Figure S1 Phylogenetic analysis of Arabidopsis SAUR proteins.

The analyses were conducted in MEGA5, using the Neighbor-Joining method. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and were in the units of the number of amino acid substitutions per site.

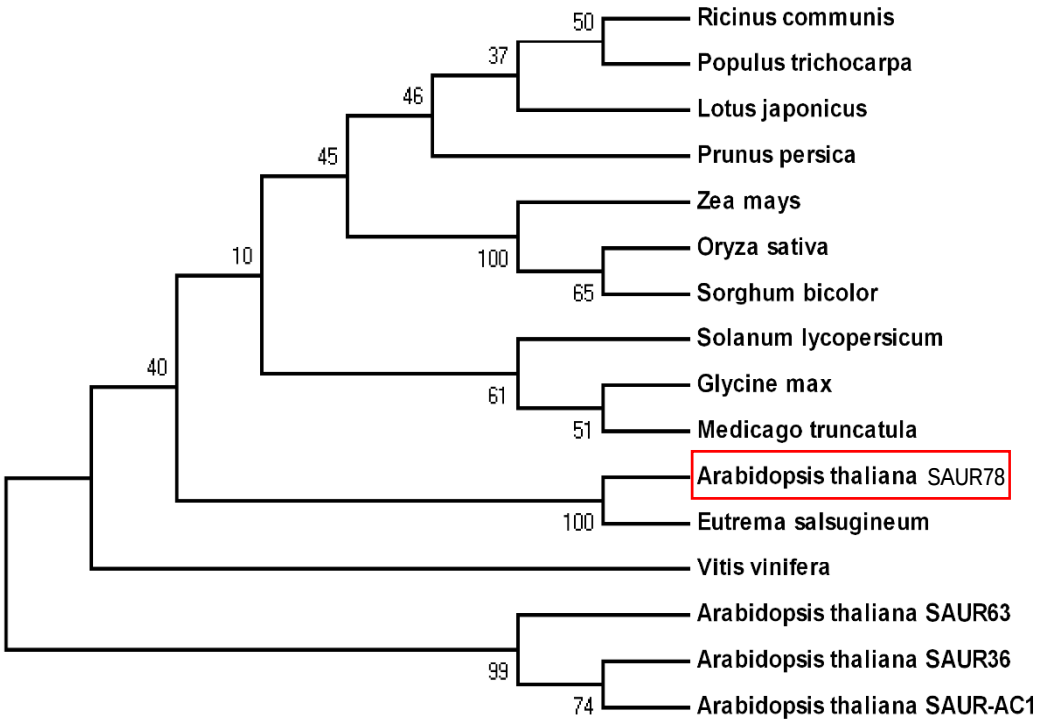

Figure S2 Phylogenetic analysis of SAUR78 homologues from different species .

Alignment of the SAUR78 with its homologues in different species. The analysis was conducted in MEGA5, using the Neighbor-Joining method, just as described in Supplemental Figure 1. Letters at right indicate the specific name and their homologous genes with accession number. Ricinus communis (XP_002529171.1), Populus trichocarpa (XP_002304244.1), Lotus japonicas (AFK34109.1), Prunus persica (EMJ18385.1), Arabidopsis thaliana (SAUR78), Eutrema salsugineum (XP_006390657.1), Vitis vinifera (XP_002268832.1), Glycine max (XP_003533801.1), Medicago truncatula (XP_003609952.1), Solanum lycopersicum (XP_004243682.1), Oryza sativa (NP_001061954.1), Sorghum bicolor (XP_002444459.1), Zea mays (NP_001266669.1). Three previously reported SAUR genes SAUR36, SAUR63 and SAUR-AC1 were also included for comparison.

