Reviewer's report

Title: Combined effect of regulatory polymorphisms on transcription of UGT1A1 as a cause of Gilbert syndrome

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Reviewer: Rene HM te Morsche

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In the report by Katsuyuki Matsui and coworkers the promoter region of a number of Japanese and Caucasian patients were sequenced. Using the most common haplotypes they constructed luciferase containing plasmids to reveal how much each haplotype contributes to the transcription of UGT1A1. This report gives interesting information about what regions of the promoter are important and how they influence the transcription of UGT1A1.

The answers given by the authors on the previous report are satisfactory.

Discretionary revisions

Discussion:

"Our results also match......Gilbert syndrome (found in 3-10% of the population)"

The authors use allele frequencies in this sentence which makes the difference between this frequency and the Gilbert syndrome frequency appear bigger than it really is. It would be more appropriate to use the genotype frequency of the homozygous A(TA)7TAA so these numbers can be seen a a better perspective. Also lifestyle plays an important role whether patients phenotypically present with Gilbert syndrome and thus patients having homozygous A(TA)7TAA do always present the syndrome.

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests.