On behalf of our authoring group I would like to thank the reviewer for his comments.

Comment 1: Title: Authors should explain why tool is "efficient"

Reply:. The big advantages of the tool, are that i) it is an all in one tool for the analysis of non-coding RNAs, ii) it includes some methods and algorithms for some of the analysis steps (miRNA prediction, miRNA target site prediction and so on) that present better accuracy metrics compared to the state of the art methods and iii) it can handle big work load and batch large scale analysis for many non-coding RNA sequences exploiting the cloud computing technology benefits. All these issues are explained in the manuscript. We agree with the reviewer though that "efficiency" might not be the right term to describe these properties and for this reason we changes the title from: "InSyBio ncRNASeq: An efficient tool for analyzing non-coding RNAs" to: "InSyBio ncRNASeq: A web tool for analyzing non-coding RNAs".

Comment 2: Abstract:"....highest accuracy metrics ..." ? I am a bit confused, does this refer to the features used in obtaining analysis scores, or does this mean it is more accurate than other tools. Since no false positive, true positive, etc. data was provided, stating that the tool is "accurate" is not correct, if this was the intention.

Reply: The term "highest accuracy metrics" refers to the results presented in table 1 of the manuscript. For the problem of locating miRNA targets the terms "Predicted Interactions present in miRTarBase / miRTarBase interactions" and "Predicted Interactions present in miRTarBase / Total predicted interactions", which are shown in column six and seven respectively, represent the equivalent true positives and false positive indicators. Furthermore, the term "highest accuracy metrics" refers to the method for miRNA target site prediction which has been compared with other state of the art methods referred in the manuscript (reference: 4).

To provide clarity in the manuscript we corrected the titles of the columns in Table 1.

Comment 3: "FASTA" format is written in all uppercase letters.

Reply: FASTA has been corrected to all of its appearances in the manuscript.

Kind Regards,

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