



## Supplementary Materials: Liposomes as a Nanoplatform to Improve the Delivery of Antibiotics into *Staphylococcus Aureus* Biofilms

Table S1. Physicochemical properties of tested antibiotics. daddy.

Antibiotics				
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MDPI, Basel, Switzer-				
land. This article is an	Molecular weight (g/mol)	Log P	pKa	Ref.
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tributed under the terms				
and conditions of the				
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censes/by/4.0/).				
LEV	361.7	2.10	6.24	[47,48]
VCM	1485.7	2.03	2.99	[49,50]
RFB	847.0	4.10	6.9	[51,52]

Table S2. Physicochemical properties of LEV-loaded liposomes.

Lipid Composition	I and improve site (up/umpl)	I.E. Ø (μm)		Zeta Potential
(molar ratio)	Loading capacity (µg/µmol)	(%)	(P.I.)	(mV)
DMPC:CHOL:SA	<b>~</b> 2	<3	0.13	+18 ± 1
(7:2:1)	<2		(<0.1)	
DMPC:DMPG	<2	<3	0.10	-17 ± 1
(8:2)	<2		(<0.1)	
DMPC:SA	<2	<3	0.13	+4 + 1
(9.5:0.5)	~2	<b>\</b> 3	(<0.1)	<b>74 ⊥ 1</b>

Initial lipid concentration, [Lip]i – 30  $\mu$ mol/mL; Initial antibiotic concentration [LEV]i – 1 mg/mL; Loading capacity – (AB/Lip)f ( $\mu$ g/ $\mu$ mol); I.E. (%) – Incorporation Efficiency, [(LEV/Lip)f] / [(LEV/Lip)i] x 100; Ø – mean size; P.I. – polydispersity index; DMPC – dimyristoyl phosphatidyl choline; DMPG – dimyristoyl phosphatidyl glycerol; SA – stearylamine; CHOL – cholesterol; Results are expressed as mean  $\pm$  SD.

**Table S3.** Physicochemical properties of rhodamine-labelled liposomes used in influence of lipid. composition in *S. aureus* biofilm interaction assays and in biofilm transwell model experiment.

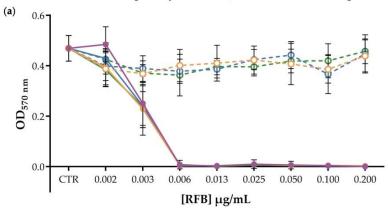
For	mulations	Loading capacity (μg/μmol)	RFB (μg) / (0.5 μmol of lipid)	I.E. (%)	Ø (µm) (P.I.)	Zeta Potential (mV)
LIP1	Unloaded				0.12 (<0.1)	-23 ± 1
	Loaded	$8 \pm 0.2$	4 ± 1	101 ± 8	3 (<0.1)	-24 ± 3
LIP2	!Unloaded				0.11 (<0.1)	-19 ± 1

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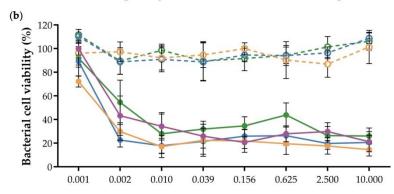
	Loaded	13 ± 1.7	7 ± 1	$75 \pm 1$ $0.12$ $(<0.1)$	-21 ± 2
LIP3	Unloaded			0.13 (<0.1)	+12 ± 1
	Loaded	11 ± 1.3	6 ± 1	$57 \pm 11  \begin{array}{c} 0.13 \\ (<0.1) \end{array}$	+10 ± 1

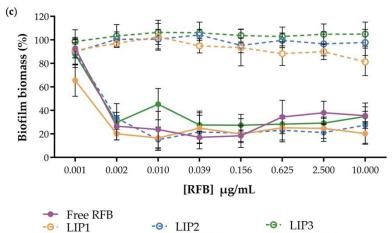
Initial lipid concentration, [Lip]i – 30  $\mu$ mol/mL; Rhodamine concentration: 0.2 mol%; (RFB/Lip)i – LIP1 = 10 nmol RFB/ $\mu$ mol of lipid, LIP2 = 17 nmol RFB/ $\mu$ mol of lipid and LIP3 = 25 nmol RFB/ $\mu$ mol of lipid; Loading capacity – (RFB/Lip)f ( $\mu$ g/ $\mu$ mol of lipid); I.E. (%) – Incorporation Efficiency, [(RFB/Lip)f] / [(RFB/Lip)i] x 100;  $\emptyset$  – mean size; P.I. – polydispersity index.

## Planktonic S. aureus susceptibility to free RFB, loaded and unloaded liposomes



S. aureus biofilm susceptibility to free RFB, loaded and unloaded liposomes





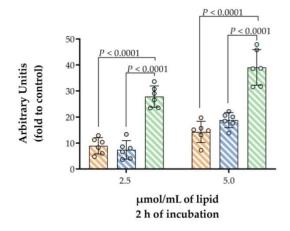
- RFB LIP2

RFB LIP1

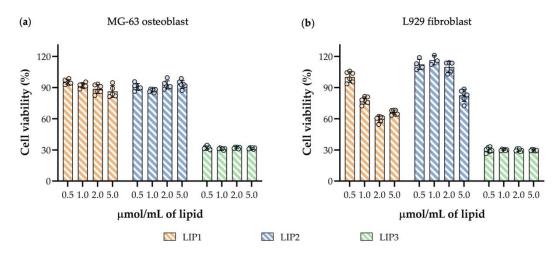
RFB LIP3

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**Figure S1.** Susceptibility of planktonic and biofilm S. aureus to RFB-loaded liposomes. (a) *In vitro* planktonic MSSA susceptibility assessment through broth microdilution method followed by turbidity measurement ( $OD_{570\,nm}$ ), after 24 h of incubation with free RFB and loaded and unloaded formulations ( $0.002-0.200~\mu g/mL$ ). The positive control corresponds to untreated planktonic MSSA in MHB represented by CTR. (b) Determination of viable bacterial cells (MTT assay) and (c) biofilm biomass quantification (CV method) after performing the broth microdilution method with a RFB concentration range of 0.001 to  $10.000~\mu g/mL$ , against mature MSSA biofilm. Results are expressed as mean  $\pm$  SD of at least three independent experiments.



**Figure S2.** Influence of lipid composition on S. aureus biofilm interaction. Mature MSSA biofilm incubated with the LIP1, LIP2 and LIP3 at 2.5 and 5.0  $\mu$ mol/mL of lipid for 2 h. Results are expressed as mean  $\pm$  SD of at least three independent experiments. Statistical comparisons were determined by two-way ANOVA (Tukey's multiple comparisons test) analysis of variance compared between formulation groups.



**Figure S3.** Cell viability of (a) human MG-63 osteoblast cell line and (b) mouse L929 fibroblast cell line, 24 h after incubation with unloaded liposomes, LIP1, LIP2 and LIP3 at lipid concentrations of 0.5, 1.0, 2.0 and 5.0  $\mu$ mol/mL. Cell viability was determined by MTT reduction assay. Results are expressed as mean  $\pm$  SD of at least two independent experiments.