

Appendix 10: Microsatellite Sequence Accession Numbers Repeats and PCR Primers.

Name	GenBank Accession	Repeat	Label	Primers
A4	EF106738.1	(CA) ₇ CC(CA) ₆	IRDye 700 5'	CGACGACGGAAGTAAGTTC GGGAAAACAAAGGAAAGTCC
A102	EF106739.1	(CA) ₇	IRDye 800 5'	GCCTTATGAGGACCATTTG GCGTGGCTATTTCAGAGAAC
A104	EF106740.1	(CA) ₁₄	IRDye 700 5'	TCTTTGGAACAATACCCACTAC GGGGAATGGGATTTACTATTC
A108	EF107741.1	(CA) ₁₁	IRDye 800 5'	ATGGATCTCACCAAGTAGACAG CACAGGACGTATGTAAACACAG
A110	EF106742.1	(CA) ₁₃	IRDye 700 5'	GGTCGGTCGATATTAGATTGC GAAGGGGAGAGACAGCTCAG
B3	EF106743.1	(ATG) ₆	IRDye 700 5'	AGGGATAAAAACACCTGGTG TTTCTGTTGACTTGCAGTAACC
B4a	EF106744.1	(ATG) ₆ ATA(ATG) ₂ CTGATGATA(ATG) ₂	IRDye 700 5'	AAGCATCAGCATCATTATTAGC AAGACGCCTTCAAGAAAATC
B6	EF106745.1	ATG(ATTG) ₂ ATGAG(ATG) ₃	IRDye 800 5'	GCATTATCGGTCTCGTC GATCCAAGGGGAGGACTG
B11	EF106746.1	(ATG) ₈	IRDye 800 5'	ATCTCGTTGTGTTATTAGAGG TCTCGACCATGAAATATACATG
B101	EF106747.1	(ATG) ₅	IRDye 700 5'	CACACCGTTTCGTTTTTAGTC TTTGGACCGCTATTCACCTAC
B105	EF106748.1	(ATG) ₂ AGG(ATG) ₂ (AGG) ₂ (ATG) ₃ (AGG) ₄ (ATG) ₂ GGGAGG(ATG) ₂	IRDye 700 5'	CCCCGTGTCTTGTTTTTC ATGAGGAAGATGAAGGTGGAG
B106	EF106749.1	(ATG) ₅	IRDye 700 5'	TGACGGTAAAAAGAAGTTTGC GCCATAATCATCATCATCCTC
B110	EF106750.1	(ATG) ₈	IRDye 700 5'	GCAGATACTTCAGGGTTGTG ACGATGACGATGATGATGTT
B114	EF106752.1	(ATG) ₉	IRDye 800 5'	GCCCAGGACACAAGAAGTG GGAGCCATAGGGAGAAAAGC
B201	EF106753.1	(ATG) ₆	IRDye 700 5'	CACTGCACATTGAGACTAACG CATCAGCAAGTACAAGGACAGT
B202	EF106754.1	(ATG) ₅ (ACG) ₂ (ATG) ₅	IRDye 700 5'	ACCTCCATCTCATCGTCAG GGCAGAAACAGAGCAGTG
B209	EF106755.1	(ATG) ₃ GAG(ATG) ₄	IRDye 800 5'	TTTCAGTTTCAGCAAGTAGACC AATCCTCTTCCATCTCCATATC
B212	EF106756.1	(ATG) ₇	IRDye 800 5'	GTGCCCCGAGATGTTTTTC ACCGCAAGATGCTACAATG

