Electronic Supplementary Material

Methods

Phylogeny

I reanalysed sequence data from a thorough investigation of rockfish phylogeny (see Hyde & Vetter 2007 for methods and GenBank Accession numbers). I used the program BEAST (http://beast.bio.ed.ac.uk/) to produce a time-calibrated tree based on 2 nuclear and 7 mitochondrial genes. I included the biogeographic calibration point used previously (Hyde & Vetter 2007), with a strong prior (normal, mean 3 m.y.a., s.d. 0.05 m.y.a.) on the divergence time between *Sebastes alutus* and a clade of four Atlantic species. I also used a weakly informative lognormal prior (mean 7 m.y.a., log s.d. 0.5 m.y.a.) on the root age of *Sebastes* based on the sparse fossil record. I ran the analysis for 20 million generations, sampling every 2500th tree for a total of 8000 samples, and discarded the first 25% as burn-in. I used the 'TreeAnnotater' utility to produce the maximum clade credibility tree (maximizing the sum of the posterior probabilities of nodes) and to calculate mean branch lengths from the posterior distribution.

The full phylogeny included 99 species of *Sebastes* as well as four outgroups (*Hozukius emblemarius*, *Helicolenus avius*, *Sebastolobus alascanus* and *Sebastiscus marmoratus*). I removed all but the 66 northeast Pacific *Sebastes* species from the tree for this study, meaning some nodes were missing from the 66 species tree. I did not include these nodes in the analyses described below, on the grounds that these speciation events occurred outside the northeast Pacific arena of diversification investigated in this study. I also excluded three morphologically cryptic species that have been proposed since the initiation of this study (Hyde & Vetter 2007, Hyde *et al.* 2008, Burford 2009). The

resulting tree (fig. S1) was highly similar to a previously published Bayesian consensus tree (fig. 3 in Hyde & Vetter 2007), with almost perfect congruence near the tips, and disagreement about earlier nodes largely coming from my decision to resolve all nodes rather than collapse weakly supported nodes into polytomies.

Simulations

To ensure that the inference method can recover known differences in ψ, I simulated growth of 66 phylogenetic trees following a birth-death process with $\lambda = 0.5$ and $\mu = 0$ or 0.1. Concurrent with tree growth, I simulated character evolution in accordance with the model assumed in this article, where evolution occurs via both Brownian motion and step change at speciation. For the 33 trees with a given value of μ, I simulated character evolution with $\sigma^2_t = 0.1$ and three replicates of each of 11 values of ψ (0, 0.1…0.9, 1). At each time step ($\Delta t = 0.01$), each lineage speciated with probability $\lambda\Delta t$ or went extinct with probability $\mu\Delta t$. Brownian motion evolution occurred at a rate of $\sigma^2_a\Delta t$, where $\sigma^2_a = \sigma^2_t(1-\psi)$, and at speciation the change in traits of each daughter species had variance σ^2_c, where $\sigma^2_c = (\sigma^2_t\psi)/\lambda$. I ran each analysis until the number of extant species matched the number of species in the rockfish tree (N = 66).

The inference method consistently recovers purely gradual evolution ($\psi = 0$). There was no bias in the estimations of higher values of ψ (0.1-1), though there was considerable scatter around these estimates (R^2 ranged from 0.6-0.78; fig. S7). There was no obvious improvement in estimation when the true λ and μ were used instead of λ and μ estimated from the tree, indicating that the estimation of speciation and extinction rates does not considerably increase the error in estimates of ψ.

