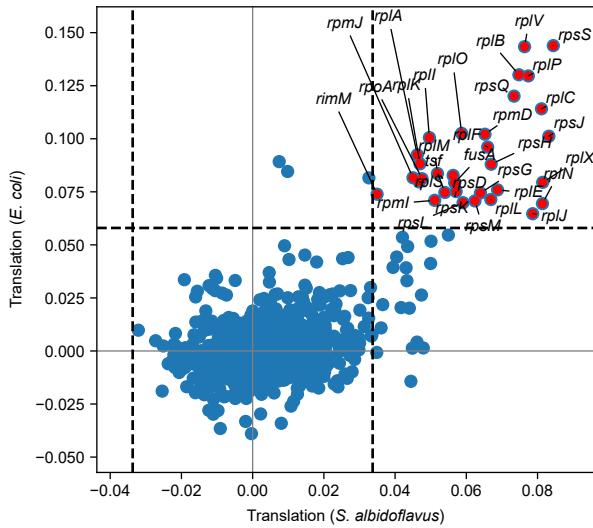
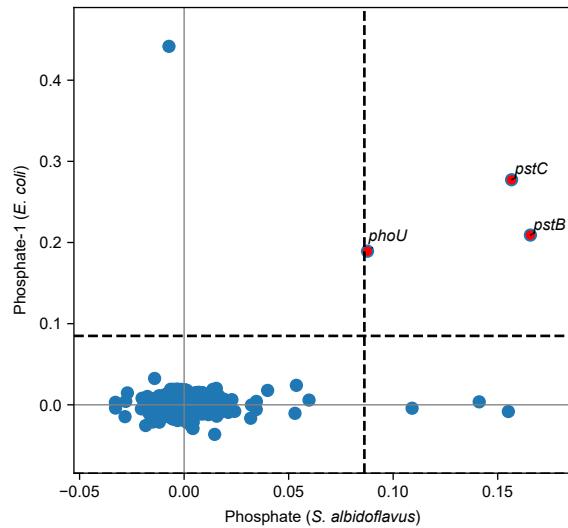


