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Soil microbial composition and abundance influence the growth of *Lotus japonicus*

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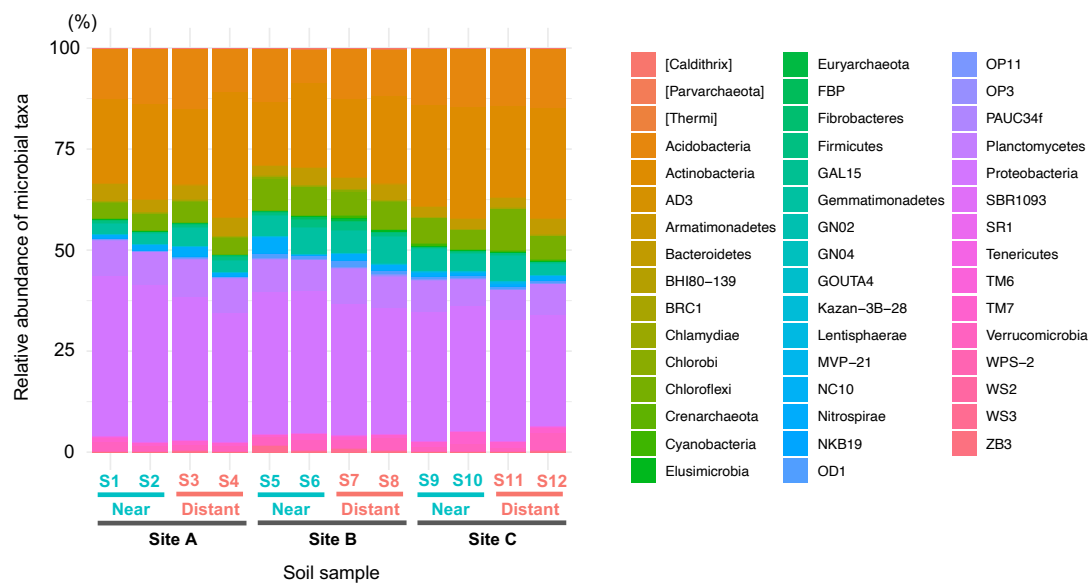
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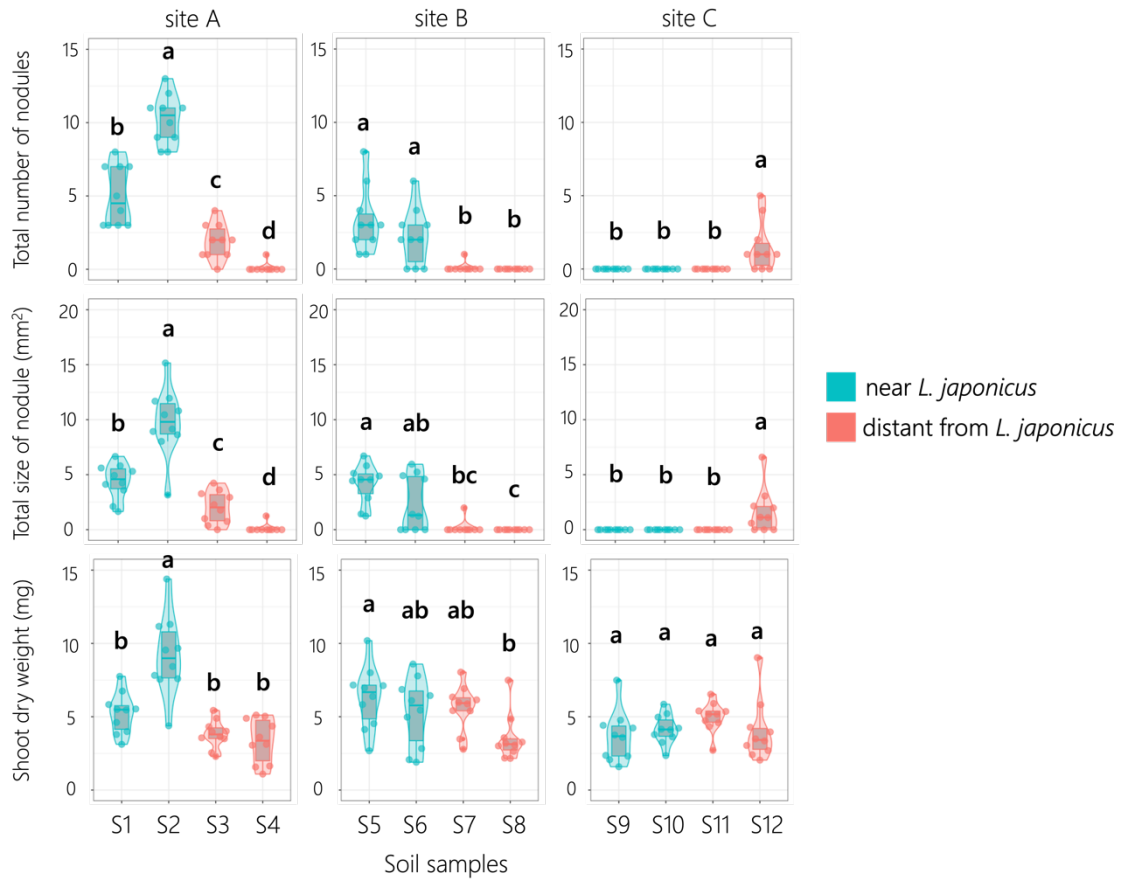
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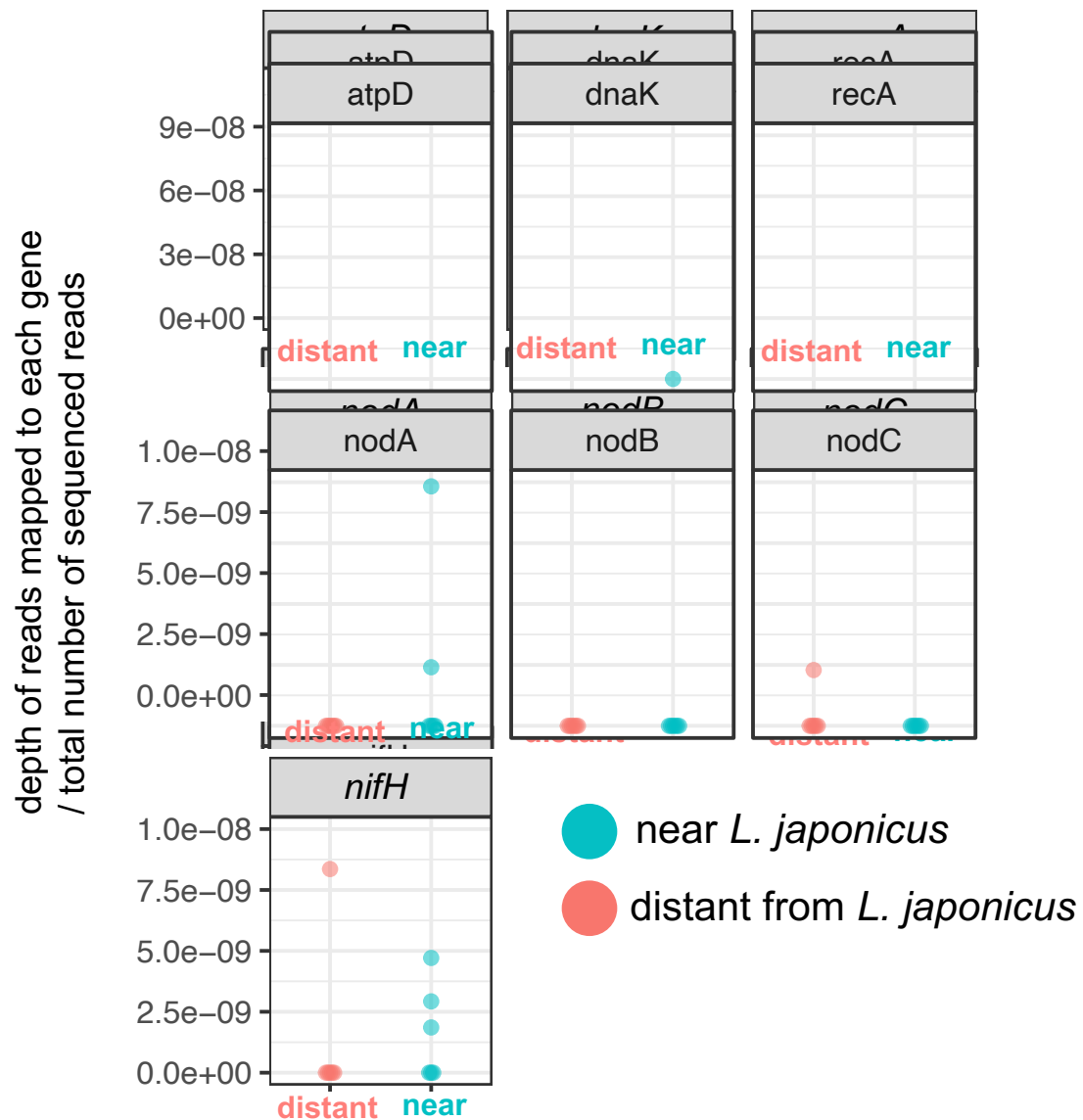
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Supplementary Fig. 1 Phylum-level classification and relative abundance of soil microbiota based on 16S rRNA amplicon sequencing analysis. Phylum names enclosed in brackets indicate unconfirmed taxonomic groupings. The color of soil sample names indicates the local presence of *L. japonicus* in sampling sites (cyan: near *L. japonicus*, pink: distant from *L. japonicus*).



Supplementary Fig. 2 Total number of nodules, total size of nodules, and shoot dry weight of *L. japonicus* seedlings inoculated with different soil-extracted microbiota. The color indicates the local presence of *L. japonicus* in sampling sites (cyan: near *L. japonicus*, pink: distant from *L. japonicus*). Different letters indicate the significant difference (Steel–Dwass test, $p < 0.05$) among inoculated soil-extracted microbiota within each soil sampling site.



Supplementary Fig. 3 The depth of short reads mapped to the housekeeping genes (*atpD*, *dnaK*, *recA*), *nod* genes (*nodA*, *nodB*, *nodC*) and *nifH* relative to the total number of sequenced short reads calculated for each soil sample. The color of the dots indicates the local presence of *L. japonicus* in sampling sites (cyan: near *L. japonicus*, pink: distant from *L. japonicus*). The y-axis scales differ between the housekeeping genes and the symbiosis-related genes.