

Table S5 - Correlation between expression pattern and sequence structural parameters for *Arabidopsis* genes.

Parameters	<i>Exp_{tot}</i>	<i>Exp_{avg}</i>		<i>Width</i>	
	ρ	ρ	partial ρ	ρ	partial ρ
Length of primary transcript	0.194	-0.039	-0.194	0.248	0.229
Length of CDS	0.073	-0.136	-0.180	0.112	0.119
Number of introns	0.251	0.019	-0.162	0.296	0.238
Average exon length	-0.170	-0.077	0.062	-0.190	-0.161
Average intron length	0.252	0.139	0.009*	0.264	0.127
Total intron length	0.289	0.069	-0.130	0.330	0.242
5' UTR length	0.447	0.227	0.014*	0.465	0.192
3' UTR length	0.451	0.229	0.012*	0.467	0.196
5' intergenic length	-0.079	0.001	0.128	-0.104	-0.179
3' intergenic length	-0.140	-0.024	0.072	-0.159	-0.124

The expression data are the microarray data Ren et al. (2006) used in their study. For each structural parameter, ρ s represent Spearman's rank sum correlation coefficients between expression pattern and structural parameters, while partial ρ s represent Spearman's partial correlations. Controlled variable for *Exp_{avg}* is expression width and that for *Width* is average expression level. *Exp_{tot}*, total expression level; *Exp_{avg}*, average expression level; *Width*, expression breadth. CDS, Coding Sequence; UTR, Untranslated Region. Level of significance: *, $P > 0.05$; **, $0.001 < P < 0.05$; ***, $1e - 10 < P < 1e - 3$; No asterisks indicates $P < 1e - 10$. Numbers in bold indicate highly significant partial correlations ($P < 1e - 10$).