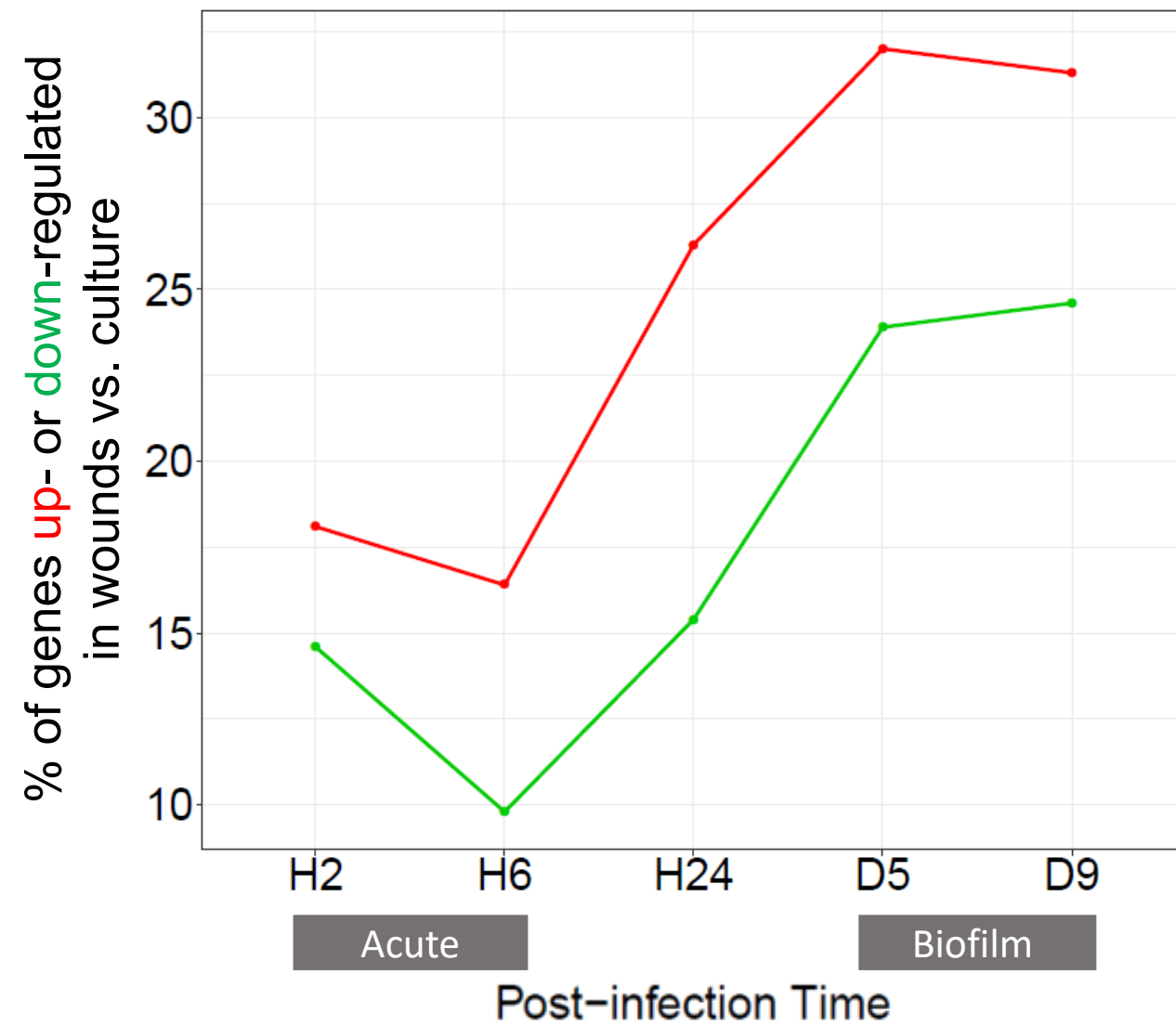
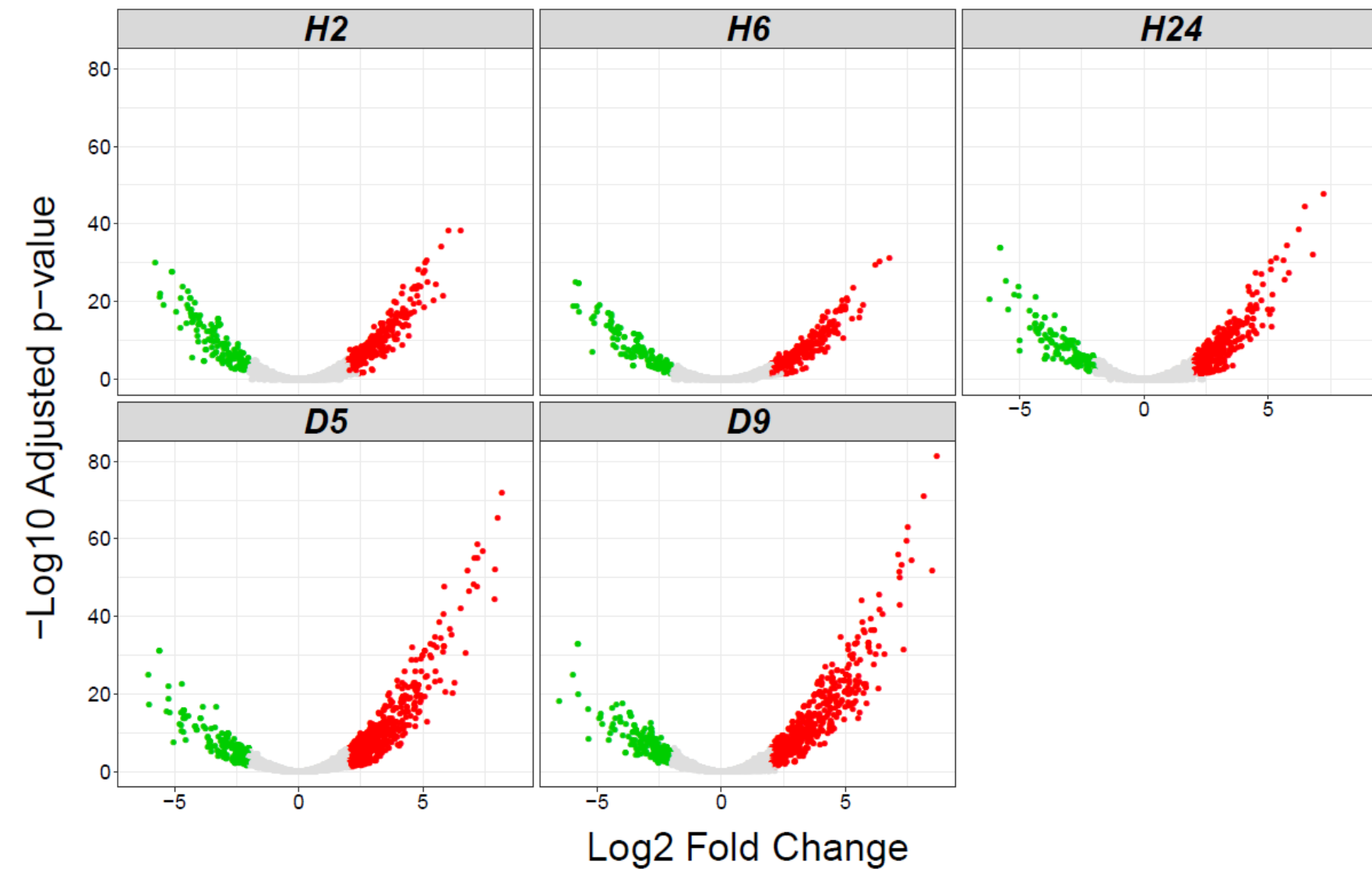


