

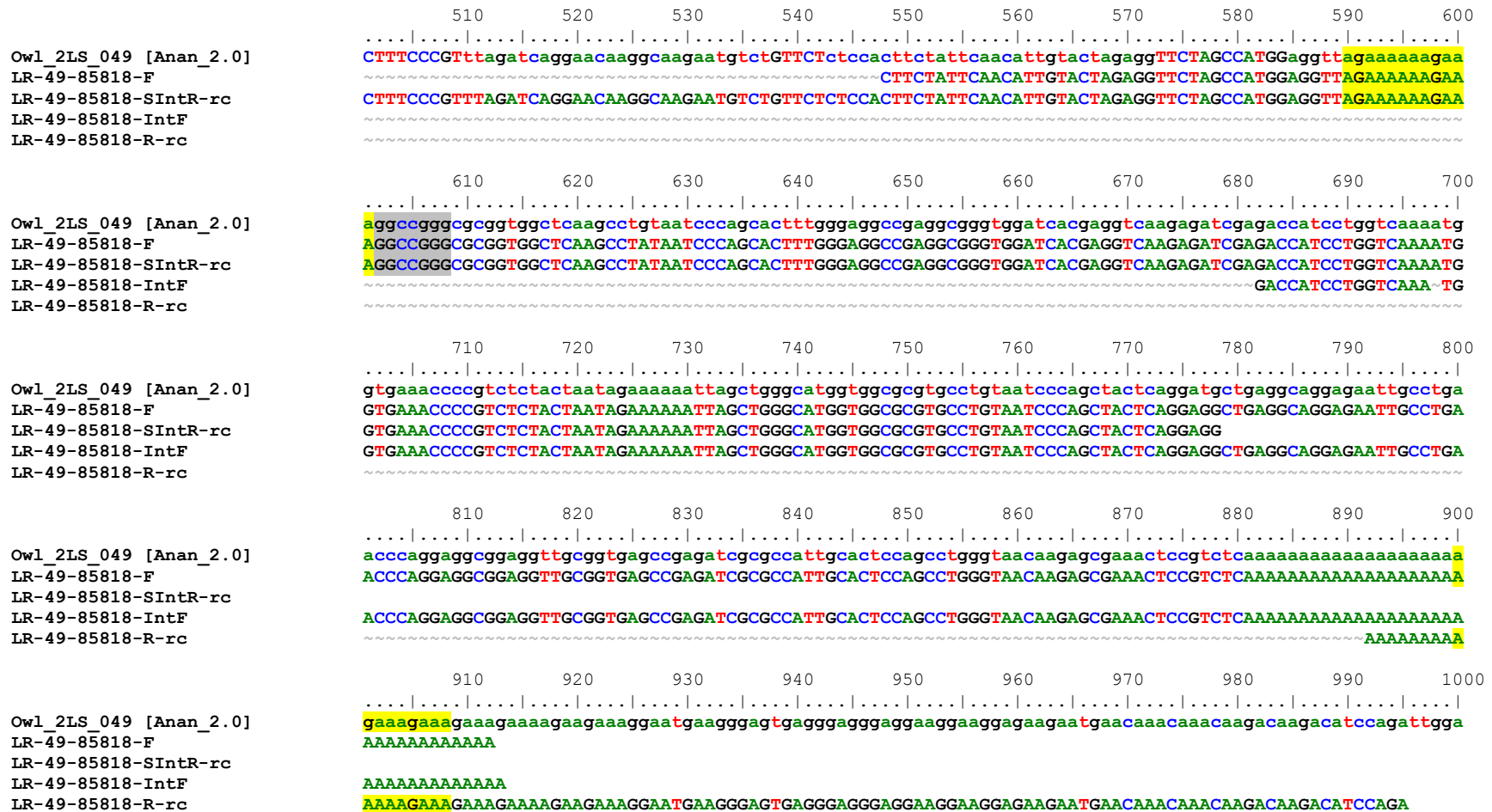
## ***Aotus Alu* Supplementary Figures Table of Contents**

- Figure S1: *A. nancymaae* and *A. azarae* shared: Locus Owl\_2LS\_049 sequence alignment
- Figure S2: *A. nancymaae* and *A. azarae* shared: Locus Owl\_2LS\_056 sequence alignment
- Figure S3: *A. nancymaae* and *A. azarae* shared: Locus Owl\_2LS\_091 sequence alignment
- Figure S4a: *A. nancymaae* and *A. azarae* shared; one *A. trivirgatus*: Locus Owl\_2LS\_095 gel image
- Figure S4b: *A. nancymaae* and *A. azarae* shared; one *A. trivirgatus*: Locus Owl\_2LS\_095 sequence alignment
- Figure S5: *A. nancymaae* and *A. azarae* shared: Locus Owl\_2LS\_111 sequence alignment
- Figure S6: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_359 sequence alignment
- Figure S7: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_420 sequence alignment
- Figure S8: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_506 sequence alignment
- Figure S9: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_592 sequence alignment
- Figure S10: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1202 sequence alignment
- Figure S11: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1203 sequence alignment
- Figure S12: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1276 sequence alignment
- Figure S13: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1507 sequence alignment
- Figure S14: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1528 sequence alignment
- Figure S15: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1534 sequence alignment
- Figure S16: *A. nancymaae* and *A. azarae* shared: Locus *Aotus*\_1559V2 sequence alignment
- Figure S17: *A. nancymaae* and *A. azarae* shared: Storer, et al. 2020\_*Aotus*\_827 sequence alignment
- Figure S18: *A. nancymaae* and *A. azarae* shared: Storer, et al. 2020\_*Aotus*\_1120 sequence alignment
- Figure S19: *A. nancymaae* and *A. azarae* shared: Storer, et al. 2020\_*Aotus*\_6430 sequence alignment
- Figure S20a: *A. azarae* novel *Alu*: near parallel insertion: Locus *Aotus*\_404 gel image
- Figure S20b: *A. azarae* novel *Alu*: near parallel insertion: Locus *Aotus*\_404 sequence alignment
- Figure S21: *A. azarae* novel *Alu*: near parallel insertion: Locus *Aotus*\_1196 sequence alignment
- Figure S22a: *A. nancymaae* and *A. azarae* shared; *A. vociferans* novel *Alu*: near parallel insertion: Locus *Aotus*\_364 gel image
- Figure S22b: *A. nancymaae* and *A. azarae* shared; *A. vociferans* novel *Alu*: near parallel insertion: Locus *Aotus*\_364 alignment
- Figure S23: *A. vociferans* novel *Alu*: near parallel insertion: Locus Owl\_2LS\_120 sequence alignment
- Figure S24a: *A. trivirgatus* novel *Alu*: Locus *Aotus*\_68 gel image
- Figure S24b: *A. trivirgatus* novel *Alu*: Locus *Aotus*\_68 sequence alignment
- Figure S25: Supports *A. vociferans* as basal: Locus Owl\_2LS\_078 sequence alignment
- Figure S26: Supports *A. vociferans* as basal: Locus *Aotus*\_1518 sequence alignment

