



Target and primer information for experimental round A.1: read ID corresponds to the read in the short read archive SRA010805, beside primer sequences PCR product length with and without primers is given, as well as the percent identity of the respective mastodon-loxAfr1 alignment, "# of hits isPCR" gives a number how often the respective primer pair anneals to loxAfr1, and a "yes" in the row "consensus for all taxa" means, that sequence information is available for all taxa. The last two rows show scaffold ID and position of the targets used in the MCMCcoo analysis aligned to loxAfr3.

target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
A001	EK3X9LI01BLRFR	TGGTCTCGAAGTCAGACAAGAG	TCAGGACTTGCCTGTTCACT	186	143	0.98	2	yes	50	16,857,885
A002	EK3X9LI02F3RBB	GCATTITGATTCGATGTTTGA	AAATITGAGATCTGTCCCAG	190	147	0.98	6			
A003	EK3X9LI02HKE1R	TATAGTCCAGGCTCCACGG	ATAAGCAGTCAAGAGCCCGA	161	121	0.95	0	yes	13	31,772,950
A004	EK3X9LI01DC8H2	TGTTGTAGGTGCCATCGAG	CGGAAAAGAGGAAGCCCTC	161	121	0.97	64			
A005	EK3X9LI01BHMHV	GCCCATGTCAATCAACAGAA	TGGCCCTCTCTATGTGT	194	154	0.92	93			
A006	EK3X9LI01A2011	AGGCGAGAATACGCTCAAA	GCTCCTACTCTGGGCTAT	184	144	0.89	435			
A007	EK3X9LI01C7BYB	TTTTCTGTGTTTGTGCATGT	AGTAATGGAAGAAATGATGAAGT	172	127	0.90	21	yes		
A008	EK3X9LI01CV00E	GAACACGGTITCCAGGAATG	GGGTCTGACAGAGTGGGA	161	121	0.90	3			
A009	EK3X9LI01C7XBW	TTTTCTATTCCTAGTAAGAACCA	CAAAACAATTTGAGAAAACAGTC	156	109	0.92	4	yes	11	58,944,724
A010	EK3X9LI01DQLE4E	AGATGAAAACGGGGAGGCTT	GCAGCAGCGGAATTTACTT	181	141	0.98	27			
A011	EK3X9LI01AQJCF	GCTTCATTCTGTGTGCGTG	ACTCTGCTGTGTGATGCTGG	136	96	0.98	8	yes	12	23,353,795
A012	EK3X9LI01BCGQI	CACTCCAGCACACCAGAC	GAGTGGGTTCATTGTCAACA	152	113	0.98	1	yes	4	2,618,296
A013	EK3X9LI02G5E9S	CAATGCCCTGAAACCAGTCC	GTAGGGCGGAGCTATGATGG	188	149	0.96	807			
A014	EK3X9LI01A1IP7	CTTCTCTGGGCAAGTCCA	CATCCTCCCAACCTTTCAA	145	105	0.87	0	yes	4	598,729
A015	EK3X9LI02JWLQA	GAGTACCAGGAGGGGGGAG	TCATCTCAGTACCAAACTTGA	192	149	0.88	1			
A016	EK3X9LI01EN54P	TGGGACCAAGCAGACCTTAC	CTGTGGCATGTGGAACAAA	151	111	0.99	4	yes	34	682,004
A017	EK3X9LI02I9G0E	CTGCTCTGCCCAACTTCT	CAGTCTGTGGGATGCTGT	177	137	0.98	2	yes	3	71,685,234
A018	EK3X9LI02GC7NK	CCATGGAGGACAGGTTTCCAG	AAGCGACTCTTCTCAGTCA	193	152	0.94	334			
A019	EK3X9LI01COK93	AACCACCATTGTCCACTTGG	CAGCTGCCAGCAACAATG	145	107	0.99	1	yes		
A020	EK3X9LI02F9G0Q	GAATAACATCAGACGGTGGC	TAGCTGGAAGCTCTTGCCTGG	173	133	0.97	0			
A021	EK3X9LI01CTJ2Y	GCTTACCACACACAATCCCC	AGAAATGACCATGAGCGGG	166	126	0.93	3	yes	3	18,742,916
A022	EK3X9LI02H02GU	ATACAGGAGGGATCCTTGGG	ACTCACATATCCCCTGGTGG	163	123	0.96	1233			
A023	EK3X9LI02GCTKJ	TGACATGTGCAAAAGAGCTTAC	TGTTCTCTGCTGCTTAAAT	149	109	0.96	269			
A024	EK3X9LI01EVLQJ	TGTCTCTCCCTCCACTCTC	GATTGGACTGGAAATGGGT	172	132	0.94	1322			
A025	EK3X9LI01C4P1K	GAATTAATTTGCCAATGACTAGA	GGTAGGGAAGCAACACTC	170	123	0.96	2257			
A026	EK3X9LI02FFWKW	CCCAGCACTTAAACAATCTTAAA	AACTAACATGTCAGCTTGC	198	152	0.98	3	yes		
A027	EK3X9LI01CDWFL	CGTGGGTAGAGAAGGACGAG	ATTATTCGTCCGGGAGG	133	95	0.97	800			
A028	EK3X9LI02IGAJD	CACAGCCAGAAGCCTCC	GGATCTGCTGAGCAAGGCG	158	120	0.93	1807			
A029	EK3X9LI02H3CND	CGTTGCTTGTGAAAGTGA	TCCTTGACAACCTCAATCTTTCTC	166	121	1.00	0			
A030	EK3X9LI02HH3QY	AGCAAAAATTACTCAAGTGGAAA	GTGAAAATGGAGCCAAAG	164	121	0.93	55			
A031	EK3X9LI02GL1UM	TGTTGAAAAGCAAGATGCTACT	TTTGCCAAACCATAATTCAA	150	106	0.93	270			
A032	EK3X9LI02G4ANS	AATAGGCCGGAAGGGAAGT	TTTTCTCCGAAAATCTCCGTT	156	116	0.94	5			
A033	EK3X9LI01B83XL	TGACTGACCAAGCAAGGCTC	GCAACATCATGATAAGTGGAGAA	195	152	0.97	1	yes	146	1,412,236
A034	EK3X9LI01AEV4R	GGTACCAAACTTGGCAT	GCTGTGTGGAGTTAGGGACC	170	131	0.98	1	yes	14	7,155,272
A035	EK3X9LI01A6LR5	CACCTTACTCCGTACTCCA	CACCTGAGACTGTGTGGCA	145	105	0.93	748			
A036	EK3X9LI01AHA1X	CATGAAAATGCTGTTAAAACCC	TCACTGTAATCTTCACTCTCCA	170	123	0.99	5	yes	3	65,357,915
A037	EK3X9LI01DFI3G	CAGTTGGTCACTGCGGGT	GACTGCTAGGCCCTTCTCC	149	109	0.94	1			
A038	EK3X9LI02IMKVX	AGGGATCAATGTTGTTTCA	TCITCCCACTTCTCAGAG	135	93	0.97	2	yes	9	48,548,100
A039	EK3X9LI02IRFTU	TCCCAAGTCAACTAGATACTCTA	GGAAAAGGCTCCTTCTCTGT	194	149	0.95	2			
A040	EK3X9LI02JSOT0	AAGGCCACTCTTGGCTTCT	GTTTGTCTCAAAGCTGGGG	174	134	0.97	2			
A041	EK3X9LI01AIALH	TGTGTGCAGGAAGATGTGTC	ATTCCGCTGCTGTTTGTAT	155	114	0.94	895			
A042	EK3X9LI01BE9T9	GACATCCAACAATTTTCAGGC	TGGAAGGTGCTCAGTCTTA	186	145	0.99	0	yes	23	26,582,346
A043	EK3X9LI02FIY9W	GAAGAGACTGGGAGAGCAGC	CACACTATGCTGTCAGGGCA	176	136	0.90	28			
A044	EK3X9LI02GFDDJ	GTGGGTCTACAATCACCCG	CACAGTGTGAAAGCGGAA	147	107	0.95	0	yes		
A045	EK3X9LI02I66QU	TGGACTGCAAAAAGAAATGA	CCATCTCATTAAGGCCCTTCT	190	148	0.96	11			
A046	EK3X9LI01A3SP9	GCTGCAGCTGCTTGAATAA	TGATGCAGTGGTTGAGGTGT	184	144	0.99	1	yes	29	18,322,968
A047	EK3X9LI01AZEP9	GGGACTCTAGGCAAACTCCAG	AAACTGCACCTGGCCATTG	151	110	0.93	1	yes	7	8,254,015
A048	EK3X9LI02GRG6Q	AGGGGAACCATGTCTGTAT	GAACTGGACAGCTGTGGTT	158	118	0.96	1	yes	86	2,349,909
A049	EK3X9LI02H25M7	TGTTGTGTTAGGTGCTGTGG	GACCTCAAGGATGGTGTG	154	113	0.87	15			
A050	EK3X9LI02JDDAK	AGGAATCGGGTGAAGTGTG	CCACCTAAAAGGGACCCAA	146	106	0.98	1	yes	27	20,268,499
A051	EK3X9LI01AX9UU	TTGTGATCAGAGTTTGGCG	ACACTCGAGGGGCTCAAC	191	153	0.95	1			
A052	EK3X9LI02G8P4Z	GTCTCTTCTGATGGTGGCT	CATGTGGAGAACTTCTTTG	157	116	0.98	2	yes	1	78,994,943
A053	EK3X9LI01E2Y6Z	TTGCCAACATCAAACTCAA	TGTTAAAACCAAGATGTCCAC	149	105	0.96	4			
A054	EK3X9LI01E21TS	CGACTCAACACATCAAGCAAA	TCCCTCAATTCACAGCAT	163	122	0.96	0	yes	37	16,375,505
A055	EK3X9LI02J0R29	GCTGAGCAAATAATCTGAGAACC	CTGAAGGCTGTGGTCTTTGA	168	125	0.97	0			
A056	EK3X9LI02JVJWB	TTTGGGTTAAATGGACAGCC	TTCTGCAATAAAGATTTGGC	147	107	0.99	0	yes	22	15,681,214
A057	EK3X9LI01DC6HA	AGCTCCAAGCCTATGCTGG	CTCGGCTGACTTCACTTCC	191	151	0.96	0	yes	75	5,427,047
A058	EK3X9LI01CQ7ZA	AACCCATCTGCGTACTGAAAG	TCITTCATTTGGGAAAGATTTGA	189	143	0.94	76			
A059	EK3X9LI01BDI18	GCCAGAATGCTCTTATGATGC	ATGCTTAGGCCATTATTTG	159	117	0.99	0			
A060	EK3X9LI02F0L3R	GCCAAAGTGGCAGCTTTTTA	TAGGAGGCCAATGAGAGCAT	172	132	0.91	5			
A061	EK3X9LI02HQFHE	TGGTTAAGAGCTCAGGCTGC	ACTCACTGCCATCGAGTCAA	134	94	0.92	20			
A062	EK3X9LI02JWOIR	TTTTGTTGGTTTCGGTGGT	GCTCCCAATGATTAAGTGT	177	135	0.95	5			
A063	EK3X9LI01BCKUW	ATGGCTGACGATGTCATTTG	CACACAGGTGAATGTCTTTGC	175	134	0.90	1			
A064	EK3X9LI02HHRV7	TAGCAAACTCTTGGCTGCT	CTCGAGTCACTCTTGCAGA	149	109	0.97	1			
A065	EK3X9LI01C7PXN	ATGGTGTGGGAGCTTTGAC	AGAAAACAGACTGCGTGCT	166	126	0.98	1			
A066	EK3X9LI01C28PT	TCTAGGGACTGGACCTCTCT	TGCATAAAAAGATGGCAATGAA	181	138	0.92	1			
A067	EK3X9LI01BV10S	ACTATCTGCCAGGGCAAC	GTTTTAGTGGAAAGGCTTG	183	144	0.91	4693			
A068	EK3X9LI01BBL1X	TGGAGGAAGCTACTACGGCT	GCACCCAGGAATATAGCAAAGT	170	126	0.97	89			
A069	EK3X9LI02II2C9	TCAGTTAAACCCACATCTGTCT	GCTCCCTTTCCTTCTTCT	202	159	0.94	3	yes	5	70,359,926
A070	EK3X9LI01AG83P	ATTTCTCTGGGCAGCGTGT	GTCTCTTTCTTCTGGCGCTG	174	135	0.91	31			
A071	EK3X9LI02HHLB0	CCAATGCCATTAATAACAGAAA	TTATGAAAGTGAATAGCACAGAAA	181	134	0.98	3	yes	0	116,134,150
A072	EK3X9LI02JM0Q8	CTGACGAAAGCGGTTAGAGG	CAAAGCGAGCTTACATTA	181	141	0.97	4158			
A073	EK3X9LI01C26R9	ACTGCATGTGCGTCACTTGT	CGTGGAGTACTGGCGG	155	117	0.96	1652			
A074	EK3X9LI02HUA09	GCTCAGAGTTTGTGACCCGT	CCGACATCCTTCTTCTGTC	169	129	0.96	749			
A075	EK3X9LI01DSV6G	CACCTGAGGGACTGAGTGTG	TTTGCTACAGAAAAGTCAAACA	171	127	0.90	4	yes	41	12,064,693
A076	EK3X9LI02FH2ZJ	CAAAATTTCACTGGCAATTCATCA	AGATCAGCCCAAGGGTTTT	197	155	0.95	3	yes	4	65,387,475
A077	EK3X9LI01CPQ0Z	GGACTGGAAGCAAAAACCT	GCTTAAGGCATTTGTGAAATCAT	206	163	0.99	3	yes	4	86,446,334
A078	EK3X9LI01C26GN	GCGGATTCCTGTGTATGTTG	TGCTGAGAGTGTGTGTGTC	167	127	0.94	6	yes	19	27,050,379
A079	EK3X9LI02H07QM	GCAGACTCTGGAAGCTGCTGG	AAAGGAGAGCACAGGCAAG	155	116	0.90	1848			
A080	EK3X9LI01B9LJB	ATAGGCCGAGTAGAGGAGC	ATTCTGGCCTGTGGGACTCT	160	120	0.92	768			
A081	EK3X9LI01DKF6W	GAGGCAATGTTTCCACCCC	ATGAAAGTATCGGGACCTTG	162	123	0.99	1272			
A082	EK3X9LI02GF929	AAAACACAGAGCCAAAGTGGTG	CAGATCTTGAATGGGCCAC	157	117	1.00	2	yes	6	941,096
A083	EK3X9LI01D541S	TCTTGTCTTGGGACGGATAC	ATGACGGGCTTCTTCTTCT	171	131	0.97	0	yes	69	2,270,628
A084	EK3X9LI01BVAL0	GCATGTGTGAGCTCTTCCCT	GCAGGATCTTCTGCTGCTC	148	108	0.97	2	yes	123	1,527,368
A085	EK3X9LI02FPCGC	GCTCCACTGTGTGAGTCAATCA	TGCTGACAGACAGAAAGAA	165	123	0.92	1	yes	173	542,484
A086	EK3X9LI01BLH35	ACACCTCTGAGCTTCCCTGA	TGCTGTGTGACTCTCTTG	154	114	0.98	0	yes		
A087	EK3X9LI02HI18H	AATTTGCAAGGCTCAGTGTCT	CTGCCGTTCTCTACTCAGG	169	129	0.95	1	yes	11	66,322,536



