**Table S4. Overlap between transcripts identified by *de novo* analysis and annotated transcripts**

|  |  |  |
| --- | --- | --- |
|  | Counts | Percent of Class |
|  | *paf1∆ vs WT* | *paf1∆ vs WT* |
|  | Decreased | Increased | Decreased | Increased |
| mRNA | 1100 | 359 | 20.32 | 6.15 |
| snoRNA | 1 | 28 | 1.30 | 27.27 |
| CUT | 72 | 34 | 2.38 | 1.41 |
| SUT | 62 | 30 | 4.14 | 1.89 |
| XUT | 77 | 57 | 2.23 | 1.81 |
| SRAT | 11 | 27 | 0.19 | 5.64 |
| NUT | 112 | 101 | 3.08 | 5.18 |
|  |  |  |  |  |
|  | Counts | Percent of Class |
|  | *paf1∆ trf4∆ vs trf4∆* | *paf1∆ trf4∆ vs trf4∆* |
|  | Decreased | Increased | Decreased | Increased |
| mRNA | 1519 | 844 | 21.47 | 16.24 |
| snoRNA | 17 | 23 | 3.90 | 24.68 |
| CUT | 294 | 70 | 22.19 | 4.11 |
| SUT | 193 | 85 | 19.86 | 6.86 |
| XUT | 372 | 172 | 18.53 | 7.91 |
| SRAT | 45 | 147 | 5.83 | 33.46 |
| NUT | 426 | 229 | 31.72 | 11.27 |

Counts and corresponding percentages of transcripts identified by the *de novo* analysis that overlap with existing transcript annotations. Transcripts exhibiting an absolute fold change of 1.5-fold or greater in some portion of the differentially expressed region were counted (see Materials and Methods for a detailed description). The percentages shown in this table were used to generate Figure 2A and the counts of mRNA overlaps were used in the comparison shown in Figure S2A. Note that any overlap between a transcript identified in the *de novo* analysis and an annotated RNA was counted. This analysis calculates overlap from the perspective of the previously annotated RNAs. Therefore, if a single *de novo* transcript overlaps with two annotated mRNAs, each mRNA is counted resulting in a total count of two. This explains the higher number of differentially affected mRNAs in this table compared to Table S5. In Table S5, we calculate from the perspective of the *de novo* transcript, so a *de novo* transcript overlapping with two annotated mRNAs would only be assigned a value of one. It is also important to note that if an overlap is detected between a *de novo* transcript and two annotated transcripts, such as a CUT and a NUT, for example, this would result in assignment of that *de novo* transcript to both a NUT and a CUT. We chose to allow this because there is overlap between and within some of the annotated RNA classes and we would consequentially lose most annotated RNAs if we excluded any with overlap within or between classes.