Figure S27a: Supports *A. vociferans* as basal: Locus *Aotus*\_1546 gel image  
Figure S27b: Supports *A. vociferans* as basal: Locus *Aotus*\_1546 sequence alignment  
Figure S28: Supports *A. vociferans* as basal: Locus *Aotus*\_1288V2 sequence alignment  
Figure S29a: *A. vociferans* and *A. trivirgatus*; share extra sequence; Locus Owl\_2LS\_042 gel image  
Figure S29b: *A. vociferans* and *A. trivirgatus*; share extra sequence; Locus Owl\_2LS\_042 sequence alignment  
Figure S30a Supports *A. trivirgatus* as basal: Locus *Aotus*\_127 gel image  
Figure S30b Supports *A. trivirgatus* as basal: Locus *Aotus*\_127 sequence alignment  
Figure S31 Supports *A. trivirgatus* as basal: Locus *Aotus*\_1602 sequence alignment  
Figure S32 Supports *A. trivirgatus* as basal: Storer, et al. 2020\_ *Aotus*\_622 sequence alignment  
Figure S33 Evidence of incomplete lineage sorting (ILS) Locus Owl\_2LS\_018 sequence alignment  
Figure S34a Evidence of incomplete lineage sorting (ILS) Locus *Aotus*\_1582 gel image  
Figure S34b Evidence of incomplete lineage sorting (ILS) Locus *Aotus*\_1582 sequence alignment  
Figure S35a Suspected incomplete lineage sorting (ILS); non-repeat sequence; Locus Owl\_2LS\_046 gel image  
Figure S35b Suspected incomplete lineage sorting (ILS); non-repeat sequence; Locus Owl\_2LS\_046 sequence alignment  
Figure S36a Suspected 2<sup>nd</sup> *Aotus* *Alu* absent from *A. vociferans*; non-repeat sequence Locus *Aotus*\_1153 gel image  
Figure S36b Suspected 2<sup>nd</sup> *Aotus* *Alu* absent from *A. vociferans*; non-repeat sequence Locus *Aotus*\_1153 sequence alignment  
Figure S37 Suspected *A. vociferans* *Alu*; non-repeat sequence; Locus *Aotus*\_1422 sequence alignment  
Figure S38 Confirmed heterozygosity: Locus Owl\_2LS\_110 sequence alignment  
Figure S39 Confirmed heterozygosity: Locus *Aotus*\_1765 sequence alignment

Abbreviations used in alignment figures:

F: Sequence trace using the forward PCR primer  
R: Sequence trace using the reverse PCR primer  
IntF: Sequence trace using the Internal-*Alu* forward primer 5' GGTGGCTCACGCCTGTAATC 3' (Konkel et al. 2015)  
SIntR: Sequence trace using the Internal-*Alu* reverse primer 5' TCTCGGCTCACCGCAACCTCC 3' (Baker et al. 2018)  
-rc: Sequence trace reverse compliment to align properly  
-E: Empty site PCR amplicon (*Alu* absent fragment) was sequenced



