Supplementary Information for

Vibrio cholerae **biofilms use modular adhesins with glycan-targeting and nonspecific surface binding domains for colonization**

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Supplementary Figure 1| **Schematic of domains and corresponding cartoon representations of Bap1 (***Left***) and RbmC (***Right***) mutants used in this study.**

Supplementary Figure 2| β-propeller anchors Bap1 and RbmC to VPS. a, Cross-sectional images of *bap1*Δ*β-prismB* at *z* = 6 µm. Cells constitutively express mNeonGreen; Bap1 was stained with an anti-FLAG antibody conjugated to Cy3. Bap1_{Δβ-prism} retains peripheral staining around biofilm clusters, suggesting that VPS binding only requires the β-propeller. **b**, Western blot analysis of the production and secretion of constructs missing the β-propeller in the VPS[−] (Δ*vpsL*) background. A significant fraction of the proteins is found in the cell pellet, indicating a defect in

secretion. Therefore, these mutants were excluded from further analysis. **c**, Western blot of *V. cholerae* strains expressing 3×FLAG-tagged WT or Bap1ΔVelcro protein (* denotes strain lacking *hapA* and *ivaP*). In the WT background, Bap1 Δ Velcro experiences degradation leading to lower signal intensity. Deleting *hapA* and *ivaP*, the two major extracellular proteases¹, resolves the degradation problem. **d-e,** Cross-sectional images of *bap1*Δ*Velcro* (d) and Δ*hapA*Δ*ivaP bap1*Δ*Velcro* (e) in the biofilm bulk $(z = 6 \mu m)$. Cells constitutively express mNeonGreen; Bap1 was stained with an anti-FLAG antibody conjugated to Cy3. Note that a functional copy of RbmC is present in these strains. Deletion of *hapA* and *ivaP* does not change the localization or aggregation of the mutant protein. **f,** Biofilm adhesion assay with *bap1*Δ*Velcro*, together with positive (Δ*rbmC*) and negative ($\Delta rbmC\Delta banD$) controls. Data are shown as the mean \pm SD ($n = 3$ biologically independent samples). Statistics were performed using an unpaired, two-tailed *t*-test with a Welch's correction. ns represents not significant ($\triangle r b m C$ *bap1*_{$\triangle V el c r o$} v.s. $\triangle r b m C \triangle b a p 1$: $p =$ 0.1144); *** $p < 0.001$ ($\triangle rbmC$ v.s. $\triangle rbmC$ bap1 $\triangle v$ elcro: $p = 0.0009$). **g**, 3D-rendering of confocal images of a biofilm from Bap1Δvelcro-3×FLAG cells expressing mNeonGreen with *in situ* immunostaining. **h**, Distribution of puncta size in *bap1*Δ*Velcro* biofilms (N = 200 technical replicates). **i**, EMSA of RbmA (*Left*) binding to VPS, RbmC's β-propeller binding to VPS (*Middle*), and Bap1*(= Bap1Δ57aa, *Right*) binding to selected polysaccharides. RbmA was used as a positive control in the EMSA as it is known to bind to $VPS²$. The protein amount per lane is 5 μ g when present. The VPS amount is 0, 0.0625, 0.125, 0.25, 0.50, 1, 5, 5, 5 µg in each lane from left to right. For other polysaccharides, 5 µg is used in each lane whenever present. Red arrows = proteinsubstrate complex, black arrows = unbound protein, green arrows = free GFP. Under the concentrations tested, we did not observe the same tight binding of Bap1 to the selected polysaccharides as seen with VPS.

