

## Supplementary data:

# Development of a microsatellite primer set to investigate the genetic population structure of *Armadillidium nasatum* (Crustacea, Oniscidea)

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**Table 1.** Raw data of the 245 reads containing microsatellite motifs from microsatellite-enriched genomic library made by Genoscreen (Lille, France).

| Loci name | Forward                      | Reverse                     | Repetition number | Repetition type | Amplification band | Label dyes | Selected                                |
|-----------|------------------------------|-----------------------------|-------------------|-----------------|--------------------|------------|-----------------------------------------|
| An_05     | AAGATATGGTGGGGAGAGGG         | TTCCGTCTCCTTTCTCACTTT       | 6                 | ga              | Yes                | NED        | Yes                                     |
| An_12     | AGACGAAAAGCAACACTAGAAACA     | TGCTGATGACTCCACTCTCC        | 7                 | ga              | Yes                | HEX        | Yes                                     |
| An_16     | CTGAAAAGACCCAGAACCA          | CGTTGTTGTCGGAGTTGTTG        | 8                 | aca             | Yes                | 6_FAM      | Yes                                     |
| An_17     | CTCCACCACACATCTTTCACA        | AAGGTTGAAATAGTCATTTGGGA     | 8                 | ct              | Yes                | HEX        | Yes                                     |
| An_20     | CAGAGGAAATGTGATAGCAAG        | TCAAGGAATAGTTGGAGAGCG       | 10                | ga              | Yes                | NED        | Yes                                     |
| An_07     | TCGAACCTCGACTGCTCAGAA        | TCTACGACCTCCTTCCAACG        | 6                 | ag              | Yes                | HEX        | Yes                                     |
| An_11     | ACAGGACGTCCAGCTGATTG         | AGTCCAACCTCTCTTAAAAATCCT    | 7                 | ct              | Yes                | 6_FAM      | No: monomorphic                         |
| An_14     | CAGATCACC AATTAGATTGTAAAG    | TGCTGATGCTTTTATTCTGTTCAT    | 7                 | aac             | Yes                | NED        | No: monomorphic                         |
| An_15     | CCATGGCAGTCAGCTGTTAG         | CCCAGCAGTTCAGTTAGTTCG       | 8                 | gga             | Yes                | 6_FAM      | No: too poor Amplification Success rate |
| An_01     | TCGTTTATTAATTCCAGTCACGA      | TTGCCTACCTTTCTGCCTGT        | 6                 | tg              | Yes                | 6_FAM      | Aspecific                               |
| An_09     | TGTATCCCTATTGTATCCACC        | GCTGAACTTGGAGAAGAGGTGT      | 7                 | ct              | Yes                | 6_FAM      | Aspecific                               |
| An_10     | AGGATGAGTGGGAGGTTTA          | TCCCTCTACCACCATTCAC         | 7                 | tg              | Yes                | HEX        | Aspecific                               |
| An_13     | CTCAATGGAGGAGGTATGCG         | ATCGTTGAGTCACTCGCTTT        | 7                 | ga              | Yes                | 6_FAM      | Aspecific                               |
| An_19     | TTCTCTCTCTCAACCCT            | GGTGCAAGTTCAGAAGCACA        | 10                | ct              | Yes                | 6_FAM      | Aspecific                               |
| An_02     | GCAACGTAATTATAAAGTGCCAA      | CGTGAGTGTGACTGTGACTGTG      | 6                 | actcac          | No                 |            | No                                      |
| An_03     | ACTGAACCCTGGGGAACAC          | GGAGGGGTGTTCATAATTGG        | 6                 | ct              | No                 |            | No                                      |
| An_04     | TTTTCGGAGAAAGGAGAAGTAGAAA    | TTTGTTAACTAGATTTGAAAAACAGGG | 6                 | taa             | No                 |            | No                                      |
| An_06     | TGAGGTCTCGGAATGACAAC         | CGTCTACCTCCTCTCCCTC         | 6                 | agg             | No                 |            | No                                      |
| An_08     | AGCGTTAGTCTTTTGCTTATG        | AAACTAACCAAACCTAACCAAACCT   | 6                 | ggtta           | No                 |            | No                                      |
| An_18     | CGATCTACGCATCTCCGTTA         | TGGAAGTTGAATGCGAAGAA        | 9                 | ct              | No                 |            | No                                      |
| An_21     | ACCAATACAACCTCAACGGC         | GTTGTCGCTTTGTTGTCGTC        | 12                | caacga          | No                 |            | No                                      |
| An_22     | AATGAGGGGTGGAGTCAITCA        | AAGGCCTTCGATTGTGTCTG        | 12                | ag              | No                 |            | No                                      |
| An_23     | ACCTACCAATCGGAAAGGTCA        | CGGTAGTTACGTCCGACTCA        | 28                | ca              | No                 |            | No                                      |
| An_24     | CGATCGAAGAGTTCGATTGC         | TTCTGATAAATGACATTGTGGAAA    | 5                 | aac             |                    |            |                                         |
| An_25     | AACAAAAAGAACAACCTTATCATCG    | TCCTGTTCTTGATGTCGTTG        | 5                 | aac             |                    |            |                                         |
| An_26     | CAACAAAAAAGCCACACC           | TTGCTGTTATTGTTCTCTGCTG      | 5                 | aac             |                    |            |                                         |
| An_27     | ATTGGTCTTAACGCCAATCTG        | TGGTGGGTAGCGTTGGTATC        | 5                 | aat             |                    |            |                                         |
| An_28     | GCAACATGAGGTAGGCTATGG        | AGTTGCGGCTAAAATGAATG        | 5                 | ac              |                    |            |                                         |
| An_29     | TCAGTCACCCAAATCACAAA         | AACTGAGCTGCTGGGGTTAAT       | 5                 | ac              |                    |            |                                         |
| An_30     | AACTAACGGACGATTGGTCTG        | TCTTGCTGTTGCTGTTGTTG        | 5                 | ac              |                    |            |                                         |
| An_31     | CGGAAATATAAATCGAAAGAGCA      | TCTCCCGTTGCATTAGGTA         | 5                 | ac              |                    |            |                                         |
| An_32     | GGCAAATTACCAACAGGTATAACA     | TTTGCCTTCTAGATTGTTT         | 5                 | ac              |                    |            |                                         |
| An_33     | CCATTCATCATCCATGTTTCA        | GACACTCTCGTAATGTATCGGT      | 5                 | ac              |                    |            |                                         |
