**Supplementary Table 4. Univariate logistic regression analysis of rs28371597 with CR in the two PegIFNα cohorts.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameters** | **PegIFNα cohort 1** | |  | **PegIFNα cohort 2** | |  | **PegIFNα cohort 1+2** | |
| **OR (95% CI)** | ***p*** |  | **OR (95% CI)** | ***p*** |  | **OR (95% CI)** | ***p*** |
| Trial (PegIFNα cohort 1 vs. 2) | - | - |  | - | - |  | 1.57 (1.08-2.29) | 0.02 |
| Male sex | 0.88 (0.38-2.04) | 0.77 |  | 1.16 (0.76-1.77) | 0.49 |  | 1.05 (0.72-1.53) | 0.79 |
| Age in years | 1.00 (0.95-1.05) | 1.00 |  | 0.95 (0.92-0.98) | 1.00×10-3 |  | 0.96 (0.93-0.99) | 3.10×10-3 |
| HBV genotype (B vs. C) | 1.57 (0.81-3.03) | 0.18 |  | 1.93 (1.31-2.85) | 9.57×10-4 |  | 1.80 (1.29-2.51) | 5.75×10-4 |
| HBV DNA#, log10 IU/mL | 0.83 (0.65-1.06) | 0.14 |  | 0.79 (0.62-1.00) | 0.05 |  | 0.79 (0.66-0.93) | 5.56×10-3 |
| HBsAg#, log10 IU/mL | 0.63 (0.42-0.96) | 0.03 |  | 0.62 (0.43-0.88) | 8.00×10-3 |  | 0.59 (0.46-0.78) | 1.20×10-4 |
| HBeAg#, log10 PEIU/mL | 0.60 (0.44-0.83) | 2.08×10-3 |  | 0.55 (0.39-0.78) | 6.13×10-4 |  | 0.57 (0.46-0.70) | 3.00×10-7 |
| ALT#, loge ×ULN | 1.69 (1.04-2.75) | 0.04 |  | 1.58 (1.02-2.44) | 0.04 |  | 1.58 (1.14-2.20) | 6.39×10-3 |
| rs7574865 genotype | 1.78 (1.10-2.88) | 0.02 |  | 1.31 (0.98-1.74) | 0.07 |  | 1.40 (1.09-1.79) | 7.78×10-3 |
| rs12614 genotype | 5.42 (0.69-42.52) | 0.11 |  | 3.57 (1.09-11.73) | 0.04 |  | 3.95 (1.41-11.06) | 8.90×10-3 |
| **rs28371597 genotype** | 3.37 (1.07-10.56) | 0.04 |  | 2.10 (1.12-3.96) | 0.02 |  | 2.32 (1.34-3.99) | 2.48×10-3 |

CR, combined response; PegIFNα, pegylated interferon alpha; OR, odds ratio; CI, confidence interval; HBV, hepatitis B virus; HBsAg, hepatitis B surface antigen; HBeAg, hepatitis B e antigen; ALT, alanine aminotransferase; ULN, upper limit of normal. #Baseline level.