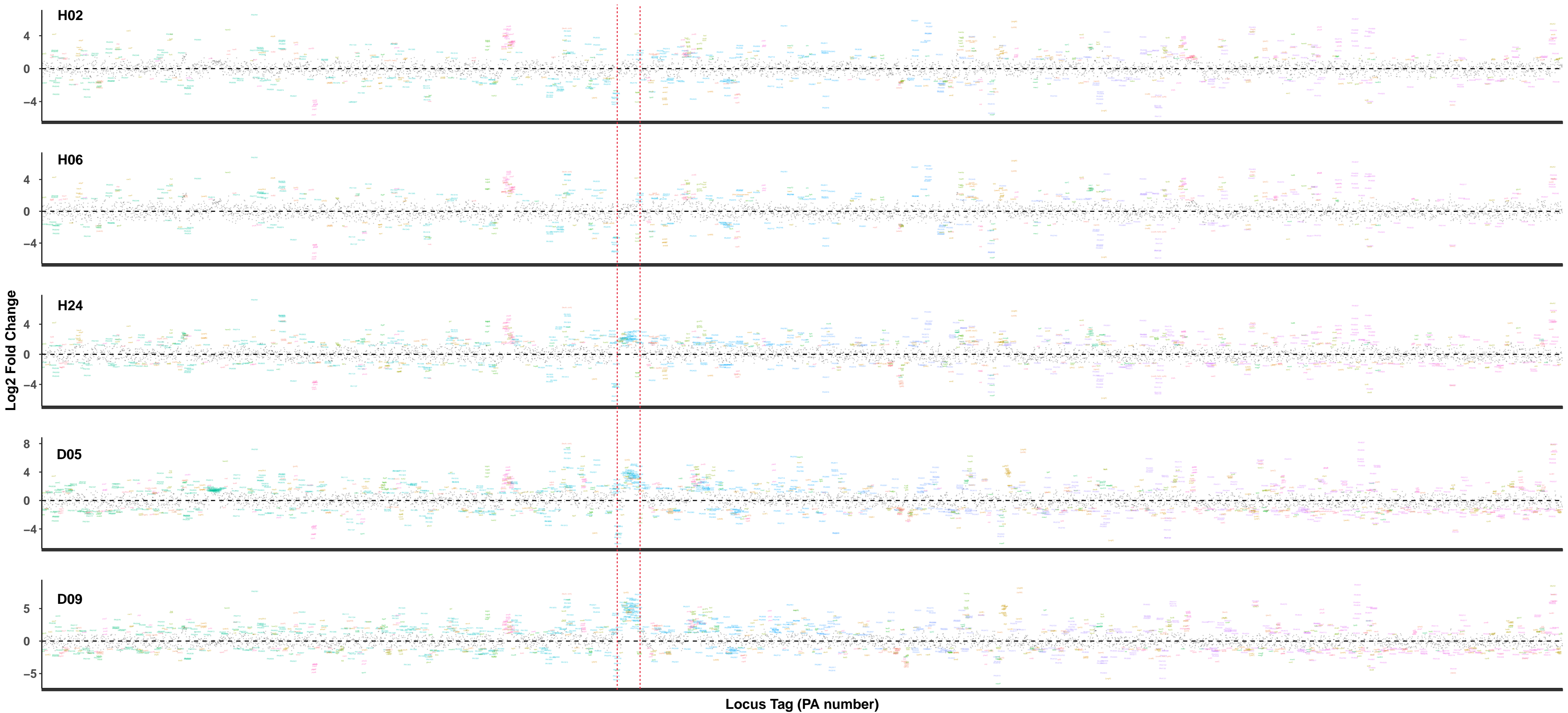
***Pseudomonas aeruginosa* transcriptome adaptations
from colonization to biofilm infection of skin wounds**