| An_34     | AACAGCAACAACGACAACGA         | TTGCTGTTTACATTGCATTG        | 5                 | aca             |                    |            |                                         |
| An_35     | TAGCGCGACAGCAAAAGAAT         | AACGCTCTGCTGATGGTCTT        | 5                 | ag              |                    |            |                                         |
| An_36     | TTGGATTCAAACCTGACGAC         | GGAGAAAAGACTGGTAAAGGTGG     | 5                 | ag              |                    |            |                                         |
| An_37     | CTTTGCGGAATCGAAATGAG         | ACAATCGTTAGGCGGAGCTA        | 5                 | ag              |                    |            |                                         |
| An_38     | GAGGCCACATTGGAACCTTT         | CCACTGCAACCATGTGAAAT        | 5                 | ag              |                    |            |                                         |
| An_39     | TGTCACGATTCTGGGATGAA         | CGCCATTACAATGGACAAAAG       | 5                 | ag              |                    |            |                                         |
| An_40     | AAAGAGGTTATTAGGCTGTAAAGGTG   | TCCACAGTAACACTCTACCTCA      | 5                 | ag              |                    |            |                                         |
| An_41     | GGAACGTGAAATAAATGGTGAAAACAAA | TCACCTCCAATATTTTACCATCA     | 5                 | ag              |                    |            |                                         |
| An_42     | CCATCAGGGGTGAAAAGGTA         | TTTCCACTTCCCTTCGATCT        | 5                 | ag              |                    |            |                                         |
| An_43     | TAAAAAGAAAGAAAGAGATAAAGTGGG  | TTATTTACATCTTCCCACCTTCC     | 5                 | ag              |                    |            |                                         |
| An_44     | GCTTGTTGGGTATGTGTATGTG       | TTTGGCCATATTTCTCAG          | 5                 | ag              |                    |            |                                         |
| An_45     | TTCTCATTGCGTAAACGACG         | CGATAAATCAGATCGGATGG        | 5                 | ag              |                    |            |                                         |
| An_46     | TGGGACAGAAAAGGATGAGA         | TGCTATGACAATGGAGACTCTG      | 5                 | ag              |                    |            |                                         |
| An_47     | AGAAGGAAGAGATCATGAATGG       | TGTA AAAACAACCAACATGC       | 5                 | ag              |                    |            |                                         |
| An_48     | GTCGTTTACATCGGGAAGACT        | CCTTGCGCTGCTAAACACTT        | 5                 | ag              |                    |            |                                         |
| An_49     | TTTCTCACAGAAAACCTGAAAGAAAT   | TGGCGCTTTATCATCTCCTT        | 5                 | ag              |                    |            |                                         |
| An_50     | TTTCTTCAAACCTACTAAGTGCATT    | TGAGAGGGGAGGGAAGATAGA       | 5                 | at              |                    |            |                                         |

Table 1 (contd)

| Loci name | Forward                     | Reverse                     | Repetition number | Repetition type | Amplification band | Label dyes | Selected |
|-----------|-----------------------------|-----------------------------|-------------------|-----------------|--------------------|------------|----------|
| An_51     | TGGTTCATGTCTTTTCCTTTCA      | AAATTTTGTGCTTAAACTTGT       | 5                 | at              |                    |            |          |
| An_52     | ATGCCGGTTTGATTTCACAG        | GCCATTCGCCAATACCTATG        | 5                 | at              |                    |            |          |
| An_53     | GGCTGTTTCTGTGTTTTTGA        | CGAATAACTTGCTTGCTCTGTG      | 5                 | att             |                    |            |          |
| An_54     | TTTTAATAACCGCAATAACTGCAA    | GGAAATAGGTGCTCAGAGACTCA     | 5                 | ca              |                    |            |          |
| An_55     | ACGTAACAGTATCGTTACAAAGCAA   | TGGTGTGCAGAAAGGATTCA        | 5                 | ca              |                    |            |          |
| An_56     | CGAGTCCGGGTATTTCTGTT        | GAAGGGATTGGTTCATGCTC        | 5                 | ca              |                    |            |          |
| An_57     | GAAACTACCATCGCAGCTC         | ATGGAGAAAAGGGGACTTGGT       | 5                 | ca              |                    |            |          |
| An_58     | TGACAAAGTCTAAGGCGGAGG       | GGAAGGTGCAAAGCAATCTC        | 5                 | ca              |                    |            |          |
| An_59     | TTCTAAATAGAATTTCCCAGCG      | ACCCTAGCAACCACTGGGAT        | 5                 | ca              |                    |            |          |
| An_60     | AAGCACACTCACCTCTCAAATC      | TTGCTCTGTATACGCGCTTG        | 5                 | ca              |                    |            |          |
| An_61     | TCATTACTTCCATTTAAGTCGCA     | AAGAGCATACCATCCTTTCAITT     | 5                 | ca              |                    |            |          |
| An_62     | CAATCACGTAACCACT            | TGATGTTGATGGTGTTTGTTG       | 5                 | cac             |                    |            |          |
| An_63     | AGGACAGCTAATGGAGAAACAAA     | TTTTGGTGGTGTGTGTTGG         | 5                 | cag             |                    |            |          |
| An_64     | TCATCGAAGAAGGATGGTCC        | GCAAAACAGCAAGGAGCACT        | 5                 | ccaca           |                    |            |          |
| An_65     | TTTGCCTTCTTCTCGGTAA         | CCAGTCCACCCATTGTTTC         | 5                 | cctc            |                    |            |          |
| An_66     | GAGCAATATGGGCAGAGTGG        | CAGAGGGAAGACTGCCAAAC        | 5                 | ct              |                    |            |          |
| An_67     | ACGGTGTCTGTCTTAATGC         | GCCGGAGTTGTCACAAAGAG        | 5                 | ct              |                    |            |          |
| An_68     | GTGCTGTCTCTACTCATGCC        | TTTTGAGAACCACAAGGGGA        | 5                 | ct              |                    |            |          |
| An_69     | TCTACCCTTCAGAAATTCGGC       | TGAGTGTAGAGCACCCTGTGA       | 5                 | ct              |                    |            |          |
| An_70     | TTCAGCATCATTTCCCTCAG        | TCATCCGGAGAGTAAGATGAGA      | 5                 | ct              |                    |            |          |
| An_71     | TTACCTATGTTCCAAATCATCCC     | AAATTCAAAAGGGGAGGGTG        | 5                 | ct              |                    |            |          |
| An_72     | CAACATACTAGTGAATTCCTTCCAC   | TGCTTAAACAAGATCGATTGGA      | 5                 | ct              |                    |            |          |
