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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Hematology
ESPS manuscript NO: 27052
Title: Identifying changes in punitive transcriptional factor binding sites from regulatory single nucleotide polymorphisms that are significantly associated with disease or sickness
Reviewer's code: 00340828
Reviewer's country: United States
Science editor: Jin-Xin Kong
Date sent for review: 2016-05-09 19:27
Date reviewed: 2016-05-31 03:56

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
[ ] Grade A: Excellent	[ ] Grade A: Priority publishing	Google Search:	[ ] Accept
[ ] Grade B: Very good	[Y] Grade B: Minor language polishing	[ ] The same title	[ ] High priority for publication
[Y] Grade C: Good	[ ] Grade C: A great deal of language polishing	[ ] Duplicate publication	[ ] Rejection
[ ] Grade D: Fair	[ ] Grade D: Rejected	[ ] Plagiarism	[Y] Minor revision
[ ] Grade E: Poor		[Y] No	[ ] Major revision
		BPG Search:	
		[ ] The same title	
		[ ] Duplicate publication	
		[ ] Plagiarism	
		[Y] No	

COMMENTS TO AUTHORS

Current manuscript applied computational approach to predict functional rSNPs in TFBS, focusing on several genes published earlier. Computational modeling and analysis for functional prediction is one of the approaches recently developed, particularly to address GWAS findings. It may expand the GWAS knowledge to potential functional identification of the SNPs. However, without experimental confirmation, the emphasis could only be limited to theoretical prediction. The author should be more elaborate in that regard, instead of using only one sentence at the end of the Discussion to briefly carry it over. For example, are there publications presented experimental results in support to computational predictions?

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ESPS PEER-REVIEW REPORT

Name of journal: World Journal of Hematology
ESPS manuscript NO: 27052
Title: Identifying changes in punitive transcriptional factor binding sites from regulatory single nucleotide polymorphisms that are significantly associated with disease or sickness
Reviewer's code: 00646254
Reviewer's country: South Korea
Science editor: Jin-Xin Kong
Date sent for review: 2016-05-09 19:27
Date reviewed: 2016-05-31 16:12

CLASSIFICATION	LANGUAGE EVALUATION	SCIENTIFIC MISCONDUCT	CONCLUSION
[ ] Grade A: Excellent	[ ] Grade A: Priority publishing	Google Search:	[ ] Accept
[ ] Grade B: Very good	[Y] Grade B: Minor language polishing	[ ] The same title	[ ] High priority for publication
[Y] Grade C: Good	[ ] Grade C: A great deal of language polishing	[ ] Duplicate publication	[ ] Rejection
[ ] Grade D: Fair	[ ] Grade D: Rejected	[ ] Plagiarism	[Y] Minor revision
[ ] Grade E: Poor		[Y] No	[ ] Major revision
		BPG Search:	
		[ ] The same title	
		[ ] Duplicate publication	
		[ ] Plagiarism	
		[Y] No	

COMMENTS TO AUTHORS

This study is technically well performed and a very interesting result. The interpretation was also sound. There are some points that the authors may consider: Major comments 1) In Abstract, there is no conclusion. Please add the conclusion to end region of Abstract. 2) You should explain the precise meaning of "punitive" word for scientists of other fields in introduction section. 3) You should more explain how you can define unique TFBS. 4) If you are not using ChIP (TF-Chromatin binding site) assay or references, you should use letter, 'potential or putative TFBS' in content of manuscript as well as table. 5) You should explain what is unique TFBS is mean in introduction by using general examples, if this finding is important in your study. 6) Please explain the reason why this study performed with rSNPs within only nine genes. Minor comments In abstract, 1) The genome-wide association studies (GWAS) has ~ ?-> The genome-wide association studies (GWASs) have ~. 2) enhances ->? enhancers ? 3) TFBS?-> transcriptional factor binding site (TFBS) In Introduction, 1) The genome-wide association studies (GWAS) has ~ -> The genome-wide association

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studies (GWASs) have ~. In Discussion, 1) these rSNPs Tables 2 & 3) -> these rSNPs (Tables 2 & 3).