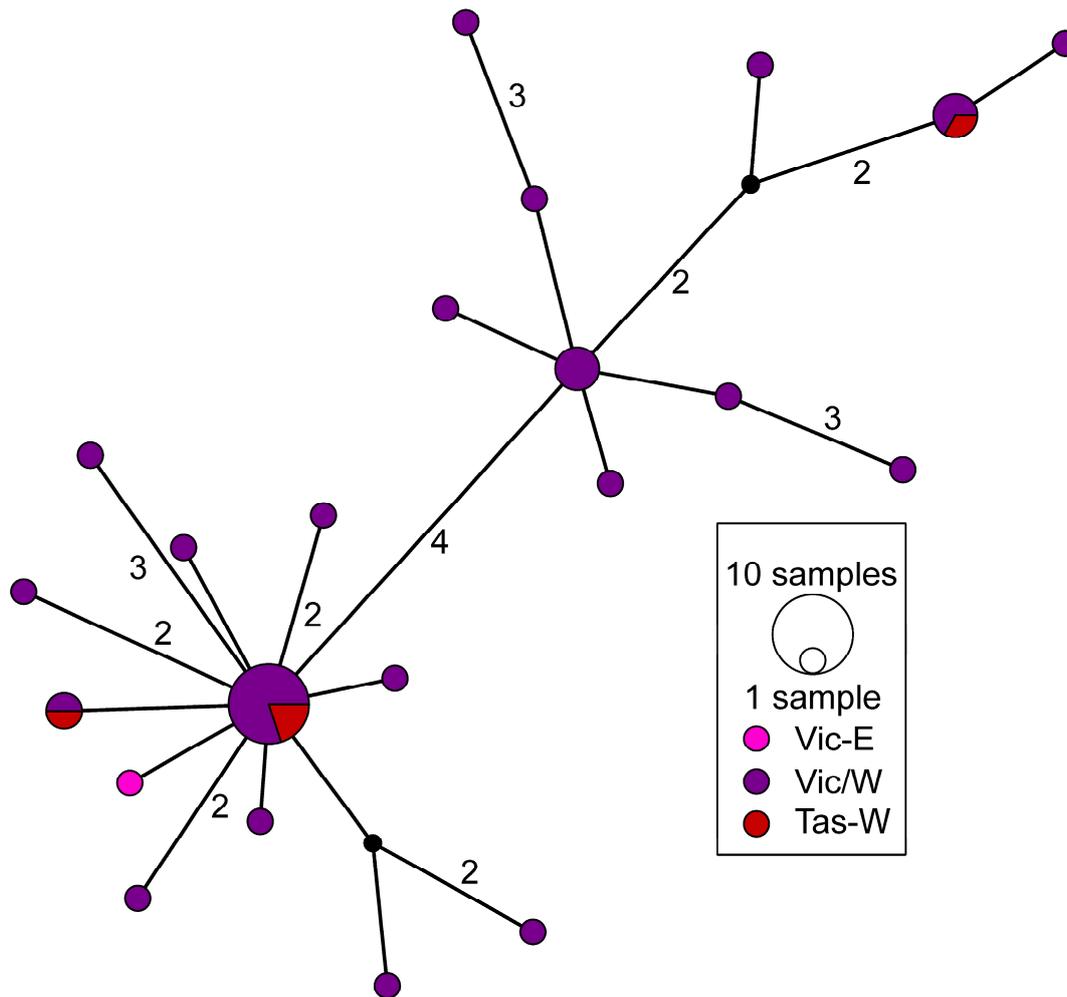
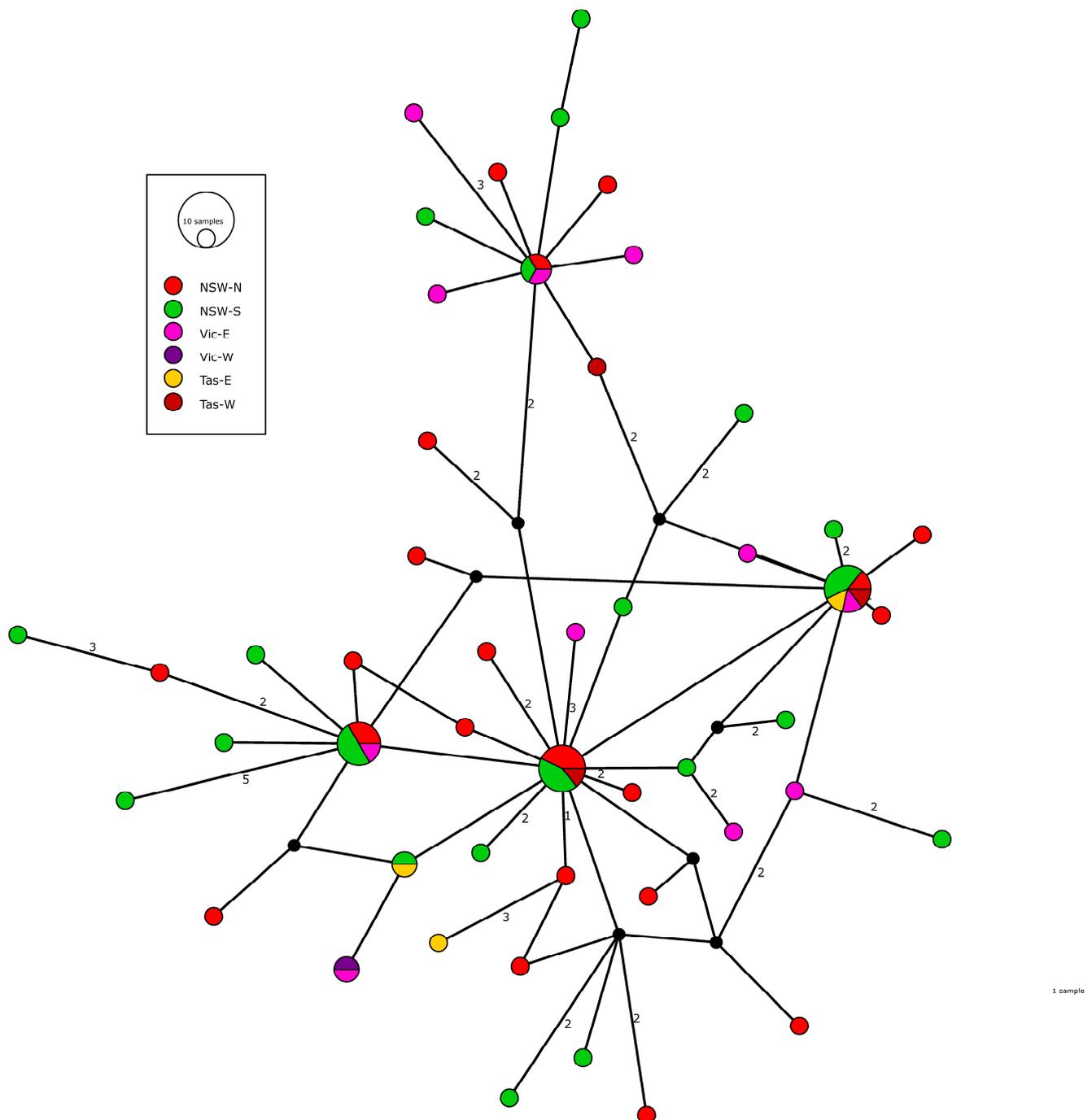


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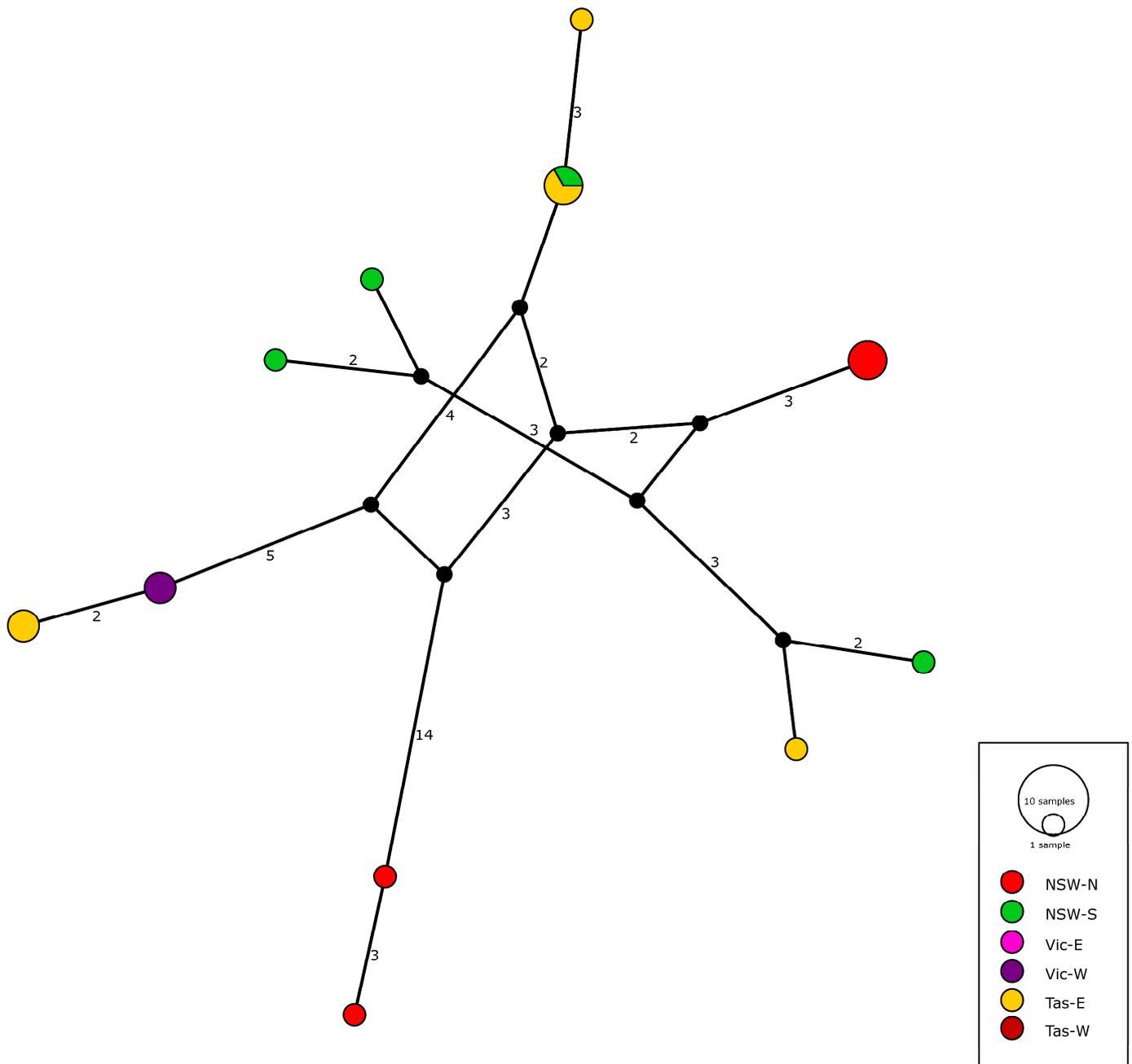
Supplementary figures for the article “Do deep DNA divergences within intertidal invertebrates reveal phylogeographic signals from earlier glacial cycles?”



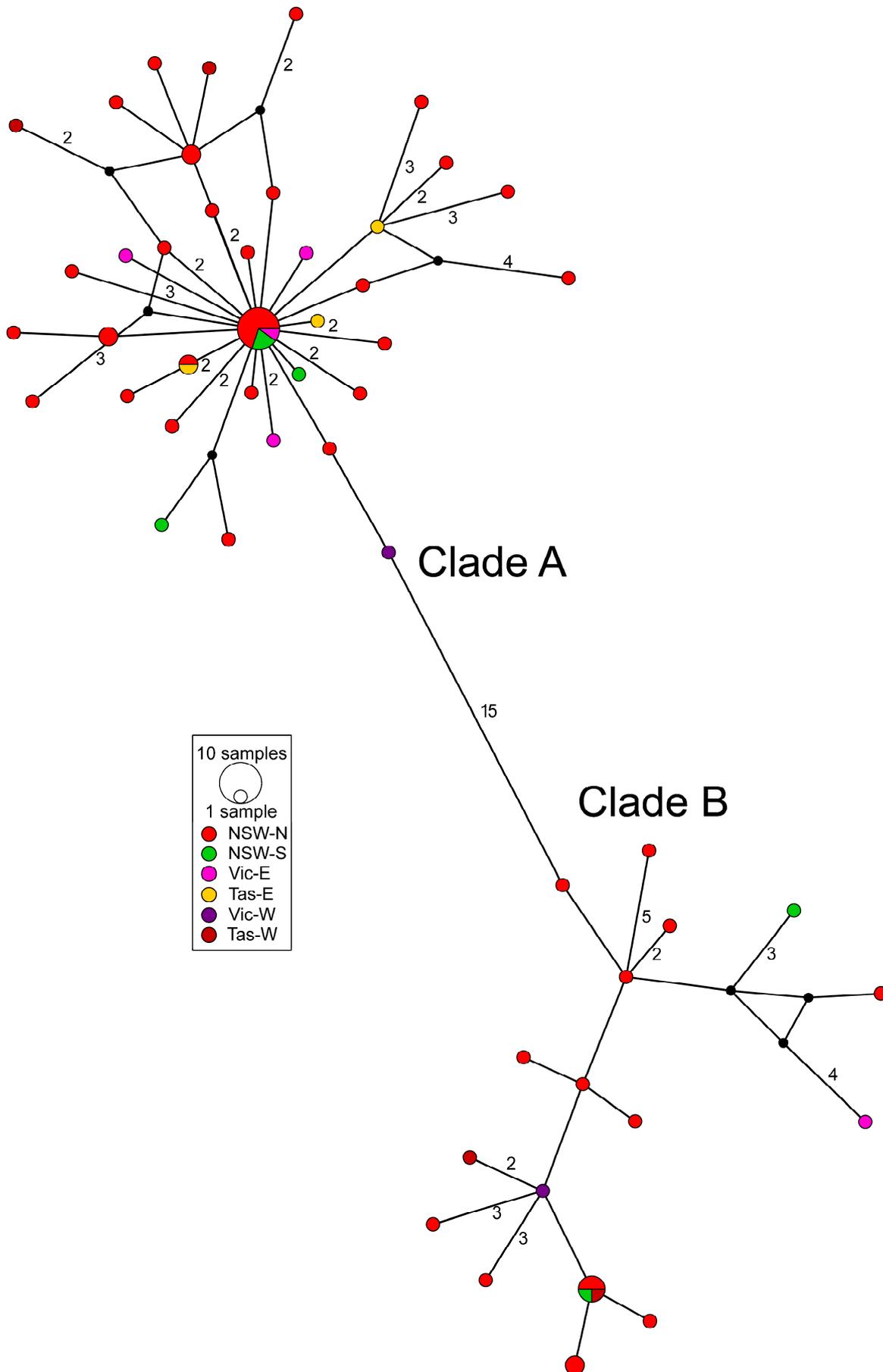
Supplementary Figure S1: *Nerita atramentosa* COI haplotype network. The numbers of mutational steps between haplotypes is one, unless specified by a numerical value written near a branch. These values are by definition one more than the number of unobserved haplotypes