| An_73     | ACCCATACATAAGTACACGAAAGAT   | AAATGACTCCAACGGTAATTAAGA    | 5                 | ct              |                    |            |          |
| An_74     | ACCATTTACCCTTGCCTTA         | GGAAGATACAAGCAGCGGAG        | 5                 | ct              |                    |            |          |
| An_75     | TCCTTCTCTAAGCATTCTCTG       | GGCTTGTAATTATGTATGCACAAAG   | 5                 | ct              |                    |            |          |
| An_76     | CCTTTTCTTCAACGCATCCC        | GAGTACGAAAAGTGGATATAGATTGGG | 5                 | ct              |                    |            |          |
| An_77     | TCATTTCCGTTCAAAGGGT         | GAAGCGCACTCCCATAAAAC        | 5                 | ctt             |                    |            |          |
| An_78     | TCAAACCTGTGTTCTGAGCTTC      | AAATGAGTGCACGCTCCAG         | 5                 | ctt             |                    |            |          |
| An_79     | ATTCTGTGACTATCCTAATTTTGT    | AGCCATTTGGGTTTGTGAAC        | 5                 | ctt             |                    |            |          |
| An_80     | GACGGCGCTTGTACTCTTGT        | CATCCCTGCAACGATATTGA        | 5                 | ctt             |                    |            |          |
| An_81     | GAGAGGGGCTGGAAATGTG         | CCCTCAAAGTGAATTCAGTCA       | 5                 | ga              |                    |            |          |
| An_82     | CGCCTTTGTCCGAAATATAAA       | GCAATTTCAAATCAAATTCATC      | 5                 | ga              |                    |            |          |
| An_83     | GAAAGGTGTAGATGTGGGAGATG     | CTTTCAAACCACCAACACC         | 5                 | ga              |                    |            |          |
| An_84     | AACGGTGCAAATTTCTGTGA        | GGTCAAAGGGTAGTTATGTTCTTC    | 5                 | gaa             |                    |            |          |
| An_85     | GTCTTTTCGACAGGCCATTA        | TTTCCGTCGCTGTAAGTTC         | 5                 | gga             |                    |            |          |
| An_86     | GAATCCTGGTCTCACAATAGTTTT    | TTTATCTTGCCACAGCGCC         | 5                 | gga             |                    |            |          |
| An_87     | TGTGAATGTAAAGATAGTGAGCTTTT  | GCAAACCACAATCGTCATGT        | 5                 | gt              |                    |            |          |
| An_88     | TTGTGTTGTGTACTGTTTTGA       | CAACTACTCGAACATGACTATCATAC  | 5                 | gt              |                    |            |          |
| An_89     | CGTCTATTTGTGTCTTCTCTCC      | CAACAACATAACCACATACTCG      | 5                 | gt              |                    |            |          |
| An_90     | TTTCAATCCCATCTATCCG         | TCTCAGTAAATCCCACGCT         | 5                 | gt              |                    |            |          |
| An_91     | CCTATGGGAAGTAAAATGATACTAACG | TTTCTCCCATCACCTTCTT         | 5                 | gt              |                    |            |          |
| An_92     | AACAATTTGGTGTAAATTTGGC      | CACAGACAGACAAAACAGATAAACA   | 5                 | gt              |                    |            |          |
| An_93     | TGGCTCAGCAAATTTTCATTG       | CACCCATGGGAAGAAACCTA        | 5                 | gtt             |                    |            |          |
| An_94     | CCCTCTCCCAACACATATT         | GGAGAGGCGGAAAAGACAT         | 5                 | ta              |                    |            |          |
| An_95     | AGTTGACCTGGGTAAGTGGG        | GGATCCCCTAAGCACATTCA        | 5                 | ta              |                    |            |          |
| An_96     | TGAATTTAAGGCGAATGAAAAG      | TGCTGTGAAAACAAGTCATCAGA     | 5                 | ta              |                    |            |          |
| An_97     | ATTACCCTGCGATCTCGGTCC       | ACTCGCTCTTTCCACCCTA         | 5                 | ta              |                    |            |          |
| An_98     | AAGAAGTGAAGAGACCATGCTG      | AAATTTGCGCTTTTTCGCTTT       | 5                 | ta              |                    |            |          |
| An_99     | GGAGAGTGTACAGAAAGTGGC       | CCCTCTTAAATTTCAAACAGATCA    | 5                 | ta              |                    |            |          |
| An_100    | ATTCAAATGAATTTCTTCGGAC      | CTTATTTTGTGTGTCAGCTCT       | 5                 | ta              |                    |            |          |
| An_101    | GGACGCGCTGTATTTATGA         | TGGATAAGTTATTTGCGGGAA       | 5                 | ta              |                    |            |          |
| An_102    | CTGCTTTACAATAAAAGCATGGC     | TCGACTTACTCGTTTGAAAATG      | 5                 | ta              |                    |            |          |
| An_103    | TTCAATCCGTTACTTTACATCC      | TGGGAGATTGGTAGCAAATAATG     | 5                 | tac             |                    |            |          |
| An_104    | TCATCTCTGTCCTCTTCCC         | CCACCCACGAGAGTAGAAA         | 5                 | tatt            |                    |            |          |
| An_105    | TTCTTTATTTCTTACCCTCCCC      | AATTAGGGATGGGGTTGAGG        | 5                 | tc              |                    |            |          |
| An_106    | TTAATCATAGCTCTATACCATTCTCA  | GTTTGGTAGCTGCTAAGAATCAC     | 5                 | tc              |                    |            |          |
| An_107    | TTCAATCGCTCACTAAATTAACCTCT  | GCAAGGAGGAAAAGTGAATGG       | 5                 | tc              |                    |            |          |
| An_108    | TATCCATCACTCTCACTCACTCC     | ATGAGAGGATAGATAGTTCTGAGAGA  | 5                 | tc              |                    |            |          |
| An_109    | TCCAATCCATTTCCCTAAC         | TGTTACACTTAGAATGATTGGTG     | 5                 | tc              |                    |            |          |
| An_110    | TGCTGGCATAGGTAACACA         | CACCATACAATCATAGAGGTGCT     | 5                 | tc              |                    |            |          |
| An_111    | CCATGCTTCCTTTAATCCCG        | TGTTAGTGAGAGTTAAATGGGGA     | 5                 | tc              |                    |            |          |
| An_112    | TGGAAGCTAGAATGATGGCA        | CAGAAGAACAATGTCCGTTGG       | 5                 | tc              |                    |            |          |
| An_113    | TCTCCAGAGTCTGCGAAACC        | GGACTGTCAGTTGTAGGAGG        | 5                 | tec             |                    |            |          |
| An_114    | CCTGAAGGCGTTACTAAACCA       | GCGAAAGTGAAGAATCGGAG        | 5                 | tec             |                    |            |          |
| An_115    | CTCCTGTAAATCTTTCTCTCTC      | AGGGATGAAGAGGCACACTC        | 5                 | tg              |                    |            |          |
| An_116    | ACCCAGATTATAGAGGGTGTCA      | AAAACCCAAAATTTCTGGAAAAG     | 5                 | tg              |                    |            |          |