**Figure S1.** Sequence alignment for *Alu* locus Owl\_2LS\_049\_018487317.1:279352-280858 (LR-49). PCR-based genotypes indicate the target *Alu* insertion is homozygous present among *A. nancymae* and *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 602 (grey highlight), with matching flanking sequence and TSDs in yellow highlight.

```

      810      820      830      840      850      860      870      880      890      900
Owl_2LS_056 [Anan_2.0] TaccaggagttaaaaaaaaatgaaacaaaacaaaaaactactATCAGGATTGTTATCCTAAaggcaatttttaattttatattttacttaaaccc
LR-56-85818-F ATCCTAAAGGCAATTTTTAATTTTATATTTTACTTAAACCC
LR-56-85818-SIntR-rc TACCAGGAGTTAAAAAAAAAATGAAACAAAACAAAAAATACTACTATCAGGATTGTTATCCTAAAGGCAATTTTTAATTTTATATTTTACTTAAACCC
LR-56-85818-IntF
LR-56-85818-R-rc

      910      920      930      940      950      960      970      980      990      1000
Owl_2LS_056 [Anan_2.0] ttaaaatatttttttaagagtgactctggcgggcggggtggctcaagcctgtaatcccagcactttgggagggcggggtggatcacgagtcaag
LR-56-85818-F TTAATAATTTTTTTTAAAGACTGACTCTGGCCGGGCGGGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGGATCACGAGTCAAG
LR-56-85818-SIntR-rc TTAATAATTTTTTTTAAAGACTGACTCTGGCCGGGCGGGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGGATCACGAGTCAAG
LR-56-85818-IntF GAGTCAAG
LR-56-85818-R-rc

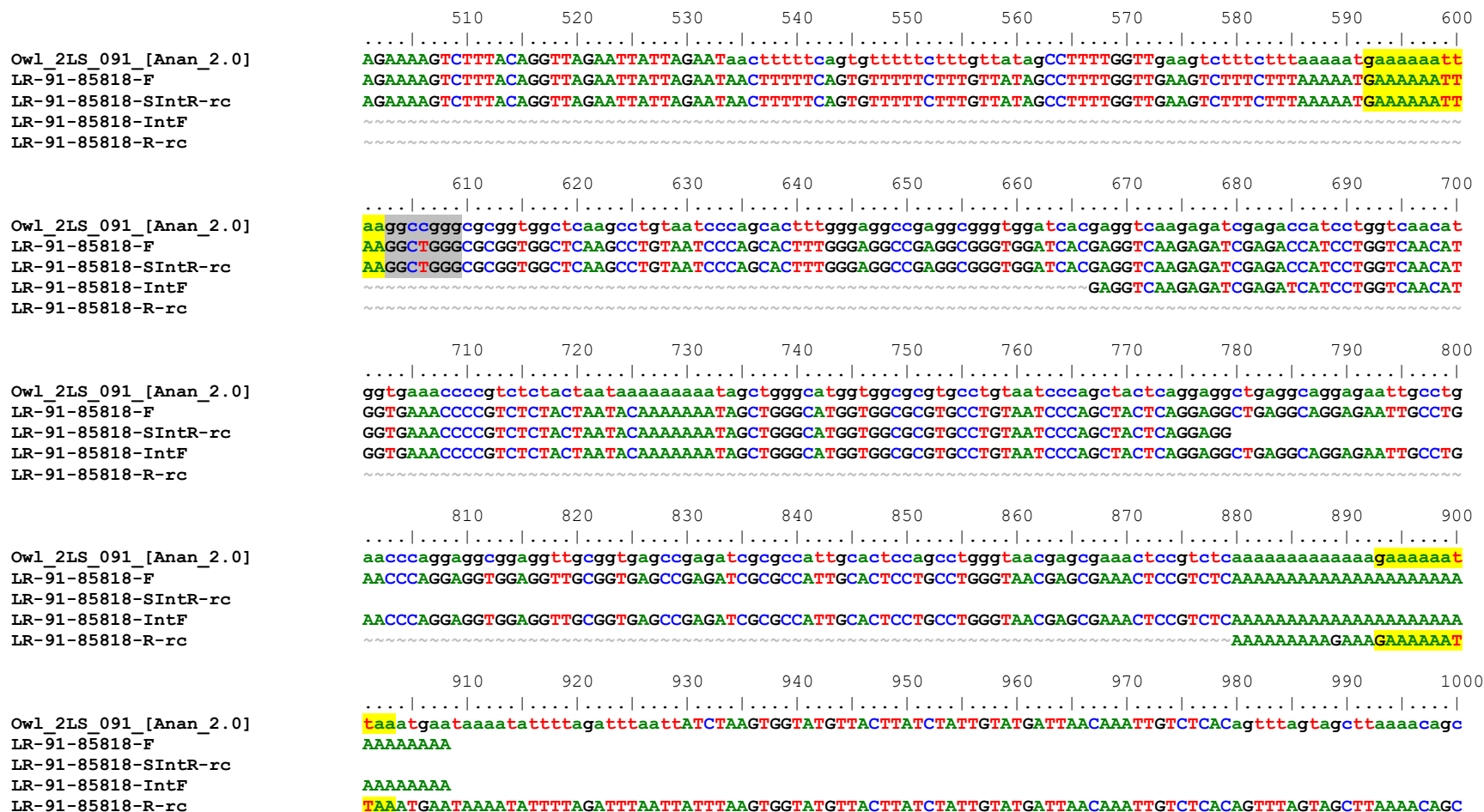
      1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
Owl_2LS_056 [Anan_2.0] agatcgagaccatccgggtcaacatggtgaaaccccgctctactaaaaatacaaaaaattagctgggacagtggtgctgctgtaatcccagctact
LR-56-85818-F AGATCGAGACCATCC TGGTCAACATGGTGAACCCCGTCTCTACTAAAAATACAAAAAATTANCTGGGCACAGTGGTGCCTGTAATCCCAGTACT
LR-56-85818-SIntR-rc AGATCGAGACCATCC TGGTCAACATGGTGAACCCCGTCTCTACTAAAAATACAAAAAATTAGCTGGGCACAGTGGTGCCTGCCTGTAATCCCAGTACT
LR-56-85818-IntF AGATCGAGACCATCC TGGTCAACATGGTGAACCCCGTCTCTACTAAAAATACAAAAAATTAGCTGGGCACAGTGGTGCCTGCCTGTAATCCCAGTACT
LR-56-85818-R-rc

      1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
Owl_2LS_056 [Anan_2.0] caggaggctgaggcaggagaaattgcctgaaaccaggaggcggaggttgcggtgagccgagatcgcgccattgcactccagcctgggtaatgagcgaact
LR-56-85818-F CAGGAGGCTGAGGCAGGAAA TTTGCCTGAA CCCAGGAGGCCGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAATGAGCGAAACT
LR-56-85818-SIntR-rc CAGGAGG
LR-56-85818-IntF CAGGAGGCTGAGGCAGGAGA TTTGCCTGAA CCCAGGAGGCCGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAATGAGCGAAACT
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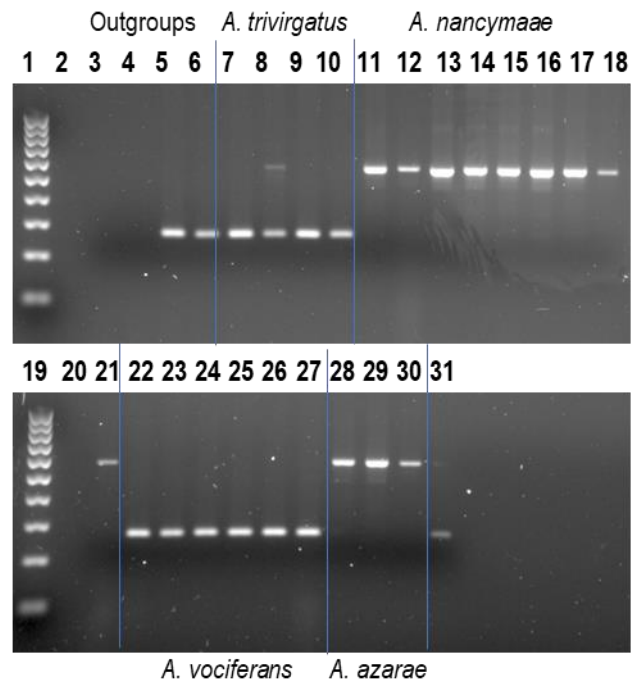
      1210      1220      1230      1240      1250      1260      1270      1280      1290      1300
Owl_2LS_056 [Anan_2.0] ccgtctcaaaaaaaaaaaaaaaaaaaaaaagagtgactcTTAGATTCTACTTAGGGCACACTTTCACCTTATAGTAAAAAGTACTGGATCACACATACCTT
LR-56-85818-F CCGTCTCAAAAAAAAAAAAAAAAAAAAAA
LR-56-85818-SIntR-rc CCGTCTCAAAAAAAAAAAAAAAAAAAAAA
LR-56-85818-IntF AAAAAAAAAAAAAAAAAAAGAGTGACTCTTAGATTCTACTTAGGGCACACTTTCACCTTATAGTAAAAAGTAC
LR-56-85818-R-rc

