

Figure S1. (A) Methacrylation and fluorination reactions involved in MAC and MACF synthesis. (B) 1H-NMR spectrum for MACF to determine degree of methacrylation. (C) Quantitative 19F-NMR spectrum of MACF to determine fluorination efficiency using d-TFA (1 nM) as an internal standard.



**Figure S2.** Viability of HDFs at different timepoints post PHMB exposure in soluble forms as well as encapsulated within MAC/MACF hydrogels. Data all n =3, mean  $\pm$  S.D. Asterisks denote significance by three-way ANOVA with Tukey's *post-hoc* (\*\* denotes *p* < 0.05, \*\*\*\* denotes *p* > 0.0001).



## (B)

- MACF Hydrogel (Non-infected)
- MACF-PHMB Hydrogel (Non-infected)
- MACF Hydrogel (Infected)
- □ MACF-PHMB Hydrogel (Infected)
- MACF-PHMB Hydrogel (Non-infected)
- MAC Hydrogel (Non-infected) MAC Hydrogel (Infected) MAC-PHMB Hydrogel (Infected)
- Tegaderm (Non-infected)
- Tegaderm (Infected)
- Kendall Dressing (Infected)



## **Days Post Wounding**

Figure S3. (A) Representative images of all wound treatments at different timepoints post-wounding. Strong infection presence visible in infected groups, indicating effective bacterial colonization. Reduction in visual bacterial load present in wounds treated with PHMB, and visualization of necrosis apparent in D21 images in Kendall dressing and MACF with continuous PHMB. (B) Wound area analyses from wound images at different timepoints post-wounding for treatment and control groups, showing a delayed wound healing response in all infected groups and successful wound closure in hydrogel-treated non-infected wounds. Data all mean ± S.D. from 3 to 5 biological samples. Significance by two-way ANOVA with Fisher's post-hoc test (p < 0.05). p values are as shown on the graph only for significantly different groups vs. Tegaderm (Non-infected) group at each timepoint.



**Figure S4.** Blood glucose measured on days 0, 7, 14, and 21 of the study by glucometer with blood collected from the tail vein of mice. All blood glucose recordings were above the diabetic level (120 mg/dL) for the entirety of the study. Data 3 < n < 14, mean ± S.D. No significance between groups as determined by one-way ANOVA with Fisher's post-hoc (p < 0.05).



**Figure S5.** Effect of sex differences on wound healing progress over time. Statistical significance was calculated using a non-parametric Mann-Whitney's test from 3 to 5 biological replicates (ns: not significant, p > 0.05).



**Figure S6**. (A) Representative images of the wounds treated with MAC-based hydrogels at the endpoints of the study (D21). (B) Wound area analyses from wound images on day 21 for MAC-based treated wounds Data all mean  $\pm$  S.D. from 3 to 5 biological samples. Significance by one-way ANOVA with Fisher's post-hoc test (p < 0.05). Groups with the same letters are not statistically significant. (C) Wound histology assessment of day 21 wounds that were treated with MAC-based hydrogels showing H&E (left) and Masson's trichrome (right) staining. Scale bars are 500  $\mu$ m and zoomed in images from the dotted portion is 5X larger (D) Analysis of the length of epithelial tongue from histology images of MAC-based treated wounds. Data mean  $\pm$  S.D from 3 to 5 biological samples. Significance by one-way ANOVA with Fisher's post hoc test (p < 0.05). (E) Representative tissue Gram-staining to visualize bacterial load and penetration for MAC-based treated wounds on day 21 in treatment groups at day 21. Black scale bars = 50  $\mu$ m and green scale bars in insets = 1.5  $\mu$ m. Arrows indicate bacterial colonization.



**Figure S7.** Overall bacterial bioburden quantified via direct qPCR from wound tissues harvested on day 21, CFUs calculated from CT values (maximum CT 35 signifying no amplification). Infected treatments with MACF-PHMB up to D14 and D21 reduced general bacterial count well below non-infected Tegaderm only controls. Treatments with no error bars show no amplification of overall bacterial load 16S rRNA gene past designated cycle end (cycle 35), indicating no measurable presence of genomic DNA. Data 5 < n <8, mean  $\pm$  S.D. Statistical significance was calculated using 1-way ANOVA and Fisher's post-hoc comparing groups to Tegaderm (infected) control (p values are shown on the graph).



**Figure S8.** *P. aeruginosa* counts via qPCR from aqueous fractions harvested on day 21, no significant difference between oxygen containing treatments (MACF) and non-oxygenated treatments (MAC) with and without PHMB on bacterial levels, CFUs calculated from CT values (maximum CT 35 signifying no amplification). Data n = 3, mean  $\pm$  S.D. No significant difference between groups as measured by one-way ANOVA with Fisher's post-hoc (p < 0.05).



**Figure S9.** (A) Neutrophil accumulation in the wound bed at day 21 as characterized by Ly6G staining for MAC-based treated wounds. Green areas are positive for Ly6G and blue are DNA staining using DAPI. Scale bars are 50  $\mu$ m. (B) Quantitative analysis of the relative fluorescent area positive for Ly6G for MAC-based treated wounds showing reduced levels of neutrophil accumulation in infected wounds treated with MAC hydrogels with or without PHMB as compared to the infected control (+Bacteria/- PHMB). (C) Macrophage accumulation in the wound bed for MAC-based treated wounds characterized by CD68 staining. Red areas are positive for CD68 and blue shows DAPI DNA staining. Scale bars are 50  $\mu$ m. (D) Quantitative analysis of the relative fluorescent area positive for CD68. Data all mean ± S.D from 3 to 5 biological samples. Significance by one-way ANOVA with Fisher's post-hoc (p < 0.05). In all graphs, groups sharing letters are not significantly different.



**Figure S10.** CD11b staining as a surface integrin marker for macrophages accumulation in the wound bed at day 21 for control (A) and treatment groups (B). Yellow areas are positive for CD11b, and blue are DNA staining using DAPI. Scale bars are 50  $\mu$ m. (C) Quantitative analysis of relative fluorescent areas positive for CD11B staining showing reduced levels of neutrophil accumulation in infected wounds treated with different hydrogels as compared to the non-infected control. Data all mean  $\pm$  S.D from 3 to 5 biological samples. Asterisks denote significance by one-way ANOVA with Fisher's post-hoc (p < 0.05). Groups with no asterisks are not significantly different.



**Figure S11.** Lipidomic profiling of infected diabetic wound healing at day 21. (A) Transform heatmap showing fold change of notable phosphatidylglycerols (PG) and sphingomyelins (SM) for MAC-based treated groups. (B) Log fold change comparison of MAC-based treatments vs. control (i.e., Tegaderm (infected) for infected groups and Tegaderm (Non-infected) for non-infected). Significance by one-way ANOVA with Fisher's post-hoc test (p < 0.05) with 3 < n < 5. Groups with same letters not statistically significant (p > 0.05).



**Figure S12.** (A) Representative images of wound different timepoints when PHMB is stopped at 3 different timepoints (D21, D14, D7). (B) Representative wound H&E staining of wounds showing the effects of stopping PHMB treatment on wound healing outcomes. Scale bars are 500  $\mu$ m. (C) Effect of stopping PHMB treatment at different timepoints on wound areas on D21 for infected and non-infected groups. All data are mean ± S.D (4 < n < 10). Asterisks denote significance by 1-way ANOVA with Fisher's post-hoc test (p < 0.05) (lower values indicate better healing).