| An_117    | TATTTCCCAAAGTGGTTCGG        | AACGCACATACAGAAGCACAA       | 5                 | tg              |                    |            |          |
| An_118    | AATGTTTTGTGCAGGTGGGT        | GCAAAGCCACTCAATTTTCATC      | 5                 | tg              |                    |            |          |
| An_119    | CGTACATTTCTGGTTAAAGAAGTAA   | CATCCAAATTTCTTTCTGTGGA      | 5                 | tg              |                    |            |          |
| An_120    | TAGTGTCTAAGTATGTTATGTCTCGG  | TTAACTTATAAACAGCAGACCTCCC   | 5                 | tg              |                    |            |          |
| An_121    | TGTGTGCATAATATAAGTGTATGTGCT | GGGGATTTGTGTTTTGTGAGA       | 5                 | tg              |                    |            |          |
| An_122    | TGTCCGGTTGTTGCTTGTTA        | ACCAACATAAAAAGCATGGGTTG     | 5                 | tg              |                    |            |          |
| An_123    | GGCTGAGGAGACATTGAAGG        | TTTAAACCAGGGCTTCCCTC        | 5                 | tg              |                    |            |          |
| An_124    | CGTAGCCGGGCTCTATGAAT        | CATGCCTTGAACCGTGAAC         | 5                 | tgggaa          |                    |            |          |
| An_125    | ATTCTCCACCTTTCTCCACG        | GGAAAGAAATGAACGTAGCACAA     | 5                 | ttc             |                    |            |          |
| An_126    | GCTTATCGTTAAAGTCATAACAGGG   | TGCAATCATACATACCAACATACA    | 5                 | tfg             |                    |            |          |
| An_127    | CAGCATCAGCAATAAACAGCA       | ACTGTTCAAGTTGTGCTTTCTGA     | 6                 | aac             |                    |            |          |
| An_128    | TCTGCTTGAATTCGTTGCAG        | CAGAACCAATCAGAGCGAAT        | 6                 | aac             |                    |            |          |

Table 1 (contd)

| Loci name | Forward                     | Reverse                     | Repetition number | Repetition type | Amplification band | Label dyes | Selected |
|-----------|-----------------------------|-----------------------------|-------------------|-----------------|--------------------|------------|----------|
| An_129    | TTTAGTATCCCATTGAAGGAGC      | CCTATTCCATGGGAGGTAGTGA      | 6                 | aat             |                    |            |          |
| An_130    | GGAGTACGCCTCTCACGC          | AGAGTTTATAAGACGAAAGGCC      | 6                 | ac              |                    |            |          |
| An_131    | ATGCACGCACACAAAACAT         | TGGAAGGAAGTCAAGGGTCA        | 6                 | ac              |                    |            |          |
| An_132    | CACGGCACATTTAAACAACG        | TGAGAGTGTGAACGTTGTATGTG     | 6                 | ac              |                    |            |          |
| An_133    | TACACGCACACTACTCACG         | GGACCGATCCATACTCAACAA       | 6                 | ac              |                    |            |          |
| An_134    | AACAAAACAATCATGCACTCA       | TGCGTGATAGAGGGTGTGAA        | 6                 | ac              |                    |            |          |
| An_135    | AAGGCGTATTTGTGGCAGTT        | TGCTGTCTTGACCTATTG          | 6                 | ag              |                    |            |          |
| An_136    | CGTCGCTTTTCGTCCAATTA        | AGTTGGAGGGAAATGAACCTG       | 6                 | ag              |                    |            |          |
| An_137    | TCGAATATCGAAAATATAGAAGTGA   | CACAACCTCAACCAGTTTCAA       | 6                 | ag              |                    |            |          |
| An_138    | TCGAACCTCGACTGCTCAGAA       | TCTACGACCTCCTTCCAACG        | 6                 | ag              |                    |            |          |
| An_139    | TGAGGTCTCGGAATGACAAC        | CGTCTACCTCCTCTCCCTC         | 6                 | agg             |                    |            |          |
| An_140    | ATTGAATGTCCGGAACAGG         | AACCTCCTCTTCCCGCTAC         | 6                 | at              |                    |            |          |
| An_141    | TCTCACGCTATGTAGGTGCAAT      | ACGCTATGTGCATTTGAGTG        | 6                 | ca              |                    |            |          |
| An_142    | ACAAACAGACAACTAACAGACCC     | CTGTTTGTCTGTGAATCTGTG       | 6                 | ca              |                    |            |          |
| An_143    | CGACTACGTATGTTAATAGCACTAAC  | TGAAGTTTGTGCTTTCATTTTGT     | 6                 | ca              |                    |            |          |
| An_144    | CTAACACCGACACCAGCACT        | TTCTATCTTCTGTGTGATGATGG     | 6                 | caacac          |                    |            |          |
| An_145    | TCTTTCTCACACTCTCACCTTTTC    | GGGAGTTAGAGGAAGACGGA        | 6                 | ct              |                    |            |          |
| An_146    | GTGTGAACACCTAGTCCGCTC       | GTCCTCCGACGCTGTGATAGG       | 6                 | ct              |                    |            |          |
| An_147    | CTCTCGTATGTGGTGCC           | ATGGTGAGCAGGGTGTCTAG        | 6                 | ct              |                    |            |          |
| An_148    | GAATAGGGGTGTGGATGACG        | TCCCTCCACCAATATTCTC         | 6                 | ga              |                    |            |          |
| An_149    | TCGACAGATAGACAGGCAATTT      | ACGGGCGGTGTTTATCAAT         | 6                 | ga              |                    |            |          |
| An_150    | TGAGCTGTTTGTGGAGTTGG        | CCAAGATCTTCTTCATCCACA       | 6                 | ga              |                    |            |          |
| An_151    | AAGATATGGTGGGAGAGGG         | TTCCGTCTCCTTCTCACTTT        | 6                 | ga              |                    |            |          |
| An_152    | GAAGAAGGAGGAAGAGAAAAGG      | GCTGTTGTGGTATTTCTCC         | 6                 | gga             |                    |            |          |
| An_153    | AGCGTTAGGTCTTTTGCTTATG      | AAACTAACCAACCTAACCAAACTT    | 6                 | ggta            |                    |            |          |
| An_154    | TTGCAACTCCAATATTGTTTTGT     | ACTCTCCAACAGCCACCAAC        | 6                 | gt              |                    |            |          |
| An_155    | ACGACTCAAATTTACCTAATCAAAA   | TGCATTAGCAACAAGACTACCA      | 6                 | gta             |                    |            |          |
| An_156    | TCTCTTCCCACTTACCC           | CAAGAAAGTAATGATGACTGGTATAAA | 6                 | ta              |                    |            |          |
| An_157    | AACAGCCCTCAATAGATTTGAGTA    | AAGATTCCGGCAAAGCTGATG       | 6                 | ta              |                    |            |          |
| An_158    | AAACTCACGATCATTCTCCTTCA     | TGGTGAGTTTATACATGGAGAGAGG   | 6                 | tc              |                    |            |          |
