

Table S1 PCR primers used to amplify InDel markers in the candidate region.

Name	Forward primer (5'-3')	Reverse primer (5'-3')	position
SIN-1	TCTATTCCATTTGTCAACACCTAA	AATCTACAAGCAACACACTTCGTC	7957221
SIN-2	GTGGAGAAAGAGAGGGGTGGG	GACAGCGAAAGTGAAGTGCGA	8192436
SIN-3	TGAGGCTGTTCTATGAACAAGATC	CGCCGTAGCCTAATCCATCT	9752949
SIN-4	CGACGAAGTCACGAAGTACATACT	TAAACACTGCCCACTCCCGTA	1.1E+07
SIN-5	TTGACTCTGGAGGGACTTGGATT	CTTGACTGCGTGCTCTACTGTTGA	1.2E+07
SIN-6	GTGAACAATGTAGATCGACGAAA	TTGGTGAAATTAAGCAAGTCATC	1.4E+07
SIN-7	AAACAAAGACTACCCTTGTTTCAGAT	GGATGGCTTAGATTTCGTTTATGA	1.4E+07
SIN-8	AGCTCGTAATCGATCAATTTTCC	CCGACTGACACTATTTCTCTGG	1.4E+07
SIN-9	GCAAGCTTATGTTATCATCCTTATAC	ACTATTTGAAGACTATCTGCCCTG	1.7E+07
SIN-10	GCAAGCTTATGTTATCATCCTTATACC	ATCATCTGCACTGGAAACCTCTG	1.7E+07
SIN-11	GCAAGCTTATGTTATCATCCTTATACC	ATCATCTGCACTGGAAACCTCTG	1.7E+07
SIN-12	TGCTTGCTTTTCTGGATCTTAAA	GATCAGTAGTGCTCCGATGGTTC	1.7E+07
SIN-13	CGGATTATAACAGTAACAACCACCA	GACTGTCTTATGAGTTTGACTTGTGC	1.7E+07
SIN-14	ACGGTCCATCAGAAACAGCC	CATAACCCGAACCCCCACTA	1.7E+07
SIN-15	GACCAAAGATCAAAACAAATGTGTA	CTGGTAAAAGAGAAAAATCAGGTTC	1.8E+07
SIN-16	TCTTGGCTATCACCGGATGG	GGGTATGAGTTCAAATGGCTTCT	1.8E+07
SIN-17	CCGATTTAGGGTTTTGGTTCAC	GATTGTGGTTAATGTATAAAGTTGA	1.8E+07
SIN-18	TAAACAGCGACAAAGGACAATGA	GGGCCTTCTTACAAATAGCACAT	1.8E+07
SIN-19	TTTCGCCGCCTAAACCTTCT	CGATCATCTCTTTCACCGCATT	1.9E+07
SIN-20	GGGTAGACCTCATTTGCGTAAT	TGTCTCGTGTGTAAGAGGCCTG	1.9E+07
SIN-21	TAGGATTACTTTTTCCCCACTTACT	AATTAGCTGTTCAATTTTTGGATTAT	2E+07
SIN-22	CAAAGAACCCAGACGACTCAAAG	GGAAAGTTGGTAGGAAAGATAATGC	2E+07
SIN-23	TGACAAATCACAAACCTAACCT	TTTGAGGGAATGTAATTTTCCAA	2.1E+07
SIN-24	TAACATCCAAAAGGAGTCAACACTT	AAGAACGAAACGGTAAAGGCATA	2.1E+07
SIN-25	TGAATCTTGAGGACGGAGGAG	TGTTTTTGTTCGCTTATTCTTG	2.1E+07
SIN-26	GTTTAGGTTTGGGGGTTTGGC	ATGAGGAAGCGCATCATGAAGTT	2.2E+07
SIN-27	GATTAAACATATCTCAATGAATCATCTAG	TTCTCTTGCTTCGCTCTCC	2.3E+07
SIN-28	TGTGAAACTACATCTCTGGACGG	AGGTAATGGGCAGCATATACTCG	2.4E+07
SIN-29	AAAGGGGCTTAAATGGAGAAACA	CTGGAAGGAGAGCGTGGTGAA	2.4E+07
SIN-30	CACCGGAAGTGAAGAGGTATGATAC	TTGATGGAACAGCGTAAGCAG	2.4E+07
SIN-31	AAACCGATTCAACCTTGTTTTCTAA	TCCATACGTGTACAGTCCTTGTCAG	2.4E+07
SIN-32	GCATTACACTACCACTAGTAGGGAAA	ACTTTAGTCCAGTTGTTAGAGTGTTTC	2.4E+07
SIN-33	GTTTCTTGTCGCTGAGTCTGG	TAACCTCAACCCGAATCCAATC	2.4E+07
SIN-34	TCTTGAGTAACCTTTGCGGA	CGAGTTATCTCACAGGACCGA	2.4E+07
SIN-35	ATTACGAGTTACCTTTTTTCCA	GAGATTCTGGTGTTACCATGAC	2.5E+07
SIN-36	GAAAGAAATAGAGAAGTTGACGAGAG	TATTACCGTTTTTATTGTTTTACCGA	2.5E+07
SIN-37	CCTTATCTTACCCGGCCCAT	CGTTGAGAGCAGCGGGAAGT	2.6E+07
SIN-38	GCCAGAAGATCAAAACCAAACCTAT	AACTCAACAAACGTATCGAGCAA	2.7E+07