

Data

There are 35 taxa with 3738 codons (3539 without ambiguous sites) in the concatenated alignment. Each of the 10 branch-site tests is on a single branch.

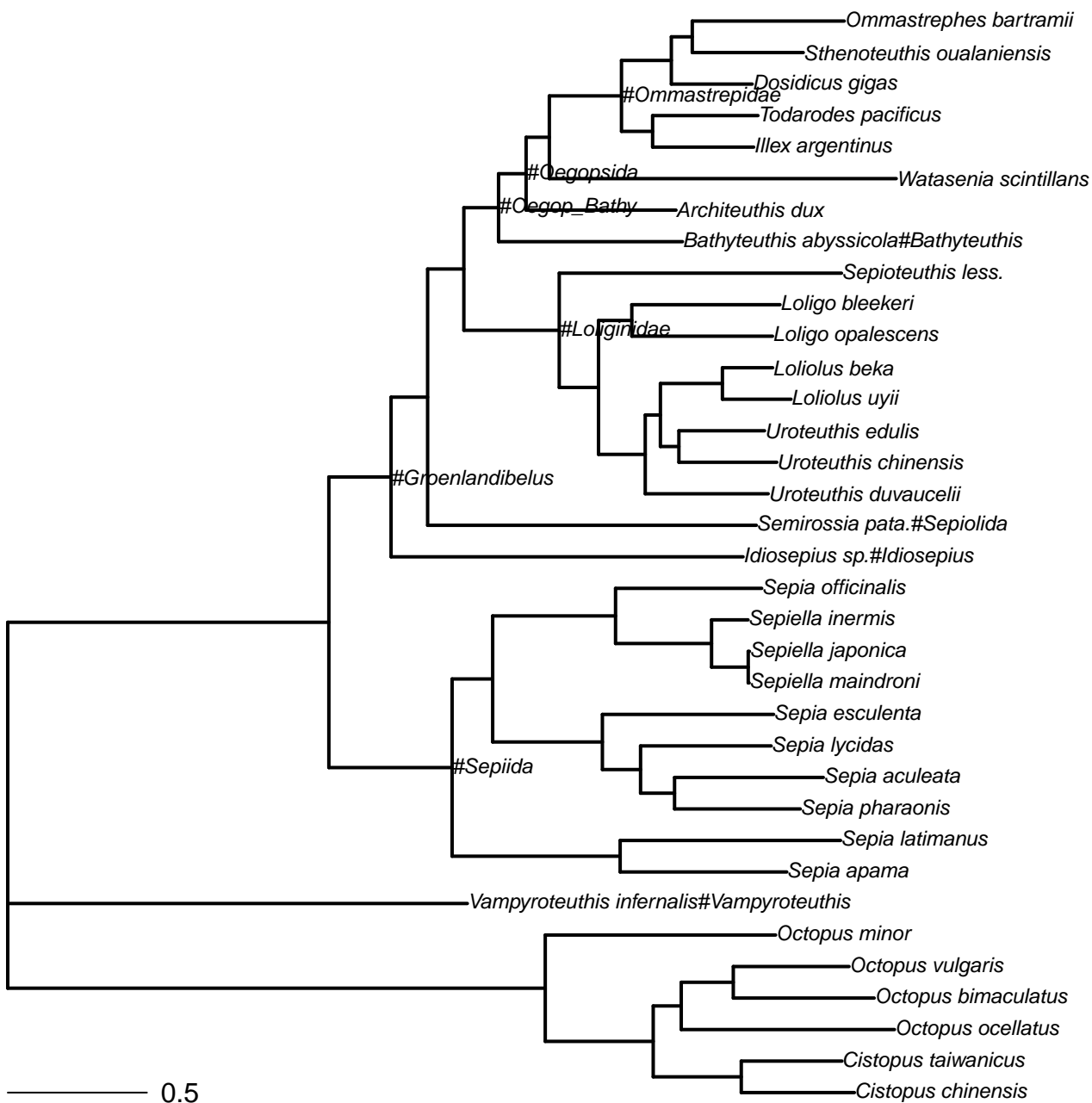


Figure 1: Tree labelled with each foreground branch tested under a branch-site model.