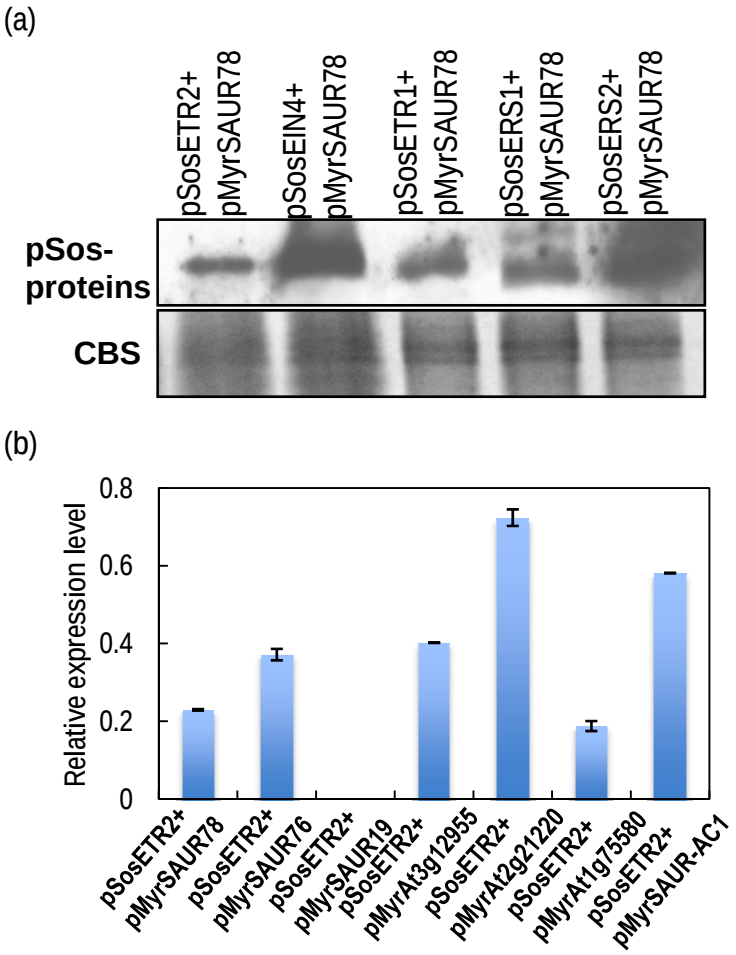

Figure S3 Expression of Sos-fusion proteins and Myr-fusion genes in yeast transformants.

The protein levels of Sos-fusion transgenes and transcriptional levels of Myr-fusion genes were detected, respectively. (a), The pSos vectors containing genes encoding different ethylene receptors were co-transfected with pMyr-SAUR78 in yeast cells. Expressions of Sos-ethylene receptor fusions in transformants were examined by Western analysis using anti-Sos1 antibody. CBS: Coomassie blue staining. (b), Quantitative PCR analysis of different SAUR genes which were co-transfected with pSos-ETR2 in yeast cells. The relative expression of SAUR78/SAUR76 served as positive controls and SAUR19 as negative control. Bars indicate SD (n=3).

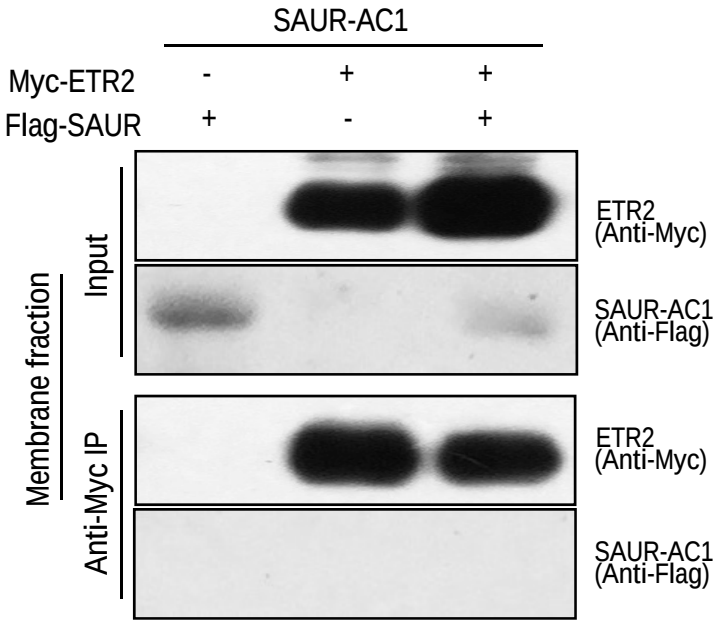

Figure S4 immunodetection of SAUR-AC1 with ETR2 by co-immunoprecipitation (Co-IP).

Co-IP was performed with agarose beads conjugated with anti-Myc monoclonal antibody. The presence of the Flag-SAUR-AC1 (negative control) in the membrane fractions was detected in input samples with the anti-Flag by Western blotting, but not in anti-Myc IP solution.

