**Supporting Information Methods and Results S1.** Data treatment, ordination and measures of disparity of Stebbins (1951) dataset.

**Supporting Information Figure S1:** Frequency of the 16 character states recorded by Stebbins (1951) for ten angiosperm subgroups. Colors highlight character states whose frequency exceeds 85 %.

#### Methods S1

#### Data treatment

We used the character states of eight binary characters that were recorded for 288 angiosperm families by Stebbins (1951). A character state combination is thus a binary vector of length eight. Polymorphic families (n=90) were recorded several times for each character state combination. We assigned each family to one of ten major angiosperm taxa (some of them non-monophyletic) according to the current classification of APG III (2009) and Soltis et al. (2011): basal angiosperms, monocots, basal eudicots, basal superrosids, fabids, malvids, Caryophyllales, basal superasterids, lamiids, and campanulids. We are aware that the taxonomic composition and therefore also the family descriptions of some angiosperm families such as Hamamelidaceae, Scrophulariaceae, or Theaceae have changed considerably since Stebbins' paper was published. Some character state combinations of Stebbins dataset might thus be differently represented in the currently delimited families. We chose angiosperm subgroups to be large enough so that most of these changes do not affect the total morphospace occupied by each category. The full dataset with all recorded character state combinations (taken from Stebbins 1951) and the subgroup assignments are given in Supplementary Table 1. The number of families per subgroup is given in Figure 4d.

## Ordination

In order to visualize the area of the space occupied by each major taxonomic group, we performed an NMDS ordination with the function metaMDS from the *vegan* package (Oksanen *et al.*, 2013) in R vs. 3.0.0. (R Core Team, 2013). This method uses an iterative process to maximize the correspondence between pairwise distances calculated from the data, and the Euclidean distances between dots in a two or three-dimensional representation (Rabinovitz, 1975). The quality of the fit is estimated by the stress value, ranging from 0 (best solution) to 1 (worst solution). We used the distance index D = 1 - S where S is the simple matching index for symmetric binary characters (Gower & Legendre, 1986), so that for two given character combinations, D is the proportion of characters that are under different states in these combinations. Finally, we tested for morphological differences among taxonomic groups using a non-parametric multivariate analysis of variance (npMANOVA; Anderson, 2001) with the function adonis from the *vegan* package in R, using the same dissimilarity index (D) and 10,000 repetitions. Post hoc tests were performed in the same way with a npMANOVA and a Bonferroni correction.

#### Measure of disparity

We computed three disparity indices for each of the ten angiosperm subgroups, following the method of Ciampaglio *et al.* (2001): the sum of variances, as the sum of the three variances associated to the scores of each NMDS ordination axis; the range, as the maximum simple matching distance between two families; and the averaged pairwise distances, calculated with the simple-matching distance index. As subgroup size varies considerably (from 15 families for basal superrosids to 84 for fabids, figure 4d), we added an analysis of rarefaction for the range (variance and average pairwise distance are relatively insensitive to sample), for which we strictly followed the method of Foote (1992). For each angiosperm subgroup, and for each possible sampling size (from 3 to the group size), we calculated the mean and 90% confidence intervals of the disparity indices obtained from 200 random samplings without replacement. The resulting curves allowed us to compare the angiosperm subgroups despite their size differences.

## **Results S1**

## Posthoc test results for the npMANOVA:

> posthoc: upper part: r2, lower part: p								
	basal angiosper	ms basal	eudico	ots basa	l superasterid:	s basal	superrosids	campanulids
basal angiosperms		NA	0.02	250	0.117	)	0.0160	0.3910
basal eudicots	0.38	95	NA		0.161	)	0.0820	0.4290
basal superasterids	0.00	02	0.0001		N	J –	0.0590	0.1080
basal superrosids	0.59	56	0.0451		0.009	2	NA	0.3420
campanulids	0.00	01	0.0001		0.000	1	0.0001	NA
Caryophyllales	0.00	25	0.0001		0.000	9	0.0038	0.0001
fabids	0.03	36	0.0055		0.000	2	0.5888	0.0001
lamiids	0.00	01	0.00	001	0.000	L	0.0001	0.0001
malvids	0.00	15	0.00	001	0.000	L	0.2683	0.0001
monocots	0.00	01	0.00	001	0.051	1	0.1058	0.0018
	Caryophyllales	fabids l	amiids	malvids	monocots			
basal angiosperms	0.1130	0.0320	0.3010	0.0630	0.100			
basal eudicots	0.2060	0.0480	0.2800	0.1080	0.121			
basal superasterids	0.0720	0.0720	0.1090	0.0790	0.020			
basal superrosids	0.1190	0.0060	0.2350	0.0170	0.024			
campanulids	0.3160	0.2140	0.1460	0.2500				
Caryophyllales	NA	0.0790	0.2380	0.1320	0.091			
fabids	0.0001	NA	0.1920	0.0230	0.070			
lamiids	0.0001	0.0001	NA	0.2180	0.102			
malvids	0.0001	0.0237	0.0001	NA	0.053			
monocots	0.0001	0.0001	0.0001	0.0002	NA			
> p #with Bonferron	i correction							
[1] 0.001111111								