| An_159    | CTTCTGATTCATCTTTCCAA        | CAGACCAAGAATATTATGTTGTTTAC  | 6                 | tc              |                    |            |          |
| An_160    | TGGGAGTTAAAATACAACTTGTGAA   | CCGTCAAGGAGATACGAAA         | 6                 | tc              |                    |            |          |
| An_161    | GTACTTCAGTCTTAATTAATTCCT    | TTTATAAGATTACGAATGTGAAGGAGT | 6                 | tc              |                    |            |          |
| An_162    | ACCTTGTGAATTACAACCTTTAAAT   | AGGTAAGACGGAAGAGCCGT        | 6                 | tc              |                    |            |          |
| An_163    | TCTACAGGTGATCTTTCCTTT       | GGAAATTAAGTTTGTGCCAGA       | 6                 | tc              |                    |            |          |
| An_164    | TTCTCTTGTCCCTCTCCCTC        | ACATGAATAATGATGTAATGGAAAT   | 6                 | tc              |                    |            |          |
| An_165    | TTTTAAAACCTACAATATTGGTTTCCA | AAAGAGCACTAAGATTAAGAGGCCG   | 6                 | tc              |                    |            |          |
| An_166    | GTGGTCACTTTAGCGAACAAC       | AGGTGATGTTAGGGTGTGGTG       | 6                 | tc              |                    |            |          |
| An_167    | TGTTTTCTGTGTATTTAATCTACC    | CAATCTCGGACCTAAAGCAGA       | 6                 | tc              |                    |            |          |
| An_168    | CGCTGATTTGGATAGAGTTTCA      | GGAAATCGGGAGTTGTTTGA        | 6                 | tc              |                    |            |          |
| An_169    | AATTAAGTTTGCCTTTCTTTCTG     | TGGTGCCTCTTCCAATGAA         | 6                 | tc              |                    |            |          |
| An_170    | GCTCTTGGATGTCAATCGAAAC      | CAGTCGTTTCGCAAGGGT          | 6                 | tc              |                    |            |          |
| An_171    | ACCACATCCCCACTCATT          | CTGCTGTTGCTTCTGAGGAT        | 6                 | tca             |                    |            |          |
| An_172    | TTTGGGAATGTCCCGAATAA        | TGTGGATGAGGATGAGGATG        | 6                 | tct             |                    |            |          |
| An_173    | CAATTTAAGGCGTCTTTTATTTTT    | TAGAAAGGGAAGTGGCGAAG        | 6                 | ttg             |                    |            |          |
| An_174    | ACTGTTTCTTTCGAGGACTGTT      | ATGTGGGTTTGTGGGTGTG         | 7                 | ac              |                    |            |          |
| An_175    | TGAACGGATAATTTCAGATGTTTG    | TCAATTAATCCAAAATGTAACCTCT   | 7                 | ac              |                    |            |          |
| An_176    | TCTTGAGAAAATATTCGAGACAGC    | TAATAAAGCAAGTCCGCGGT        | 7                 | ac              |                    |            |          |
| An_177    | CCCTCAATCTGGAGCTGAG         | GGTAGCAGTCTGTTGGTT          | 7                 | act             |                    |            |          |
| An_178    | GACTTCTAAACGTAAGAGTTGATGC   | CTCACTATCACCATTAGTCACA      | 7                 | ag              |                    |            |          |
| An_179    | GTCATGGTTTTGGTGGATACG       | ATATTCAAATCCTTCAGCAATGG     | 7                 | ag              |                    |            |          |
| An_180    | CAGACACAGAAACGAGGAATGA      | TCCTCTATTTCTTCCCTATATGC     | 7                 | ag              |                    |            |          |
| An_181    | GAATAGGGAGGGATGGAGGA        | CCTCTTTGTTTGTGTTGCCA        | 7                 | ag              |                    |            |          |
| An_182    | TGCGAAAGGGACCTCTGATA        | GCATCTTCACTTCTCCCA          | 7                 | ag              |                    |            |          |
| An_183    | AACCGATACCGATATGTGCC        | TGCAACTAACGTTGTGGAGAA       | 7                 | ca              |                    |            |          |
| An_184    | TACGCAACGACATCTGAGG         | TCAAAGACAAAACAAGAGTGCAA     | 7                 | cata            |                    |            |          |
| An_185    | TTTACCATTACCTTCCCA          | GCAGAGGACAGAGTGAGGTG        | 7                 | cccaca          |                    |            |          |
| An_186    | GCGACTCCATGCCTACAAC         | GGTCTGACGGAGACGAGAAT        | 7                 | ct              |                    |            |          |
| An_187    | TTTCTGTGTGTACAGATGCCG       | GGCTGATAATGGCTTCTCAAG       | 7                 | ct              |                    |            |          |
| An_188    | GCGGTGAACATTGAAATCAC        | TGCCTTCTACGTTTAAATTCAT      | 7                 | ct              |                    |            |          |
| An_189    | CCTCGAATACACTTTCAGATTCAA    | GACAAACCGTGATCCTGATG        | 7                 | ct              |                    |            |          |
| An_190    | TCCGGAGCTATTACTCCTCT        | CAAAGTCAAGGACCGTACACC       | 7                 | ct              |                    |            |          |
| An_191    | TTGCGTAATGCAAAACAGATGA      | TCACTTCCGCCGTTACTTC         | 7                 | ctt             |                    |            |          |
| An_192    | AGTCGTTGAAGGAGATAGGAAA      | ATATCTCCAATTTGTAGCAAGCG     | 7                 | ga              |                    |            |          |
| An_193    | GAAAAGGTAGAGGGTGTGCG        | CCCTTCAATAAACTTCTCC         | 7                 | ga              |                    |            |          |
| An_194    | TGTGTCTTCGTGGATGTCTGA       | GCTAGCAGGAATCATAAAATCTATCT  | 7                 | gt              |                    |            |          |
| An_195    | TTTGATGTACGCTCTTTGC         | CAGACTTCCGGTGTGATCTCT       | 7                 | ta              |                    |            |          |
| An_196    | TGGTGGAGTCTAGGACTTTTCG      | TTTGTCTTCCAATGGCAATA        | 7                 | tc              |                    |            |          |
| An_197    | AGGTTTCAGAAATCAAAATTTACACA  | CGAATTTCCGGTGAATCACTTG      | 7                 | tc              |                    |            |          |
| An_198    | TCTCTCTTTCATAATTTCTGATTTT   | TTAACAGATTCATAGGATGGGC      | 7                 | tc              |                    |            |          |
| An_199    | AATTCTCATGAAGGAGGGAGG       | TGGTGTCTGGCGATTATTCA        | 7                 | tc              |                    |            |          |
| An_200    | ACTGTTCCACCGTAAGTGGC        | AGGAGGGAAAGGGAATCAGA        | 7                 | tc              |                    |            |          |
| An_201    | CCTCTCCTTCTTCTTCTCAG        | GGGAGTCTGATAGTGTCTTGA       | 7                 | tcc             |                    |            |          |
| An_202    | TGTTTTCTTCCCTTCACTCA        | TGGGTATGAAGTTGGGTATGTG      | 8                 | ac              |                    |            |          |
| An_203    | CACTCCCTTCAAAGTAATTATCG     | CTTAAAGTTAATGGGTGCAACTC     | 8                 | ag              |                    |            |          |