Peter D'Arpa, S. L. Rajasekhar Karna, Tsute Chen, Kai P. Leung

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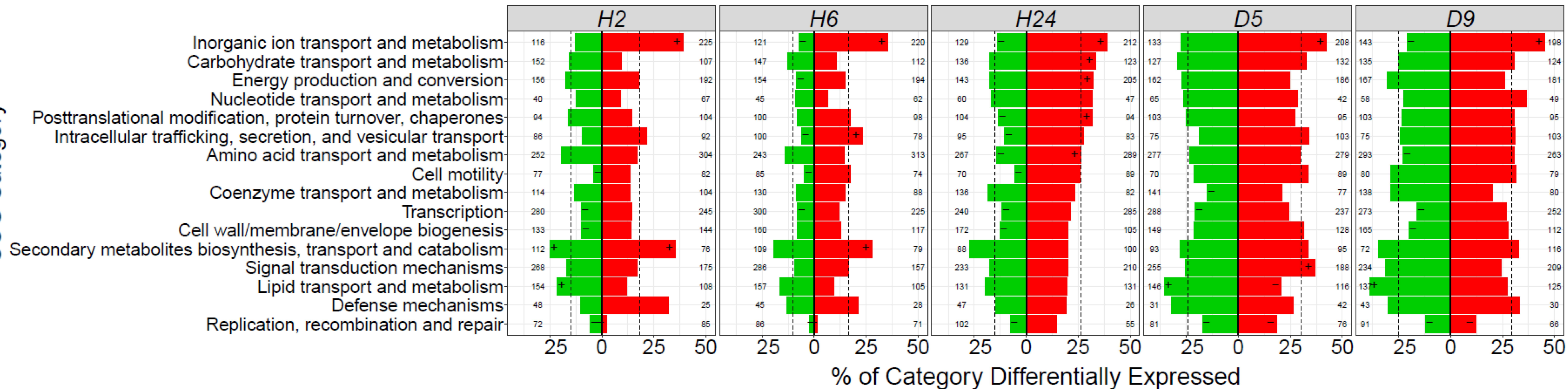
A**B**

S1 Fig. Global gene expression of PAO1 in wounds vs. log-phase culture. (A) The percentage of genes with up- (red) and down(green)-regulated expression in wounds (false discovery rate, FDR < 0.05). (B) Volcano plots.

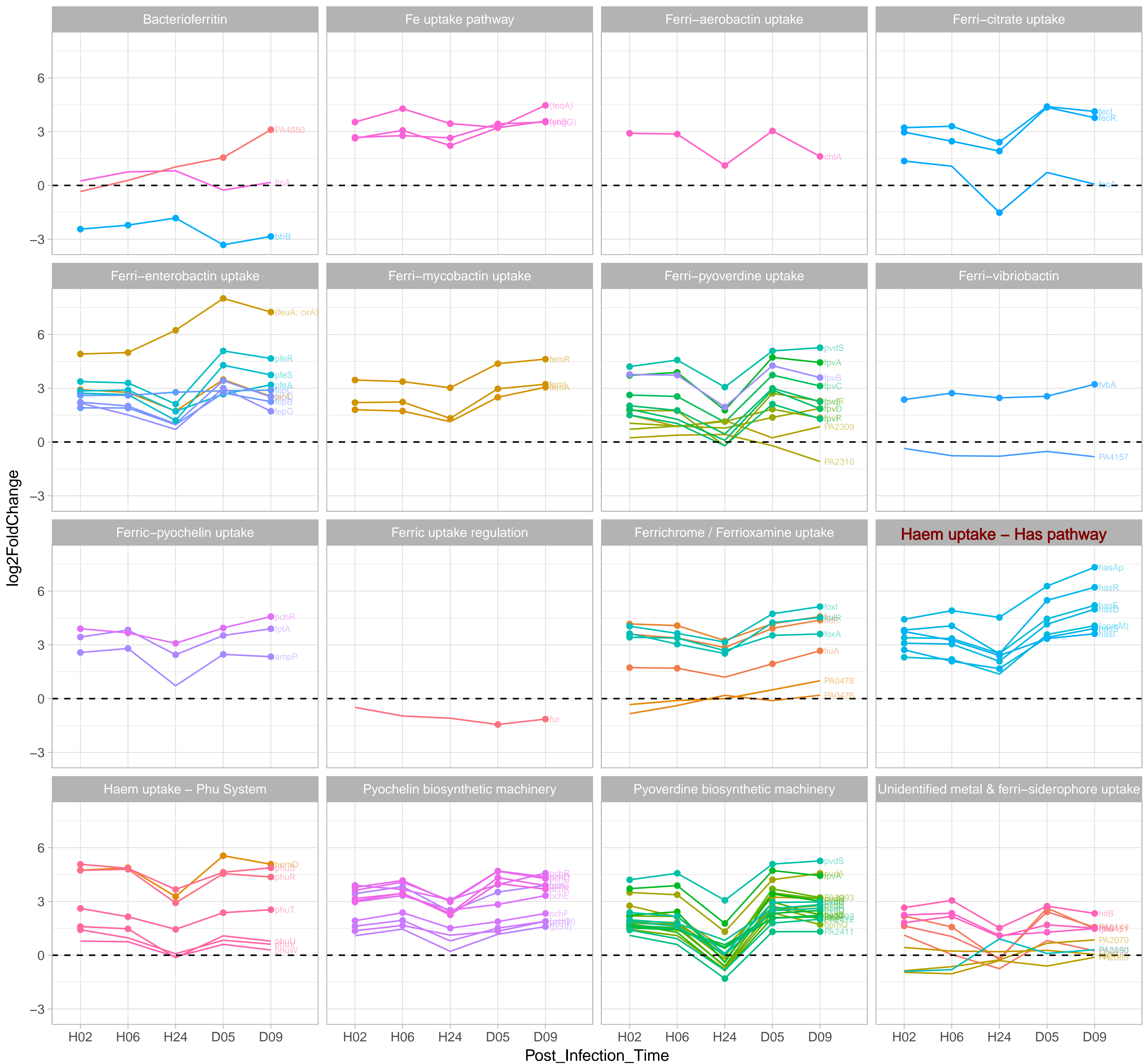


S2 Fig. Log2 Fold Change of PAO1 genes at in-wound times vs. log-phase culture. Genes are ordered by their position in the genome. The red dotted lines delineate PA2134 to PA2193. Gene color is alphabetical.