#### > posthoc2: significance of p after the Bonferroni correction

	basal angiospe	rms basa	l eudico	ts basal	superasterids	basal	superrosids	campanulids
basal angiosperms	<1	NA>	<n2< td=""><td>A&gt;</td><td><na></na></td><td></td><td><na></na></td><td><na></na></td></n2<>	A>	<na></na>		<na></na>	<na></na>
basal eudicots		ns	<n2< td=""><td>A&gt;</td><td><na></na></td><td></td><td><na></na></td><td><na></na></td></n2<>	A>	<na></na>		<na></na>	<na></na>
basal superasterids		*		*	<na></na>		<na></na>	<na></na>
basal superrosids		ns	1	ns	ns		<na></na>	<na></na>
campanulids		*		*	*		*	<na></na>
Caryophyllales		ns		*	*		ns	*
fabids		ns	1	ns	*		ns	*
lamiids		*		*	*		*	*
malvids		ns		*	*		ns	*
monocots		*		*	ns		ns	ns
	Caryophyllales	fabids	lamiids r	malvids	monocots			
basal angiosperms	<na></na>	<na></na>	<na></na>	<na></na>	NA			
basal eudicots	<na></na>	<na></na>	<na></na>	<na></na>	NA			
basal superasterids	<na></na>	<na></na>	<na></na>	<na></na>	NA			
basal superrosids	<na></na>	<na></na>	<na></na>	<na></na>	NA			
campanulids	<na></na>	<na></na>	<na></na>	<na></na>	NA			
Caryophyllales	<na></na>	<na></na>	<na></na>	<na></na>	NA			
fabids	*	<na></na>	<na></na>	<na></na>	NA			
lamiids	*	*	<na></na>	<na></na>	NA			
malvids	*	ns	*	<na></na>	NA			
monocots	*	*	*	*	NA			

#### **References:**

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http://www.mobot.org/MOBOT/research/APweb/welcome.html. [accessed 1 January 2014].

# Chartier et al. The floral morphospace. Supporting Information Figure S1

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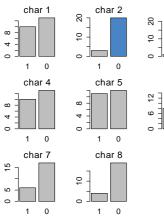
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# basal angiosperms



## basal superrosids

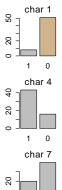


# basal superasterids

- 20

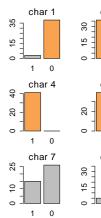
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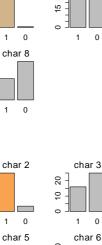
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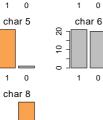




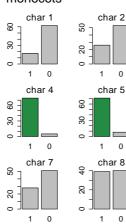
lamiids



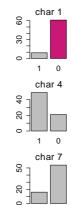




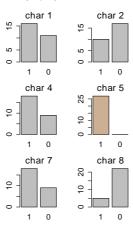
# monocots



# malvids



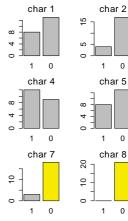
# Caryophyllales

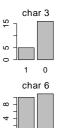


#### Table 1 Ch

able 1.	
haracter	State "0"
1	Calyx and corolla both present (dichlamydous)
2	Petals separate (polypetalous)
3	Calyx and corolla regular (actinomorphic)
4	Stamens more numerous than perianth members (polystemonous)
5	Carpels separate (apocarpous)
6	Seeds more than one per carpel (many)
7	Placentation axial
8	Carpels not united with the receptacle or perianth (hypogyny or perigyny, i.e. superior ovary)

# basal eudicots







char 2

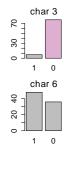
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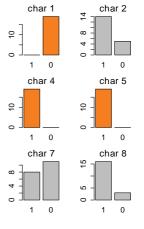
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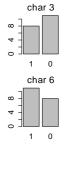
g





# campanulids





State "1" Corolla or entire perianth absent (monoor achlamydous) Petals (sepals in monochlamydous forms) united (sympetalous) Perianth irregular (zygomorphic) Stamens the same number as or fewer than perianth members (oligostemonous) Carpels united (syncarpous) Seeds not more than one per carpel (few) Placentation parietal, basal or free central Carpels united with receptacle, perianth,

or both (epigyny, i.e. inferior ovary)

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