

Electronic Supplementary Material

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

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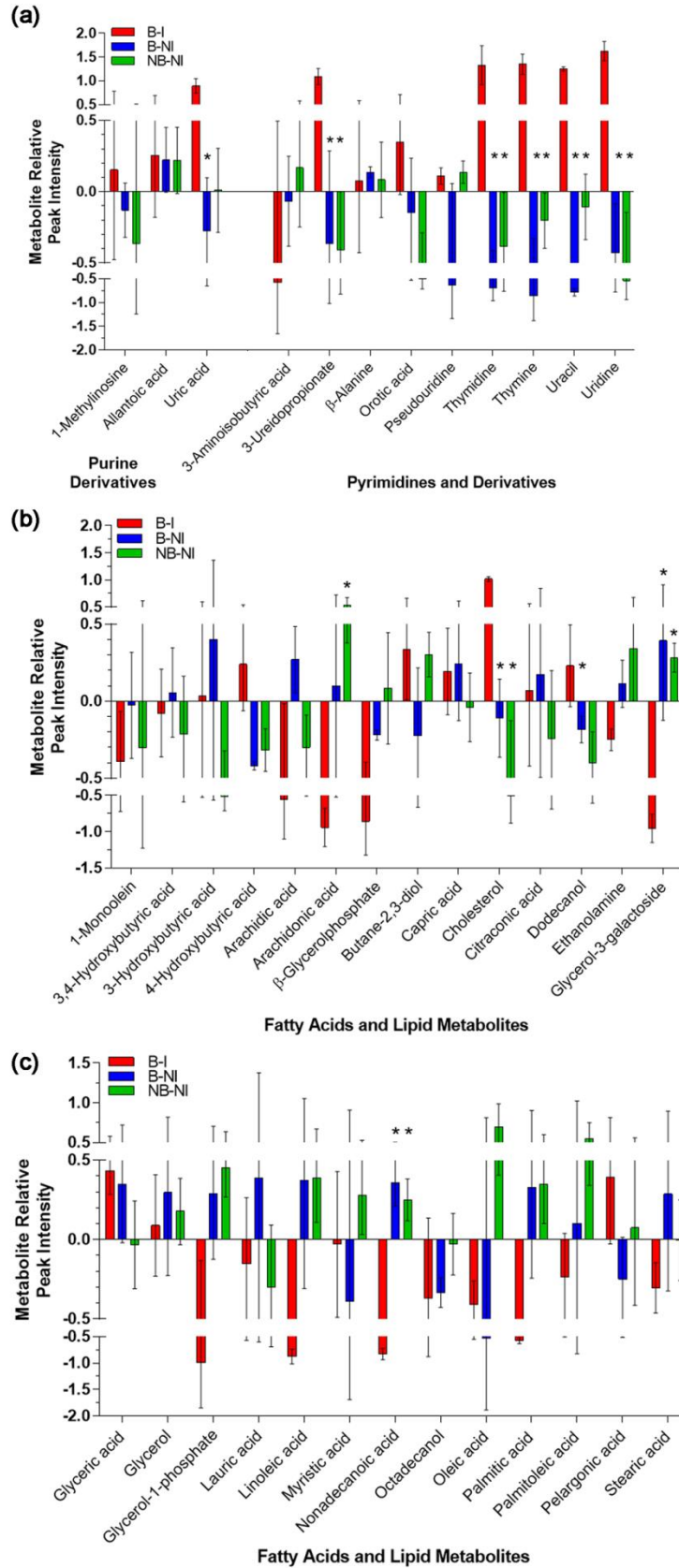
⁴Department of Medical Education, Texas Tech University Health Sciences Center, Lubbock, TX, USA