Supplementary Figure 3| **Bap1 is the major biofilm adhesin on abiotic surfaces. a,** Absorbance at 550 nm in crystal violet assays for the indicated strains. Data are shown as the mean \pm SD ($n =$ 3 for rugose and $\triangle rbmC$, $n = 4$ for $\triangle ban1\triangle rbmC$, $n = 9$ for $\triangle rbmC$, all biologically independent samples). Statistics were performed using an unpaired, two-tailed *t*-test with a Welch's correction. ns represents not significant (Rg v.s. $\Delta rbmC$: $p = 0.0751$); ** $p < 0.01$ (Rg v.s. $\Delta ban1$: $p = 0.0026$); **** *p* < 0.0001. **b**, Biofilm adhesion assays performed on polystyrene, untreated glass, or NaOHtreated glass (following an increasing order of hydrophilicity), for various mutants with a single or double deletion of *bap1* and/or *rbmC*. Data are shown as the mean ± SD (*n* = 3 biologically independent samples). On NaOH-treated glass that is more hydrophilic and negatively charged³, a single deletion of *bap1*, but not *rbmC*, is sufficient to lead to an adhesion defect. **c,** Representative cross-sectional views of the bottom layer and side views of different mutant biofilms. The two defective mutants Δ*bap1*Δ*rbmC* and Δ*rbmC bap1*Δ*β-prismB* form floating clusters not attached to the surface. The Δ*rbmC bap1*Δ*57aa* displays a hole at biofilm core (yellow arrow), indicating a slight adhesion defect. **d**, Biofilm adhesion assays performed on polystyrene, untreated glass, or NaOHtreated glass, for various *bap1* mutants in the presence of 1 mg/mL BSA. Data are shown as the

mean \pm SD ($n = 3$ biologically independent samples). The Bap1_{Aβ-prismB}+57aa construct, although functional on bare glass, does not adhere to NaOH-treated glass, suggesting that β-prism**B** still contributes to abiotic surface adhesion to some extent. **e**, Negative control for the microbead adsorption assay. *Top*: a representative image of 5 μm silica bead (*Left*, bright field) and FITC adsorbed on the bead (*Right*). *Bottom*: a representative image of 5 μm silica beads coated with lipids, labeled with RhPE (*Left*) for lipids and the FITC adsorbed on lipid layer (*Right*). [FITC] = 1.5 µM. FITC molecules adsorb minimally to these two types of surfaces. See main Figure 3f for quantification. **f**, A representative image of 5 μm silica beads incubated with RhPE. RhPE does not adsorb onto silica surfaces unless coated with lipids. The intensity scale in e and f is the same as that in main Figure 3e.

constructs. **a**, Western blot analysis of the production and secretion of RbmC protein constructs in VPS[−] *V. cholerae* strains. All constructs are secreted into the supernatant at a level comparable to WT. **b**, Western blot analysis of the production and secretion of Bap1 protein constructs in VPS⁺ (*Left*) and VPS[−] (*Right*) *V. cholerae* strains. Among the defective mutants, Bap1Δβ-prism**B** shows reduced intensity due to degradation and potentially also secretion. To verify that the defective phenotype seen with Bap1Δβ-prism**B** is not due to these confounding factors, we overexpressed *bap1*Δ*β-prismB* from an arabinose-inducible plasmid. **c**, Western blot analysis of induction,

production, and secretion of *bap1*Δ*β-prismB***-**3×FLAG from a plasmid in the VPS+ (*Left*) and VPS[−] (*Right*) background, with and without 0.2% arabinose. In the presence of arabinose, the level of secreted proteins is restored to a level higher to that of WT Bap1. **d**, Adhesion assay of the strain overexpressing $bap_1_{\Delta\beta\text{-prism}}$ in the presence of 1 mg/mL BSA. Data are shown as the mean \pm SD $(n = 3$ biologically independent samples). Even in the presence of arabinose that leads to elevated levels of the secreted protein, *bap1*Δ*β-prism^B* is unable to adhere the biofilm to the glass surface, suggesting that the protein is inherently defective. **e,** Adhesion defective mutants can be complemented. Shown are results from adhesion assay (from left to right) of Δ*rbmC*Δ*bap1*, Δ*rbmC bap1*Δ*Velcro*, Δ*rbmC bap1*Δ*57aa*, *and* Δ*rbmC bap1*Δ*β-prism^B* mutants with a plasmid containing PBAD-*bap1* induced with 0.2% arabinose in the presence of 1 mg/mL BSA. Data are shown as the mean \pm SD ($n = 3$ biologically independent samples). The complementation assay validates that the defective phenotype of these strains is due to the specific mutations in Bap1.

