Bayesian Analysis of the the 55 vertebrate ectodomain sequences listed in Table 1, plus three IR family invertebrate homologous ectodomain sequences.
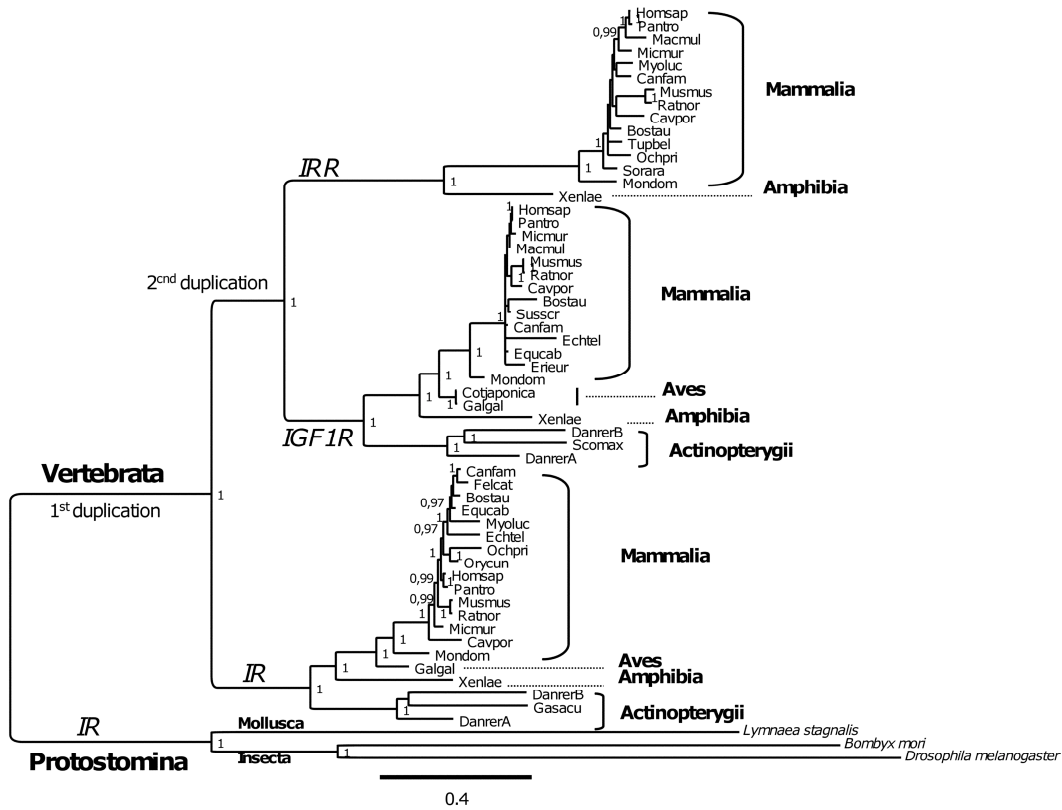

Figure S1. Bayesian phylogeny of the IR family.

Bayesian phylogeny of the IR family ectodomain inferred from amino acid sequences. Two independent MC3 runs, each replicated twice, yielded identical topologies, indicating excellent convergence. The numbers at the bipartitons correspond to their posterior probabilities (only shown if ≥ 0.95), estimated from their proportion of occurrences among 8002 source trees (4001 x 2, after discarding the first 1000 trees of each run as burnin) used to calculate the majority rule consensus tree shown. The scale indicates the number of expected substitutions per site under the best fitting JTT+G model (shape parameter α = 0.96), which had a posterior probability of 1. Compare this figure with Fig. 1 in the paper, which shows the corresponding ML phylogeny.

Statistical analysis of the four Bayesian MC³ runs.

