


## Erratum to: Temporal characterization of serum metabolite signatures in lung cancer patients undergoing treatment

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The original version of this article unfortunately contains a mistake. The presentation of Fig. 2e and its caption are incorrect. The corrected Fig. 2e and its caption are given below.

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The online version of the original article can be found under  
doi:[10.1007/s11306-016-0961-5](https://doi.org/10.1007/s11306-016-0961-5).

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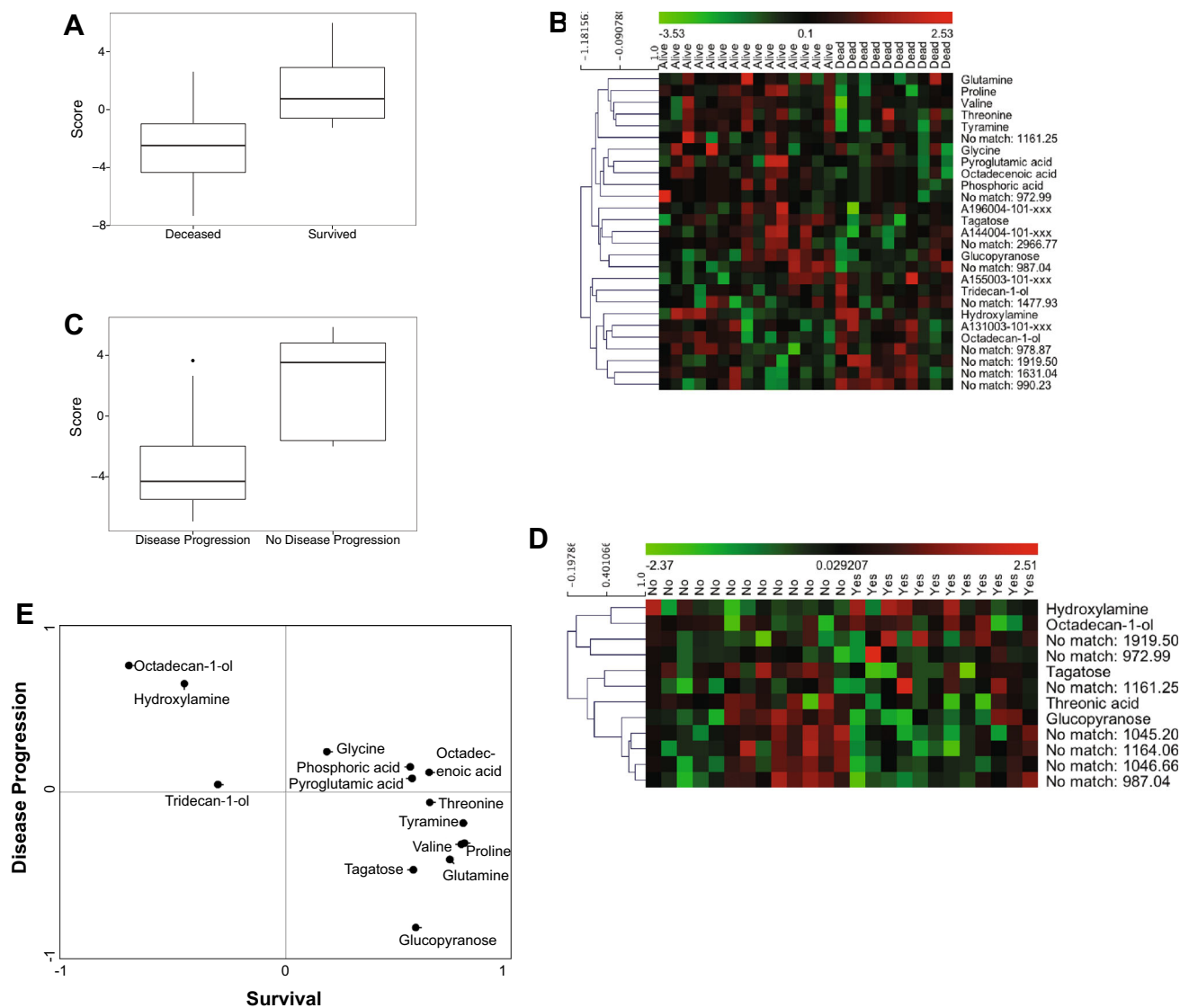
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**Fig. 2** GC-MS metabolite bioprofiling facilitates prognostic evaluation of clinical outcomes based on survival and disease progression. **a** Box and whisker plot based on scores from OPLS-DA model of patient survival at pretreatment as a function of the eventual survival status; **b** Heat map showing clustering of metabolites with respect to patient survival (**c**, **d**) Progression: **c** as in **a**, with samples stratified by

evidence of progression; **d** Heatmap showing progression-related metabolites; **e** Shared and unique structure (SUS) Plot, highlighting the strong relation between the two variables of disease progression and survival. The metabolites that line up along the diagonal running from the upper left corner to the lower right corner are common to both the disease progression and survival models