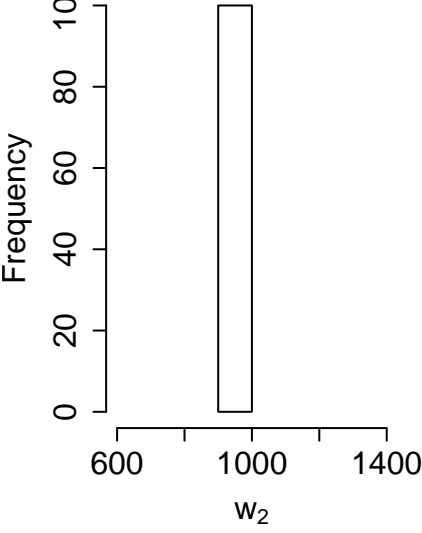
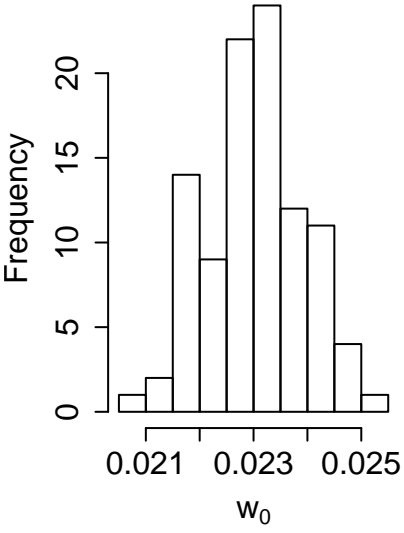
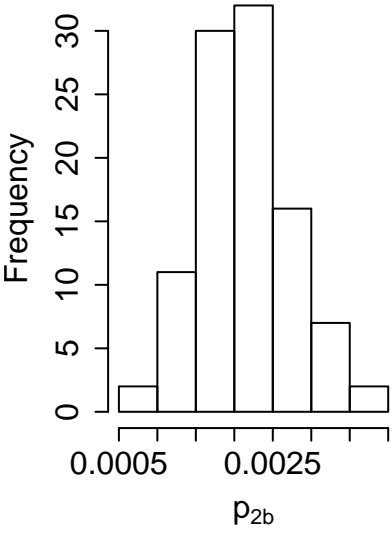
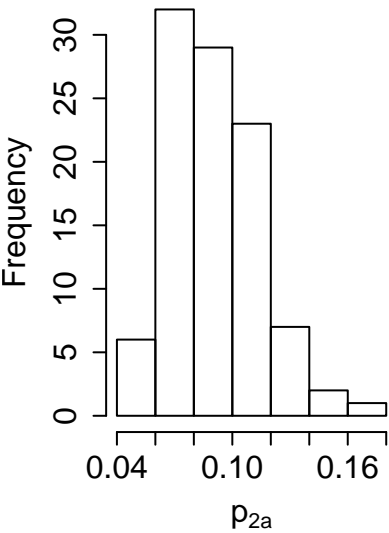
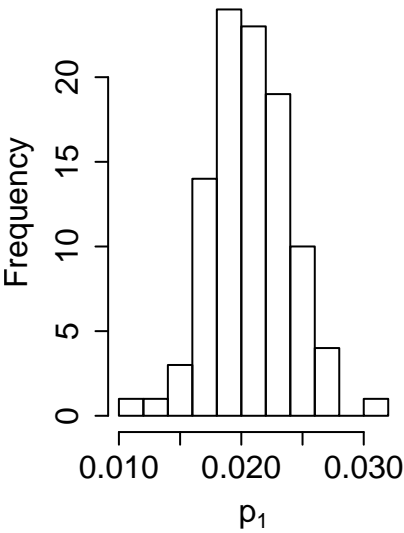
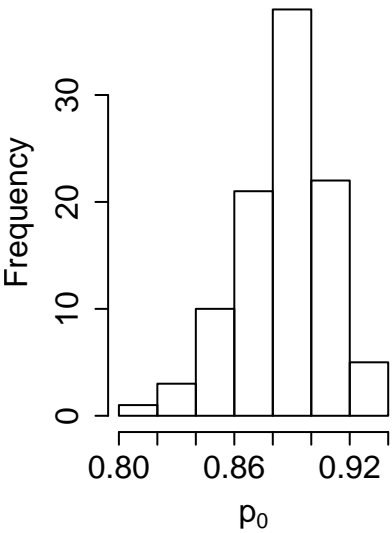
Branch-Site Tests