Generation plots of ln*L* values for the four Bayesian MC³ runs. Notice the good mixing and convergence of the individual runs
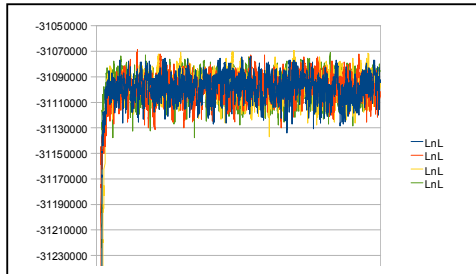
Generation plots of tree length values for the four Bayesian MC³ runs. Notice the good mixing and convergence of the individual runs
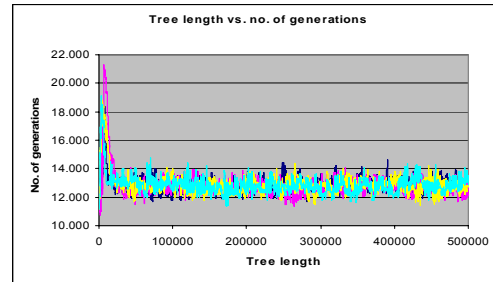
Estimated marginal likelihoods for replicate 1 and 2 of *Run1*:

Rep	Arithmetic mean	Harmonic mean
1	-31078.29	-31129.18
2	-31078.93	-31123.45
TOTAL	-31078.56	**-31128.49**

Estimated marginal likelihoods for replicate 1 and 2 of *Run2*:

Rep	Arithmetic mean	Harmonic mean
1	-31076.18	-31128.40
2	-31080.54	-31125.36
TOTAL	-31076.86	**-31127.75**

Model parameter summaries over the replicate 1 and 2 of *Run1*:

Summaries are based on a total of 8002 samples from 2 replicated runs. Each run produced 5001 samples of which 4001 samples were included.

		95% Cred. Interval				
Parameter	Mean	Variance	Lower	Upper	Median	PSRF *
TL	12.766011	0.196148	11.965000	13.689000	12.751000	1.017
alpha	0.960459	0.002124	0.873029	1.053529	0.958775	1.000

* Convergence diagnostic (PSRF = Potential scale reduction factor [Gelman and Rubin, 1992], uncorrected) should approach 1 as runs converge. The values may be unreliable if you have a small number of samples. PSRF should only be used as a rough guide to convergence since all the assumptions that allow one to interpret it as a scale reduction factor are not met in the phylogenetic context.

Model parameter summaries over the replicate 1 and 2 of *Run2*:

Summaries are based on a total of 8002 samples from 2 replicated runs. Each run produced 5001 samples of which 4001 samples were included.

		95% Cred. Interval				
Parameter	Mean	Variance	Lower	Upper	Median	PSRF *
TL	12.726446	0.183333	11.876000	13.535000	12.739000	1.008
alpha	0.962038	0.002120	0.875532	1.054901	0.961335	1.001

* Convergence diagnostic (PSRF = Potential scale reduction factor [Gelman and Rubin, 1992], uncorrected) should approach 1 as runs converge. The values may be unreliable if you have a small number of samples. PSRF should only be used as a rough guide to convergence since all the assumptions that allow one to interpret it as a scale reduction factor are not met in the phylogenetic context.

Model selection using reversible jump MC³ replicate 1 and 2 of *Run1*:

Model selection using reversible jump MC³ replicate 1 and 2 of *Run2*:

```
Amino acid model probabilities:                  Amino acid model probabilities:

              Posterior   Standard                             Posterior   Standard
      Model   Probability Deviation                     Model  Probability Deviation
      --------------------------------             --------------------------------
      Poisson    0.000     0.000000                Poisson       0.000     0.000000
      Jones      1.000     0.000000                Jones         1.000     0.000000
      Dayhoff    0.000     0.000000                Dayhoff       0.000     0.000000
      Mtrev      0.000     0.000000                Mtrev         0.000     0.000000
      Mtmam      0.000     0.000000                Mtmam         0.000     0.000000
      Wag        0.000     0.000000                Wag           0.000     0.000000
      Rtrev      0.000     0.000000                Rtrev         0.000     0.000000
      Cprev      0.000     0.000000                Cprev         0.000     0.000000
      Vt         0.000     0.000000                Vt            0.000     0.000000
      Blosum     0.000     0.000000                Blosum        0.000     0.000000
      --------------------------------             --------------------------------
```