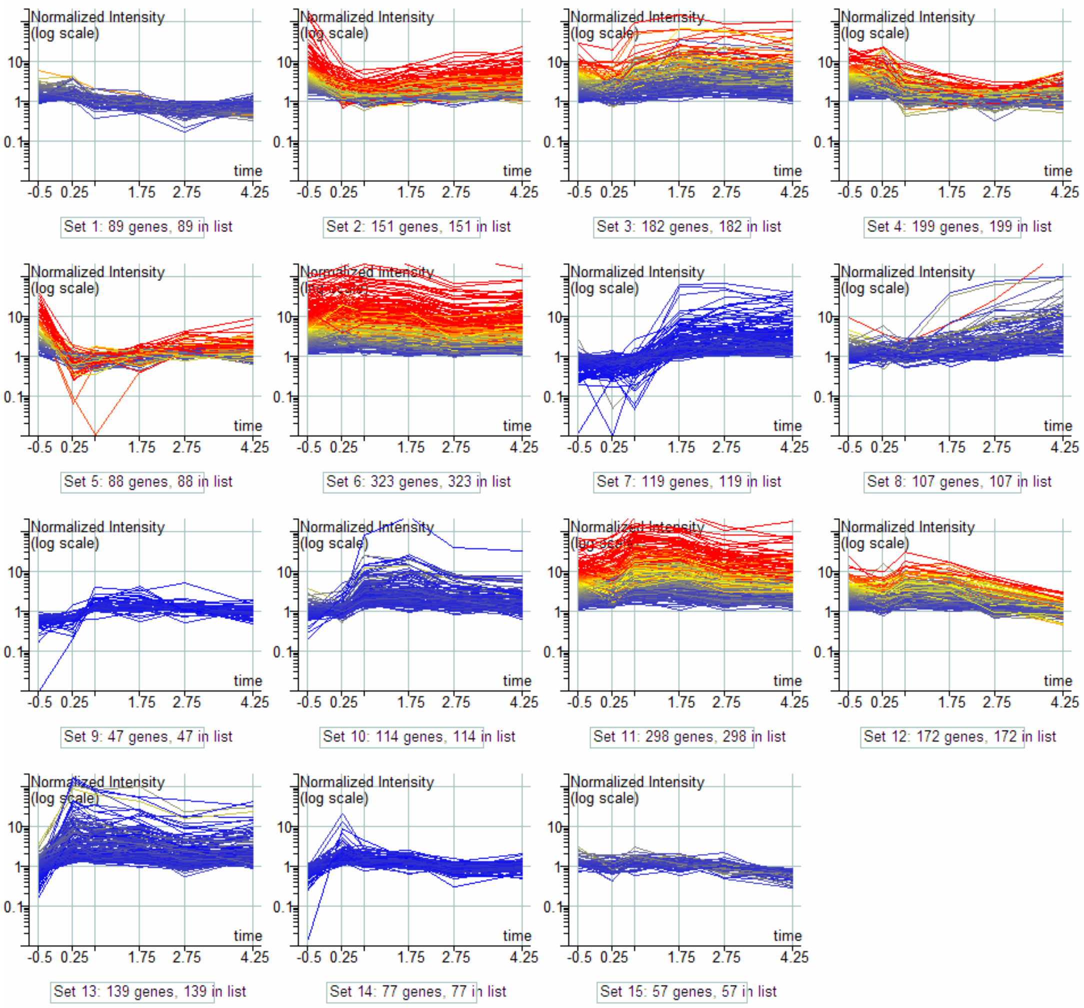
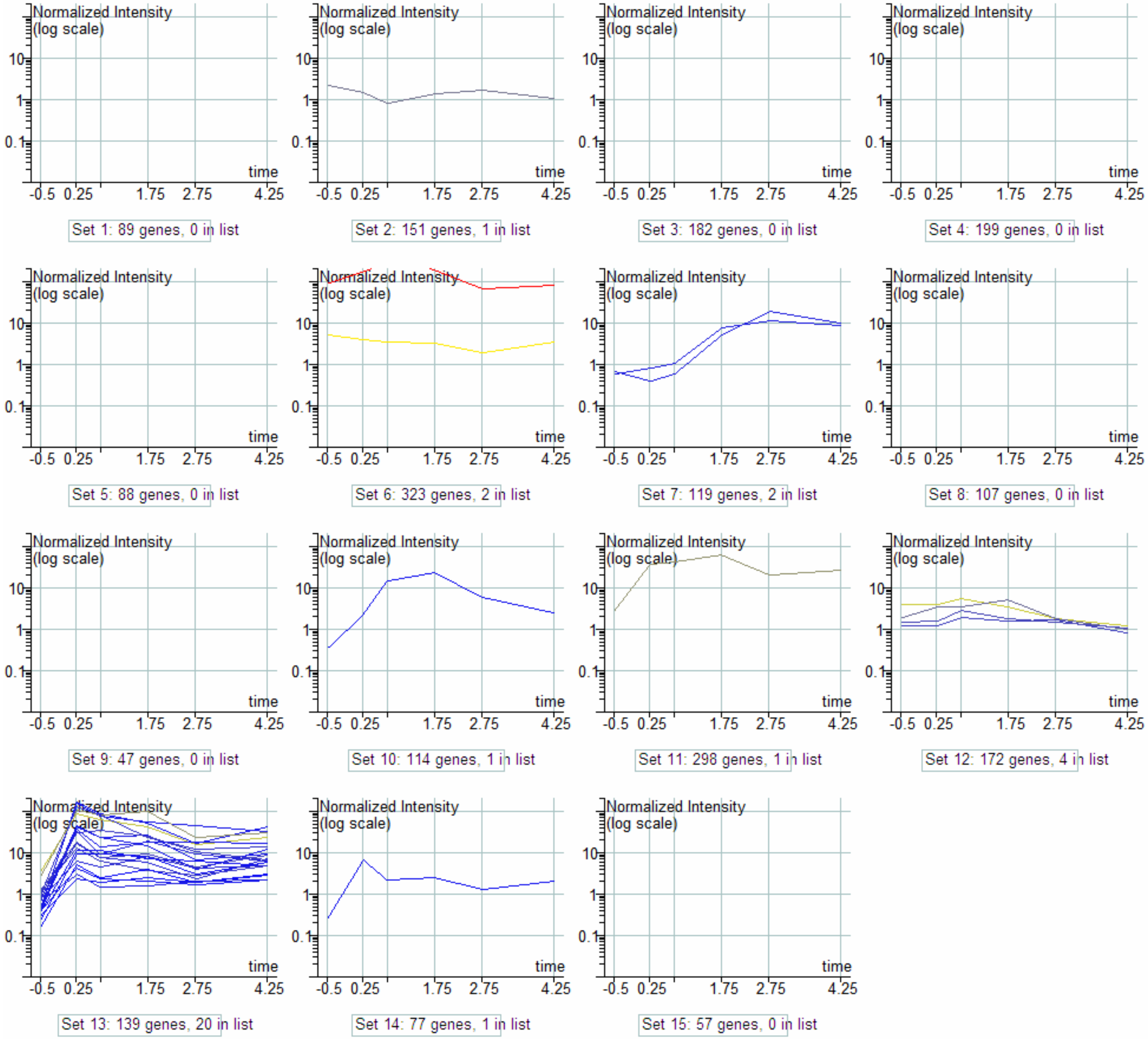
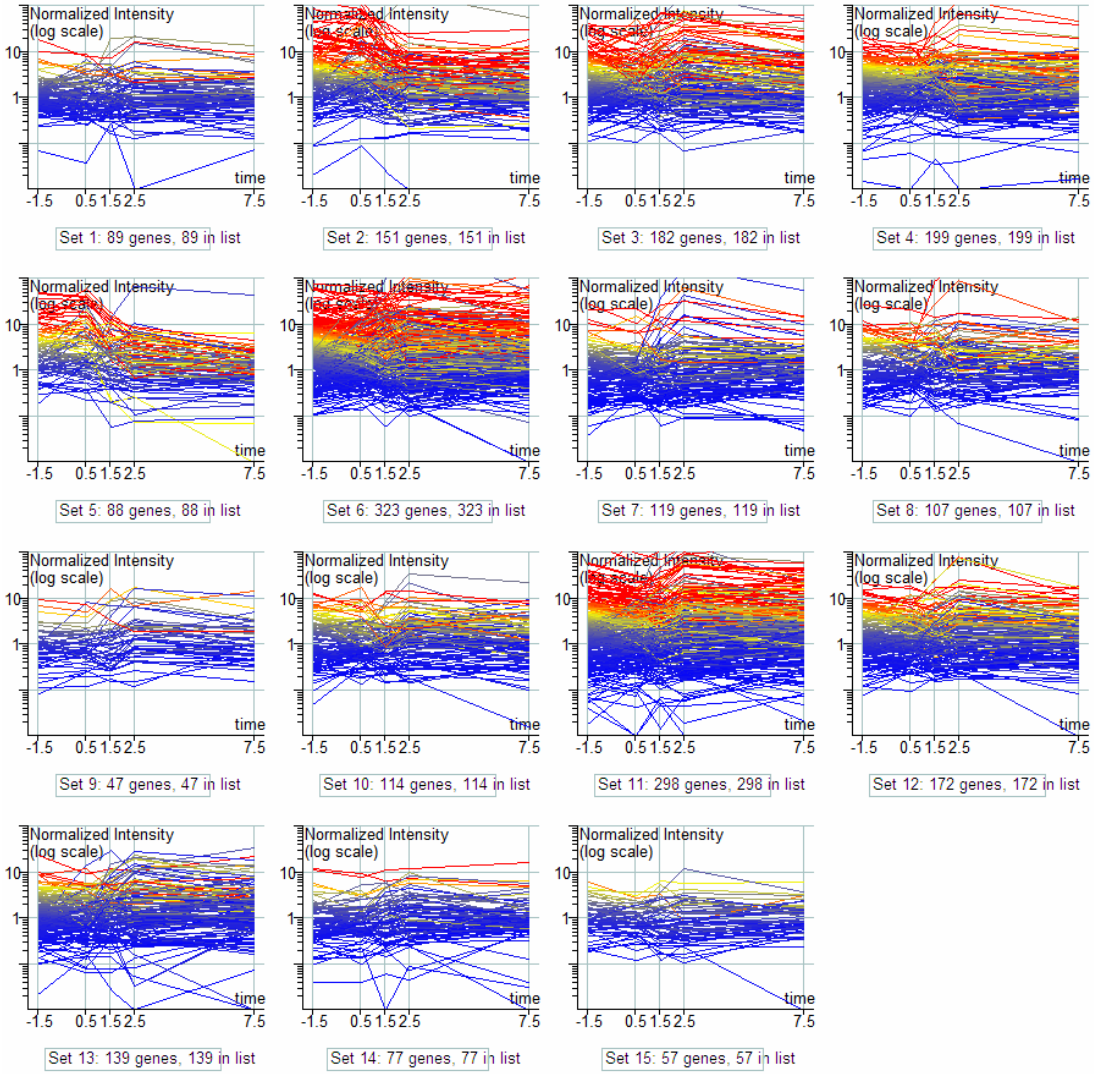


Supplementary Figure 1. K-means clustering of *B. subtilis* phosphate starvation transcriptional profiles. Clustering was performed on 2162 genes that had expression levels between 1 and 1905 normalised intensity with the *sigB*-null mutant dataset used as the source data. Standard correlation was chosen as the similarity measure, the number of clusters was arbitrary chosen to be 15. The data are coloured by expression levels at $T_{-0.5}$.



Supplementary Figure 2. K-means clustering of *B. subtilis* phosphate starvation transcriptional profiles, showing the location of members of the PhoP regulon. Most PhoP regulon members cluster to set 13. Clustering was performed on 2162 genes that had expression levels between 1 and 1905 normalised intensity with the *sigB*-null mutant dataset used as the source data. Standard correlation was chosen as the similarity measure, the number of clusters was arbitrary chosen to be 15. The data are coloured by expression levels at $T_{-0.5}$.



Supplementary Figure 3. K-means clustering of *B. subtilis* phosphate starvation transcriptional profiles in a *phoR* mutant. Clustering was performed on 2162 genes that had expression levels between 1 and 1905 normalised intensity with the *sigB*-null mutant dataset used as the source data. Standard correlation was chosen as the similarity measure, the number of clusters was arbitrary chosen to be 15. The data are coloured by expression levels at $T_{-0.5}$.