target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
A088	EK3X9LI02JBXZW	TGCTGTGTGCAAAAGCCTGAG	AACGGCAATCCCATTTTACA	154	114	1.00	1	yes		
A089	EK3X9LI02IOGIR	TGCAGGTATCAGGAAGACCC	TTTACTGCCTGCACCTTCGTG	185	145	0.89	1			
A090	EK3X9LI01AVFGZ	TACATTCGCCTACCTCCCTG	TGGGCAGGATTCATAGGAG	174	134	0.95	1	yes		
A091	EK3X9LI02HYK2I	CCTTCTGACCTCGGAAGTA	CATTTCACCCAGATCCAC	154	114	0.96	1	yes	48	3,590,814
A092	EK3X9LI02GY7B7	GTAGGCTTCCAGGGTGTG	CATGGAGACAGTCCCACCAC	148	108	0.98	1548			
A093	EK3X9LI02F4X94	GACTTCTCCTACCGGCTGC	CGAAGTACTACGGGGAAGCA	163	124	0.99	239			
A094	EK3X9LI01ET8NT	CAGACATCAGGATCTGGAGG	TCCATGGGGTAACTTTTGAA	161	119	0.99	2	yes	61	591,902
A095	EK3X9LI01C591E	GGGAAGCAAGAGGTCATTA	TGGGCTAGGCACACCTTAGT	177	135	0.96	10			
A096	EK3X9LI02ITBQL	TTGGAGCTTTGATGTCCAT	AACACCTTGCCTCTTAAG	167	127	0.96	2			
A097	EK3X9LI02JWQHI	ATGCCCCCTCCTGAGATAAT	TCTGCGGTACATAGGGCTG	170	131	0.96	1	yes	13	5,005,567
A098	EK3X9LI01A8R7J	CACCCATGGAAGAGCAGTC	CCTTATTCATTGTCCAGCATCA	180	138	0.99	1			
A099	EK3X9LI02IKMWQ	AGCAGGTGTTGAGTGTGTG	GTGCTTGGCCTAGGAAACAA	181	141	0.94	1	yes	44	3,564,342
A100	EK3X9LI01CU5LO	GAGGTTGCATCTGCCAC	GAGAGAGCCTAGAGACGGCA	168	130	0.90	515			
A101	EK3X9LI02IYRPJ	AGAAGTCACTGTAAAGTCGGAA	ACTGGCTTTTGGCAAAATCA	186	144	0.96	2	yes	4	15,013,685
A102	EK3X9LI01EAN2W	GGCTAGACATTTGGTTTCAGT	CCCTTGGCCATGCTGTGAT	176	134	0.99	5			
A103	EK3X9LI01DG80A	GGTGTGTGCTGAGAAGGTGA	ATTCGCTGCTGCTTTGTAT	143	103	0.94	1353			
A104	EK3X9LI01D826E	TTCAGAGTACTTCTGGCTCC	GCCAACTTTCAGACAGGGA	156	116	1.00	32			
A105	EK3X9LI02HUL5N	GGGGAAGAATCTAGGGTCCA	ACTAGCTGCGCACCCACTC	176	136	0.97	1	yes	11	7,758,960
A106	EK3X9LI01DD6LB	TCAGCTGATCTGAGTGCACAA	TACAGGATGCACGAGGCATA	170	128	0.95	5			
A107	EK3X9LI02JTI0F	GAAGCATTTGAAATAGTGCCT	TTGGACTTTTAAACCATCTACCTG	172	126	0.98	1	yes	34	1,459,684
A108	EK3X9LI02GWF6A	CACITGGCCAGGACGAAACAG	GGCCACACAGATCACAGA	180	140	0.97	23			
A109	EK3X9LI01CREZQ	GCAGGCACACAAGGGGCTCT	GGCGCGGGGCTAGATTT	133	95	0.93	1	yes	34	3,759,193
A110	EK3X9LI01D0Z43	TAGATGAAAACCCCGCATTCT	GCTGGGTCAACTAATTTGGAATA	183	140	0.97	0			
A111	EK3X9LI02HJ5E6	CGTGTGTTGGACGAGCTGTA	GCCTCTGGATTTGGTTTGA	171	131	0.98	1			
A112	EK3X9LI01D2RKE	GTCTGCTTTGAAGGGAGCAG	CCCATAGGGTTTCCAAGGAG	161	121	0.98	0	yes	75	7,727,987
A113	EK3X9LI02G11JT	GACCTCACTGGTCTTGGCTC	CTTGGCAAGAGCAGTGTTC	176	136	0.97	2	yes	53	15,437,941
A114	EK3X9LI02FWX64	CTAGTTTCTCCACAGCCCTCG	TTTTGGCTGAGCAATTTGG	175	135	0.98	1			
A115	EK3X9LI01ANZ5L	ATAAGCCCGCTACTCTTC	ACCGGCCACATTAATTTTT	150	110	0.96	15			
A116	EK3X9LI01BAG0E	GGAAAGTCAAGCTAATTTGGA	TGGGATGCAGAATTTTTCA	166	126	0.98	235			
A117	EK3X9LI01EFDHQ	CAGGAGCCAGAGCTTGGAAA	TCTGTGTTGCACTGTAGCC	178	138	0.99	1	yes	86	4,337,419
A118	EK3X9LI02ITWWD	ACCTTGAGCACCTTCCCTT	TCCTTAGTCCCTGTTGTGG	176	136	0.98	335			
A119	EK3X9LI01AOC2E	GCTGTGACAGTCTGAAATTTG	TTGCCGTTTATGTTGGTGA	159	119	1.00	1652			
A120	EK3X9LI01BVY8E	CCCACACTCACATCCCT	TTCACTGCCTGCCTATTC	145	107	0.93	70			
A121	EK3X9LI02F5KTB	GCTGCTTCCAGTCTCTTC	GACTTCAACCAGCCCTCTG	194	155	0.92	147			
A122	EK3X9LI01ETJ69	GTTCACACTCACAGCAACC	CTGCAAGACCCAGGAATTA	151	111	0.98	3	yes	3	37,511,028
A123	EK3X9LI02I0H9I	GTGGAGCGGCTTCTCTGA	ACGGATAGATTTAGTGGGT	186	148	0.99	1	yes	94	3,410,871
A124	EK3X9LI02IJEPM	CGAACCCAAGATTGGTAGGA	GGGCTTTTGCTAGTTCTGGA	171	131	0.93	9			
A125	EK3X9LI01EHT4U	TGATCAGGGCTCCTAGGTTG	TGTTCAAGTGCAGACTTTG	174	133	0.97	1			
A126	EK3X9LI01EBDG8	AACTAAAACAAGAGCCGCC	TCTCTGCTGAGACTGCC	189	149	0.97	1			
A127	EK3X9LI01BJV3L	TGCGATTTCTCAAATGAAAGA	TCATATGCTGCTCCTGAAA	184	142	0.95	4	yes		
A128	EK3X9LI02FXPPF	GGTTTGAGTCCATCCAGAGG	TGTGTTCTGTGTGTGACCA	165	124	0.92	4	yes	190	544,216
A129	EK3X9LI02IM99N	CTGACCTAGGCTGCCTCTG	CAGAGAAGCCTCAGCCCC	169	131	0.88	279			
A130	EK3X9LI02H1ZVD	TCCCATGTGGTCTGACAGT	AGGTTAGTACCCACCCCTCC	161	121	0.88	2			
A131	EK3X9LI01C1TEE	ATAGCCTGTTCCAGGAGGC	CCTTGTAGGCTGAGGGAAAC	163	123	0.97	1			
A132	EK3X9LI02JZRK0	TCCAAGTCAATTAAGCCGCAC	TCTCAAGACATTAGCCAGTGA	150	108	0.96	52			
A133	EK3X9LI02F6FN8	TTCTGATCTATGGCTCGGTG	TTATGCCCTTTTGAAGGGGG	163	122	0.96	1	yes		
A134	EK3X9LI01DOC2A	TGGCATTAGTGGTGTGTG	TGCCAGGAATGACAAATAAA	173	132	0.93	507			
A135	EK3X9LI01C8N0Q	CTGTGTTTCCCAAGCAAGT	AAAGGAGCTTTCTCCCTC	157	117	0.98	4129			
A136	EK3X9LI02I36U7	CTAGCAGGCTGGGGCTGT	CCCCCAGAAAGTCACTTTGT	184	146	0.97	0			
A137	EK3X9LI01EDFZR	ATGTCAGATGGATCCTGGCT	AGGTTCTCATGAGCACAATTA	163	121	0.94	1232			
A138	EK3X9LI02GH9IC	CCCAGCCCTAGACATT	GGTTCAAGGCTCTCGCTG	166	127	0.93	3	yes		
A139	EK3X9LI01DWNEV	CAGCAGTGTCAAGGCGAGT	TGGCCTTCACTTCACTTACC	181	141	0.97	701			
A140	EK3X9LI02INCWL	AATCTTAGCTCCTCAAAGCGC	TGGCTGACCCCAATACAGTA	159	118	0.97	1	yes	9	48,345,794
A141	EK3X9LI02GMTFT	CCTCAAGTCTGAGGACCTT	TTTTAACTCTGAGCCCTC	170	130	0.95	1	yes	69	9,882,985
A142	EK3X9LI02GNGBB	ACTCTGCAAGGCGGTACATC	ATCAGATAAATACGCCGAC	165	125	0.99	1			
A143	EK3X9LI02GKZUQ	TTATTGGCCAGTGTGAGG	TTGAAGAAGAATGGGGCATC	189	149	0.96	70			
A144	EK3X9LI02GYYTB	ATGGCTGCAAAATTAAGTGG	GATCGGACTTAGGAGCCC	184	145	0.98	1	yes	5	24,165,720
A145	EK3X9LI02G8NUG	CCCCTCTCTGTGTTTGTGA	GATGTGTTTCAATAAGACTCAGTA	153	108	0.95	5	yes	3	70,689,859
A146	EK3X9LI01E5Q3R	TGAGTATCTTCCACCTGGC	CGAGCCAGCAAAATAGGTAG	162	122	0.96	1	yes		
A147	EK3X9LI02IQHZQ	AACATAGGCCCGAACGGT	CTTGTTTCTGACCGGT	161	125	0.91	61			
A148	EK3X9LI01BADUP	AGGGCCCTAGGATTTTCAGA	GCTGGCTACACTGAACCCA	194	154	0.96	3	yes	72	1,311,673
A149	EK3X9LI01CEAIR	GTCCTGATGGGAACACAAC	TGTCTGGGAATGGTTCTGT	174	134	0.94	100			
A150	EK3X9LI02FF96G	GGTTCCTCATGAGCAAAATTAAG	GATCTGGCTGAAAGCAGAG	152	109	0.96	17			
A151	EK3X9LI01E0TRO	TGTACGTGGCAAGAGGTTGA	AAGGAGGACACAGGCAGAT	191	151	0.92	1527			
A152	EK3X9LI01EPXIX	TCTTTGAATATGGTGTGGTGA	TCCAAGGAGTGGTCTCTCTG	169	125	0.93	6			
A153	EK3X9LI02INS8N	GGAGAAAAGTGGGATGCGA	CATGCTCACCAGTATCATTT	193	151	0.91	196			
A154	EK3X9LI02FZCNA	CCGCAATAAAATGAGTCTGG	GCTAGCTGAATGAACGGG	176	135	0.95	3	yes		
A155	EK3X9LI02G11L8	ACACTGGAGCACAGGCAAG	CACGTACCTCAAGGTGCTCA	183	144	0.93	0	yes	8	42,387,873
A156	EK3X9LI01CD6WH	GTCCCCAGTCTGCTCT	ATGGGGGCACAGTGTTAAG	183	145	0.93	2	yes	97	3,528,068
A157	EK3X9LI02GUVFP	AGGCAAGAATAGAGGAGCCC	TGCTGTGGGACTCTATTGG	183	143	0.88	780			
A158	EK3X9LI02GM7LC	CTTGGGTCAAGTGCACCTTT	GAATCCACAATTTGACACCA	151	111	0.91	6			
A159	EK3X9LI01B76F7	CAGCGCTCCTCGCCGAC	GCGTCGCCAGGGGACACCAC	147	108	0.96	10			
A160	EK3X9LI02IKVA4	ATAGCAACCTTGCACAAC	GACACAGTGGCTGCAACAAT	162	122	0.96	0			
A161	EK3X9LI02F8K36	ATCTTGTCTCCGGGAATCG	CATACGCTGAACGGAGATT	190	151	0.92	1076			
A162	EK3X9LI02HLJ9S	GGTCAGGCCACCTTAGTCT	CAAGGATTTTCAATTTGCTTGG	156	115	0.99	14			
A163	EK3X9LI02I2Z3L	CTGTGTTGGCATTTCTCTGTC	ACAAGTCAAGTCACTGTGCACAT	172	128	0.95	1503			
A164	EK3X9LI02FL5QN	AACTCGGCATTTATCCGTTG	TCCGCTACATGAATTAAGCAA	189	148	0.90	0			
A165	EK3X9LI02GFCPO	CATAATCCCCAGATATGCAG	TGCCCTGAAGTTACAAATGATG	163	120	0.98	1	yes	32	18,723,414
A166	EK3X9LI02JUKUM	ATGGCTGTTTGGAAATGG	AGCAGGCTACTGGGGTACTG	160	120	0.97	3			
A167	EK3X9LI02I4GH3	GCCAGAGAAATCTAGCAA	AATTGGCAACAGCCTCACTT	146	106	0.94	1			
A168	EK3X9LI02GZ29S	GGACTGATCCCTCTGACAA	CCTTTGAATTTGGTGTGG	164	124	0.97	0			
A169	EK3X9LI01CFY6E	CAAGTCTTGAACCTCTCCC	CCTTCTGGTGAACCTCTGACA	162	121	0.92	3			
A170	EK3X9LI02I8SJM	GGTTGAGAGGAGGTTGGGAT	AATACGTTAGGGGGCGGAC	187	149	0.97	3			
A171	EK3X9LI01CDP0M	CCTGTACGTGGCAAGAGGT	AAGTCACTGAAGCCCGTGT	177	137	0.94	1734			
A172	EK3X9LI01B941C	TAAAGTCCCGTCCAGAGAA	GACACCGTTCGGGTCTATTC	164	124	0.95	557			

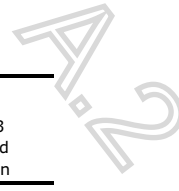


target ID	read ID GenBank	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
A173	EK3X9LI01COG9U	GGACAAGTAGTCCAATGTTGCC	TCGGGAATATGCTCTCAACA	157	115	0.97	1	yes	7	41,888,057
A174	EK3X9LI02FPNPZ	CACAAGGTAATTATGAGCCCAA	ACTGCTGCTGCTCCTTCA	156	114	0.98	185			
A175	EK3X9LI02HKA5F	CCGAGCAGTACCTCAGAAGA	GTCAACAGGCCTTCTTCC	181	142	0.94	130			
A176	EK3X9LI02JYAKH	CGGGGCTCTGCTATTTCAG	GTCCCGCAGACCAGATAG	164	127	0.96	22			
A177	EK3X9LI01DNN7S	TCCCCATCCTTTCTCTTGA	TGACCAACCAACAAACAGG	186	146	0.96	2			
A178	EK3X9LI01A38EU	CAATTGTGGAAACATCAAAACTG	CCATTGGCTAGTCCCAACAT	160	117	0.96	3	yes		
A179	EK3X9LI01DLN0U	GGCTATGGTGTCATCCACC	GCCGAACGAAGGAGAAAATC	184	144	0.97	1	yes	20	38,002,468
A180	EK3X9LI02GECMC	TGACAGATAAAGGGCAAGTGG	TGCCTCCCTCTTGATTATGG	151	110	0.95	3	yes	53	5,839,203
A181	EK3X9LI02JOYBY	TAGGATCTCCCTTTGGGTTG	TGTGCAGGGTGTATGTGCT	185	145	0.92	1			
A182	EK3X9LI01BKX6S	AGGACTGGAGCTCGGTAACA	CAAGGTGATGGAGTACCCTGA	170	129	1.00	0	yes		
A183	EK3X9LI02JX96K	GCTGGTGAGGAGTGAGCTTC	TCTCCCTAATGTGACAGCC	161	121	0.96	95			
A184	EK3X9LI02IDCDD	GCTTAAATGAGCCATCCCA	CAGTCTCGTGTCTCCTGGT	165	125	0.90	11			
A185	EK3X9LI01D32G7	AGGTGAGAAAGCCCGAG	ATTCTTGGCCGGGAATCTC	165	127	0.96	6			
A186	EK3X9LI01BIKBU	CCCCAGGCAATTAAGCTTCT	AGTCTGCATCATAGCCAGGG	187	147	0.95	0	yes	83	4,825,814
A187	EK3X9LI02FRKY4	GATGTCTCAGGATTTGAGGGA	CACCCTGTGCATTATTGGT	180	140	0.98	1			
A188	EK3X9LI01DOV2U	ATTTCTGGCAGTTCCTGTG	GGAAGAAGTCCAAGCCACAC	184	144	0.94	152			
A189	EK3X9LI02JN1NO	AGCCCTGGAGCAGTGTTTA	ATCTCCAGACAGGAGTTGCC	140	100	0.97	2			
A190	EK3X9LI01A00Z0	GACCCAAGTGACCCCTCTCT	CATGGAGCTGCAGTGAGTTG	151	111	0.96	1	yes	22	39,379,180
A191	EK3X9LI02ILR5V	AACTGACTGACAGGGTGC	GGGATGGTCCCATAGATCAC	173	134	0.96	0	yes	14	6,513,068
A192	EK3X9LI01BZ6AP	TATCCCCAATGGTTTGTGCT	TGTTGTTGTTAGTTGCCACAGA	175	133	0.98	7			
A193	EK3X9LI01BF8WX	CCTGCTGTACGAGGCAAGAC	TCAAGATTTTGCCCTCTGCT	157	117	0.97	639			
A194	EK3X9LI02HHLCV	GGGCCTAAGGCTTCTTCTC	GATTTTGTGGCCAAGGACAG	186	146	0.96	1165			
A195	EK3X9LI01D9AK9	ACTTGTGTCCGGGGATAGC	AGGCCGAAGGAGTAGGTGTT	174	135	0.91	1	yes	3	20,250,612
A196	EK3X9LI02I4J7D	CCCCCTATGGGATACCTTGA	GCAAAAGCTCAGACTCTTTGTAA	139	96	0.95	1	yes		
A197	EK3X9LI01ES0QL	TCCTGATGCTGCATTCTTCT	CATTCAAACAGAACACGGG	157	116	0.92	82			
A198	EK3X9LI02GB3Q1	TGCTGCGGTTTTTCTTCTT	TGTAGGGATGAAAGCCCAAG	179	139	0.96	130			
A199	EK3X9LI02I3BZM	CACAGCTGAGGGAAGAGAGG	CACATGGCCTAACCAAGTTAAT	181	139	0.98	3	yes	9	82,155,052
A200	EK3X9LI02I9BMY	CTCAGCCCAGGAACACATTA	CTCTCAGCCCTCATGGCA	177	139	0.97	1	yes	28	6,496,546
A201	EK3X9LI02J0BXR	TGAAAGAGGTAGAGGCAGGC	TAAAACCACGGACCTTTTGG	153	113	0.98	0	yes	23	11,204,208
A202	EK3X9LI02GX158	GAAAGCAAAGAAGTCAACCTGA	TCTCCAACACCACAATTCAAA	144	101	0.88	1			
A203	EK3X9LI02HICTO	CGGGGTTAGTTCAGGAGG	AACAAGTGAATCGATCACATACAT	179	137	1.00	1288			
A204	EK3X9LI01B6NX6	TGAACATGTAATCAAGATGCATTG	GCCGTTTACGTTGGTGA AAA	187	143	0.87	36			
A205	EK3X9LI01DH4GJ	GGTGATACTCTTGCTAAATAAGTGG	TGCTGTAATAAAAACCATTTCTCTC	162	112	0.96	5	yes	3	24,751,797
A206	EK3X9LI01EYOLN	CGAGGAGACTGCCATTTT	GTCCCAACGTCATAAAACC	148	109	0.94	1346			
A207	EK3X9LI01AG3Z2	TGCCATACACTCCTGATTGC	TCTTGGATCAGGTGGACACA	164	124	0.97	6			
A208	EK3X9LI01CGJW5	CACCCTGCAAGAGAGGAGAG	GTGTTTGGACTCCCAGGATG	197	157	0.92	0	yes	8	60,121,961
A209	EK3X9LI02J346Q	AAAGGCTTCTTGGGGTAGGA	TGACAGCATGTTTTCAAGTTTCT	180	137	0.97	6			
A210	EK3X9LI02F0NW3	ATAGGCCCGAGTAGAGGAGC	AATTCTGGCCTGTGGGACT	161	122	0.90	955			
A211	EK3X9LI02HV00D	CTATCGTGAAGGCTCGCTT	GAGTCTCCCTTTCACCGAG	171	132	0.93	89			
A212	EK3X9LI02HAW50	AAGTAATGGCATGCGGAATC	AGAAGCCCTATCCTTCCAA	171	131	0.97	2	yes	43	4,093,612
A213	EK3X9LI02GE17J	AGGCAAGAGATGCTGAGTGG	CACACCCTGGGAAAGGCTAC	144	104	0.97	2182			

A2

Target and primer information for experimental round A.2: read ID corresponds to the read in the short read archive SRA010805, beside primer sequences PCR product length with and without primers is given, as well as the percent identity of the respective mastodon-loxAfr1 alignment, "# of hits isPCR" gives a number how often the respective primer pair anneals to loxAfr1, and a "yes" in the row "consensus for all taxa" means, that sequence information is available for all taxa. The last two rows show scaffold ID and position of the targets used in the MCMCcoal analysis aligned to loxAfr3.