COG Category

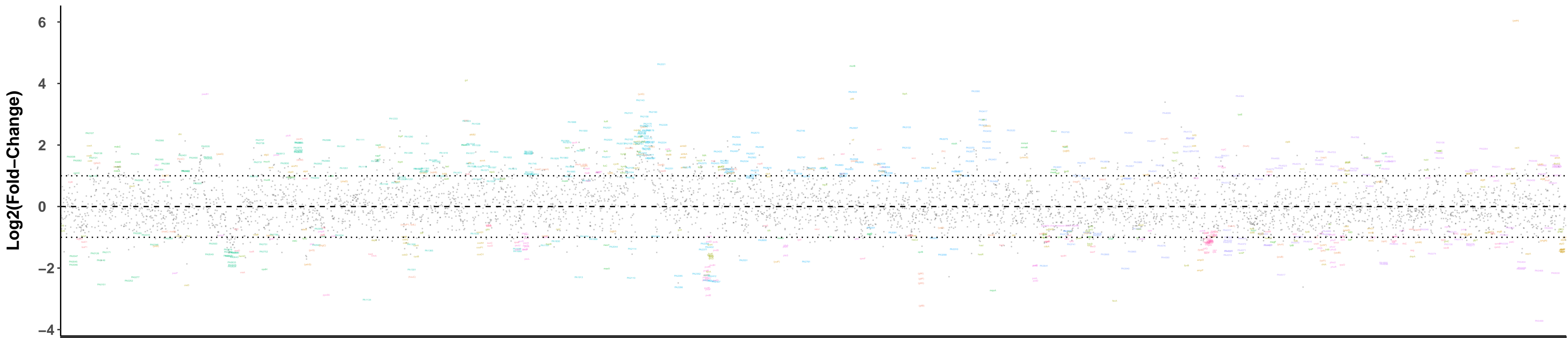


S3 Fig. Percent of genes in COG categories differentially expressed at each in-wound time (vs. log-phase culture). COG categories significantly overrepresented (+) or underrepresented (-) relative to the proportion of all significant up-regulated or down-regulated genes (Fisher's exact test, $p < 0.05$, implemented in R package GeneOverlap version 1.10.0). Dotted lines indicate the percent down- and up-regulated genes averaged across all COG categories. The COG categories are arranged from top to bottom in descending order of the percent of significantly up-regulated genes at 24 hrs. The numbers in the panels are the counts of genes per COG category (*Pseudomonas Genome DB*, PAO1 COG mappings) expressed less or more so than in log-phase culture (regardless of fold-change or FDR).

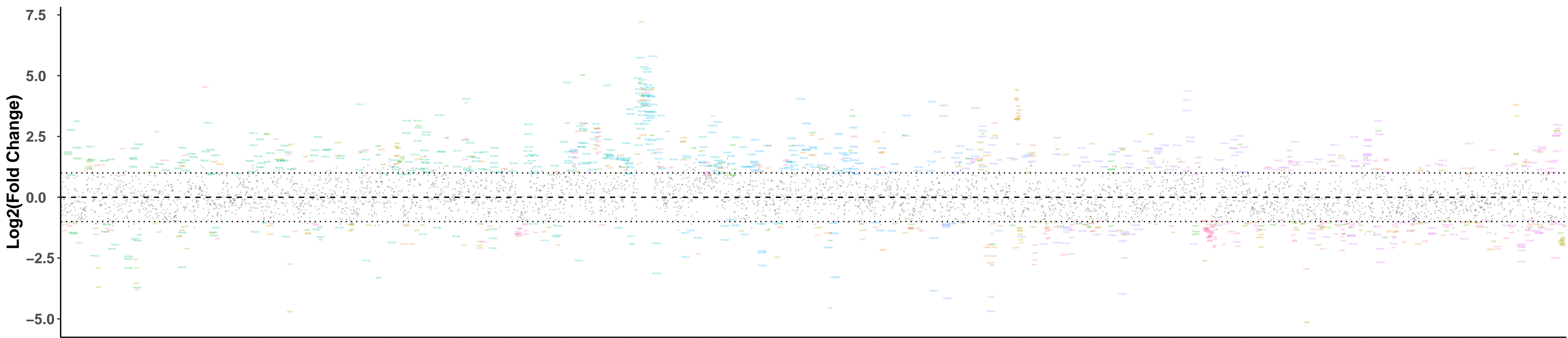


S4 Fig. Expression of COG, 'Inorganic ion transport and metabolism', genes in wound infection vs. log-phase culture. A solid circle indicates a significant difference in the expression of the gene in the wound vs. culture.

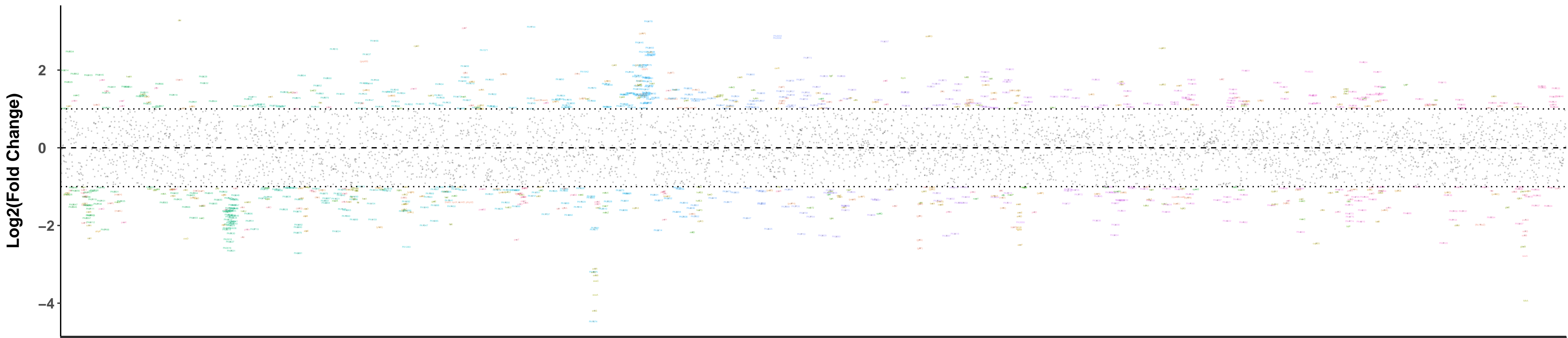
Acute infection (H24) vs. Colonization (H2&H6)



Biofilm infection (D5&D9) vs. Colonization (H2&H6)