B222	EF106757.1	(ATG) ₂ AATTTG(ATG) ₄ ATA(ATG) ₃	IRDye 700 5'	CTGCGTAGAATGGTCTTAGTTC CTTTGAAAACAGGGGTATGTC
B227	EF106758.1	(ATG) ₇	IRDye 700 5'	TTTTTACGCTTGTGGTTTGAC TCGCACTTTGCCCTGATTC
B228	EF106759.1	(ATG) ₆	IRDye 800 5'	GACCACTGAAGTGAACCACTTC TTTTTCATGGCGAGTTAGGAC
B231	EF106760.1	(ATG) ₈	IRDye 700 5'	AGGGTATAGGAGACCCATCAG GCTTACTCAGCCACTTGAGAG
B234	EF106761.1	(ATG) ₆	IRDye 700 5'	TGGGTGACTTGTGATGAAC TGAATGTTGGACTTGATGTG
B236	EF106762.1	(ATG) ₅ ATA(ATG) ₃	IRDye 800 5'	CCACAACAAGTGCTCAAAC ATCAAGTATCGCCAACCTGTC
C8	EF106763.1	(CAG) ₄ CAACAT(CAG) ₄ CAC(CAG) ₂ CAACCG(CAG) ₄	IRDye 700 5'	TTACGGCAGTAGAACCCAC TGGAGGAGTCAAAGGTGAG
C104	EF106764.1	(CAG) ₁₁	IRDye 800 5'	GCTGACTTTGTGGCTTGAC AATCGGTTTGTGCTGTCC
C107	EF106765.1	(CAT) ₄ (CAA) ₃ GAA(CAA) ₂ GAA(CAA) ₅ GAACAAAAA(CAA) ₆ (CAG) ₈ CAACAG(CAA) ₃ (CAG) ₃	IRDye 700 5'	TTATGACACCATTTCCCATATC CCATATCCCCTTGATCTCTC
C111	EF106766.1	(ACC) ₃ AGCAT(CAG) ₄	IRDye 700 5'	TTGCCACTGCTGTTGTAGG GCCAAATCGTGACAGGTG
C112	EF106767.1	(CAG) ₃ (CAA) ₂ (CAG) ₃ (CAA) ₂ (CAG) ₅ CAACAG(CAA) ₄ (CAG) ₇	IRDye 700 5'	TTTTGTGCGGGACTGAACTTC GTTTGAAAGCAGCCTGAGTG
C113	EF106768.1	(CAG) ₇	IRDye 700 5'	CCCAGGCACACTTGATTG TCGGTTGGACCACTTTTG
C114	EF106769.1	(CAG) ₇	IRDye 700 5'	GTGGCAAGGATACCTCGTC GGGTTGACAAATCGTGGAG
C115	EF106770.1	(CAG) ₈ CAA(CAG) ₃ (CAACAG) ₄ (CAG) ₂	IRDye 700 5'	GATGGTCCTGTGTGTTACGAC TTGTTGGGCAAGCAGTTG
C204a	EF106771.1	(CAG) ₂ CAA(CAG) ₅ (CAACAG) ₂	IRDye 800 5'	GTTGCTGTTGGTTTGGATAC ATCTTCTGCCATTTTCAGTTC
C207	EF106772.1	(CAG) ₄ CACCAA(CAG) ₂ CAA(CAG) ₃ (CAA) ₂	IRDye 800 5'	TATGCCAGAGGCTATTGAGA CTTGTTGCGAGGGAAGAG
C210	EF106773.1	(CAG) ₅ (CAA) ₈ CAT(CAG) ₂ (CAA) ₄ CATGAA(CAG) ₁₀ (CAA) ₅	IRDye 700 5'	CAGTTTTCAACAACAGCAGATG GGTGGTATCATTGGAGAGTAGC
C212	EF106774.1	(CAA) ₃ (CAG) ₃ CAA(CAG) ₂ CAA(CAG) ₃	IRDye 800 5'	GCTTGATTTTTTTTCTCTCAC CACTGCTGCTGGTGTTACTG
C213	EF106775.1	(CAG) ₉	IRDye 700 5'	CTCTCGGCAATCCTCATAG GACCAAGCAAATCTACAAAGAC
C216	EF106776.1	(CAG) ₇	IRDye 700 5'	GACCTGTCTATGATGCCCATAC CAACCAGACTTACCTGTTGGAC
C219	EF106777.1	(CAG) ₃ CA(CAG) ₃	IRDye 700 5'	CTGCTGTTGTTGCTGTTTC TGGAAGTTACCCGACTCC
C227	EF106778.1	(CAG) ₇	IRDye 800 5'	GCACACTTGTCGTAGCACTTG TCGGTCATCCAACACACAC
C231	EF106779.1	(CAG) ₄ CAA(CAG) ₄ CAA(CAG) ₂ CAA(CAG) ₃	IRDye 700 5'	CCACAATAGGAAATCGGTTAC GAAGCCAAGAAACAGAAGAAG

C232	EF106780.1	(CAG) ₄ CAACAGCAACTGCAGTGG(CAG) ₆ CAA(CAG) ₂ CAA(CAG) ₂	IRDye 700 5'	TTGCTCAGGGAAGTGTCC
				GCGGAAGTGTGTTGATTG
D8	EF106781.1	(TAGA) ₇	IRDye 800 5'	CGTGTTTGTATGTGTGTGTTTG
				GTCAGTTGGAAGTACGATGTGTC
D114	EF106782.1	(TAGA) ₁₂	IRDye 800 5'	AAACGGAAGGCACAGTTC
				TCTCAAATGTCACCCATCTG
D127	EF106783.1	(TAGA) ₁₆	IRDye 700 5'	ACGGCCAAATCCAAAATG
				GGAGGGAACAAGCATTGC

Primer oligonucleotide sequences (5' to 3') are shown for each clone. Forward primers (top sequence for each microsatellite) were labeled with LI-COR infrared dyes (IRDye 700 or 800).