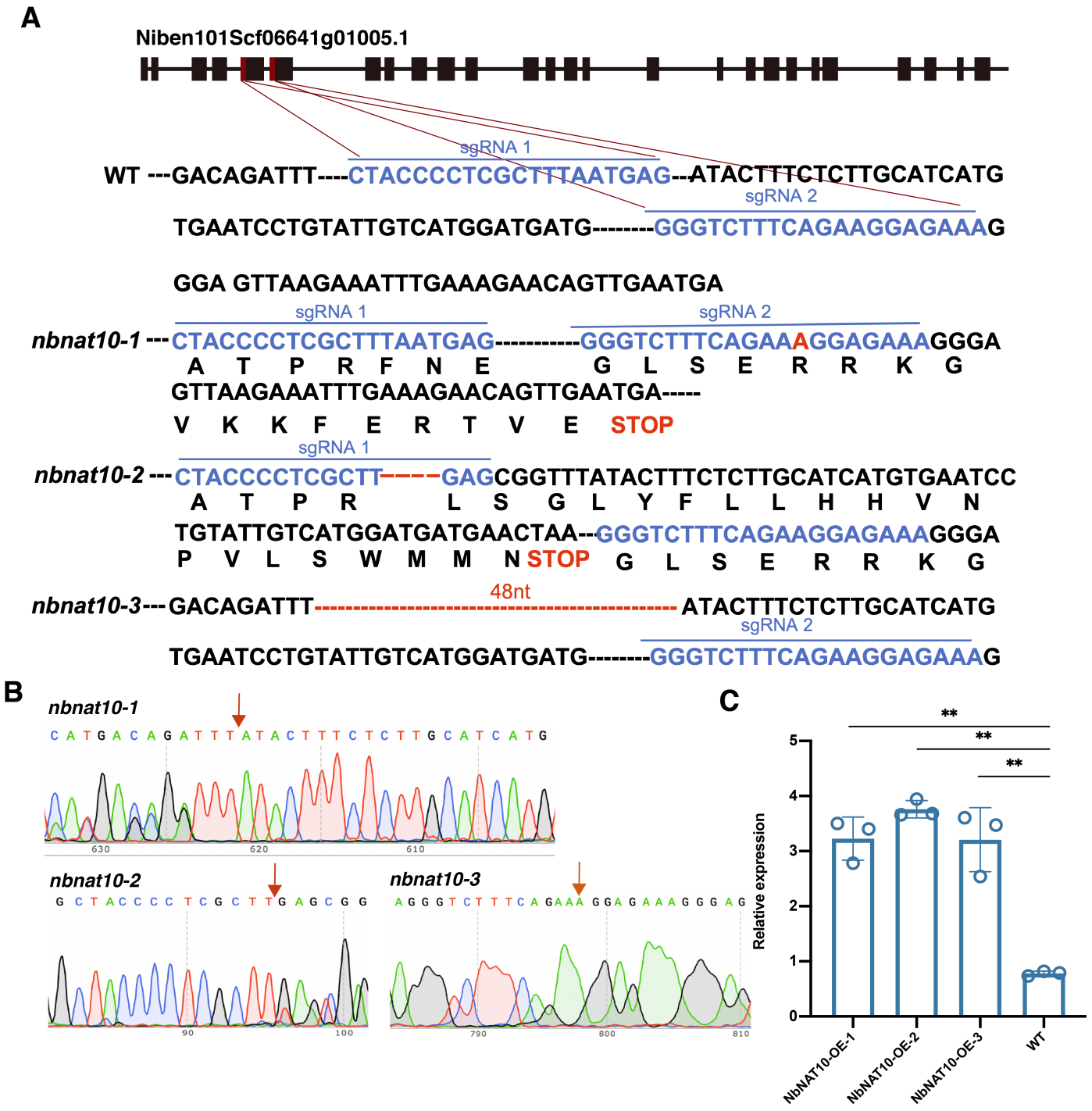

Extended Data Fig. 1 Genotyping of *nbnat10* and NbNAT10-OE mutants.

a. The positions of the two sgRNA target sites (T1 and T2) for CRISPR/Cas9 editing *NbNAT10*(Niben101Scf06641g01005.1) (upper panel). Black rectangles indicate exons, red rectangles indicate sgRNA target sites. DNA sequences of three independent *N. benthamiana nbnat10* mutant lines (lower panel). In the *nbnat10-1* mutant, an additional adenine was inserted at the sgRNA-2 target site, resulting in a frameshift mutation and the generation of a premature stop codon. The *nbnat10-2* mutant has a 4-base deletion at the sgRNA-1 target site, resulting in a frameshift mutation and a premature stop codon. The *nbnat10-3*

mutant exhibits a large 48-nt deletion at the sgRNA-1 site.

b. Sanger sequencing chromatograms of CRISPR/Cas9-targeted DNA regions in *NbNAT10* knockout lines (*nbnat10-1, nbnat10-2, nbnat10-3*). The red arrows indicate the mutation sites.

c. The relative expression levels of *NbNAT10* in WT and three independent NbNAT10-OE lines. The expression of *NbNAT10* was significantly higher in all three NbNAT10-OE lines compared to WT. Statistical analysis was performed using one-way analysis of variance (ANOVA) (* $p < 0.05$, ** $p < 0.01$). Data are means ± standard deviation (SD) (n = 3 biological replicates).