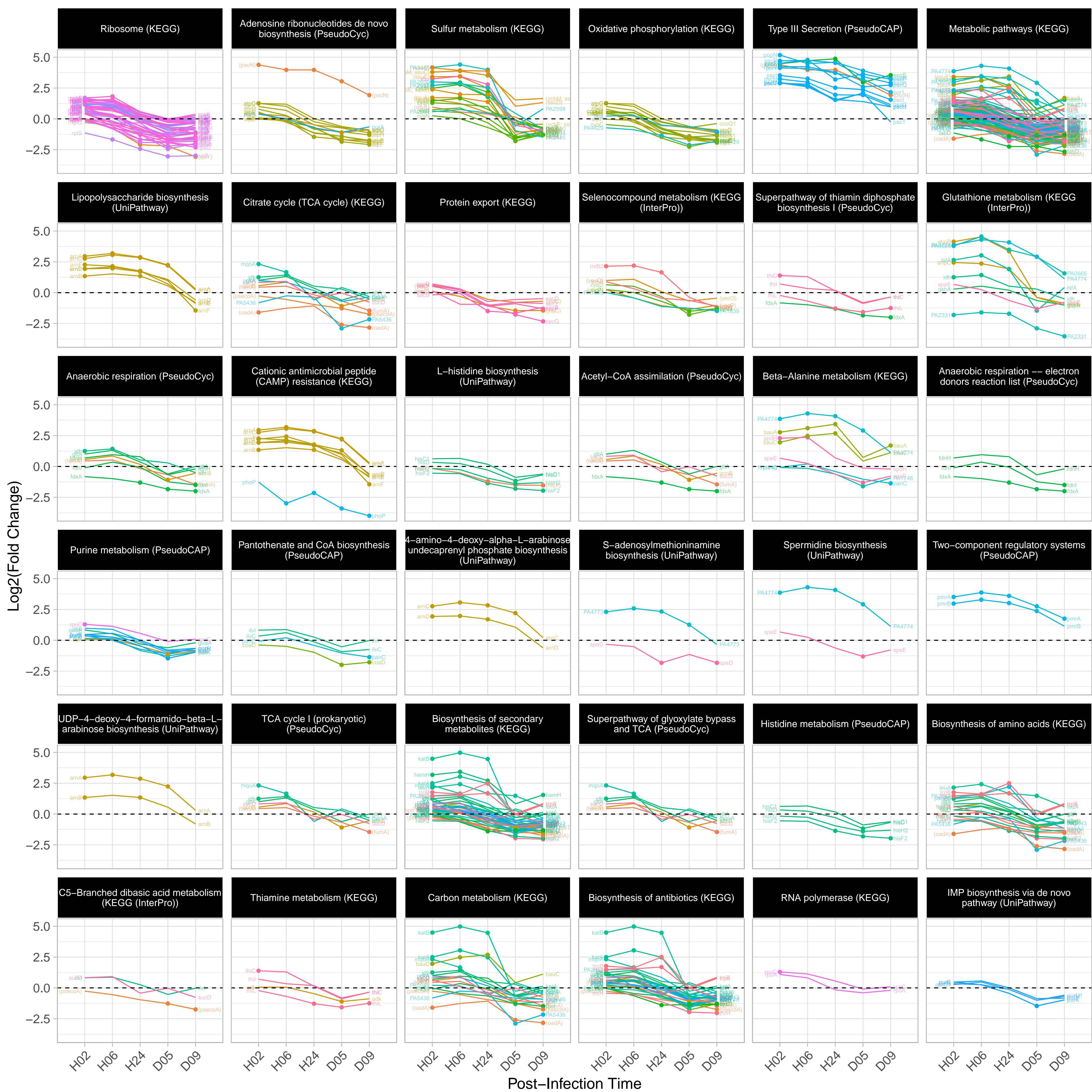


Late biofilm (D9) vs. Early biofilm (D5) infection



Locus Tag (PA number)

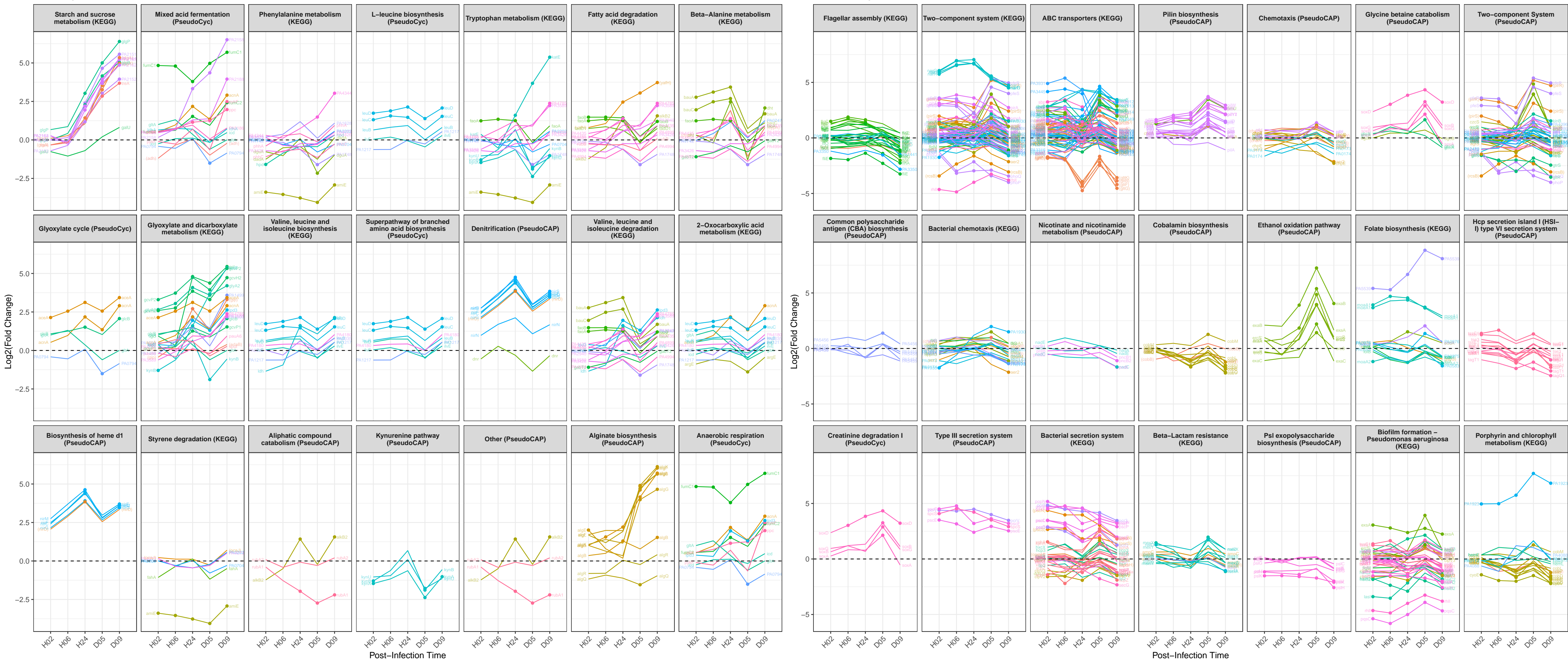
S5 Fig. Changes in PAO1 gene expression as wound infection developed: colonization to acute infection, colonization to biofilm infection, and earlier to later biofilm infection.