Table 1: Branch-site model likelihood ratio tests. Correcting for multiple tests does not change the results. Tests along the Groenlandibelus, Loliginidae, OegopBathy, Oegop_Bathy, and Sepiida branches are significant.

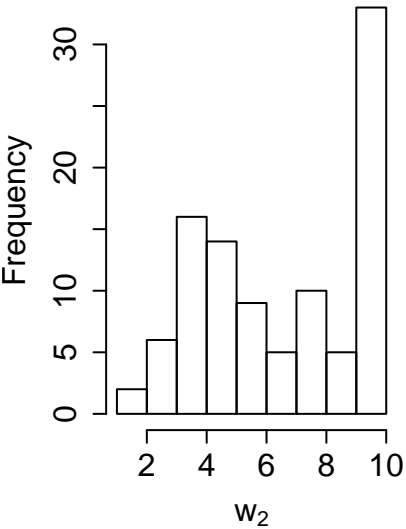
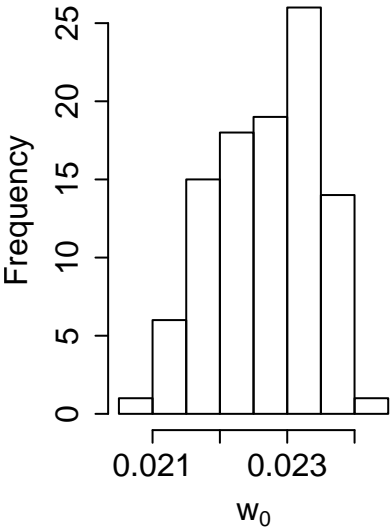
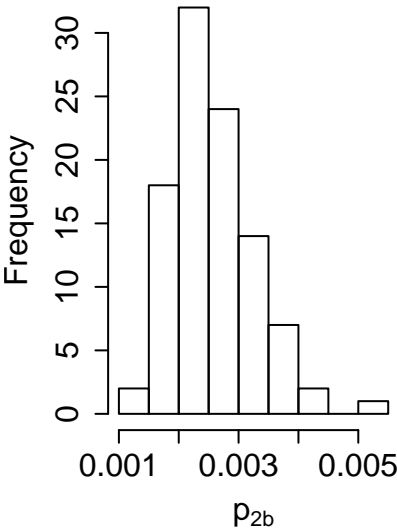
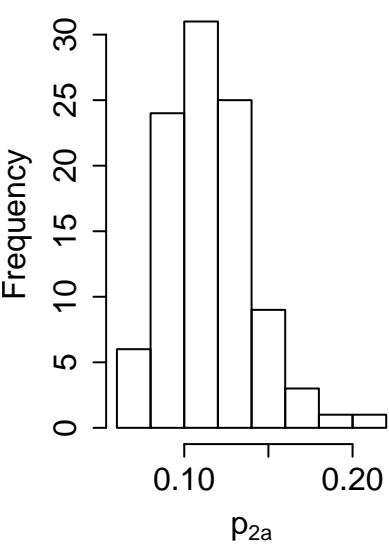
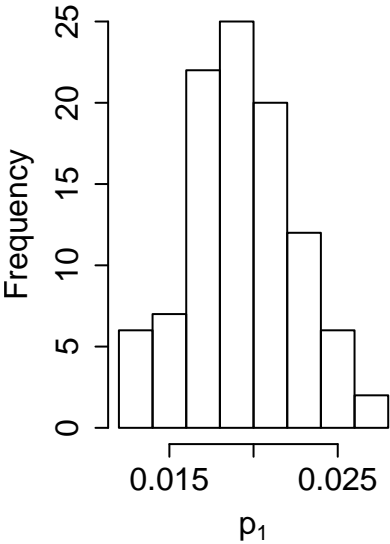
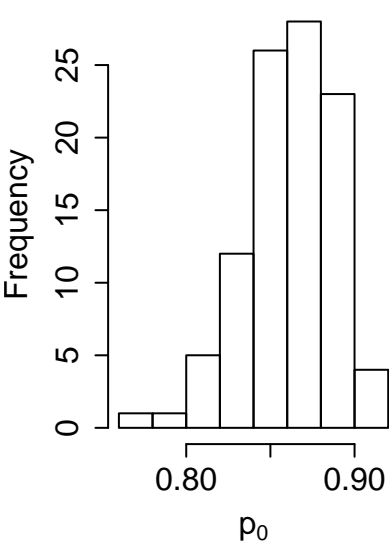
Branch Tested	H0	Ha	LRS	p-value
Bathyteuthis	-156044.3	-156044.3	0.000000	0.5000000
Groenlandibelus	-155990.8	-155974.3	32.971196	0.0000000
Idiosepius	-156004.9	-156004.7	0.332972	0.2819571
Loliginidae	-155953.6	-155945.5	16.195108	0.0000286
Oegop_Bathy	-156012.1	-156005.1	14.102188	0.0000866
Oegopsida	-156033.4	-156028.6	9.690420	0.0009262
Ommastrepidae	-156027.4	-156027.3	0.177430	0.3367956
Sepiida	-155926.7	-155898.3	56.892882	0.0000000
Sepiolida	-156021.7	-156021.7	0.000000	0.5000000
Vampyroteuthis	-156007.8	-156007.8	0.000000	0.5000000

