**Supplemental table 1** The primers for *LPR5*/*AXIN1* gene amplification and sequencing.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **SNP** | **1st-PCR primer**  | **2nd-PCR primer** | **UEP-DIR** | **UEP-SEQ** |
| LPR5 | rs61887821 | ACGTTGGATGTCCTTTTGTCTGCCCCTGAG | ACGTTGGATGTTGCCTCTTCCCAAACCAAC | R | CTTGGATTATAAAAAGCTTTTCTTAA |
| rs11228219 | ACGTTGGATGGAGTCTCTCTCTGTCACCTA | ACGTTGGATGTAATCGCTTGAGCTCAGCAG | R | ggggtGCAGAGGTTGCAGTTAGC |
| rs4988321 | ACGTTGGATGGACACATCAAAGTCCAGGGC | ACGTTGGATGTCTCCCTCGAGACCAATAAC | F | CGAGACCAATAACAACGAC |
| AXIN1 | rs11228240 | ACGTTGGATGGGAAGACCCAAAACAAACAG | ACGTTGGATGGCAGAGCTTAGCCTATTTAC | R | CAGTCAATGTTATTATTGATAAGT |
| rs2301522 | ACGTTGGATGTCACATTCCCGTAAGTACCG | ACGTTGGATGTTTCCCGCGGACCAGTTCAC | F | GGAGGACGATGGGCTGAGG |

SNP, single nucleotide polymorphism; UEP-DIR, Unique extension primer-direction; UEP-SEQ, Unique extension primer-sequencing.**Supplemental Table 2** SNP–SNP interaction models of *LPR5*/*AXIN1* analyzed by the MDR method.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Model** | **Training Bal. Acc** | **Testing Bal. Acc** | **OR (95% CI)** | ***p* value** | **CVC** |
| *LPR5* | rs11228219 | 0.525 | 0.509 | 1.35 (1.02-1.80) | 0.0366 | 8/10 |
| rs11228219, rs11228240 | 0.536 | 0.508 | 1.32 (1.05-1.66) | 0.0171 | 10/10 |
| *AXIN1* | rs2301522 | 0.534 | 0.534 | 1.35 (1.07-1.72) | 0.0127 | 10/10 |
| rs2301522, rs9921222 | 0.544 | 0.526 | 1.45 (1.15-1.83) | 0.0019 | 10/10 |

MDR, multifactor dimensionality reduction; Bal. Acc., balanced accuracy; CVC, cross-validation consistency; OR, odds ratio; 95% CI, 95% confidence interval.

*p* values were calculated using χ2 tests; *p* < 0.05 indicates statistical significance.