

doi: 10.1590/0102-33062018abb0393

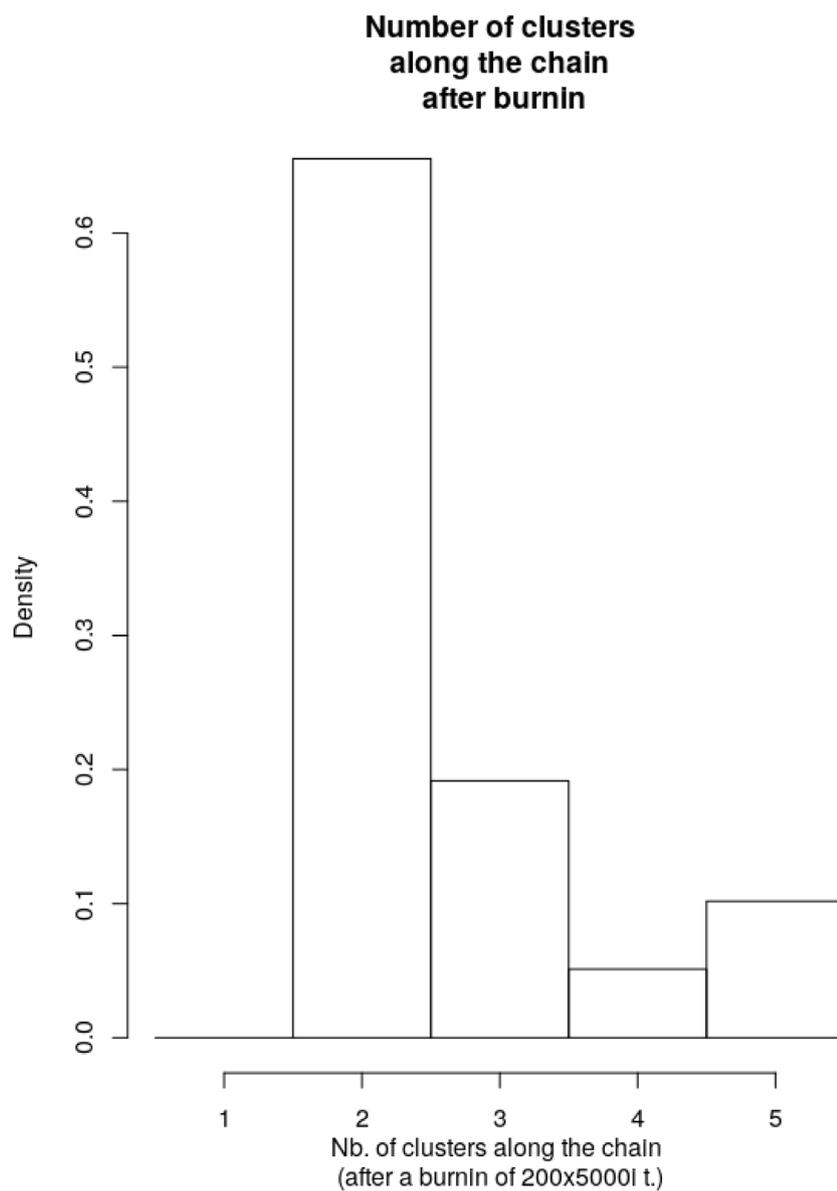


Figure S1. Posterior distribution of the estimated number of genetic clusters inferred by Geneland.

Table S1. Sequences of *primers* selected for amplification .

Primers	Sequences (5'-3')
Manny	CACCACCACCACRC
John	AGAGAGAGAGAGAGY
Terry	GTGGTGGTGGTGRC
Omar	GAGGAGGAGGAGRC
844	CTCCTCCTCCTCCTCCTCCTRC