

Fig. S4 - Extreme transcript lengths versus expression levels (microarray data) for plant genes.

Figure (a), extreme transcript lengths of *Arabidopsis* genes scales as a power-law of average expression level; Figure (b)-(f), extreme transcript lengths of *Arabidopsis* and rice genes scale as logarithmic functions of expression levels. In each figure, points represent the whole dataset, whereas triangles represent data points used to fit the darkviolet linear line; dashed red curve represents the extreme energy-cost of transcription; dotted vertical line indicates the maximum point of the energy-cost curve. Equations show the functional form for corresponding curves. Figures at the left side represent *Arabidopsis* genes, whereas that at the right side represent rice genes. The adjusted r-squares for the linear regression analyses range from 0.80 to 0.91, and analyses of variance indicate high statistical significance ($P < 2e-16$ in all cases). Similar trends could be observed for other structural parameters, such as total intron length per gene and intron number per gene.

