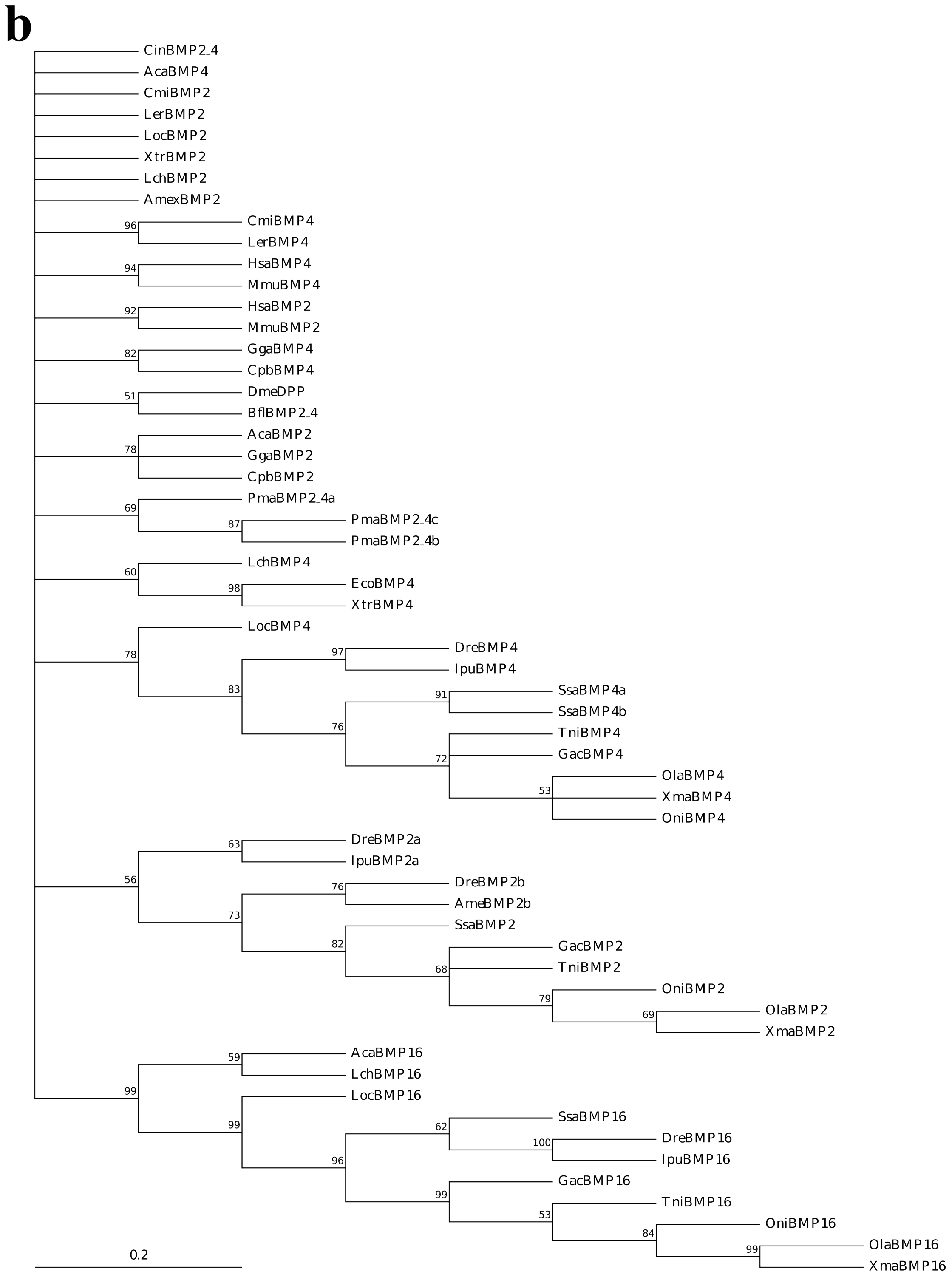
Online resource 2. Phylogenetic analyses of 58 BMP gene sequences. (A) RAxML 7.8.4-MPI ML optimal tree search GTR+Γ+Fest 400 replicates. Likelihood: −lnL = 17343.6220; (B) RAxML 7.8.4-MPI ML bootstrap GTR+Γ+Fest 400 replicates; (C) MrBayes MCMC GTR+Γ+I marginal likelihood: −lnLh = 17419.5992. 