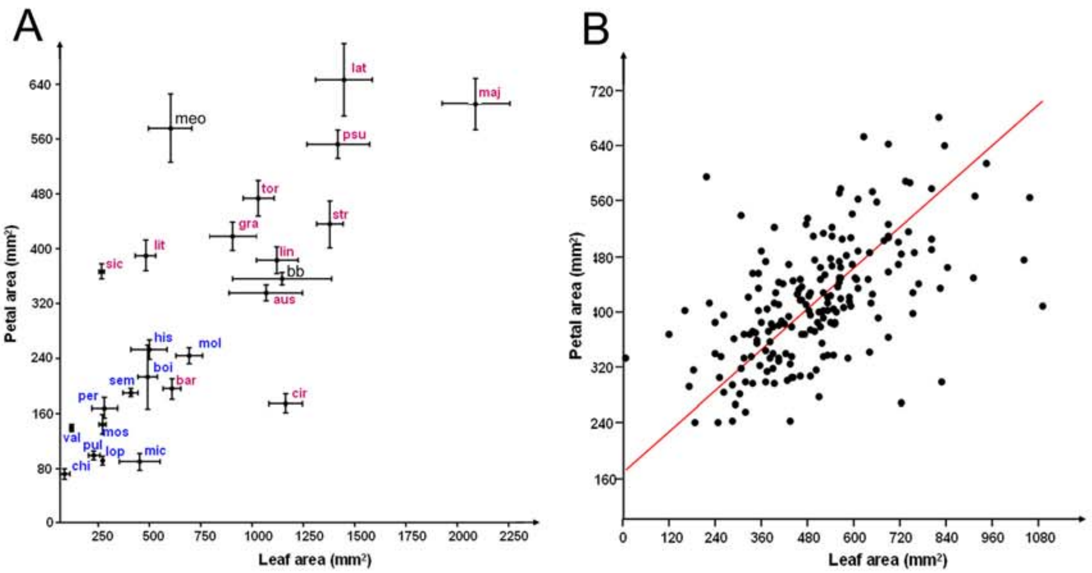
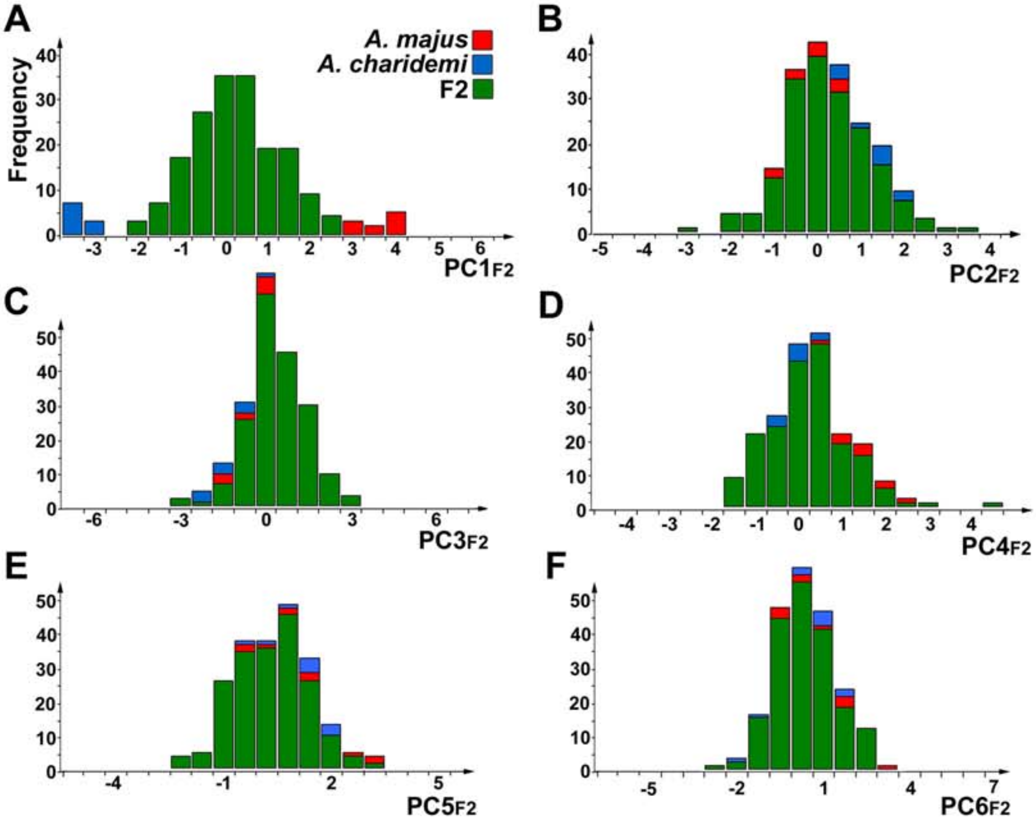