Figures

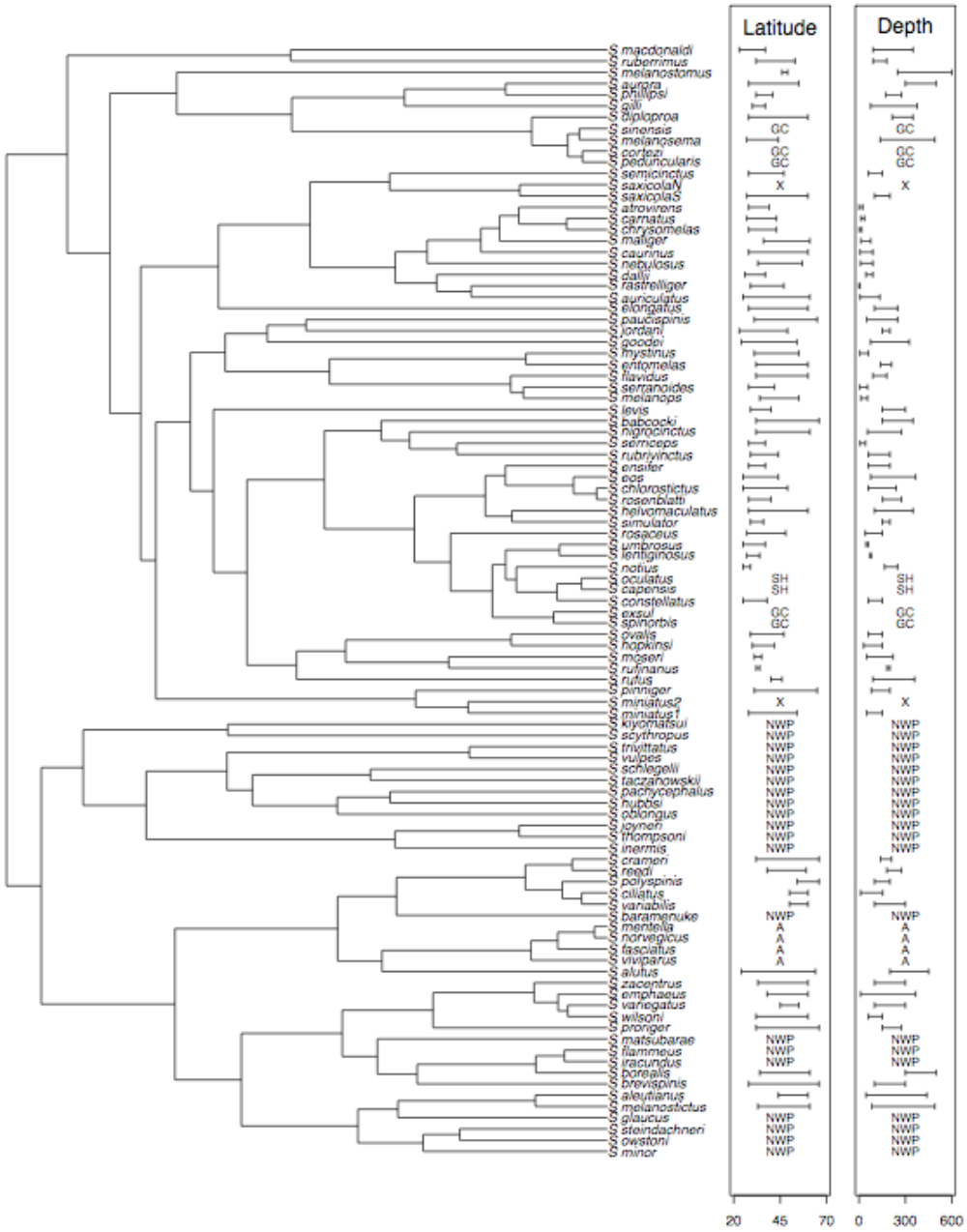


Figure S1. *Sebastes* phylogeny used for the main analyses presented in this paper. To the right of each species' name is its latitudinal (º) and depth (m) ranges. Species not in the northeast Pacific dataset are labeled (NWP = Northwest Pacific; A = Atlantic; GC = Gulf of California; SH = Southern Hemisphere; X = recently described NEP species, no data).

