

Fig. S2 - Boxplots of structural characters versus expression level (microarray data) for *Arabidopsis* and rice genes.

In each graph, x-axis represents gene-expression level, boxes represent the value range of parameters for each gene group, with bold central lines represent the medians, lower and upper boundaries represent the first and third quartiles respectively, whereas whiskers extend to the most extrem points within $1.5\times$ interquartile range from the boxes. Horizontal darkviolet lines indicate the population median for each parameter. Presented parameters are: CDS length in (a) *Arabidopsis* and (b) rice; total intron length per gene in (c) *Arabidopsis* and (d) rice; number of introns per gene in (e) *Arabidopsis* and (f) rice. Differences in structural parameters between different expression groups are statistically significant (all Kruskal-Wallis rank sum test $P < 2e-16$).

