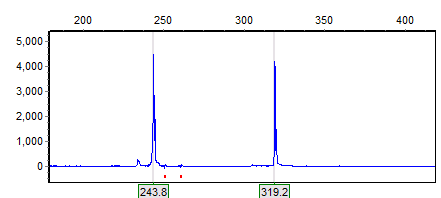
**Supplementary material**

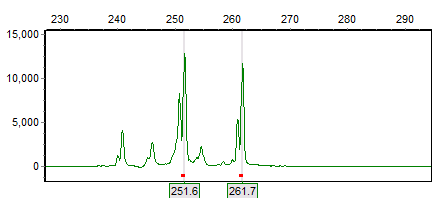
**Table S1** Characterization of polymorphic microsatellite loci used for ploidy identification in *M. anguillicaudatus.*

|  |  |  |
| --- | --- | --- |
| Primers | Sequences 5’-3’ | Motifs |
| MATS2-33 | CAAACTTTAGCAGCAAAACGAGT | (AACA)5 |
| TATGAAAATGTTGGTCACAGTGC |  |
| MATS2-48 | TTTGGTTTGTTTTTGTGTTGTTG | (ACAG)6 |
| AAGTGACAAACGGCAAATACTGT |  |
| MATS3-55 | TATCCAACGCTTCTTCATTTCAT | (ATG)6 |
| TGTATCCCCATCACAAGAAACTT |  |
| MATS3-65 | TTGTATAGAGAGCCATCTGAGCC | (TGA)7 |
| ACAACACCTCACCTCTTCTGAAC |  |
| MATS3-74 | GAATGCAGAGACGTGTGAAGATA | (TGA)7 |
| ACTCACTGGAGTTTCATCAGCAT |  |

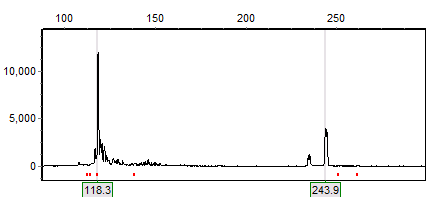
The data presented are a compilation from Feng *et al*., (2017)



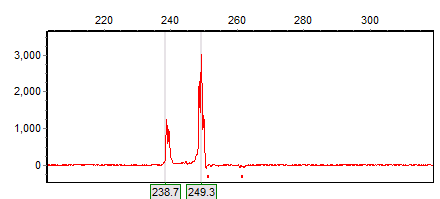
MATS2-33



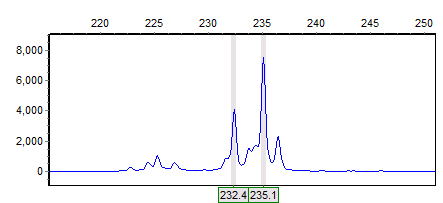
MATS2-48



MATS3-55



MATS3-65



MATS3-74

**\**

**Figure. S1** PCR products of microsatellite locus (MATS2-33, MATS2-48, MATS3-55, MATS3-65, MATS3-74) in *M. anguillicaudatus* as a material for genome sequencing.

**Table S2** The four fluorescent joints

|  |  |  |
| --- | --- | --- |
| Joints | Sequence5’-3’ | Fluorescent color |
| FAM | TGTAAAACGACGGCCAGT | Blue |
| VIC | CAGGAACTCAGTGTGACACTC | Green |
| NED | CGACAGACAGTAAGGTCTCTG | Yellow |
| PET | CACGACGTTGTAAAACGAC | Red |

**Table S3** Distributions of mono- to hexanucleotide motif types with different repeat numbers (from 5 to >10) in the assembled genomic sequences of *M. anguillicaudatus.*

