Table S6. The primers of pyrosequencing for validation

Individual	Position	Forward primer	Reverse primer	Sequencing primer
ACC1-II-1	15:80878576	AGGTTGCTTAAAGAGAAATGGCTCAAA	GCTTGCCAAGACAATATATCTGGAAATC	CTCCAAGTGTGGCATA
ACC1-II-1	4:165099831	TTGGGTCTGTACTTTCCATCAGAT	AAAACACGAACCCATCCAAATA	ATATCACTACAGTGTTAATTACTAT
ACC1-II-1	6:85605629	GGAATGAGAATGTCAAGGAGTGTA	TGTTCCACTTTTCCTCTGTTGTAG	GTAGATGCAATACTGTGTGA
ACC1-II-1	10:115352263	CCGTAAAAGGCTTCAGCTCTAA	AGGAACAGCACTTTCAGCATGTAG	CTCTAAGCCCCCAAC
ACC1-II-1	6:154692299	CCACATATAACGGGCATGTATAGA	TATCCTTCTTGGCAGCTACTGG	GGAGTTTGAACAAAATGA
ACC1-II-1	18:31333885	GGAAGCCACTAACACATTTTATACCC	GTGAGGACGTTCAGTGAGTATTTATC	AAGATTTTATCAAAAATATGC
ACC1-II-1	15:45732364	GTTGCCTGTTTGTACACTACTTAGCTTT	TTTTTAAAATAGTATGCCCACTCTCC	CAACTTGCTCATTCACTT
ACC1-II-1	6:76955874	TACCTTCCACCCCAATAGGAATAT	TGTGATAGTCCAAGTGCAAACTTT	GATAGGTGATAATGAAGCA
ACC1-II-1	3:158917393	TACAGTTAAAGCGACAATCATTGATG	TTTCTTCTGAGTAGTACCCTCATAACC	GACCAGCTTTCCTCC
ACC1-II-1	8:11688362	CATAAAAAGAACCTGGTCCGGTAG	TCTGCAATACTTGGTAAAGGCAACTAA	AAAAAGTGTAAGTTCCTAGC
ACC1-II-1	19:4032107	GGGAGAAGGAAGAGCCCACTG	GCCTGAAACACCACTTATCTCTGC	CTCTGCCCGCTTGGGAGCCA
ACC1-II-1	7:19343958	GGGAAGACAGAGCAGTAAAAGTTG	TAAGTACATACCTTGGACAAGCTAACA	GTAAAGAAAATAAGTAAATGACTC
ACC1-II-1	18:70512197	CAGCACTGAAGCGCAGGTCT	ATGGCATGTGCGTAATGTGG	GGAGGAGAAGTGGGTAAC
ACC1-II-1	7:147539364	ACACCCAAGTGAAATACTTTACCA	TATGAATCTGCAACAAATTGTCTG	TTGCTTATATGTGTCTCTCA
ACC1-II-1	6:123036854	GGGCTCACAAGATAACCAAACAT	CAAATCCCCATAATGCACATAGTTAGC	GAACTTTAACAAACTTTTAGATATA
DS1-II-2	17:52287119	CGGATTTGCATAATGTGTATTCA	GTGATAGTGTTGTGATGCCCTTGT	AAGAGAAAATATTATGAGGA
DS1-II-2	19:55529705	CCAGGTGCCTACAGTCTGTGTG	GCACTGCTCCCAGGATGAA	CTGTGATCCAGGTATTTAAT

DS1-II-2	19:56343191	CCATAAGGCTATGATGACGAGTT	TTACCTTTCTGGCCGATTTG	GAGCTTGGCCTGCCC
DS1-II-2	20:4339054	GGGGCAGAATGCAGTCAAG	TCAACTCCCCTCTTTTCACCTG	GAGTGAGGATGAAGGTAAC
DS1-II-2	4:190179317	TTTTGAGAAGGGCAAATTTTATGA	AAAAAATTGGGAGCAATGTGA	CGCATTGTGTCTATTGAGT
DS1-II-2	14:71380614	GGTGACTAAAACAGGGATTTTCAT	GTAAAGGGCACAGGCTAATAGATC	AAGTATTATTTTCTGCATCC
DS1-II-2	16:84073033	ACGCTCTAAGCTCCCTGAAGACT	GGCCAGGATGGTCTCGAT	GGGCCTGACAAATGC
DS1-II-2	7:132334892	CCCTGAGCATCATGCAGTTT	AATGGGGGAAAGCAGACACTA	GCAGTTTTCCTTTCTAGATA
DS1-II-2	13:79932615	GGTCTGCAAACAAAATTCAAGTTA	GTGGATCAGAAGTGGAAAGTAACA	TTATTCCCTTGTATTTGGT
DS1-II-2	2:166848782	GGCCGAATCCTACGTCTGATC	AGTAGGAGGCCGATGTTAAACAAC	CCGATGTTAAACAACGC
DS2-I-1	1:72008400	TGCAATGTTTCACCACAACAA	TGAGGAGCAAAGGTTATCATAGG	TGCTAAAAACACTTGGCTC
DS2-I-1	16:64312186	GCCCTGACTTTAGCCACTACATA	GGCTTACAACCTGAGTCATCACAA	CATCCTTCACATGAGATTAA
DS2-I-1	X:68611473	TCTCTGGGCCCCCTTCAA	GGTGGGCAGAATGAAATGG	GGGAGTGGGGATAATTT
DS2-I-1	20:60500224	AGCAGGAGGCATGAGACCC	AGGAAGGGGTGGCTGCTTCT	TGGGCTGGGCAGAGA
DS2-I-1	22:18619901	GCTCAGAGATGGAGGGAAATAGG	CCAACAGGTCAGCATTGTGTAAAC	CAGCCCATACAATGTTC
DS2-I-1	2:166854673	ATTCCCCTTTGGTAGGTGGAACTC	CAAGGTGAAGAAGGACCCAAAGAT	TTTGGTAGGTGGAACTC
DS2-I-1	6:35755658	CGCCAAGGTCGAGGTCAA	CATAGGCGATGCTAAGCCATT	CCAGGTGTTCTTTGG
DS2-I-1	13:89662020	AGCATTTGAAAATTCCGTTGACT	AAACACACACAAAACGGCATAT	ATAATTTTCCAAATTGAGAT
DS2-I-1	2:79895035	GGGGTGATTAAACTTTAATGCATG	TAGAGACGGGGTTTCACCTTGTT	GGTATAGGACTTCAGAATAA
DS2-I-1	4:3472325	GTGGCGTCCGTGAATCAGAA	GATTTGGCCCAGAGACCACA	TTGCCACGACGGCTT
DS2-I-1	16:48880245	TGCCAAAGCCATGGTATAGC	TCTGGAATCTGGGGTTGG	TACACATTTGGTTTATTGTT

DS2-I-1	18:11785347	TGCTCCTGGATTCTGCACTCTT	GTTCTACTTATTGGGGGCTTGGAG	GTGTCCACAAGGCAG
DS2-I-1	17:59415198	GAGACAGAGAAAGCCTCCTTGTT	TGCAGGACTGGTGGAAATATTCA	TGGTGGAAATATTCACAG