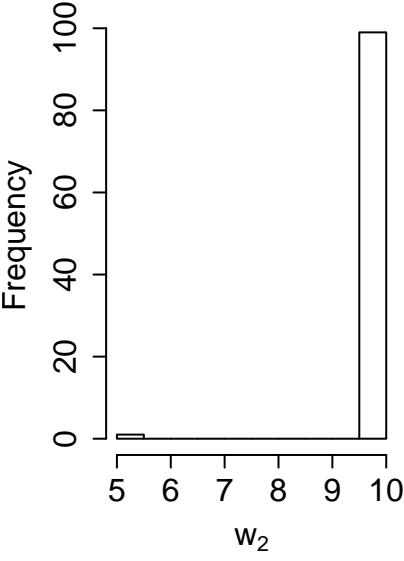
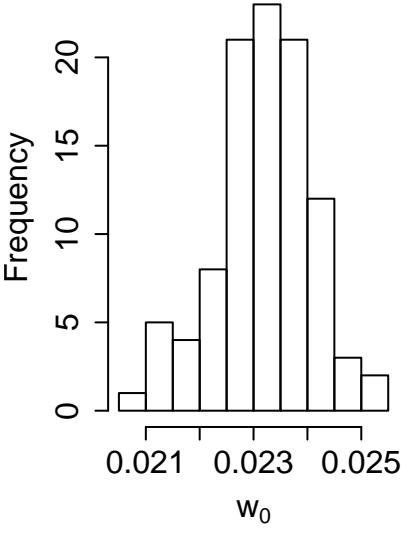
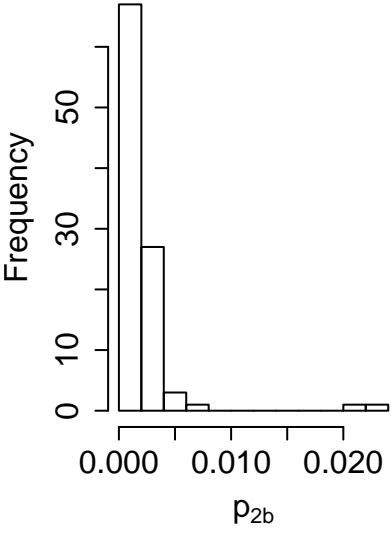
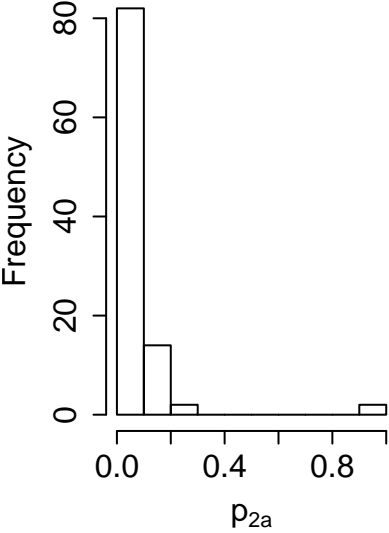
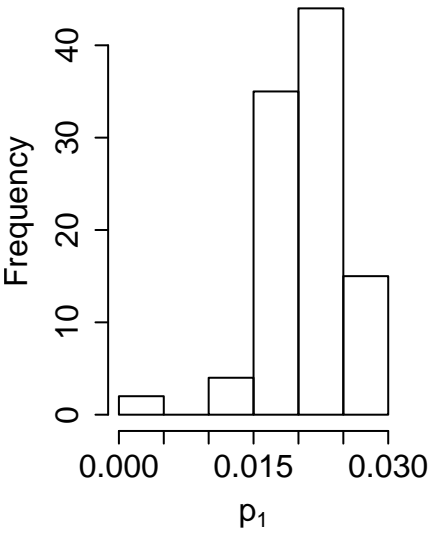
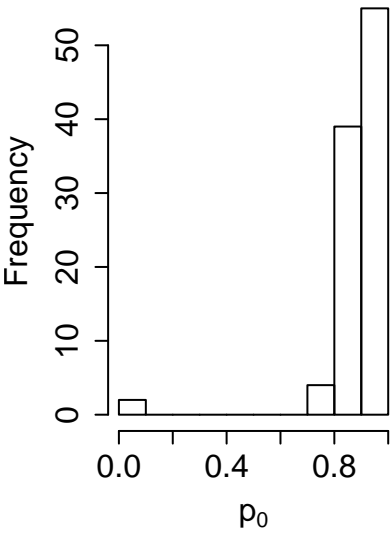
SBA MLE Distributions

