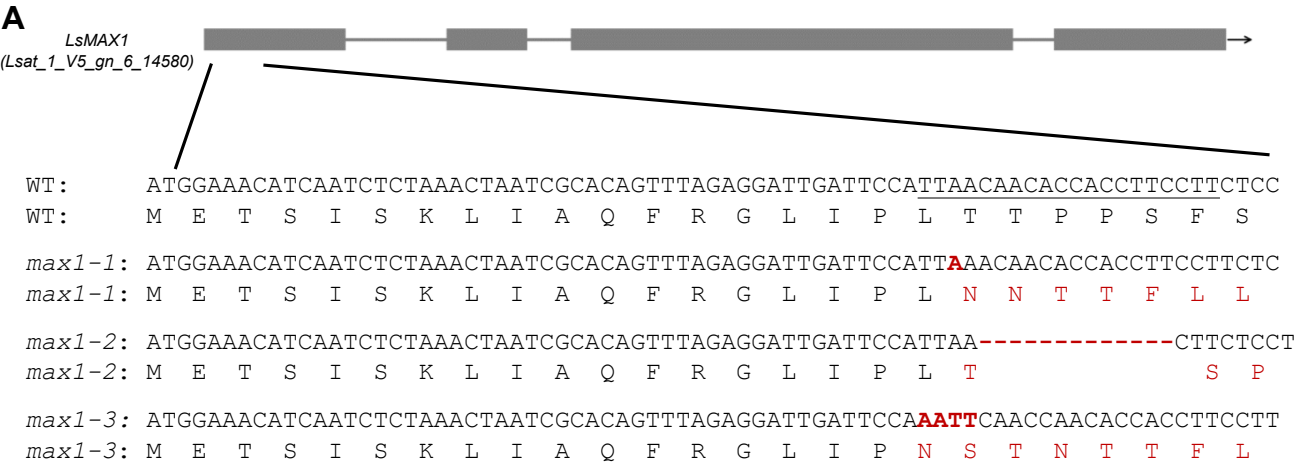
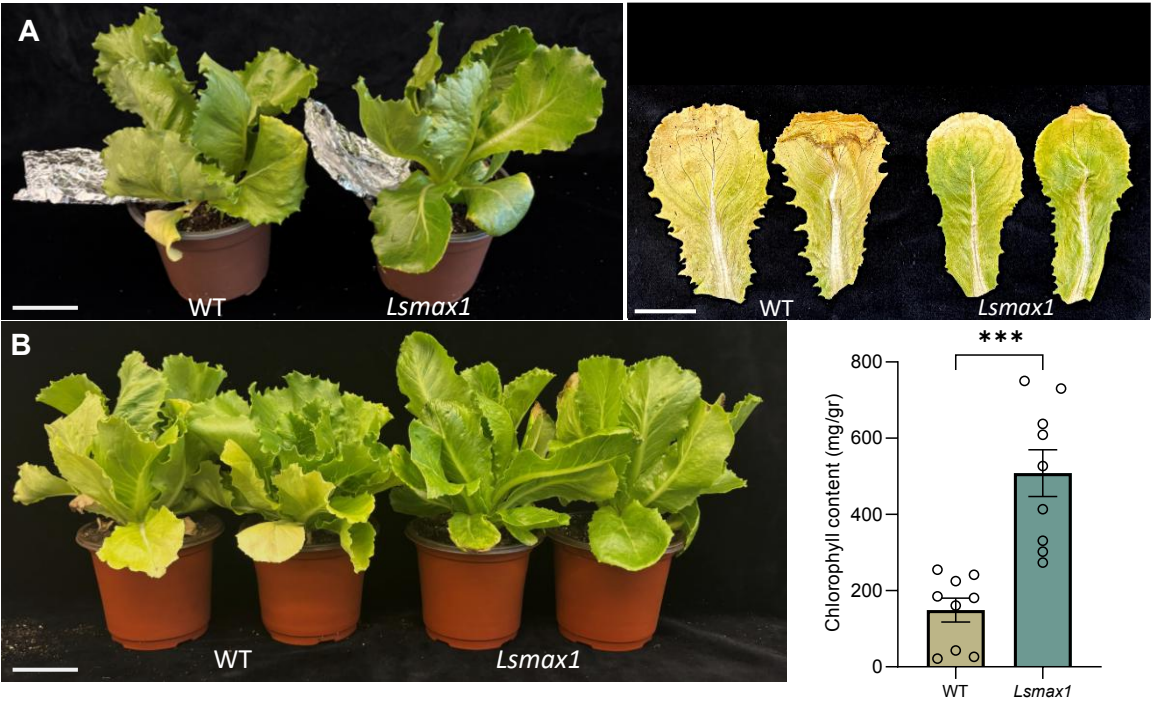




Supplementary Figure 2. CRISPR/Cas9-generated *Lsmax1* alleles with delayed senescence phenotype. **A.** Schematic representation of the *LsMAX1* gene structure with exon-intron organization (top). Partial nucleotide and corresponding amino acid sequences of WT and *Lsmax1* CRISPR/CAS9-generated mutant alleles (*Lsmax1-1*, *Lsmax1-2*, and *Lsmax1-3*) are shown below. Mutations relative to WT are indicated in red; dashes denote deletions. Predicted amino acid changes resulting from each mutation are shown beneath the nucleotide sequences. **B.** Representative detached leaves of WT and *max1-1* (left) and WT and *max1-2* (right) following dark incubation, demonstrating that the delayed senescence phenotype is shared across independent CRISPR/Cas9-generated alleles. Scale bar = 2 cm.



Supplementary Figure 3. *Lsmax1* shows delayed senescence during both dark-induced and natural age-dependent leaf senescence. **A.** WT and *Lsmax1* plants with the fourth leaf covered with aluminum foil for 14 days. Left: whole-plant view showing the covered leaf. Scale bar = 5 cm. Right: close-up of the treated leaf after 14 days of coverage. Scale bar = 3 cm. **B.** Representative images of 60-day-old WT and *Lsmax1* plants, showing more pronounced senescence in the lower leaves of WT compared with *Lsmax1*. Chlorophyll content of randomly selected lower leaves confirms this difference, with WT leaves showing significantly lower chlorophyll content than *Lsmax1* ($n = 9$ per genotype, mean $\pm$ s.e.m., t-test, $p < 0.001$). Scale bar = 5 cm