The Association of Polymorphisms in IncRNA-\textit{H19} with Hepatocellular Cancer Risk and Prognosis

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Supplementary Table S1. The primer information for the H19 polymorphisms

| ID    | Primer_AlleleFAM | Primer_AlleleHEX | Primer_Common | AlleleFAM | AlleleHEX |
|-------|------------------|------------------|---------------|-----------|-----------|
| rs2735971 | CCGATTCCACAACCTCAACAACC AATTCT | CGATTCCAACACTCAACAACCAATTCC | CTTCACTCACC GCGCGGAT | A | G |
| rs2839698 | AGTGAGGAGTGGAGTAGGC | CAGTGAGGAGTGGAGTAGGT | GATGTCGCCCTGTCTGACGAT | C | T |
| rs3024270 | CCACCATCTCACTGCCCG | CCACCATCTCACTGCCCG | CACCAGCTAAGGTGTTCTCTAGAA | G | C |
### Supplementary Table S2, The baseline of the subjects

| Variables         | Hepatocellular cancer patients (%) | Controls (%) | P   |
|-------------------|-----------------------------------|--------------|-----|
|                   | n=472                             | n=472        |     |
| Gender            |                                   |              | 0.805 |
| Male              | 382(80.9)                         | 379(80.3)    |     |
| Female            | 90(17.3)                          | 93(19.7)     |     |
| Age               |                                   |              | 0.821 |
| Mean±SD           | 56.6±10.8                         | 56.7±7.2     |     |
| Median            | 57                                | 56           |     |
| Range             | 21-90                             | 26-85        |     |
| Smoking           |                                   |              | <0.001 |
| Never             | 224(73.9)                         | 199(60.7)    |     |
| Ever              | 79(26.1)                          | 129(39.3)    |     |
| Drinking          |                                   |              | <0.001 |
| Never             | 256(84.8)                         | 235(71.9)    |     |
| Ever              | 46(15.2)                          | 92(28.1)     |     |
| HBsAg             |                                   |              |     |
| Negative          | 38(15.0)                          | ND           |     |
| Positive          | 216(85.0)                         | ND           |     |
| Anti-HCV          |                                   |              |     |
| Negative          | 111(86.0)                         | ND           |     |
| Positive          | 18(14.0)                          | ND           |     |

ND, not known.
Supplementary Table S3, HCC patient clinical features and univariate analysis of overall survival

| Factors          | All HCC | Death, n=43 | MST<sup>a</sup> (M) | P-value |
|------------------|---------|-------------|----------------------|---------|
| Grade            | n=130   | n=43        |                      |         |
| High             | 31(23.8%) | 5(11.6%)   | 50.7<sup>b</sup>     | 0.170   |
| Moderate         | 73(56.2%) | 28(65.1%)  | 48.000               |         |
| Low              | 26(20.0%) | 10(23.3%)  | 45.000               |         |
| Smoking          | n=205   | n=71        |                      |         |
| Never Smoker     | 172(83.9%) | 60(84.5%)  | 69.000               | 0.380   |
| Ever Smoker      | 33(16.1%) | 11(15.4%)  | 98.9<sup>b</sup>     |         |
| Drinking         | n=205   | n=71        |                      |         |
| Nondrinker       | 186(90.7%) | 66(93.0%)  | 90.000               | 0.383   |
| Drinker          | 19(9.3%)  | 5(7.0%)     | 87.0<sup>b</sup>     |         |
| Family history   | n=309   | n=123       |                      |         |
| No               | 252(81.6%) | 106(86.2%) | 51.000               | 0.123   |
| Yes              | 57(18.4%) | 17(13.8%)  | 95.6<sup>b</sup>     |         |
| HBV              | n=168   | n=58        |                      |         |
| No               | 30(17.9%) | 11(19.0%)  | 27.000               | 0.102   |
| Yes              | 138(82.1%) | 47(81.0%)  | 86.5<sup>b</sup>     |         |
| HCV              | n=118   | n=51        |                      |         |
| No               | 102(86.4%) | 44(86.3%)  | 28.000               | 0.984   |
| Yes              | 16(13.6%)  | 7(13.7%)    | 27.000               |         |

<sup>a</sup>, MST, median survival time (months). <sup>b</sup>, mean survival time was provided when MST could not be calculated.
Supplementary Figure S1. The LD figure of the $H19$ genetic polymorphisms

Figure legend. The studied polymorphisms of IncRNA-$H19$ were selected the HapMap data. TagSNPs were selected by Tagger via Haploview with the following criteria: pairwise tagging of HapMap population with $r^2 \geq 0.8$; a minor allele frequency (MAF) $\geq 5\%$; and Chinese Han Beijing (CHB) ethnicity. And we expanded 10kbp both upstream and downstream of $H19$. Then, the LD figure of the $H19$ genetic polymorphisms was shown.
Supplementary Material. The results of the haploview software for the selection of the H19 genetic polymorphisms.

captured 81 of 81 alleles at $r^2 >= 0.8$
captured 100 percent of alleles with mean $r^2$ of 0.956
using 17 Tag SNPs in 17 tests.