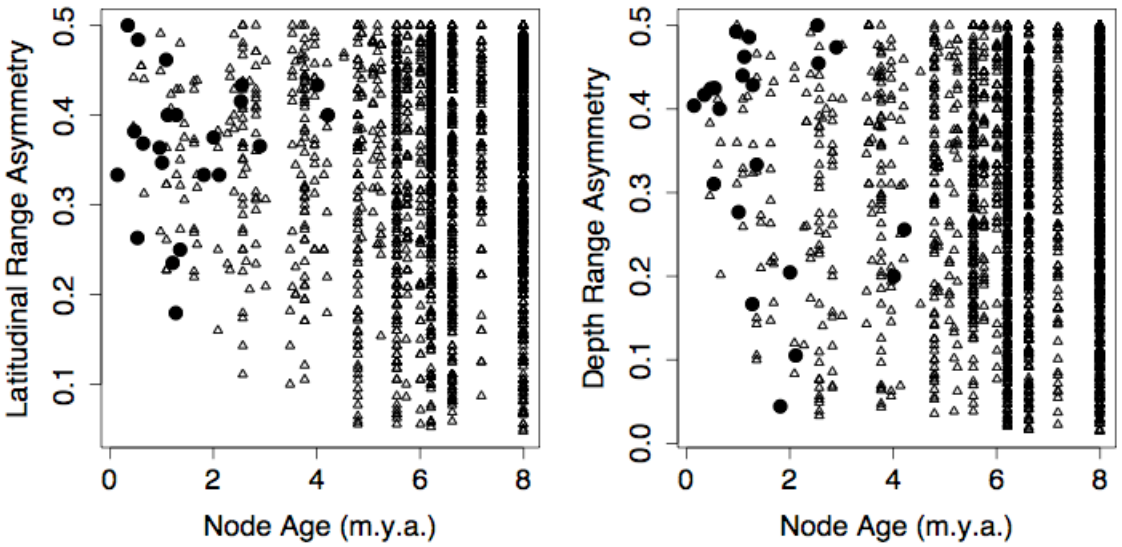


Figure S2. Asymmetry in range sizes in both latitude and depth, against time since divergence for pairs of rockfish species. Asymmetry is calculated following Barraclough & Vogler (2000) as (smaller range size)/(sum of range sizes). As in Figure 1, sister species are denoted with filled symbols. There was no relationship between asymmetry and node age for either latitude (Mantel test, $p = 0.40$) or depth ($p = 0.56$).

