Figure 4 Continued.

Considering the variables of phosphate and $NO_3 + NO_2$ concentrations in more detail, peaks in relative hybridisation values for the Prymnesiophyceae tended to be linked with lower PO_4 concentrations. Large prymnesiophytes in the Ross Sea are responsible for the export of higher N:P organic matter than that attributed to diatoms (Arrigo *et al.*, 1999), and it is possible that pico-prymnesiophytes might co-vary with these larger prymnesiophytes. Samples with peak Chrysophyceae relative hybridisation values tended to have higher PO_4 values (especially along the AMBITION, BIOSOPE and AMT transects). Marine production is constrained by nutrient availability, and phytoplankton N:P ratios differ with group. For example, green algae have higher ratios than red algae and growth strategies also alter this ratio (Falkowski *et al.*, 2004; Arrigo, 2005). Generalist strategies have a near Redfield N:P ratio of 16:1, opportunistic strategies rely on low N:P ratios and survivalist strategies rely on high N:P ratios (Arrigo, 2005). The average N:P ratio of the water samples analysed in this study was calculated to be 14:1 by linear regression, similar to the study of Tyrell (1999) that reported a 15:1 N:P ratio. When considering only samples for which Prymnesiophyceae relative hybridisations were $>30\%$, the average N:P ratio was 25:1, whereas when considering only samples for which Chryso-phyceae relative hybridisation values were $>30\%$, the average N:P ratio was 12:1. According to Weber and Deutsch (2010), phytoplankton may influence the N:P ratio of their surrounding water because of their differing metabolism. Alternatively, phytoplankton may be adapted to the N:P ratio of their surroundings, resulting in niche differentiation that may underlie the distribution patterns of the Prymnesiophyceae and the Chrysophyceae (see Litchman and Klausmeier, 2008). However, it should be considered that both classes had peaks at very low concentrations of these nutrients and it is likely that other factors in complex interactions also exerted influence over their distributions.

Plastid 16S rRNA gene sequences: global distribution analyses. In order to better understand global distributions of PPEs at a higher taxonomic level, all currently available plastid 16S rRNA gene sequences (this study; Fuller *et al.*, 2003; McDonald *et al.*, 2007; Lepère *et al.*, 2009; Kirkham *et al.*, 2011a, b; Shi *et al.*, 2011) obtained using the PLA491F/OXY1313R primer pair were analysed via Unifrac. This primer set is considered to best encompass the extent of PPE diversity currently observed using other 16S or 18S rRNA