

Stress related epigenetic changes may explain opportunistic success in biological invasions in Antipode mussels

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Supplementary Figure 1.

Neighbor-Joining phylogenetic tree constructed with MEGA6 software, bootstrap 10,000 and Jukes-Cantor evolutionary model (the best model obtained with MEGA6). It is based on 225 bp from Nelson sequences (NEL) and Havelock sequences (NZ) from this study, together with GenBank references from 4 different lineages described in Hilbish et al.³ (AF179451.1, AF179452.1, AF179453.1 and AF179459.1).

