The utilization of RNA sequencing has revealed the highly complex nature of Eukaryotic transcriptomes. With massive amounts of transcription coming from intergenic regions or in antisense to known genes, there is widespread effort to characterize these novel transcripts. Long intergenic non-coding RNAs (lincRNAs) are an enigmatic yet abundant class of Eukaryotic transcriptomes. LincRNAs are defined as RNA molecules greater than 200 nucleotides in length, have little to no protein coding potential, and do not resemble other classes of noncoding RNAs. Molecular characterization of lincRNAs in plants has significantly lagged behind protein coding genes and other classes of non-coding RNAs. To identify potential candidates for molecular characterization, we employed a bioinformatic approach to identify lincRNAs conserved at the genomic and transcriptomic level across Brassicaceae, with the expectation that conservation implies function. In this study, we identify a highly conserved lincRNA (At1NC031460) across Brassicaceae, a trait rare among lincRNAs. Mutant analysis of At1NC031460 suggests early senescence, which is a unique phenotype among disrupted lincRNAs. We utilize CRISPR genome editing to generate additional mutant alleles of this lincRNA, and to generate dominant activators or repressors at this locus. The dominant CRISPR activator preliminarily suggests that overexpression of At1NC031460 delays senescence, in accordance with our hypothesis that At1NC031460 is involved in senescence. Finally, we identify deletions alleles generated by CRISPR that will inform future functional studies of At1NC031460. In conclusion, we identify a conserved lincRNA across Brassicaceae that is involved in senescence in Arabidopsis thaliana and are using CRISPR to characterize the gene in further detail.