S6 Fig. Pathways down-regulated from acute to biofilm infection. Pathways with over-represented down-regulated genes in biofilm infection (D5&D9:H2&6) are shown with their genes plotted vs. in-wound time. Dashed lines indicate the expression level in log-phase culture. Solid circles indicate a significant gene expression difference (FDR < 0.05) between log-phase culture and wounds at each in-wound time

Up-regulated pathways from less-mature to more-mature biofilm wound infection

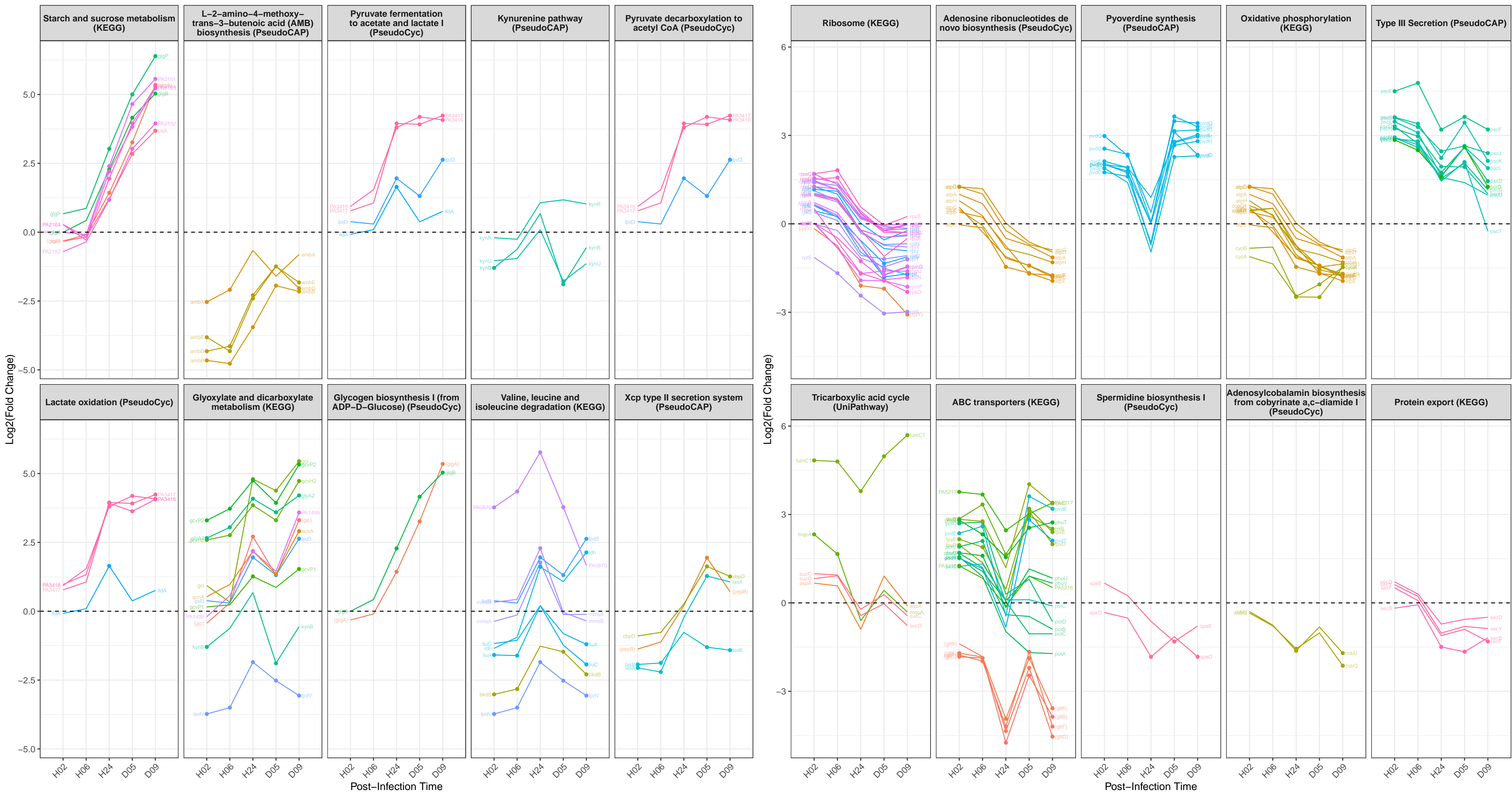
Down-regulated pathways from less-mature to more-mature biofilm wound infection