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SSR motif | Number of repeats | | | | | | | Total |
| 5 | 6 | 7 | 8 | 9 | 10 | > 10 |  |
| A/T |  |  |  |  |  | 72011 | 71959 | 143970 |
| C/G |  |  |  |  |  | 4781 | 11475 | 16256 |
| AC/GT |  | 22289 | 11249 | 6761 | 4741 | 3580 | 22872 | 71492 |
| AG/CT |  | 14762 | 8832 | 5195 | 3396 | 2347 | 15554 | 50086 |
| AT/AT |  | 10122 | 5540 | 3617 | 2527 | 1875 | 7910 | 31591 |
| CG/CG |  | 361 | 98 | 23 | 9 | 4 | 1 | 496 |
| AAT/ATT | 7749 | 3893 | 2178 | 1439 | 842 | 734 | 1211 | 18046 |
| ATC/ATG | 1511 | 690 | 332 | 166 | 86 | 54 | 55 | 2894 |
| AAC/GTT | 1659 | 584 | 216 | 99 | 57 | 28 | 43 | 2686 |
| AAG/CTT | 820 | 302 | 149 | 58 | 41 | 27 | 37 | 1434 |
| ACT/AGT | 389 | 219 | 150 | 94 | 79 | 63 | 138 | 1132 |
| AGG/CCT | 457 | 117 | 46 | 21 | 10 | 5 | 7 | 663 |
| AGC/CTG | 413 | 115 | 39 | 19 | 9 | 2 | 12 | 609 |
| ACC/GGT | 426 | 92 | 34 | 11 | 3 | 3 | 5 | 574 |
| Other Tri | 110 | 29 | 5 | 3 | 3 | 1 | 2 | 153 |
| ACAG/CTGT | 4474 | 2608 | 1667 | 1088 | 376 | 53 | 90 | 10356 |
| AGAT/ATCT | 664 | 497 | 527 | 1037 | 1064 | 21 | 95 | 3905 |
| AAAT/ATTT | 2051 | 669 | 226 | 126 | 157 | 4 | 6 | 3239 |
| ATCC/ATGG | 1278 | 770 | 492 | 311 | 164 | 10 | 36 | 3061 |
| AAAG/CTTT | 966 | 515 | 394 | 384 | 348 | 12 | 42 | 2661 |
| AAAC/GTTT | 940 | 358 | 152 | 81 | 46 | 5 | 1 | 1583 |
| ACAT/ATGT | 462 | 272 | 190 | 144 | 125 | 8 | 4 | 1205 |
| ACGC/CGTG | 407 | 226 | 137 | 77 | 51 | 13 | 9 | 920 |
| ACTC/AGTG | 261 | 148 | 122 | 97 | 77 | 7 | 7 | 719 |
| AATG/ATTC | 304 | 144 | 68 | 63 | 79 | 9 | 2 | 669 |
| AATC/ATTG | 203 | 103 | 55 | 35 | 62 | 7 | 3 | 468 |
| AAGG/CCTT | 166 | 91 | 40 | 27 | 15 | 2 |  | 341 |
| ACTG/AGTC | 78 | 55 | 23 | 18 | 15 | 3 | 3 | 195 |
| AATT/AATT | 119 | 40 | 10 | 8 | 6 | 1 |  | 184 |
| ACGG/CCGT | 89 | 40 | 16 | 8 | 5 | 4 |  | 162 |
| ACCT/AGGT | 65 | 27 | 22 | 13 | 8 | 2 |  | 137 |
| AGGC/CCTG | 65 | 18 | 13 | 5 | 6 | 1 |  | 108 |
| Other Tetra | 279 | 120 | 58 | 26 | 30 | 19 |  | 532 |
| AAAAT/ATTTT | 179 | 123 | 271 | 8 |  | 1 | 5 | 587 |
| AATAT/ATATT | 135 | 86 | 245 | 3 |  |  | 2 | 471 |
| AATAG/ATTCT | 108 | 95 | 186 | 10 | 3 |  | 9 | 411 |
| AATTC/AATTG | 229 | 48 | 35 | 8 |  | 1 | 0 | 321 |
| AAATT/AATTT | 38 | 30 | 137 | 10 |  | 1 | 4 | 220 |
| ACTAG/AGTCT | 50 | 26 | 17 | 6 |  |  |  | 99 |
| AATAC/ATTGT | 45 | 27 | 16 | 6 |  |  |  | 94 |

**Table S3** Continued

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SSR motif | Number of repeats | | | | | | | Total |
|  | 5 | 6 | 7 | 8 | 9 | 10 | > 10 |  |
| Other-Penta | 511 | 235 | 299 | 175 | 7 |  | 8 | 1235 |
| AAATAT/ATATTT | 19 | 45 | 1 |  |  |  |  | 65 |
| ACATAT/ATATGT | 34 | 23 |  |  |  |  |  | 57 |
| AACCCT/AGGGTT | 18 | 4 |  |  |  |  |  | 22 |
| AGATAT/ATATCT | 14 | 8 |  |  |  |  |  | 22 |
| ACACAT/ATGTGT | 12 | 7 | 2 |  |  |  |  | 21 |
| ACACGC/CGTGTG | 15 | 4 |  |  | 1 |  |  | 20 |
| AAAATT/AATTTT | 3 | 7 |  |  |  |  |  | 10 |
| Other-Hexa | 80 | 86 | 8 |  | 1 |  |  | 175 |
|  |  |  |  |  |  |  | Total | 376357 |

