Corrigendum

Corrigendum to "Genetics Variants and Serum Levels of MHC Class I Chain-related A in Predicting Hepatocellular Carcinoma Development in Chronic Hepatitis C Patients Post Antiviral Treatment" [EBioMedicine 15 (2017) 81–89]

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The authors wish to point out that there is an error of abbreviation in the Abstract (Background paragraph) of this article. The correct Background paragraph of the Abstract should read as follows:

Background

The genome-wide association study has shown that MHC class I chain-related A (MICA) genetic variants were associated with hepatitis C virus (HCV) related hepatocellular carcinoma (HCC). The impact of the genetic variants and its serum levels on post-treatment cohort is elusive.

Also in the Abstract (Results paragraph), "HR/CI: 5·93/1·86–26.38·61, $P = 0·002$" should read "HR/CI: 5·93/1·86–26·38, $P = 0·002$". The correct Results paragraph of the Abstract should read as follow:

Results

Fifty-eight (8·2%) patients developed HCC, with a median follow-up period of 48·2 months (range: 6–129 months). The MICA A allele was associated with a significantly increased risk of HCC development in cirrhotic non-SVR patients but not in patients of non-cirrhotic and/or with SVR. For cirrhotic non-SVR patients, high sMICA levels (HR/CI: 5·93/1·86–26·38, $P = 0·002$) and the MICA rs2596542 A allele (HR/CI: 4·37/1·52–12·07, $P = 0·002$) were independently associated with HCC development. The risk A allele or GG genotype with sMICA >175 ng/mL provided the best accuracy (79%) and a negative predictive value of 100% in predicting HCC.

Finally, in the Results, Section 3.5. Impact of MICA SNP and sMICA on HCC Development in Non-SVR Patients, the last sentence should read as follow:

Cox regression analysis revealed that the factors independently associated with HCC development among cirrhotic patients without an SVR were high sMICA levels (HR/CI: 5·93/1·86–26·38, $P = 0·002$) and the MICA rs2596542 A allele (HR/CI: 4·37/1·52–12·07, $P = 0·002$).