

Charles Thompson

From: Yan Liu
Sent: Thursday, June 23, 2022 9:44 PM
To: Charles Thompson; Zheng Xia
Cc: Yang Yang
Subject: Re: 10x scRNA-seq case study copywriting outsourcing request.

Categories: Office Email

Hi Charles,

Sorry for the late reply because it takes me times to read the paper and compare the draft. Below please find my thoughts.

1. Please draft the Introduction according to the paper writers' original consecution and logical sequence. For example, the therefore part below in red box is the result of the '*current primarily targets single specific cells and/or molecules, lacking of targeting multiple key elements simultaneously*'

170 1 year, indicating GBC is extremely poor prognosis[4-7]. Given GBCs are sophis
171 ecosystems characterized with spatiotemporal interactions between heterogeneous cell
172 such as malignant cells and stromal cells in the tumor microenvironment (TMI
173 heterogeneity has evidently dampened therapeutic efficacy of anti-tumor management
174 current primarily targets single specific cells and/or molecules, lacking of targeting m
175 key elements simultaneously[8-15]. Therefore, it is worthwhile to globally understa
176 cellular heterogeneity and their intimate interactions underpinning tumor malignancy in

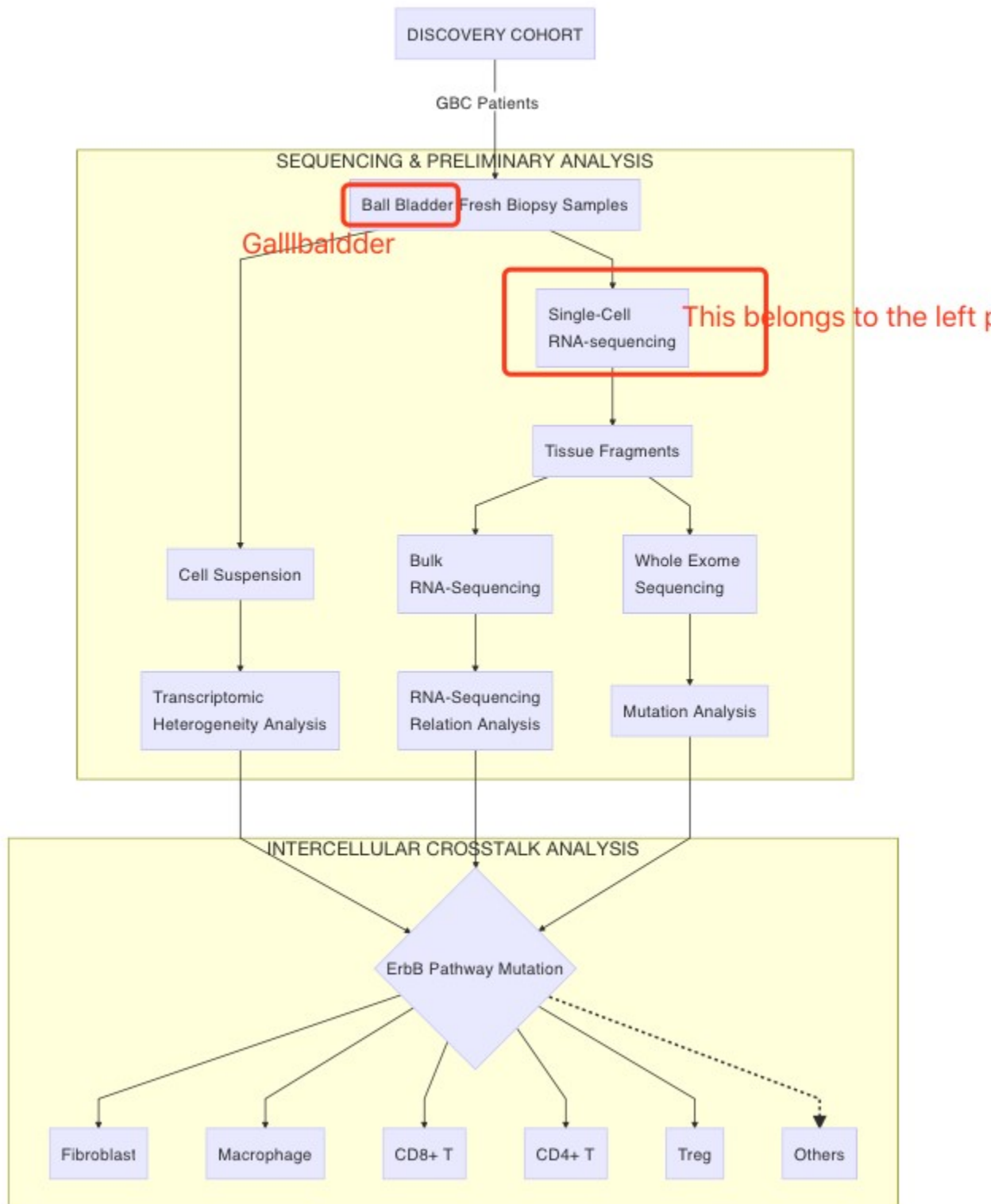
but seems not so suitable if put after the limitation of ⁸ *these studies*.

1.1.1 Introduction

- ErbB signaling is the most extensively mutated pathway that mediates anti-tumor immunity
- Elevated ErbB-mutation levels are correlated with a worse outcome in patients with GBC.
- However, these studies generally relied on data from bulk tumor profiling, limiting their ability accurately decipher tumor heterogeneity and genomic variations between individual cells.
- Therefore, it is worthwhile to globally understand cellular heterogeneity and the intimate interplay underpinning tumor malignancy in order to develop new therapeutic approaches to improve treatment.

Primary reference, (Zhang et al. 2021)

2. Please note that in research strategy part, scRNA-seq part belongs to the left part if you want to add this summary.



3. There are too many results, please list three main results according to the summary contents in the Results part.

4. Please delete the 1.2.2 Graphical Results part which we do not show to client considering the copyright issues.

5. The reference format: please use APA style, exported from googlescholar.

<https://scholar.google.com>

Google Scholar

Google Scholar provides a simple way to broadly search for scholarly literature. Search across a wide variety of disciplines and sources: articles, theses, books, abstracts and court opinions.

scholar.google.com

Lastly, a word file should be fine for me, and we will make the marketing design based on that before releasing.

Any questions, please let me know.

Best ,

Yan (Sophie) LIU Product Specialist

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From: Charles Thompson <charles.thompson@novogeneusa.com>

Sent: Friday, June 24, 2022 0:44

To: Zheng Xia <Zheng.Xia@novogeneusa.com>

Cc: Yang Yang <yang.yang@novogeneusa.com>; Yan Liu <yan.liu@novogeneusa.com>

Subject: RE: 10x scRNA-seq case study copywriting outsourcing request.

Hi Yan,

Any thoughts or feedback?

Best,

Charles Thompson (he/him) – EukmRNA Product Specialist

Phone: (916)-252-0068 ext. 361

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