```

**Figure S2.** Sequence alignment for *Alu* locus Owl\_2LS\_056\_018502759.1:6075589-6077089 (LR-56). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals, homozygous present in all three *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 929 (grey highlight), with matching flanking TSDs in yellow highlight.



**Figure S3.** Sequence alignment for *Alu* locus Owl\_2LS\_091\_018503592.1:8635400-8636896 (LR-91). PCR-based genotypes indicate the target *Alu* insertion is homozygous present among *A. nancymae* and *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 603 (grey highlight), with matching flanking sequence and TSDs in yellow highlight.

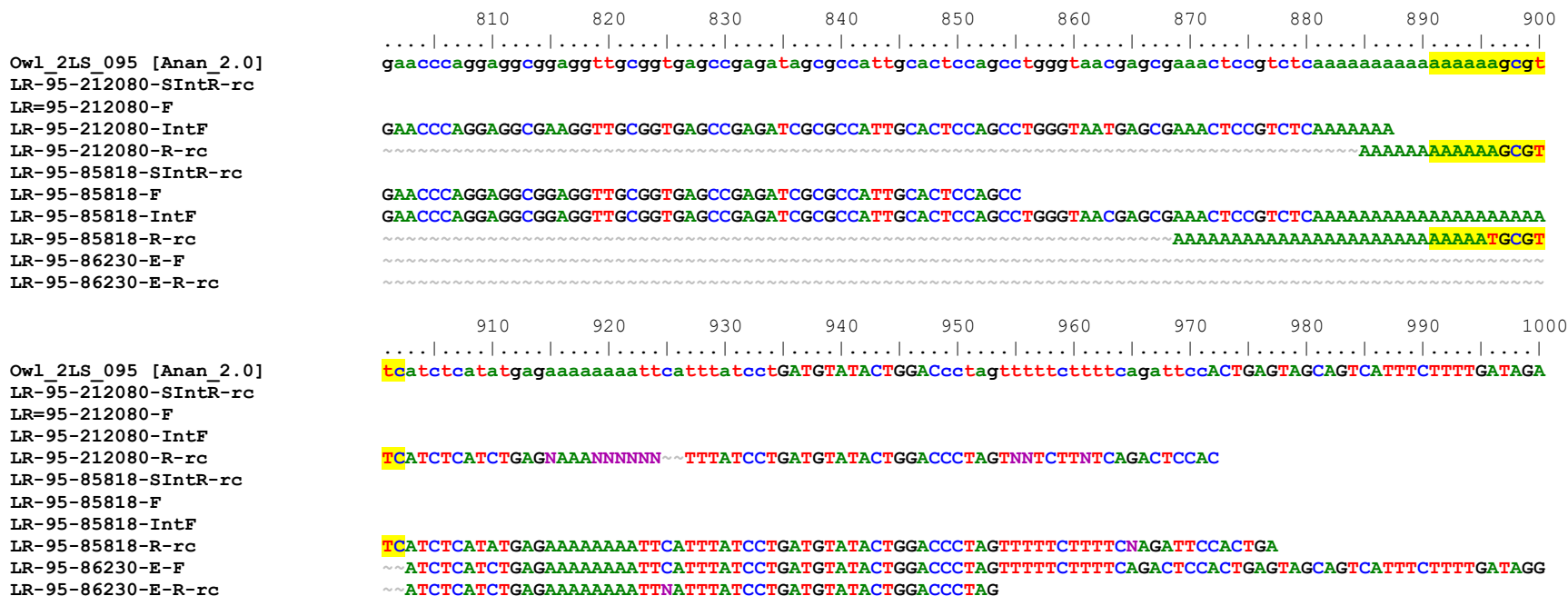


**Figure S4a:** *Alu* locus Owl\_2LS\_095\_018496424.1:3086922-3088414 (LR-95): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3-TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. Vertical blue lines superimposed on the gel image visually separate the species groups. The predicted amplicon sizes are 563/266 bp. PCR-based genotypes indicate that the target *Alu* insertion is homozygous present (563 bp fragment) in *A. nancymae* (lanes 11-18, & 21) and *A. azarae* (lanes 28-30), while homozygous absent (266 bp fragment) in *A. vociferans* (lanes 22-27), yet appears to be heterozygous for the insertion in *A. trivirgatus* sample MSB-212080 (lane 8). DNA sequencing was performed to confirm these genotypes (See Figure S4b).

```
510 520 530 540 550 560 570 580 590 600
Owl_2LS_095 [Anan_2.0]
LR-95-212080-SIntR-rc AAGATTCAATTCATATAAAGGTATGttgatataaaaatTTTTAAAGAAAACACTTTGAAAAtg-aaaagcataaaTAGCTCGGATGGTTTAAAAATGcg