Greonlandibelus

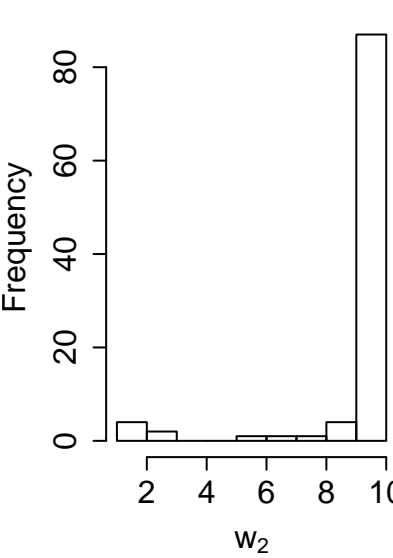
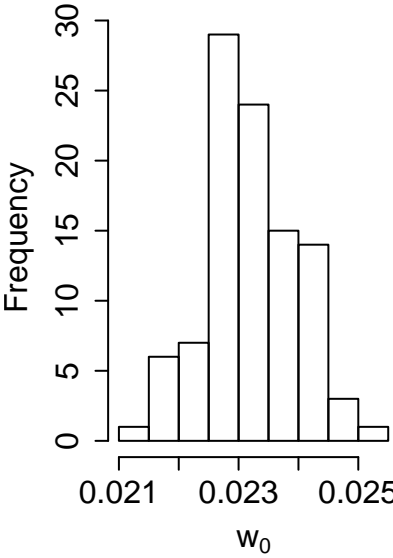
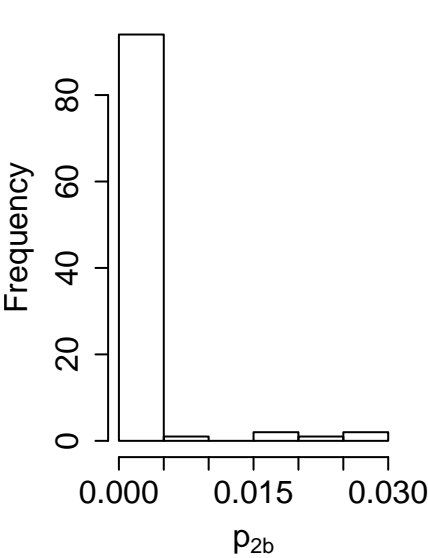
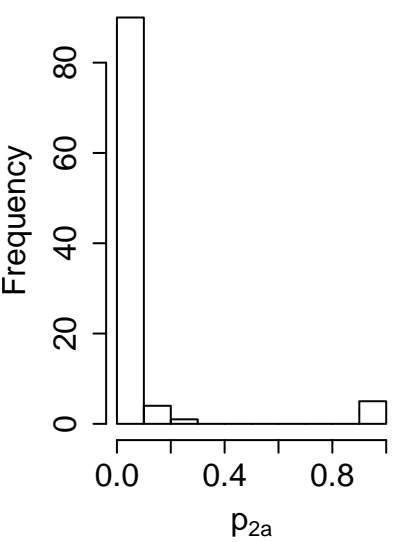
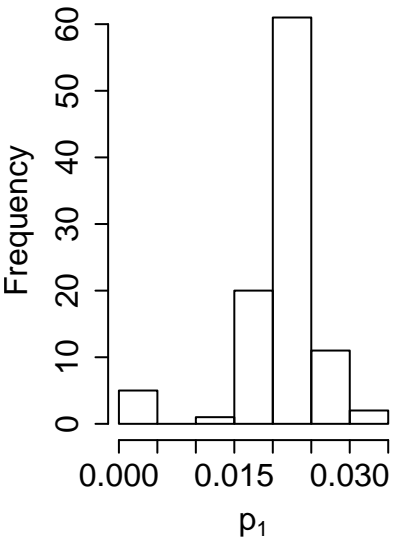
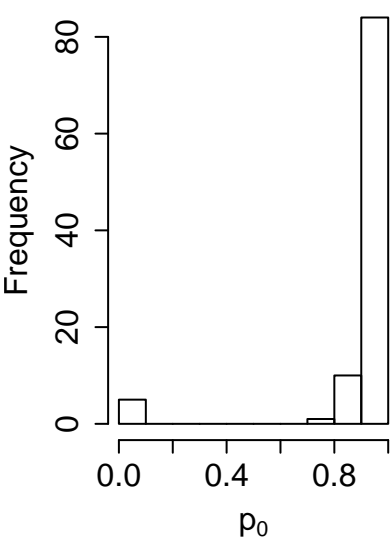


