

**ESPS Peer-review Report****Name of Journal:** World Journal of Gastroenterology**ESPS Manuscript NO:** 8936**Title:** Association of MYO9B gene polymorphisms with IBD in Chinese Han population**Reviewer code:** 00505564**Science editor:** Gou, Su-Xin**Date sent for review:** 2014-01-23 13:26**Date reviewed:** 2014-01-28 23:48

CLASSIFICATION	LANGUAGE EVALUATION	RECOMMENDATION	CONCLUSION
<input type="checkbox"/> Grade A (Excellent)	<input type="checkbox"/> Grade A: Priority Publishing	Google Search:	<input type="checkbox"/> Accept
<input type="checkbox"/> Grade B (Very good)	<input type="checkbox"/> Grade B: minor language polishing	<input type="checkbox"/> Existed	<input type="checkbox"/> High priority for publication
<input type="checkbox"/> Grade C (Good)	<input type="checkbox"/> Grade C: a great deal of language polishing	<input type="checkbox"/> No records	<input type="checkbox"/> Rejection
<input type="checkbox"/> Grade D (Fair)	<input type="checkbox"/> Grade D: rejected	<input type="checkbox"/> Existed	<input type="checkbox"/> Minor revision
<input type="checkbox"/> Grade E (Poor)		<input type="checkbox"/> No records	<input type="checkbox"/> Major revision

**COMMENTS TO AUTHORS**

ESPS 8936 Review Association of MYO9B gene polymorphisms with IBD in Chinese Han population  
Jing Hu, Qiao Mei, Jian Huang, Nai-Zhong Hu, Xiao-Chang Liu, Jian-Minh Xu The paper possesses a logical presentation of facts with regard to the description of the patient cohort, the performance of experiments and analysis of data. However, this reviewer highly recommends that the paper should be read and corrected by a professional proofreader before being reconsidered for publication. Concerning the contents of the paper. It would be helpful if it contained a definition what constitutes the Han population. Also, the description of the PCR method should include the sequences of primers and probes used, as well as methodological details regarding the quantification of nucleic acids, and testing of inhibition. The method of statistical analysis should be specified under the tables to explain the origin of the p values shown. Speaking of statistical analysis: as far as I know, genetic analyses such as exploring frequencies, often contain multiple comparisons of data, so a correction of the significance levels may be needed.