target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
A214	EK3X9LI01A6YMK	GAAGCCAGGTTCTCAGCAT	TCCATTAACCCCAACAGA	161	121	0.97	2	yes	97	479,593
A215	EK3X9LI01DAICP	CCGGCTTAACCCAGTAGTTG	TGTGGCTTTATGCAGATTGG	183	143	0.99	2	yes	110	1,274,053
A216	EK3X9LI01BAUW5	GGATGAATAGGGCAATCAA	TGAGTTGGCCCTCATCAAAA	177	137	0.92	1	yes	13	16,032,688
A217	EK3X9LI01C10D3	CAGGACTCGCTTCTCCACT	CACACACACACTGCT	176	137	0.99	1	yes	92	2,467,920
A218	EK3X9LI02J0Z1A	GAGGTCTCACCCTCTCA	GGCAGTCACTCACAGTCCT	182	142	0.92	2			
A219	EK3X9LI01CI39V	CAGCTTCCAGCCAGGTCTA	ATGGGAGTTGAACCAAGCT	148	108	0.99	2	yes	84	5,711,232
A220	EK3X9LI01EW96T	ACAGTCGCTTACCTCCTG	TAGGCAGGGAATCTTGAGGA	197	157	0.89	1	yes	53	8,525,170
A221	EK3X9LI01AZE43	CCTCCCTCTCTAAAATCTCC	CAGGAAGACAGAAAGAAAGAA	151	108	0.98	2			
A222	EK3X9LI02JH9W9	TCCCTCTAGCCAGATGCTGA	AAAGCCTACAGCCCACTCA	168	128	0.96	0	yes	0	59,325,869
A223	EK3X9LI02FUTMC	ACTTGGTGTCTGTGGGAAA	TGGCCGACACAATCTCTCT	154	113	0.97	1	yes	7	81,324,383
A224	EK3X9LI01DAMAT	CCAGTTTCCAGTTTGGTGA	CTCCATGACAGTCAAAAAGTGC	175	131	0.90	2	yes	30	24,735,311
A225	EK3X9LI02GKBWR	AGGGCGCCGCAAGGACT	CTGCCCTGCCCTACCC	148	112	0.95	1	yes		
A226	EK3X9LI01BJT69	TGGAAGGTGTGATGACTGA	GAGAGCACCAACCAAGATT	160	120	0.99	2			
A227	EK3X9LI01DR5D4	AGGAAGGCGCTGGAAGAATA	GCTGAGTCTGTGCCTTCCTT	170	130	0.99	1	yes		
A228	EK3X9LI01CSRAY	CTTTTGGCATCTCCGAAGTA	CCAATCCCTCATCTGGTGT	189	149	0.88	1			
A229	EK3X9LI02GJUXQ	GCAAGACAGTAATAACAGGCA	GAATTTGGACTTGGGAGACAGA	196	152	0.98	1	yes	15	50,273,886
A230	EK3X9LI02F7W3P	GACCCCTCCAGGATCTAACG	GCCAGGAAAATGCCAAATTA	187	147	0.96	0			
A231	EK3X9LI02FMHVI	CAGGATCAGGATCAACTTGGGA	TAGTACTTGGCCCAAGCAGG	162	121	0.98	1			
A232	EK3X9LI02J8V9	GTGTCGCATCTCCCTTAC	CCAATTCACITTTGAGCCT	171	131	0.97	1	yes	12	31,489,001
A233	EK3X9LI01C2U0	GCCTTAGAACCTTTATGACACAAGA	TCCTTCTCACTCGCAGGAT	172	127	0.96	1	yes	18	26,323,125
A234	EK3X9LI01BQPYQ	TCTTATCTCTCTCCGCCC	CAGTTTGGAGTTTGTGGGG	166	126	0.98	1	yes	28	12,171,137
A235	EK3X9LI01EUZ9D	ACGGGCATGTGTAGGATTT	GTGGCCTCTAGCTCCACTCA	173	133	0.94	1	yes	25	12,455,405
A236	EK3X9LI01AHPM0	GGACTGGGTGGTGTTCATTC	GAACTGTCAAGGATTTGACCT	163	122	0.95	1	yes	57	4,986,525
A237	EK3X9LI02H570X	TGGCAAACCATGAGAATCA	TCAGGTGGATGTCCTGAGT	166	126	0.95	2	yes	12	52,770,539
A238	EK3X9LI02ICHTZ	CAGTGGATTTGACCCCTAT	TTTCTAATAATCACTCCACTGCC	151	107	0.98	1	yes	137	501,356
A239	EK3X9LI01AZKE2	CAACAACAACAGCACCAACC	GGTAGCCTGACCTCACACT	171	131	0.95	2	yes	12	34,447,175
A240	EK3X9LI01BNVRE	CAGATTGGCCAAATGCAAG	TGGATTGCACCTCAACCTAA	168	129	0.94	1			
A241	EK3X9LI01CS96W	TGGAATAAGTGAGCAAGAGCA	GCACCTGAGTAGAAGATGCAA	158	116	0.96	2	yes	5	2,099,580
A242	EK3X9LI01DBT28	GTCTATGGTCTCGGGAAATA	GGACTGTCCATCCCCAC	168	130	0.90	1			
A243	EK3X9LI02GXGIC	TGGTCCACATCTGCCTTCT	GCCTGACTAATGATCAAAATGTT	184	139	0.99	2	yes	2	96,260,218
A244	EK3X9LI01C5BXG	GAGATGATCAGCCAGGTTTC	AAGGTGAAAATTCATTAATCCAGA	171	126	0.98	1	yes	31	3,190,302
A245	EK3X9LI02HHH91	CCCTCTGTGATGTCAGTGT	TGTCAGTTCGTCTGGGAAC	201	161	0.93	1	yes	55	10,557,275
A246	EK3X9LI01CUAQF	ACCATTTCCTGTTCCGCTCA	CCCTGAGGTGCAAAAAGT	200	160	0.96	2	yes	101	4,362,706
A247	EK3X9LI02HHXNO	AGGCATCCAGAACTGCTCT	AGTGAAGCCTGTGCTGGG	142	105	0.98	2	yes	12	20,904,563
A248	EK3X9LI01C88FU	ACCAACCCATTGCCATCTA	AGTGGTTAAGAGCTCGGCTG	151	111	0.96	0			
A249	EK3X9LI01C41XA	TAGCAGCTTTTGGTTTGCCT	ACAAGCACACTGAGAGATGTGT	182	140	0.97	2	yes	97	2,757,461
A250	EK3X9LI02H0GIE	CCTTCAGAAGCCCTATGAAA	ATCTTATCCGATGGGGGAG	123	93	0.97	1			
A251	EK3X9LI01EVMCB	GTCCGTTCTGACTCATGGTG	AGTCCCTAGATTGCTGGGT	197	157	0.99	1	yes		
A252	EK3X9LI02IU90W	AACAACCCAGGGTAGCCACAA	TTCTCCTCTTAGGGGGACT	159	119	0.94	1	yes	19	9,704,021
A253	EK3X9LI01DMCVW	AGACCACAGCTTCAAGTATGG	TTTCTTACTGCTGCTTCCA	167	126	0.99	0			
A254	EK3X9LI01DE35N	GGACTTACAGCAGTAAATCAGGA	ACGTTTGGGACTGCAGCATA	167	123	0.94	1	yes	68	3,515,241
A255	EK3X9LI01E3ANB	ACTTGGGAGCCCTGTTTAG	CTGGCCAGAAAGGAGGACTA	168	128	0.98	1	yes	0	90,319,470
A256	EK3X9LI02HCP5E	AGGGAACCTGCCAGAAATCCA	GATCTGCAGAGTCAAATGCC	150	110	0.94	0			
A257	EK3X9LI02IX36P	TATAGCTTGGGGGCTTTTTC	TGCAGAGGAGAAACAGTTTG	177	136	0.98	1	yes	6	19,705,800
A258	EK3X9LI01B5YLH	TAAGTCAGGCTCCTTTTGG	CTGATTTCAAAGCCCAAGCA	178	139	0.96	1	yes	18	25,385,818
A259	EK3X9LI01BYU3U	AACCACTATGCCACCAGGTT	CTGGGAGTCTAACCCACCAC	189	149	0.95	0	yes	8	62,591,951
A260	EK3X9LI01B2CXX	GTATGATGTCTTCCGCGAGG	TTTGAATTGTGTTTGGGG	180	140	0.92	2			
A261	EK3X9LI01C04JU	CTCGAGGGCTCGGCTCGG	GTGTGCTCCGAGGATGCTG	188	151	0.96	0			
A262	EK3X9LI01D78CW	GCTAATCGCAAAATACGTAAGCA	CAAATAATGATATCACTGCC	182	142	0.97	1	yes	4	100,302,354
A263	EK3X9LI01A36MQ	TGGATACCAGAGGTGTCTTCAA	TGAGGCAGAAAAACATCCC	190	148	0.89	2			
A264	EK3X9LI01C31CQ	TGTGGTAGCATGGCTTTATGG	CATTGAGAACTGAAAGACTGGT	172	127	0.98	1	yes		
A265	EK3X9LI01AXUGS	GGTTGAACCTGAATGAGCGT	GCACGCTCCTGGAGTTCTC	166	127	0.97	1	yes		
A266	EK3X9LI02IP80Q	GCCTCATGGGAAGTAAAAC	ATGGATCAAAGGTGACGACC	155	115	0.96	1	yes	16	15,855,345
A267	EK3X9LI01DW9XM	AAGCAATGTCTTACTACTGGTGA	TGCAACAAGCAACAACATGA	138	94	0.96	0	yes	14	50,048,147
A268	EK3X9LI01BA2KU	CTTTTCTCTGAGCCTAGCCC	TCCACCATCACTTCAAATGG	137	97	0.97	2	yes	11	27,188,476
A269	EK3X9LI01EQMZH	ATGAGCTGAGCTGGAAGCAT	GGAAGACTTCGTTTCTTG	136	96	0.99	1	yes		
A270	EK3X9LI02GJE0M	TTTCTGCGGCTTCTCCTAGT	TGCAGGTTGACATTTAACGA	154	114	0.98	0	yes		
A271	EK3X9LI01AG73T	TCTCAGTGTAGGGACCTATGG	CCTTCCAACGGGATCATTTTA	156	116	0.91	1	yes	4	89,117,088
A272	EK3X9LI01DSCFL	TCCGGTACAGGCTTCTCTGG	TGTGTGTCTCAGATGACTGGGTG	177	114	0.98	1	yes	11	9,150,261
A273	EK3X9LI01E0MTG	AAGTGGCAGCATCGAGAGAC	CTCTGCCACAAAGTGCCT	184	146	0.95	0	yes	45	4,466,640
A274	EK3X9LI02HISXL	CTTCCCTCAGAGGAATAACCA	CTTCTGTGAGCAACTGCCT	203	162	0.95	1			
A275	EK3X9LI01EMD03	AGTAGACAGTGTGTGGGGC	CTCTCGTGGTGAAGGCAC	174	136	0.96	1			
A276	EK3X9LI01C61ZJ	GCACCCTGGGGAAGGTATAG	CTGCCTGAGATTTACTGCGA	171	131	0.98	0			
A277	EK3X9LI02F2KAX	AGGTGCTGCTCATCTGAGC	GACAGCGGCAGACAGAT	170	134	0.93	0	yes	5	79,715,844
A278	EK3X9LI02GYCYN	TTTGTGATCCTGCAAGGTCG	TTTTTCTGTATGCATATATGCTGT	156	111	0.94	1	yes	23	18,612,615
A279	EK3X9LI01BL8TH	CTCCAATCAACAGTGAACCCC	CCACCGGAGGCAGATAGG	142	104	0.96	0	yes	8	78,972,721
A280	EK3X9LI02IM216	TACTGATTGGAAAAGGGGGG	ATGGCGGAGCCAAATACAG	159	119	0.92	0	yes		
A281	EK3X9LI02JRGTA	AGGAAGAAAGGCTGGTGTAT	GCTGCTGCATGCTCACTCT	164	124	0.98	0			
A282	EK3X9LI02IDB6R	GGCTGAGGTCCTCTTGTGT	TTTTTCTCTTATCCCTTGGGA	170	128	0.96	1	yes	18	34,832,978
A283	EK3X9LI02GUA05	ACGCTTGGAGCAGACAGTGT	TGCACACTTGAAGCATCTCT	159	119	0.98	0	yes	90	5,612,392
A284	EK3X9LI01E0S03	TCAAAGACACAGCCCTTCA	GCCTTCTCGGTTTCTTTCAG	181	141	0.89	0			
A285	EK3X9LI02HCAW0	AAATGACAGAAAATTTGGCCT	TAAACCTTCTCTGTGGGG	152	111	0.99	1	yes	27	33,846,061
A286	EK3X9LI01APTFF1	TCTTCTCACAGTCCCTTTT	GCAGCATCTTGGAGTGACA	175	135	0.87	1	yes	14	51,320,467
A287	EK3X9LI01DKQC1	CAGTCTCCCTGTGCTCTGG	GCTGTAGAGTGTGGGCACA	190	150	0.97	0			
A288	EK3X9LI02I5B92	GTGGAGCGCCTTCTCTGA	ACGGATGAGTATGTGGTGGT	186	148	0.99	1			
A289	EK3X9LI02H7DWQ	CCAGGATGACTTTAAGGGATTTT	TGTAAGTGTGTAAGTGGGAG	182	138	0.99	1	yes	2	91,796,234
A290	EK3X9LI01EL68Y	GGGTACAGGCTTACCGATG	GTAGGCCCTCCAGCACC	179	140	0.92	0			
A291	EK3X9LI02FGJW8	CAGGAATCCAGCAGCTAAA	GGTGTGAGCAACCACTGAGA	185	145	0.96	1	yes	26	25,202,384
A292	EK3X9LI01CEPH4	TGGCCACAGGATGACTCAG	GACGAGCATCTGACACCAC	186	147	0.96	1			
A293	EK3X9LI01ESOP1	CACCTCTGGCTCCTGTG	CCCTTGGCCACCACTAAA	176	138	0.99	1			
A294	EK3X9LI01EFXA0	CCTGGCTCTGAGTAGAGGATTT	CCTGACCTTCAAAAATCACCA	200	157	0.98	0	yes	31	2,675,757
A295	EK3X9LI02I1W1WN	GACTTGTCTGGCATTTCCCT	AGGGTGCACCTTCAAGGAT	196	158	0.94	1			
A296	EK3X9LI02HERS2	TATCTTCTGCGCTTCTCT	TGGTATGACCCCACTCTG	175	135	0.97	1			
A297	EK3X9LI01D261C	TGGTTTGAACAAGCATTAA	ACCAATGTGGGAAGGATGGT	150	110	0.87	1			
A298	EK3X9LI01EKU3Q	GTGGGAAACAGTATGGTGG	ACCAGCCATAAGTCTGCTC	174	136	1.00	0			
A299	EK3X9LI01EGAXM	ACCCTCTCACCAACCT	ACACTGGCTGAAAGACCCAG	165	127	0.95	1	yes	8	44,369,514
A300	EK3X9LI02IFNCG	CCTCTCCGTGATGAGCCTAC	CCCCATGTTGATGAGCGAAA	157	116	0.96	0	yes	48	1,875,618
A301	EK3X9LI01DWCAZ	GATCTACTTGGTTATAAGCCTGC	CCACACAATGATGCTTGA	165	120	0.96	1	yes		
A302	EK3X9LI02G0MB9	TCTGGCCTTAGTGCTTTGT	AAAGGGTCGCCAGTTCAAAT	165	125	0.95	0	yes	96	1,758,331



