Supplementary Information

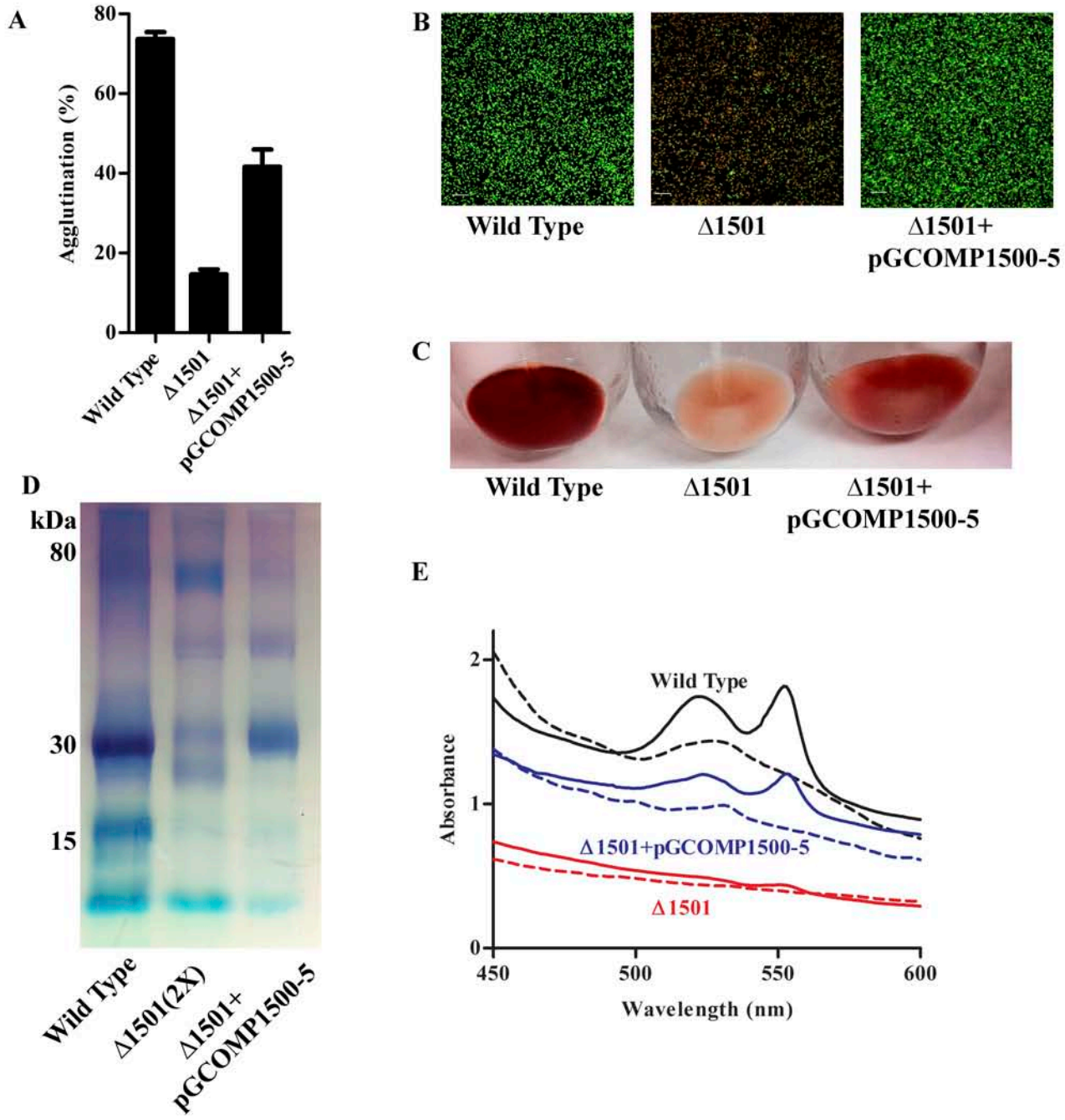

FIG. S1. Complementation of the *G. sulfurreducens* Δ1501 mutant required expression of multiple genes from the *xap* cluster. (A) Percent agglutination in wild type, Δ1501 mutant, and complemented mutant (Δ1501+pGCOMP1500-5) as determined by change in OD_{600} before and after aggregate disruption. Error bars are standard errors of the mean for three replicates. (B) CLSM images of wild type, Δ1501 mutant, and Δ1501+pGCOMP1500-5 after 24 hours with electrode poised at +0.24 V vs. SHE. CLSM images are maximum projections (bar = 20 µm) of electrode-attached biofilms stained with a LIVE/DEAD kit. (C) Extracellular material isolated from wild type, Δ1501 mutant, and Δ1501+pGCOMP1500-5. (D) Stain of total extracellular heme-containing protein in wild type (lane 1), Δ1501mutant (lane 2) and Δ1501 +pGCOMP1500-5 (lane 3), 10 µg protein loaded in lanes 1 and 3, while lane 2 was double loaded (20 µg protein) in order to detect heme-containing proteins in the Δ1501 extracellular material. (E) UV/visible spectra of isolated extracellular material, oxidized shown by dashed lines, dithionite reduced as solid lines.