**Supplementary Materials**

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**Supplementary Table 1. Variables and calculation of the four HCC risk models**

|  |  |
| --- | --- |
| Risk score | Calculation |
| CU-HCC | Age (> 50 years = 3; ≤ 50 = 0) + albumin (≤ 35 g/L = 20; > 35 = 0) + total bilirubin (> 18 µmol/L = 1.5; < 18 µmol/L = 0) + HBV DNA (< 4 log copies/ml = 0; 4-6 = 1; > 6 = 4) + cirrhosis (yes = 15; no = 0) |
| GAG-HCC | 14 \* gender (male = 1; female = 0) + age (in years) + 3 \* HBV DNA (log copies/ml) + 33 \* cirrhosis (presence = 1; absence = 0) |
| REACH-B | Gender (male = 2; female = 0) + age (1 point for every 5 years) + ALT† (15-44 IU/L = 1; ≥ 45 IU/L = 2) + HBeAg status (positive = 2; negative = 0) + HBV DNA (4-5 log copies/ml = 3; 5-6 log copies/ml = 5; ≥ 6 log copies/ml = 4) |
| PAGE-B | Gender (male = 6; female = 0) + age (16-29 years = 0; 30-39 years = 2; 40-49 years = 4; 50-59 years = 6; 60-69 years = 8; 70 years = 10) + platelet (≥ 200,000/mm3= 0; 100,000-199,999/mm3 = 6; ≤ 100,000/mm3 = 9) |

† ALT: alanine aminotransferase.

**Supplementary Table 2. Cumulative incidence of HCC development between the IFN and NAs group in CHB patients at different HCC risks**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| HCC  Risk | HCC development at 3 years | | |  | HCC development at 5 years | | |  | HCC development at 10 years | | |
| NAs | IFN | P value |  | NAs | IFN | P value |  | NAs | IFN | P value |
| CU-HCC |  |  |  |  |  |  |  |  |  |  |  |
| Low | 1 (0.4%)\* | 0 (0.0%) | 0.38 |  | 2 (1.0%) | 1 (0.7%) | 0.72 |  | 3 (2.7%) | 1 (0.7%) | 0.47 |
| High | 14 (4.6%) | 0 (0.0%) | 0.01 |  | 20 (7.5%) | 0 (0.0%) | 0.00 |  | 26 (12.3%) | 1(5.3%) | < 0.001 |
| GAG-HCC |  |  |  |  |  |  |  |  |  |  |  |
| Low | 2 (0.7%) | 0 (0.0%) | 0.16 |  | 4 (1.6%) | 1 (0.4%) | 0.16 |  | 5 (3.3%) | 1 (0.4%) | 0.08 |
| High | 13 (5.3%) | 0 (0.0%) | 0.08 |  | 18 (8.2%) | 0 (0.0%) | 0.03 |  | 24 (13.3%) | 1 (11.11%) | 0.031 |
| REACH-B |  |  |  |  |  |  |  |  |  |  |  |
| Low | 0 (0.0%) | 0 (0.0%) | - |  | 0 (0.0%) | 1 (2.5%) | 0.17 |  | 1 (2.9%) | 1 (2.5%) | 0.75 |
| High | 15 (3.5%) | 0 (0.0%) | 0.00 |  | 22 (5.6%) | 0 (0.0%) | < 0.001 |  | 28 (9.3%) | 1 (2.6%) | < 0.001 |
| PAGE-B |  |  |  |  |  |  |  |  |  |  |  |
| Low | 0 (0.0%) | 0 (0.0%) | - |  | 0 (0.0%) | 1 (1.1%) | 0.32 |  | 0 (0.0%) | 1 (1.1%) | 0.32 |
| High | 15 (3.8%) | 0 (0.0%) | 0.00 |  | 22 (6.2%) | 0 (0.0%) | 0.00 |  | 29 (11.1%) | 1 (3.1%) | < 0.001 |

\* All these data were presented as HCC cases (Cumulative HCC incidence). Cumulative HCC incidence was estimated by Kaplan-Meier method. P value was compared by log-rank test.

NAs: Nucleos(t)ide analogues; IFN: interferon.

**Supplementary Figure 1 (Fig. S1)**

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Fig.S1: The PS distribution between the IFN and NAs group in the entire cohort before (A) and after (B) PSM. Group “1” represented the IFN group while group “0” indicated the NAs group.

**Supplementary Figure 2 (Fig. S2)**



Fig.S2: The PS distribution between the IFN and NAs group in the naïve cohort before (A) and after (B) PSM. Group “1” represented the IFN group while group “0” indicated the NAs group.