Supplemental Figure 1 Correlations between leaf and petal areas

(A) Mean dorsal petal area plotted against mean leaf area (± standard errors) for each of the species ($r = 0.65$ for all individuals; please see Supplemental Table 1 for details of sample sizes). Members of subsection Antirrhinum are shown in red, subsection Kickxiella in blue and Streptosepalum in black. aus = *A. australe*, bar = *A. braun-blanquetii*, boi = *A. boisieri*, chi = *A. charidemi*, cir = *A. cirrhigerum*, gra = *A. graniticum*, his = *A. hispanicum*, lat = *A. latifolium*, lin = *A. linkianum*, lit = *A. litigiousum*, lop = *A. lopesianum*, maj = *A. majus*, meo = *A. meonanthum*, mic = *A. microphyllum*, mol = *A. molle*, mos = *A. mollissimum*, per = *A. pertegasii*, psu = *A. pseudomajus*, pul = *A. pulverulentum*, sem = *A. sempervirens*, sic = *A. siculum*, str = *A. striatum*, tor = *A. tortuosum*, val = *A. valentinum*.

(B) Dorsal petal area plotted against leaf area for the F2 mapping population. The reduced major axis regression line is shown in red, $r = 0.55$.



Supplemental Figure2 Segregation of PCF2 values in F2 hybrids

Each histogram shows the distribution of F2 hybrids (green) along the first six PCs of the F2 allometry model (A-H), in relation to the values for their parents, *A. majus* (red) and *A. charidemi* (blue). PC values are shown on the x-axis in standard deviations from the mean of the F2 population.

Supplemental Table 1 Antirrhinum accessions

Species^{a}	**Population**^{b}	**Mothers**^{c}	**Offspring**^{d}
A. australe Rothm.	Benamahoma, Cádiz, S	2	2
	Grazalema, Cádiz, S	1	1
	Villaluenga del Rosario, Cádiz, S	1	1
	Cortes de la Frontera, Málaga, S	1	1
	Benaoján, Málaga, S	1	1
	Gaucin, Málaga, S	1	1
	El Burgo, Málaga, S	1	2
	Torcal de Antequera, Málaga, S	1	1 (10)
A. barrelieri Boreau	Alora, Málaga, S	3	3
	Padul, Granada, S	3	4 (7)
A. braun-blanquetii Rothm.	St Pietro de Villanueva, Asturias, S	1	2 (2)
A. boisieri Rothm.	Guadahortuna, Granada, S	1	2
A. charidemi Lange	Cabo de Gata, Almeria, S	1	10 (10)
A. cirrhigerum Welwitsch	Gala, Coimbra, P	2	3
	Praia de Mira, Coimbra, P	2	3
	Lisboa, Lisboa, P	1	1
	Sagres, Faro, P	2	3 (10)
A. graniticum Roth.	Bragança, Bragança, P	1	2
	Gallur, Zaragoza, S	1	1
	Fuentidueña deTajo, Madrid, S	1	1
	Chinchón, Madrid, S	1	1
	Celorico da Beira, Guarda, P	1	1
	Tornavacas, Cáceres, S	1	1
	Navalperal de Tormes, Toledo, S	2	2
	Navacepeda de Tormes, Ávila,S	1	1 (10)
A. hispanicum Chavannes	Mecina Bombarón, Granada, S	2	2
	Balcón de Canales, Granada, S	1	2
	Almargen, Malaga, S	4	6 (10)
A. latifolium Millspaugh	Roubion, Alpes-Maritime, F	3	6
	Bagà, Berguedà,S	1	1
	Entrevaux, Alpes-de-Haute-Provence, F	2	3
A. linkianum Boissier & Reuter	Serra d Arrábida, Setúbal, P	1	2
	Almada, Setúbal, P	1	2
	Sintra, Lisboa, P	1	1
	Pernes, Santarém, P	2	2
	Porto de Mós, Leiria, P	1	1
	Coimbra, Coimbra, P	2	2 (10)
A. litigiosum Pau	Mas de Barberans, Tarragona, S	1	1
	Cheste, Valencia, S	1	1
	Traiguera, Castello, S	1	3
	Santes Creus A, Tarragona, S	1	2
	Santes Creus B, Tarragona, S	1	2
	Borja, Zaragoza, S	1	1 (10)
A. lopesianum Rothm.	Alfaiao, Bragança, P	1	10 (10)
A. majus L.	John Innes Centre, inbred line	1	10 (10)
A. meonanthum Link	Manteigas, Guarda, P	4	4
	Sobradelo, Ourense, S	1	1 (5)
A. microphyllum Rothm.	Sacedón, Guadalajara, S	5	7 (7)

