Fig. S1. Phylogenetic analysis of the 26 *Microbacterium* strains isolated from the rhizosphere and endosphere of sugar beet seedlings (green circle) and type strains (black circle). Neighbor-joining phylogenetic tree was constructed with MEGA6 using the 16S rRNA gene sequences. *Microbacterium* strains used in this study for functional analyses are highlighted with filled green circles.
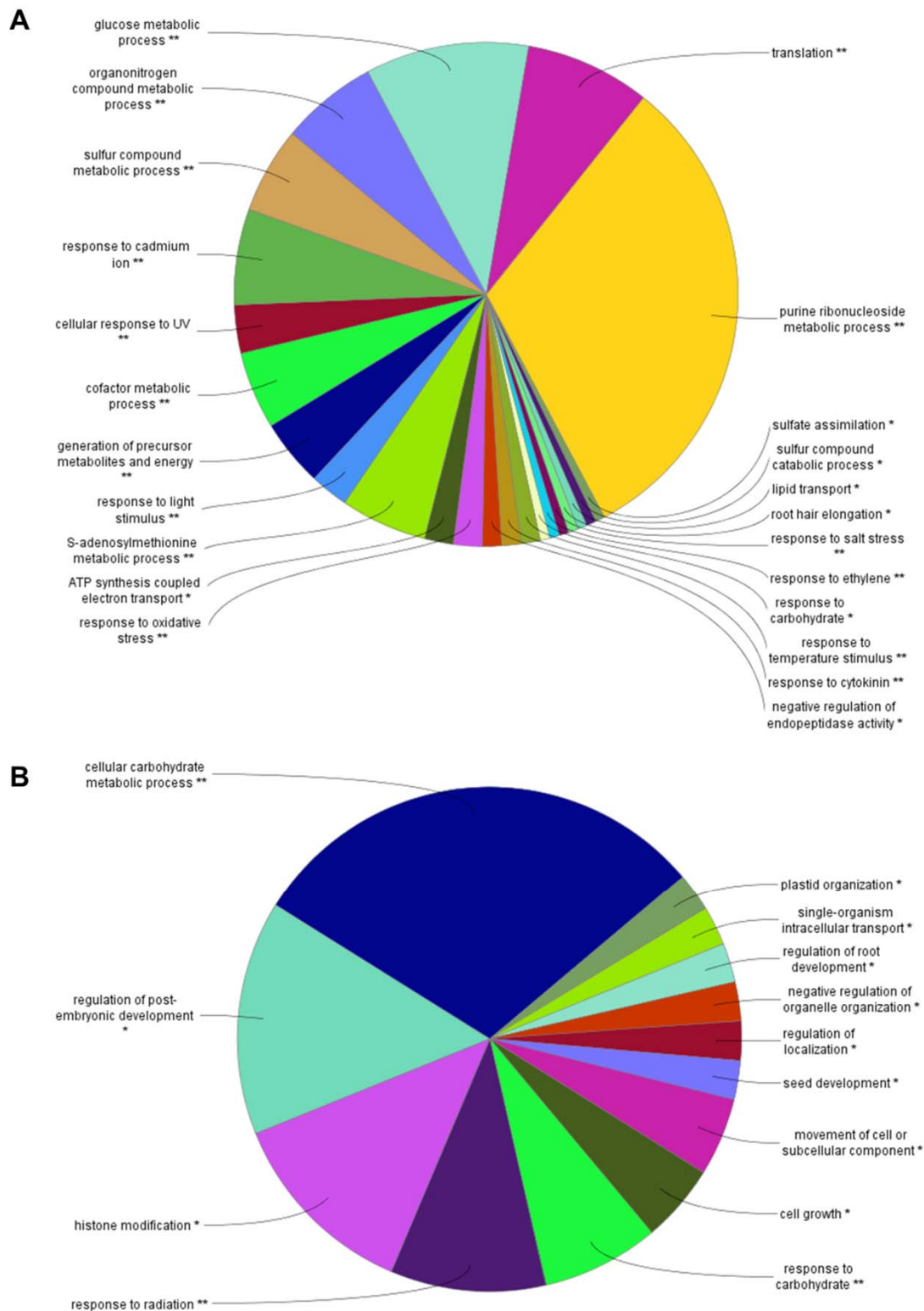
A

