Table S7. The primers of Sanger sequencing for validation

Individual	Position	Forward primer	Reverse primer	T_m (℃)
ACC1-II-1	15:80878576	ACATCCTGCACACTGCGTTA	ATGGACATGCTGTTGCTTGC	60
ACC1-II-1	4:165099831	AGGCCTGACTGAGGGATACA	TGGGGTGGTTCTAGGGGAAG	60
ACC1-II-1	6:85605629	TGCTTGGCACTGTCCTGAAA	GCCCAGAAGTGCCTACGTTA	60.5
ACC1-II-1	10:115352263	AACTCATCAGTGACCGCAGG	GCCTCTATCGGTGATGTGGG	60
ACC1-II-1	6:154692299	TTCTGTTCCAGCCTCCGATG	TAAGTCGGCATCCCTGTGGA	60.5
ACC1-II-1	18:31333885	TCTGGGATGTTACAGCGTCG	AGGTGAGGACGTTCAGTGAG	59
ACC1-II-1	15:45732364	TGTTTGACTATATCAGTTGCCTGT	ATGCCCACTCTCCAAATAAGCA	69
ACC1-II-1	6:76955874	GGGAACCGGTCATAGAGACA	GTGATGGTGGCTGACTTCTCA	59
ACC1-II-1	3:158917393	TCTTCTGGGTATCTGCCTCCA	CTCCTGTGGGTCTTGGTGTC	60
ACC1-II-1	8:11688362	GTGGATACGGGGCTAAAGGG	CAATGCCAGGGGGAGAACAA	60
ACC1-II-1	19:4032107	CCGGGCTTAACTCCTCAGTG	GTAGCTCAGGAGAGACCCCA	60
ACC1-II-1	7:19343958	CAGGAACCCAGACAGAGTGG	GAAAGCACCGACACTTTGTAGT	59.5
ACC1-II-1	18:70512197	CGTATCTGGCGTCTCACTCA	CATGTGCGTAATGTGGGGTG	59
ACC1-II-1	7:147539364	TGGTCAAAGTTGCCATTAATTGTT	CCCCTTGTTCTCAGAGCTGC	59
ACC1-II-1	6:123036854	ATGTACCATGGGAGGGCTCA	AGCACTCAGGCATGCAAATC	60
DS1-II-2	17:52287119	GCTCCAGGAAGCAAAGACCAT	CCAAGGCTTCAGGCTATGAAA	62
DS1-II-2	19:55529705	GGCCTGGAGCGGTTAGAAG	GCTAGAGCATGGGTGCAGAGT	62

DS1-II-2	19:56343191	GCGTGTGCCTGTCATTCCT	TTCTTCCCGCTGCCTAGCT	58
DS1-II-2	20:4339054	GGGAGACGCTGATGGAAAGA	ACATTGACTGGTGCCTACCTTATG	62
DS1-II-2	4:190179317	TCTTTTTGAGAAGGGCAAATTTTATG	TCTGGAAGTAAAAGGAACAATGCTATAA	58
DS1-II-2	14:71380614	GGGTGACTAAAACAGGGATTTTCATAT	TGTGCCATGACCAGTTATGGA	62
DS1-II-2	16:84073033	GGAAACAGACACATGCAATTGTAAA	CACCCTGCTAGTTTTTTGTGATTTT	62
DS1-II-2	7:132334892	GGTCCCATAGCTCATGCAGATAG	GCACTATTCTATGGGCTGGGATT	58
DS1-II-2	13:79932615	TTCCCTAAACAGAAAGAAGAGATAACAA	AAGTAGAGGTGGATCAGAAGTGGAA	58
DS1-II-2	2:166848782	TGTTGAGAATGGGTGCTAGCAAT	TCCGAGTGATCCGTCTTGCT	62
DS2-I-1	1:72008400	TGGCCTTTTCACTCCCAATC	CCAGAATTGGTTGGATCAGGAA	62
DS2-I-1	16:64312186	GGAATGGTGAGAGGGTTGGA	CACAAGGTTCACATAGCATAGTCATG	55
DS2-I-1	X:68611473	CCAGAAGGCCCAGGTGAGA	GTCAGCCTGTCCATCAACCA	64
DS2-I-1	20:60500224	CACTGGAATCAGGTCCACAGTTT	ACTTGGCAGAGGAGGAAACTGA	55
DS2-I-1	22:18619901	AGGGAGAGGGTTTGGAGATCA	CATTACTTCCAACAGGTCAGCATT	58
DS2-I-1	2:166854673	CTTTTTCTGCTGGTTGAAATTATCTATG	AAAGGCCAATTTCAGGGATGT	62
DS2-I-1	6:35755658	GACATAGAGGTCCTGCGATGGT	CTCTTTATTTCAATCACTCCCCACTT	58
DS2-I-1	13:89662020	CCGTTGACTTTTATTTCTCAAAATTCC	CATCATGCTGGACACAATACATATATACA	62
DS2-I-1	2:79895035	TGCTCTTTAGCATGTATTTGGAGTTC	TTTACTAGTATGAATTTCAGTTGGTATAGGACT	58
DS2-I-1	4:3472325	GCTGCTGCGTTCAGACAATC	CCGACGTCACCCTTTTGG	55
DS2-I-1	16:48880245	CCATGGTGAGCCCAGGATT	GGCAAGTCAGAAGCTTCAGTGAT	58

DS2-I-1	18:11785347	CCCAGTCCCACGCTCAGTT	AAACTCTGAAAGGCTGGATGGA	58
DS2-I-1	17:59415198	CAGGTCTTCCTCTTGGAGCAA	GCCCCCGCCAGAGACT	58