Microsatellite primer sequences and locus information for Scarlet Macaw (*Ara macao*)

Locus name	SMACv1.1 scaffolded contig number	Forward primer sequence 5'–3'	Reverse primer sequence 5'–3'	Repeat motif	*Fluorescent tag
SCMA01	s_1_1NewScaffoldedcontig_720	*ATGGTAGAGGGAGGCACTGA	GCATGGTATAAGGCCCATCT	$(AC)_{22}$	NED
SCMA02	s_1_1NewScaffoldedcontig_3573	*TCAACCTCCAGGTGTCTTCC	TCCTTCAGTCACCAGCTTCA	$(GT)_{21}$	NED
SCMA04	s_1_1NewScaffoldedcontig_8801	*TAAGCCCTGCTCATCAAAGG	CGACAGGAGCTGATAAGGGT	$(AC)_{20}$	VIC
SCMA05	s_1_1NewScaffoldedcontig_11956	*CAGAAAGCCAGGAGTCCAAG	TTTCTGACTTTGCTGGTTGG	$(AC)_{20}$	NED
SCMA06	s_1_1NewScaffoldedcontig_12019	*AGTCTGAGCAGGTGCAGGAT	ACAGACTCTGCACCACATGC	$(CT)_3T(TG)_{21}$	VIC
SCMA07	s_1_1NewScaffoldedcontig_14086	*CTGATGATGGTGGAAAGCCT	ATGTTCCACTGCATGTCCTG	$(TG)_{21}$	NED
SCMA08	s_1_1NewScaffoldedcontig_18034	*CTTGCCAGATGCTGACACTC	TCATGACCTTTCTGCCTTCC	$(TG)_{22}$	FAM
SCMA09	s_1_1NewScaffoldedcontig_19117	*CACTACCAGCAAGTAGCAGGC	TGAATTCTAACAAGCAGCGG	$(CA)_{20}CG(TA)_3$	VIC
SCMA10	s_1_1NewScaffoldedcontig_19611	*TCCAGGAACTGAAATACCTCAT	TGGCTTATCATTTCTTAGCCAG	$(GT)_{21}$	NED
SCMA11	s_1_1NewScaffoldedcontig_19941	*TCCTTCGTCCCTCCTTCC	AGGCAAATGACAGAACTGGG	$(AC)_{21}$	NED
SCMA12	s_1_1NewScaffoldedcontig_20383	*GGTGGAGCACATTGCTGAAA	CAAAGATGCCCACCCAAA	$(AC)_{22}$	VIC
SCMA13	s_1_1NewScaffoldedcontig_21269	*GTTGGCCACTGCTTCAGAAC	GCTGCAAGAAATTCCAGTCC	$(TG)_{21}$	VIC
SCMA14	s_1_1NewScaffoldedcontig_25432	*CGCATACTTTACACCCACCA	TTGTGACAGGGCTAGGCAG	$(AC)_{20}$	FAM
SCMA15	s_1_1NewScaffoldedcontig_26647	*GACTGGCAGTTAAGGTGGTTG	AATGACTTTCCTCTTGCTCCC	$(GT)_{20}$	NED
SCMA16	s_1_1NewScaffoldedcontig_32560	*AAAGCTTCCACACATCATGG	TTGCTTTATCCAAACATTTGTGTC	$(AC)_{20}$	NED
SCMA17	s_1_1NewScaffoldedcontig_34586	*CACAGCTGCACATTTGATCC	GCCTCATGGGTAGAACAGTTT	$(TG)_{20}$	VIC
SCMA19	s_1_1NewScaffoldedcontig_35385	*AGCGCATCTGCCTAGATGTT	TAATCCACAGCACCACCAAG	$(GT)_{24}$	VIC
SCMA20	s_1_1NewScaffoldedcontig_36691	*ATGCTTCCAAATCAGAATGC	CCAGGGACATAGTAGCTGCAC	$(AC)_{20}$	VIC