target	read ID GenBank	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
A303	EK3X9L102GXPG5	GGTGCACCTTAGTCTTCAAGG	GCAACATCATGATAAATGGAGAA	189	145	0.92	0			
A304	EK3X9L101AP2KK	ACACGTCTTCGAGTGCAGAG	AAATATAACCCCAAGCAGGCC	178	138	0.93	1	yes	2	67,326,190
A305	EK3X9L102F2W14	ACCTTCCAGGACTGGTATGGAT	CGGGCCAGACTAGGTAAGGT	155	115	0.95	1	yes	31	11,774,220
A306	EK3X9L101B6D8U	TGGAAATCCAGTGGAAAGGAG	TGAGTTTGCCAGTAGTGCCTT	166	126	0.95	1	yes	55	11,051,588
A307	EK3X9L102JVNVO	TCCCTGGCTTCCAGCAT	CTGGTAATCCGTCATGTT	174	134	0.98	1			
A308	EK3X9L102H2Y5V	TGTCCTGACCTTCTCCAGT	TATATTTACCGCACCCCGG	177	137	0.94	0			
A309	EK3X9L101BV7SL	TTCACCACTATAGCAACCA	CTGTGATGTTCTGGAGCC	185	145	0.92	0	yes	17	30,851,947
A310	EK3X9L102HEM7N	GTCCTCTCCACCCCTGCTG	AGGCCAGGGTACAACCTTA	188	148	0.91	1			
A311	EK3X9L102SHAS	CCTTTGAAGGGTGGCTAATG	AGAAAAATGTGAGCGCAGGAG	156	116	0.98	0	yes		
A312	EK3X9L101BATY4	GTCATGGGCAGAGAGGTAC	CTGCCGTGCTCTCCACT	164	126	0.99	1	yes	5	11,867,225
A313	EK3X9L101D26AB	AAAGCCCAATAGATTAGCATTG	ACCACCAGACTAGAGCCC	147	104	0.98	1	yes	13	9,741,987
A314	EK3X9L101C5E1W	GGGTACCCTCTATGGCCCT	GGAGGTGGGACTCAGAGGA	152	113	0.98	0	yes	19	37,637,919
A315	EK3X9L102I7G1A	ATCTCTGAGCTCCAGGGG	AACATCAGTTCCAGGCACAA	185	145	0.96	0	yes	3	2,970,325
A316	EK3X9L101B101E	AAGCAGAAAAGGTGTCAGGG	TCCAAGTTCTCACTACTTTCAGCA	175	131	0.98	0			
A317	EK3X9L102H6HJK	CATGAAGTGGAGGCTGAAC	CAGCTCGTTTCTGCTCTCC	168	128	0.96	1	yes	123	1,762,385
A318	EK3X9L102JWOZV	AAACCCCTGGTGTGTAGTGG	TCTAAAACTCAACTTAGTGCCG	164	121	0.96	0			
A319	EK3X9L102GZSQ8	CCCCGTTGGTTATGGTAATG	CCAGCACCAAGGCTAGT	170	131	0.98	1	yes		
A320	EK3X9L102JNZU2	TGGAACCAGCTGAACATAGG	AGGCTCCCTTATTTTCAA	144	104	0.98	1	yes	114	1,404,004
A321	EK3X9L101BN7F6	GAGATTACCCCTTCTCCCTG	GAGCTGGGAGGTGCAGAT	164	125	0.95	1	yes	16	34,910,293
A322	EK3X9L102HJXEE	TTGGGCATGAAGGCTATTGT	GCTCTGCTCAATCTCTGAAC	168	128	0.96	1			
A323	EK3X9L102IHQWE	AAGAAAGCCTGCACCCCTC	TCCAGCCAGGAGTAGTAGCC	180	140	0.98	1			
A324	EK3X9L101C3BAK	AAATTGAGAAAGCCAAAGCA	TCACTTGGGACATGTAGCC	180	140	0.99	1	yes	13	28,007,158
A325	EK3X9L101BJ5ZM	AGGGGCTAACCATGTCTCTC	GCAGAAGCCAGGTAGGTGG	171	132	0.88	1			
A326	EK3X9L102I1MLE	GCATGCTTGTAGTAACCTTTTTC	CCACTGTGCACAAGTCACTT	189	145	0.94	1	yes	73	4,835,113
A327	EK3X9L101A6DKU	ATCAAGAGCAGTGTTCGGG	TCTTCTCCAATCCGTATGC	173	133	0.94	0			
A328	EK3X9L102I1GYF	TCTTCGCAAGTAAGGCGAAA	GCAGATAAGCAGCTGTTTCC	167	127	0.95	0	yes	132	1,763,628
A329	EK3X9L102HAYZJ	CTCCTTGCCTGGCTTCCAC	CTTCTTCCGGCCTCTCC	151	114	0.90	1			
A330	EK3X9L102H06PN	ATGTTAGCCCTGATGACCC	ATTCTGGTTCACTTCCCCC	165	125	0.98	0	yes	140	582,722
A331	EK3X9L102GJELN	GCAAAATGAAATGAGCACTTG	CTCAAACTCAACCCATGTGA	180	139	0.99	1	yes	0	64,893,892
A332	EK3X9L101D79PM	TGAAGGCTCCAGTATACCA	AATGACACCTTGGGCCTGTA	170	130	0.98	0	yes	6	64,713,931
A333	EK3X9L101ATT8N	TTTTTGGAGCTTATGACGGTT	CTGTTTCTTCCCACTCCCA	154	112	0.98	0	yes	102	646,152
A334	EK3X9L102JCVGO	CTGGAGAGAACAGAGCCAC	GCCTTCTGAACCTTCTCCCTCA	191	150	0.95	1	yes	48	17,101,706
A335	EK3X9L102I1RUJ	CTTCGCAACACTGCATAAA	CACCTGCACATCAGACAGGCT	150	110	0.98	1	yes		
A336	EK3X9L102GKDNX	CGAGCAGTACGAAACAGCCT	GCCTCGCTCATGACATAAT	171	131	0.95	1	yes		
A337	EK3X9L101D9NMD	AGAAGTACTGTTGGGCTGC	TCTCTTCTCCAGCAGTGCC	152	112	0.99	1	yes		
A338	EK3X9L101C3W4S	AGCCTGTTGACAGCTGGAAT	TGGATATGTAATAACAGGCAGAAA	188	143	0.96	1	yes	5	66,366,555
A339	EK3X9L102FW3PT	AGCGACACATCTGTTAAGCG	TGATTCACACCCCAACTCCA	161	121	0.97	1	yes	11	10,327,481
A340	EK3X9L102HFC44	TGACCCAGGCACTGGTATT	CCTCTAAGGAGCACTCTGGC	189	149	0.93	0			
A341	EK3X9L102I1H3N	TAGCCGTATTCTGGGAGTGG	CTGTGGCTCTCTATTTGGGA	172	132	0.94	0			
A342	EK3X9L101D26Z5	TCTGCTAACCAAAAGCTCGG	GACCCAGGCTTGTGCTAAT	177	137	0.95	0	yes	49	3,448,120
A343	EK3X9L101CV1K0	GGCCCTTAGTACTTCTCTATT	CACAGTTCAGATCCCTCAG	198	156	0.96	1	yes	33	23,320,683
A344	EK3X9L101BQZYB	CTTCAATTCATGGCAGCTC	CTTGCCTATGCATTCCACA	171	131	0.99	1	yes	11	21,526,888
A345	EK3X9L101AHLK0	AGTCATTTTCACTGCGGCTC	TTTCTGGCCTTGGAAATTTG	172	132	0.94	1			
A346	EK3X9L101CGF48	CCCTGTGGCATAGAGGTTA	AACCAAAACCAAGCTGTTC	160	120	0.94	0			
A347	EK3X9L102HHBR7	GAGGGCTTTTTCATTACACAGG	TGGTGGTGCAGTGGTTAAGA	182	140	0.94	0			
A348	EK3X9L102I5TH7	CAAGAAATCAAAAGCAGCTTG	TTCTTATTCAITGTCCAGCTT	167	123	0.97	0			
A349	EK3X9L101AGNDJ	TGGCGTAGTGGTTAAGTGCT	CAAACAAAATGAACAGGGC	192	152	0.91	0			
A350	EK3X9L101DOOZ2	CTGGAATCCCATTCTTTG	ATTGCTGATGACGGATGGAT	142	102	0.96	0			
A351	EK3X9L101C4567	TAGCACAAACCAACCCAA	AAAAAGCCCTGCAATCATTT	185	145	0.97	0	yes		
A352	EK3X9L101CK5FS	ACCATGGACTGCCAAAAGAG	GGCCCTCTGCTTACCAGG	161	122	0.95	0			
A353	EK3X9L101EEV1K	GGGGGATTTCAGAAAACAGG	GGATTCAGACCCGGCTTTAG	162	122	0.96	7			
A354	EK3X9L102ICLCR	CGGCCATTTTGAATGATCT	TGCCAAGAAGTTGGAAGACA	166	125	0.93	7			
A355	EK3X9L101DY4ZE	AGCCCAAGGTAAGCAGAA	CATCTTTGTTCTCTGGCAG	149	108	0.99	2	yes	19	44,681,437
A356	EK3X9L101AOG35	TATCTTGGCAGGAAGTTGG	GAAAAGAGAAGCAGGGAATGA	146	105	0.97	2			
A357	EK3X9L102GVD2Y	ACCATCCAGCAATTCACCTC	CCATTCTCACCCCTCACAT	164	124	0.97	2	yes	4	201,844
A358	EK3X9L101BZFRW	AGCCTTCAGGCTTCTCTG	CATTTGCAAAATGGACACCTT	166	126	0.92	2	yes	72	7,242,987
A359	EK3X9L102JGWHQ	ATACGCTGAAACGGAGATTG	GGGGCTCTACTTCTGTCAC	167	127	0.97	14			
A360	EK3X9L101CSTA6	GGTAGCACTTCACTCAGCCG	GCACGCCCTCTGTAATTTT	166	126	0.98	2	yes	9	72,773,335
A361	EK3X9L102F2DRH	AACACACCATCAGACCAACC	GAGTCAGGCTGGAGATTTGG	194	154	0.98	4	yes		
A362	EK3X9L101CT3DB	TACCAGGACTGCCAAAAG	GCATGGTATCTCTTCCAGG	146	105	0.96	6			
A363	EK3X9L101AULJ8	GGTGTGCTCTGATGCTGAA	AATGGAATGAAACACTGCC	168	128	0.97	5			
A364	EK3X9L102H1MD3	TGTATTTCCATGTTGCTCC	TGTCAAAACAGAAACAGCCA	151	111	0.95	2	yes	18	474,687
A365	EK3X9L101ES7D3	CTCGGGAAGCAAAATCTCG	TGTTTGTGTTTTCAGGTTG	196	156	0.95	6			
A366	EK3X9L102FHQAQ	GGACCCAGCCTGTACAGATA	TTGGTGGGCTTCAAAAT	201	162	0.93	2	yes	58	7,346,355
A367	EK3X9L102I6LIN	ACTGCCAGAGCCCAAGTAA	GTCCTTTTCCCACTTCT	173	133	0.97	2			
A368	EK3X9L102JX8L2	GGAAACGCACTGTGTTGCA	GATTAAGCATATGTTCCCAA	165	122	0.97	2	yes	8	76,341,113
A369	EK3X9L102GWT1S	GACCTCTCCTGTTGGCTCAG	GTCATTGGCCGACATCTTT	191	151	0.96	23			
A370	EK3X9L102JBOOT	CAACATTCAGCATTTCAGC	AGTAACTTTCAGTGCCG	156	116	0.90	9			
A371	EK3X9L102GSG4U	CCTACCAACTGACTGGAAGA	TTTTCTGGGAGTTCTGGTTG	171	130	0.91	13			
A372	EK3X9L101DD81C	TGTGTGATGCAACTACAAGG	AGCGGCCAGAAACCAACA	155	115	0.98	17			
A373	EK3X9L102GJN13	GGCCTGTGACTCAGCACTTT	TGCACCACTTTCATTTT	191	151	0.94	2	yes	57	5,155,828
A374	EK3X9L102HM0KE	TGCAGTCTCCAGCAACAT	TGGCCTTGGAGAAAGATAA	189	149	0.92	6			
A375	EK3X9L101CNIJ4	ACCCTCGACTTACCAAGCA	CCATGAACTGCCAAAAGAAA	167	127	0.97	2			
A376	EK3X9L101DYFL4	TGAAATGTGCAAGAACCCTGG	CAATGGCTCTGTGTTCTCT	185	144	0.97	7			
A377	EK3X9L101DFG2C	GCGGAAGATTGATGACAAGG	TGCTGCTAAGCAGAAATACCAAC	159	114	0.88	5			
A378	EK3X9L102F97Q0	AGCCCTACAGCAGCTTCGG	GTAGGCTGACAGACCTGGCT	183	145	0.92	8			
A379	EK3X9L102JNZE5	CCTTTGAATATGTTGTTGGC	TTCTCTGTGATACTGTCCAAA	157	113	0.98	11			
A380	EK3X9L102IIZCH	TCTCTGGCACTTCAAAGGC	TGATGGAGAAAAGGGTCTG	169	129	0.99	2	yes	186	543,457
A381	EK3X9L101CQR52	CGAGACTTCGCTTGCACAC	AATGAAACTGCCCCAGTCC	166	126	0.94	9	yes	12	1,357,538
A382	EK3X9L102HT88N	GGCTGTTGACTGTTGTGAA	TTGGGTTTAAACACTTCTGA	154	113	0.95	1	yes		
A383	EK3X9L101DKL12	TGACAAGCTAGGAGCTGTGAA	CAGGGGATTTGGCTGAG	144	105	0.96	5			
A384	EK3X9L102G2N3R	TTGAGCACTTCCCTTTTG	TGAGTAGTGGGAGCTTGG	156	117	0.94	6			
A385	EK3X9L102I7ONA	TCCACACTTATCCAGAGGG	TAGAAGCTGAGGGGAGGTT	136	96	0.96	1	yes	146	1,412,413
A386	EK3X9L101BNWGF	CCCACCTTACAGGCTGAGG	TTTGCTTTAATAACCCAGACA	192	149	0.98	1	yes	74	2,692,157
A387	EK3X9L101EVFH1	CAAGTTGTTCCCTTGTCTGA	CCACTGATTGTGATTTGACTG	167	124	0.89	1	yes	10	24,477,942
A388	EK3X9L102INT62	TGTAAGCCACCTGCTTCAAT	ATTCTGAGCTGGCCATCTT	168	128	0.96	2	yes	41	6,205,165
A389	EK3X9L101EW5JW	GGCCGCAATTGATGACATTC	ATGTGGCTGTCTGTAACCCC	142	104	0.98	2	yes		
A390	EK3X9L102FEYRB	CTCACGTGCGGAGAAATAGG	TTCTGATCTTTTACGCGCT	192	152	0.99	1	yes	39	17,610,294
A391	EK3X9L101BR66V	GACAAGGGAACCACTCTGG	CAAGTTTTCTGGGACTGGA	170	130	0.98	1			
A392	EK3X9L101DS72Y	ATTGGACGAGACAATGGGAT	TACCCCTAACTGCTCTCCC	204	164	0.89	2			
A393	EK3X9L101EGYU4	GATTGTGTGGCTCCCAATG	ATGGCTCAGATCCTTGCACT	176	136	0.94	1	yes	74	4,368,719
A394	EK3X9L102I8NU3	AACCAACCTGTTCCGTTG	AGCCCTGGCAGACTAGTT	155	115	0.97	8			
A395	EK3X9L101BROU1	ACAATTGTGAGGATGGACA	TGTGGCTGGGTTGTTGTA	157	117	0.91	10			
A396	EK3X9L102H9XCH	GTTCCACACTCAAAGGGGG	TGGAGTGAAAAGACACATGG	162	121	0.97	2	yes	15	33,021,381
A397	EK3X9L102I4R9E	GGAAATGCTTTCGCAACT	AGGTTGAGCAACACTGATGC	185	145	0.97	2			
A398	EK3X9L101EJ2CR	CAGAAATCCCACTGATCTCA	GCCTGGTCTGCTCCCTC	179	140	0.93	1	yes	15	22,588,500

A2

target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
A399	EK3X9LI01EU20A	GACTAAATGGGCACACCAGC	TCCATTTCATTTTGGACAATTTC	168	124	0.97	7	yes	18	2,631,071
A400	EK3X9LI021SJEZ	CTCCAGCCCCCACTTTT	GGTCTTGGAGGAAGGAAAGC	192	154	0.98	4			
A401	EK3X9LI02FGAXJ	TCCAGAAGGGACATGGTAATG	CTCCTGAAGCCGTGTCTCTC	176	135	0.95	1	yes	4	66,397,755
A402	EK3X9LI02HLL0U	GTGAAAAGCTGCATGCTGAA	CCAAGTTACTCCAGGGGTT	163	123	0.91	7			
A403	EK3X9LI02HN8L1	AAGGTGACCCTATGTAAAGC	TGCAATTTAGGCTGTCACTTG	182	140	0.97	1			
A404	EK3X9LI02GSBFJ	AGTGGAAATGTGGTGGGTGAT	TCCTGGGTTATTTGGGTTG	144	104	0.99	2	yes		
A405	EK3X9LI01CSU10	TCCAGAGCCAACACAGACAG	TCATTCTCTGTTCTCTGTCACTTTC	177	132	0.98	19	yes	14	2,295,033
A406	EK3X9LI02HCWKX	ACTCTGACTGTGTGGCCT	TGTGCAGAAGGACAACCTCAA	172	131	0.98	3			
A407	EK3X9LI01BR75A	TGCTCTCCAACCTCAGAGT	ATCTAGCCCTGGCAGCAGT	148	109	0.90	2	yes	4	25,548,875
A408	EK3X9LI01CG92M	TCCTAGGGCCCTGACTGAG	GAGGTGTCACTGAGGCCG	177	140	0.99	1			
A409	EK3X9LI0214LVA	CACGTACATCCACCCTCT	CGAGTGGTGGTGACAGAGAA	175	136	0.98	1	yes	1	55,090,741
A410	EK3X9LI0216U6P	TAGTTCCTCTGTCCCCAGC	TGGAAGCATGATGTAGCAGC	174	134	0.98	1	yes	1	26,114,494
A411	EK3X9LI01DY40E	GAAAAGTTTCTCCGCAAAA	TATGGCTTTGCCAGGATTTTC	143	102	0.99	1			
A412	EK3X9LI01D7D35	GAAATAAGCTGATGAGAGGAAACC	GGACAGAGAGCCAACACAG	181	137	0.96	1	yes	5	71,661,785
A413	EK3X9LI02HY1W8	GCCTGTCTCAAAGGCTCAT	AGAAGCAGAAAGTGGCAGT	172	132	0.93	24			
A414	EK3X9LI01CR2K5	TGAGAAATGTGGGATAAAGGG	AGCCACTCTCAACTCACTGGG	167	124	0.96	1	yes	43	7,175,416
A415	EK3X9LI02FZ53G	TACCAATGATGCAGCAGCC	CGAGATCCCAAGAAGCTAGTG	146	105	0.92	6	yes	22	13,947,214
A416	EK3X9LI02F0KPQ	ACAAATCACTGTCTCTCACAT	TGTTGCATCTCCTGTCTGG	186	142	0.96	10			
A417	EK3X9LI02FK9G5	CCCTCTGCACAGCTGAAAC	CTGGAAACAGACAGGAGCCG	176	137	0.88	4			
A418	EK3X9LI02ICEX4	AGATGAGCTCCCCAGGCT	TGAATGTTTGGCTATTGGCT	158	118	0.97	3	yes	6	46,290,310
A419	EK3X9LI01AXH9B	ATCGTTGGTGGCTATTGTGC	CCTGATGGATCAGAACAAACA	165	123	0.95	3			
A420	EK3X9LI01CN0BK	GCAGGGAGCATCAAAGAAG	TTTTTGGCAAGCCCTCAGT	153	113	0.92	3			
A421	EK3X9LI02F7KM5	CACATGGCTATGCCAACAA	TTGCTTTGAATGATCTCCAG	172	131	0.92	5	yes	72	2,595,307
A422	EK3X9LI01CWJLJ	CTTCTCTGGAGCTCTGGTGC	AAATCCGTTGCTGTCTGAGTC	161	121	0.87	7			
A423	EK3X9LI02FQPRM	CCACAAGTTTCCCAAATATC	CAGGCAAGAAAGAAAGACCTTG	189	146	0.97	3	yes	9	16,167,935
A424	EK3X9LI01D0RFU	GACCAAGGAAAGGTCATGGA	CCACTTTAAGACCCAGACGC	182	142	0.94	4			
A425	EK3X9LI01BLD35	GTCAGCTACAGCGACTTCGG	GACCTGGCTGGTGGGGTC	174	136	0.89	8			
A426	EK3X9LI01ANCQQ	ACTGGCTGATCTTTCCGGA	CCCCACATGTCTGTCACTG	175	135	0.90	16			
A427	EK3X9LI02FKADD	AAGAATTTCCATCATCAGCTT	GAGCTTCCAGAGCTGTTGT	197	155	0.99	13			
A428	EK3X9LI02JA4H2	GGGAGAGAACACGCAAGTC	GCAGACTCTGGACTGCTGG	152	113	0.92	5			
A429	EK3X9LI0212D2J	GGGAGGTCAGCCTAATGGGA	TGGGATGTGGAAATGTTTTCA	166	126	0.98	21			
A430	EK3X9LI021S177	GCTGCACTCTGCTTATCAAGC	CCATGGACTGCCAAGAGAAT	165	122	0.97	3			
A431	EK3X9LI021HJ80	TCATTCCAACAGAACAGAGGA	TGCAGGTTGTAATATGTCTATCC	156	111	0.98	26	yes	1	93,100,472
A432	EK3X9LI02H27IT	TGTCAGGGTCAACACCAGTC	CTTTCTTGTGGGGAGGT	143	104	0.98	3	yes	15	49,396,357
A433	EK3X9LI02H51B0	GCGCACCTTAGTCTTCAAGG	CGAAGAAAAGTTGAAGTTGCA	172	129	0.91	5			
A434	EK3X9LI02HK8QF	GGGAGAGGTCCAAACCTGCAC	ATTTCTTCCAGCTGGTTGGC	167	127	0.94	3			
A435	EK3X9LI01C7EDZ	TGATACTGGTGAGGAAATCTTGAA	CATGGTATATTCATTACAGGGCA	179	132	0.91	2	yes	88	692,684
A436	EK3X9LI01EG202	TATGTACTGGAGCCCTGGTG	TACCCAACCCATTGTCATCC	166	126	0.88	7			
A437	EK3X9LI02HV0XV	TAAACACTAGCAAGGGGGCCA	TCTGTTGTACCCAGGCATCA	181	141	0.94	2			
A438	EK3X9LI021XGA3	ATAGGGACCATTTCTTGGC	AAAGTGGCCATGATTTGGAG	166	126	0.94	2	yes	81	531,445
A439	EK3X9LI01A679X	TGGATTCCACAGCAAAAGCA	AATCCTCCAACTCACAGGCT	179	139	0.98	3	yes	43	2,511,708
A440	EK3X9LI01BCLJT	TGGGTGACATCCAGCAAGT	TGTCCAAAACACTGATTAATAACA	191	147	0.96	6			
A441	EK3X9LI02GSTFP	CAGAGGGAAGGTTGAAGGAA	GGCAAACTCACTGGCTGCT	180	140	0.92	2			
A442	EK3X9LI02HBFQX	TGTTCTTACTCTGTCTTAGCTCCA	TGTTGATTGCTCTTAGAGTGTG	173	126	0.92	3	yes	23	4,746,893
A443	EK3X9LI01B6FSD	TCITTTTACTTCTCCAGTAAACCA	ATCTGAGGGCTGAGCTGCTA	152	107	0.96	3	yes		
A444	EK3X9LI02GB207	TGGAGTAAATTTCCAGCAG	CCTACGCTCCATTTTCCCA	145	105	0.87	2			
A445	EK3X9LI01AXKEV	AGGCAACAAGGACAAAGCTAA	AAAGCAACAATAATGTGGGG	154	113	0.98	3	yes	54	1,474,214
A446	EK3X9LI01AT135	TAGCGTTTGTCTGGACCC	CCTGAAGCCTAACTTCAACTGT	175	133	0.93	4			
A447	EK3X9LI02G13TL	TTTACCCACATGAACAGTGA	GCCTTTGAGCAGTTGATGTT	165	124	0.91	2			
A448	EK3X9LI01EV5K6	CATTGTCCAGTTGTGAGGA	GGCATCAGCATTGGAAGAAG	177	137	0.98	2			
A449	EK3X9LI01BMRPD	CTGCTAGTGAGGGAAGGCAC	GTAATGACCTCAGCCGCTT	180	140	0.98	3			
A450	EK3X9LI0214W2R	GCAGGCCTACATTTAAAGTTCA	AAGGGTCCAACTGAATGTC	148	106	0.99	2	yes	87	1,987,911
A451	EK3X9LI01D1YJ5	AGCACITGGAATTTCCCTTCA	TTCAAGTGAAGGAAGGCTCTC	176	134	0.91	5	yes		
A452	EK3X9LI02HI63G	GGGTCCCTGGTGTAGT	TCTTCTCTCCCTGAGT	183	144	0.99	26			
A453	EK3X9LI02H1M9M	TGTGCCATCTCACAAATCAT	GAATGCACTTTAGAAGCGAGG	184	143	0.97	10			
A454	EK3X9LI01CFAU6	TGTATGGTCTTGTCTGGAGC	TACATTAACACTACTGTACAGGGA	181	136	0.95	2	yes	1	53,667,867
A455	EK3X9LI01BU2XL	GGGGTTTACAAGTAGGAAGTTCA	CCATGCTGACATTGAGGATAAC	187	142	0.99	26			
A456	EK3X9LI021BDAS	TCTCTGATCTGTGCTACTAAATTGG	AACCCCAAAATTTGATCCAAG	181	136	0.96	2	yes	59	4,864,244
A457	EK3X9LI02FUTXB	AAAACATAGTGACTTCCCTGA	ACCATGAACTGTGGCCTCT	171	129	0.97	4			
A458	EK3X9LI01D2PV3	AGGTGAAGTATTGCTGGGTG	GACACACTCAGCTCTCAA	148	107	0.98	14			



Target and primer information for experimental round B: read ID corresponds to the read in the short read archive SRA010805, beside primer sequences PCR product length with and without primers is given, as well as the percent identity of the respective mastodon-loxAfr1 alignment, "# of hits isPCR" gives a number how often the respective primer pair anneals to loxAfr1, and a "yes" in the row "consensus for all taxa" means, that sequence information is available for all taxa. The last two rows show scaffold ID and position of the targets used in the MCMCcoal analysis aligned to loxAfr3.