along the branch. Small black circles represent unobserved nodes at branch points. The number of observed sequences at each node is according to the scale in the legend which also specifies the provenance of the sequences according to regions which are colour coded as detailed in Figure 1 in the article.



Supplementary Figure S2: *Nerita melanotragus* COI haplotype network. The numbers of mutational steps between haplotypes is one, unless specified by a numerical value written near a branch. These values are by definition one more than the number of unobserved haplotypes along the branch. Small black circles represent unobserved nodes at branch points. The number of observed sequences at each node is according to the scale in the legend which also specifies the provenance of the sequences according to region as detailed in Figure 1.



Supplementary Figure S3. *Ascorhis tasmanica* COI haplotype network. The numbers of mutational steps between haplotypes is one, unless specified by a numerical value written near a branch. These values are by definition one more than the number of unobserved haplotypes along the branch. Small black circles represent unobserved nodes at branch points. The number of observed sequences at each node is according to the scale in the legend which also specifies the provenance of the sequences according to region as detailed in Figure 1.



Supplementary Figure S4. *Phallomedusa solida* COI haplotype network. The numbers of mutational steps between haplotypes is one, unless specified by a numerical value written near a branch. These values are by definition one more than the number of unobserved haplotypes along the branch. Small black circles represent unobserved nodes at branch points. The number of observed sequences at each node is according to the scale in the legend which also specifies the provenance of the sequences according to region as detailed in Figure 1.