Loliginidae

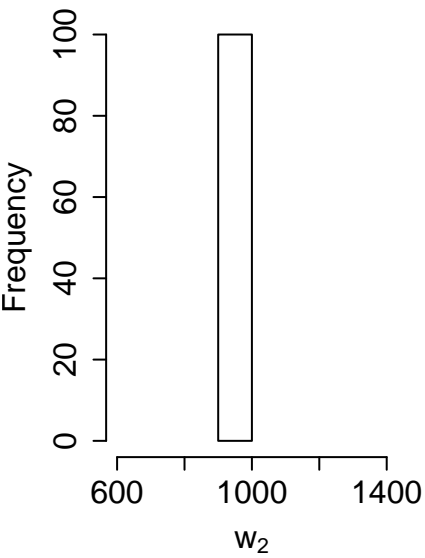
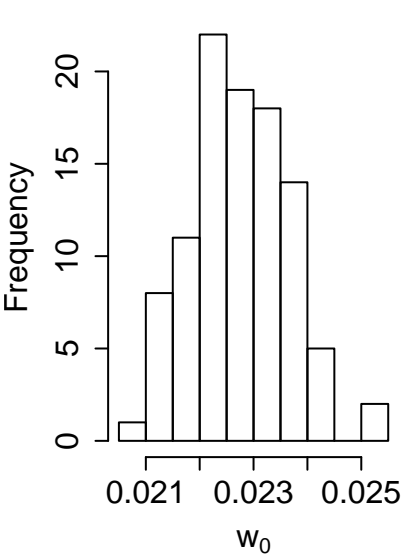
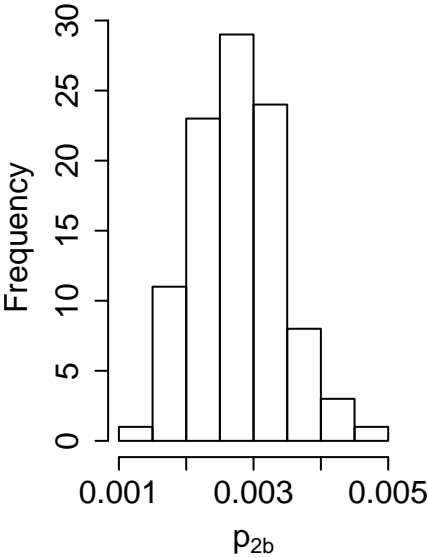
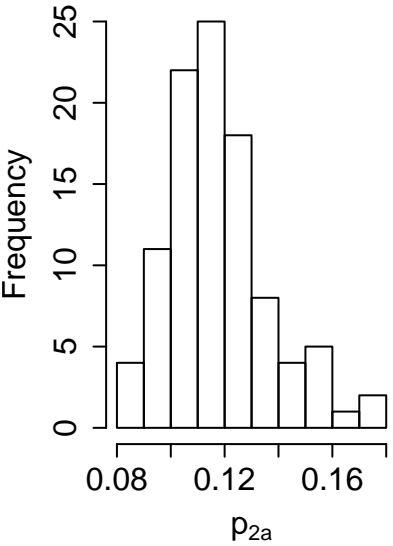
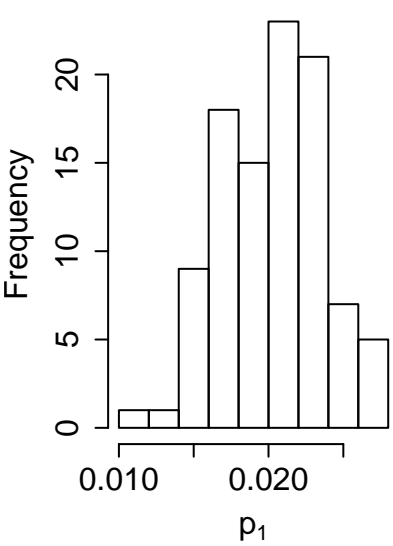
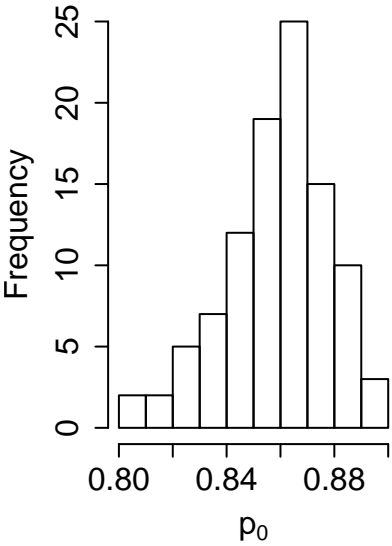




Oegopsida



Sepiida



Site Classification

Branch	BEB			SBA (mean)			SBA (median)		
	0.5	0.95	0.99	0.5	0.95	0.99	0.5	0.95	0.99
Groenlandibelus	0	0	0	127	38	9	132	51	17
Loliginidae	163	19	13	141	12	7	143	86	12
Oegop_Bathy	0	0	0	66	18	2	71	32	16
Oegopsida	0	0	0	29	10	2	32	15	6
Sepiida	50	1	0	201	77	56	201	91	67

Table 2: Number of sites classified to be under positive selection for BEB, SBA (mean posterior probabilities), and SBA (median posterior probabilities) for three posterior probability cut-offs: 0.5, 0.95, and 0.99.