A. molle L.	Gerri de la Sal, Lleida, S	1	2
	Seu de Urgell, Lleida, S	2	2
	Saldes, Berguedà, S	1	2
	South of Seu de Urgel, Lleida, S	1	2
	Bagá, Barcelona, S	1	1
	Martinet, Lleida, S	1	1 (10)
A. mollissimum Rothm.	Capileira, Granada, S	1	1
	Felix, Almería, S	1	1
	Enix, Almería, S	1	1
	Canjáyar, Almería, S	2	2
	Bayárcal, Almería, S	1	1
	Juviles, Granada, S	1	1
	Trevélez, Granada, S	1	1
	Bubión, Granada, S	1	1
	Lanjarón, Granada, S	1	1 (10)
A. pertegasii Rothm.	Near Pego, Alicante, S	2	4
	Albacete, Albacete, S	1	1 (5)
A. pseudomajus Rothm.	Ribes de Freser, Girona, S	2	5
	Minerve, Aude, F	3	4
	Prats-de-Mollo-la-P., Pyrénées-Orientales, F	1	1 (10)
A. pulverulentum Lazaro	Pelegrina, Guadalajara, S	1	1
	Alcorlo, Guadalajara, S	6	9 (10)
A. sempervirens Lapeyrouse	Héas, Hautes-Pyrénées, F	1	5
	Col d'Aubisque, Pyrénées-Atlantiques, F	4	5 (10)
A. siculum Miller	Taormina, Sicilia, I	2	5
	Palermo, Sicilia, I	1	1
	Vicolo del Gargano, Puglia, I	1	1
	Unknown, ex IPK Gatersleben genebank	2	3 (10)
A. striatum Rothm.	Alet Les Bains, Aude, F	1	1 (1)
A. tortuosum Bosc	Casas de El Cañizar, Cuenca, S	1	1
	El Tempul, Cádiz, S	1	1
	Casares, Málaga, S	1	1
	Marbella, Málaga, S	1	1
	Almargen, Málaga, S	1	1
	Loja, Granada, S	1	1
	Priego de Córdoba, Córdoba, S	1	1
	Alcaudete, Jaén, S	1	1
	Cerro Muriano, Córdoba, S	1	1
	Gibraltar	1	1 (10)

a: Taxa sometimes regarded as subspecies of *A. majus* are considered to rank as separate species for clarity. *A. majus* refers here only to the inbred parent of the F2 mapping population, derived from cultivated stocks.

b: The location of each population from which seeds were sampled. S = Spain, F = France, P = Portugal, I = Italy. The number of populations sampled for each species broadly reflects its geographic range.

c: The number of maternal parents sampled from each population.

d: The number of offspring from each population that were used in allometric analysis. The figure in parentheses against the last population of each species shows the total number of individuals analysed for that species.