target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
B001	FBUJGPD11GZ51K	CGGAGGGGTCATATAGAGGG	CTGCTCCAAGCCATACCTA	279	239	0.97	0			
B002	FBHG2QE12HD6LJ	CACGCCCTAGTCTTCAAGGTG	GCCAAAAGTGAGTGAGGAGG	299	258	0.95	2			
B003	FBHG2QE07EDHIV	TGAGTGAGACAACAGCATCCA	GATCTGATCCACAACCAGTCA	253	211	0.89	2	yes	98	2,965,472
B004	FBHG2QE16JWWC2	GCCTTTGCATAGTCAATAAAAACA	TATTTGTGCCGTTCCAAAG	258	215	0.97	0			
B005	FBUJGPD11GXNVE	ATCCTGGCTAAAGCAGAGA	GGATTAATTTGCTCAGCATCG	285	245	0.92	0			
B006	FBHG2QE09FLWZM	CCTTGTCTGCAGAAAACAAA	AGCAAAAAGGTACACCAGGG	269	229	0.97	1			
B007	FBUJGPD16J0WE2	TGATGAACAGCCACAGACA	CAAAATCTGGATGGTAATCAGTGT	247	203	0.90	1			
B008	FBHG2QE09FMB5Z	CCCAAGGGGTATCGTTACTT	CCTGGCCCTTTTCTAGTCT	257	216	0.99	1	yes	58	11,372,720
B009	FBHG2QE16JSW1W	GAAGCTGTCCAGGACGTGTGT	GACTGTCACTTGTCTGGAGCC	267	227	0.91	0			
B010	FBUJGPD12HGXD	TTACTGGTTCAITGGAGCCCT	TTCTAGTCAATGTAAACCGAATGA	221	177	0.90	1	yes		
B011	FBUJGPD14I1254	CTGAATGTCTATCCAGGGC	CCCTGCTGATTTTCTCTTG	255	215	0.97	1	yes	58	11,826,278
B012	FBHG2QE11GSC9C	GGAGTGAGGAAGCTGGTTTG	ACGCTGAGTTTGTGGGAAA	249	209	0.92	1			
B013	FAGAMMR16JW3QK	CTGGTGCAAGCCAATAGTGA	CCTGCCAGCTCAACAGTA	229	189	0.91	2			
B014	FBHG2QE07D419I	TCCTGGAGGGAACTTCACTG	GTCACCTCTGTGGCTTGG	255	215	0.97	1	yes	1	12,744,769
B015	FBHG2QE16JWYU8	GGAGCATGCTGGTGTACTTC	GCATTGCGTTAGGCAAACT	263	222	0.91	1			
B016	FBUJGPD12HN83D	GGCAATAGCAAGGGAAGCTG	GCGATCCAGAGTCAAAAGG	224	184	0.96	1			
B017	FAGAMMR16JSX5T	TGGCTTCGAGAATGGTTTTTC	AAAGAGAAGGAGGCCACAT	252	212	0.97	2	yes	36	23,445,001
B018	FBHG2QE12HLRU	ACACAGGCAAGCTTGAAC	ATATGGGATGGGATGAG	241	204	0.96	2			
B019	FBUJGPD10F6XEK	AAGGCACCATGAATTTGGTC	GTGAATCTCTCGCTGCTC	252	212	0.95	2			
B020	FBHG2QE08EPYQS	TCACAACCTGGACCAATAAGCA	TTGTTTGTCTTTCACATGCC	261	220	0.93	0			
B021	FBHG2QE12H88LV	TCCCATTGTCTCAGTTTCC	TTCCAACCTATAGGACCCCT	242	202	0.95	0			
B022	FAGAMMR16JUS2T	ACTAGTCTGGCAGAGTTGGTTT	TCAGGGTCCAGAATGAAAGG	244	202	0.99	1	yes	7	83,494,142
B023	FBHG2QE12HMIZ6	CAGTGAACAGCCCATATATCCA	GAGAGGCTCACTGTCCAGG	244	201	0.92	1	yes		
B024	FBUJGPD12HFLXV	AGAGTCCCTCTCTGTTCTGACA	TACCGCCTGAGTCAACCTCT	242	199	0.95	2			
B025	FBUJGPD11GYZSZ	TTTATTTTCATCTTATGGAGGCA	CCAGCAGGAATGTGCTGTT	243	200	0.97	2	yes	19	35,638,888
B026	FBHG2QE07EC90R	CTTGTATGCTCCAGGAAAT	GCACTGTCTATTTGGCCCTC	245	205	0.99	0			
B027	FAGAMMR16JY40W	CATAGGGACTGTGGGACA	TGTCATAGGCTTTGGATGT	232	192	0.99	1			
B028	FBHG2QE07D41FW	TTGTGGCCACTGTCAATGAG	GGTTCAGTGTGGCTGCACT	257	217	0.96	2			
B029	FBUJGPD11GPK4Y	ATGAGCTGCTGGAAACATCC	GCAAGTGTGGAAACAGACAAA	241	201	0.96	2	yes	10	20,603,229
B030	FBHG2QE09FJ6P0	TTGATACTGACTCTGGGGA	GCAACCGTATAGGGCAGAGA	233	193	0.92	2	yes		
B031	FBUJGPD10GCK4V	GCAAAACCAACCTTCAAATCCA	GTGGTTTGACACAGTGGCTG	238	197	0.96	2			
B032	FBHG2QE11G06BN	AAAACAATCAGCACCCGAAAG	TGGATGTCTCAGGCTCTTCT	240	200	0.98	2			
B033	FBHG2QE11GXV6K	AGTTGGTGTTCACCCAGG	CCAGCCATCTGGTAAGAGCA	231	192	0.97	1	yes	28	34,196,601
B034	FBUJGPD14I07WJ	GATGATCCCGTAGCTGGGA	GGAAGCACTCAAGGAAGGAA	242	202	0.95	0			
B035	FBHG2QE16JZZ3C	TGGCTTGGACTCAAAGGAAA	AGCAGCTCACCCCAAGT	242	204	0.94	1	yes	9	77,702,870
B036	FBHG2QE09FOE7E	CACAACCTGAAAATGGGCA	GCGTATTCGGAAGACCTGTT	261	221	0.98	2	yes	84	991,369
B037	FBUJGPD16JWU00	GGGGATATCCACGCTGACT	GATGATTGAGGTGGGGAATG	245	206	0.99	1	yes	31	18,100,580
B038	FBUJGPD11GZYE3	CCACCACTCTCTAGGGTCT	TGATGAGCCCATCTGCTGT	223	184	0.96	1	yes		
B039	FBHG2QE11GW4A7	GCCAAAGCTAGGCCAAATA	TCCTGGGCAAAACCTTTTA	241	201	0.88	1			
B040	FBUJGPD14I0UNS	CTGTCACTGTTGTGATTTGTC	GAGCTGAAGTGAAGGGATCG	218	176	0.98	1	yes	29	28,748,390
B041	FBHG2QE07D82HF	GTACTGCCTGTGGTGTGGG	ACAGCTGCCTGCACAACT	213	174	0.98	2	yes	32	27,727,719
B042	FBHG2QE14IYSKF	CCCTTGTGGCAGCCACT	CCATGGACTACCAAAAGAACG	221	182	0.91	0			
B043	FBHG2QE06DG3P0	GGCAAGCTAGTCGAATGTT	GCTCAGGTCACTCCACTTT	233	193	0.97	2			
B044	FBUJGPD13H5NWL	CCAGGGACCTCTGTCTTAGC	CTGATCAGCTTGTATTGCTCC	241	200	0.99	2	yes		
B045	FAGAMMR16JSCSH	CCCAGACTGGCTTACCTCTG	AGTGGACTGCTGTTTCTCTG	232	192	0.98	0	yes		
B046	FBUJGPD12HL41T	CCCACCCACCACTTCTTCC	GGGTCCAGCCAGGCTCTC	224	186	0.98	0			
B047	FBHG2QE09FTUFS	CTACCTTGTAGCCCTGTGGG	TGGCAATGATTTAGAAAGCTTAGA	239	195	0.98	1			
B048	FBHG2QE12HNQFY	TGCTACCTTTGAAGCTGATTG	CGCTCTTGTTAATGCTCACA	227	185	0.99	1	yes	34	14,004,436
B049	FBHG2QE12HNFYE	GCTTTGCAACTCCAGTAGG	ACCAATCTCAACAACCCAA	220	180	0.95	2			
B050	FBUJGPD14I08KG	CTTCTGGCTACCCAGCTC	CCATGTGTCATCACATCCCT	244	204	0.92	0	yes	72	8,627,248
B051	FBHG2QE14I0W8D	CTTCAAGCTCTTCACTTTCA	CAAGGAGCAGTGTTCAGACA	238	194	0.94	0			
B052	FBHG2QE06DPH8U	GGAGTGTCAAGGATTTCAATTT	TTCTTATTCACTGCCAGC	226	183	0.89	1			
B053	FBHG2QE10F9B25	AGGAGTCCAGTTCGGGCTC	CCAGGTCCGAAAGGTTGTA	233	193	0.87	1			
B054	FBHG2QE15I9HEY	AGCACCAACATCACCCCTC	CATCAACAACAGGATGCC	230	190	0.94	1	yes		
B055	FBHG2QE15JFTE6	GGATGCTGTTCCCGTATTA	AGCCCTGTTTGTTGAACGG	232	192	0.99	2	yes		
B056	FBHG2QE15I9ECF	AAACGTATACCATGTGCCAGG	AGTCAGGTAAGGCATCGGA	217	177	0.96	2	yes		
B057	FBHG2QE07EA7D4	ATGGTTAAGCCGTTGGCTG	CGTTTAGCATGGATTGCGTA	221	182	0.91	0	yes	0	94,946,559
B058	FAGAMMR16JY0BL	TCTTTCACCTAAAGCAGAAAA	TGATGGCACCTAACAAACA	255	215	0.98	2			
B059	FAGAMMR16J28Z2	GAGGAGACTCTTGCTGCCAT	GGCTGCTGTGGCTTACTTTT	250	215	0.97	0			
B060	FBHG2QE09FK8Y2	AACATCGCCAGGAAACAG	GACTTTCATCGCTTGACAGATG	237	197	0.92	0	yes	0	95,646,240
B061	FBHG2QE14IQCGK	TACTGGTCACTTTGTGGCCC	GGGCTCTCTGCTGTTCTCT	227	187	0.98	0			
B062	FBHG2QE12HEX4Q	ATTCCCTCTGAGTCCCTTA	AAAGGCACACATAAGCAGGG	242	202	0.96	1			
B063	FBUJGPD16J0V4R	TTCAAGCTGTTTCAACAAGAGA	TATTTGAAGCCCGGCCATA	237	196	0.98	1	yes		
B064	FBHG2QE07D6YR8	CCCTGAGCACTCTATCCAC	CAAGGCTCTTGAACTAAGGG	225	184	0.99	1			
B065	FBUJGPD13H8C94	CCTTTGACGACAGATTACCC	TTAACGGATCGCAACCTTAAT	229	188	0.94	1			
B066	FBHG2QE12HEX4Q	TGCAGGTTGTTAATGGGTCA	TGTGCTCAGGAGGACCTGTA	215	175	0.96	1			
B067	FBHG2QE16J219W	TGGACCAATAAGCCACATCA	AAAATACCCAGGATGGGTCA	220	180	0.90	2			
B068	FBUJGPD16J21D6	ACTCAGCTGGTGGCTCTCAC	CCGAGAGGATGGACTAGAGG	203	163	0.97	2			
B069	FBHG2QE07EBJ5T	GGACCCCGTTTGACTGTG	GGGAAAATATCCCACTCACTT	218	179	0.96	0			
B070	FBUJGPD10F58F6	GTTGTCGTTGATTTGCTTT	GGCCTTCTATCTTATGCT	213	173	0.94	1			
B071	FBUJGPD11GZ08X	ATAAATACCCAGACCCGAG	AAGTCAGTCAGTCAGGCTC	209	169	0.94	1			
B072	FBHG2QE06DI9V4	TAGTGGCCACAGGATTTGAG	AAGCTGTGAGATGACTGGGG	241	201	0.93	2			
B073	FBUJGPD11GRPKL	CCACTGTACCTAACGGATGAA	TGCTTCCCACTAATTTGGCT	264	221	0.97	1			
B074	FBHG2QE06DM9RM	GGCAATAGCAGAGGAAAAA	GGAAGGCAATTTCTGTGGAA	262	222	0.96	2			
B075	FBHG2QE15JAS8I	CCCTTCTGTTAGTGGTGA	ACTGGAGCCACAGGCAATG	264	224	0.90	1			
B076	FBHG2QE12HEW2T	TCTCTCTTAGGTTTTCGACTG	CAAAGCACCATAACAATGTTCAA	234	189	0.91	2			
B077	FBHG2QE16JVLHW	GGCACACAGTTTCTCTTGA	CGCACTTAAATACCCAGGACA	237	196	0.97	0			
B078	FBHG2QE10F6FS2	CCCAAACTTGGTGTGGTAGC	CCCAAAAGGTCACTCCAA	267	227	0.97	1			
B079	FBHG2QE12HGBVQ	GAGGAGTGCCTGGTGGTGG	AACCTCCCTTACAGAGACCC	249	209	0.98	2			
B080	FBHG2QE07D6807	CTCGTTTCCCAACAGATCAC	TCTTGGATTTCACTACAGTGC	222	180	0.99	0			
B081	FBHG2QE12HGIHL	AAATTCCTGAGGCACTGAA	CTCTGAGGCCACAATTAGCC	237	197	0.98	2	yes		
B082	FBHG2QE11GSXF6	TTTCTATATGATTTCCAGAAAA	GGGTCTGATGTCCCAAG	261	216	0.98	1	yes	57	12,897,274
B083	FBUJGPD11GQ5ME	TGAGGGGAGAAAAGCAACT	GTTGGAAGTTATGGGCAAA	258	218	0.99	2	yes	19	34,250,944
B084	FBHG2QE15JC08Y	CCTGGCTTGGCTGACCTG	ACACAGCAACCTAAACATCC	232	193	0.98	0	yes	47	1,420,135
B085	FBUJGPD16J2J79	CTGACCCCTTCTTCTGTGT	CTATGTGTGTGCTCATCTC	247	207	0.94	0			
B086	FBUJGPD16JVC7N	GATGTGTCAAGTCCCACTT	AAGAGGTGAAGATGAGGAGG	224	183	0.96	1	yes	60	8,341,199
B087	FAGAMMR16J25MU	AGGACAACTGAACACTGGC	GGTTGCAATTTCTGCTCACTT	242	201	0.94	2			
B088	FBUJGPD11GUBBF	TGCATATCAGGAAACCTCA	TGTGGTACTGCTGAAAA	226	186	0.97	2	yes	45	15,439,266
B089	FBUJGPD13HYV38	GAAGGCAGCAGATATATGG	CCCTCAAGGAGATGGATTGA	234	194	0.90	1			
B090	FBHG2QE09FIK66	TCCAACCACTGGGGAAAC	GACAAAGTTGGCTCAGGGA	236	196	0.94	1	yes		