| An_204    | ACCCTACCCACTCAC             | AAAGGAACATGACGACGAGG        | 8                 | ca              |                    |            |          |
| An_205    | TTTCTACTCTGTGTAGTGGTGC      | GAGGTTTGAATGTGGACGAGA       | 8                 | ca              |                    |            |          |
| An_206    | TCGAAGTTACCCTCTACTTGG       | CGATGAGCAAGAAAACCAGA        | 8                 | ca              |                    |            |          |

Table 1 (contd)

| Loci name | Forward                     | Reverse                     | Repetition number | Repetition type | Amplification band | Label dyes | Selected |
|-----------|-----------------------------|-----------------------------|-------------------|-----------------|--------------------|------------|----------|
| An_207    | CAGCAAATCAAACACCTTAGC       | TGATGTTGATGATGTGATGATG      | 8                 | cat             |                    |            |          |
| An_208    | GTCTCTTTCATCCCGTCGAA        | TAGTTGGAGGAGGGTATGCG        | 8                 | ct              |                    |            |          |
| An_209    | GAGCCTCTCGTCTTGCAATTC       | TCCGCCTAGATATCCACGAT        | 8                 | ct              |                    |            |          |
| An_210    | ACCAGAATTTCTAAAACAACCTGGTTA | GGCAACCAGTTAAAATGCCA        | 8                 | ct              |                    |            |          |
| An_211    | ATCGTATGCCCTCGTATGGA        | GTGACGCCAACAGTTCGAAAA       | 8                 | ct              |                    |            |          |
| An_212    | CTCCACCACACATCTTTCACA       | AAGGTTGAAAATAGTCATTGGGA     | 8                 | ct              |                    |            |          |
| An_213    | TGGGGCACGGAAAGTCTTAT        | CCTCTCGTTATTCTTTCCTT        | 8                 | ga              |                    |            |          |
| An_214    | ATGCTCCACCTTCTCAAGGA        | ATTACTTCACGCCATCCCAA        | 8                 | ga              |                    |            |          |
| An_215    | GAACTTGTGCCAAGTATGAAAAC     | TCAAGACGTACATGAAGACTCACA    | 8                 | gt              |                    |            |          |
| An_216    | GGAAGTGTGCTTCTGAGCTG        | TTAGAAGGATCAGAGTCGGC        | 8                 | tc              |                    |            |          |
| An_217    | ATGAACACCCCACTTTCGTT        | GCCCTCGATCAACAGGATTA        | 8                 | tc              |                    |            |          |
| An_218    | TCTACGTGAATGGAGTGGTTTTG     | AGGTTTTACGTGTCACCCAAG       | 8                 | tg              |                    |            |          |
| An_219    | GAAGTTGAAGGGCTTCGGTT        | CACACCTCAAATCCACTCA         | 8                 | tg              |                    |            |          |
| An_220    | AACACCAACGAAACAATACCATAA    | AATGTTGCTGTGTTGATCATT       | 9                 | aac             |                    |            |          |
| An_221    | CCCAGAACCAACAACGACAT        | TTCTTTTGTGAACCTTCAGGC       | 9                 | aca             |                    |            |          |
| An_222    | AGTTGAAAAGTGGAGCAATCCAT     | AAGACAGCACTACGATTAGTAAAGAGA | 9                 | ct              |                    |            |          |
| An_223    | AGGGTCTTCTTGACAGGT          | GAAGAGCGGTATCCGTTGAA        | 9                 | ct              |                    |            |          |
| An_224    | TGAAAGTTAAATCGCATTCTCC      | CACTATTACAGCGGACACTGC       | 9                 | ga              |                    |            |          |
| An_225    | AGTGTGACACCTGAAAACCTGA      | CTCATCCTGTTATGCTCCTC        | 9                 | gag             |                    |            |          |
| An_226    | ATACTCCGCAGCTCTCATGC        | AAGGCCAAAAGTAAAGGAGCA       | 9                 | tc              |                    |            |          |
| An_227    | AGACACTTCGATTCTGCGG         | CCTGAATTGCACGAGAACAA        | 9                 | tc              |                    |            |          |
| An_228    | AGGCCAATAAGGACTTGATTTT      | TAATGGCCAATCTGAACTCG        | 9                 | ttg             |                    |            |          |
| An_229    | TTCCAAGTGTAACACATTCAAATAA   | CGATAACCTCTGAAGGCAGC        | 10                | ac              |                    |            |          |
| An_230    | AGGGTAGTGTCTCGTGTGC         | TTCTATCTTCTTTTTCGTCTG       | 10                | ag              |                    |            |          |
| An_231    | ATAGACCACCGTTTTCCCAA        | CAAAAATAAATCCTTGGTTCGG      | 10                | ga              |                    |            |          |
| An_232    | CAGAGGGAAATGTGATAGCAAG      | TCAAGGAATAGTTGGAGAGCG       | 10                | ga              |                    |            |          |
| An_233    | AGACAGGCCGAAAGAAATTG        | TCCTTCTCTCTTCTTATTAGCA      | 10                | gata            |                    |            |          |
| An_234    | AGAGGTCCGTTCTTCTCCA         | AAGAATGATGGGTTGCAGTTG       | 11                | act             |                    |            |          |
| An_235    | TGTGAGAGAAGTACTCCATGCAA     | TCCGACTATCTTGCTTCAA         | 11                | gt              |                    |            |          |
| An_236    | GGAGTGCGATAGGTCAGCTC        | TCCCTACCTTCTAAACTACCC       | 12                | ag              |                    |            |          |
| An_237    | TTTCTCATATCCCGTTCTGATG      | CCTAGAGGAAACCATGGGAAA       | 12                | ct              |                    |            |          |
| An_238    | TGCACATACACATGCACATACA      | TTCCGCTGTCTCTTACAGT         | 13                | ac              |                    |            |          |
| An_239    | GACAAGGCAGGGGTGGTTAT        | TCTGGAGGTGTGTTAGTTACCTACT   | 15                | ga              |                    |            |          |
| An_240    | AGGAGAGGAAAATAGACCGCA       | CAGCCTCTCAAACGTACC          | 16                | ag              |                    |            |          |
| An_241    | GAAGACCTCAGGGCCTTCAT        | TGTGGTACAGCGTATGAGCC        | 16                | ttc             |                    |            |          |
| An_242    | ATATTCCGACAAAATAATAGATACACC | CTGTCTTGTGTTAATGTTCTTTG     | 17                | caa             |                    |            |          |
| An_243    | AACACGGTCTCAATTTTCGCT       | CCCACCCATTAGGAAACAAC        | 19                | gta             |                    |            |          |
| An_244    | TTACGTTTTTGTGTTTTGTTTTG     | AACGAACCGACCTACCCTA         | 23                | gtt             |                    |            |          |
| An_245    | ACCTACCAATCGGAAAGGTCA       | CGGTAGTTACGTCCGACTCA        | 28                | ca              |                    |            |          |