**Table S4** Organization of the mitochondrial genome of *M. anguillicaudatus*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Positions | |  | Codon | |  |  |
|  | Start | End | Size | Start | Stop | Space/overlap | Strand |
| tRNA-Phe | 1 | 69 | 69 |  |  | 0 | + |
| 12S | 70 | 1022 | 953 |  |  | 0 | + |
| tRNA-Val | 1023 | 1094 | 72 |  |  | 0 | + |
| 16S | 1095 | 2773 | 1679 |  |  | 0 | + |
| tRNA-Leu | 2774 | 2848 | 75 |  |  | 0 | + |
| ND1 | 2850 | 3824 | 975 | ATG | TAA | 1 | + |
| tRNA-Ile | 3831 | 3902 | 72 |  |  | 6 | + |
| tRNA-Gln | 3901 | 3971 | 71 |  |  | -2 | - |
| tRNA-Met | 3973 | 4041 | 69 |  |  | 1 | + |
| ND2 | 4042 | 5088 | 1047 | ATG | TAG | 0 | + |
| tRNA-Trp | 5089 | 5158 | 70 |  |  | 0 | + |
| tRNA-Ala | 5159 | 5227 | 69 |  |  | 0 | - |
| tRNA-Asn | 5229 | 5301 | 73 |  |  | 1 | - |
| tRNA-Cys | 5332 | 5397 | 66 |  |  | 30 | - |
| tRNA-Tyr | 5398 | 5466 | 69 |  |  | 0 | - |
| COX1 | 5467 | 7017 | 1551 | GTG | TAA | 0 | + |
| tRNA-Ser | 7019 | 7089 | 71 |  |  | 1 | - |
| tRNA-Asp | 7092 | 7163 | 72 |  |  | 2 | + |
| COX2 | 7177 | 7911 | 735 | ATG | TAA | 13 | + |
| tRNA-Lys | 7939 | 8014 | 76 |  |  | 27 | + |
| ATP8 | 8016 | 8183 | 168 | ATG | TAA | 1 | + |
| ATP6 | 8174 | 8857 | 684 | ATG | TAA | -10 | + |
| COX3 | 8857 | 9640 | 784 | ATG | T-- | -1 | + |
| tRNA-Gly | 9641 | 9713 | 73 |  |  | 0 | + |
| ND3 | 9714 | 10064 | 351 | ATG | TAG | 0 | + |
| tRNA-Arg | 10065 | 10132 | 68 |  |  | 0 | + |
| ND4L | 10133 | 10429 | 297 | ATG | TAA | 0 | + |
| ND4 | 10423 | 11805 | 1383 | ATG | TAG | -7 | + |
| tRNA-His | 11806 | 11874 | 69 |  |  | 0 | + |
| tRNA-Ser | 11875 | 11942 | 68 |  |  | 0 | + |
| tRNA-Leu | 11943 | 12015 | 73 |  |  | 0 | + |
| ND5 | 12016 | 13854 | 1839 | ATG | TAG | 0 | + |
| ND6 | 13851 | 14372 | 522 | ATG | TAA | -4 | - |
| tRNA-Glu | 14373 | 14441 | 69 |  |  | 0 | - |
| CYTB | 14448 | 15588 | 1141 | ATG | T-- | 6 | + |
| tRNA-Thr | 15589 | 15660 | 72 |  |  | 0 | + |
| tRNA-Pro | 15659 | 15728 | 70 |  |  | -2 | - |
| D-loop | 15729 | 16646 | 918 |  | 918 | 0 | + |

**Table S5** The mitochondrial genome sequences for phylogenetic analysis in this study

|  |  |
| --- | --- |
| **Species** | **Accession No.** |
| *Danio rerio* | NC\_002333.2 |
| *Cyprinus carpio* | NC\_001606.1 |
| *Botia udomritthiruji* | NC\_031601.1 |
| *Leptobotia taeniops* | NC\_026130.1 |
| *Leptobotia pellegrini* | NC\_031602.1 |
| *Parabotia kiangsiensis* | NC\_053270.1 |
| *Parabotia fasciata* | NC\_026128.1 |
| *Lefua echigonia* | NC\_004696.1 |
| *lefua costata* | NC\_029385.1 |
| *Triplophysa bleekeri* | NC\_018774.1 |
| *Triplophysa dorsalis* | NC\_029423.1 |
| *Triplophysa rosa* | NC\_019587.1 |
| *Pangio anguillaris* | NC\_008675.1 |
| *Pangio oblonga* | AP011336.1 |
| *Pangio kuhlii* | NC\_031599.1 |
| *Cobitis lutheri* | NC\_022717.1 |
| *Cobitis macrostigma* | MK156771.1 |
| *Cobitis sinensis* | NC\_007229.1 |
| *Cobitis striata* | NC\_004695.1 |
| *Misgurnus mohoity* | NC\_022712.1 |
| *Misgurnus nikolskyi* | NC\_008678.1 |
| *Misgurnus anguillicaudatus* | DQ026434.1 |
| *Misgurnus anguillicaudatus* | HM856629.1 |
| *Misgurnus anguillicaudatus* | MF579257.1 |
| *Misgurnus anguillicaudatus* | NC\_011209.1 |

**Table S6** SSR sequences for *M. anguillicaudatus*

**MA-SSR-04**

**>scaffold1424239**

AGCCACTTGACTTCACTGGGTGGGTTGGAGTCCACGATACACACACAGACTGTAAGAGGCTCTGATTTACAGGAAGACTCGTTTTTAATCTCAGGGGGATCTATGATAGATAA**ATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAGTAGATAG**ATATAGACAGGGTAAGTTAACATGTTAGTTTAGTGTTTTAGCCAAACACAGGGTTATATTAAATAATATCCTGTTTTATTAACACCTTTATCAATATTTTCCCTACAACTCAGACTTCTCGTAATTTAGATTGTGTGATTTTTCTTTCCGTGTTACTCTTAAAAAGTATTGTACTTTCATCCTTCGTTTTGCTGAGTTTCATATTAATTTACACTGTAAGCCTGGATAAGTTGAGTTTACTTAAAAAATGAAGGTAACTCGTTGCCTAAAAAAACTTTAT

