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ESPS PEER-REVIEW REPORT

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ESPS manuscript NO: 20058

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Reviewer's country: Italy

Science editor: Jing Yu

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CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
<input type="checkbox"/> Grade A: Excellent	<input checked="" type="checkbox"/> Grade A: Priority publishing	Google Search:	<input type="checkbox"/> Accept
<input checked="" type="checkbox"/> Grade B: Very good	<input type="checkbox"/> Grade B: Minor language polishing	<input type="checkbox"/> The same title	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C: Good	<input type="checkbox"/> Grade C: A great deal of language polishing	<input type="checkbox"/> Duplicate publication	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D: Fair	<input type="checkbox"/> Grade D: Rejected	<input checked="" type="checkbox"/> No	<input checked="" type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E: Poor		BPG Search:	<input type="checkbox"/> Major revision
		<input type="checkbox"/> The same title	
		<input type="checkbox"/> Duplicate publication	
		<input type="checkbox"/> Plagiarism	
		<input checked="" type="checkbox"/> No	

COMMENTS TO AUTHORS

This is an interesting review, which helped me to clarify a few concepts I had never clearly understood. The three examples they provide to support the use of metabolomics in systems medicine are relevant, and among the most commonly used to support this approach. I have very few suggestions to improve readability: 1) in the introduction, the authors discuss the several potential techniques providing the metabolomics analysis. It would be important to have a comparative table summarizing the advantages and disadvantages of the different techniques at a glance. 2) The authors do not discuss the results in terms of superiority compared with standard analysis. Hopefully, the metabolomics approach might improve diagnosis and prognostic accuracy, but at a cost in terms of analytical burden and time which is not irrelevant. They provide several examples: how does metabolomics compare with the standard analytical approach in these examples? How much is the cost of a single analysis? How long does it take from bed to bedside and back?