



**Supplemental Figure 1. RNPA2000 bactericidal and human cytotoxicity measures. Panel A.** Graphed are the colony forming units (CFUs) per milliliter of *S. aureus* strain UAMS-1 following 16 hr incubation with the indicated concentration of RNPA2000; starting inoculum and standard deviations (N=8) are shown. **Panel B.** Human HepG2 cell viability as measured by the MTT proliferation assay following 24 hr treatment with DMSO (negative control), mitomycin C (positive control), and the indicated concentration of RNPA2000.



**Supplemental Figure 2.** *S. aureus* **RNase P activity assays.** Shown are RNase P ptRNA<sup>Tyr</sup> activity assay results for reactions performed in the absence (-) or presence of increasing concentrations (0, 31.25, 62.5, 125, 250, 500 µM) of mupirocin (**Panel A**), linezolid (**Panel B**), erythromycin (**Panel C**), and vancomycin (**Panel D**).



Supplemental Figure 3. S. aureus rnpB activity assays. Shown are rnpB ptRNA<sup>Tyr</sup> activity assay results in high salt buffer conditions performed in the absence (-) or presence of increasing concentrations (0, 31.25, 62.5, 125, 250, 500 µM) of RNPA1000 (Panel A) or RNPA2000 (Panel B).



**Supplemental Figure 4. RnpA Western-blotting.** *S. aureus* RnpA levels within cells harboring pML100 (vector; control) or pML100::AS-*rnpA* (*rnpA* mRNA directed antisense molecule; RnpA Depletion) following growth in the absence (-) or presence (+) of 5 ng ml<sup>-1</sup> anhydrotetracycline (ATc).



**Supplemental Figure 5. Cellular RnpA levels do not influence** *S. aureus* susceptibility to RnpAindependent classes of antibiotics. Serially diluted *S. aureus* vector (pML100) or isogenic RnpA Depletion (pML100::AS-*rnpA*; *rnpA* mRNA directed antisense molecule; RnpA Depletion strain) cells plated on TSA agar containing low induction conditions (5 ng ml<sup>-1</sup> ATc; **Panel A**) or medium supplemented with 0.25X MIC vancomycin (0.5 µg ml<sup>-1</sup>; **Panel B**), rifampicin (1.95 ng ml<sup>-1</sup>; **Panel C**), mupirocin (0.125 µg ml<sup>-1</sup>; **Panel D**), daptomycin (0.5 µg ml<sup>-1</sup>; **Panel E**), or ciprofloxacin (0.25 µg ml<sup>-1</sup>; **Panel F**).



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## 5'CCCGGCAAACTGAAAATCCCCTCCTTCGGGTTCGGCAGTTCAAATCTGCC3'

5'CCGCGGCGGACTGTAAATCCGCTCCTTCGGGTTCGGCAGTTCAAATCTGCC3'



5'TTCAGTAGCTCAGTTGGTAGAGCAATGGATTGAAGCTCCATGTGTCGGCAGTTC GACTCTGTCCTGAACCATTTCTTAGCCGGCCTAGCTCAATTGGTAGAGCAACTGAC TTGTAATCAGTAGGTTGGGGGGTTCAAGTCCTCTGGCCGGCACCATTTATGGAGGG GTAGCGAAGTGGCTAAGCGCGGCGGACTGTAAATCCGCTCCTTCGGGTTCGGCA GTTCAAATCTGCCC3'



**Supplemental Figure 6. 5' Rapid Amplification of cDNA Ends (RACE) sequencing results. Panel A.** RNA isolated from mock treated *S. aureus* cells generated a single 5'RACE product representing a 5' truncated tRNA<sup>Tyr</sup> species by sequencing. **Panel B.** Three predominant 5'RACE products were detected following 5'RACE of RNA isolated from *S. aureus* cultures treated with 2x MIC RNPA2000, corresponding to tRNA<sup>Tyr</sup> species, and two polycistronic tRNA<sup>Tyr</sup> species by sequencing (tRNA<sup>Asn,Glu,Val,Tyr</sup> and tRNA<sup>Phe,Thr,Tyr</sup>); secondary structures are approximate and were generated using tRNAscan.