Table S 1: Total number of endogenous small RNAs from CSRDB [1], MPSS [2] 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*. (a): Stem. (b): Germinating seedlings. (c): Nipponbare immature panicles-90 days old plants. (d): Germinating seedlings infected with Magnaporthe grisea. (e): Seedlings treated with ABA.(f): Seedling control for ABA treatment. (g): total number of unique small RNAs. The small RNAs were downloaded from MPSS small RNA database([2]).

number of siRNAs mapped to	our libraries			CSRDB	MPSS						unique
	control	drought	salt		STM$^{(a)}$	SNU$^{(b)}$	FLR$^{(c)}$	SNM$^{(d)}$	ABA$^{(e)}$	UNT$^{(f)}$	total$^{(g)}$
protein coding gene	3904	2208	2389	4237	13807	7662	30989	7264	8193	13254	84940
cis-NAT genes	200	124	160	73	391	177	937	208	248	359	2592
cis-NAT overlapping region	22	19	27	3	23	17	103	29	21	34	258
trans-NAT genes	8072	4635	4386	2710	8161	4440	14466	4177	4895	7821	56790
trans-NAT overlapping region	7522	4242	3680	1590	3020	1684	3811	1576	1786	2971	27509

References

[1] C. Johnson, L. Bowman, A.T. Adai, V. Vance, and V. Sundaresan. CSRDB: a small RNA integrated database and browser resource for cereals. *Nucleic Acids Res*, 35(Database issue):D829–33, Jan 2007.

[2] K. Nobuta, R.C. Venu, C. Lu, A. Belo, K. Vemaraju, K. Kulkarni, W. Wang, M. Pillay, P.J. Green, G.L. Wang, and B.C. Meyers. An expression atlas of rice mRNAs and small RNAs. *Nat Biotechnol*, 25(4):473–7, Apr 2007.