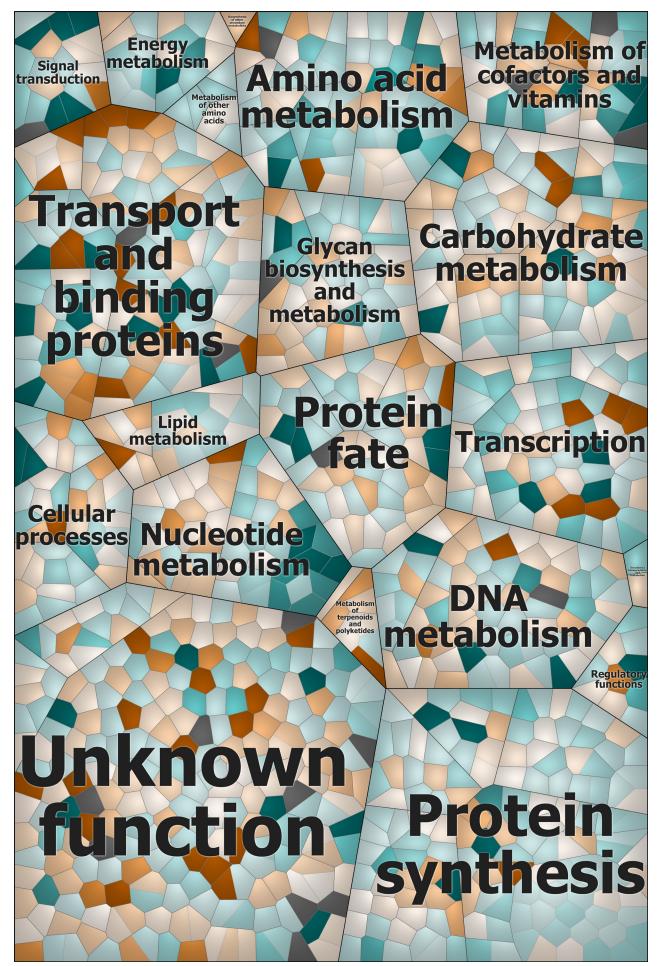
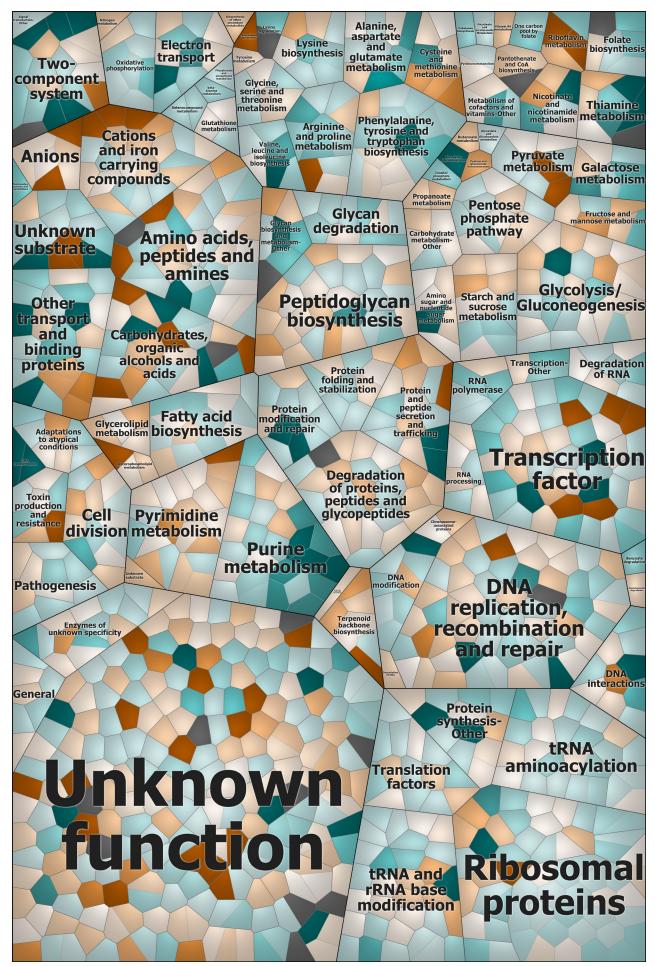
Supplementary Image 1 A

