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**Supplementary Figure S1**. Patterns of gene presence/absence variability (PAV) across individuals. (**A**) Simplified phylogeny and PAV of big defensin genes in *Crassostrea gigas*, based on data gathered from genome assemblies (Zhang *et al*., 2012; Wang *et al*., 2019). (**B**) Complete PAV profiles of *Cg*-BigDef1, *Cg*-BigDef2 and *Cg*-BigDef3 in 163 *C. gigas* individuals. Data extracted from Rosa *et al*. (2015). (**C**) Simplified phylogeny and PAV of big defensin genes in *Mytilus galloprovincialis*, based on the analysis of the genome of 16 different individuals from Gerdol *et al*. (2019). “Lola” indicates the reference genome (a female mussel from Galicia), “Pura” indicates the individual sequenced in a previous effort (Murgarella *et al*., 2014) whereas the “GAL” and “ITA” prefixes indicate mussels collected in Galicia and Italy, respectively. “M” and “F” indicate male and female mussels, respectively.

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