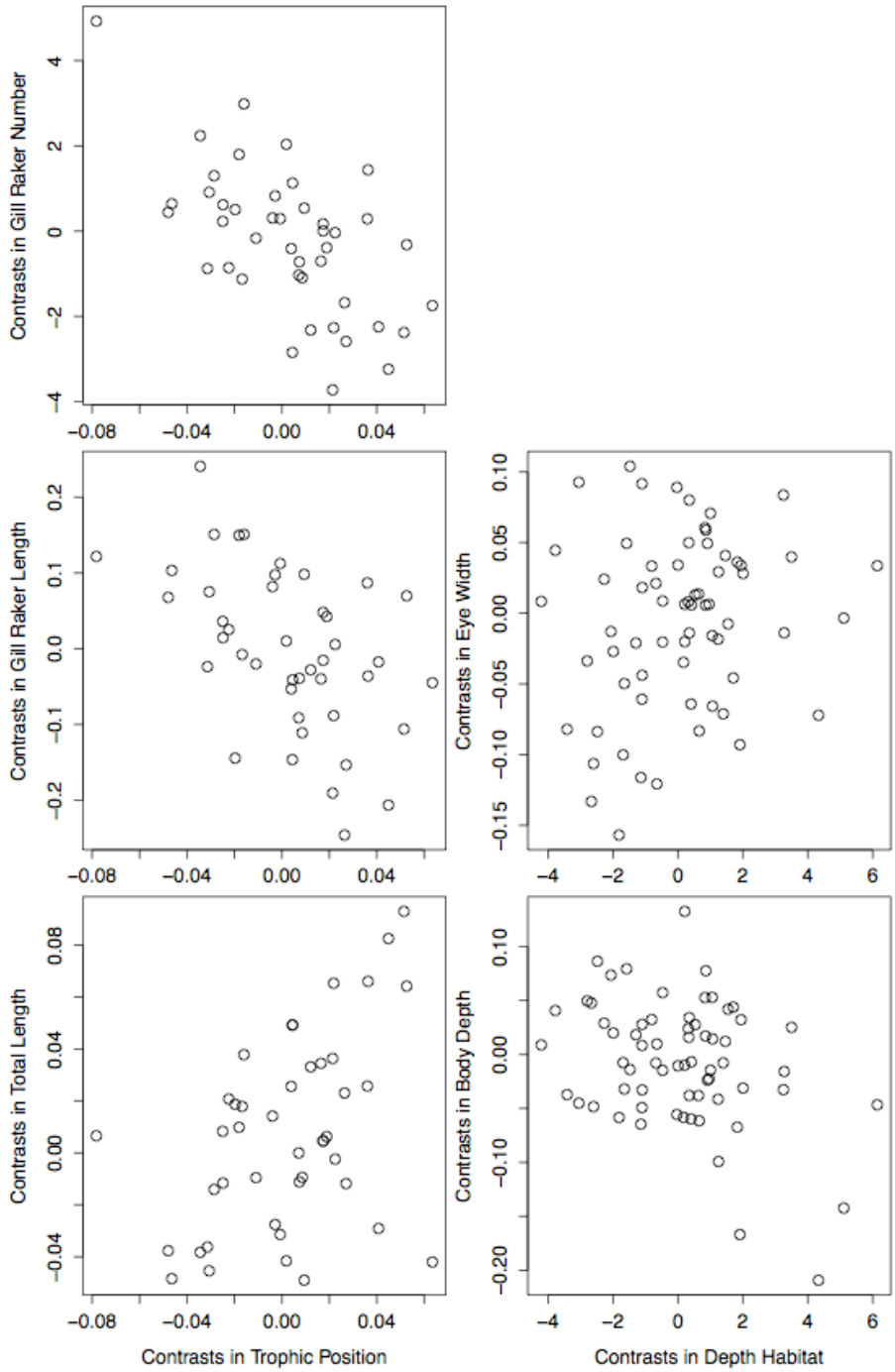
