3407 and Δ atu4761 and the Δ atu3407 Δ atu4761 double KO-mutant) were similar in AB medium supplemented with sucrose and GABA.