Supplemental Table 2 A molecular recombination map for the *A. majus* x *A. charidemi* F2 population

Marker[a]	position (cM)[b]	Dominance[c]	Type[d]	Plants genotyped[e]
1:01	0	c	CAPS	175
1:02 (AJ568102 *46*)	14	c	CAPS	198
1:03	20	c	synth	204
1:04	22	c	synth	203
1:05	24	dm	synth	203
1:06	25	c	synth	203
1:07	27	dc	AFLP	197
1:08	34	d	AFLP	201
1:09	37	c	SSLP	170
1:10	39	dm	AFLP	187
1:11	41	dm	AFLP	191
1:12	43	c	synth	203
1:13	46	c	synth	204
1:14	52	dc	AFLP	191
1:15	53	c	CAPS	183
1:16	57	d	AFLP	185
1:17	63	dc	AFLP	171
1:18	82	dc	AFLP	200
1:19 (X03710 *NIV*)	84	c	CAPS	135
1:20	85	dc	CAPS	95
1:21	87	dc	AFLP	203
1:22	90	dm	AFLP	201
2:01	0	dc	CAPS	162
2:02	13	dc	SSLP	147
2:03 (X92369 *SBP*)	23	d	CAPS	138
2:04	32	dm	AFLP	165
2:05	43	dm	SSLP	152
2:06 (X63701 *SQUA*)	46	c	CAPS	198
2:07	52	dc	AFLP	203
2:08	54	c	SSLP	191
2:09	55	dm	AFLP	200
2:10	57	c	synth	192
2:11	60	c	synth	203
2:12 (S53900 *PLE*)	66	c	CAPS	132
2:13	68	dm	AFLP	199
2:14	71	c	CAPS	105
2:15	76	c	synth	192
2:16	82	dm	AFLP	198
2:17	85	c	synth	192
2:18	87	dc	AFLP	197
2:19	92	c	synth	202
2:20	94	dc	AFLP	189
2:21	99	dc	AFLP	199
2:22	104	dc	AFLP	185
3:01	0	dm	AFLP	184
3:02	14	dc	CAPS	190
3:03	15	dc	AFLP	185
3:04	18	c	synth	203
3:05	19	dm	AFLP	200
3:06	21	dc	AFLP	190
3:07	24	dm	AFLP	204
3:08 (AJ568098 *42*)	24	c	CAPS	198
3:09	26	dm	AFLP	190
3:10	27	dm	AFLP	190
3:11	27	dm	synth	203
3:12	28	dm	CAPS	194
3:13 (M55525 *FLO*)	30	dm	CAPS	193
3:14	32	dm	AFLP	191
3:15	34	dm	AFLP	201
3:16	37	c	synth	203
3:17	45	dm	AFLP	190

3:18	49	c	synth	202
3:19	52	dc	AFLP	199
3:20	53	dc	AFLP	203
3:21 (AJ804282 *214*)	58	c	CAPS	94
3:22	59	dc	AFLP	199
3:23	60	dm	AFLP	191
3:24	69	c	CAPS	191
3:25 (AJ250397 *CYCD3A*)	78	c	CAPS	198
4:01	0	c	CAPS	107
4:02	7	c	synth	203
4:03	12	c	synth	203
4:04	16	c	CAPS	182
4:05	19	dm	AFLP	188
4:06	24	dm	AFLP	191
4:07	33	c	synth	204
4:08	38	c	CAPS	133
4:09	41	c	synth	203
4:10	44	c	synth	202
4:11	48	c	CAPS	87
4:12	50	dm	AFLP	165
4:13	52	c	synth	204
4:14 (AJ803243 *74*)	53	dc	CAPS	106
4:15	54	c	CAPS	202
4:16	56	dc	AFLP	190
4:17	58	c	CAPS	197
4:18	60	c	synth	204
4:19	62	dm	AFLP	173
4:20	66	c	synth	203
4:21 (AY072735 *INA*)	69	c	CAPS	197
4:22	74	c	synth	201
4:23	77	dm	AFLP	191
4:24	80	dm	synth	204
4:25	85	dm	AFLP	201
4:26	89	dc	AFLP	191
4:27	92	c	CAPS	190
4:28	94	dm	AFLP	191
4:29	98	dm	AFLP	185
4:30	104	c	synth	192
4:31	115	c	CAPS	191
5:01	0	dm	AFLP	203
5:02	17	dm	AFLP	201
5:03	20	c	SSLP	189
5:04 (AJ568103 *48*)	21	dc	CAPS	132
5:05	29	dc	synth	202
5:06	29	d	synth	192
5:07	32	c	synth	192
5:08	34	dc	AFLP	201
5:09 (AJ568044 *113*)	38	dm	CAPS	174
5:10	48	dm	AFLP	201
5:11	55	c	synth	192
5:12	62	dc	AFLP	188
5:13	65	dm	AFLP	204
5:14	70	dm	AFLP	191
5:15	76	dm	AFLP	187
6:01	0	dm	AFLP	188
6:02	17	dc	AFLP	191
6:03	22	c	CAPS	179
6:04 (AF208341 *CYC*)	35	c	CAPS	105
6:05 (AJ804396 *203*)	49	c	CAPS	201
6:06	54	dm	AFLP	187
6:07	55	dc	AFLP	187
6:08	64	c	CAPS	138
6:09	67	dm	AFLP	192
6:10	68	dm	AFLP	192
6:11	71	dm	AFLP	182
7:01	0	c	CAPS	117