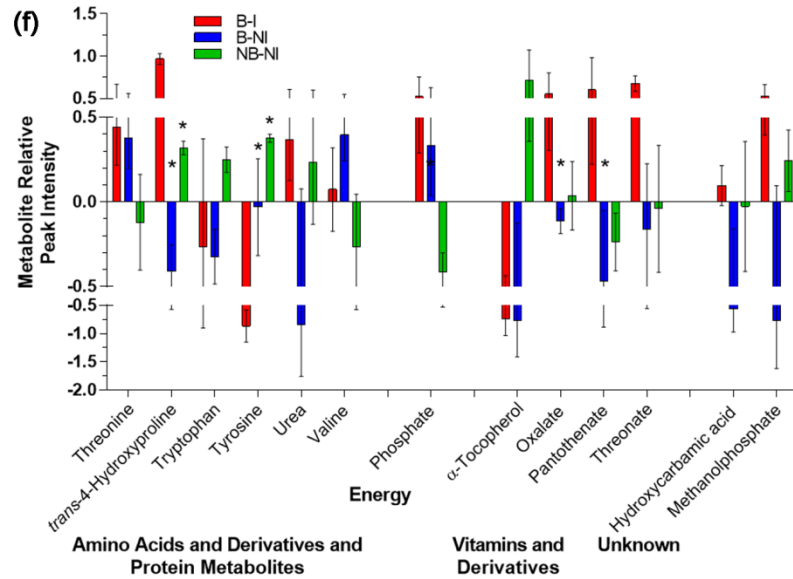
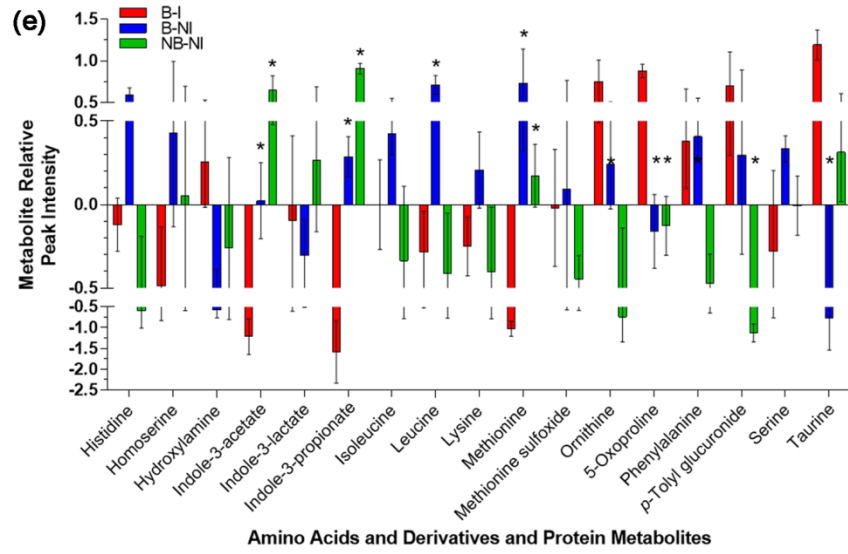
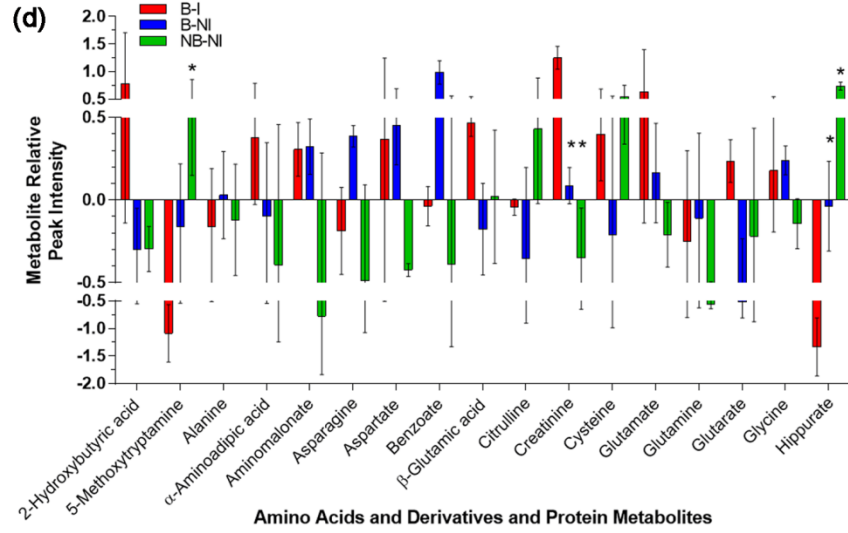
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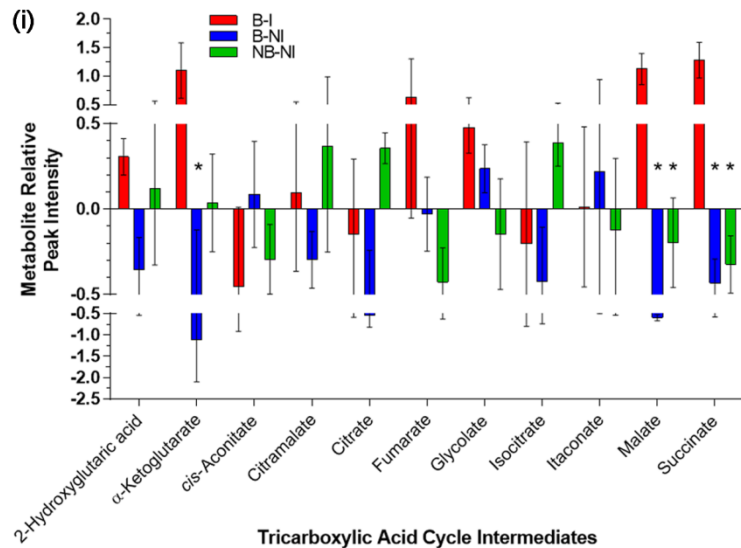
