**Supplementary Table S2** Candidate causal variants selected for validation study from target sequencing.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| SNP | Chr. | Positiona | Alleleb | r2 c | MAF |
| rs4743305 | chr9 | 101760026 | C/T | 0.877 | 0.41 |
| rs7021675 | chr9 | 101752965 | G/A | 0.779 | 0.415 |
| rs1572136 | chr9 | 101740604 | C/G | 0.768 | 0.402 |
| rs10988451 | chr9 | 101741666 | A/G | 0.749 | 0.407 |

MAF, Minor allele frequency; SNP, singlenucleotide polymorphism.

a Position is GRCh37.

b Major allele/minor allele.

c r2 of linkage disequilibrium between variants with rs1413299.