

Reviewer #1: comments: 1. In the Introduction section 3rd paragraph: The authors stated that 'lncRNAs are more than 200 nucleotides long...as "transcriptional noise"..... In fact, although the non coding RNAs do not encode proteins but they may regulate intracellular biological processes at post-transcriptional levels rather than being only 'noise'. **Correction made.**

2. Are there any information regarding the role of HOTAIR in post-transcriptional levels in any types of cancers? **Answered in text. Please refer to Introduction p. 6**

Reviewer #2: I reviewed with interest the manuscript ID-03251786 submitted to World Journal of Gastrointestinal Oncology by Lampropoulou and colleagues. In this manuscript the authors evaluated the association between genetic polymorphisms in HOTAIR long non coding RNA (lncRNA) and cholangiocarcinoma (CCA). The study is highly relevant given that CCA is a deadly cancer with limited therapeutic option due to a late diagnosis. Early phases of CCA carcinogenesis are usually asymptomatic and biomarkers for CCA diagnosis lack specificity and sensitivity. Thus the identification of cancer susceptibility markers is clinically relevant in CCA. The authors genotyped 3 HOTAIR SNPs (rs920778, rs4759314 and rs7958904) in 122 CCA patients and 165 healthy controls. The study provides the first evidence of the potential association between carriers of HOTAIR rs4759314 AG and GG genotypes and CCA risk. Overall the study sounds and is clearly presented. The message is clear and supported by the data.

Minor comments p.3 "... significantly increased risk of CCA risk" (risk x2) **Correction made.**

p.4 and p.7 "cholangiocarcinoma" vs "cholangiocarcinoma" **Correction made.**

p.6 I would not mention HOTAIR as "a relatively new lncRNA"; this lncRNA has been well characterized for a long time. **Correction made.**

p.7 "The rs7958904 polymorphism genotyping was determined using for allele specific PCR" should be rephrased. **Correction made.**

It would be interesting to determine whether rs4759314 AG and GG genotypes were associated with an increased expression of HOTAIR. **We agree unfortunately we did not have available RNAs for all the cases.**