target ID	read ID GenBank ID	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
B091	FBUJGPD16JTCBG	ACCCAAGGCCTCAGAAC	CTCCCACTTCGGAGCAG	249	213	0.95	0	yes		
B092	FBUJGPD11GXN09	GTTTCGTAGGTTGGCTTGAG	TTCCATCTTCTTCATGATCC	209	169	0.89	0	yes		
B093	FBUJGPD10GB1KI	GCAATGCTCAACAAGTTTGAC	AATAACAAGTAGCAACAATGCGT	236	191	0.95	1	yes		
B094	FBUJGPD109F6MU	GAAACCCCTTGGTTTAAGGC	GGAGGGATCAAGACACAA	236	196	0.88	1	yes	750	2,039
B095	FBUJGPD14IM969	CCTGCATTTGTAAAGCTGA	TGTTATTTGCTTGTCTCAGGG	236	194	0.99	0	yes		
B096	FBUJGPD16JV99F	TTACCTAAATCACAAITGAAAA	TATCAGCCCAATTTGCCTTTC	257	213	0.88	1	yes		
B097	FBUJGPD15JD9FZ	AGCACTGCACGTGGACCT	AAGTGTGAAGGTGACGGCAGG	228	189	0.97	0	yes		
B098	FBHG2QE12HGRZ5	TCAAATCTGCTGCAAAAGACC	TTCTTTGGGTAGTCCATGGTATG	216	172	0.96	0	yes		
B099	FBHG2QE08EZLLY	ACAAGACTATCCCGCAGAGA	CCATCTTTGACCGTCACTGA	244	204	0.93	1	yes		
B100	FBUJGPD10GEEFQ4	GCATAGAGGGCTGTAGGGTG	TAAAGTCTGTCAAGGAGGCT	223	183	0.98	1	yes		
B101	FBHG2QE13H59FF	TGATGACACCATTTTGGAGC	CTACCACAGGTCTATCCAGC	216	176	0.97	0	yes	1	75,524,245
B102	FBHG2QE13H9Q2Q	AATGGCCAGGCTATGAGAGA	GCATAATCTCCCCCATCTC	243	203	0.97	1	yes	10	34,024,629
B103	FBHG2QE16J11CA	CCGGCACATTATGAACCTTC	TGAACAGGGTGAAGGAGGTG	230	190	0.99	1	yes		
B104	FBHG2QE06DQBLA	CACGAGCTTTAGACAGGGGA	CTGTGCAGGGTGAATGCTG	223	185	0.95	2	yes		
B105	FBHG2QE09FSDM3	ACCTAAGAGCTGTTGGTTCG	TGAATCTGCTCAAAGACTACG	221	178	0.97	1	yes	9	74,552,276
B106	FBHG2QE16JUE6S	GCTCCAGGTAGGCCCTTCACT	TCCTGAGGCCAGAGTAAAA	233	193	0.94	1	yes	64	2,463,063
B107	FBHG2QE09FVL3O	TCAACATTTGTCAACATCCCA	CCTCACTCAGCCCTGAA	208	169	0.91	2	yes	17	27,878,148
B108	FBHG2QE06DGS5W	CCTGATTTCTCTGTITGGAA	GGCCATCAATCAGCTTCAG	235	194	0.97	2	yes		
B109	FBHG2QE06DQ7N0	CATCAGGAACAAGCCAAAGG	CCCCAGGCCATATGTGATAC	234	194	0.88	1	yes	10	49,857,693
B110	FBHG2QE07ECR9G	GGATGAAAAAATTCAGCCACC	GTGTAGGTCCTGTCACTCC	227	188	1.00	1	yes	5	95,301,740
B111	FAGAMMR16JZQNT	CTCCTTCTGTCACATTCGA	AGGGACAGGAATTAAGGGGA	231	191	0.99	1	yes	27	12,707,099
B112	FBHG2QE16J1QTV	CCCAGACCTGTGATGAAAGAA	TTATTCCTGAAATGGGGCT	231	190	0.91	2	yes	1	17,440,473
B113	FBUJGPD12HMUFW	GGAGGGAGATTCACAAATCA	CAAGGCCCTTATATGAGTCAA	249	206	0.98	1	yes	1	
B114	FBHG2QE14IKKAG	CTTTACCTGGGCTGATCCAA	TTCAAGTCACTATCAACCCA	207	166	0.91	1	yes	1	50,767,865
B115	FBUJGPD13H3H2E	TTTGTGTCAATCTGCTATTTC	TACTGACCGCTGAAACAGG	201	157	0.93	1	yes		
B116	FBHG2QE06DNXY7	AGTCACTACCCCTGCTGCT	CCTCTCAACCCATGCTGTT	220	180	0.96	1	yes	19	7,098,600
B117	FBHG2QE09FRUFI	TTCTAAGGAGCATTCTGGCTG	TTTAAAGTGTAAAAAGCAAGACG	237	191	0.93	0	yes		
B118	FBHG2QE10GE4QZ	TGTTCTCTTGGCTTGTGAGA	TTCAACAATAATCCCTTCCC	226	186	0.96	1	yes		
B119	FBHG2QE11GR20R	CCAAGTGCACATGAGCAAAC	CAGCTAGGTTGTTTCCAA	230	190	0.96	1	yes		
B120	FBUJGPD10F7MV4	GGGTCAAGGCTCCTCACTCTT	TGAAGAAGGAACACAGCAA	232	192	0.96	1	yes	4	47,945,658
B121	FBHG2QE06DTL01	CAGAACAATCCAAAGGGCAT	CCGGGCTGAACCTTTGTT	211	173	0.96	0	yes	12	32,920,038
B122	FBHG2QE13H8P08	ATAACCTTTGCCAGACTCG	GTGGTCAAGTGGAAAGGGAA	221	181	0.96	0	yes	9	74,542,366
B123	FBUJGPD12HB5AH	CAGGTGTCTGGAAGGAGGG	GGCAGAGATGTCAGTTC	216	177	0.91	0	yes		
B124	FBHG2QE13HX17R	CACCTTTGTCCGAGGAG	CCGTGATTTTCCGCTXTTA	225	187	0.98	0	yes		
B125	FBHG2QE08ERFJ9	GGAGGAAAACCTGTAGTCTG	GACTCCTTCTAAGCTCCA	248	206	0.95	1	yes		
B126	FBHG2QE08EY9HT	GTGGAGCTGGCTCACTAGC	TTTGCAAGTGGCCAGAAAAT	203	163	0.95	1	yes	13	36,001,336
B127	FBHG2QE07EA6ID	AAATTTTGCTGTGCTCCAGC	TAAAGGCCACTTCAGAAAC	242	202	0.92	2	yes		
B128	FBUJGPD15I63MK	TTCCAGGACTCCAGGGCC	GTCTTTGCCATGATAAGCATCTT	209	167	0.92	2	yes		
B129	FBHG2QE13H3JXD	CTACAGGCCCGGCAAAC	ATGTGGCTGCATCCAATAG	218	180	0.87	1	yes		
B130	FBHG2QE07D8BBZ	CGGTACTTAATGGTTTACAATACA	CCGTGGATATCCCATTTGTC	213	168	0.96	1	yes	117	1,875,586
B131	FBHG2QE16JVU2K	CTCAAGTCTAGTGGAGGCCA	GCTCAGTAGCATAACATGGCT	212	170	0.93	1	yes		
B132	FBUJGPD10GBS7	TAGCGCTAGAAGAAGCCCG	TGTTACATGAGTGATCGAGTTAAA	213	168	0.99	1	yes		
B133	FAGAMMR16JUSZ4	GGCTTAGAAAAGGCCCTCAG	TGCATAAATTTACTGGCCAA	220	179	0.98	2	yes		
B134	FBHG2QE06DPANW	TTGGACAGTATCTCGTGTGA	GGGAAGTCCACAACCTATCTG	226	184	0.98	0	yes		
B135	FBUJGPD14IT09Z	TAATTTGGCTGGCTAAAAG	TCCTGTGATGTGCCCTACA	219	179	0.95	0	yes	22	30,306,397
B136	FBHG2QE06DPQ7U	TGCAGACAGACTATGGGCAC	TTGGCAGATTTGCACTGTT	208	168	0.98	1	yes		
B137	FBUJGPD16JQ2KC	AGTTCCTAACACACAGGGGG	TGGCAATGCTTACTGAGGA	215	174	0.98	2	yes	121	1,727,613
B138	FBHG2QE07D5K9N	GAGGAACTGGACAAGTCAAGC	AGCAATCAGAGGCCAAAAC	230	189	0.89	2	yes		
B139	FBUJGPD16JSZ0Z	TCGGAGATCAGCAGCAAAAC	GTCTAGGCTGAGCCAAAAT	216	176	1.00	2	yes	5	32,465,128
B140	FBHG2QE12HJC1A	TCTTTTAAAGGCCACGCAGT	GCCTTAGCTGATCCCTTCA	213	173	0.99	0	yes	13	51,371,453
B141	FBUJGPD16JZ2UT	TCTAATCAGGAAGGAGGAGGG	TGTCACAGAATGAGGACCCA	190	149	0.95	1	yes		
B142	FBHG2QE13H9BA4	CTGCATAATTTGGACAGCC	AACGCAATTAACAGCTTGC	240	200	0.96	1	yes		
B143	FBHG2QE15I6EUU	GGGAGCCCAACAAATTATG	GAAATTTGATCAGATGTGCAA	207	169	0.95	1	yes	5	16,516,502
B144	FBHG2QE16JT4ZQ	GAAGCTGTTCAAGACCAGG	GGGCACTAGCACCTTTGAGT	225	185	0.94	2	yes		
B145	FBHG2QE08EYAEJ	TGCTGTGACTTCCAAAAGTG	CATGAACATCAGGACGGCTA	217	177	0.97	2	yes		
B146	FBHG2QE08EQ74W	TCGCTTGTGCTGAAAGTGAAGA	TGCAACCCATTTGTTGATT	234	194	0.93	0	yes		
B147	FBHG2QE14IPW59	CCTTTGAAATTTGGTGTGG	TTCTCTTTTCTGCTGACCC	216	176	0.96	0	yes		
B148	FBUJGPD14IPVHA	CACCTGGAATCTTGTGGCTTG	TCAAACTTCCPCCACTT	212	172	0.88	2	yes		
B149	FBUJGPD14I06H1	AGTAGGCTGACAGGGCAGAT	AACTGTTTCACTGTCCAGAGG	227	187	0.91	2	yes		
B150	FAGAMMR16JV03I	CCCTCAGCTGGGTAACCTC	ATTGTCAAGCTGGTGCAG	216	176	0.96	2	yes		
B151	FBHG2QE12HME5J	CATACAGGACCAAATCCCT	GTCTGTGAACTGGCTGCT	231	191	0.90	0	yes		
B152	FBHG2QE09FND0V	TGATGCTCTACCATAGCACTTCA	CCAATGGCTGAACCTTTGGG	217	172	0.95	1	yes	6	53,782,150
B153	FBHG2QE10F52CK	CACCTCCCTTCACTTCC	GGCCTCAGCAGGCTTATCT	213	173	0.96	2	yes		
B154	FBUJGPD13H1JEF	GGCTTCAATTTTCTCCAG	TTTCTGAGTGGGATATTGA	224	182	0.97	2	yes	64	5,960,942
B155	FBHG2QE15I9JM5	CCCGCTTCCCTTATAAT	CCAGGATCAGAATGCAATGA	213	174	0.99	0	yes		
B156	FAGAMMR16JV2WU	TCAACTTAGCTTCCAGGGCT	AGGGGTGTCCAAGGGAGAT	206	167	0.97	1	yes	47	16,627,053
B157	FBHG2QE12HI088	GTTCTAGGGAGGAAAAATTG	GGGCATCAGAGCTGAAACAT	226	186	0.98	2	yes	63	9,693,741
B158	FBHG2QE08EZHEP	CCATGTTAGCCGGTGTAG	CTTGTTTTGAAGAAAGTTGACA	226	182	0.96	0	yes	18	21,157,709
B159	FBHG2QE12HF0FW	CCTTCTTCAAGAAAGTGA	CTCTCTCTGACCCAGATG	234	193	0.97	0	yes	45	18,085,112
B160	FBHG2QE11GZUFX	TAAACAAAAGGTTGTGGCT	TAACTAAGGCTGAATGGCCG	214	174	0.96	0	yes		
B161	FBHG2QE16J13WZ	CTCAAGTGGTGTATGGCC	CTGGACGGTCTGTCAAGATA	237	197	1.00	1	yes		
B162	FBHG2QE13HZKRS	TCAAGACGTGGCTTAGTCA	AAGGGAACTGAGCAACAGA	248	208	0.98	2	yes		
B163	FBHG2QE08EQTPH	AAGACTGTCAACTGCAAAAGG	GACACATTTTGAGTTCCC	226	185	0.99	0	yes	33	21,481,153
B164	FBHG2QE16JUNV8	AAAATTTCCCAACAGCCAGC	CGATACAAGTTAGCGCTC	214	174	0.97	0	yes		
B165	FBHG2QE09FLS0H	AGGCTGTGTCAATCTTTC	TCGGAAATCCAGGAACTACC	212	172	0.96	1	yes		
B166	FBHG2QE09FRK7H	TGCTGTAAAGGACTTCTGG	CCACACAAGGACAGCAGAGC	195	155	0.98	1	yes	29	31,534,560
B167	FBHG2QE14ISS79	TGAAACAAGTTAAGGCTCAC	GCTGTACAACCTTCTGGGG	227	186	0.96	1	yes	65	11,353,589
B168	FBHG2QE13HXK49	CACCTCAGTGAAGCTGTCA	TTGCTCCTCTTTTCTTAGC	211	169	0.99	2	yes		
B169	FBHG2QE10F65PN	TGTTTTGGGATTTGCCTTTT	TGGGAAACCTTTATGGAGCA	240	200	0.97	1	yes	6	54,694,957
B170	FBHG2QE16JZVQN	AAGTCAAGGGGACCACTC	AGAAGATTTGGCCAAAACCA	187	147	0.96	1	yes	67	5,778,372
B171	FBHG2QE11GRHMU	CATCTGCTACCCTAAGCCCA	GCAAGGTGCATAGGATGTGA	210	170	0.98	1	yes	1	101,862,519
B172	FBUJGPD14IUNDT	AAACCAGTCTCAGAAAGGGA	GAGAATTCACGATAGCGAGC	219	177	0.97	1	yes	18	34,656
B173	FBHG2QE10F601J	GCATTTGGGCTTTGGTTTTA	TATCAGGAAATCCAGGCTT	242	202	0.98	0	yes		
B174	FBUJGPD10F6USF	TGTTGGCAGCTGGTAAAGA	TCTGTTGTTGGCTTATGTGA	224	181	1.00	0	yes	50	9,445,613
B175	FBHG2QE15JGYUA	ATGAAGTGTGGAGGGATGG	CACCTAGCCTTTTGGGCTA	216	176	0.99	0	yes	3	78,448,534
B176	FBUJGPD10GGSAK	TTGTGAATTCAGAGGCAAC	TTCCAAGTCAAGGATAGGAAAGT	235	191	0.96	0	yes	19	35,050,101
B177	FBHG2QE14IUSWE	TCTGCTGCTGTCTGCAAT	TAACAATCTCCCTCTGCC	223	183	0.96	1	yes		
B178	FBHG2QE12HNAEL	CAGGAAGGCCATGTCTGTG	TCGAAATAGTGGCAAGCTGT	194	154	0.98	2	yes	99	715,849
B179	FBUJGPD10F5PKB	CCAGCTCTGGAACCATCTC	CCACAGGCTGGCAAATATAGA	199	178	0.98	2	yes	21	15,471,258
B180	FBUJGPD10GB711	TTATCTGGGAGAGTTTGGC	AACCTTTGTCACAGGCTTC	218	178	0.97	2	yes	58	10,358,110
B181	FBHG2QE08ESODZ	AGAGGCTTGTGCTTGCTAT	GGTGGCTGTAGTAGTAGGAG	213	173	0.93	1	yes	18	11,408,461
B182	FBUJGPD15I845X	GCAAGATAGGTTAGGGGCTTG	CTGAGAGGACAGGGAGAAA	209	168	0.93	1	yes		
B183	FBUJGPD15JENB8	ACAATGCCCTACTGAAAG	GCCAAGCTCTTGTCTCTA	204	164	0.99	1	yes		
B184	FBHG2QE15I6HZ8	TTTTCCCAAGTTGATGGGAG	CCTTACCAGCTTGTCTCCA	232	192	0.95	2	yes	37	19,442,139
B185	FBUJGPD10F4FGQ	TGGACAAGAAATGAGGAAGCA	ATGTCCTTCCAGGGACTG	212	169	0.93	0	yes		
B186	FBHG2QE13H08E0	TCCAGCTCACTATGAGGCA	TGGAATGAATATCCCCCA	225	185	0.94	1	yes		



target ID	read ID GenBank ID	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
B187	FBHG2QE09FLVCG	AGCTCCCAGATCAAACGAGA	GGGGTTCATCCAGCCTCTAT	233	193	0.96	1	yes		
B188	FBHG2QE14IS2J2	TCCACTTGAGGCATTGGAAGA	TGAAAGTCCACAGCCCTCAG	232	192	0.99	1	yes	8	28,743,344
B189	FBHG2QE09FKAVU	CCTGGACTGGCTACAGGCTA	AACAGGTCAGCCCAAGA	199	161	0.99	2	yes	64	10,988,385
B190	FBUJGPD12HEBCW	AGCCACTGAAGTGTGCCG	GTCTGTCACTGGGAGGGTGT	208	169	0.96	2			
B191	FBHG2QE07EDNG2	AATTTCCAGGAGTTAATGGCTT	TCTGTCTGTGTTAGTGTTCAGC	218	173	0.96	2	yes	30	7,557,074
B192	FBHG2QE14IK2L7	ATTGATCTCCATGACCACC	GTCTGTGGGAAAGATTGGG	221	181	1.00	0	yes	18	30,278,164
B193	FBHG2QE10F6LX1	AAGCGTGGTATGTGTGTGT	ACCTAGATTTCTCGAGGGGA	215	175	0.94	0	yes	27	13,377,102
B194	FBUJGPD11G0IU9	GCAGGTAAGAGAGCAGGCAG	CCTCCATGATGCAATCTGATA	229	188	0.91	0	yes	18	40,691,157
B195	FBHG2QE14II3P2	TCCTATTGGAACATCTTCTCT	TGAACCTGAGGCTAGTITGG	212	168	1.00	1	yes	12	34,660,356
B196	FBUJGPD16JYHN2	TCAGTGGCTTTGACTGTGTGG	CCTGGCTCTTAACCTGCTTA	214	172	0.97	2	yes	16	24,765,073
B197	FBUJGPD14IKZ7Q	AAACCACCTGCAACTATGG	CTCATGCTCTGAAACCTT	204	165	0.95	1	yes	3	9,545,026
B198	FBHG2QE07EE7F1	TGTGTGTCTGACCACCCATAG	ATTAAGGAGACAGGACGGCA	193	152	0.99	1	yes	28	12,702,582
B199	FBHG2QE06DMMPO	TGGTACCCTTTGACCTCGG	GGACAATGTGGATTGAGGGAG	210	170	0.98	1			
B200	FBUJGPD14IKWYZ	CCAGGAGCTGGTATCTGTC	GACACTCAAGGTGGACAGGC	218	178	0.97	1	yes	29	26,771,641
B201	FBHG2QE16JWNC8	CAATTTGGTGGCAGATTTGA	GGCCTAGGACACCAACCTAG	216	176	0.98	0			
B202	FBUJGPD13HW1Y2	GCAGGAGTAAAGCAGCAGT	ACCAAAAACCAACCCAGTG	212	172	0.95	0			
B203	FBHG2QE06DIG65	GGGACTCCACAGAAATGT	TGGCACTGTGAGGAAGAGA	209	169	0.98	1	yes	122	2,400,993
B204	FBHG2QE11G0GDB	TTGGCAGAAATGGAAGCCT	AGTGGCTACGTGGACTCAGG	213	173	0.99	1			
B205	FAGAMMR16J3WD	AAACCCGCAATTTGGTGAAC	GAGTATCCCATGACTGCTT	211	171	0.98	0	yes	3	30,984,529
B206	FBHG2QE15J5B3B	TTAATGTACCTGCAACCCCT	CTCAGCTGGAGGACCAAGGT	209	169	0.96	0			
B207	FBUJGPD13H9U0T	ACAAGTTCCTGATCTCCCA	CTGGCACTCATGCTCTCT	226	188	0.92	1	yes	319	48,206
B208	FBHG2QE08EP2Y4	TTCAAAGTCTGCACTATCTTC	GCACATTAACAGTCTTGGATGC	192	147	0.92	1			
B209	FBHG2QE12HGN7U	TCAGCAGATCTCCAGTGTGG	AGCCAACAACCTGAGAGGG	205	165	0.95	2	yes	42	9,116,261
B210	FBHG2QE13H5MMY	GCTTCTTCCACTTCTGGG	TGTGGTCAATATGCCCTCACA	229	188	0.99	2	yes		
B211	FBUJGPD12HJ3JY	CCCAGCAAGAAAGGCTTTTA	GGGATTAATCTGGAGTCAAA	241	201	0.99	1	yes		
B212	FBHG2QE10GCB5E	GTGGCAACTGTTCACTGTC	CATCCTTCCCAACAGTCTGC	218	178	0.96	1	yes	14	47,737,118
B213	FBUJGPD13H01SL	TTCTTTCACTGGATCTGTGG	TTACTTGGATGACAAAGGGG	221	180	1.00	2	yes		
B214	FBUJGPD13H2RBJ	ACTTCCCCTCACTCCCTTCC	TCACATGAGGTAAAAATGGCA	237	195	0.96	2	yes	36	21,174,749
B215	FBHG2QE12HM20S	CCTGTACTGAGTCCCAAGGC	CTTCACTCCACTCTCAGCA	196	155	0.96	1	yes	127	820,250
B216	FBHG2QE09FMQNN	GTCCACAAAGTGCAAGACC	GCATTGAGGCGAGGCTAAA	191	151	0.96	1			
B217	FBHG2QE15JE7E6	TATTTTGAAGGGAGGAGGGG	TCAGCGCACTTAGCTGTTC	216	176	0.99	0	yes	65	11,061,277
B218	FBHG2QE08EV9NS	TTGTGTTCTATGTGGAAGTG	TCTCTCCAATCTGATGCTG	199	159	0.90	0			
B219	FBHG2QE13H4M8U	CCTGGGCGAGCTCCAGCTT	GGGTGGGGAAGACGCTT	207	169	1.00	1	yes	6	93,344,124
B220	FBHG2QE10F8IHA	TGTCATGAAAGGATGAGTGAGC	TTTGTGTGTAACCTGCAATACT	205	159	0.95	1	yes	22	10,273,074
B221	FBHG2QE11G1LGC	CGTGTCTATCCAAGCTCCC	GTGGGACCATGAGAAGCAGT	225	185	0.94	1	yes	72	7,687,676
B222	FBHG2QE06DNX08	GACAACTGCATTCTGACTTGC	GACCATGTCTAGGGCTCTG	224	182	0.95	1	yes	28	3,604,923
B223	FBHG2QE11GTYCW	GATTAGCTGAGGAGGAGGAGA	GGCACAATTTGGAGGATGT	197	147	0.99	2	yes		
B224	FBUJGPD15I75TP	CCATCTTGGACTCACCAGAA	TGCAGCGTGTCCCTTAAGTA	237	196	0.95	2			
B225	FBHG2QE10GAJZB	GAGTGATGAAAGCTGCCCT	TGGTGCATTTCTGTGTTC	207	167	0.98	2			
B226	FBUJGPD14IMZ37	TTCAACAATAAGATGCAATGCTG	TCGATGTACCCGTGAAAGC	220	178	0.99	0	yes	102	4,393,297
B227	FBUJGPD11GXMS7	TACGGCACACTTGTCTCT	AAAGAAAACAAAATCTCACAA	225	182	0.93	0			
B228	FAGAMMR16JU81N	TTGCTGTTGCACTTACCAG	AAAAGGAATGGTGGACTG	236	197	0.98	1			
B229	FBHG2QE10GEREW	TCTGGGCGAGCTCTGATTT	AACGTTCTTGGAAATCTGACA	211	170	0.93	1	yes	507	66,245
B230	FAGAMMR16JZF2Q	TGGTGGTTCACAGCTGGG	GTCTGGGCACTTAGCTGGT	233	165	0.96	1	yes	71	941,543
B231	FBHG2QE14ISADM	GAAGGCTTCTCTCCCTGTC	GGCCTGACCACTCTTATC	233	193	0.95	1			
B232	FBHG2QE06DH180	GCATGACGTGGGAGGTGAT	CCAGCAGCACTCACTCAG	226	187	0.95	1			
B233	FBHG2QE12HK8W8	CGCTGGTAACTGAGAGTCA	CCTGAAGCGCTTCTCTG	242	203	0.99	1	yes		
B234	FBHG2QE06DHUJT	TCTAGCCTGCGACTCACAC	GCACCAGGTAGACCAGAGA	150	110	0.93	1	yes	9	83,036,813
B235	FBUJGPD15JG9ZV	GGCCCTTCCCTAATCAAG	AGTGACATCAGATTTGGTCTC	206	164	0.93	1			
B236	FBUJGPD12HDZ32	GGAATGTGGAAAGCAGAGC	GGACTGCAATTTCTGGCT	192	152	0.96	2	yes	9	40,645,422
B237	FBUJGPD14IMZAP	TTTCACTGTGTGAGAAGATCAGA	GCATCTGACATCTAGCTCCTT	224	180	0.96	2	yes	50	5,580,361
B238	FBHG2QE15JDH47	ATTTCAAATGGCATCGGTAG	GAAGTTCCTGCTAGACCCC	204	164	0.99	2			
B239	FBUJGPD10F88N4	TGGATGAAAGCAAGAAAGAGA	GATTCTGACTATGTATCGGAG	227	182	0.98	2			
B240	FBHG2QE07D7KLN	TTCTGTACCACCTTGACACA	TGATAGTCTGTCTCACCACA	216	174	0.98	0	yes	151	80,293
B241	FBHG2QE10F3Y9Z	CTGGGACTTCTCTCTGGG	GCAATTCAAGGAGAAAGCA	210	172	0.91	1	yes		
B242	FBHG2QE10GA3BL	CCGTGCCAATTTTACAAGGA	TCGAAAGCTAAGCCGAAATG	244	204	0.93	1	yes	127	1,455,825
B243	FBHG2QE14IVSUR	GTGTGCCAGTCCATGCTA	TAGTAGCTGGCTGCTCTG	204	164	0.95	1	yes	5	94,097,177
B244	FBHG2QE13H1STR	CACCAAGAACCTCACTATTCA	AACCTTACTAGGCGCTGCT	212	170	0.96	1	yes	129	1,478,153
B245	FBUJGPD10F35ZZ	TGCTTCAGCACTTCTTGTG	AAGCCATCTGGTTCCTTT	201	161	0.96	1	yes	49	296,180
B246	FBHG2QE08ET8Z0	ACACACTGCTCAAGCTCCT	CGGGTCAAGCTCAGAG	200	161	0.99	1	yes	27	367,552
B247	FBUJGPD13HWCT3	CCCAGTCTGGCAAAAATACC	CTCCCAATAGGAAGCTCTCA	197	157	0.99	2	yes	8	39,229,258
B248	FBUJGPD10F7U4S	TGCTCCCTGATGTGTGTG	AGCCTGGTAAAGGAGAGGG	223	183	0.99	2	yes	11	49,000,000
B249	FBHG2QE16JHCHY	GGTAAACAGCTTTTCTCTCT	GAAAAAGTGGGAGGAAGCTG	231	189	0.99	2			
B250	FBHG2QE08EWP1T	CAGGGGTACAGTTTCACTGATG	TGTGAGAAAGCAATGTGAGGCA	199	154	0.98	2	yes	11	27,980,216
B251	FBHG2QE09FK0SU	TGGGTGAACGAACAGTTTCA	CCATGATTTATGCTCTCTCT	191	150	0.98	0	yes	47	12,040,065
B252	FBUJGPD12HMH24	AATACCATGGCTGGGTGAG	CCGGAACAATAAGCAACATC	220	180	0.94	0			
B253	FBHG2QE09FI2XG	CCGTCTGCTCCATCATT	TGAGGGCTCTCAACCTTT	230	191	0.97	0	yes	3	10,675,793
B254	FBHG2QE11GTJ16	GCATGACCTCACTGTTTACC	AGCCATCGTCTGAGACATTT	206	165	0.94	0			
B255	FBUJGPD11GVQJ3	TAGGGGACTGATCCACAGC	GGTTTGGAAAGTGGAAAGCA	189	149	0.89	1			
B256	FBHG2QE06DQMJ2	GGGACGGGTGATGAGTAATG	CAGGGCAATTTAAAAAGCA	196	156	0.96	1	yes	86	3,693,404
B257	FBHG2QE10F6PFZ	TCAAGAGTTTGTACCAAGGG	ATAGGGCTTTTGCAGAGGGT	224	182	0.97	1			
B258	FBUJGPD11GU0Q6	AGACATCAGCCGTAAGCTGG	TCAGACCTCACTGTGCAAGAA	233	192	0.98	1			
B259	FAGAMMR16J1N29	CCCCACCTACTGATTTAT	TTGAGTGTATCTGACTCGTAGTG	199	154	0.87	1	yes	99	1,861,855
B260	FBUJGPD12HD8EE	TCTGGCAGTCTCTGAAAGC	CAGCAAGCAAGTCTTGTGA	215	175	0.88	1	yes	20	10,655,556
B261	FBHG2QE07D6R67	TTCTCTGCGTCTTTTCTCA	TCCAGAGGTGGGCTCATAG	237	196	0.98	1	yes	1	5,314,690
B262	FBUJGPD15JGOXJ	CTAGATGCAAAATCGGGAG	CTCTCGGGTGGCTGAAAC	238	199	0.93	1	yes		
B263	FBHG2QE13H4KT3	TTTTCCGACTCATAGTGAACCT	AAGGATGGGCACTTCATC	238	197	0.91	1			
B264	FBHG2QE12HEUHS	CCTTCTCCATCCAGGACAC	TGGAGGAACCTTTGTCAAC	155	115	0.96	2	yes	21	4,340,823
B265	FAGAMMR16J56GX	TTTTATAAAGGGGAGGTGGC	CACTCTCCATCCCTGAAGA	197	157	0.98	2	yes	63	10,535,568
B266	FBUJGPD10GFGEX	CATATTTTGGGTTCAAGGAA	GCACAGGCTGAACTGTCTAT	195	154	0.99	2			
B267	FAGAMMR16JFND	CTCCAGCTCACTCACTCAT	AGAGGGGCTTATGAGACT	215	175	0.95	0	yes		
B268	FBHG2QE09FMKKE	TGCCCAAGTCAATCTCTGA	CATAATGAAATGGGAGCCCTG	201	161	0.99	0			
B269	FBHG2QE09FVFT2	CCTCACCACTCTCACTCT	GCCAGTGTCTTTCGAGTIT	205	165	0.97	1	yes	9	45,296,098
B270	FBUJGPD15JEXC	GCTCCTCACAGCAGACTT	CCTGTCTGAAGCTAAGCTT	226	186	1.00	1			
B271	FBHG2QE09FHSI6	TGAGACCATGACTGCACTTG	AAGTTCCTTCTGACTGAACTT	217	174	0.87	1	yes	9	31,042,083
B272	FBUJGPD11G1BQ0	CTGCCAATGATTTGTAAAGA	GGTTGCCAGTGGTAAATG	231	189	0.97	1			
B273	FBHG2QE16JWZPH	CATGGGCTCAAAAAGAAAGA	GCAACCCCAACCCCTAAAGT	211	171	0.93	1	yes	113	2,459,782
B274	FBHG2QE06DMSFL	TTCATATGACCCTGAAGAACTTG	TCAGGGTAGTAACCAATAGGCTCA	228	182	0.99	1			
B275	FBHG2QE10GCMX19	GAGAAGGAAGACGCAGATGG	AGGTTCTCAGCATCGGTAAGC	219	179	0.98	1			
B276	FBHG2QE13H66FP	GGACTGGCTCTCTGTATA	ACGCAAGCAGGATTTACAAC	229	189	1.00	2			
B277	FBUJGPD15JAI0D	TGCTGAAATAAAGACCCCTCA	CCCTCCAGAGGAAATCGTAG	206	165	0.91	2	yes	43	11,627,841
B278	FBHG2QE13H2TW1	GAAAGTTGGCCTTATTTTCTTCA	GAGCAAGGAGACTCCACAGG	220	176	0.94	2	yes	16	43,716,062
B279	FBUJGPD16JR8R	AGGAAGGTTCTCCATGGGT	AACAGTCACTGGGAAGGAT	186	146	0.98	2			
B280	FBHG2QE07D5ZS6	TGCAATTTGGTCCATGAGA	GGTGGTGGATTCTAGGACA	228	189	0.99	2			
B281	FBHG2QE09FIDOD	AGGTCTGCCAACCTAGGGAC	ACAGTTGAGCTCAGGCATC	225	185	0.98	1	yes		
B282	FBHG2QE10F9I2L	CAAAGCATAGACGAGCCAT	CAGAGATGACTCCCGTTGG	232	192	0.89	1			