LR-95-212080-F AAAATTCATTTTCATATAAAGGTATGTTGATATAAAAATTTTTAAAGAAAACACTTTGAAAAAGCAATAAATAGCTCGGATGGTTTAAAAATGCG
LR-95-212080-IntF ~~~~~~ATTTTCATATAAAGGTATGTTGATATAAAAATTTTTAAAGAAAACACTTTGAAANTGANNAAAGCATAAATAGCTCGGATGGTTTAAAAATGCN
LR-95-212080-R-rc ~~~~~~
LR-95-85818-SIntR-rc AAGATTCAATTTTCATATAAAGGTATGTTGATATAAAAATTTTTAAAGAAAACACTTTGAAAAAGCAATAAATAGCTCGGATGGTTTAAAAATGCG
LR-95-85818-F ~~~~~~TATAAAGGTATGTTGATATAAAAATTTTTAAAGAAAACACTTTGAAAAAGCAATAAATAGCTCGGATGGTTTAAAAATGCN
LR-95-85818-IntF ~~~~~~
LR-95-85818-R-rc ~~~~~~
LR-95-86230-E-F ~~~~~~TATAAAGGTATGTTGATATAAAAATTTTTAAAGAAAACACTTTGAAAAAGCAATAAATAGCTCGGATGGTTTAAAAATGCG
LR-95-86230-E-R-rc AAAATTCATTTTCATATAAAGGTATGTTGATATAAAAATTTTTAAAGAAAACACTTTGAAAAAGCAATAAATAGCTCGGATGGTTTAAAAATGCG
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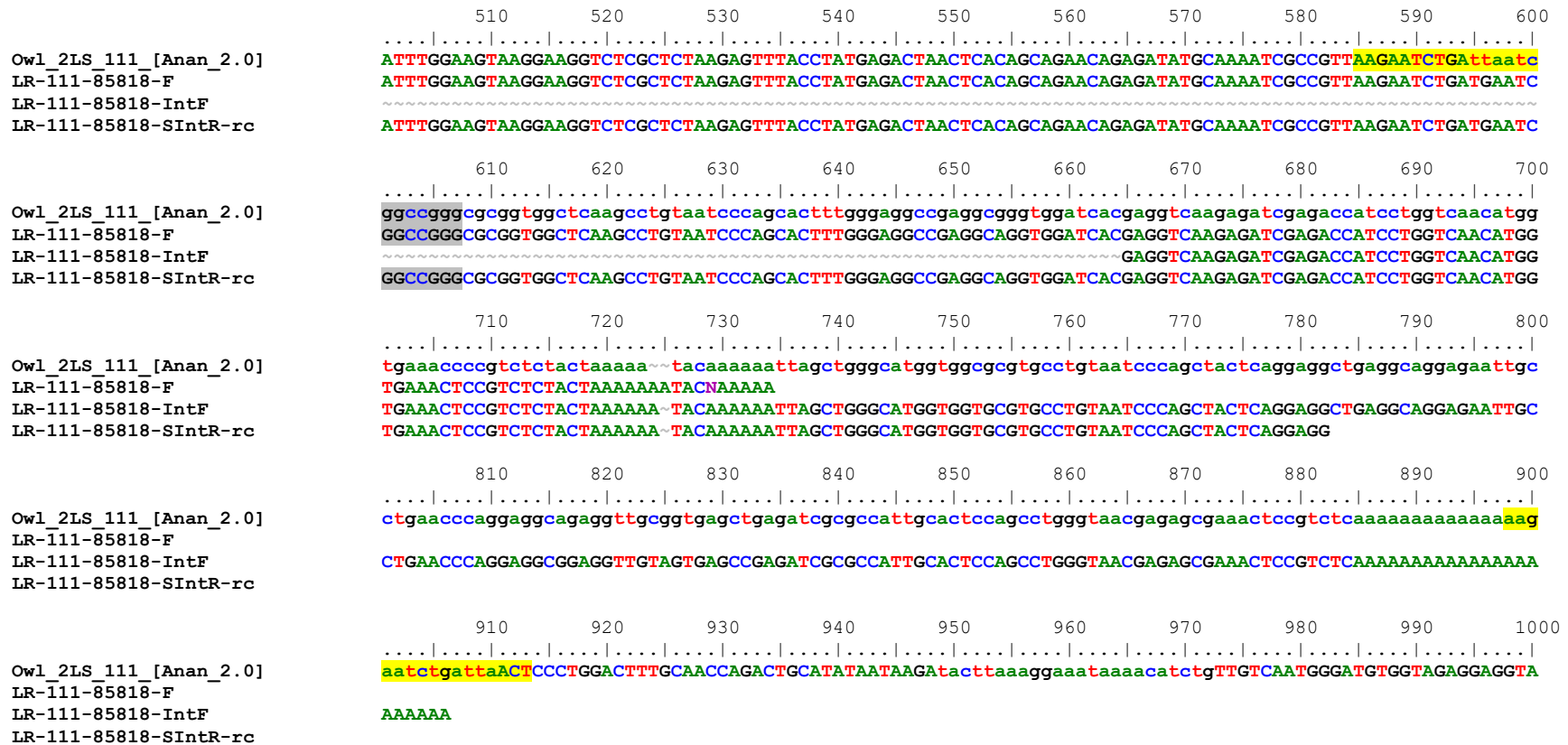
```
610 620 630 640 650 660 670 680 690 700
Owl_2LS_095 [Anan_2.0]
LR-95-212080-SIntR-rc ttctggcgggcggggtggctcaagcctgtaatcccagcacctttgggaggccgaggcggtggatcacgaggtcaagagatcaagaccatcctggtaaca
LR-95-212080-F TTCGGCCGGGCGGGTGGCTCAAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAATAGATCAAGACCATCCTGGTCAACA
LR-95-212080-IntF NNCTTNCGGGCGGGTGGCTCAAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAATAGATCAAGACCATCCTGGTCAACA
LR-95-212080-R-rc ~~~~~~GAGGTCAATAGATCAAGACCATCCTGGTCAACA
LR-95-85818-SIntR-rc TTCGGCCGGGCGGGTGGCTCAAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAAGAGATGGAGACCATCCTGGTCAACA
LR-95-85818-F TTCGGCCGGGCGGGTGGCTCAAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAAGAGATGGAGACCATCCTGGTCAACA
LR-95-85818-IntF ~~~~~~GAGGTCAAGAGATGGAGACCATCCTGGTCAACA
LR-95-85818-R-rc ~~~~~~
LR-95-86230-E-F TTC
LR-95-86230-E-R-rc TTC
```

