# *UGT2B28* genomic variation is associated with hepatitis B e-antigen seroconversion in response to antiviral therapy

Kung-Hao Liang[1,3#], Chih-Lang Lin[1,2,4#], Chao-Wei Hsu[1,4], Ming-Wei Lai[1,4], Rong-Nan Chien[2], Chau-Ting Yeh[1,3,4*]

#These two authors contributed equally

**Affiliations**

[1] Liver Research Center, Chang Gung Memorial Hospital, Taoyuan, Taiwan

[2] Liver Research Unit, Keelung Chang Gung Memorial Hospital, Keelung, Taiwan

[3] Molecular Medicine Research Center, Chang Gung University, Taoyuan, Taiwan

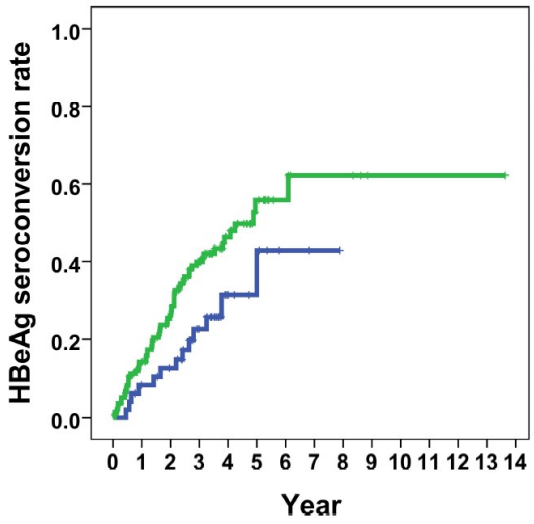
[4] Chang Gung University, College of Medicine, Taiwan

**Supplementary Table S1: Cox regression analysis of the entecavir-treated patient group with respect to time-to-HBeAg seroconversion**

| | Baseline Statistics | Univariate | | |
|---|---|---|---|---|
| | | Hazard Ratio | (95% CI) | P |
| **Subject number** | 257 | | | |
| **Gender-Male (%)** | 173 (67.32%) | 0.660 | (0.397-1.1) | 0.111 |
| **Age (year)** | 41.41±11.83 | 0.980 | (0.957-1.003) | 0.086 |
| **HBV DNA (log copies/ml)** | 8.03±1.27 | 1.124 | (0.905-1.396) | 0.292 |
| **Cirrhosis (%)** | 57 (22.18%) | 0.626 | (0.333-1.176) | 0.145 |
| **platelet (1000/uL)** | 189.1±70.58 | 1.001 | (0.997-1.005) | 0.534 |
| **ALT/AST** | 1.59±0.64 | 1.337 | (0.921-1.939) | 0.127 |
| **ALT (IU/L)** | 212.04±325.44 | 1.000 | (1-1.001) | 0.105 |
| **AST (IU/L)** | 330.67±480.27 | 1.000 | (1-1.001) | 0.250 |
| **SNP rs2132039 TT (%)** | 172 (66.93%) | 1.256 | (0.726-2.174) | 0.415 |

CI, confidence interval

**A**




**B**

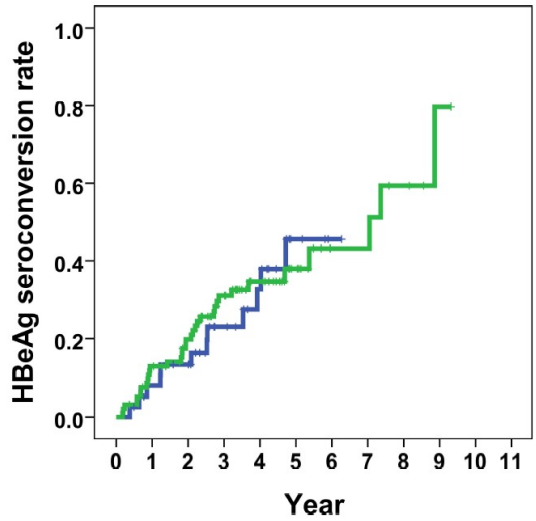



**Figure S1.** The Kaplan-Meier analysis curves for the patients with HBV genotype B (A) and genotype C (B). The HBeAg seroconversion rate between *UGT2B28* genotypes "TT" (green) and "non-TT" (blue) were significantly different in genotype B (log-rank P = 0.037, Hazard ratio = 1.872, Confidence interval = 1.027 – 3.412) but not in genotype C patients (log-rank P = 0.848, Hazard ratio = 1.067, Confidence interval = 0.548 – 2.080).