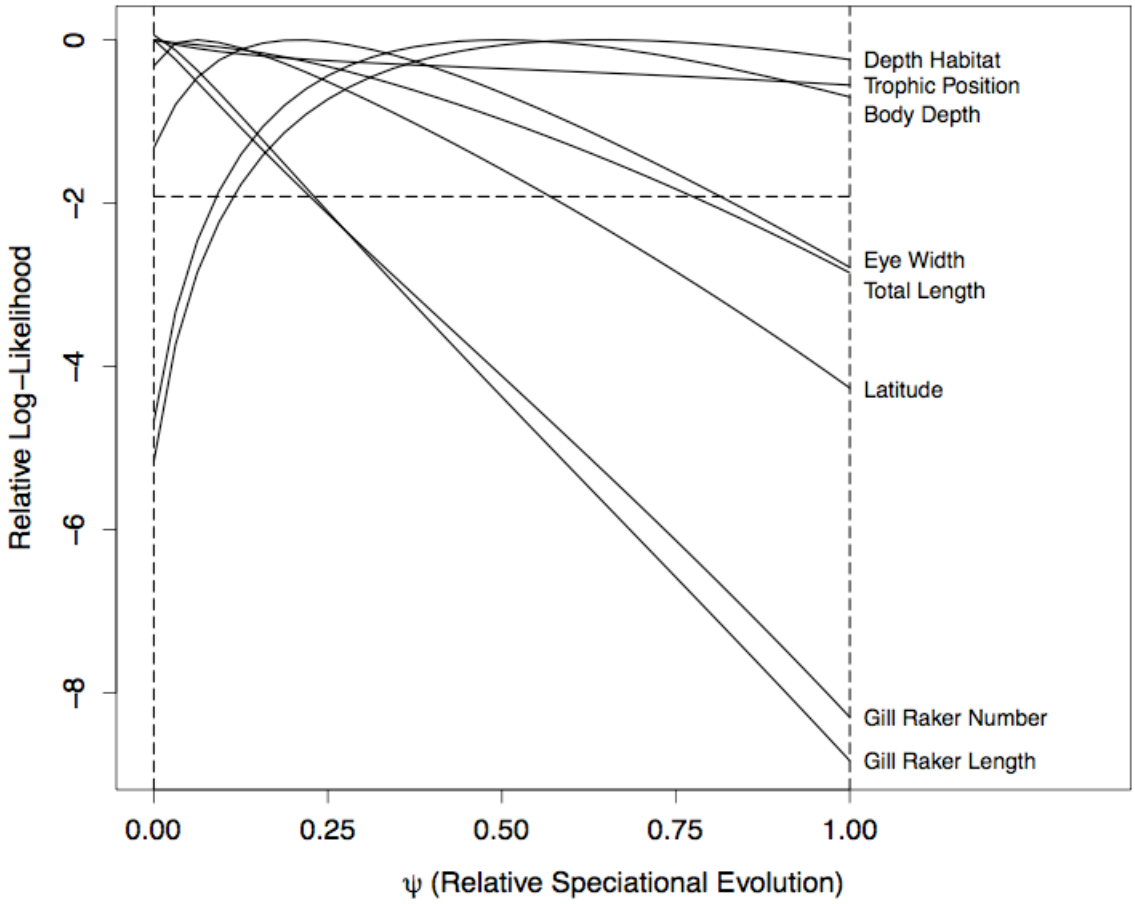