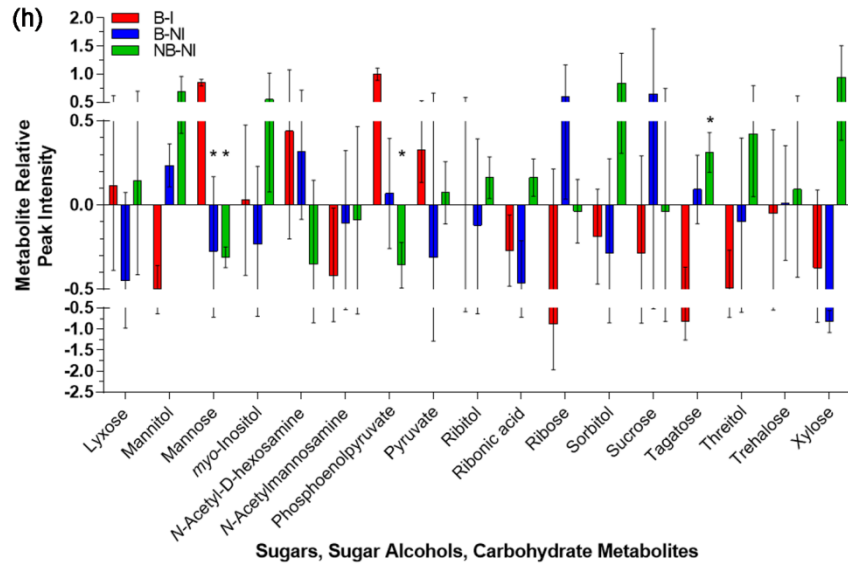
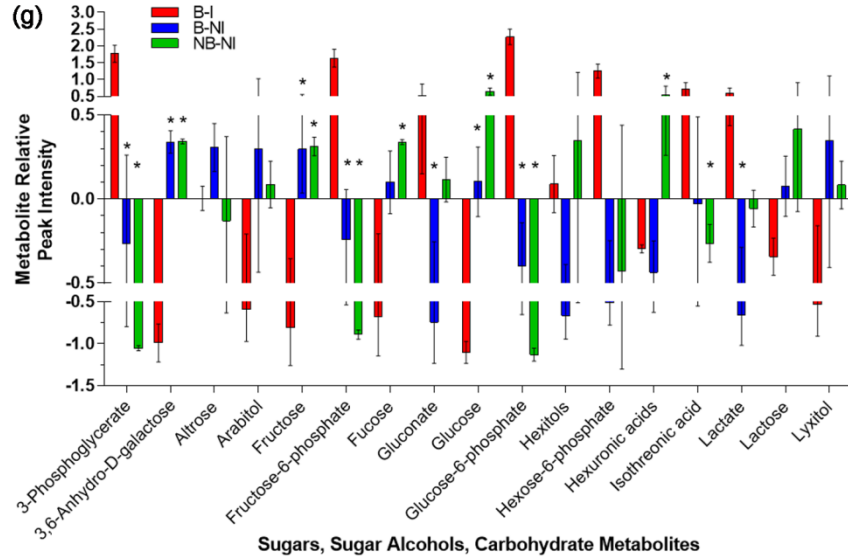
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Online Resource 4: Fig. S1 Relative peak intensities of the 148 identified metabolites