SCMA21	s_1_1NewScaffoldedcontig_41388	*TGAATTTCCGTGCCTAAAGC	TCACCCAAACAAGCAACTTTC	$(GT)_{20}$	FAM
SCMA22	s_1_1NewScaffoldedcontig_44385	*AACTGTGATGAAGTTCGTGGC	CAACGGCTACACACAGTGCT	$(TG)_{22}$	VIC
SCMA25	s_1_1NewScaffoldedcontig_58183	*AAATGCTGCCCTGAGTTCAT	TCTTATAGCTTTGTGATAGTCATTGAA	$(GT)_{20}$	FAM
SCMA26	s_1_1NewScaffoldedcontig_61104	*AGCAAAGGTAAGGAGCAGCA	GGCACCTCTATCATCTATTGCAG	$(TG)_{21}$	VIC
SCMA27	s_1_1NewScaffoldedcontig_62371	*TTCTGCAGCAGTTCCCAAA	TGGACTCTGTATTCCAGTCGC	$(CA)_{22}$	FAM
SCMA28	s_1_1NewScaffoldedcontig_65504	*GAAGGCAAAGTTCTCATGCTG	CCATTATGATCAGATTTCCGC	$(TG)_{21}$	NED
SCMA29	s_1_1NewScaffoldedcontig_66792	*GGTGGGCAGATAGCCTGAT	GTTGAATGCAAAGTGCATGG	$(TG)_{20}TA(TG)_3$	FAM
SCMA30	s_1_1NewScaffoldedcontig_68479	*TTGCCAGGTCCTTCTCTACC	ACCACCTTCTCTTGACTTGTAATTG	$(CA)_{24}$	FAM
SCMA31	s_1_1NewScaffoldedcontig_70421	*TGTGCTCCCTACAGTTCCAA	AACGCTGAACTTGGTGTGGT	$(AC)_{21}$	FAM
SCMA32	s_1_1NewScaffoldedcontig_77138	*GGCATGGCTCTTTACTTGCT	TTGCCACTGAGGCTTCTACC	$(TG)_{21}$	VIC
SCMA33	s_1_1NewScaffoldedcontig_77453	*GAGGCACTATTTCTGGCAGC	GCTAAGCAGATTTGTCTAAACATTCA	$(AC)_{21}$	VIC
SCMA34	s_1_1NewScaffoldedcontig_78919	*TTTGGCAGTAGTCGGGATTT	AACTTGGGAATACATCGCTGA	$(AC)_{22}$	VIC
SCMA35	s_1_1NewScaffoldedcontig_81206	*CTCGATCTGGACAGCACACT	GGGTTGTCTGCTGGTACTAAAG	$(GT)_{20}$	VIC
SCMA37	s_1_1NewScaffoldedcontig_91851	*TCACATGCATGAGCTGGG	CCTGTAAGGTCAGGAAGGACA	$(GT)_{20}$	VIC
SCMA38	s_1_1NewScaffoldedcontig_92645	*TCACTGAATCTCATTGCCCA	CATCCTAATCAGGCAGGGAA	$(AC)_{20}$	FAM
SCMA40	s_1_1NewScaffoldedcontig_109156	*GCCTGCACCAAATTCATACC	TTTGGTGGAAACTGGACCTA	$(AC)_{24}$	FAM
SCMA41	s_1_1NewScaffoldedcontig_115612	*AATTTGGGTAGCAATGTGGA	CAGCAGATGTGGATTCTGGTT	$(TG)_{20}$	NED
SCMA43	s_1_1NewScaffoldedcontig_127204	*GTGATCACAGAAACACGGG	GGCTGGAGAGTGCCTTACCT	$(GT)_{20}$	VIC
SCMA44	s_1_1NewScaffoldedcontig_132550	*GGTGGAGCACATTGCTGAAA	CAAAGATGCCCACCCAAA	$(AC)_{22}$	NED
SCMA46	s_1_1NewScaffoldedcontig_181852	*TGTGGCATCTCATATTGTGC	CATAAACATGCGGAGCAGC	$(AC)_{21}$	NED