Comparison of protein abundances $\Delta phpP/WT$. Voronoi treemap of the quantified proteome (1,070 proteins of 1,918 theoretical proteins) of pneumococcal phosphatase mutant in comparison to WT assigned to specific functional main roles. Within the treemap all tiles symbolize single proteins which are colored according to their abundance in a divergent color gradient. Turquoise cells indicate proteins that are less abundant or "Off" in $\Delta phpP$ in comparison to the WT whereas higher abundant or "On" proteins are illustrated in orange. Grey fields represent proteins that could not be quantified in the compared strains.



Supplementary Image 1 B

Comparison of protein abundances $\Delta phpP/WT$. Voronoi treemap of the quantified proteome (1,070 proteins of 1,918 theoretical proteins) of pneumococcal phosphatase mutant in comparison to WT assigned to specific functional sub roles. Within the treemap all tiles symbolize single proteins which are colored according to their abundance in a divergent color gradient. Turquoise cells indicate proteins that are less abundant or "Off" in $\Delta phpP$ in comparison to the WT whereas higher abundant or "On" proteins are illustrated in orange. Grey fields represent proteins that could not be quantified in the compared strains.



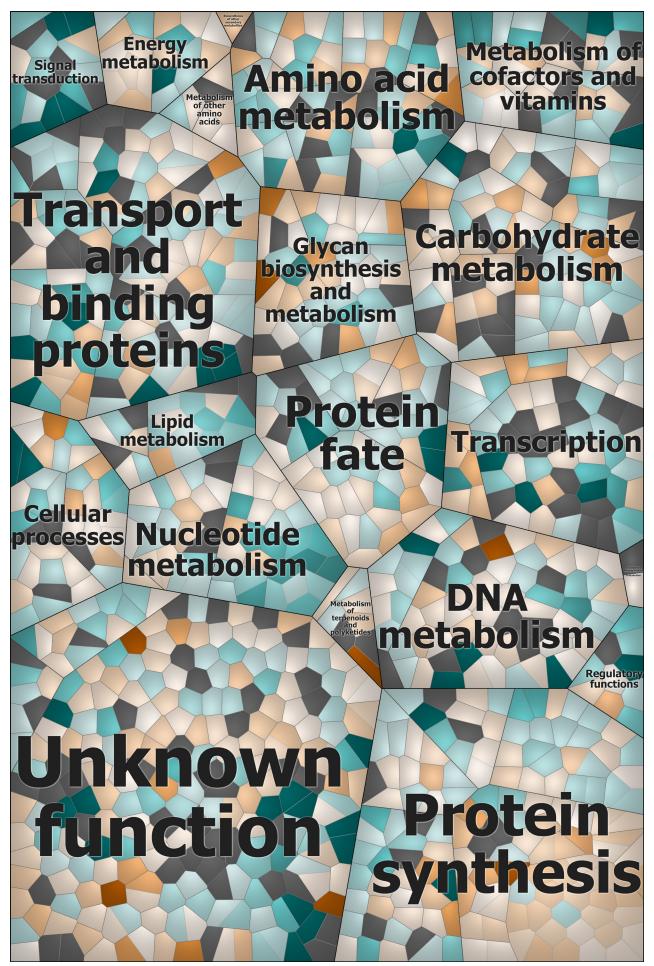
Supplementary Image 1 C

Comparison of protein abundances $\Delta phpP/WT$. Voronoi treemap of the quantified proteome (1,070 proteins of 1,918 theoretical proteins) of pneumococcal phosphatase mutant in comparison to WT labelled with single proteins. Within the treemap all tiles symbolize single proteins which are colored according to their abundance in a divergent color gradient. Turquoise cells indicate proteins that are less abundant or "Off" in $\Delta phpP$ in comparison to the WT whereas higher abundant or "On" proteins are illustrated in orange. Grey fields represent proteins that could not be quantified in the compared strains.



