**Table S3. Summary of differential expression results obtained from the annotation-guided analysis of the tiling array data**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| *paf1∆ vs WT* | | | | | | |
|  | | Increase | | | Decrease | | Sum | |
| Transcript Class | | Count | | Class Percent | Count | Class Percent | Count | Class Percent |
| mRNA | | 126 | | 1.9 | 348 | 5.3 | 474 | 7.2 |
| snoRNA | | 12 | | 15.6 | 1 | 1.3 | 13 | 16.9 |
| CUT | | 8 | | 0.9 | 2 | 0.2 | 10 | 1.1 |
| SUT | | 4 | | 0.5 | 3 | 0.4 | 7 | 0.9 |
| NUT | | 9 | | 0.6 | 5 | 0.3 | 14 | 0.9 |
| XUT | | 10 | | 0.6 | 5 | 0.3 | 15 | 0.9 |
| SRAT | | 2 | | 0.4 | 0 | 0.0 | 2 | 0.4 |
| Sum | | 171 | |  | 364 |  | 535 |  |
|  |  | |
| *paf1∆ trf4∆ vs trf4∆* | | | | | | |
|  | | Increase | | | Decrease | | Sum | |
| Transcript Class | | Count | | Class Percent | Count | Class Percent | Count | Class Percent |
| mRNA | | 281 | | 4.3 | 320 | 4.8 | 601 | 9.1 |
| snoRNA | | 21 | | 27.3 | 2 | 2.6 | 23 | 29.9 |
| CUT | | 14 | | 1.5 | 86 | 9.3 | 100 | 10.8 |
| SUT | | 5 | | 0.6 | 31 | 3.7 | 36 | 4.3 |
| NUT | | 16 | | 1.0 | 61 | 4.0 | 77 | 5 |
| XUT | | 30 | | 1.8 | 54 | 3.3 | 84 | 5.1 |
| SRAT | | 21 | | 3.9 | 5 | 0.9 | 26 | 4.8 |
| Sum | | 388 | |  | 559 |  | 947 |  |

Counts of RNAs with an absolute fold change of 1.5 or greater in the annotation-guided analysis of the tiling array data. The analysis was performed using the *limma* Bioconductor package in R. These data are graphically presented in Figure 1. Percentages of transcripts within each class that show an expression change greater than 1.5-fold are also shown. The differentially expressed mRNAs detected in the *paf1∆ trf4∆* vs *trf4∆* comparison were used in the comparison shown in Figure S2A.