Appendix 1

Table A1.1 Primer sequences and genetic polymorphism observed in 24 individuals from leopard grouper from Puerto Libertad among 5 microsatellite loci previously described (Jackson et al. 2014) and eight new loci described here, including repeat motif, size of the expected PCR product, range of observed allelic variation, number of observed alleles (Na), observed (Ho) and expected (He) heterozygosity and P values for deviations from Hardy-Weinberg equilibrium (HWE): * 0.05, ** 0.01, *** 0.001, NS = not significant.

Locus	Repeat motif	Primer Sequence (5'-3')	Size (bp)	Allelic range (bp)	Na	Ho	He	HWE
Jackson et al. 2014								
Mros03	$GT_{(43)}$	F: CCATCATGAAGCTTTGACCA	104–160	120-180	18	0.944	0.912	NS
		R: TTGACTTTATCTCCAAGGCAAA						
Mros05	$CA_{(36)}$	F: GGGACCTGAATGAGATCAACA	117–199	159-200	14	0.786	0.890	NS
		R: ATCCTCAAGGACTGCTGGTG						
Mros07	$GT_{(36)}$	F: CATTAGTGCTGCAAGGCTCA	140–216	161-210	15	0.786	0.908	NS
		R: CAGTGAAAGGCTTGGTGTCA						
Mros11	$TCTA_{(19)}$	F: ATCGAGACGAAAGGATGCAG	83–181	128-192	13	0.706	0.896	NS
		R: TCCGTCAGCAGTTTACTCCC						
Mros12	$TAGA_{(16)}$	F: GTCCTGCACTCAGCTTCCTC	186–302	208-289	16	0.889	0.901	NS
		R: TTCCATGACTGATCCAGCCT						
New loci:								
Mros17	$AAAG_{(14)}$	F:CTTGTCCGAGGTAAGGCTTG	154	157–182	6	0.778	0.793	NS
		R:AACAGCAGTTAAGACTGTTTCTTCA						
Mros18	$AGAT_{(14)}$	F:TGAGATTTTACCAGATTCAAAAGTCA	178	178–232	8	0.500	0.837	*
		R:TGCTCATGAATTCCTTACCTTG						
Mros22	$AAAG_{(12)}$	F:TGGGAATTGTAGGATCTGGC	213	210–244	9	0.824	0.851	NS
		R:GTACGTAAGGGGCATTCCAG						
Mros25	$AGGT_{(12)}$	F:GAAGCTTGATTTAGAAGATCTTACCC	190	180–210	7	0.667	0.684	NS
		R:GCAAGTGCATGCGAAAATTA						
Mros26	$AATC_{(12)}$	F:TGGAGGCTTCAAAACTGGAG	162	152–176	6	0.833	0.682	NS
		R:TCACTGGCTATTCATGTGCAA						
Mros27	$AGAT_{(11)}$	F:TTCTACATGTAACAAATTTCCCC	140	144–190	8	0.889	0.855	NS
		R:TTGAGCCTCATGTGAAGCAG						
Mros29	$AAAG_{(11)}$	F:GATCCCTCTAAACTGTTCTTGTTG	169	172–234	8	0.778	0.793	NS
		R:CCTGACACTTTGGGTCCCT						
Mros32	$AACT_{(11)}$	F:GACAACTGTTCAAGCAGGCA	205	206–278	14	0.944	0.907	NS
		R:TGTAAACCCATTTGGGCAAG						