**Table 2.** Raw data of the 50 microsatellites primer pairs selected for the cross species amplification.

| Locus name | M13-forward                                  | Reverse                     | Repetition number | Repetition type | Amplification band on 1.5% agarose gel | Selected  | Label dyes                              |
|------------|----------------------------------------------|-----------------------------|-------------------|-----------------|----------------------------------------|-----------|-----------------------------------------|
| AV/0009    | TGTAAAACGACGGCCAGTGTGATGATCATATAATTTTGTGTGC  | TTTCAATCTTTAGAGTTTGGGG      | 5                 | tg              | Yes                                    | Yes       | HEX                                     |
| AV/0018    | TGTAAAACGACGGCCAGTGAAGAAATTCACCTCACCTCA      | CTTTGAAACGACTACGATTAACATC   | 6                 | caa             | Yes                                    | Yes       | 6_FAM                                   |
| AV/0024    | TGTAAAACGACGGCCAGTAAATCGGGTGACAGAGAAGC       | GGCAGCTCAATCCCTATGAG        | 7                 | ag              | Yes                                    | Yes       | HEX                                     |
| AV/0028    | TGTAAAACGACGGCCAGTCCCTACCCCTTCAGAAATTCG      | CTGAGTGTGAGCATCACTGT        | 7                 | ct              | Yes                                    | Yes       | HEX                                     |
| AV/0037    | TGTAAAACGACGGCCAGTGAATGCTGAGGGAGGAC          | CATGAAAAGACTGGAGAAAGGA      | 5                 | cat             | Yes                                    | Yes       | 6_FAM                                   |
| AV/0049    | TGTAAAACGACGGCCAGTACCCTATGCTTATTCAC          | CTTTATTAGGCAAGTCTTTTGA      | 7                 | aca             | Yes                                    | Yes       | 6_FAM                                   |
| AV/0005    | TGTAAAACGACGGCCAGTGGCTGTCTGTGGAGCTTT         | ATCACATGCTTATTTCTATGGCAA    | 5                 | ga              | Yes                                    | No        | No: too poor amplification success rate |
| AV/0007    | TGTAAAACGACGGCCAGTGGATGCTGGAATTTGAATTT       | CAGGAATGATTTCTGTGACC        | 8                 | gt              | Yes                                    | Aspecific |                                         |
| AV/0041    | TGTAAAACGACGGCCAGTGGATGCTGGAAGAAAGACA        | CCTTTAGCCATGCACCTTC         | 5                 | gga             | Yes                                    | Aspecific |                                         |
| AV/0030    | TGTAAAACGACGGCCAGTATATGTCATTTCCCTCCG         | GGCACATATAAGGGTGTGGGA       | 9                 | tc              | Yes                                    | Aspecific |                                         |
| AV/0039    | TGTAAAACGACGGCCAGTGAACATTAAGCAACAGGG         | GTATGTGCGGTGTGCGTATG        | 5                 | ac              | Yes                                    | Aspecific |                                         |
| AV/0046    | TGTAAAACGACGGCCAGTATCCGACTTCCCATTT           | TCCGAGTAGATCGGATCAGG        | 5                 | gaa             | Yes                                    | Aspecific |                                         |
| AV/0012    | TGTAAAACGACGGCCAGTTCACACCTCAGTCTGG           | TACGGAGAGAGACATGGAG         | 5                 | tc              | Yes                                    | Aspecific |                                         |
| AV/0013    | TGTAAAACGACGGCCAGTCTGTGTAAGAAAGCGGTGTG       | TTCTAACCTTTGAATTTGTGCAT     | 7                 | ga              | Yes                                    | Aspecific |                                         |
| AV/0021    | TGTAAAACGACGGCCAGTCAACAGGACCGTACGTTTT        | GGCTTCAACCCCTCTAACT         | 12                | ag              | Yes                                    | Aspecific |                                         |
| AV/0035    | TGTAAAACGACGGCCAGTGGCTGCTATAAGGAGAGA         | GGGACTCACGTCTACAACC         | 8                 | ag              | Yes                                    | Aspecific |                                         |
| AV/0042    | TGTAAAACGACGGCCAGTGAAGATGAATTTGGCGGTG        | TGCTCTCATCTGGTCTACGA        | 5                 | aag             | Yes                                    | Aspecific |                                         |
| AV/0044    | TGTAAAACGACGGCCAGTCTCCACCATGTTTCTTTG         | GGTTTCAATCTTGGTCTCA         | 5                 | ect             | Yes                                    | Aspecific |                                         |
| AV/0047    | TGTAAAACGACGGCCAGTGGAAACATCAAGGAATTAAGG      | GGGCTAGCATTCATCATCA         | 5                 | gt              | Yes                                    | Aspecific |                                         |
| AV/0045    | TGTAAAACGACGGCCAGTGGTTTACACGACAACAG          | TCATCGCTTTACCAATAACAA       | 9                 | tg              | Yes                                    | Aspecific |                                         |
| AV/0001    | TGTAAAACGACGGCCAGTATACACAATACATTCAGACGA      | TTAAATAGAAGTTAGGCTTCTTGAGGA | 13                | ac              | No                                     | No        |                                         |
| AV/0002    | TGTAAAACGACGGCCAGTCCGACTCCGACTCCGAAATG       | TTCCGACATGACGATTTATCA       | 5                 | actcgg          | No                                     | No        |                                         |
| AV/0003    | TGTAAAACGACGGCCAGTACGAGGAGAAATTTTAAAGCTG     | TCAAACTGGTTGAATAACAAATAA    | 13                | ag              | No                                     | No        |                                         |
| AV/0004    | TGTAAAACGACGGCCAGTCACTCCCTATTTGCTATAGCC      | ATGCAACGACAAACGACAGC        | 10                | lgctgt          | No                                     | No        |                                         |
