Comments to the Authors,  
  
  
In present study, Dr.Menif and colleagues reported Regulatory network analysis of microRNAs and genes in Imatinib-resistant chronic myeloid leukemia. The discovery is quite interesting and would be a model to connect miRNA, host-genes, target genes, TFs in specific disease. This research assembled comprehensive knowledge including epidemilogical, bioinformatics and clinical cancer research together and then provided very interesting finding and would be helpful on the understanding to Imatinib-resistant of chronic myeloid leukemia. However, several small problems should be considered to make the manuscript acceptable. In general, I would recommend acceptance if the authors can address my concerns as the following,  
  
Major:  
  
1, the Method section were too brief, including Data Collection and standardization and Three networks construction section. Since actually the paper was including huge information and the protocol of the manuscript should be with lot of special strategy. However, from current version, all these decision-making process were absent. Such as Line 4-5 in page 4, the authors said the data were downloaded from Ensembl database, However, Ensembl database is really huge database including all the biological information. In the present study, such kind of brief description would be useless. It would be helpful for the author to think how to make the study more repeatable.   
  
2, The author didn't consider the role of SNP and DNA methylation, Is there any special reasons? If these two biological element were included in this paper, it would make the network more plenary. At least, it should be discussed in the last section, if it is hard to finish it.   
  
3, I recommend one of the paper could be cited in the background section to show the miRNA important in cancer research. Shenglong Lin, Pan Lili, Guo Shicheng, Wu Junjie, Jin Li, Wang Jiu-Cun, Wang Shaoyuan: Prognostic role of microRNA-181a/b in hematological malignancies: a meta-analysis. PLoS One 2013, 8:e59532.  
  
4, Actually, this work enrolled huge database and some database might be the choice and we might have some other choice, and this would be the section which can be updated, such as TFs can be used the data from ENCODE project. It would be great for the authors to make some discuss on which database can be replaced in the future at last section.

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