**MA-SSR-09**

**>scaffold756577**

TAAGACAACTGTACATAGGATACATAGTCCCATACTATAATGCACATACTATGTCCTATACAAATTTATTTAAGAATGCAGGAATGCATGCAGACACACATCCACCCAGAGGTGCAGTGGGGAAAATCTGTCTGAGCCTCTGTAAACCTTTCACCCCTGTGCCAACCTGAGAGAAAGCTGTTGGTTGCCAGATTGTCTAGGTCTGTGTTTTTTTCTCCTGGTCTTGGGCATTAGCCGCTCTTTGAAAAGCACCCAGACTGATGAAGACCAGGTGTGACTATGTGTCTGAATATGTGCGACAGAGACATATAGTACAGC**GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCACAGA**GGCACAAAGCTTATGTGAGTATTGGATCTGCTGGTAGGAATGATTGCTATGTAAGTGTGTATTGAGATGTATCTTCCTTCAGTTCAAGTGTGTGTGTCTATTTGCTCCTTCTGACACATACACTCACACGTACACACACACACACACACACGCACACACGCATGCACATGCACACACACAGTCGTTTCTTGTAGGTCAAGTTTGCATCTTTTACCTTAACTAAAACACAGAAAGGGTCAGACTCAGAAGTTTAATGTAGTATTCAGATACTTTGGAAATATGTGAACACATGCATGTGACTTTGTGTGTGAACTCCAGGCTAAAGTCTCATAATGCATTTATTACTGTATATTATGGGCATCAAAGTTTGACATTCTTTGACTTAGTCAATATTAAAGATATCAA

**MA-SSR-10**

**>scaffold454499**

CAATTATTTTTGCCCTATTACTTTGTTACAGTATTACAATACGTGTCATTTTTACCGTATTACTTTGTTATTA**CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT**CTCGTTTTGCATGGGAAACATTAGTATACACACATGAAAGAAAAATATTGAAAAGGTTAAATGCATACACACAAAATTAATTCCAAAATAATTTAGTATTTTACCTCTCTTAGGGTCAGGATGGACCTTGTGCTGAATGTTGCGGATTATTACTTCTTCACTCCGTATGTGTATCCATCATCATGGGCTGAGGATGAACCGCTGCGCCAGATCATCGGTTTAATGGTGGTCACCAACCTGGGTGCTGCAATCCTGTATCTTGGCCTGGGTGCTTTAAGCTACTTTTTTGTTTTTGACCACAAATTAAAGCAACACCCTCAGTTTTTGGAGGTTGGTTTATCCACGTCTATCTTCTTACGTTTAGTATAACAGGAGTATATTAATGTGTTTTATTATTTTTGCCCACAGAACCAGGTGCAACGAGAAATAAAGTATGCGTTGTGGTCTTTACCCTGGATTAGTATTCCTACAGTGGCGTTGTTTTTTGCCGAGGTCAGAGGTTACAGCAAACTGTACGACAATGTTGACGAGTCGCCGCTTGGTAAGAGAACAGAGCTGTTTCCTTTAATGTCAGTCAAAGTTCATATTAAGTCAGTGCTACACAGGCTTATCAACTGGGTTATAGTTGTTTATAGATAAATAAGCGATTTAAAAATACAAATCAGATGAAATGAAAATTATGAAATCTAGATCAGACAATCTGATAACCCCAACTGTAGAATA

**MA-SSR-11**

**>scaffold604377**

AAAAAAAATAAAAATCAAAGTAAATAAAAAAAAATGCTCGGTCTACATGACCTACCGCATCGCACTGCTGGGTGCGGATACTGGTGCAAAAAAAAAAAACTGAGTAAGAATGATATTTTTCTGTTTGGTCTTCCGAGAGCCTGAGCTTCTAATAGCGGCAATGTGCCGCTGGGATCCCCTTCTACAGCCACAGAACAGACGCACAGCTTTACTGGCCTACGTCAGCACGCAAGAGACGCACAGACTTACTGACCACGCCCCCACGTACGAT**TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGA**CAGATAGATATTAACAATATAAGTTTTTAGTACGTTTTTTAGTAATCAAGTCATTCCCTACCCTGTAAGCTTTGTGCATATGTCGTGTGTCATTTTTTGCCTCTTTAAATTATTCTCAAAGCTGAGCTTCAGTTTACAAAATTTTTAATACATCTTCAATGTGTTTTTTTAGATCTTAGTTACCACCTCAGCTACTGCATTCACACATATTTCTAATTTTTA

**MA-SSR-17**

**>scaffold812085**

ATTATCAGATACAACCTAGAACTGATAACACAGCCTCTTCTTGGTAATACGAGTCATTTTGAATG**GAATTGAATTGAATTGAATTGAATTGAATTGAATTGAATT**GAATGGGAAAACGCTGTGATGGAGAAGACCAGCAGGTTAATTTGTGCCATCCTGTCCATGGGAAGCAGGAACTTCAGGTACAATTCTGCCAAAGAGAAAGCCTCAATCAAGTGATGCCTGATGGTAGGACAAAGTAATGAATAAATAATTCATTTTACATTTATGTCTCTATTGCAGTCTCTGTTTTCATCTCTTAACCGGTATTGAAAAACAACTGACGTTCTCCAGGAAAAACGACCTGACAAATCAACTTATCAAACTTTATAATAAACTTATACCATTGTGAATATGTGTAAGATAAGGAGATACGTGTTACATTACAGATTTTTGACTTTAATATTGCGCAAAATATTTTTCACAGGAAAGTGCTACTCAAGTTTGCGTCATAAGGTTTTGGTTTCATCATTCTGTATATGAACAGCTTTATTTTGTAGAACTGCTAGGTCCTGGGGTTTCTGGTCTTCTTCTATCATTTGCAGTATGCCACCATCACTGACAAGAAATTATATATTTTTCCCCAAGAAACATTTGTGTTTGATCACTCTGTACAAGAGATCTTGTACAGTAAAAAAACATTACAGACTCTAATTCTCTAATGATTCTCCTGCTTCCAGTTGGTACTGTATCCTGTACATAGGTCTGTCAGGCTCTGCTTATTTCCTAGGGGCAATTAA