| AV/0006    | TGTAAAACGACGGCCAGTACGAAAGCAAACTTTCA          | AGTGTGGTGTGAGTCTGTG         | 5                 | tc              | No                                     | No        |                                         |
| AV/0008    | TGTAAAACGACGGCCAGTGGTCCATTTCTTCCAAAGC        | CACATCACTTAAACACCTTAAAGCA   | 9                 | tg              | No                                     | No        |                                         |
| AV/0010    | TGTAAAACGACGGCCAGTATCAAATAGCAGTACACAACA      | TGAAGAGAAAGATCCGAGGA        | 7                 | tct             | No                                     | No        |                                         |
| AV/0011    | TGTAAAACGACGGCCAGTCAAGATGCATTTAGAAATTTG      | AACTAATCTATGACTCAATAGGCAAT  | 9                 | ca              | No                                     | No        |                                         |
| AV/0014    | TGTAAAACGACGGCCAGTGTGATTTCTTTCTGTGG          | GACTATGTTAAGAACTGTCCGCGTT   | 5                 | gga             | No                                     | No        |                                         |
| AV/0015    | TGTAAAACGACGGCCAGTCTATTAAGAAAGAAATTAAGCAA    | GCACCAATGGCATAACAAA         | 5                 | ac              | No                                     | No        |                                         |
| AV/0016    | TGTAAAACGACGGCCAGTCTATTTATGATCTGTCCG         | CTCCCACTGGTGTGATCTTC        | 5                 | tc              | No                                     | No        |                                         |
| AV/0017    | TGTAAAACGACGGCCAGTGGGTGAGTGGAGGTAATTTG       | TTCTCTCCCTACCCCTCGAT        | 7                 | tg              | No                                     | No        |                                         |
| AV/0019    | TGTAAAACGACGGCCAGTCCAGTGTGACGAAATAAGAAA      | TCTGATCTCGCAGATCTCTC        | 8                 | ag              | No                                     | No        |                                         |
| AV/0020    | TGTAAAACGACGGCCAGTGAACCTTAAAGCAGTGTCTGA      | CAAAACCCACTCTACATAATAAATA   | 14                | gft             | No                                     | No        |                                         |
| AV/0022    | TGTAAAACGACGGCCAGTGAAGAAAGCAAAATGCTGATATGC   | TCTAAGCCCGACCAACGATA        | 6                 | ca              | No                                     | No        |                                         |
| AV/0023    | TGTAAAACGACGGCCAGTGGAAATTTATTTGGAGAGGG       | GAGGTTAAGTCTGGGTCTGG        | 6                 | ag              | No                                     | No        |                                         |
| AV/0025    | TGTAAAACGACGGCCAGTCAATATATGCGTAGCCGAG        | CCTCAAAGACTAACCCTCCA        | 8                 | tg              | No                                     | No        |                                         |
| AV/0026    | TGTAAAACGACGGCCAGTAAACAGATGAATCAAGATCAAGAA   | CTCTGAATCTCAGGCAATC         | 7                 | aag             | No                                     | No        |                                         |
| AV/0027    | TGTAAAACGACGGCCAGTGGTCTTAAAGCTTAAAGGAA       | GAAAGACTGAAGATTCACGC        | 8                 | tg              | No                                     | No        |                                         |
| AV/0029    | TGTAAAACGACGGCCAGTGTGATTAAGTCAAGGCTTAAAGGAA  | AAAATCATGCCCAAAATGC         | 5                 | tg              | No                                     | No        |                                         |
| AV/0031    | TGTAAAACGACGGCCAGTGTATTAAGTCAAGTATTAACATTTCA | CCTCAGTTCGTAATGTCGTGG       | 9                 | tc              | No                                     | No        |                                         |
| AV/0032    | TGTAAAACGACGGCCAGTTCACCTCTCAACCAAAAC         | TTGTTTTATATCCACCCATCC       | 7                 | tc              | No                                     | No        |                                         |
| AV/0033    | TGTAAAACGACGGCCAGTATCCCTCAACACTCTTTGACA      | AAAAGGTAATTCAGAAAGTGGAGTGT  | 7                 | ct              | No                                     | No        |                                         |
| AV/0034    | TGTAAAACGACGGCCAGTCTGATTTCACTCTTTCTCACC      | GAAAGGAGACTGAAGACTGAGAGA    | 8                 | tc              | No                                     | No        |                                         |
| AV/0036    | TGTAAAACGACGGCCAGTATAAATTCAGAAATTAACCAACA    | GGAAATGATGATAAATTTGTTG      | 7                 | ca              | No                                     | No        |                                         |
| AV/0038    | TGTAAAACGACGGCCAGTACGAAAGCAAGCAAGAGATC       | GTGTGCTTCAATTTGTTGTTTC      | 9                 | aca             | No                                     | No        |                                         |
| AV/0040    | TGTAAAACGACGGCCAGTATCCCAAGATGCCCTTCA         | TTTCAGTATTTCTAAACCGAATGT    | 11                | tgt             | No                                     | No        |                                         |
| AV/0043    | TGTAAAACGACGGCCAGTATCCAGGAAAGCGGCTTTTA       | GCTTTTAAAGAACTCCGGAATA      | 5                 | tig             | No                                     | No        |                                         |
| AV/0048    | TGTAAAACGACGGCCAGTGTGAATTTCTTTGTTCTTCTTTG    | TTAACATCAACCTCAATATCATCG    | 13                | tig             | No                                     | No        |                                         |
| AV/0050    | TGTAAAACGACGGCCAGTATTCGGGGTGTGTTCTACT        | TGAGGAGAAAAGGGGATGTC        | 5                 | ta              | No                                     | No        |                                         |