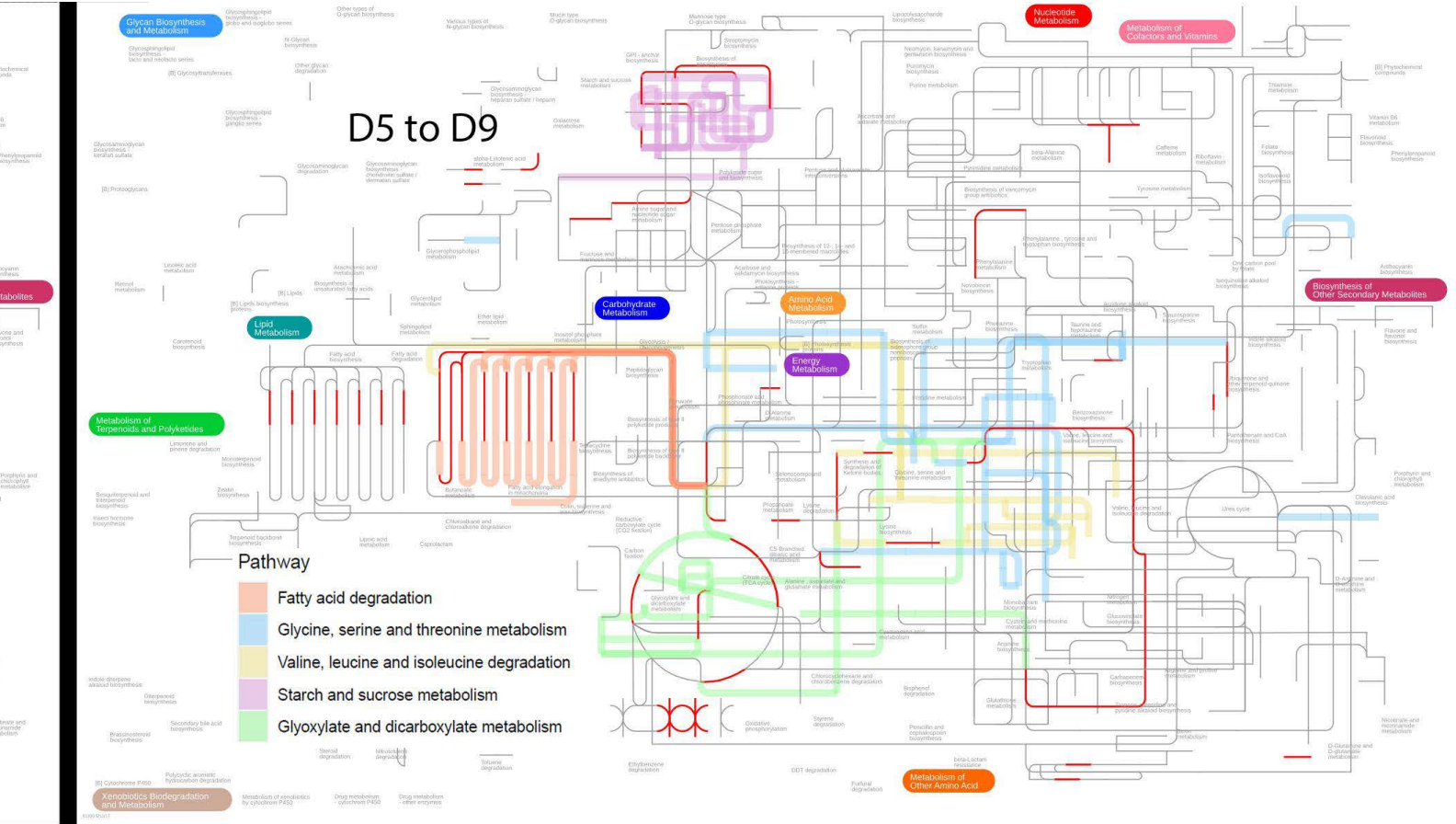
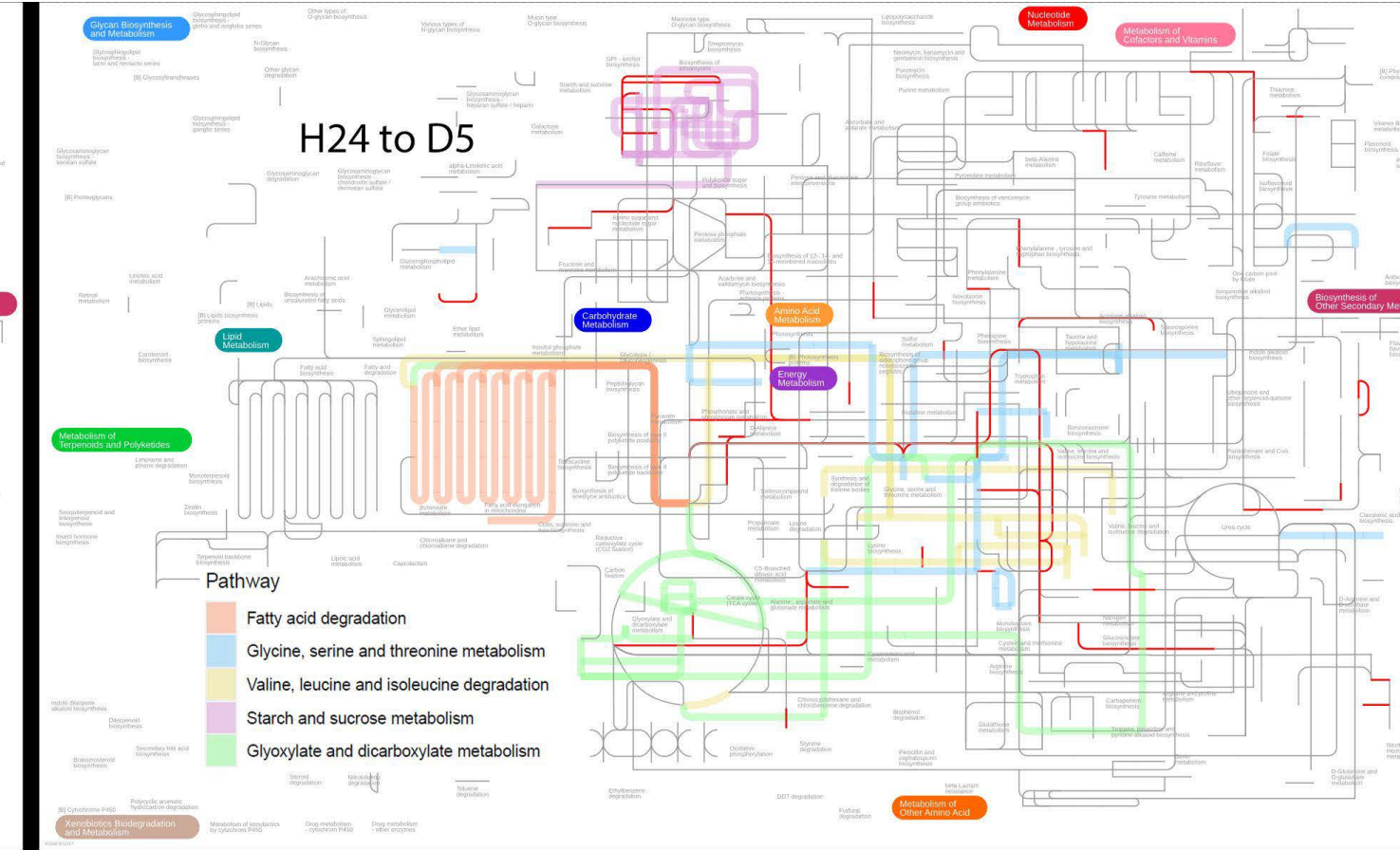
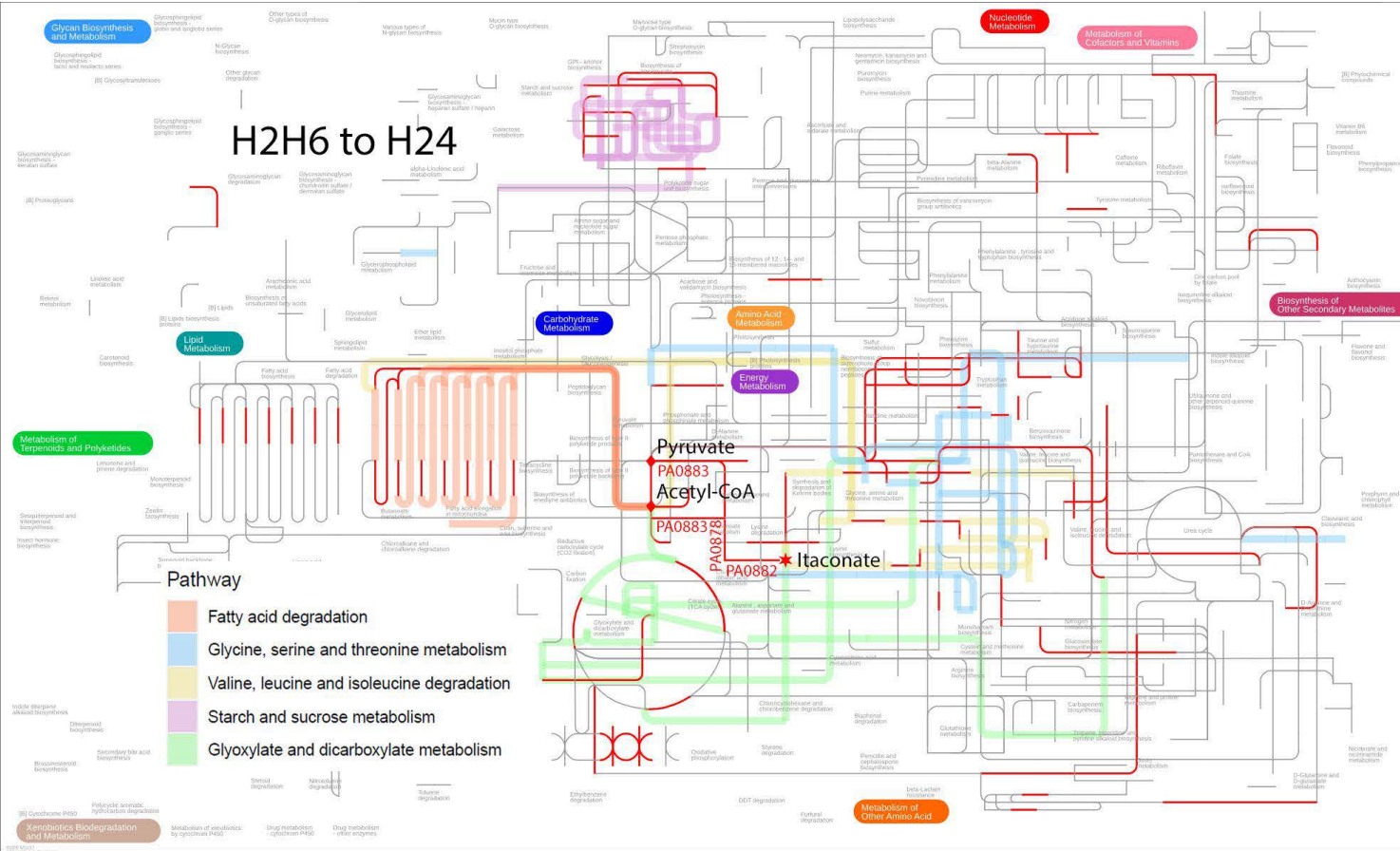
S7 Fig. Pathways up- and down-regulated from less-mature (D5) to more-mature (D9) *P. aeruginosa* wound infection. Genes in the pathways are plotted vs. post-infection time. Dashed lines indicate the expression level in log-phase culture. Solid circles indicate a significant gene expression difference (FDR < 0.05) between log-phase culture and wounds at each post-infection time.

Up-regulated pathways from colonization to acute wound infection

Down-regulated pathways from colonization to acute wound infection



S8 Fig. Pathways up- and down-regulated from colonization (H2&H6) to acute (H24) infection. Pathways with over-represented up- or down-regulated genes in biofilm infection (H24:H2&6) are shown with their genes plotted vs. time after infection. Dashed lines indicate the expression level in log-phase culture. Solid circles indicate a significant gene expression difference (FDR < 0.05) between log-phase culture and wounds at each post-infection time.



S9 Fig. Mapping of up-regulated genes onto KEGG pathways specific for *P. aeruginosa* strain PAO1. Up-regulated genes, about 450 for each comparison (selected by adjusting the FDR cutoff), were mapped (red lines) onto *P. aeruginosa* PAO1 metabolic pathways (pae01100) using Interactive Pathways Explorer v3 ([42](#)).