**Table S5. Counts of transcripts identified by the *de novo* analysis that fall into various categories based on position relative to mRNA coding regions**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | *paf1∆ vs WT* | | *paf1∆ trf4∆ vs trf4∆* | |
|  | Decreased | Increased | Decreased | Increased |
| sense mRNA Overlap | 872 | 275 | 1111 | 687 |
| antisense mRNA overlap | 23 | 47 | 256 | 353 |
| no overlap with mRNA | 39 | 12 | 151 | 88 |
| Sum | 1268 | | 2646 | |

Counts of transcripts identified by the *de novo* analysis with an absolute fold change of 1.5-fold or more (calculated as described in Table S3) that either overlap with mRNAs in the sense or antisense direction. The counts shown in this table were used in the generation of Figure 2B. The sum of all transcripts identified in each strain background is shown in the bottom row representing the total number of transcripts identified in the *de novo* analysis (used in Figure S2C Venn diagram). Note that the mRNA overlap shown here does not match with Table S4. This analysis calculates overlap from the perspective of the *de novo* transcripts, meaning that if a transcript overlaps with more than one mRNA it is only counted once in this analysis. This leads to a lower number of mRNA overlaps being counted in table S5 than in table S4, because some *de novo* annotations encompass more than one mRNA.