

Table S9: Size of intron 5 in orthologs and putative orthologs of the *APETALA3* and *DEFICIENS* genes.

Organism	Gene name	Genomic (size)	sequence	mRNA (size)	sequence	Largest intron / presence of intronic TE sequences
<i>Oriza sativa</i> japonica	<i>SUPERWOMANI</i> (<i>SWI</i>)	AF424549.1 (4.84 kbp)		Gramene LOC_Os06g49890.1 (1,349 nucl)		i5 (2.1 kb) / yes
<i>Zea mays</i>	<i>SILKY1</i> (<i>Si1</i>)	Maize GDB GRMZM2G139073 (4.68 kbp)		NM_001111481.1 (1,004 nucl)		i5 (2.0 kb) / yes
<i>Sorghum</i> <i>bicolor</i>	<i>SbMADS16</i>	NC_012879.1 (4.26 kbp)		XM_002438958.1 (681 nucl)		i5 (2.4 kb) / yes
<i>Brachypodium</i> <i>dystachion</i>	<i>BdMADS16</i>	NC_016131.1 (8.07 kbp)		XM_003560499.1 (702 nucl)		i5 (4.7 kb) / yes
<i>Asparagus</i> <i>officinalis</i>	<i>AoDEF</i>	AB180962.1 (8.55 kbp)		AB180962.1, annotated CDS (678 nucl)		i5 (4.7 kb) / yes
<i>Arabidopsis</i> <i>thaliana</i>	<i>APETALA3</i> (<i>AP3</i>)	TAIR10 AT3G54340 (2 kbp)		NM_115294.5 (1,037 nucl)		i5 (275 nucl) / no
<i>Medicago</i> <i>truncatula</i>	<i>MtAP3-like</i>	NC_016409.1 (3.85 kbp)		XM_003603673.1 (900 nucl)		i4 (2.5 kb) / yes
<i>Solanum</i> <i>lycopersicum</i>	<i>TAP3</i>	NC_015441.1 (3.20 kbp)		NM_001247148.1 (771 nucl)		i4 (803 nucl) / yes
<i>Populus</i> <i>trichocarpa</i>	<i>PtMADS3</i>	NW_001492764.1 (1.82 kbp)		XM_002327739.1 (948 nucl)		i4 (332 nucl) / no
<i>Vitis vinifera</i>	<i>VvAP3</i>	NC_012024.3 (6.06 kbp)		XM_0022779699.2 (1,211 nucl)		i4 (4.1 kb) / yes

The presence of TE-related sequences in the largest intron was assessed using CENSOR (<http://www.girinst.org/censor/index.php>).