

## Supplementary Information

### **A miR172 target-deficient AP2-like gene correlates with the double flower phenotype in roses**

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**Supplementary Table 2. Rose cultivars used in this study.**

Phenotype	Rose species/variety	Code
Simple flower roses	<i>R. wichurana</i>	WIC
	<i>R. gigantea</i>	GIG
	<i>R. chinensis</i> 'Spontanea'	SPO
	<i>R. chinensis</i> 'Sanguinea'	SAN
	<i>R. chinensis</i> 'Mutabilis'	MUT
	<i>R. moschata</i>	MOS
Double Flower roses	<i>R. chinensis</i> 'Old Blush'	OB
	<i>R. x hybrida</i> 'Rouge Meilland'	RME
	<i>R. x hybrida</i> 'La France'	FRA
	<i>R. odorata</i> 'Hume's Blush'	HUM
	<i>R. x hybrida</i> 'Bébé Fleuri'	BFL
	<i>R. x hybrida</i> 'Bengale d'Automne'	BENG
	<i>R. x hybrida</i> 'Cramoisi Supérieur'	CRAM
	<i>R. x hybrida</i> 'Comtesse de Cayla'	COMT
	<i>R. x hybrida</i> 'Ducher'	DUS
	<i>R. x hybrida</i> 'General Shablikine'	GEN
	<i>R. x hybrida</i> 'Blush Noisette'	NOIS
	<i>R. x hybrida</i> 'Hérodiane'	HERO
	<i>R. x hybrida</i> 'Louise d'Arzens'	LOUI

**Supplementary Table 3.** Primers used in this study.

Genotyping primers	RcAP2L_TE_left_border_F	GTGGTGAGAAGTAGTTCCTAGCTAG
	RcAP2L_TE_left_border_R	AGACCAAATAGTAGATCCTCACACG
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	RcAP2L_TE_right_border_R	GAGACTCTTCCACTTTGTTTCCTTG
	RcAP2Lwt_F	ATTGCTATGTCATGTCTTCACAACC
	RcAP2Lwt_R	TATGGATGGGAAAGAAGTTGGAGTT
cDNA sequencing primers	RcAP2L_F	CACCATGCTAGATCTCAACCTCAA
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## Supplementary Data File 1

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