2 chains, 5,000,000 generations, 10,000 samples, 2,000 burnin each chain; (D) P4 MCMC GTR+Γ+I marginal likelihood: −lnLh = 17430.2044. 2 chains, 1,000,000 generations, 5,000 samples, 200 burnin each chain. Posterior predictive simulations of χ2 statistic of composition homogeneity: original statistic = 469.8018, the distribution goes from 43.1524 to 142.2298, the tail-area probability = 0.0000; (E) P4 MCMC GTR+Γ+I+CV2 Marginal likelihood: −lnLh = 17045.6169. 2 chains, generations, samples, burnin each chain. Posterior predictive simulations of χ2 statistic of composition homogeneity: original statistic = 469.8018, the distribution goes from 248.3454 to 772.3124, the tail-area probability = 0.4613; (F) CodonPhyML GY+ω+κ+Fest non-synonymous/synonymous ω parameter value of 1.0 fixed for all sites. Likelihood: −lnL = 19333.7, κ = 2.3671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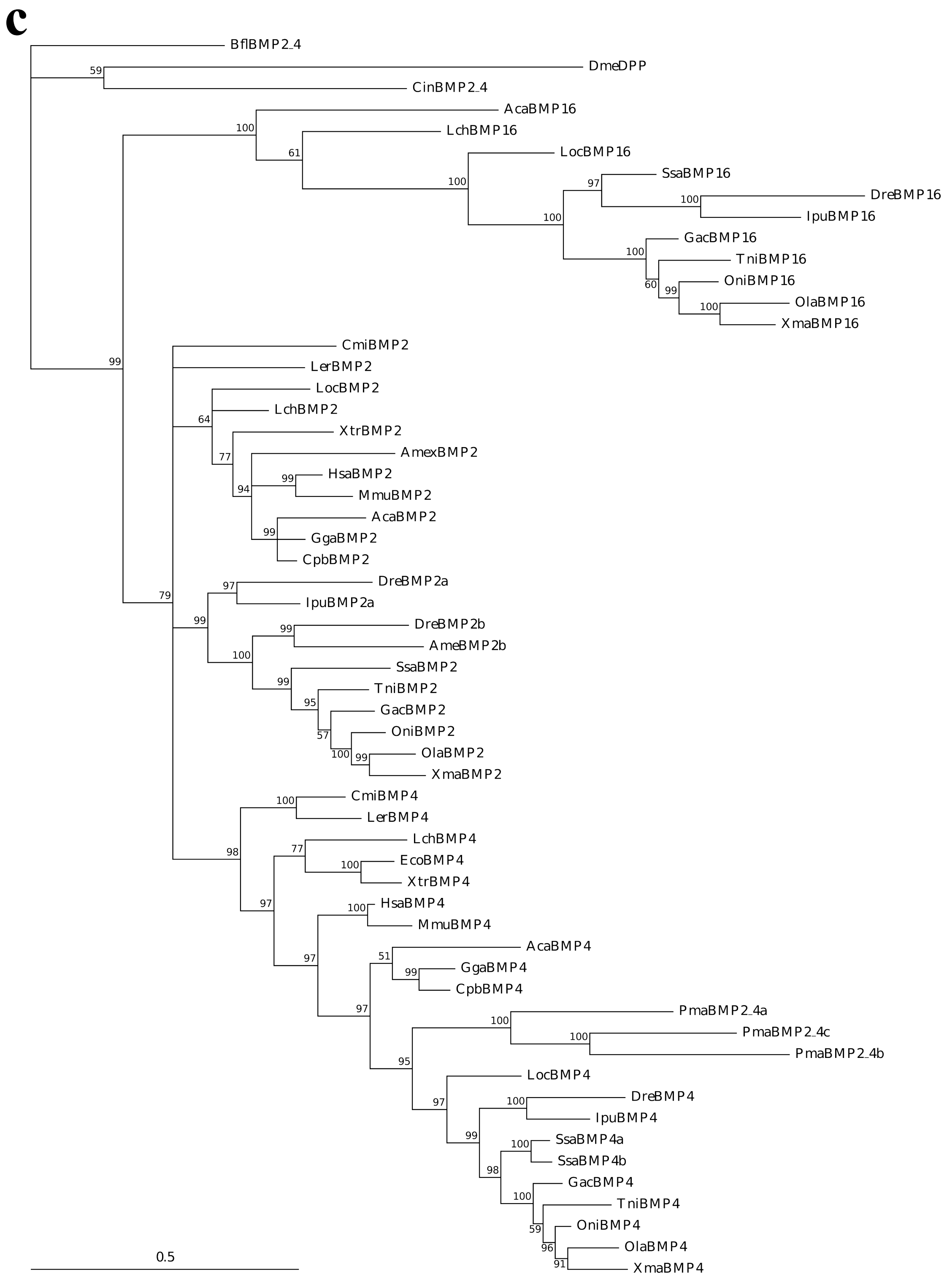
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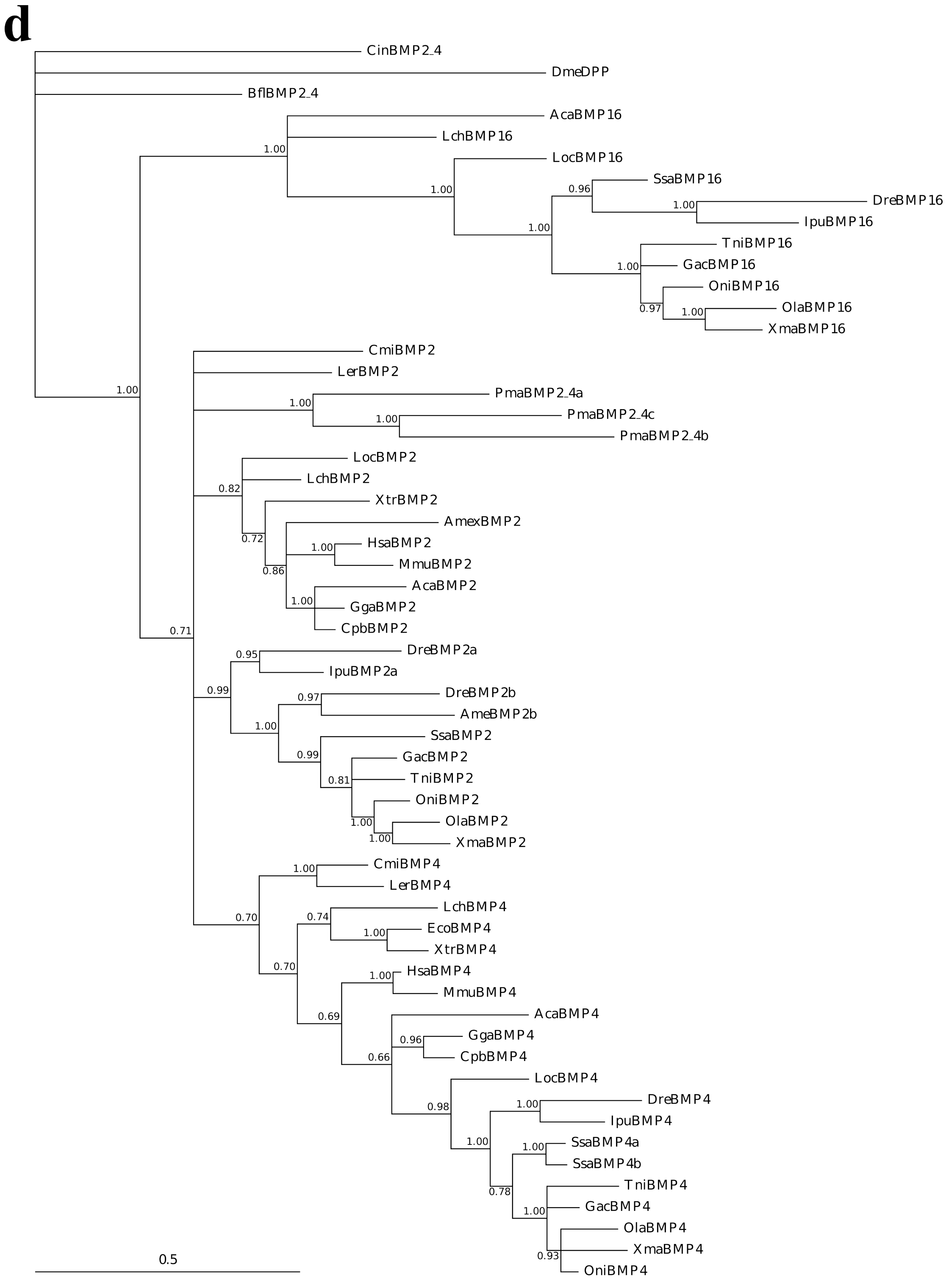
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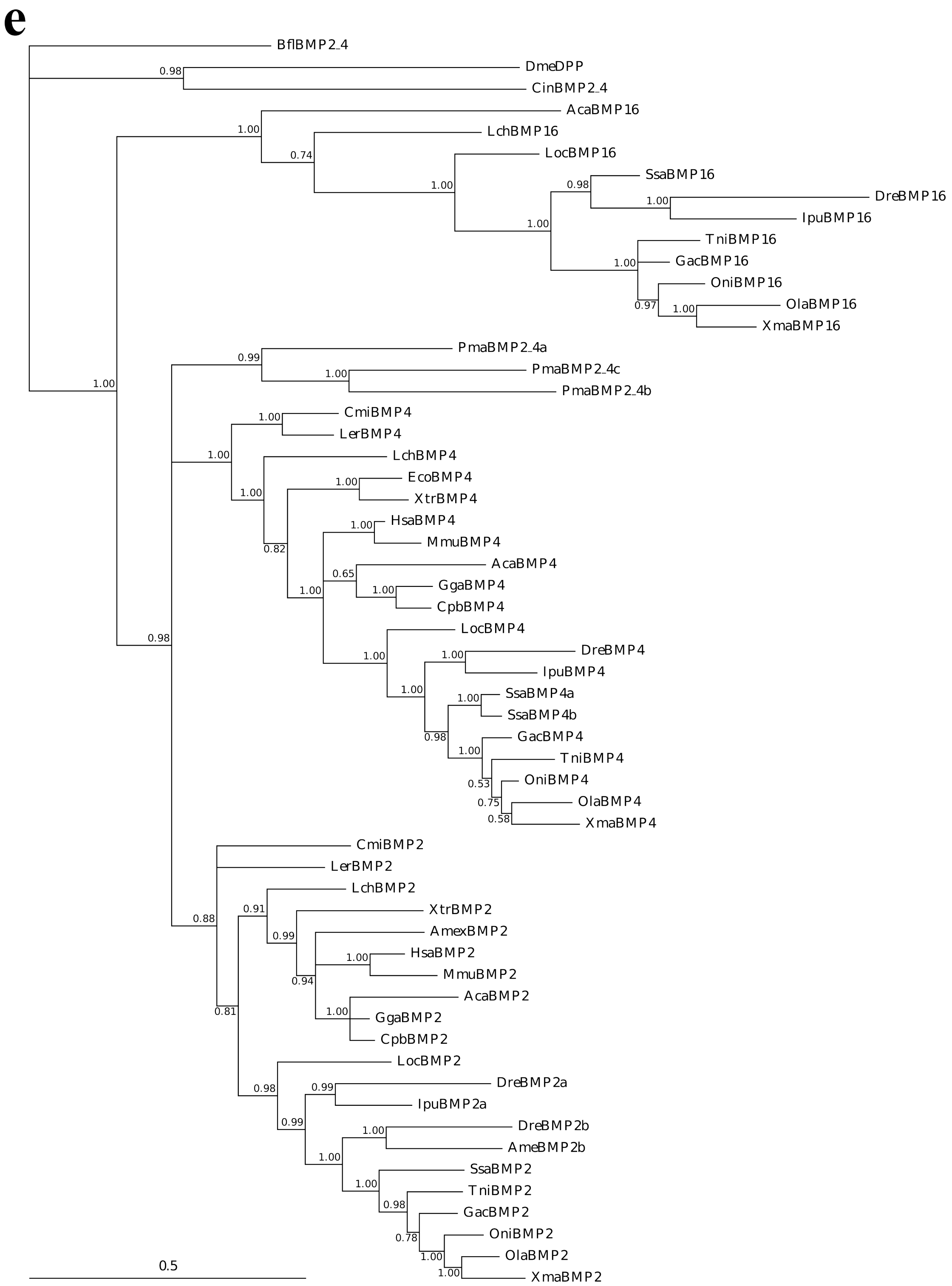
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