Author's response to reviews

Title: Extracellular Matrix Signatures of Human Primary Metastatic Colon Cancers and their Metastases to Liver.

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Author's response to reviews: see over
June 23rd, 2014

Dear editor,

Thank you for considering the revised version of our manuscript and finding suitable for publication pending minor editorial changes. We have uploaded the revised version of the manuscript that includes all the editorial changes requested. We have summarized the changes in our point-by-point response (see below).

Of note, the raw mass spectrometry data are now publicly available at MassIVE: ftp://MSV000078555@massive.ucsd.edu.

Thank you again for considering our manuscript. We hope you will find the editorial changes satisfactory and our article suitable for publication in BMC Cancer.

With best regards,

Alexandra Naba and Richard Hynes
RESPONSE TO THE EDITORS COMMENTS:

1). Please include email addresses for all authors on your title page.

We have now included the email addresses for all authors on the title page.

2). Please improve the grammatical quality of this sentence, "We obtained for three patients panels of three tissue samples: normal colon, colon tumor and metastases to liver.

We have now changed this sentence: “For each of the three patients included in this study, we obtained a set of three samples: normal colon, colon tumor and its metastasis to liver.” (see page 4)

3). Please state in the Methods section whether written informed consent for participation in the study was obtained from participants or, where participants are children, a parent or guardian.

Informed consent was obtained from all of the patients and none of the specimens came from minors. The anonymized specimens were obtained from the MGH tissue bank and were removed for medical reasons unrelated to this project. The specimens were analyzed in accordance with a protocol approved by the Massachusetts General Hospital’s Institutional Review Board. We have now stated this in the Methods section of the manuscript (see page 4).

4). Currently the link you have provided to your mass spec data is password protected, please provide a link that is openly available to the public. Please include the accessions to the data available in MassIVE in your manuscript.

We have now lifted the password protection on the data deposited in MassIVE and have included in the manuscript the accession ID of the data (see pages 5 and 18).

5). We encourage authors whose supporting data are available in an open access repository to include an “Availability of supporting data” section in their manuscript, before the Competing interests and Authors’ contributions. The section should state the name of the repository in which your data is deposited and include a link to the dataset DOI. If all the supporting data are included as additional files the section should state this. If your manuscript has any supporting sequence data, microarray data, or proteomic data this must be deposited in the appropriate repository and a link to the dataset should be included in the Availability of supporting data section.

We have now included an “Availability of supporting data” section and provided the data set’s accession ID in addition to the link to the raw proteomics data (see page 12).

6). Nucleic acid sequences, protein sequences, and atomic coordinates should be deposited in an appropriate database in time for the accession number to be included in the published article. In computational studies where the sequence information is unacceptable for inclusion in databases because of lack of experimental validation, the sequences must be published as an additional file with the article. Where appropriate, authors should adhere to the standards proposed by the Microarray Gene Expression Data Society (http://www.mged.org) and must...
deposit microarray data in MIAME-compliant format in one of the public repositories, such as ArrayExpress (http://www.ebi.ac.uk/arrayexpress), Gene Expression Omnibus (GEO; http://www.ncbi.nlm.nih.gov/projects/geo) or the Center for Information Biology Gene Expression Database (CIBEX; http://cibex.nig.ac.jp).

This does not apply to the data generated for this study. As noted above (see #4) all the proteomics data will be publicly available.