**MA-SSR-19**

**>scaffold530079**

ATTTAAACGATAAACCATACCATACAGAACTTACCTGGAAGTTAAATAGGCTAAATTAACCGAACAAGCCAACT**ATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCA**ATTTTATTTATATAGCGCTTTTCACAATTTGGTAATTGTATCAAAGCAGCTTTACATTAATAGAAGGAGTGAAAGCGCAGAAAATCGACAGTTAGCACAACATAATACACGATAGCACAAGCAGCTAAATTTG

**MA-SSR-31**

**>scaffold465339**

AGGCAATAAATCAGCTATGCCTTCACAAAAACAACTTTTTATTTAAATTTTTAATGTGTTGACACAATCGACTTTATTTTAATGTTTAATTGATACAATAAATGCGTAGTAAACCGGTGAATCTGCTTTTTGAACCAGTTCGATGAGCCGAACTGTCCGAAAAGAGCCGGTTCGTGAAAATGAATCGGACTTTGCATTATTAAGCCCTAGACTAGACTAGACT**AGACCAGACCAGACCAGACCAGACCAGACCAGACCAGACC**ATACAAATACTAGGAATTTGGTTCGGTATTCTCCATGCAGGCAACACACAGTACAACATACAACATGCAAATTAATTTAAGTTAAGAGTCATTTAGAAGGGCTATTGCATGGGGGAAAAAACTGTTGCGATGGCGTGATGTTTTGAGGAAAAATAAACAAGATAACGAGAGAAGGTCAGGTGAGGGGAGTTAAC

**MA-SSR-34**

**>scaffold656427**

AAGTTGATACAATGGTTGTAAAATGAAAATATTTGTCTTTCTTTCTTATAGTGTAAAAGACAGCCTATATAATGTAGATCCACTGATCAAACTGATTTTATTAAGTGCATTTCCA**TATCTATCTATCTATCTATCTATCTATCTATCTATCTATC**CTAATTAACACTTAATACTAACCGGAAATGTAAATCTCACATTTTTCAAACAAATAGTTTCAGATTTTACAAATTATGACAAATGAATATTCAGATTTCATGCCCTTATTCAATTCGTTTTCATTTTCTTTTGTAATTTAATGATAAGTGTGTTTAGTGTCCACCTCTATAAATGATGATGGGTTCATTGAGCTCAGTGTCATCTCTTCTGACTGGTCACTGGGGAGAAAAAGGAAATCGCCACTCAATTAGCAGCCCTTGACCTGTCACTCTGAACTTTGACCTCCGTTGTTTAAGTCGGGTTTATTGTCCTCCAGGGAGCGACCGGTCGGTCTCTGTCCATCTGA

**MA-SSR-35**

**>scaffold635637**

AAATGTAAAGGCTACAAGTGAACTTGAATTTTACTAGCTAATAACATCTTTGTGTTTTCCCCAGTTTATGTATGGTACCAGTTACCCTGACGTTGTCCAACTGTTCCCTGGCTCAGGTAGACGTCATCATTGATCTGCGACACAAAACGACCAGGTACATCTTAGTTTTTGAACTGATGGCCAAAATTAATTTTAGATAGATAGATG**GATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATATAGATATAGATA**GCATTAAAGGGTACCCCGACTATAAACACATGGATGGCTTAATAGATTAATAATACTGGGATTGGCTATATCAATGTTAAATTTAAAACTGTACAAATGTTAACATGTAAAAAATATAACTTTGAAAGAATCTTTTCACTTGGAGGCCGCCATTTTGTTTGCATCACAATTCATGTTGTCAAAAGGTAGCAAGCAAAACTCGTTCTATTAACGTTACACTATGAGAAGTTTTTAAGTTAACTTAAAAAATACTTAATTAACACCTAAAATAATTTCAGTTTAATTGAGAAAATAAATTTGAAAAAGCTTACATTTTTTTGGTATTTTTCTGACTTTAAAGGAACAGTAT

**MA-SSR-38**

**>scaffold659133**

AATGAATCAAATTATGAGCTAGCATACAAAACAACTTTTTTTGAGTGATTGCACACCGTAAGAAAAATGGTAAAAAATATTATCAAGCAGTGACTGGGACAGTACCCTTAAAAAGATCCTATTTAAGTACAGATTTGTATACACTGAACAACTTAAAACAACTTGCAAGTCAATTCACTTATAAGTTAAAGTAGCATAAAATATATGTTGATTTTGACAAAAGTGTACATTTGGTACCAATTTGTTCCTTTGCAGTACTAATGTGCACTCTTTGCTACACATCTATGTACAAATGTGTGATTTTTGAAAGGGTACTATCCCATTGACAGCTAGG**GAATGAATGAATGAATGAATGAATGAATGAATGAAT**GAACACGCTATAATTATTGCAATGTTGATCCAAGAACATGTCCTGCTTGTTGAATTCCCATCCACCCACCAGGCATCAGGAGATACCGCCACAGCTTTGTGGTCAGTATGCTCAGTGATGAGGACCTGCAATTTAATTTGCATGCAGGGTCATGAGGTTGTGCAGAAATCTGACTGCAGTAGAGACACACACACACA

