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CONFIDENTIAL: request to review Scientific Reports manuscript SREP-16-04775

1 message

scientificreports@nature.com <scientificreports@nature.com> Thu, Mar 10, 2016 at 7:14 AM
Reply-To: scientificreports@nature.com
To: scguo@ucsd.edu

Dear Dr Guo,

A manuscript has been submitted to Scientific Reports, which we were hoping you would be interested in reviewing. The manuscript comes from Prof Qian et al. and is entitled "Identification of a Functional SNP rs17079281 at 6q22.2 Locus That Is Associated with Lung Cancer Risk"; the abstract is appended below.

Scientific Reports is an online multidisciplinary publication which is committed to providing a rapid and fair review process. We would hope to receive your comments within 7 days if you are able to review the manuscript. However if you would like to assist us, but require a few extra days to review the manuscript, please do not hesitate to contact us.

To respond to our request, please use the following link:
http://mts-srep.nature.com/cgi-bin/main.plex?el=A7CG1Cvr1A2Bzpu4J3A9ftdIkFNoSyNIz9FuXot5m12gZ

From there, simply follow the link to manuscript SREP-16-04775, where you will be able to view general manuscript information followed by options to accept or decline our request.

If you are unable to help on this occasion, we would appreciate any suggestions for alternative reviewers - perhaps someone in your own laboratory might be suitably qualified?

Many thanks in advance for your help; I look forward to hearing from you. Please do not hesitate to contact me by replying to this e-mail if you have any questions.

Best regards,

Jiucun Wang
Editorial Board Member
Scientific Reports

Yu Wang, Ben Liu, Jinyu Kong, Jingxiin Li, Rongna Ma, Ming Gao, Herbert Yu, and Biyun Qian

Abstract
Genome-wide association studies (GWAS) have identified numerous genetic polymorphisms that are associated with cancer risk, but their biological relevance to the disease is not known for many of them. The study performed linkage disequilibrium (LD) analysis on a GWAS-discovered SNP rs9387478 and identified four potentially functional SNPs (rs17079281, rs6911915, rs9320604 and rs4946259) in DCBLD1 with high LD. Associations of these SNPs with lung cancer were examined in 766 Chinese cases and 773 matched controls. The results suggested that lung cancer risk was associated with SNP rs17079281. Genotype C/T and T/T had lower risk compared with genotype C/C (OR=0.78, 95% CI=0.63-0.98). Luciferase assays demonstrated that YY1 had higher binding-affinity to the T alleles of rs17079281 than C alleles, and the binding was associated with reduced transcription of DCBLD1. We further observed a trend showing a decrease in DCBLD1 expression in the C/T and T/T carriers compared to C/C
carriers. DCBLD1 knockdown inhibited lung cancer cell migration and invasion. Our findings suggest that rs17079281 (C>T) may affect the binding affinity of YY1 to DCBLD1 and influence the risk of lung cancer.

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