target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer	Mastodon-loxAfr1 alignment % identity	# of hits isPCR loxAfr1	consensus for all taxa	aligned loxAfr3 scaffold ID	loxAfr3 scaffold position
B283	FAGAMMR16JZKFE	GTGGGGTTATTGGAAGGTT	TGCCTGCTCAACAGAAGATG	214	174	0.95	1	yes	25	21,228,071
B284	FBHG2QE15I8O26	ACTGGGTGGGCTCTAGGTTT	TTTGATTTCCAGCCAGGAG	219	179	0.95	1	yes	11	55,035,949
B285	FBUJGPD11G0VYR	CTGTTCCACAACCAAGCCTC	AATGACATTCGATGGAAAAGAA	194	152	0.95	1	yes	64	7,081,948
B286	FBHG2QE07D9OIX	TGGAACAGTTGACTGGGTTT	TGTTGGCAATTATGGCAATG	195	155	0.99	1	yes	9	52,027,714
B287	FBUJGPD13H6T03	ATGTTTGAAGTCCAGGCT	TTACGTCCTATGGTTCCCC	217	177	0.93	1	yes		
B288	FBHG2QE15I88E1	CATGGAGATGGTTCATAACACAC	TGTGAATTCGTTCCAACAAGA	215	171	0.94	1	yes		

A1-long

Target and primer information used for sequencing error rate estimation using direct Sanger sequencing, read ID corresponds to the read in the short read archive SRA010805, PCR product length with and without primers is given.

target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer
A002	EK3X9L102F3RBB	GCCTTCTTCTGGCTGATGAT	AGCTTTCTGGGCTTCTTTTC	746	706
A004	EK3X9L101DC8H2	GAAGTGCCCGTTATACACCAA	GCGAAAGCTGGACAATGAAT	749	708
A005	EK3X9L101BHMHV	GCAGTGTTTCTCTCGATTTCC	CTGAGCCAACAGGAGAGGTC	750	710
A008	EK3X9L101CV00E	TTCCTTCTCTGCCTTCTCA	GGACATCTACATCAGCTGGC	749	709
A010	EK3X9L101DQL4E	ACGTGGACAGGTTCCGACATA	GCAAACAGGTCATCCGAGTC	750	710
A012	EK3X9L101BCGQI	CTGGTCTACAACACAGGATT	TGAGTTGGACTTGACAGCCC	746	705
A013	EK3X9L102G5E9S	ACTCAGCCAGGATTTGCAT	CCTTTATCCCAGATGCTGACA	746	705
A015	EK3X9L102JWLAQ	TTTGTGGATGTTTGCAGGTG	TTGGTATCACGTGGGTATAGCTT	743	699
A016	EK3X9L101EN54P	TGACAACAGAGTTACCCACACC	TGCTGGGTAAATACAGTATGAGG	732	687
A019	EK3X9L101C0K93	CATGCTCGTTGCTCTGCTC	GCTAAAGGGCCATGCAATTT	749	710
A020	EK3X9L102F9G0Q	ACTCAAATCTGTCTCAGAATGGC	AATAGATTGCACCTGCCACC	737	694
A021	EK3X9L101CTJZY	TGACGTCAGGAGTCTCTCCC	ACCTGAAACACCCAATCAGG	749	709
A022	EK3X9L102H02GU	ACACACACCTTCTCTGCACA	CTCTGCCATTGGCTCAGTCT	748	708
A023	EK3X9L102GCTKJ	CAAGAGGCAAGAGGTCAATAAA	TCTGGCATTCCCTGCAAT	750	708
A026	EK3X9L102FFWKW	AAACACACTCTTCCAAGCCC	CAGGCAGTCTGTCTCCTTGG	748	708
A028	EK3X9L102IGAJD	GCAGTGTTTCTCTCGATTTCC	CTGAGCCAACAGGAGAGGTC	750	710
A030	EK3X9L102HH3QY	ATAGTGGTCTGCTGCCTTT	GTCTCGGGTCAACGAAGACA	750	710
A032	EK3X9L102G4ANS	GAACGGAGATTGTCGGAGG	CTTATTCTTGTCTGCCGGAC	748	709
A034	EK3X9L101AEV4R	GGTCAGGGTTGAGTTGGCT	GGAGGCAGATAGGAGAGGCT	742	702
A035	EK3X9L101A6LR5	TGGACCAATGAGCGACATTA	TCACACGACAATAAGAGCCC	748	707
A036	EK3X9L101AHAIX	CATTGACAATCGTCTGAGCTTT	TGTCGTCTTGTGGATTGAC	748	706
A038	EK3X9L102IMKVX	ACCTATCTGGGAAATGCTCG	AACAATTGTGAGGACGGCTC	740	700
A039	EK3X9L102IRFTU	TCATCAATACAACCTGCCCT	AAAGGCTCCGGTAAAGAGTC	750	710
A040	EK3X9L102JSOT0	GGGTTGTAGGTAAGGGCCAC	ATTCCCAGGTACAGGACAGC	750	711
A041	EK3X9L101AIALH	ATGTGGGAAACATGCTATCG	TTCCGACTACTGGGACAGCA	747	707
A043	EK3X9L102FIY9W	ACCCAGCTTCTCTGAGCAA	GGGTCTGCTGAGATTTCTTCC	748	707
A044	EK3X9L102GFDDD	CTTGGAAACCTTATGGAGCA	CAGCAGAGCTAAGGAAACC	750	710
A048	EK3X9L102GRG6Q	TTAACATGCTTGGTCCCTGC	AGGTCAGTCCCACAGTCCC	750	711
A049	EK3X9L102HZ5M7	GCGAAGCATGGTTGATAGC	ATATACCACGGACTGCCAGC	746	706
A051	EK3X9L101AX9UU	TAGGGAGAGCCATTTGCTCT	AAGCGCTAGAGCCAATGAGA	750	710
A052	EK3X9L102G8P4Z	ACTTCCGGCAATAGAGCCTT	GGAGGGCTGGGTTTCTCTTA	747	707
A054	EK3X9L101E21TS	TCTGGGATCATCTCCCTCTG	CGACTCGATGGCACTAGGTT	750	710
A055	EK3X9L102J0R29	GAACCTTTACATAGATCAAGAGGCA	TGAAATCCTTGAAAACCTCAATCTT	391	341
A057	EK3X9L101DC6HA	CCTGGAGCATGAGAAACTGG	AATGTGTGAATGGAACCGGAG	750	709
A059	EK3X9L101BDI18	TGGAAGGAGCAGTCAAGAAA	GCCATCAAGGAAATGCAAAAT	750	710
A061	EK3X9L102HQFHE	TTTCTTTAGCCCTTTCTTT	GGGTCTCAGATGAGTAAGGCA	750	708
A062	EK3X9L102JWO1R	ATTTCAACTTCCAGTGCAGG	TTGGTCTTCTCACTGATCC	750	710
A063	EK3X9L101BCKUW	TTGGAAGAGCTCGCTTGT	TTGCTTTCTTATGTTGAGGTG	750	708
A064	EK3X9L102HHRV7	TTGTTCCAACGCCACTCAT	ACTCTGGCATTGAAACAGCA	750	710
A070	EK3X9L101AG83P	TGAACGCTAACACTGCATACG	CAAAGAAGAGAGCGCACAGG	750	709
A072	EK3X9L102JM0Q8	AGGGATTCTTCCAGAGGAGC	CCTGCTTTGCTCAGAGGACT	750	710
A075	EK3X9L101DSVGO	TGAGTGACACAGTAAATCACAA	TCTTTGGCTGAAGGGTGAAC	750	707
A078	EK3X9L101C26GN	GGAGTTGCACCTGGCTGATTT	TGTGTGAAGCCTTCTTTGTG	746	706
A079	EK3X9L102H07QM	ACTCAGAGTGGTCGGAGCTG	ACTTACACCTTGGAGTGCC	746	706
A081	EK3X9L101DKF6W	GGACTGAAGATCCCAACCTG	CATGAGCTCCACCACTCTT	750	710
A082	EK3X9L102GF929	AACCACCGACTTGTGACAGTT	CAGCTTCACTCGGGTTACAC	750	707
A088	EK3X9L102JBXZW	TGAAAGAAGAGGCCAACACA	CCAGCCCTCAAAGTGTCTT	749	709
A090	EK3X9L101AVFGZ	CAGGCAGGAGGAGCTATGAG	GCTGACAAATGGGAAGCAAT	750	710
A091	EK3X9L102HYK2I	AGGTTGGCCATTAGGCTAGG	TAACGCATCCCTGGGTTAAG	745	705
A092	EK3X9L102GY7B7	TTCAGAGAACGAACATCCA	CGATGACATGTTTCCACAT	720	679
A093	EK3X9L102F4X94	CCTCCAGGAGACTTCTCTTA	AAAGGGTTGGAGGATCAAGG	743	703
A094	EK3X9L101ET8NT	ATGCGGTCTGGAACAACAGC	TGTGCCAAGGACTGTGCTAA	749	709
A097	EK3X9L102JWQH1	CGTCTCTTCTGAATCTGGC	CTCCTTTGAAGCAAGGATGG	750	710
A099	EK3X9L102IKMWQ	TGGGAGTGAGGATGAAGCTC	TTGGTTGGTCCGGAGTGTAT	750	710
A101	EK3X9L102IYRPJ	CCCTACTATAITGTCTGCGGG	TAACGGCCACTGCTCCTCA	750	708
A102	EK3X9L101EAN2W	GTTGCCATGAGATGGAACCT	CTGCTTGCCTTGTATGTGATG	746	706
A103	EK3X9L101DG80A	CACGTCATTAACCACTGGA	CAGTAGGCAACCCGTGATGT	750	710
A104	EK3X9L101D826E	AGTTCTCTTGTCTGCGCCC	TGCATCAATTTGCTCAACC	737	697
A106	EK3X9L101DD6LB	GTGAAGCAGGGTGACAAGGA	TGGTTAACTGAAAGGTGGATGA	748	706
A107	EK3X9L102JTIFO	TGTTTCTGGTGTCTCGGATG	CCCAACTGAACCAGAAGGAG	746	706
A111	EK3X9L102HJ5E6	GATGTGGCAGTCTGCTTCTG	CTGGCTCCAGTCTCTCACT	747	707
A113	EK3X9L102G11JT	TAGGAGGTAACCTGCCACGG	CCAGATGAACTGAGAGCTTGG	750	709
A115	EK3X9L101ANZ5L	ACCAGATCTTGTCTGCCCAT	AGCGATGTTTCTCCACCAT	750	710
A118	EK3X9L102ITWWD	CCTGAGGTAGACCTGGTGA	TTCACTTTGGAGCTCTGGT	743	703
A120	EK3X9L101BVY86	GCTGACCCTCACTCAGACCT	AATCCGCTGCTGCTTCTTA	747	707
A121	EK3X9L102F5KTB	CACACAATCTGATGTGGCCT	GCAGTGTTTGCCTTCACTA	749	709
A124	EK3X9L102IJEPM	TGGCACTGACTCAATAAGGA	ATACGCCTGGACATCTGCAA	750	710
A125	EK3X9L101EHT4U	GAGTAGGCTGTGGCTGG	GAGTTTGGTGTACTGAGGCA	750	710
A126	EK3X9L101EBD6G	CACCAGGGCTTGCACACAT	TTGCAACATAGTGGAGGGA	737	697
A127	EK3X9L101BJV3L	TGTCAAGTGGATCCCAAAC	CCCTGTGATGATGAGTCTGC	750	710
A129	EK3X9L102IM99N	AGCTCCACCACTGCCACTAC	CTCTAGGCCCTCTGTCAGGC	750	710
A130	EK3X9L102H1ZVD	GTCAGCCACCAAGGATTTCT	GGACCAGGACCTGATTGAGA	749	710
A131	EK3X9L101C1TEE	GAAGTCCCTTCCACAGGTGT	GCTGAGCTTTCTCTGAAAC	749	708
A133	EK3X9L102F6FN8	CAGCTTTCAGGTAGCATGGG	TTCTCCACCTTCTGGTC	750	711
A137	EK3X9L101EDFZR	GGGACCGATTGAGATGTTTC	TCCATACTGGAGGCTGTGGT	750	710
A138	EK3X9L102GH91C	TGCAGTCATCTCAAAGGGCT	AGAGAGAAGGCGCTTGACATA	750	710
A139	EK3X9L101DWNEV	CCGACAGCTCCAGTGGTTC	AGGCAAGAGATGCTGAGTGG	747	707
A141	EK3X9L102GMTFT	TGTTTGTGTTTTCAGGGTTC	GGATGGCTCCATCAATTAAG	746	706
A144	EK3X9L102GYTBB	CTCGGCTGTAACCGAAATA	GATGGCAACGAGCTTGGTAT	749	709
A146	EK3X9L101E5Q3R	GGAAACTGAGTTCAGCTCCAT	AGCTCCCTACCTCTTGTGTA	750	709
A149	EK3X9L101CEAIR	GCACACCTGGATTAACCGAA	ATACTCCCACTGCTCTCCC	750	710
A151	EK3X9L101EOTRO	CTCCATGGTATTGGGAAAG	TGACACATACCTGCCAGAGC	745	705
A152	EK3X9L101EPXIX	ATGATGGGCTCAGGCATAAC	GGCTAGTGACGAGGCAACTT	749	709