**MA-SSR-39**

**>scaffold674301**

GATTTTAGATAAGCAAGTTTTCATTTGTGTTTAGGAAACTGCTGGTTTTTGGCCTCATTTGGGGCACTTAGCTGTCAACAGGATATTATGGACAAAGTCATTCCAGTTGAACAGTCATTCGACAAGGATTATGCTGGAATATTTCATTTCAGGGTAAGCACGTAGTATATAATTTACTTAATTTTCATATATAAATATTATATTATCACTCATTGACTTAGAATTTCTGTGTTTTGTGTATTGCACAGTTCTGGCGGTTTGGGAAATGGATTGATGTTGTCATTGATGACCAACTGCCAACAATTAACGACAGGCTAATTTTTGTTCATTCAAGAACGCCTAATGAATTTTGGCCTGCTTTACTGGAGAAAGCTTATGCAAAGTAAGTGCCAGGACACCATTTATGATTACGATAACATCTGAATAATCTGTAAAACTATTCATCTCATAGACGACGGGAGATAACTTCACAAATGCGATG**GATAGATAGATAGATAGATAGATAGATAGATAGATA**TAAACAATTAAATGAGTAACATACCTTTAGCAAGTACTGCTCTTTAATGTGCGCCCGATCAAAGCTCACATTGTGTCCAACCACAAGCCTCTCCTGCCACTCGCCGCCTGGTGGTAGAGGGATTCGGTTCTCCCGCCCAAACTGGATGCCAGTGCATTATTGTTTGATGAGTCAGACAATGTTCGCGTGCCTCGCAGTTTGAGCCCCGCCCCGACTGGTCTATTGAATGTGACACAAATATGAGGAGTTGATAGAGATTATAACTCGCATGTCAGTTTCTCCCGCCCCAACCAGTGGCCAGTGCGTCATTGTTTGATGAGTCAGACAATGATATCATGTTTCACACGTTTGATAAGGCATTCAATAAAGTTTACACAAG

**MA-SSR-40**

**>scaffold688025**

ATTAGAACTTTAGTTTCTTTAACCAGATGTTCTTCCATTTTATAAAAAGAATGTTATTGGAAAGAGAATGTTACTGCAGTATTGTTGAAGTTGGGGGTATGTTGACTAGTAAAAAAAAAAATCATCTATCTTCAAATGTTCTGAAATAAAAAATCTAGACTTATTTTTACCAAATCACCCAGCCTTAATTTGCTACAGAAAATATAGCATGTGGCAGTATACAGCAGCACAGTAACATTCAAAGATTGCAGATGTTTACTATTTTAAAAATATCACATAAAATCACATGCTTCCTCTGGCTGTAAACAATCTAATGCAAAGTAAACAATCTAATGCAAACCAATACATCACTGTATACATGACAAATGAAAAACAACAATAAATCTGTGATCGTGTTTTGAACAGGCCCAGGCTGTTACTAGCTGGTAAGGATTCCCCAAAATTAAATCAATAAAGTTTTCTCCTT**TGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTC**CTGTTCCTTCTCCTAAAAAGGTAATGTCTGACACAGTCTTTAAGGGTTTGTGCTTTTTTTATTATTTATAATTATTTATTACCATAAATAAACATTGACACAATATTTACACTAATCCTAAATACAAACAACTATTAAGAACATGCAATGAAACATACACATTTGAAAACCAAGTCTTTAATTTAACCACCAAAGAGATAACAGTCAAAAGAAGAATATGCTTAACGTATATACAATTATGTCGATATATTTAAGCTTACATGCCACTCCAGTGACATCAGCACTGATACGTGAGCATTGAGCAGGGAGATTCCTCCTGCTGCTCCACAGTTACTATGGCAACAGAGGAGAGCAGGTCTGCTCCCGCTAT