Figure S3. Relationships between five morphological traits and the niche axis each is most associated with. Phylogenetically independent contrasts in three traits are shown against contrasts in trophic position (TP; left column), and contrasts for two traits are shown against contrasts in depth habitat (right column).



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65 Figure S4. Profile likelihood surfaces for ψ for characters analysed in this study. Log-
66 likelihoods were calculated using the maximum likelihood value of σ^2_t corresponding to
67 different values of ψ between the bounds of 0-1, then scaled relative to the maximum
68 log-likelihood for each trait. The horizontal dashed line is -1.92, the nominal cutoff for a
69 95% confidence interval using a χ^2 approximation with 1 d.f.

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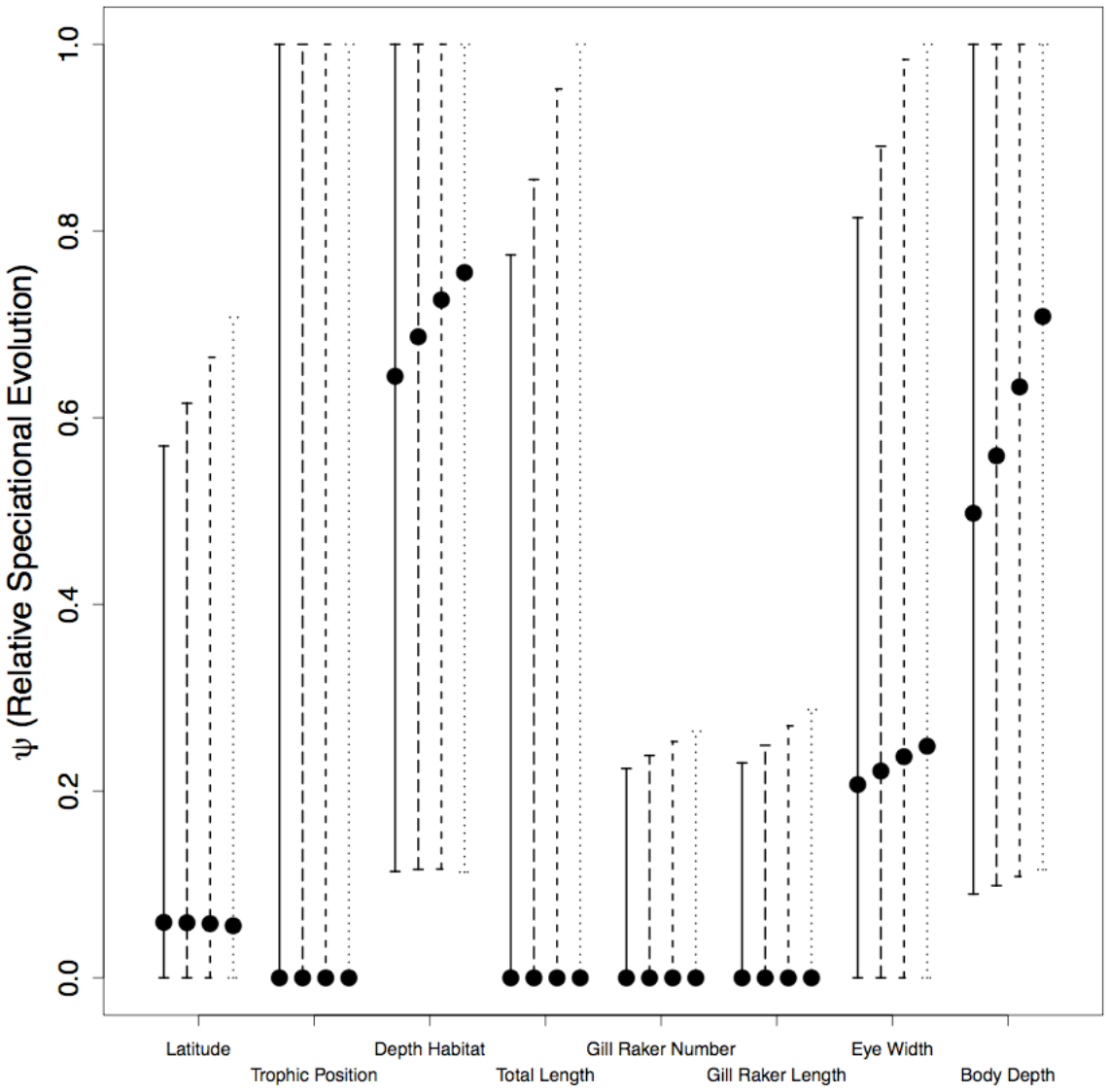

Figure S5. Effect of a non-zero extinction rate on estimation of ψ. Likelihood analyses of speciational evolution in each character were repeated using turnover rates (μ/λ) of 0 (solid line, equivalent to fig. 2), 0.25 (long dashed line), 0.50 (short dashed line) and 0.75 (dotted line). These turnover rates correspond to values of λ = 0.35, 0.39, 0.44 and 0.47, and μ = 0, 0.10, 0.22 and 0.35, respectively.

