

**Table S1 - The correlations between expression pattern and sequence structural parameters for *Arabidopsis* and rice genes.**

Parameters	Arabidopsis			Rice		
	<i>Exp<sub>tot</sub></i>	<i>Exp<sub>avg</sub></i>	<i>Width</i>	<i>Exp<sub>tot</sub></i>	<i>Exp<sub>avg</sub></i>	<i>Width</i>
Length of primary transcript	0.187	-0.091	0.288	0.139	0.134	0.234
		<b>-0.228</b>	<b>0.286</b>		<b>-0.100</b>	<b>0.216</b>
Length of CDS	-0.027	-0.184	0.048	-0.064	-0.071	0.012*
		<b>-0.203</b>	<b>0.090</b>		<b>-0.136</b>	<b>0.116</b>
Average exon length	-0.142	-0.065	-0.184	-0.188	-0.167	-0.220
		0.038***	<b>-0.215</b>		-0.0005*	<b>-0.157</b>
Average intron length	0.205	0.071	0.251	0.161	0.165	0.222
		<b>-0.054</b>	<b>0.225</b>		-0.033***	<b>0.157</b>
Number of introns	0.221	-0.002*	0.303	0.272	0.260	0.343
		<b>-0.151</b>	<b>0.282</b>		-0.032***	<b>0.228</b>
Intron density	0.266	0.102	0.321	0.317	0.307	0.360
		<b>-0.058</b>	<b>0.286</b>		0.027***	<b>0.194</b>
Total intron length	0.243	0.016*	0.333	0.259	0.254	0.343
		<b>-0.158</b>	<b>0.320</b>		<b>-0.046</b>	<b>0.240</b>
5' UTR length	0.472	0.146	0.507	0.112	0.113	0.184
		<b>-0.052</b>	<b>0.331</b>		<b>-0.048</b>	<b>0.153</b>
3' UTR length	0.473	0.145	0.509	0.217	0.199	0.260
		<b>-0.055</b>	<b>0.336</b>		-0.003*	<b>0.165</b>
5' intergenic length	-0.078	-0.022**	-0.124	0.009*	-0.011*	-0.013**
		<b>0.066</b>	<b>-0.167</b>		0.038***	-0.039***
3' intergenic length	-0.129	-0.011*	-0.167	-0.099	-0.089	-0.120
		<b>0.062</b>	<b>-0.142</b>		0.012*	<b>-0.078</b>

For each structural parameter, the first line shows Spearman's rank sum correlation coefficients with expression pattern, while the second line shows Spearman's partial correlations. Controlled variable for the columns of *Exp<sub>avg</sub>* is expression width and that for the columns of *Width* is average expression level. Intron density was defined as the ratio of intron number to coding sequence length, i.e. the number of introns per coding base for each gene. *Exp<sub>tot</sub>*, total expression level; *Exp<sub>avg</sub>*, 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 ( $P < 1e - 10$ ).