Supplemental Information

for

Human Serum Alters the Metabolism and Antibiotic Susceptibility of

Staphylococcus aureus

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Figure S1. Representative 1D ¹H NMR spectra.

Figure S2. Representative 2D ¹H-¹³C HSQC NMR spectra.



Figure S1. Representative 1D ¹H NMR spectra. A stack plot depicting the extracted metabolome from 616 TSB-DEX cells cultivated in medium supplemented with (blue) and without (green) 55% serum, and the extracted metabolome from 703 TSB-DEX cells cultivated in medium supplemented with (red) and without (black) 55% serum. The boxes highlight spectral differences between the four groups that correspond to lactate and branching amino acids, glycolysis and TCA cycle, and energy metabolites and amino acids.



Figure S2. Representative 2D ¹H-¹³C HSQC NMR spectra. A stack plot depicting the extracted metabolome from 616 TSB-DEX cells cultivated in medium supplemented with (blue) and without (green) 55% serum, and the extracted metabolome from 703 TSB-DEX cells cultivated in medium supplemented with (red) and without (black) 55% serum treatment. The top ten metabolite from Figure 4 are labeled.