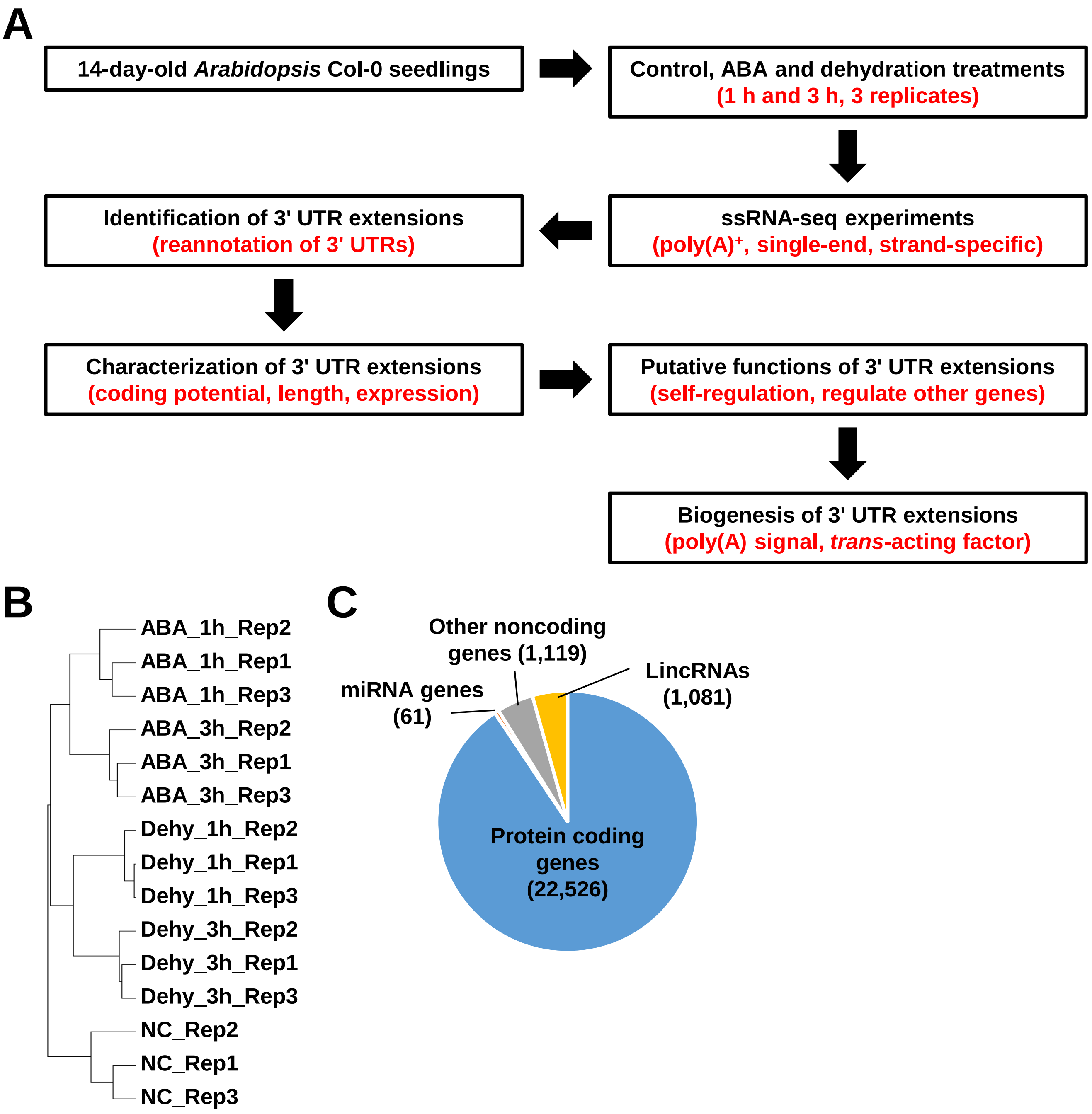
Supplemental Figure 1



Supplemental Figure 1. Global view of ssRNA-seq results.
(A) Schematic diagram showing experimental procedure for the identification and functional analysis of stress-induced 3' UTR extensions. **(B)** Correlation analysis of all ssRNA-seq samples from normal condition (NC), ABA treatment for 1 h (ABA_1h), ABA treatment for 3 h (ABA_3h), dehydration stress for 1 h (Dehy_1h) and dehydration stress for 3 h (Dehy_3h). Hierarchical clustering of expression levels (FPKMs) of all detected genes segregates NC from ABA-treated and dehydration-stressed samples. **(C)** Composition of ssRNA-seq detected genes in all ssRNA-seq samples. Other noncoding genes are genes annotated as “transposable_element_gene”, “pseudogene”, “pre_trna (tRNA)”, “small_nucleolar_rna (snoRNA)”, “ribosomal_rna (rRNA)”, “small_nuclear_rna (snRNA)” and “other_rna” by TAIR10.