A11-long

target ID	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer
A153	EK3X9LI02INS8N	AGTCAGAACCGACTCAACGG	TGTGTCGTCTTAATCTCCTCCA	750	708
A154	EK3X9LI02FZCNA	GAAGGACTACAGTGGAGGACTGA	CCACCATTGCTAGAACCTG	749	706
A158	EK3X9LI02GM7LC	TTAGGTGCCGTTGAGTTGGT	TTGCTTGCCAAGAGTGAAGA	750	710
A160	EK3X9LI02IKVA4	TCCATGTGGTGCACAAAC	GCTCCTCCATGTGGAATACG	750	710
A164	EK3X9LI02FL5QN	CAGAGTCTGCTGTGTGGC	AAGCTTCCAATAGACATTTGCT	750	708
A165	EK3X9LI02GFCPO	GGTCTTGTGGCCTGACATT	CTCTAGGAAACACGCCAACA	750	710
A166	EK3X9LI02JIUKM	ACACACATGGGTGGGATTCT	CCCACCAGCAATGAACAAG	750	711
A168	EK3X9LI02GZ29S	CTGTGAGTCGGTTTGGACT	CACAACCTTGCTTGCTGAAA	750	710
A169	EK3X9LI01CFYE6	AGGTTAGTGGAGCTGGCAGA	TCGTACCAACACATGTTCA	746	706
A170	EK3X9LI02I8SIM	CCCACGTCCATAAACCAATTG	ATGTGGACAGGTTGACACA	739	699
A171	EK3X9LI01CDPOM	TGACCTGTGACACTGCAGAC	CTCTGGCTCTACTGGTTGCC	750	710
A177	EK3X9LI01DNN7S	CACATCGCAGATCAGTGGAC	CAGTGTGGCCATGAAGACTG	750	710
A179	EK3X9LI01DLN0U	CTCTGTCTGCTTGTCTCCC	TGGAAACAGAAGCCAACAGAT	749	708
A180	EK3X9LI02GECMC	AGAAGGGCCACAGAGTCTCA	AAATCGAATGCTTCAGGGTG	750	710
A181	EK3X9LI02JOYBY	ATTGGAACACTTGCCACAGC	CCCAGTCTCTGAGCCACG	655	617
A184	EK3X9LI02IDCDD	CCCAAGTGCCTGTCTGAGT	TCCGACTCTCTCAGTCCCTC	750	710
A186	EK3X9LI01BIKBU	GACACTGCCTGGTGAAGGAC	AGTCTGGAAGCTCCACCAAA	745	705
A187	EK3X9LI02FRKY4	GGGACCCAAACAAGCAAATA	TCTCATGGCTATCACAAAGC	749	709
A188	EK3X9LI01DOVZU	CCAATCCTGATGCTCTGTTT	CAAGTTGAAAGAACGGGAAGAAA	750	708
A190	EK3X9LI01A0OZO	TGTTTGTGCCACCTAGGCTT	AAGGCACCACAGAAGAAAGG	748	708
A192	EK3X9LI01BZ6AP	CCCTTCTCTTCTTGCTGC	TGCTCAGCCTTCTGAAAGAAA	750	709
A195	EK3X9LI01D9AK9	GTCCGAGGCGTAGGAAGTG	TTGATGTTACAGGATTGGG	750	711
A200	EK3X9LI02I9BMY	CTTCTGTCCGTCCCTCTCA	TGTCTCAGCTCCTGTAGCCC	749	709
A206	EK3X9LI01EYOLN	ATAATTCCGCTGCTGCTTTG	CTTGCTGACCCCTCACTCAGA	750	710
A207	EK3X9LI01AG3ZZ	CTGAAATGCTTTGATGGCAA	AGAACGCCAAAGACACAAGG	749	709
A211	EK3X9LI02HVV0D	TCAGCTATTGTGAAGGCTCG	CACACTATCTCGTCAGGGCA	749	709
A213	EK3X9LI02GE17J	TGAGTTGCTGGAGACCAGG	GGCCAGGTAGGTGAAGTCAA	750	711

A1 = short

Target and primer information used for sequencing error rate estimations of the mastodon shotgun sequencing: read ID corresponds to the read in the short read archive SRA010805, PCR product length with and without primers is given. Targets (see round A.1) were divided into two targets, primer set α uses the already existing forward primer from round A.1 and primer set β utilizes the existing reverse primer from round A.1, the corresponding (sometimes degenerated) primer per pair was designed using all available sequence information (modern elephants, mastodon and mammoth).

target ID	primer set	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer
A001	α	EK3X9L01BLRFR	TGGTCTCGAAGTCAGACAAGAG	TGTCAGAATTGCTTCCTTG	96	54
A002	α	EK3X9L02F3RBB	GCATTTTGATTGCATGTTTGA	ATATTATCCAAATTTATAAACCAACCA	112	64
A003	α	EK3X9L02HKE1R	TATAGTTCCAGGCTCCACGG	TGGAGTATTTCAGGCAGAGAGA	122	80
A007	α	EK3X9L01C7BYB	TTTTCTGTGTTTGTGCATGT	GGRTRRCTCAAGGAGGCAAAA	123	81
A009	α	EK3X9L01C7XKW	TTTCTATTCCATGAATGAACCA	TGGCAATTCACAGAAAACCTCA	122	77
A011	α	EK3X9L01AQJCF	GCTTCATTTGTTGTGCGTG	AGCTGGCTTCCTGTTGTTGT	76	36
A012	α	EK3X9L01BCGQI	CACTCCAGCAGCACCCAGAC	AGGTGCAGTTTGCCGAGTAG	103	64
A014	α	EK3X9L01AIIIP7	CTTCTCTGGGCAAAGTCCA	YATYCTTGYGTTGATGTR	101	61
A015	α	EK3X9L02JWLAQ	GAGTTACCGAGAGGGGAAR	TGCAAAACAAAGACTCAAAGGA	128	86
A016	α	EK3X9L01EN54P	TCGGACAACAGGACCCCTAC	RGATGAATGGGTCACTACGG	109	69
A017	α	EK3X9L02I9G0E	CTGCTCTGCCCAATCTTC	GGCTGTGAGGAGCCAGA	100	62
A019	α	EK3X9L01C0K93	AACCACCATTTGCCACTTTG	GGCAGTTGAGAAGTTGCACT	103	62
A020	α	EK3X9L02F9G0Q	GAATAACATCAGACGGTGCG	AGCCACCCCACTGACT	103	65
A021	α	EK3X9L01CTJZY	GCTTACCACACAAATCCCC	TGTGAGTTTTGACCYATTAGAGTG	110	66
A026	α	EK3X9L02FFWKW	CCCAGCATTAAACAATCTTAAAA	AAACACAAAGCTGTTAACCA	101	55
A033	α	EK3X9L01B83XL	TGACTGACAACAGCAAGGCT	GGAAAGCAGTTCAGGAAAT	118	78
A034	α	EK3X9L01AEV4R	GGTACCAAACTTGCAT	RCCAGGGCTTAGCTAGAGAG	108	69
A036	α	EK3X9L01AHAIX	CATGAAAAATGCTGTTAAAAACC	TCTGTTTACATRTTCTTGG	112	67
A038	α	EK3X9L02IMKVX	AGGGATCAAATGTTGTTTCA	CATTCTGAGCTGCGTTGTG	101	59
A040	α	EK3X9L02JSOT0	AAGGCCACTCTGGCTTCT	GCAGAAGGATGRGTCTCARAGC	128	86
A042	α	EK3X9L01BE9T9	GACATCCAAACATTTTCAGGC	TCTGGRATGAAGGACATCA	112	71
A044	α	EK3X9L02GFDDDD	GTGGGTCTACAAATCACC	GCTTGGCACCATTGCTTAG	107	67
A046	α	EK3X9L01A3SP9	GCTGCAGTCTTTGAATAA	GTGCCAGTTCCAAAGAAAGG	111	71
A047	α	EK3X9L01AZEP9	GGGACTCTAGGACAATCCAG	GTCCACCTGCCCTGTAG	99	59
A048	α	EK3X9L02GRG6Q	AGGGGAACCATGTCTTGTAT	GAGAGTCTGTGCTTTGGACA	113	71
A049	α	EK3X9L02HZSM7	TGTTGTGTAGGTGCTGTGG	CAAYGATTGAGKATGGTK	101	60
A050	α	EK3X9L02JDDAK	AGGAATCGGGTGAGTGAGTG	CTTCCAGGACAGGACTG	99	59
A051	α	EK3X9L01AX9UU	TTGTGATCAGAGTTTTCGGG	GGRGTGAGTCCCCCAAG	126	88
A052	α	EK3X9L02G8P4Z	GTCTCTCTGATGTTGGGCT	ATGACTGGTGGGRRAGTT	99	60
A054	α	EK3X9L01E21T5	CGACTCAACACATCAAGCAAA	CAACTCAAACCTTTACAAAAGCAA	125	79
A056	α	EK3X9L02JVJWB	TTTGGGTTAAATGGACAGCC	TTGGTAGTGGTGTATTGAA	98	56
A057	α	EK3X9L01DC6HA	AGCTCAAGACCTATGCTGG	CCTYYAAACCCATCSAGAAG	125	85
A061	α	EK3X9L02HQFHE	TGGTTAAGAGCTCAGGCTGC	GGGCCATAAGACAGGGTAG	101	61
A064	α	EK3X9L02HHRV7	TAGCAAACCTTGGCTGCCT	TTYAYTGTGCTTAGGGTTG	101	61
A065	α	EK3X9L01C7PXN	ATGGTGATGGGAGCTTGTAC	CAACATTTGCCAATCAACG	108	68
A066	α	EK3X9L01C28PT	TCTAGGGACTGGACCCTCCT	TGCCAGAAGAATAAACAGGTCT	108	66
A069	α	EK3X9L02II2C9	TCAGTTAACACCCACATCTGTCT	CTTSCCTTCCSTTCCCTTC	135	93
A071	α	EK3X9L02HHLB0	CCAATGCCATTAATAACAGAAA	AGGCTTCAATGGGTGAGTG	108	65
A075	α	EK3X9L01DSVGO	CACCTGAGGACTGAGTTG	ACYAGATGCCACTACCAA	107	68
A076	α	EK3X9L02FH2ZJ	CAAATTCATGCGCATTATCA	ACAATTTCTTCTCTGACTTCC	97	51
A077	α	EK3X9L01CPQOZ	GGACTGGAAAGCAAACCCCT	TGGCTTTAGCKGAAAGATT	125	85
A078	α	EK3X9L01C26GN	GCGGATTCCTGTATGGTT	CAGGYAGAGCCGAGACAT	108	70
A082	α	EK3X9L02GF929	AAAACAGAGCCAAAGTGGTG	AGAGTCTCTGGYGACAAT	108	69
A083	α	EK3X9L01D5415	TCTTGTCTTGGGACGGATAC	AGTGGCCGAGRTGGTTTG	120	82
A084	α	EK3X9L01BVALO	GCATGTGTGAGCTTCCCT	GCAGTAAAGSCTGGGAAGG	117	78
A085	α	EK3X9L02FPCGC	GCTCCACTGTGTGAGTCATCAT	GTAGCAGGGCAGGAGAGGAG	113	71
A086	α	EK3X9L01BLH35	ACACCTCTGAGCTCCCTGA	GGGSCAATCCTTAYTGTGTG	95	55
A087	α	EK3X9L02HII8H	AATTTGCAAGGCTCAGTGTCT	GGGGTTTACGCTTAGAGG	112	73
A088	α	EK3X9L02JBXZW	TGCTGTGTCAAAGCCTGAG	CTTGAAGGGGCTTTGAGAGA	107	67
A090	α	EK3X9L01AVFGZ	TACATTCGCTACCTCCCTG	TCTGTGTACAGACTGCTTTGG	110	67
A001	β	EK3X9L01BLRFR	AGGGCTTTGTAACAGTGAACAC	TCAGGACTTGCCTGTTCAGTT	140	96
A002	β	EK3X9L02F3RBB	CAATTTCTCATCTTTGGCTTT	AAATTTGAGATCTGTCCCGAA	135	91
A003	β	EK3X9L02HKE1R	AGGGAGAAGCTTGGGACAG	ATAAGCAGTCAAGAGCCCGA	121	81
A007	β	EK3X9L01C7BYB	CCTTGACACTGATAACTGGAG	AGCTAATGGAAGAAATGATGAAGT	131	85
A009	β	EK3X9L01C7XKW	AKTCCCYRATTACTACTAAGATTGT	CAAACAAATGAGAAAACAGTGC	108	59
A011	β	EK3X9L01AQJCF	AGGCAGGGCTGACTCSAT	ACTCTGCTGTGATGCTGG	106	68
A012	β	EK3X9L01BCGQI	AAAGGCTCTGCCCTGCA	GAGTGGGTTTATTGTACCA	124	87
A014	β	EK3X9L01AIIIP7	GYCCTTGAAWRTCACTGMTT	CATCCTCCCAACCTTTCAA	90	50
A015	β	EK3X9L02JWLAQ	AACAGAAGTATGGCTTCTTGG	TCATCTCAGTGACCAAACCTGAA	110	65
A016	β	EK3X9L01EN54P	TGACACAGGACCTATGAGTG	CTGTGCCATGTGGAAACAAA	110	69
A017	β	EK3X9L02I9G0E	GGAGAGAGCCCTCTGAGCC	CAGTCTGTGGCATGTCTGT	123	83
A019	β	EK3X9L01C0K93	GGAGGTCCAGGAGAGCTTTT	CAGCTGCCAACAACATG	109	71
A020	β	EK3X9L02F9G0Q	GCCAGTGTGGTRGGTGACC	TAGCTGGAACCTTGCCTGG	110	71
A021	β	EK3X9L01CTJZY	AAAAATTTGGTCAACTCACTG	AGAAATGACCATGAGCGGG	117	73
A026	β	EK3X9L02FFWKW	TGATTTGGTTATACGCTTCACTCA	AACTAACATGGTCAGCCTTGC	106	62
A033	β	EK3X9L01B83XL	AARAGGCTTTTGCAGCAGATT	GCAACATCATGATAAGTGGAGAA	119	74
A034	β	EK3X9L01AEV4R	TCACCTCTCCCTCCTAAC	GCTGTGTGGAGTTAGGGACC	120	80

A.1 = short

target ID	primer set	read ID GenBank SRA010805	F-Primer 5'-3'	R-Primer 5'-3'	product length in bp amplicon	product length in bp w/out primer
A036	β	EK3X9LI01AHAIX	TCACACACACCACCTGTTC	TCACTCTAATTCTTCATCCTTCCA	115	71
A038	β	EK3X9LI02IMKVX	TTCTCTGCYCTTCAAATTCA	TCTTCCCATTCTCAGAGG	94	54
A040	β	EK3X9LI02JSOT0	TGTGTGCTATCAGCCCTCAC	GTTTGCTCAAAGCTGTGGG	125	85
A042	β	EK3X9LI01BE9T9	GTGAAGCTCTGTGAGGAGCA	TGGAAGGTGCTCAGTGCTTA	119	79
A044	β	EK3X9LI02GFDDD	AACRCGCCCTTCTGRITTY	CACAGTGAYTAAAGCGGAA	92	54
A046	β	EK3X9LI01A3SP9	AATTTCTCACTCTGTTGGATCA	TGATGCAGTGGTTGAGGTGT	116	73
A047	β	EK3X9LI01AZEP9	GCTRCRYGTCTAGTACTG	AAACTGCACCTGGCCTTATG	90	50
A048	β	EK3X9LI02GRG6Q	AATGTCCYCAAAGGAGCTG	GAACGGACAGCCTGTGGTT	118	78
A049	β	EK3X9LI02HZ5M7	GCMACCCATGTACAACAGA	GACCCCTAAGGAGATGGTTG	116	76
A050	β	EK3X9LI02JDDAK	AGGCTGTCTATGGGGCTTG	CCACACTAAAAGGGACCCAA	107	69
A051	β	EK3X9LI01AX9UU	AGGGCCAGCTGCTTCAG	ACACTGCAGGGGGCTCAAC	105	70
A052	β	EK3X9LI02G8P4Z	TGCCCTTTCGAGTATCMCA	CATGTGGAGAACCTCCTTTC	99	58
A054	β	EK3X9LI01E21TS	TCTCCCTGGTCTCATCATCA	TCCCTCAATCCAACAGCAT	116	76
A056	β	EK3X9LI02JVJWB	TTGTGGTGAGAGCTCCTTT	TTCTGCAATAAAGATTGGC	100	60
A057	β	EK3X9LI01DC6HA	AAGCAAACAACARGCAGTCC	CTCGGCTGACTTTCCTTCC	115	75
A061	β	EK3X9LI02HQFHE	CAAAAGCCRRGGAATCAGA	ACTCACTGCCATCGAGTCAA	110	70
A064	β	EK3X9LI02HHRV7	ATGTTCTTTCTGGGGCTGCT	CTGCAGTCAGTCTTGACAGA	109	69
A065	β	EK3X9LI01C7PXN	TCACTAAATGCACMCCTGAAAA	AGAAAAACAGACTGCGTGCCT	103	60
A066	β	EK3X9LI01C28PT	CAAAGTCTGCCATCCTCAC	TGCATAAAAAGATGGACAATGAA	127	84
A069	β	EK3X9LI02H2C9	TGGGTCTTTGGCTAGGAAG	GCCTTCTTTGCTTTCTTCTT	117	77
A071	β	EK3X9LI02HHLB0	AAGGGTGGAGCATTCTATG	TTATGAAAGTGAATTAGACACGAAA	120	75
A075	β	EK3X9LI01DSV0	TGTAAGAAAAATGTTCTACATCCAA	TTTGTACAGAAAAGATCAAACA	108	59
A076	β	EK3X9LI02FH2ZJ	GCACCATCCCTGTGATTCTC	AGATCAGCCCAAAGGGTTTT	124	84
A077	β	EK3X9LI01CPQ0Z	TGGRATGCTTGACTTCCAGA	GCTTAAGGCATTTGTGAAATCAT	101	58
A078	β	EK3X9LI01C26GN	TTTTCTTTGCAAGTCCACTG	TGCTGAGAGTGTGTGTGTGC	113	72
A082	β	EK3X9LI02GF929	CTTTTGGCCCAATGGAAG	CAGATCTTGAGATGGGCCAC	106	68
A083	β	EK3X9LI01D5415	TTAACGCTCACAGCCTGCTA	ATGACGGGGCTTCTTCTTT	118	78
A084	β	EK3X9LI01BVALO	AGGAAGGAGAAGAGCAGYCTTG	GCAGGATTCTTGCTTGCTTC	110	68
A085	β	EK3X9LI02FPCGC	CTCTAGCCCAAGTGGCYTTC	TGCTGCAGAGACAGAAGGAA	115	76
A086	β	EK3X9LI01BLH35	AGGGTCTTGCTRCCTTCTCCT	TGCTGTGTCGACTCCTCTTG	107	67
A087	β	EK3X9LI02HII8H	CATGAATTTCAAGAAGGAGATGT	CTGCCGGTTCTCTACTCAGG	115	72
A088	β	EK3X9LI02JBXZW	CATGTTGCCATCAGCTCTT	AACGGCAATCCCATTTTACA	120	79
A090	β	EK3X9LI01AVFGZ	GAACCTCAGTTAAATCCAATAGTAGTC	TGGGCAGGATTCAATAGGAG	128	81