```
710 720 730 740 750 760 770 780 790 800
Owl_2LS_095 [Anan_2.0]
LR-95-212080-SIntR-rc tggtagaaaccccgctctactaatacaaaaaatagctgggcatggtggcgctgctgtaatcccagctgctcaggaggctgaggcaggagaattgact
LR-95-212080-F TGATGAAACCCCGTCTCTACTAATACAAAAACTAGCTGGGCATGGTGGCGCGTGCTGTAAATCCCAGCTACTCAGGAGGC
LR-95-212080-IntF TGATGAAACCCCGTCTCTACTAATACAAAAACTAGCTGGGCATGGTGGCGCGTGCTGTAAATCCCAGCTACTCAGGAGGC
LR-95-212080-R-rc ~~~~~~
LR-95-85818-SIntR-rc TGGTGAACCCCGTCTCTACTAATACAAAAACTAGCTGGGCATGGTGGCGCGTGCTGTAAATCCCAGCTACTCAGGAGGC
LR-95-85818-F TGGTGAACCCCGTCTCTACTAATACAAAAACTAGCTGGGCATGGTGGCGCGTGCTGTAAATCCCAGCTACTCAGGAGGC
LR-95-85818-IntF TGGTGAACCCCGTCTCTACTAATACAAAAACTAGCTGGGCATGGTGGCGCGTGCTGTAAATCCCAGCTACTCAGGAGGC
LR-95-85818-R-rc ~~~~~~
LR-95-86230-E-F ~~~~~~
LR-95-86230-E-R-rc ~~~~~~
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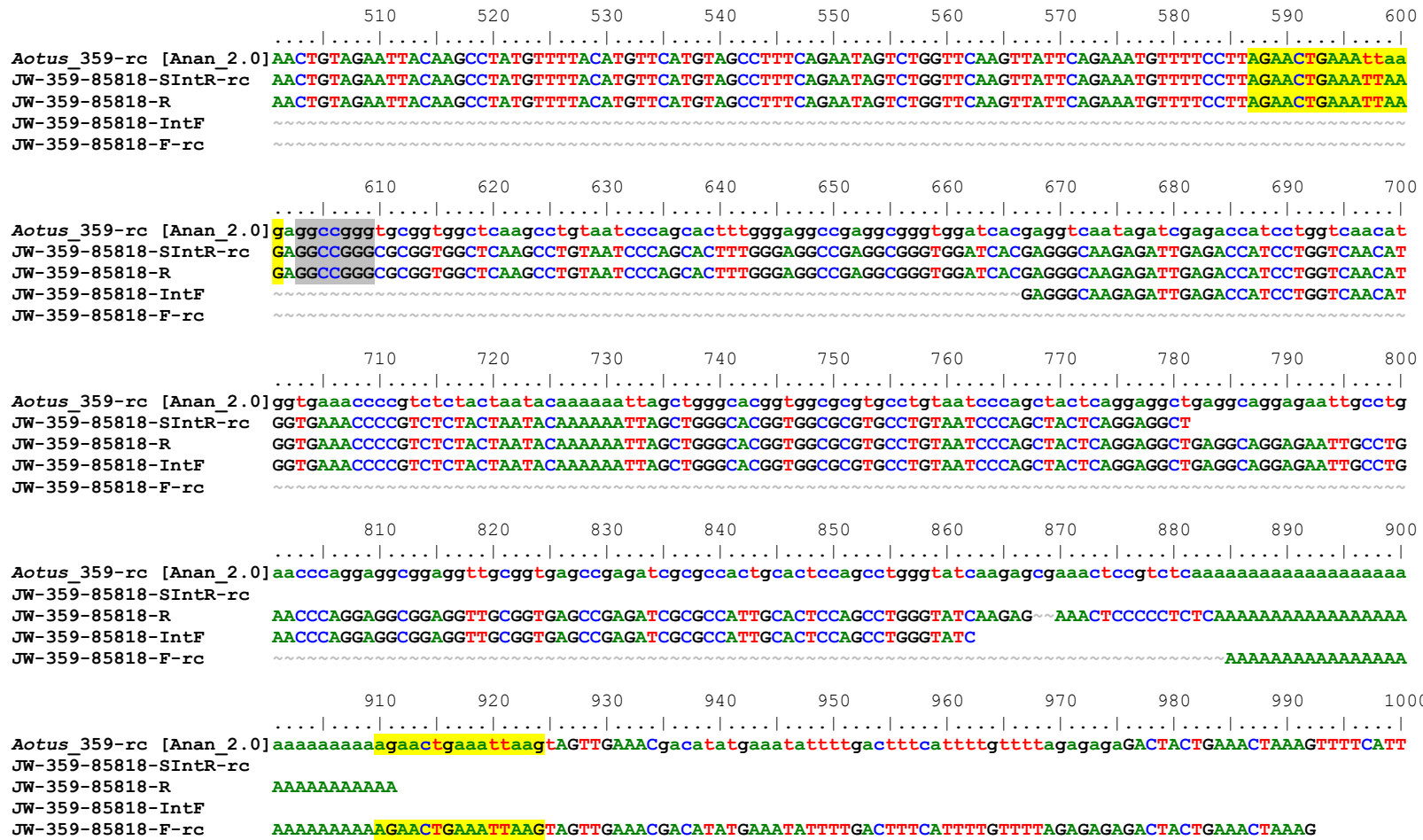


