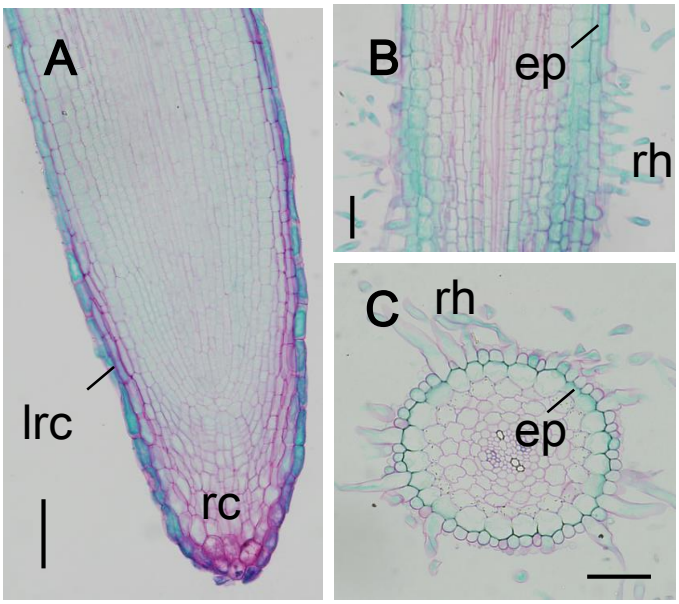

Figure S1. GUS staining of *ProNUP1::GUS* hairy roots. Thin sections of 10 μm-thickness were counter-stained with Neutral Red. A, Longitudinal section of a root tip. B, Longitudinal section of a root differentiation zone. C, Cross-section of a root differentiation zone. rc; root cap, lrc; lateral root cap, ep; epidermis, and rh; root hair. Bars, 100 μm.

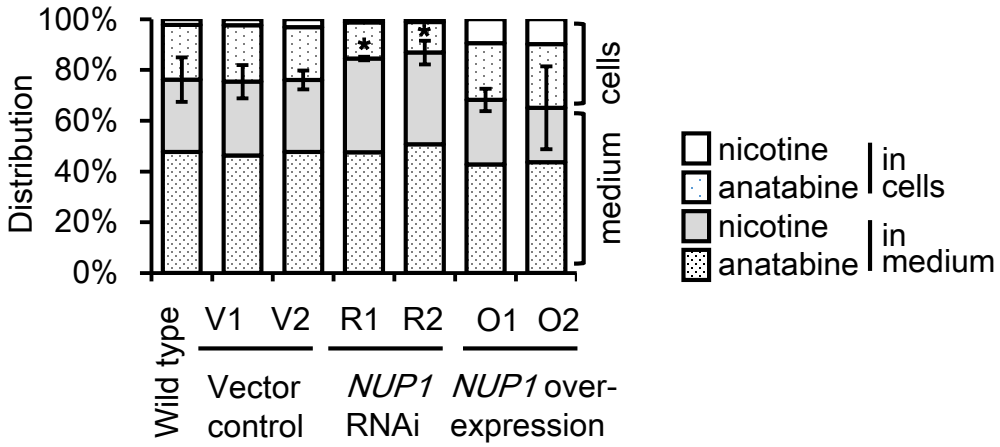

Figure S2. *NUP1* expression affects the distribution of tobacco alkaloids in cells and the culture medium. Tobacco alkaloids were measured in wild-type, vector control (V1 and V2), NUP1 RNAi (R1 and R2), and NUP1 overexpression (O1 and O2) lines of cultured tobacco BY-2 cells after they were treated with 100 μM MeJA for 72 h. The data are the mean values (±SD) of three biological replicates. Significant differences between total alkaloids in cells and the culture medium were determined by Dunnett's test and are indicated by asterisks (* for $P < 0.05$).

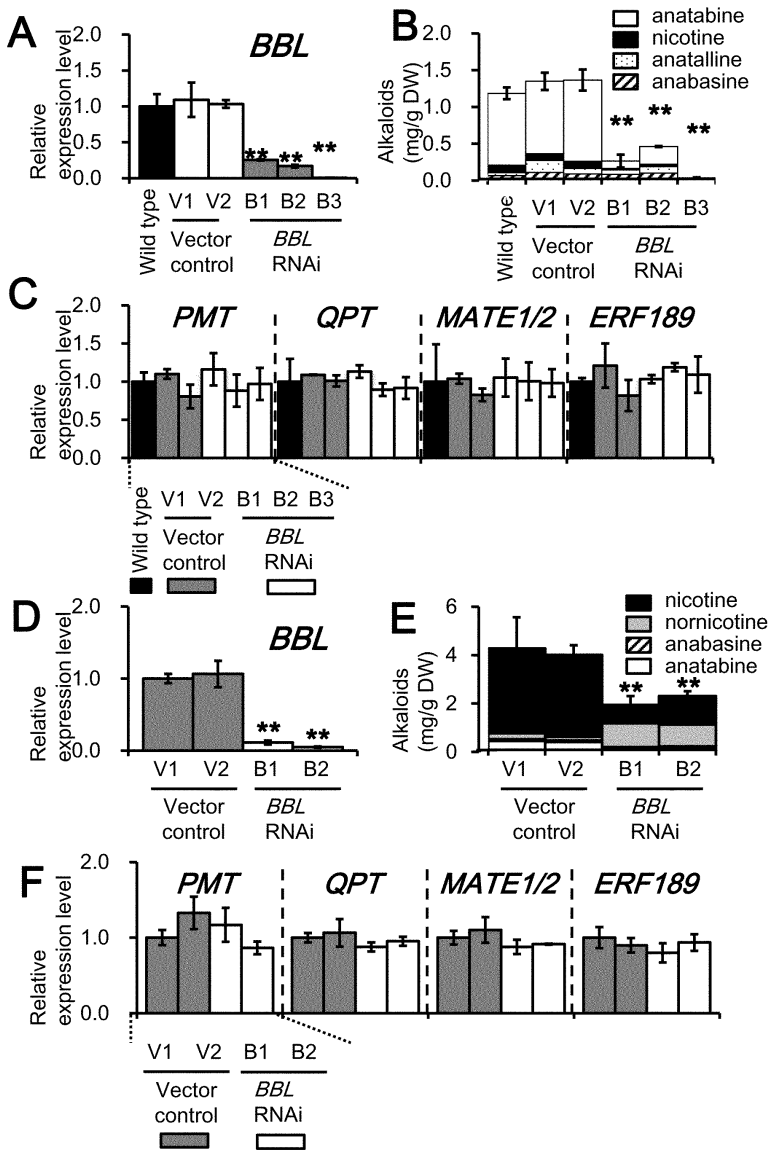

Figure S3. Down-regulation of *BBL* does not affect the expression of genes involved in alkaloid biosynthesis and transport. Data from cultured tobacco BY-2 cells are shown in A-C, whereas data from tobacco hairy roots are shown in D-F. Quantitative RT-PCR analysis of *BBL* (A and D), *PMT*, *QPT*, *MATE1/2*, and *ERF189* (C and F) expression, and the accumulation of tobacco alkaloids (B and E) in wild-type, vector control (V1 and V2), and *BBL* RNAi (B1, B2 and B3 in A-C, while B1 and B2 in D-F) transgenic lines. The cultured tobacco cells were treated with 100 μM MeJA for 24 h for RNA extraction and for 72 h for alkaloid analysis. The data are the mean values (±SD) of three biological replicates. Significant differences between the wild type and test samples were determined by Dunnett's test and are indicated by asterisks (* for $P < 0.05$ and ** for $P < 0.01$).