Genome-wide efforts reveal that a large fraction of the DNA in eukaryotic genomes is transcribed. The functional analysis of such ‘dark matter transcripts’ led to the identification of long non-coding RNAs (lncRNAs) with regulatory potential, though the functionality in gene regulatory network is still not well understood. Previously, for this purpose, we previously used an AP1-based floral induction system in Arabidopsis and identified thousands of flower-related long intergenic RNAs (lincRNAs) which display distinct characteristics compared with protein coding genes such as transcript length, expression specificity and association with transposable elements. We proposed that TF-dependent enhancer associated lincRNAs transcription can act as components of TF-dependent gene regulation networks. As a preparatory work for a new project, diverse RNA-seq samples from public databases (e.g. EBI ENA) in 26 land plant and algae species were collected. We propose to perform genome-wide analyses of identified lncRNAs datasets by comparative genomics in order to obtain insights into lncRNA evolution and functionality of lncRNAs, and also provide resources to facilitate selection of individual conserved lincRNAs for further experimental analyses in the research community. Therefore, we propose this project utilizing the HLRN resources.