



**Figure S4:** Hierarchical clustering and heat map made using log normalised expression data for the 128 protein spots of sperm samples that showed significant differences in expression level ( $p \leq 0.05$ ; before applying any multiple testing correction method) between the two *Mytilus* species and populations (SW: Swansea, VG: Vigo). Each column and row contains information for an individual mussel and protein spot respectively. Cells are coloured according to z-scores, showing up-regulation (red) or down-regulation (green) of protein spot volumes in the individual mussels compared with average expression values calculated from all mussel samples.