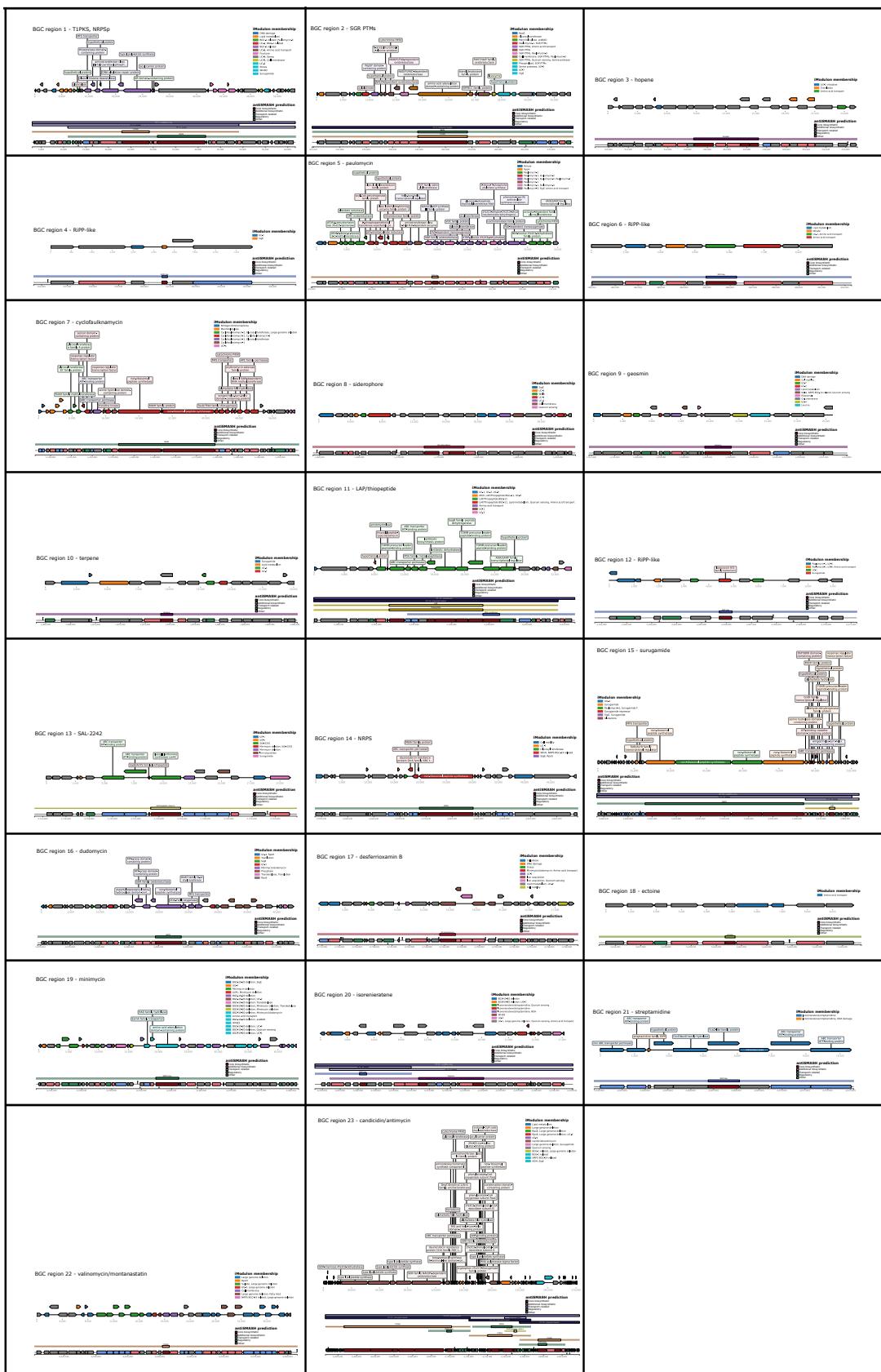
**Figure S1. Overview of the iModulome, related to Figure 2.** Each node represents an individual iModulon. Node fill color depicts the species the iModulon was detected in as per the legend. Node size reflects degree and edge thickness and colour represent edge weight as per legend. The network represents the 1500 most highly weighted edges (< 0.648 edge weight) and was clustered using the MCL clustering method from the clusterMaker app in Cytoscape v3.10.2.