Supplementary Figure 5| Purified functional RbmC constructs but not Bap1 constructs bind to glycans prevalent on host surfaces. a, Merged z-stack of confocal images of DAPI-stained Caco-2 cells incubated with 1 μM purified and GFP-tagged Bap1 domains. The total size of each image is $80 \times 80 \times 32.5$ µm. The intensity scale is the same as that in Figure 4a. None of the Bap1 domain(s) shows positive staining with Caco-2 cells. **b**, Confocal images of jejunum tissue slices stained with DAPI, FM 4-64, and 1 μM purified and GFP-tagged β-prism**C1** (*Left*), β-prism**C2** (*Middle*), and β-prism**B** (*Right*). **c**, EMSA of RbmC_{M1M2} (*Left*), RbmC_{M2} (*Middle*), or StcE_{C-term} (*Right*) binding to bovine submaxillary mucin (BSM). The protein amount per lane is 5 µg when present. The BSM amount is 0, 0.5, 1, 2, 4, 6, 8, 10, 10, 10 µg in each lane from left to right. Red arrows = protein-substrate complex, black arrows = unbound protein, green arrows = free GFP.

directing adhesins to bare and functionalized glass surfaces. a, Distribution quantification for Bap1 and RbmC in the presence of BSA or asialofetuin. Shown are the ratios between the signals of 3×FLAG-tagged proteins at the biofilm-glass interface and the total signal integrated over the entire biofilm cluster, for each indicated strain. The relative order of the two proteins localized to the biofilm-glass interface is opposite in the two cases, showing different preferences of the two adhesins for different types of surfaces. **b-c,** Asialofetuin binding requires a functional β-prism. **b**, Cross-sectional image of a biofilm from Δ*bap1 rbmC*Δ*β-prismC2 D539A*, in which N-glycan binding was abolished due to a point mutation in a key aspartate residue in the binding pocket⁴ (schematically shown on the right). The surface localization of RbmC signal is lost due to the loss of N-glycan binding, as quantified in panel **c**. For **a** and **c**, individual points are from different biofilms in one sample (technical replicates), and no statistics were derived.

Supplementary Figure 7| Validation of enteroid monolayers. Shown are maximum projection images of a representative monolayer with nuclei stained with DAPI (cyan), crypt domains stained with CD44v6 antibody (yellow), goblet cells stained with MUC2 antibody (magenta) in **a** and enterocytes stained with Villin (magenta) in **b**. Scale bars: 20 µm. **c,** Representative maximum projection images of enteroid monolayers stained with nuclei stained with DAPI (blue), an F-actin probe conjugated to Alexa FluorTM 647 dye (magenta), and 1 μ M labeled proteins. All proteins are labeled with GFPUV, and the 57aa peptide is labeled with FITC. The bottom right panel shows a control without any protein/peptide staining. Shown on the left column are the overlay images of all three fluorescent channels and on the right column are the signals in the 488 nm channel.

Supplementary Figure 8| **Validation of the role of the biofilm adhesins in the wild-type background. a**, WT *V. cholerae* biofilms with different constructs grown in microfluidic chambers under a flow rate of 0.6 μL/min. Shown are both cross-sectional views of biofilms at *z* = 6 μm, both in the absence (*Top*) and presence (*Bottom*) of 0.4 mg/mL BSA. **b,** Quantification of biomass for different WT biofilms (mean \pm SD, *n* (biologically independent samples) = 4 for $\triangle r b m C$ and $n = 3$ for all other mutants, two-tailed *t*-test with Welch's correction. * $p < 0.05$, ** $p <$ 0.01, $ns = not significant$). *p* values from left to right (in the absence of BSA): 0.8139, 0.5010, 0.0232, 0.0284, 0.0253. *p* values from left to right (in the presence of BSA): 0.2340, 0.0081, 0.0072, 0.0071, 0.0072. Note that the surface layer was excluded from the analysis; WT *V. cholerae* cells can attach to glass surfaces via pili and form a monolayer independent of their ability to form biofilms⁵.

Supplementary Figure 9| **Phylogenetic analysis of RbmC and Bap1 among Vibrio species. a**, Phylogenetic tree of 20 Vibrio species adapted from Ref.6, showing the distribution of RbmC/Bap1 homologues. The branch lengths are approximate. Filled circles indicate where a RbmC gene was recovered. Open circles indicate where a potential RbmC gene with low conservation was recovered. Stars indicate where Bap1 was recovered. Scale bar: the number of substitutions per site. **b**, Phylogenetic analysis of Bap1 and RbmC homologs in Vibrio species. Scale bar: number of amino acid substitutions per site*.*

Supplementary Table 1- Strains used in this study

Supplementary Table 2. Primers Used in this Study.

*****lowercase nucleotides indicate overlapping sequence for SOE or nucleotide change for aa mutations

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