**Figure S4b.** Sequence alignment for *Alu* locus Owl\_2LS\_095\_018496424.1:3086922-3088414 (LR-95). PCR-based genotypes (Figure S4a) indicate the target *Alu* insertion is homozygous present (1/1) in all *A. nancymae* and *A. azarae* individuals and homozygous absent (0/0) in all *A. vociferans* samples, yet a single *A. trivirgatus* individual (MSB-212080) appears to be heterozygous (1/0) for the insertion. DNA sequencing was performed to confirm this pattern. The reference genome [Anan\_2.0] is shown at the top followed by *A. trivirgatus* MSB-212080 (filled site amplicon) and *A. azarae* 85818, both of whom share the target *Alu* insertion starting at position 604 (grey highlight) and flanked by TSDs in yellow highlight. Sequencing of the empty site amplicon for *A. vociferans* 86230 displays a precise pre-integration site with forward and reverse sequence traces spanning the target region, confirming the genotypes. This pattern supports grey-neck and red-neck grouping and supports *A. vociferans* as basal to *A. trivirgatus* among the *Aotus* species on our panel.





**Figure S5.** Sequence alignment for *Alu* locus Owl\_2LS\_111\_018494522.1:1204876-1206375 (LR-111). PCR-based genotypes indicate the target *Alu* insertion is homozygous present among *A. nancymae* and *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 601 (grey highlight), with matching 5' flanking sequence. Sequencing using the reverse primer failed to produce sequence traces so 3' flanking sequence is unavailable. The target insertion TSDs are shown in yellow highlight.



**Figure S6.** Sequence alignment for *Alu* locus *Aotus\_359\_018505794.1:22106446-22107953* (JW-359). PCR-based genotypes indicate the target *Alu* insertion is homozygous present (1/1) in all *A. nancymae* and *A. azarae* while absent in other *Aotus* species. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target insertion starting at position 603 (grey highlight) with flanking TSDs in yellow highlight. Sequencing confirms the genotypes linking *A. nancymae* and *A. azarae*.

510 520 530 540 550 560 570 580 590 600  
Aotus\_420\_[Anan\_2.0] AGGAAATGCCATGAGAAAATGGCACTGCATTTACCAAGTCATCCCTAGATTCTTGTGCAAAGAAAAAGATTGAGACTATGTATTAACAATTTCATAAACAA  
JW-420-85818-F TGGCACTGCATTTACCAAGTCATCCCTAGATTCTTGTGCAAAGAAAAAGATTGAGACTATGTATTAACAATTTCATAAACAA  
JW-420-85818-SIntR-rc  
JW-420-85818-IntF  
JW-420-85818-R-rc

610 620 630 640 650 660 670 680 690 700  
Aotus\_420\_[Anan\_2.0] ataatcaggccgggcgcggtggctcatgccgtgtaatcccagcactttgggagggccgagggcggtgatcagaggccaagagatcgagaccattctggtc  
JW-420-85818-F ATAATCAGGCCGGCCGGTGGCTCACGCCGTAAATCCCAGCACTTTGGGAGGCCGAGCCGGTGGATCACGAGGTC AAGAGATCGAGACCATTCTGGTC  
JW-420-85818-SIntR-rc ATAATCAGGCCGGCCGGTGGCTCACGCCGTAAATCCCAGCACTTTGGGAGGCCGAGCCGGTGGATCACGAGGTC AAGAGATCGAGACCATTCTGGTC  
JW-420-85818-IntF GAGGTC AAGAGATCGAGACCATTCTGGTC  
JW-420-85818-R-rc

