



**Supplemental Figure 3 Identification of stored mRNA in aged wheat seeds by Illumina RNA-seq.**

(a, b) Transcripts Per Million (TPM) analysis of RNA-seq data showing the number of genes found to have a detectable transcripts level (TPM  $\geq 1$ ) under natural aging treatment (NAT) for 0, 1, 3, and 8 years and controlled deterioration treatment (CDT) for 0, 5, 15, and 25 days in the embryo (Em) and aleurone layer (Al). CDT for 0 day seeds were NAT for 3 years seeds. (c) Venn diagram of comparisons of stored mRNAs for the different tissues (embryo and aleurone layer).