**MA-SSR-43**

**>scaffold743313**

AGAGAGAGAGAGATGAAATAGGAATGTCTGTGGCTATTTTGTGTGGGTGTTGGGGAAAGACTATATTTGTGTGATGTGATGGAGGGCTGGAGAGAGGAGCTGAATGACATTGGATACACAGAGGAGGAGGAGAATATGGTGGTATAAAGAGTTGCAGTGATTAAGCCACCAATGTTGTTGCCACTGTAAAAATAATGGGAAACACATGACTAAATTTGTTAATTCATTCAGTCTGCTCTCTCAAATTAACTCACTGTCTCTCCCTCTCCTTTCTTCAAAATGCCCCTCACTTCCTTTTATGCATAATCATACACCTAAACACACATTTTATTATTCTCGTTCACCTCTTTAATTACGAAGAATTGCCACTCCTTCAGGTCTCTTTGGCTAACCATCATTCCTCCCTGTTGCTATGGTAACAACATTTCTCAATGGGACTGGCATGATTCTATTTATGTTGTAATACAGTGATATGATTTATTATAATCTCAGTGTATCTGTCAATCTATCAATCTATCAAAAAAATC**TCTATCTATCTATCTATCTATCTATCTATCTATCTA**CTCTACGATATCCCATTTCCTCTTCCTGCGGGTACTACAGGTATCAAAAGAGTAACGCATTAACATCTCACAGGAACACAAACCAGCAAAGAAAAGGAGATCATCTGACCTTTGTCAAAGATGTTTGTGGCCTTTGTTGATGTGGTTATTCTTCAAAATGAATTTGAGCTTCAGGCACAATGTGACAGGCTTTATCAATTCACATTGTAGAAAAGCAAAGAAACAGCACTGTTCAGTAACCCAGGAATTTAACTTTATTTACATTCGTTTTCTGTGTAAGAGCTATTTTGAGCTGCATTGTTAATAATAACACACCGCTGACCTGGAAATAAAGGGCAGCAGATAAGAACACGGTTAATCAATGAGCGGCACATATAAGTGACTGTTCGCATGCATTCAGTGACTCGATATAAAACAAAATGTGCCTTCAGTAAAAGACATAAACACAGAATTTCTAAAAGAGTTTGACCTTTACAAAATATGTTC

**MA-SSR-48**

**>scaffold831599**

TGTGCAGGGATGAAGTAAGGTGTTGCGCAGGTGTTGGTGAACATGTGAGGTAAAGGCAAAATTGGGGTTAAAGGCAAAATGACATATTACCGTGCATCAGTCATGATGGGCGATCAGACCTACCCAGTCTCCTGAGGATGCTTATAAATTGCTCTACTATGGTGTGCTTTCTGTGGAGCGAACTCAGTTTTTTTTATTATGAGCATATCAGTGCTTTGAAGCATTGAAGCAGACTCGTTAGCCGGATACTGTAACGC**ATTATTATTATTATTATTATTATTATTATTATTATT**GATAGCAATTTCTGACTTTGTCATGCACTTTCATTAGTAATAATACCATGCATCCACTACTACTACGATAATTACCCTCTAACAAATGCAGGGCTATTTTTTAAAAGAACGTGTATTATTATTATTATTAGTAGTAGTAGTAGTAGCAGTAGTAGTAATAGTAATAGTAGTAGTATTAGTAAAAGTAGTGGATTTATTAGTAGGCCTATTTGTTTTATTATATTTGAGAGAGCACCCAAACTAGCCGTTTTATAAATAAATGAACTAATTCGCAATAGCATCTGGCTTTAGGATCTACATTAATTCCCATATATTTCGATGACATTAACACATTCCTCATATTTACAGTTGTACATTAGGTAGATGCCTTTATTCAATGCGACGTACCAACAAATCTTTATGAATTTACAGTAATTTTAAGTAATGTTTTTAGTATGTGTGTGTTCTCTAGGAATCCACACACAATATTTGCTTTACAAGCAATAAA>

**MA-SSR-51**

**>scaffold422743**

TGTAATGTAACGTAACATACTGTAGCATAACGTAGCGTAACGTAAGGTTACGTAACGTAAAACAACATATTGTAACATAACATAACATAACATAGCATAACAAAGCGTAACAAAGTGCAACATAACGTAACATAACATACTTTAACATAACATACTGTAGTGTAACATAGCATAACGTAACGTAACGTAACGCAACGTAACGCAACGTAAAATAGCATACTGTAACATAACATAACGTAACGTGGCGTAACAAAGTGTAACA**TAACATTGGGTAACATTGGGTAACACTGGGTAACATTGGGTAACATAACATAACATAACATAACATAACATAACATAACA**GAATTATAAGAAAATAATGCACACCCAAGGTGGTTATACAGCACAACACGAAGTGTGCATTATTTTCGAATAATTTAAAGGACCGAAAGTAAAATAACGTAACATACTATAACATAACAACGTAACATGGCATAACATAGTGTAACATNTAACATACAGTAACATAACGTAACATAATATAACATAACAACGTAACATGGCATAACATAGTGTAACAT

**MA-SSR-58**

**>scaffold539485**

ACAGACAGACAGACACACAAACAGACACCCACACACACTAACAGACACAGACAGACAGACAA**ACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACACAAACAGACACACAG**CTGGTGTGTATAAAACATCCTGCTGCACACAGATGAAGTAGCGAGTAATGAGAAATGAGGGGAGAGGATCGAACCCGTGAGGGGGGGTCAAGTGAGTCAGAGTCGCTCCCGCAGGACTGTGAGGAGGAGGAAGACGTCACAAGAACTGAAGATAGGTGAGGAAGAGACAATCCCATCACAAAATCATCCCACACCAACCACTGCAAGAAACTATGATATTACACTGCAACATTTTCATGATTATTGTGCACCATGATCAAACTGTTTTCATTTAATTCCCAGGAGTCAATAGATTCTCATTCTGTGATACAGTAAGTGTTAATACTATAAAACAGCTGAGCTTCATTCAAATAAAACACATAATACACTTAGACCTGACACAAATATATTTTGGTCAAATCAAATGAATTCAGAAGAAC

