Reviewer's report

Title: Expression profile and specific network features of the Apoptotic Machinery explain relapse of Acute Myeloid Leukemia after chemotherapy

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Reviewer: Ruoping TANG

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To the authors:
The paper by Ragusa et al. has studied 84 AM gene expression in AML patient cells with high CD34 mobility after CR. 37 AML patients were selected and analyzed chemo-sensitivity in vitro; three patients were selected from both chemoresistance and highly chemosensitive groups for further molecular analysis. The studies are interesting, but results were poorly interpreted.

Major compulsory revisions:
1. English revision is required throughout the paper. If possible using a professional service to revise and copyedit the paper for proper use of the English language.
2. The results shown in the table 1 are −##CT values, not 2−##CT values. If it is 2−##CT value, it should not be negative. When −##CT=0, 2−##CT = 1; When −##CT<0, 2−##CT <1; When −##CT>0, 2−##CT >1. It is better put 2−##CT values, means the RQ values for reader.
3. High network centrality is poorly defined in the introduction. What means the significance of betweenness, closeness, radiality, stress? In the abstract, authors showed that the up regulated genes are characterized by high network centrality, however, in the results, authors showed that differentially expressed genes, in other words, the up regulated or down regulated genes.
4. In the results: AM Expression Profile in AML Patients: 24 AM genes from the Bcl2, Birc, Bnip…… had a similar expression profile in both classes. It is difficult to understand that in the table1, because Birc2 and Birc3 expression was very different in two classes. For some genes, when you consider as up or down regulation, it is not very different from similar expression. It is should be better give some definition in the table for similar, up or down expression. For example, when −##CT>1.5, you consider that it is up regulation…..
5. In the conclusion, is it possible that authors precise the genes which have a important AM profiling before chemotherapy and transplantation?
6. When we read the abstract, we can not understand why they studied AM profiling rather than the differential gene expression in CD34+ with high or low mobilization.

Minor essential revisions:
1. It is better to display important up or down regulated genes by one table and classed them depend on their function.

**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Not suitable for publication unless extensively edited

**Statistical review:** No, the manuscript does not need to be seen by a statistician.

**Declaration of competing interests:**

I declare that I have no competing interests.