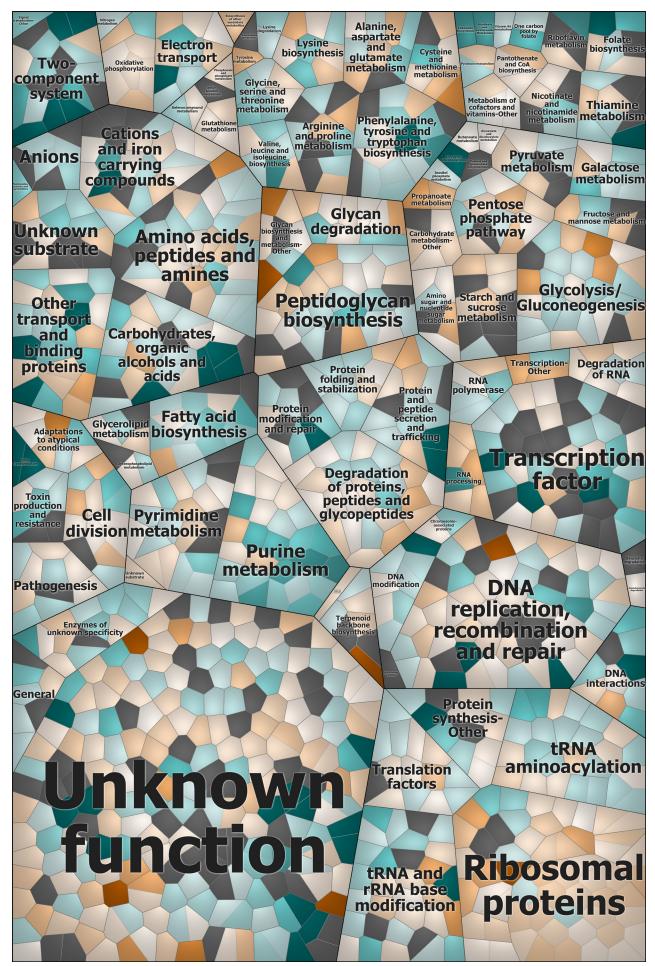
Supplementary Image 1 D

Comparison of protein abundances $\Delta stkP/WT$. Voronoi treemap of the quantified proteome (1,070 proteins of 1,918 theoretical proteins) of pneumococcal kinase mutant in comparison to WT assigned to specific functional main roles. Within the treemap all tiles symbolize single proteins which are colored according to their abundance in a divergent color gradient. Turquoise cells indicate proteins that are less abundant or "Off" in $\Delta stkP$ in comparison to the WT whereas higher abundant or "On" proteins are illustrated in orange. Grey fields represent proteins that could not be quantified in the compared strains.



Supplementary Image 1 E

Comparison of protein abundances $\Delta stkP/WT$. Voronoi treemap of the quantified proteome (1,070 proteins of 1,918 theoretical proteins) of pneumococcal kinase mutant in comparison to WT assigned to specific functional sub roles. Within the treemap all tiles symbolize single proteins which are colored according to their abundance in a divergent color gradient. Turquoise cells indicate proteins that are less abundant or "Off" in $\Delta stkP$ in comparison to the WT whereas higher abundant or "On" proteins are illustrated in orange. Grey fields represent proteins that could not be quantified in the compared strains.



Supplementary Image 1 F

Comparison of protein abundances $\Delta stkP/WT$. Voronoi treemap of the quantified proteome (1,070 proteins of 1,918 theoretical proteins) of pneumococcal kinase mutant in comparison to WT labelled with single proteins. Within the treemap all tiles symbolize single proteins which are colored according to their abundance in a divergent color gradient. Turquoise cells indicate proteins that are less abundant or "Off" in $\Delta stkP$ in comparison to the WT whereas higher abundant or "On" proteins are illustrated in orange. Grey fields represent proteins that could not be quantified in the compared strains.

