Supplemental materials:
Genome-wide identification and characterization of small RNAs originated from natural antisense transcripts in *Oryza sativa*

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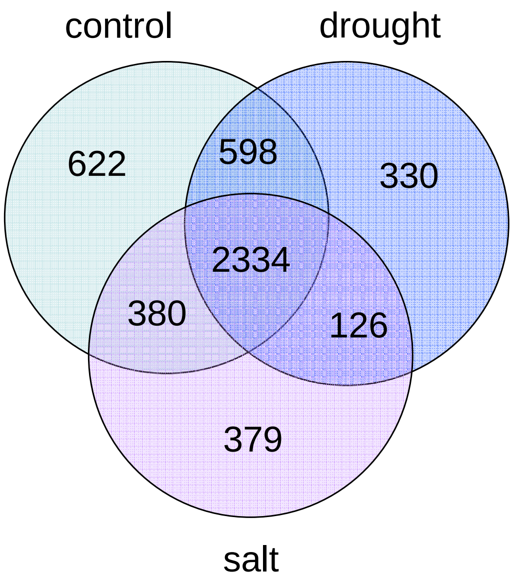
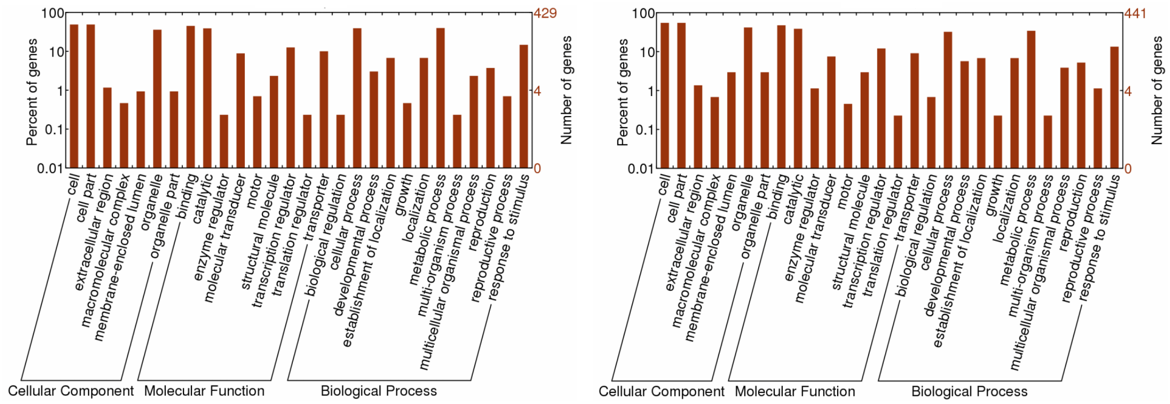
- **Table S1:** Total number of endogenous small RNAs from CSRDB, MPSS and our stress library dataset that match all protein-coding genes, cis-NATs, overlapping regions of cis-NATs, trans-NATs, and overlapping regions of trans-NATs in O. sativa.(see file suppl_table1.pdf)
- **Table S2:** List of cisNATs in *O. sativa* that give rise to small RNAs in the control, drought and salt libraries.(see file suppl_table2.pdf)
- **Table S3:** Numbers of trans-NATs in *O. sativa* that spawn small RNAs under different conditions/stages in MPSS dataset.(see file suppl_table3.pdf)
- **Table S4:** All cisNATs identified from genome.(see file Table_S4_all_cisNAT.xls)
- **Table S5:** *O. sativa* cisNATs whose overlapping regions give rise to small RNAs.
  (see file Table_S5_cisNAT_deriving_sRNAs.xls)
- **Table S6:** *O. sativa* transNATs whose overlapping regions give rise to small RNAs. Totally, we identified 7,142 transNATs in *O. sativa* genome, 7,141 of them derive small RNAs from their overlapping regions. (see file Table_S6_transNAT_deriving_sRNAs.xls)
- **Table S7:** All unique small RNAs that derived from the overlapping regions of *O. sativa* cisNATs. (see file Table_S7_all_cisNAT_overlap_sRNA.txt)
- **Table S8:** All unique small RNAs that derived from the whole regions of *O. sativa* cisNAT genes. All of these cisNAT give rise to small RNAs from their overlapping regions.
  (see file Table_S8_all_cisNAT_genes_sRNA.txt)
- **Table S9:** All unique small RNAs that derived from the overlapping regions of *O. sativa* transNATs. (see file Table_S9_all_transNAT_overlap_sRNA.txt)
- **Table S10:** All unique small RNAs that derived from the whole regions of *O. sativa* transNAT genes. All of these transNAT give rise to small RNAs from their overlapping regions.
  (see file Table_S10_all_transNAT_genes_sRNA.txt)



Supplemental Figure 1: Numbers of trans-NATs that produce small RNAs under control, salt and drought conditions.



Supplemental Figure 2: Enriched GO terms in genes involved in trans-NATs that spawn siRNAs exclusively under drought (left) or salt (right) stress conditions, respectively.