

**Fig. 5- figure supplement 8. Coregulation of genes incorporated into HPPGs of different origin in the model diatom *Phaeodactylum tricornutum*. Panel A** shows boxplots of the correlation coefficients between the expression profiles of genes encoding members of ancestral HPPGs of red algal origin (**i**), green algal origin (**ii**), prokaryotic origin (**iii**) or host origin (**iv**), compared to genes encoding members of other HPPGs. Each HPPG is separated by evolutionary origin on the x-axis of each graph: for example, the box labelled “green algae” on the “red algae” graph shows the correlation coefficients between genes encoding members of ancestral HPPGs of red origin, and ancestral HPPGs of green origin. **Panel B** shows the P value statistics of mean separation calculated when comparing genes encoding members of ancestral HPPGs of the same origin (shown by row) to members of ancestral HPPGs of different origin (shown by column). For example, the intersect between the “red” row and “green” column shows the difference in mean correlation coefficient between pairs of genes that both encode members of ancestral HPPGs of red origin, and gene pairs of which one encodes an ancestral HPPG member of red origin, and the other an ancestral HPPG member of green origin. None of the P values calculated are significant, i.e. there are no categories of ancestral HPPG in which the internal correlation coefficients of gene expression are any different to those observed across the dataset as a whole.