glucose metabolic process **

organonitrogen compound metabolic process **

sulfur compound metabolic process **

response to cadmium ion **

cellular response to UV **

cofactor metabolic process **

generation of precursor metabolites and energy **

response to light stimulus **

S-adenosylmethionine metabolic process **

ATP synthesis coupled electron transport *

response to oxidative stress **

translation **

purine ribonucleoside metabolic process **

sulfate assimilation *

sulfur compound catabolic process *

lipid transport *

root hair elongation *

response to salt stress **

response to ethylene **

response to carbohydrate *

response to temperature stimulus **

response to cytokinin **

negative regulation of endopeptidase activity *

B

cellular carbohydrate metabolic process **

regulation of post-embryonic development *

histone modification *

response to radiation **

plastid organization *

single-organism intracellular transport *

regulation of root development *

negative regulation of organelle organization *

regulation of localization *

seed development *

movement of cell or subcellular component *

cell growth *

response to carbohydrate **

Fig. S2. Functional analysis of differentially expressed genes (DEGs) of Arabidopsis shoots exposed to volatile compounds from *Microbacterium* strain EC8. Pie charts display the distribution of Gene Ontology (GO) terms grouped by a representative molecular function enriched among the up-regulated **(A)** and down-regulated **(B)** in shoot tissue exposed to *Microbacterium* volatile compounds.
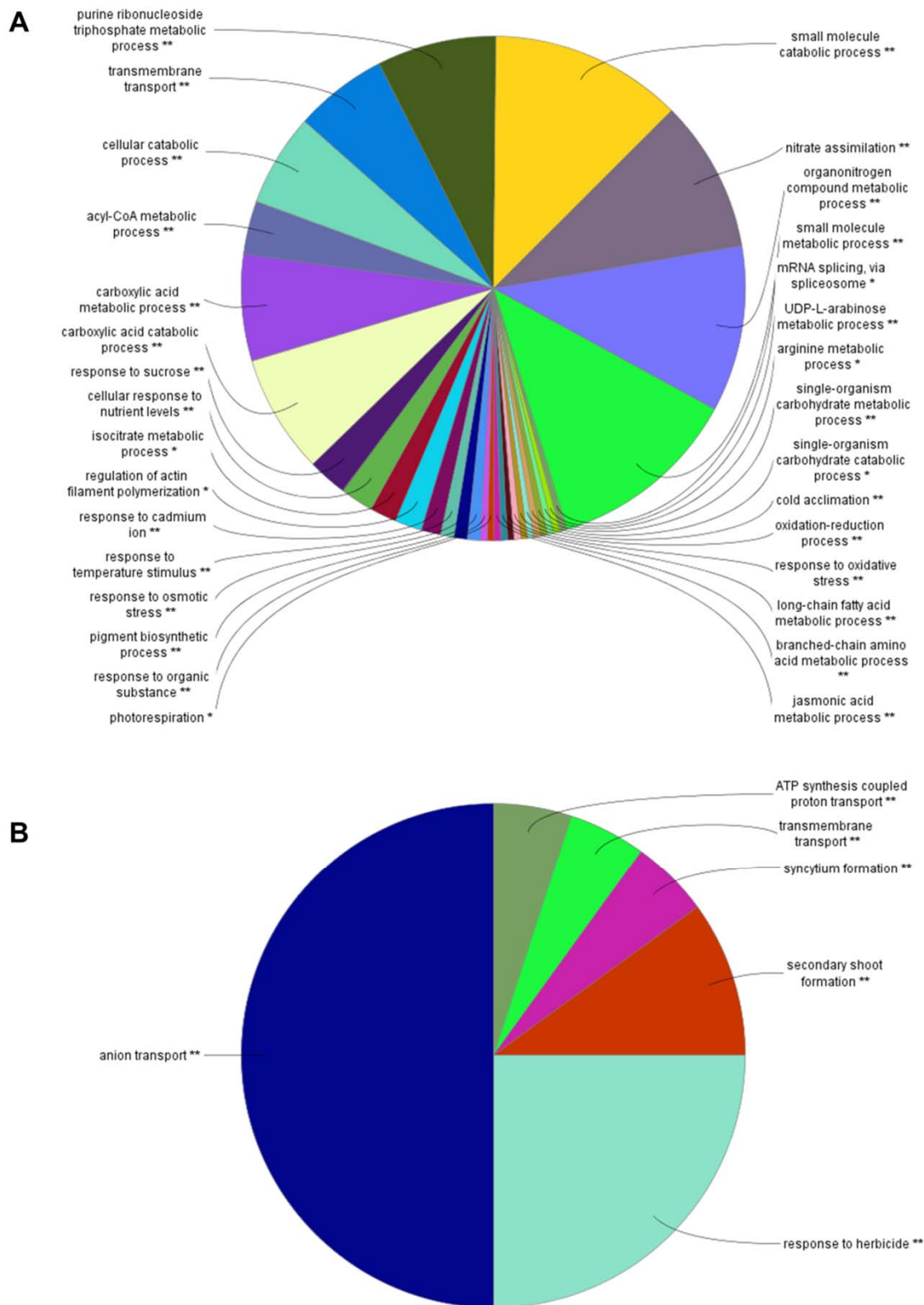
Fig. S3. Functional analysis of differentially expressed genes (DEGs) of Arabidopsis roots exposed to volatile compounds from *Microbacterium* strain EC8. Pie charts display the distribution of Gene Ontology (GO) terms grouped by a representative molecular function enriched among the up-regulated **(A)** and down-regulated **(B)** in root tissue exposed to *Microbacterium* volatile compounds.