| Allele       | Best Test   | $r^2$ w/test |
|--------------|-------------|--------------|
| rs75196800   | rs75196800  | 1.0          |
| rs76028799   | rs75196800  | 1.0          |
| rs77773409   | rs75196800  | 1.0          |
| rs217217     | rs217217    | 1.0          |
| rs77677619   | rs75196800  | 1.0          |
| rs76396712   | rs75196800  | 1.0          |
| rs217710     | rs217710    | 1.0          |
| rs77092197   | rs75196800  | 1.0          |
| rs12806111   | rs2525883   | 0.878        |
| rs170101     | rs4930101   | 0.858        |
| rs1706879    | rs1706879   | 1.0          |
| rs217718     | rs217718    | 1.0          |
| rs12575654   | rs2525883   | 0.9          |
| rs217716     | rs217716    | 1.0          |
| rs11564745   | rs2525883   | 0.9          |
| rs217714     | rs4930101   | 0.858        |
| rs77452354   | rs75196800  | 1.0          |
| rs184277     | rs4930101   | 0.925        |
| rs60976394   | rs217231    | 1.0          |
| rs59447588   | rs217231    | 1.0          |
| rs58781599   | rs75196800  | 0.962        |
| rs2285935    | rs4930101   | 0.9          |
| rs217229     | rs217231    | 0.981        |
| rs217230     | rs4930101   | 0.925        |
| rs217231     | rs217231    | 1.0          |
| rs117154195  | rs75196800  | 0.962        |
| rs217232     | rs217231    | 1.0          |
| rs217233     | rs217233    | 1.0          |
| rs217728     | rs2525883   | 0.939        |
| SNP               | SNP               | R2  |
|------------------|------------------|-----|
| rs11564741       | rs75196800       | 0.962 |
| rs3741219        | rs4930101        | 0.925 |
| rs2839704        | rs4930101        | 0.925 |
| rs2839703        | rs4930101        | 0.925 |
| rs3741216        | rs75196800       | 0.962 |
| rs217727         | rs2525883        | 0.939 |
| rs10840159       | rs4930101        | 0.925 |
| rs2839702        | rs4930101        | 0.925 |
| rs2839701        | rs4930101        | 0.925 |
| rs3024270        | rs217710         | 0.864 |
| rs3825028        | rs75196800       | 0.89  |
| rs2067051        | rs4930101        | 0.95  |
| rs2075745        | rs4930101        | 1.0   |
| rs2075744        | rs4930101        | 1.0   |
| rs2839698        | rs4930101        | 1.0   |
| rs2525881        | rs4930101        | 1.0   |
| rs2251375        | rs2525883        | 0.8   |
| rs2251312        | rs2735971        | 1.0   |
| rs2158394        | rs2525883        | 0.979 |
| rs2071095        | rs4930101        | 1.0   |
| rs11042167       | rs4930101        | 1.0   |
| rs4930098        | rs4930101        | 1.0   |
| rs2107425        | rs2525883        | 0.816 |
| rs2071094        | rs4930101        | 1.0   |
| rs10732516       | rs4930101        | 1.0   |
| rs2735972        | rs2735971        | 1.0   |
| rs11042170       | rs4930101        | 1.0   |
| rs2735971        | rs2735971        | 1.0   |
| rs2735970        | rs2525883        | 0.816 |
| rs2525882        | rs2525882        | 1.0   |
| rs4930101        | rs4930101        | 1.0   |
| rs2525883        | rs2525883        | 1.0   |
| rs10840167       | rs4930101        | 1.0   |
| rs61520309       | rs57889360       | 1.0   |
| rs61383602       | rs61383602       | 1.0   |
| rs57889360       | rs57889360       | 1.0   |
| rs2525886        | rs2525886        | 1.0   |
|       |       |       |
|-------|-------|-------|
| rs4930103 | rs2525887 | 1.0    |
| rs4929983  | rs2525887 | 0.852  |
| rs4929984  | rs4930101 | 0.823  |
| rs80047492 | rs2525887 | 0.961  |
| rs59121562 | rs2525887 | 0.961  |
| rs74584156 | rs75196800 | 0.888 |
| rs4930110  | rs4930101 | 1.0    |
| rs75051114 | rs75051114 | 1.0   |
| rs114138752 | rs75196800 | 0.888 |
| rs2525887  | rs2525887 | 1.0    |
| rs11042194 | rs2525887 | 0.961  |
| rs3890907  | rs2525887 | 0.801  |
| rs10840180 | rs4930101 | 0.95   |
| rs4929987  | rs4930101 | 0.95   |
| rs56781071 | rs75196800 | 0.852 |

Test Alleles Captured

**rs2839698:**
rs2067051, rs4930098, rs2075744, rs2071095, rs170101, rs184277, rs2839702, rs2525881, rs4930101, rs10840167, rs2839704, rs4929984, , rs10840180, rs3741219, rs10840159, rs4929987, rs2285935, rs2839701, rs11042167, rs2071094, rs2839703, rs2075745, rs10732516, rs4930110, rs217230, rs217714, rs11042170
rs75196800:
rs77452354, rs75196800, rs77773409, rs117154195, rs76396712, rs114138752, rs77092197, rs58781599, rs74584156, rs11564741, rs56781071, rs3741216, rs77677619, rs3825028, rs76028799
rs2525883:
rs11564745, rs2107425, rs2251375, rs12575654, rs217727, rs217728, rs2735970, rs2525883, rs12806111, rs2158394
rs2525887: rs11042194, rs59121562, rs2525887, rs3890907, rs4930103, rs80047492, rs4929983
rs217231: rs217231, rs59447588, rs217232, rs217229, rs60976394
**rs2735971:** rs2251312, rs2735972, rs2735971
**rs3024270:** rs217710, rs3024270
rs57889360: rs57889360, rs61520309
rs2525882 rs2525882
rs217716 rs217716
rs2525886 rs2525886
rs217233 rs217233
rs217217 rs217217
rs1706879  rs1706879
rs217718  rs217718
rs75051114  rs75051114
rs61383602  rs61383602

Then, we referred a published literature and took the intersection as the considering promising aiming SNPs. Ultimately, there were 3 SNPs covering lncRNA-H19 gene selected to proceed our study which were rs2839698 (G>A), rs2839698 (C>T), rs3024270 (G>C).