Author's response to reviews

Title: Patterns of chromosomal copy-number alterations in intrahepatic cholangiocarcinoma

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Author's response to reviews: see over
Dear Editor,

We thank the two reviewers for their positive comments regarding our manuscript entitled “Patterns of chromosomal copy-number alterations in intrahepatic cholangiocarcinoma”. In the revised version, we took into account all the minor essential revisions and modified our manuscript, accordingly.

Best Regards,

On behalf of the authors,

Philippe Broêt

Answers to the reviewers:

Minor Essential Revisions

1. The sentence in the abstract "These latter areas are those showing the highest level for copy loss (resp. copy gain) together with the lowest level for copy gain (resp. copy loss)." is not clear!

We agree with the reviewer that our sentence lacked of clarity. Exclusive recurrent genomic areas are those showing the highest estimated propensity level for copy loss (resp. copy gain) together with the lowest level for copy gain (resp. copy loss). The sentence has been modified in the abstract in order to increase clarity for the readers.

2. The sentence in abstract "None of the CNAs nor the tumor groups were associated with the outcome" is inconsistent with the results shown in the main text/results.

We thank the reviewer for pointing out this sentence. We modified the sentence in order to better summarize our main results: “We found no relationship between the number of altered cytobands or tumor groups and time to recurrence.”

3. Can the subgroups identified by CNA profiling qualify to be subtypes of ICC?

The CNA-derived tumor subgroups have no prognostic impact but may be potentially useful for therapeutic prediction purpose. Thus, these CNA-derived subgroups can be candidate for new subtypes of ICC based on therapeutic taxonomies.

4. Fig 4, labels on x-axis are difficult to read.

We modified the Figure 4.