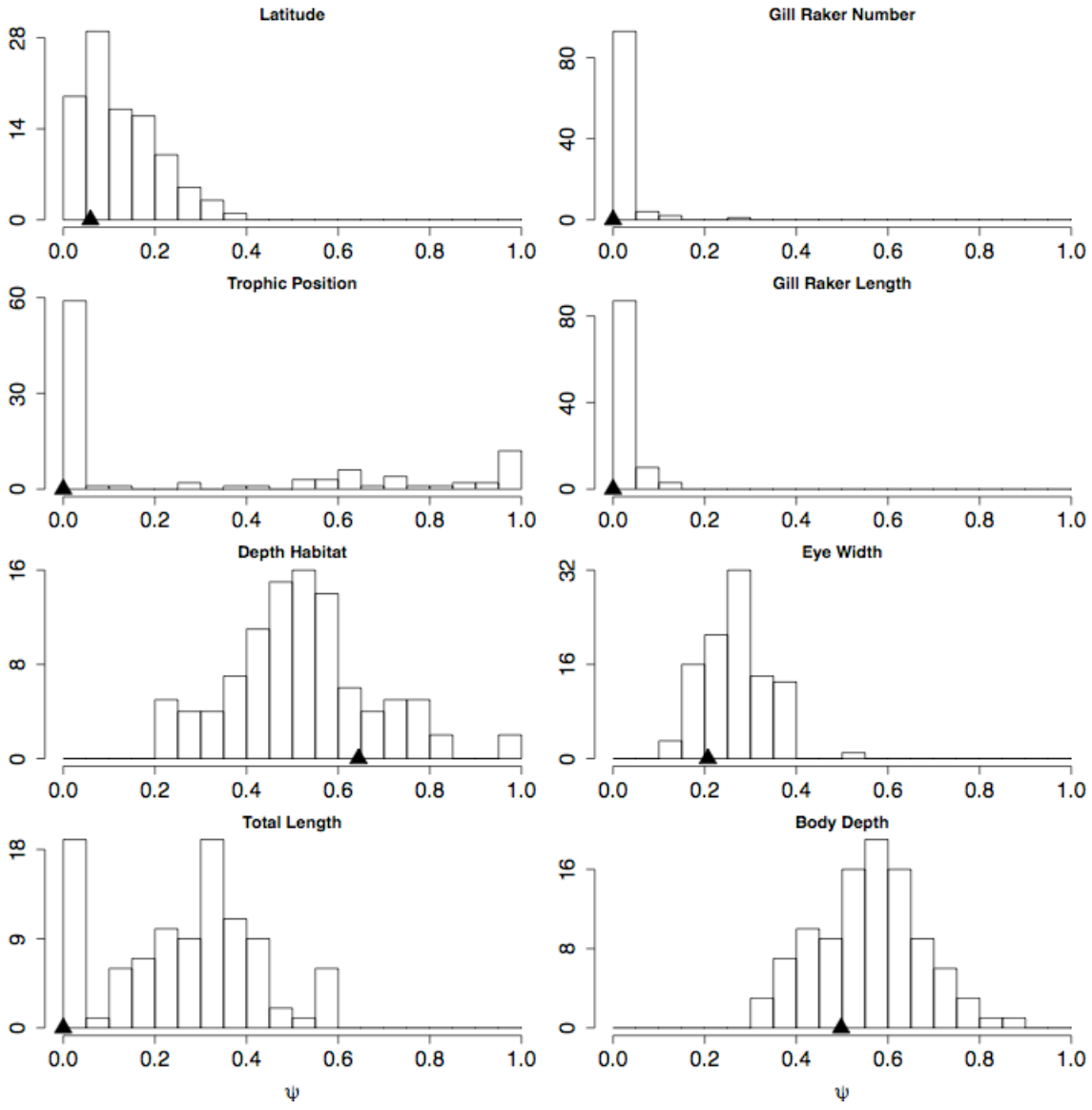

Figure S6. Distribution of parameter estimates across 100 trees from the posterior sample. For each character, the distributions of the parameter ψ (relative speciational evolution) are shown. Filled symbols indicate parameter estimates for the maximum clade credibility tree, as shown in fig. 2.