**MA-SSR-67**

**>scaffold755367**

ACAAAAAACTGTTCTAAAACTCAACATTTTAATAGAAAAAACATTAAATTATCCAAAAAAGTTGTGCTTTTGGTTAATAGCCTTATTTTTTTAGGTTTAATTACACAGAATTCATGATAAATTAATGTATTTCATAAAATGTCATAAAACTGGGGCCCCCCTGGCACCATCTCGCGGTCCCTCTGTTGGCCCCGGCCCCCAGTTTGAAAACCACTGGCATAGCACGTTTAAATAAATGCAATACAAATCTATTATCTTAATAAATGCAGCAGCAGATGTTGAAATTGCTGCCTTTTAGTGAAGGGAGGGTGTGGCTTGTACAGTGTTTTTTCTGTGTCATCCTTTGACCCGCATTTATGTATTTT**TATTCTATTCTATTCTATTCTATTCTATTCTATTC**NTAAAATGGCCTCTGGACTGTTCACATAACGAGAGAGATGATAAAATGTGAATAACATTGGATTTACAGTGGTGAAGAGTTCAAAAGGTCCATCATGCATTTATTATTTATTTGGGCGAAATGAATGAAACAATACAGCAATAAATATAAGCAACTCTTTTGATTCAATACAAGCCTTTATCAAGCACATTTGCAATCCACCTGCGGAAGTTCTTAAGTATAAATAATTAAGAATTATAAAAATCTCAAGTTAACAGCTGCAGTGCGCTTTATATGCATGCATTAGGAATTTTAGTCACATCATAAACACGTCAATAATCATTTGCATATGAAAATACATGGTGTAACAAG

**MA-SSR-68**

**>scaffold767455**

ACGCACACAAAGGGATTTGTTTTAAAATATCGATAGTAGAGCTTGAAATATCGATACACTATTGTGAAAAGTTTTATCACAATAGTTAGCTGTATCGATATGTTTGCACAGCCCTAATAATGGGTTAAGCCATGTAGTGTTTGGTCCATATTGCTGC**AAATAAAATAAAATAAAATAAAATAAAATAAAATA**AATACTTTTCCTTTTTTGTTTATCTAAAATGTCAACAAAAAAATTCTTTACTTTTTTTAAGCCAATGTGCTTTCACACGCTTTTACATTTTCTGCCATTTTCTGGCCGAATGGCCGTATATGACAGACAACGGGACAGTGACAACTACAGTAGCAGCGGAGGAGGTCGTTTGCAGTACGGACCTGCAAAACGTAACTGTGACATCAATTGTACAACGTTAGCATATAGCATTAACTAGCATATAGTGCTAACTC

**MA-SSR-69**

**>scaffold634523**

GATATATTCAACAAGGACTAGTTAAACAACAGGATGGTAAGCTGAGAACTCATTTACTAAACACATCTACACAATCTGAATCATAATACCAACCTGATCAACTAAATATAACAAACACTTTAAACAAGCCACGTGTTTGAAAGAGATTTAATATTTTAATGGTTGATATATAAAAGAAATATACAACTACAACACAATGTTTTATAAAGAAGAAGTCTTGTTCAGTATTAAATTAACAGCTAATGTGTTCATTTACACTTAACTTACATTCAAGTTGTCATGTATAGTTCACAGTTTGCAGTGTTTTGTTAATTGTTTTGTAGTATTTGTTGATGATGTACTTTATGTATACGGTCATACACGTCACCTGTAACTCTGGGTCAATTTCTTGTCCTCTTTCATAAAAGCTGTATTTTTTATCTTTTACCCATAAAACTGCAACTGAACTT**ACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG**TCCACCGTCTGCAATGATTTTAAGTGATTTGATTTCCATAAATATACCTGACAAAATGTTGTCAAGAAACTAAATTTGACAGAGACGGCGGCCTCAATATTCTGTTTGTTCATTTAGTCATCATCTCAGCTCACAGATTTCTGTAGTTTTGTTTACCTTCATGTTAGGAACCGCAAACATGTTTTAAATTTTTCTCATCAAATTAATTATGCATTTAAGTTATACATACACTGCTGGATAAATAAGAATATCTGAAGTGCACCAAAGCTTAGGGTCGGGTGCTTTGACAGATTGTAATGTTTAAGTGAATCCAGATGTTTTCTCA

**MA-SSR-70**

**>scaffold398107**

ATCTTCGCTTGCATTCATTCACTGTAAAAAAAGAAATATGTATATATAAATATTTATTTATGTTTATATAATACAATATTACAACTAACACTTCTGAATTTCTTTTACAGATATCTTGCAACTTGGGAGAGTTTTACCAGCCTGGCATTCCAGTATTGATTAGGGATAAGCACCGACCTGCAAAGCCATTGAGAGTGAAATGATGGCCCGTGTACACGGACAATAAAGTG**CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTTTCTATCTATCTAT**CTGTCACCCCTCTTGGATGTCCGTGAACGTGCCAAAAAGGTTCAATGTATGAACGTCTGTTTGGTTCACCCTATGGGCGTCTGTGGACGTGCAGTACACAGCAGTGAAGAACACAGAGACACTGTGACATGTTTGACGCTGTGAGTATGAAAGGAACATGTTTTATATTGACCAAATTTAATGTGTTAATGTATCTTT