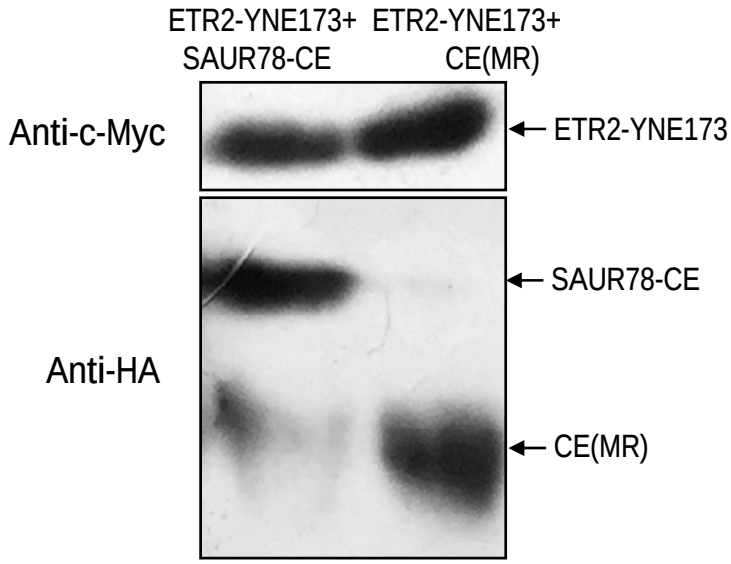

Figure S5 immunodetection of recombinant proteins expressing in tobacco leaves from BiFc assay.

The protein level of recombinant proteins, YNE173- and CE(MR)-, was examined by western blot. Infiltrated tobacco leaves were frozen in liquid nitrogen and homogenized in SDS buffer (50 mM Tris, pH 7.2, 10% glycerol, 2% SDS, 2 mM EDTA, 1 mM PMSF) . The samples were heated at 95° C for 10 min and then centrifuged at 16,000 g for 30 min at 4° C. 50 μg supernatant protein was used for SDS-PAGE. For immunodetection of recombinant proteins, c-Myc antibody (MBL) was used for ETR2-YNE173 construct ,while HA antibody (EARTHOX) was used for SAUR78-CE and CE(MR).

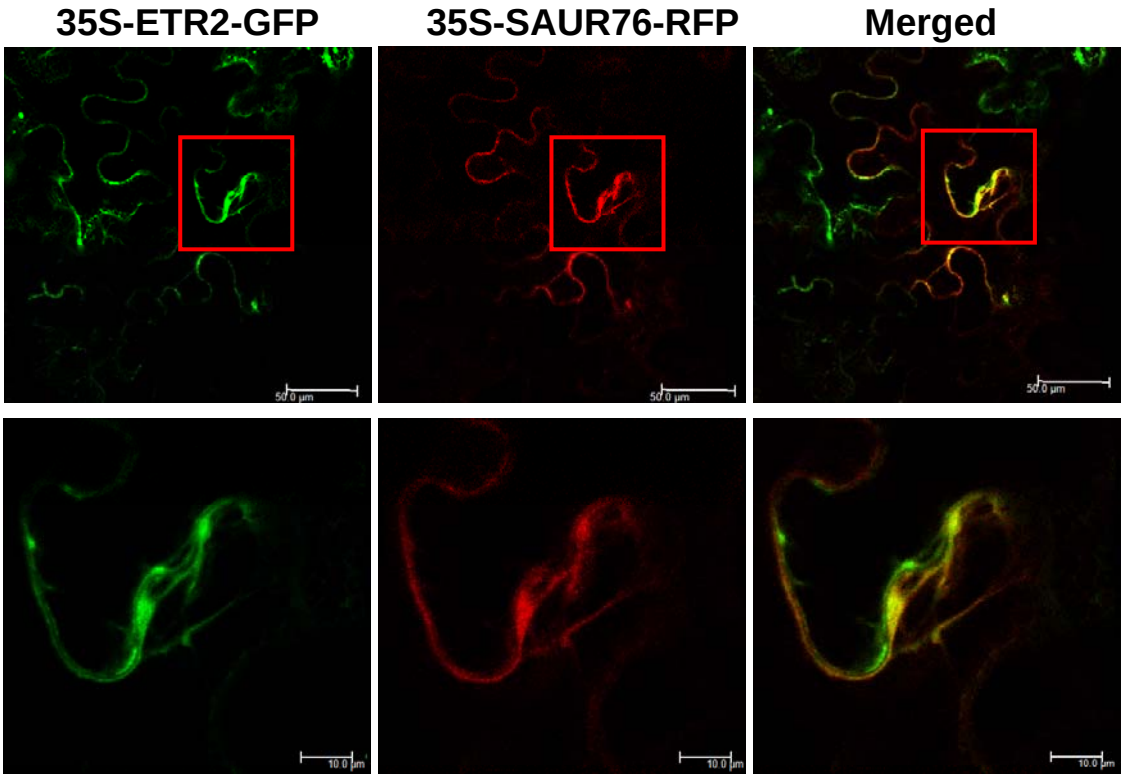

Figure S6 Co-localization analysis of ETR2 with SAUR76 in tobacco leaf cells.