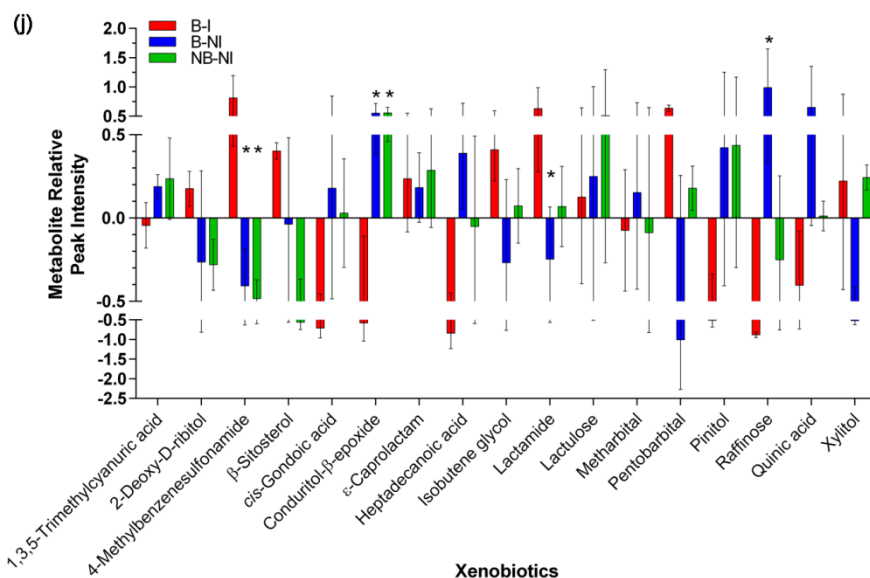


Fig. S1 Relative peak intensities of the 148 identified metabolites. Peak intensities of the identified metabolites were normalized using vector and median normalization methods. Relative peak intensities were log-transformed and scaled using Pareto scaling in the MetaboAnalyst program (<https://www.metaboanalyst.ca>; accessed 18 Aug 2019) (Chong et al., 2018)¹. Values shown for the thermally injured/*P. aeruginosa* infected group (B-I), the thermally injured but not infected group (B-NI), and the sham control group (NB-NI) represent means \pm SEM ($n = 3$ /group). Asterisk (*) represents significance of at least $P < 0.05$ as determined by one-way ANOVA (all pairs) followed by Fisher's least significance difference test. **a** purine and pyrimidine derivatives; **b, c** fatty acids and lipid metabolites; **d, e, f** amino acids and protein metabolites; **f** energy, vitamins and derivatives, unknown function; **g, h** sugars, sugar alcohols, and carbohydrate metabolites; **i** tricarboxylic acid cycle intermediates; **j** xenobiotics

¹Chong, J., Soufan, O., Li, C., Caraus, I., Li, S., Bourque, G., et al. (2018). MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. *Nucleic Acids Res*, 46(W1), W486-W494. doi:10.1093/nar/gky310.