7:02 (Y14857 *FAP2*)	13	c	CAPS	196
7:03	17	dc	CAPS	105
7:04	17	dm	AFLP	190
7:05	23	dm	AFLP	192
7:06	24	dc	AFLP	199
7:07	31	c	synth	199
7:08	34	dm	AFLP	190
7:09	39	dm	CAPS	181
7:10	41	dm	AFLP	200
7:11 (AJ568042 *107*)	43	c	CAPS	201
7:12	44	dm	synth	192
7:13	45	c	synth	204
7:14	46	c	synth	203
7:15	50	dc	AFLP	192
7:16	53	c	synth	203
7:17	59	dm	AFLP	192
7:18	61	dc	AFLP	202
7:19	70	dm	AFLP	183
7:20	74	dc	AFLP	203
8:01 (X62810 *DEF*)	0	d	CAPS	191
8:02	17	d	AFLP	199
8:03	20	c	CAPS	177
8:04	22	c	CAPS	138
8:05	24	c	synth	192
8:06	26	d	AFLP	190
8:07	29	c	synth	202
8:08	32	c	synth	204
8:09	35	c	synth	204
8:10	36	d	AFLP	203
8:11	40	d	CAPS	158
8:12	47	c	synth	203
8:13	51	c	synth	203
8:14	52	d	synth	204
8:15 (AJ568075 *26*)	55	c	CAPS	197
8:16	56	c	synth	204
8:17	59	c	synth	203
8:18	62	c	synth	203
8:19	64	d	AFLP	177
8:20	72	d	AFLP	190
8:21	75	d	AFLP	189
8:22	78	c	CAPS	122
8:23	86	c	CAPS	197

a: Each locus is named according to its relative order within the eight linkage groups of Antirrhinum – e.g. 1:02 is the second marker from the top of Linkage Group 1. The map was estimated with *Joinmap 2.0* software, taking a LOD value of 7.0 as the minimum support for a linkage group and using default parameters for estimating marker positions within groups. For loci that were used in a previous recombination map for Antirrhinum (Schwarz-Sommer et al., 2003), sequence accession numbers are given in parentheses with the previous name of the locus in italics. The linkage groups are numbered and oriented as in the previous map.

b: The estimated position of the locus relative to the first marker in the linkage group, in centiMorgans estimated from recombination fractions using the Kosambi function.

c: Dominance of markers. *c* denotes a co-dominant marker, *dc* a dominant marker originating from the *A. charidemi* parent and *dm* a dominant marker from the *A. majus* parent.

d: Amplified fragment length polymorphisms (shown as *AFLP*) were generated from *Pst*I – *Mse*I restriction fragments, using six different combinations of selective primers. To simplify QTL analysis, AFLPs that mapped to the same position were combined to create synthetic loci (*synth*) with a dominant allele if the AFLPs came from the same parent or co-dominant alleles if the AFLPs were in repulsion. *CAPS* denotes a marker amplified from a protein coding gene and detected usually as a restriction fragment length polymorphism. *SSLP* denotes a microsatellite marker located in a non-coding sequence.

e: The number of F2 individuals from the population of 204 plants that were genotyped at each locus.

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