**File S10 [A-G].** Prior (black) andposterior (blue) distribution for PopABC [[1](#_ENREF_1)] analysis of region one versus region two (Fig. 1). Parameters investigated are mutation rate (mut rate [A]), migration into sampling regions one and two (labelled mig1 [B] and mig2 [C] respectively), effective population size of sampling regions one and two (labelled Ne1 [D] and Ne2 [E] respectively), effective population size of the ancestral population (NeA [F]) and time since divergence of sampling regions one and two (labelled t1 [G]).

 

G

F

E

D

C

B

A

References

1. Lopes JS, Balding D, Beaumont M (2009) PopABC: a program to infer historical demographic parameters. Bioinformatics 25: 2747-2749.