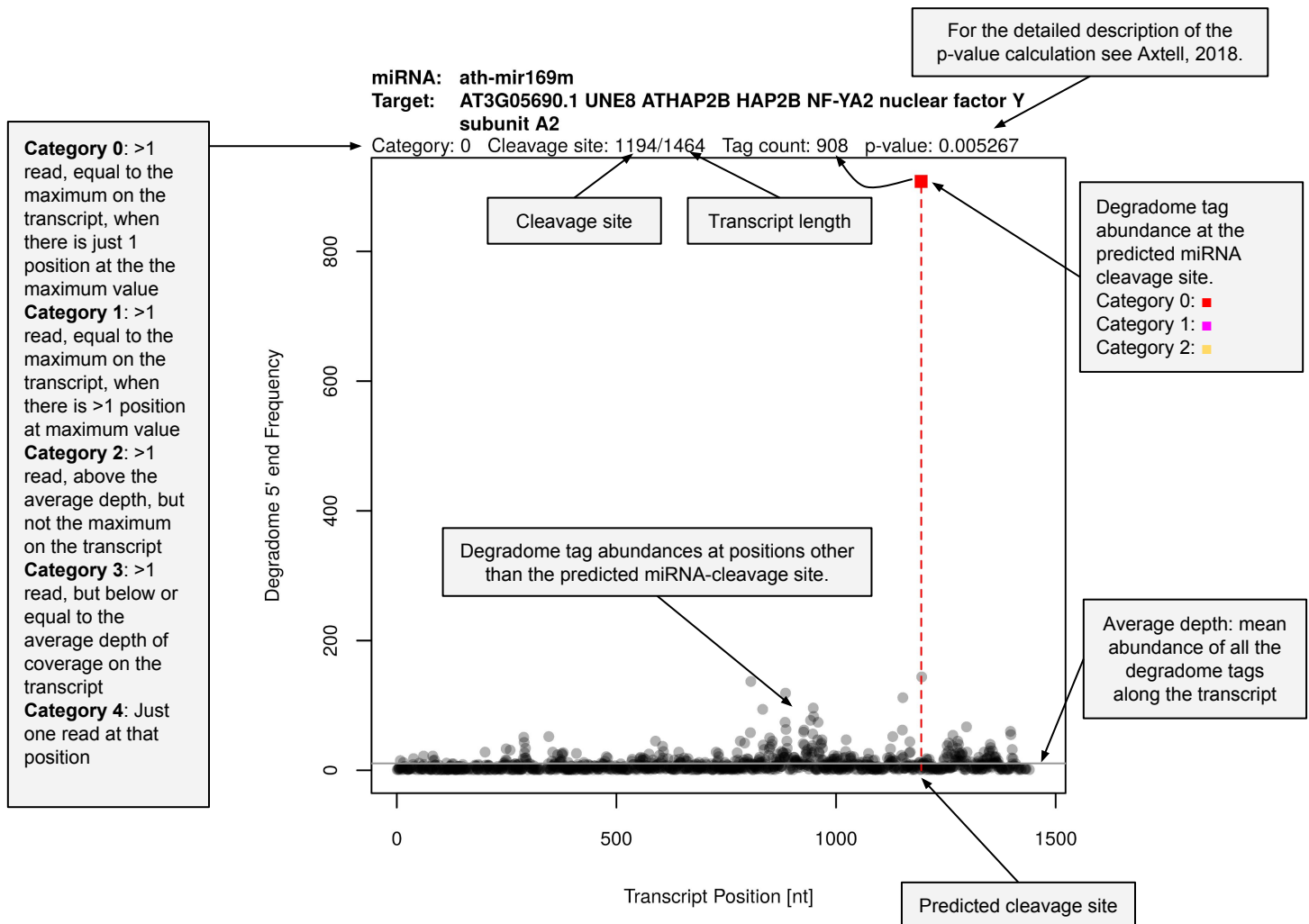


## Fig S5. Degradome target plots.

The degradome libraries were prepared from seedling, root, leaf, and flower samples at 15, 21, and 27 °C in two biological replicates. For the analysis, we merged all the libraries to detect possible cleavage events with higher sensitivity. Therefore, the plots presented here show the cumulative degradome tag abundances across all the tissues and temperatures. In some cases, it is possible that a cleavage occurs only in a specific tissue or at a certain temperature (i.e. when a miRNA or the target gene expresses in a tissue-specific manner).

The degradome analysis was performed with CleaveLand4 (Axtell 2018). The TAIR10 annotated transcriptome file called `TAIR10_cdna_20101214_updated.fasta` was tailored to make it suitable for the analysis (long annotations were simplified, dots were replaced with dashes, miRNA genes were removed). The original CleaveLand4 script was also modified to include additional details in the figures and to change some graphical elements but the functionalities of the program were not modified. Only hits of category 0-2 with p-value < 0.1 are presented.

The explanation of the figure elements is presented below:



## References

Axtell M. (2018) *CleaveLand4: Analysis of degradome data to find sliced miRNA and siRNA targets*.

<https://github.com/MikeAxtell/CleaveLand4>