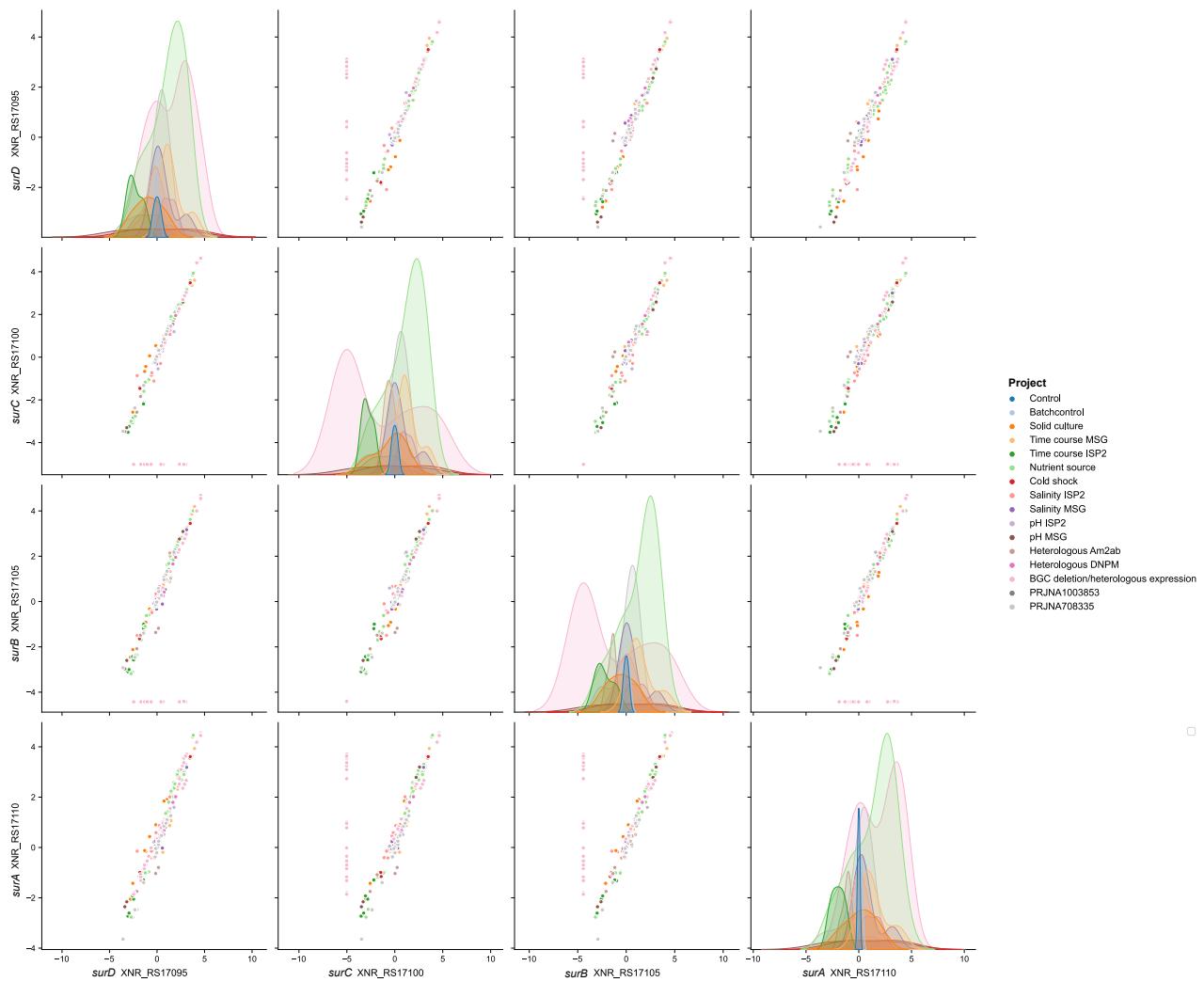
**Figure S2. Pairwise Translation-related iModulon comparison between *S. albidoflavus* and *E. coli*, related to Figure 2.** Gene weight correlation of the Translation iModulons of *S. albidoflavus* and *E. coli*. The dashed lines indicate the threshold values for the two iModulons. Genes highlighted in red and labelled, depict genes that are present in both the *S. albidoflavus* and the *E. coli* iModulons based on bidirectional BLAST results. These results indicate that these two iModulons are very similar to each other.



**Figure S3. Pairwise Phosphate uptake-related iModulon comparison between *S. albidoflavus* and *E. coli*, related to Figure 2.** Gene weight correlation of the Phosphate *S. albidoflavus* iModulon and the Phosphate-1 *E. coli* iModulon. The dashed lines indicate the threshold values for the two iModulons. Genes highlighted in red and labelled, depict genes that are present in both iModulons based on bidirectional BLAST results. The *pstSCAB* operon appears in both iModulons along with several putative lineage-specific members of the iModulons.



**Figure S4. antiSMASH predicted BGC regions and iModulon gene memberships, related to Figure 3 and Figure 4.** Genomic overview of all 23 endogenous BGC regions, as predicted by the antiSMASH software. For each BGC the iModulon memberships of all genes are depicted by color according to the legend. Labelled genes are members of iModulons containing the core biosynthetic genes for respective BGC. The images below are outputs from antiSMASH.



**Figure S5. Correlation between *surABCD* activities, related to Figure 3.** Pairwise plot depicting the gene activities of *surABCD* across different experiments (color). The expression of this operon is highly correlated across all conditions except for *surBC* which appear to have been deleted in some of the BGC deletion/heterologous expression samples. This deletion appears to be the main reason why these two genes are not part of the Surugamide iModulon, and instead placed in a separate iModulon (Surugamide F).