Reviewer's report

Title: Subtypes of primary colorectal tumors correlate with response to targeted treatment in colorectal cell lines

Version: 1 **Date:** 9 November 2012

Reviewer: Scott Kopetz

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Schlicker et al utilized new and existing datasets and innovative bioinformatic techniques to determine molecular subsets of colorectal cancer with functional and potential clinical implication. They have identified 5 subtypes defined at the highest level by epithelial and mesechymal features, and driven by further iterative clustering techniques. These subsets are subsequently defined by enriched pathways/ontology and sensitivity to disparate molecularly targeted agents. Molecularly homogeneous subsets of colorectal cancer will be critical to spur further research in biomarkers and molecular therapeutics. This work should be considered the most robust approach to clustering published to date and will add to the development in this area.

With this revision, this reviewer appreciates the access to AZTS gene expression dataset, inclusion of the EC50 data as a supplement, and acknowledges the lack of reviewer access to AZCL gene expression and the lack of plans to include this data with the current publication (but instead with a future publication). While I understand the stated desire to publish further studies based on the AZCL dataset, the standard is to provide such gene expression datasets with the original publication and exceptions to this should be made judiciously.

Minor Essential Revision: The addition of Table S16 is appreciated but is incomplete as it only includes the Src inhibitors.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

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