Plasmids harboring 35S-ETR2-GFP or 35S-SAUR76-RFP were transfected into Agrobacteria EHA105. After co-infiltration, the infected tobacco leaves were maintained for three days and observed for protein co-localization under a confocal microscope for fluorescence.

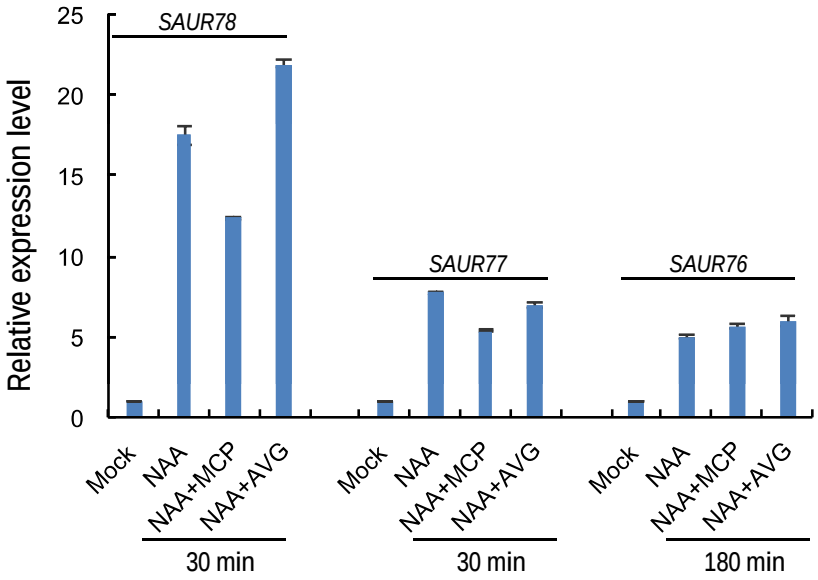

Figure S7 Expressions of *SAUR76-78* by quantitative PCR in response to NAA plus ethylene perception blocker MCP or ethylene biosynthesis inhibitor AVG.

Relative expressions of *SAUR76-78* under different treatment conditions were measured by quantitative qRT-PCR. Total RNA was extracted from six-day-old wild-type seedlings 30 min or 180 min after treatment with NAA (50 μM) ,MCP (5 ppm) or AVG (10 μM). At the treated times, the genes showed relatively higher expressions compared to the initiation point. Data represent the average of three biological repeats (±SD).

