

Electronic Supplementary Material

New markers for sepsis caused by *Pseudomonas aeruginosa* during burn infection

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Online Resource 5: Fig. S2 Box-and-whisker plots of the 21 metabolites that did not distinguish *Pa*-sepsis from niSIRS

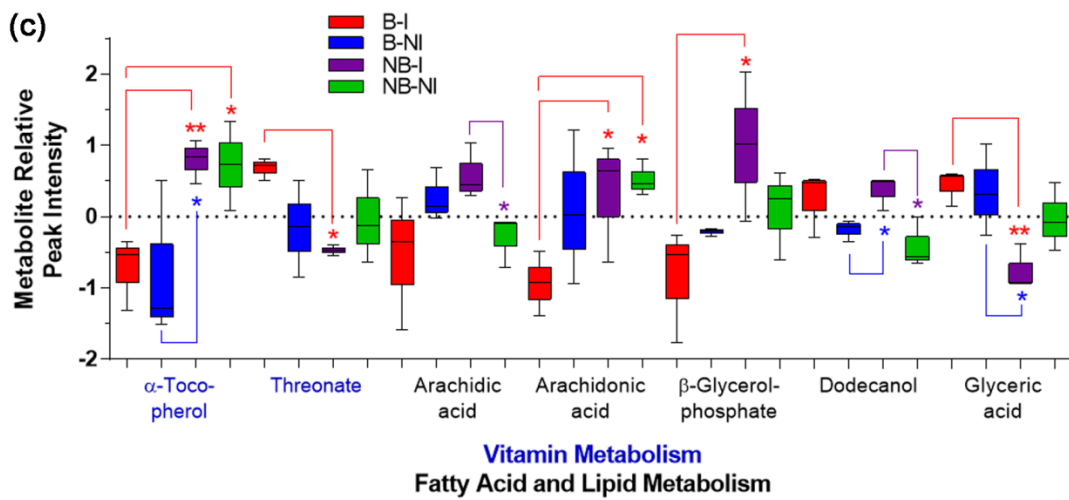
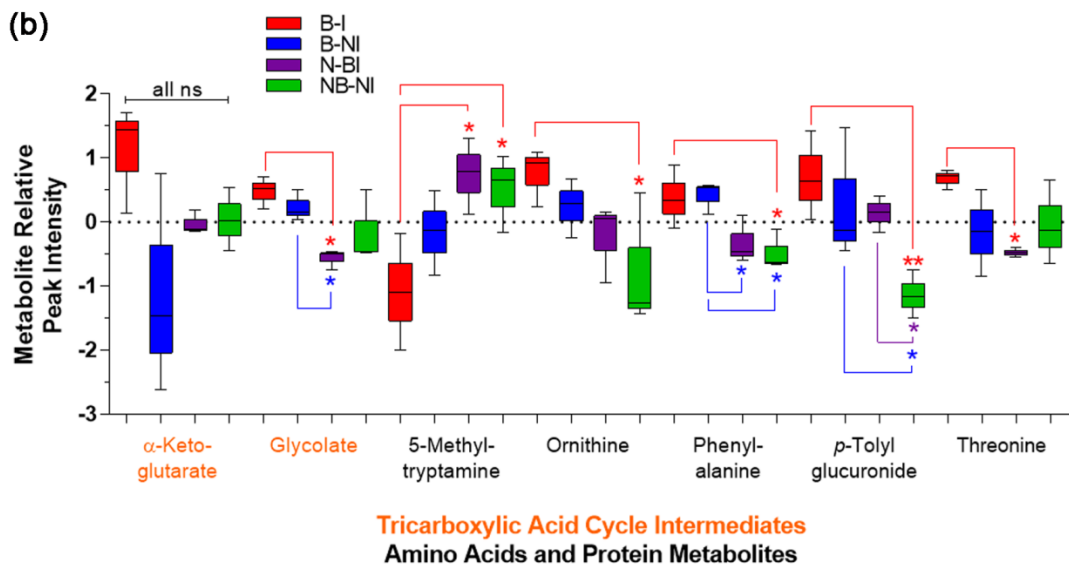
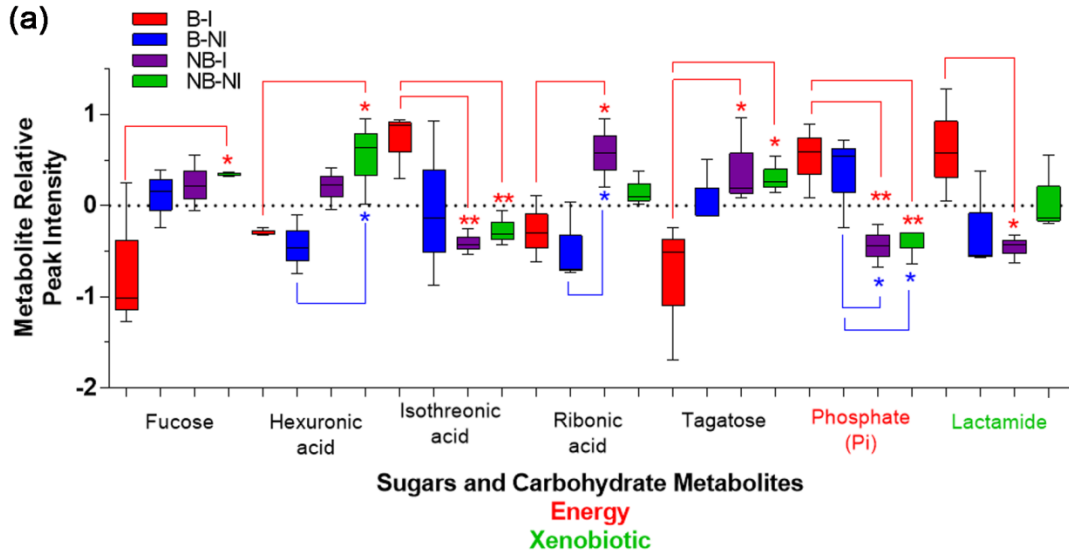


Fig. S2 Box-and-whisker plots of the 21 metabolites that did not distinguish *Pa*-sepsis from niSIRS. Evaluation of those 21 metabolites that did not distinguish B-I (thermally injured/*P. aeruginosa* infected; *Pa*-sepsis) from B-NI (thermally injured/not infected; niSIRS). Peak intensities were normalized using vector and median normalization methods and significance was determined using one-way ANOVA using B-I as the comparator to NB-I (no thermal injury/*P. aeruginosa* infected) and NB-NI (noninjured and noninfected control; healthy), BN-I as the comparator to NB-I and NB-NI, and B-I, BN-I and NB-I without NB-NI. This analysis was followed by Fisher's least significant difference test; ns, no significance; *, $P < 0.05$; **, $P < 0.01$. Each box plot represents 3 biological samples and whiskers represent their distribution. **a** sugars and carbohydrate metabolites, energy metabolite (Pi), and xenobiotic; **b** tricarboxylic acid cycle intermediates and amino acids and protein metabolites; **c** vitamins and metabolites and fatty acid and lipid metabolites. There are different patterns of discrimination among the metabolites – B-I from NB-NI and B-I from NB-I, B-NI from NB-I and B-NI from NB-NI, and even NB-I from NB-NI. Further investigation will be necessary to determine if these metabolites would be useful in discriminating between individuals with niSIRS related to trauma or other causes and those with infections who do not manifest sepsis