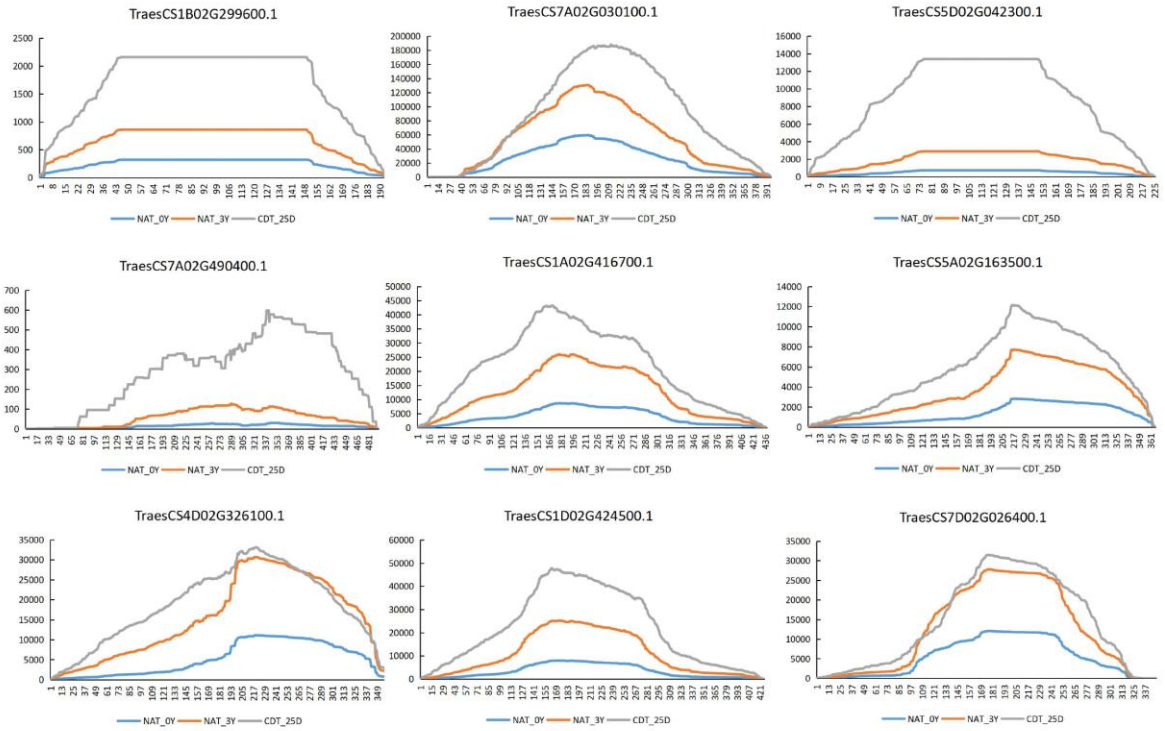
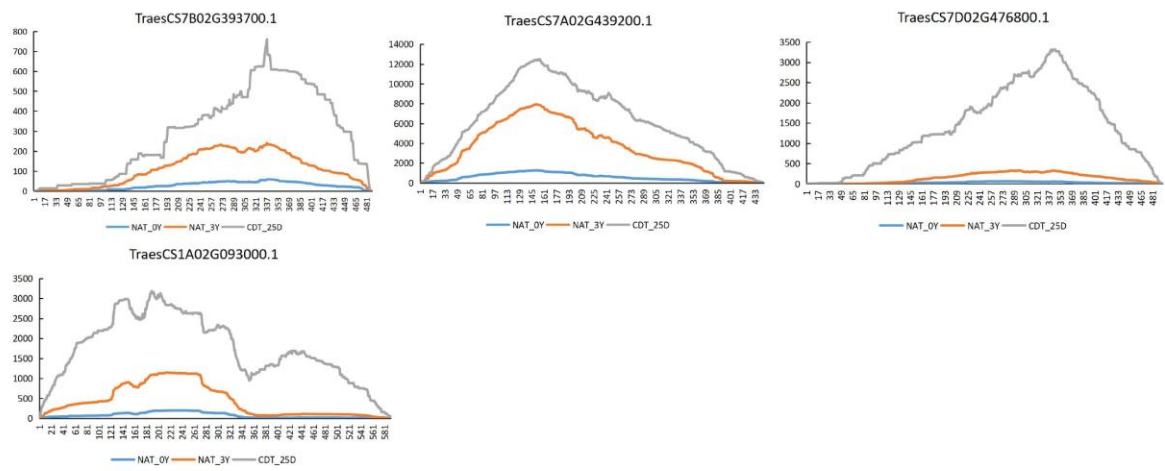