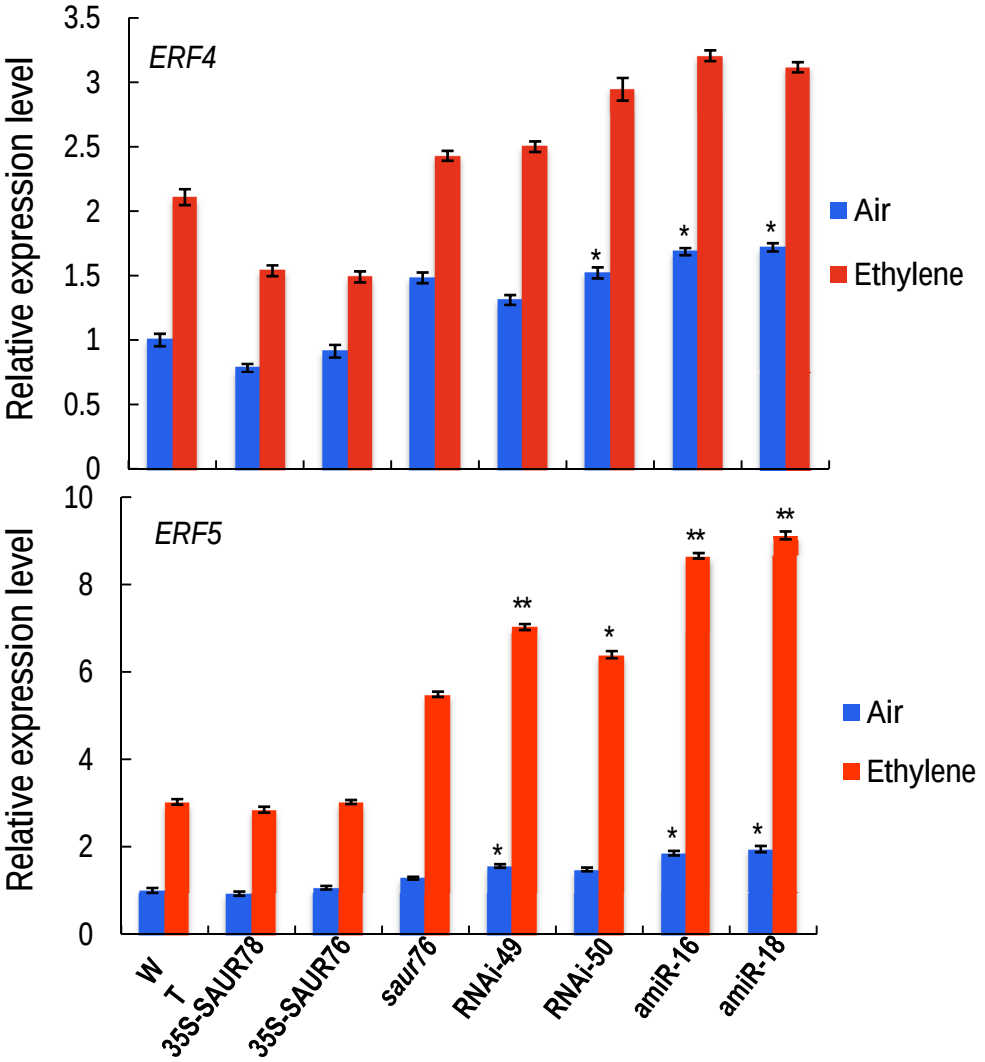

Figure S8 Expressions of *ERF4* and *ERF5* in response to ethylene.

The expressions of *ERF4* (upper panel) and *ERF5* (lower panel), which could be induced by ethylene, were examined by quantitative PCR. Six-day-old transgenic seedlings were treated with 10 ppm ethylene for 1 h. Bars indicate SD (n=3).

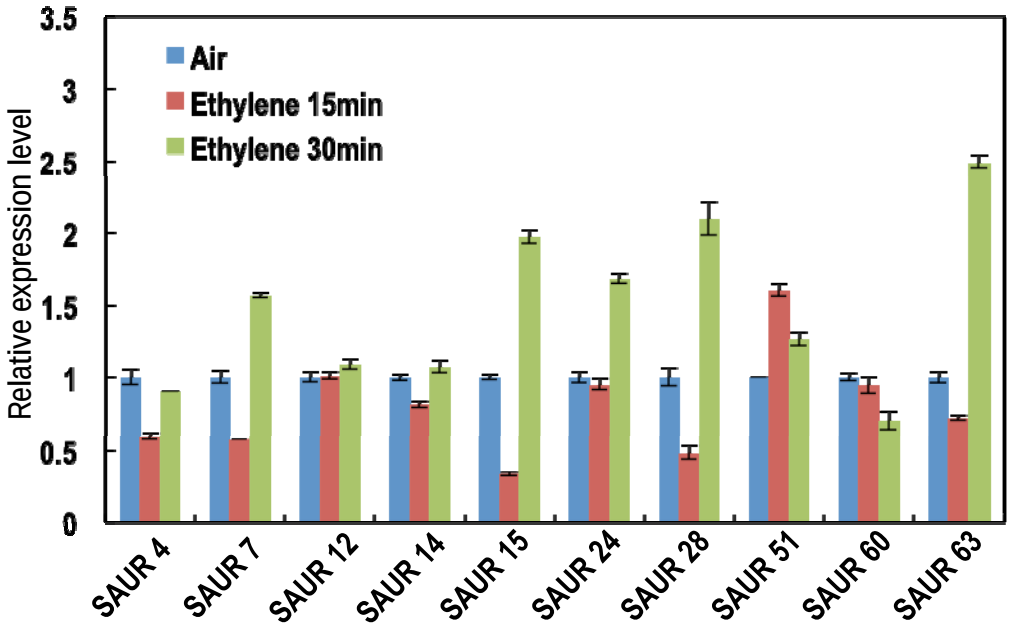

Figure S9 Expressions of 10 *SAURs* in response to ethylene.

The expressions of ten other *SAUR* genes, which were not grouped with *SAUR76-78*, were examined by quantitative PCR. Among them, SAUR12 (At2g21220), SAUR15(SAUR-AC1) and SAUR51(At1g75580) were verified not to interact with ethylene receptors (Figure 1c). Six-day-old light-grown seedlings were treated with 10 ppm ethylene and sampled at specified time points. Bars indicate SD (n=3).