Author's response to reviews

Title: EMT is the Dominant Program in Human Colon Cancer

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Editor:

Enclosed please find the manuscript entitled: “EMT is the dominant “intrinsic” program in human colon cancer that predicts recurrence” by Laboda et al. for submission to BMC Medical Genomics. The manuscript describes an unsupervised analysis of microarray data from 326 colon cancer to identify the first principle component of (PC1) of the most variable sets of genes. We report that the most dominant pattern of intrinsic gene expression in colon cancer was tightly correlated with the EMT program of gene expression in both gene identity and directionality. In a global micro-RNA screen we further identified, the most anti-correlated microRNA with PC1 as MiR200, known to regulate EMT. Moreover, the intrinsic PC1 subtypes predicted recurrence of the disease in multiple independent data sets.

The outcome demonstrates that the biology underpinning the native, molecular classification of human colon cancer--previously thought to be highly heterogeneous was clarified through the lens of comprehensive transcriptome analysis.
As indicated in your routine in-house assessment we have addressed the following issues:

• Data availability and deposition- Both mRNA array data for 326 colon samples and the miRNA data for the colon FFPE samples have been deposited in Gene Expression Omnibus (GEO) database.

• Ethics and Consent- All patient samples and clinical information for the 326 colon samples were obtained through a protocol approved by The University of South Florida Institutional Review Board. (please see page 3 of the manuscript).

• References: We added a reference which outlines the use of lung cell line data (Please see page 5).

• Authors and Contributions- In response to the suggestions made on this section we added an author to the main manuscript. Additionally, we added a section titled authors contributions. (please see page 13).

• Funding Information- In response to the suggestions made, we added an area outlining the funding source for the work outlined in the manuscript (please see page 14).

Please feel free to contact me should you require additional information regarding this manuscript.

We thank you in advance for your consideration.

Sincerely,

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