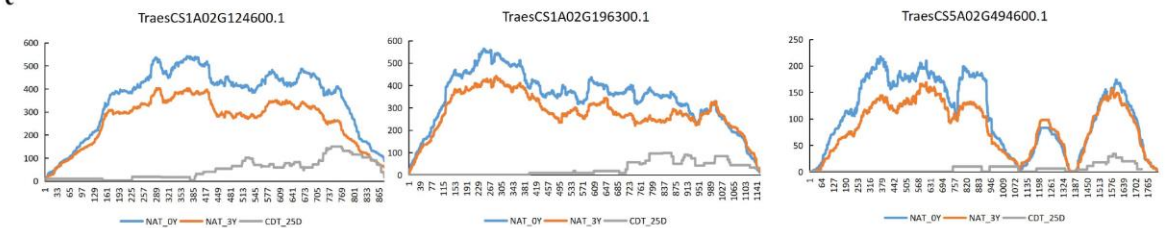
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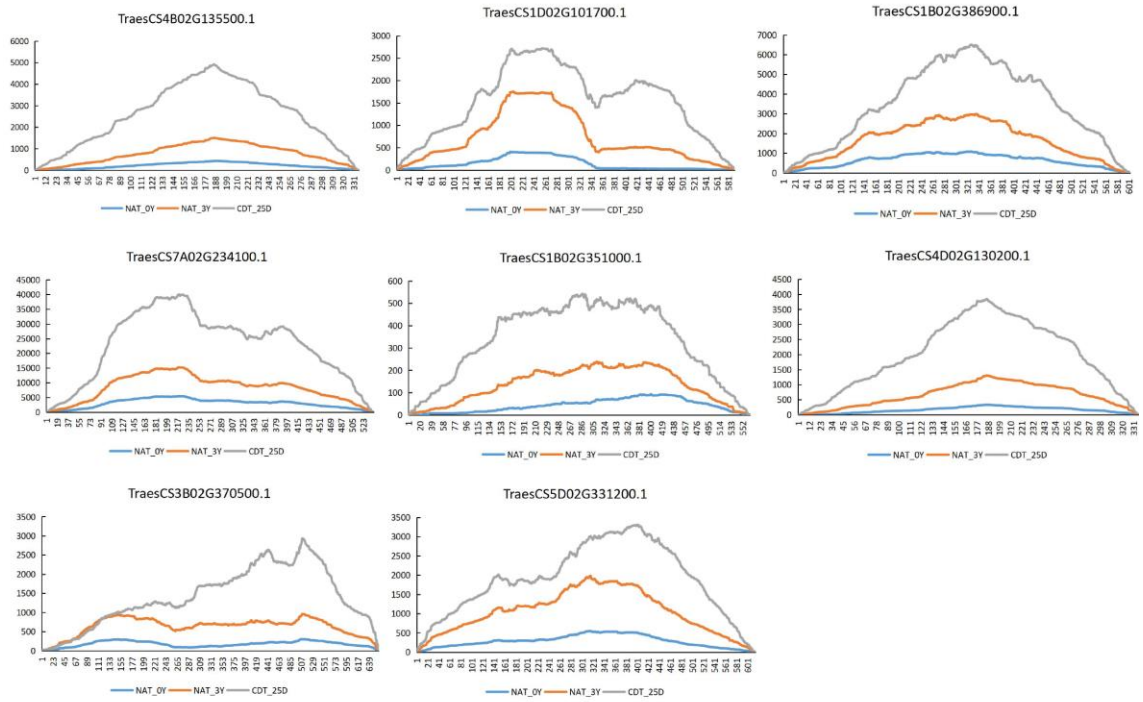
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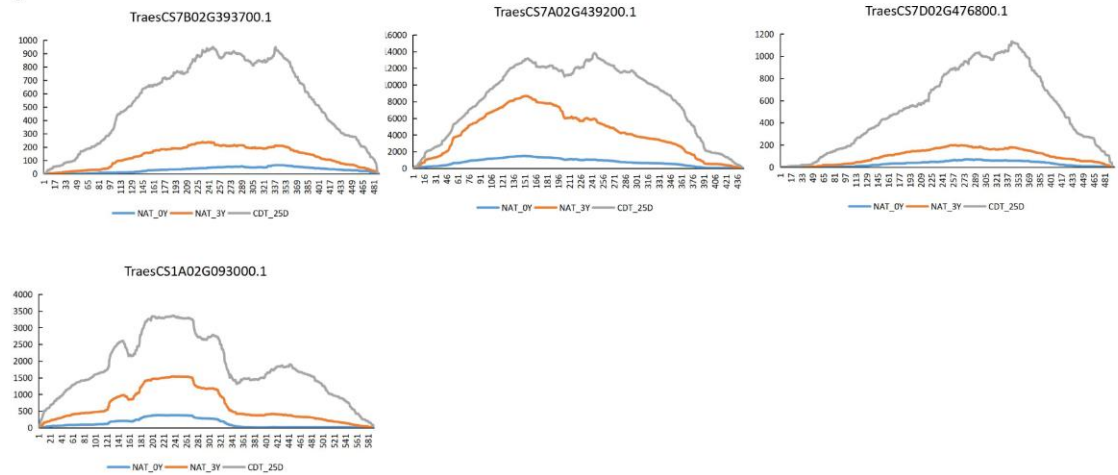
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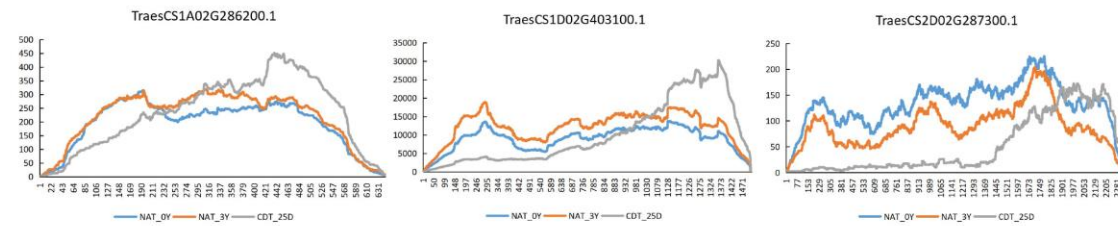
d



e



f



Supplemental Figure 5 The sequencing depth from 5' to 3' of the most stable long-lived mRNAs (LLRs) and easily degraded mRNAs.

Comparison of sequence depth between reads from fresh seeds, Natural aging treatment for 0 years (NAT_0Y, blue solid line), Natural aging treatment for 3 years seeds (NAT_3Y, orange solid line) and controlled deterioration treatment for 25 days (CDT_25D, gray solid line) at each position in a transcript. Sequencing depth distribution of the thirteen most stable LLRs identified in the embryo (a, b), the twelve most stable LLRs identified in the aleurone layer (d, e), four LLRs identified as the most stable in both tissues (b, e) and the mRNAs that degraded during aging of embryo (c) and aleurone layer (f). The x-axis represents the gene coding sequence in the 5' to 3' direction, with the 5' end on the left and the 3' end on the right.