

Supplementary Material

The *Staphylococcus aureus* Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures

Kumari Sonal Choudhary¹, Nathan Mih^{1,2}, Jonathan Monk¹, Erol Kavvas¹, James T. Yurkovich^{1,2}, George Sakoulas³, Bernhard O. Palsson^{1,2,3*}

¹Systems Biology Research Group, Department of Bioengineering, University of California, San Diego, CA

²Bioinformatics and Systems Biology Program, University of California, San Diego

³Department of Pediatrics, University of California, San Diego

***Correspondence:**

Bernhard O. Palsson

palsson@eng.ucsd.edu

SUPPLEMENTARY FIGURE

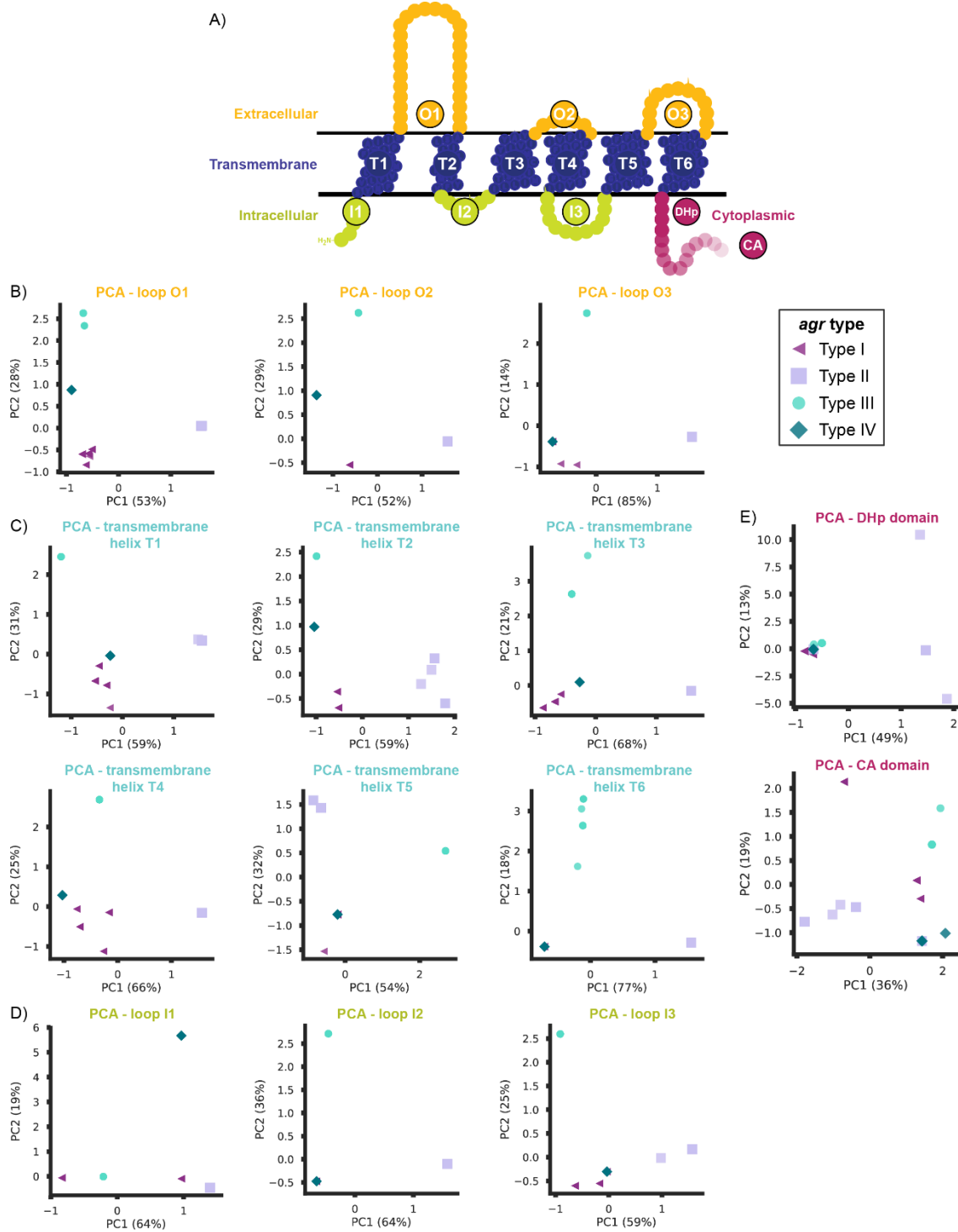


Figure 3: Biochemical property PCA between multiple *agr* types, per domain as defined by location in A). Locations are B) extracellular loops, C) transmembrane helices, D) intracellular loops, or E) cytoplasmic domains. It can be seen that both the extracellular loops

and transmembrane domains cluster the *agr* types well, although this clustering may be due to the short sequence of the domains being used for property calculation.