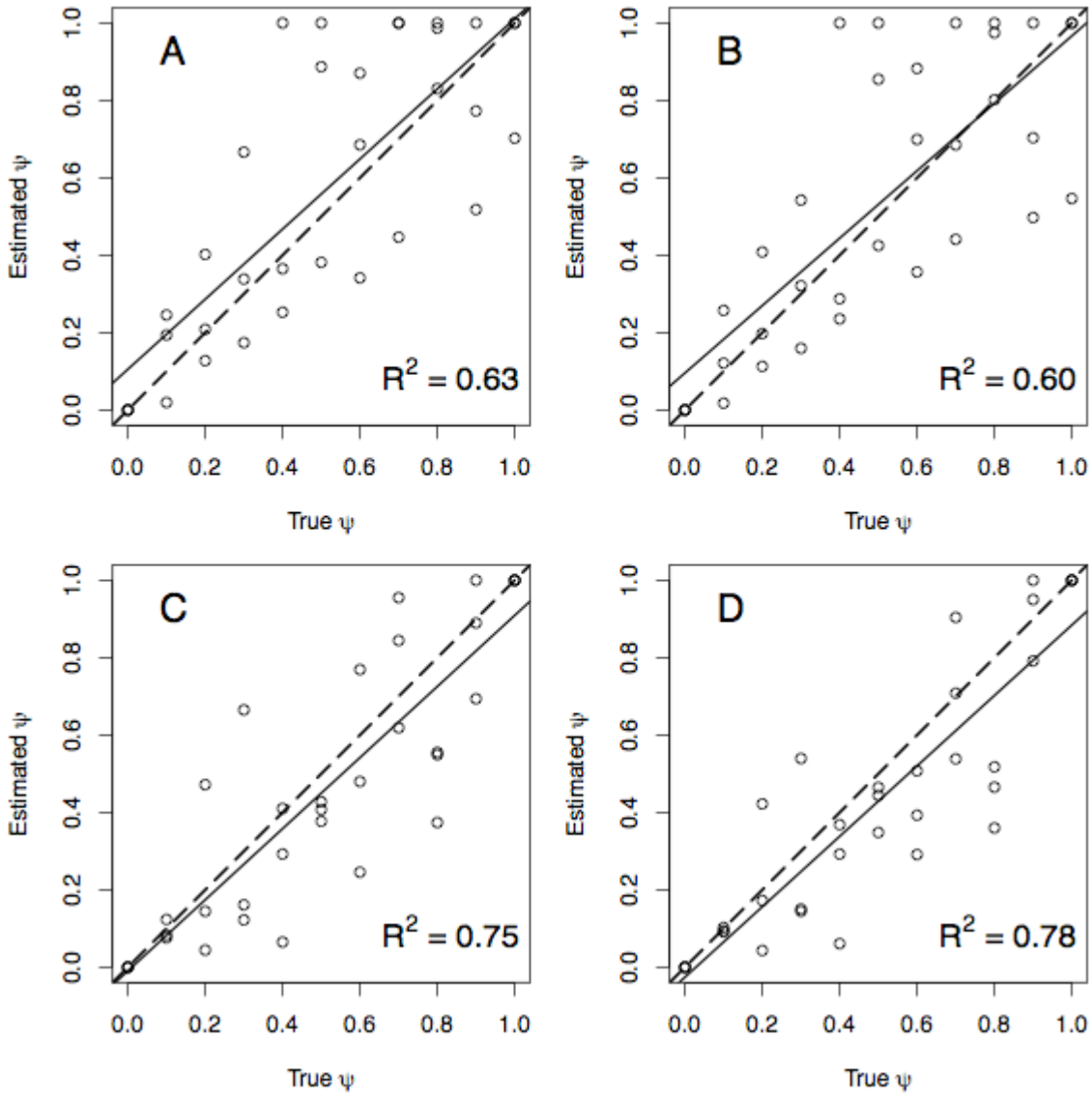

Figure S7. Recovery of known ψ values by carrying out maximum likelihood inference on simulated phylogenetic trees and trait values. Trees were simulated with no extinction (μ = 0; AB) or with μ = 0.1 (CD). λ and μ were either estimated from the phylogeny (AC) or their true values were used (BD). Shown in each panel are the 1:1 line (dashed), the least-squares regression line of estimated ψ against true ψ (solid), and the R^2 for this linear fit as a measure of precision.