

Table S1. Homologues of *LFY/FLO* and *AP3/DEF* cloned previously or in this study. Gene names conform to the cited reference for previously cloned homologues, or follow the nomenclature for *Antirrhinum majus* if cloned in this study. For species with more than one homologue, an A or B designation describes the paralogy group within which genes cluster in phylogenetic analyses (Aagaard et al., 2005). Species with multiple A or B copies are given a further numeric designation. An abbreviation incorporating both species and gene names is used to label terminal branches in gene trees.

Species	Gene	Abbreviation	Reference	Accession
<i>Petunia hybrida</i>	<i>ALF</i>	PetHyALF	Souer et al., 1998	AF030171
	<i>PMADS1</i>	PetHyPMADS1	Kush et al., 1993	X69946
<i>Solanum esculentum</i>	<i>FA</i>	LycEsFA	Molinero-Rosales et al., 1999	AF197935
	<i>AP3</i>	LycEsAP3	Kramer et al., 1998	AF052868
<i>Syringa vulgaris</i>	<i>FLO</i>	SyrVuFLO	Aagaard et al., 2005	AY524037
	<i>DEF</i>	SyrVuDEF	Aagaard et al., 2005	AY524007
<i>Antirrhinum majus</i>	<i>FLO</i>	AntMaFLO	Coen et al., 1990	M55525
	<i>DEF</i>	AntMaDEF	Sommer et al., 1990	S12378
<i>Chelone glabra</i>	<i>FLO</i>	CheGrFLO	Aagaard et al., 2005	AY524029
	<i>DEF</i>	CheGrDEF	Aagaard et al., 2005	AY524008
<i>Verbena officinalis</i>	<i>FLOA</i>	VerOfFLOA	Aagaard et al., 2005	AY524030
	<i>FLOB</i>	VerOfFLOB	Aagaard et al., 2005	AY524038
	<i>DEFA</i>	VerOfDEFA	Aagaard et al., 2005	AY524009
	<i>DEFB</i>	VerOfDEFB	Aagaard et al., 2005	AY524014
<i>Pedicularis groenlandica</i>	<i>FLOA</i>	PedGrFLOA	Aagaard et al., 2005	AY524033
	<i>FLOB</i>	PedGrFLOB	Aagaard et al., 2005	AY524039
	<i>DEFA</i>	PedGrDEFA	Aagaard et al., 2005	AY524010
	<i>DEFB</i>	PedGrDEFB	Aagaard et al., 2005	AY524017
<i>Paulownia tomentosa</i>	<i>FLOA</i>	PauToFLOA	Aagaard et al., 2005	AY524034
	<i>FLOB</i>	PauToFLOB	Aagaard et al., 2005	AY524040
	<i>DEFA</i>	PauToDEFA	Aagaard et al., 2005	AY524011
	<i>DEFB</i>	PauToDEFB	Aagaard et al., 2005	AY524018
<i>Maxus reptans</i>	<i>FLOA</i>	MazReFLOA	<i>this study</i>	AY530546
	<i>DEFA</i>	MazReDEFA	<i>this study</i>	AY530538
	<i>DEFB</i>	MazReDEFB	<i>this study</i>	AY530542
<i>Mimulus ringens</i>	<i>FLOA</i>	MimRiFLOA	<i>this study</i>	AY530547
	<i>DEFA</i>	MimRiDEFA	<i>this study</i>	AY530539
	<i>DEFB</i>	MimRiDEFB	<i>this study</i>	AY530543
<i>Leucocarpus perfoliatus</i>	<i>FLOA</i>	LeuPerFLOA	<i>this study</i>	AY530548
	<i>FLOB</i>	LeuPerFLOB	<i>this study</i>	AY530550
	<i>DEFA</i>	LeuPerDEFA	<i>this study</i>	AY530540
	<i>DEFB</i>	LeuPerDEFB	<i>this study</i>	AY530544
<i>Mimulus kelloggii</i>	<i>FLOA</i>	MimKeFLOA	<i>this study</i>	AY530549
	<i>DEFA</i>	MimKeDEFA	<i>this study</i>	AY530541
	<i>DEFB</i>	MimKeDEFB	<i>this study</i>	AY530545
<i>Mimulus lewisii</i>	<i>FLOA</i>	MimLeFLOA	Aagaard et al., 2005	AY524035
	<i>FLOB</i>	MimLeFLOB	Aagaard et al., 2005	AY524041
	<i>DEFA</i>	MimLeDEFA	Aagaard et al., 2005	AY524013
	<i>DEFB</i>	MimLeDEFB	Aagaard et al., 2005	AY524019
<i>Mimulus guttatus</i>	<i>FLOA</i>	MimGuFLOA	Aagaard et al., 2005	AY524036
	<i>FLOB</i>	MimGuFLOB	Aagaard et al., 2005	AY524042
	<i>DEFA</i>	MimGuDEFA	Aagaard et al., 2005	AY524012
	<i>DEFB</i>	MimGuDEFB	Aagaard et al., 2005	AY524020

Table S2. Likelihood ratio test (LRT) statistics comparing branch-specific models (R1-R4) and fixed-sites models (C and E). The test statistic ($2 \Delta \ln L$) is calculated as twice the difference between log-likelihood values for models, and compared with a chi-square distribution with degrees of freedom equal to the difference in the number of parameters between models (Table 1).

Gene	Models Compared	$2 \Delta \ln L$
<i>LFY/FLO</i>	One-ratio (R1) vs. Two-Ratio (R2)	7.104**
	Two-ratio (R2) vs. Three-Ratio (R3)	1.236
	Three-ratio (R3) vs. Four-Ratio (R4)	58.992**
	Model C vs. Model E	59.590**
<i>AP3/DEF</i>	One-ratio (R1) vs. Two-Ratio (R2)	5.770*
	Two-ratio (R2) vs. Three-Ratio (R3)	2.012
	Three-ratio (R3) vs. Four-Ratio (R4)	0.010
	Model C vs. Model E	0.212

*Significant at $p \leq 0.05$. **Significant at $p \leq 0.005$.

Table S3. Likelihood ratio test (LRT) statistics comparing sites models (M1a-M8) and branch-sites-models (A and B). The test statistic ($2 \Delta \ln L$) is calculated as twice the difference between log-likelihood values for models, and compared with a chi-square distribution with degrees of freedom equal to the difference in the number of parameters between models (Table 2).

Gene	Models Compared	$2 \Delta \ln L$
<i>LFY/FLO</i>	Neutral (M1a) vs. Selection (M2a)	0.000
	Beta (M7) vs. Beta & ω (M8)	8.984*
	ModelA vs. ModelA _{null}	0.000
<i>AP3/DEF</i>	Neutral (M1a) vs. Selection (M2a)	0.000
	Beta (M7) vs. Beta & ω (M8)	3.682
	ModelA vs. ModelA _{null}	0.000

*Significant at $p \leq 0.05$. **Significant at $p \leq 0.005$.