710 720 730 740 750 760 770 780 790 800  
Aotus\_420\_[Anan\_2.0] aacatggtgaaaccccgctctactaatacaaaaaattagctgggcatggtggcgctgtaatcccagctactcaggaggctgaggcaggagaatt  
JW-420-85818-F AACATGGTGA AACCCCGTCTCTACTAATACAAAAATTAGCTGGGCATGGTGGCCGCTGCCGTAAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATT  
JW-420-85818-SIntR-rc AACATGGTGA AACCCCGTCTCTACTAATACAAAAATTAGCTGGGCATGGTGGCCGCTGCCGTAAATCCCAGCTACTCAGGAGG  
JW-420-85818-IntF AACATGGTGA AACCCCGTCTCTACTAATACAAAAATTAGCTGGGCATGGTGGCCGCTGCCGTAAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATT  
JW-420-85818-R-rc

810 820 830 840 850 860 870 880 890 900  
Aotus\_420\_[Anan\_2.0] gcctgaaacccaggaggcggaggttgcggtgagccgagatcgcgccattgcaactccagcctgggtaacaagagcgaaaactcctctcaaaaaaaaaaaaa  
JW-420-85818-F GCCTGAACCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACTCCAGCCTGGGTAACAAGAGCGAAAACCTCCGTCTCAAAAAAAAA  
JW-420-85818-SIntR-rc  
JW-420-85818-IntF GCCTGAACCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACTCCAGCCTGGGTAACAAGAGCGAAAACCTCCGTCTCAAAAAAAAA  
JW-420-85818-R-rc

910 920 930 940 950 960 970 980 990 1000  
Aotus\_420\_[Anan\_2.0] aaacaataatcaacaATTTCACTCCATTATTTGATGTTGGGTAAGCCTGAAATGTGGTGTCAAGTTTTTCCATTTGCATTACATAAATTTCTGTCT  
JW-420-85818-F  
JW-420-85818-SIntR-rc  
JW-420-85818-IntF  
JW-420-85818-R-rc

1010 1020 1030 1040 1050 1060 1070 1080 1090 1100  
Aotus\_420\_[Anan\_2.0] ACTATGGATATTTGATATGACAAAGACTAAATTCCTATTGAAACATTTGCCATTTACTACACTCACATAACTTCTCTTAGGATATAGATTTTTTGTATGTT  
JW-420-85818-F  
JW-420-85818-SIntR-rc  
JW-420-85818-IntF  
JW-420-85818-R-rc

```
          1110        1120        1130        1140        1150        1160        1170        1180        1190        1200
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_420_[Anan_2.0] GGGTGTGACCGAATGtcctcacacacatacacgtttattacatttataatatttttgcataGGCATGAATGATACAAAACAAGGTAGTTTCTTTGACTGA
JW-420-85818-F
JW-420-85818-SIntR-rc
JW-420-85818-IntF
JW-420-85818-R-rc
~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
          1210        1220        1230        1240        1250        1260        1270        1280        1290        1300
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_420_[Anan_2.0] TGGCTCTTTCACACTCATTGCGGTAATGGAATTTTATTCCCGTATGATTTTTCCAAATGTGACTaaagttagaaaaattatgacatgAAAAATTACC
JW-420-85818-F
JW-420-85818-SIntR-rc
JW-420-85818-IntF
JW-420-85818-R-rc
~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
          NGGCTCTTTCACACTCATTGCGAGTAATGGAATTTTATTCCCGTATGACTTTTCCAAATGTGACTAAGTTATGAAAAATTATATAGCA
```

**Figure S7.** Sequence alignment for *Alu* locus *Aotus\_420\_018497736.1:502088-503587* (JW-420). PCR-based genotypes indicate the target *Alu* insertion is homozygous present (1/1) in all *A. nancymae* and *A. azarae* while absent in other *Aotus* species. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target insertion starting at position 608 (grey highlight) with flanking TSDs in yellow highlight. The reverse primer sequence trace initiates at position 1287 but does not extend back to the A-tail of the target insertion, however the forward and SIntR traces confirm the genotypes linking *A. nancymae* and *A. azarae*.

```
          510        520        530        540        550        560        570        580        590        600
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_506_[Anan_2.0] GTGGCTTTGCTCCTGtagttaataaagaagaaagagagagagagagagagaagag~cattcCAAGAAGAGAGAATAGTTTATGCAAAAACCTCTATg
JW-506-85457-F
JW-506-85457-SIntR-rc GTGGCTTTGCTCCTGTAGTTAAATAAGAAAAGAAAGAAAGAGAGAGAGAGAGAGAGAAGAGCATTCCAAGAAGAGAGAATAGTTTATGCAAAAACCTCTATG
JW-506-85457-IntF
JW-506-85457-R-rc
~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
          610        620        630        640        650        660        670        680        690        700
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_506_[Anan_2.0] gctggcgggcgggctggctcacgctgtaatcccagcactttgggaggccgaggcaggtggatcaogaggccaagagatcgagaccatccttggtcaaca
JW-506-85457-F
JW-506-85457-SIntR-rc GCTGGCCGGGCGGGTGGCTCACGCTGTAAATCCCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACAAGGTCAAGAGATCGAGACCATCCTGATCAACA
JW-506-85457-IntF
JW-506-85457-R-rc
~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
          710        720        730        740        750        760        770        780        790        800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_506_[Anan_2.0] ttggtgaacctgtctctactaaaaatacaaaaaattagctgggcatggtggcgcatgccgtgtaatcccagctactcaggaggctgaggcaggagaattg
JW-506-85457-F
JW-506-85457-SIntR-rc TGGTGAATCACCGTTTCTACTAAAAATA
JW-506-85457-IntF
JW-506-85457-R-rc
~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
          TGGTGAATCACCGTTTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCACGTGCCGTAAATCCCAGCTACTCAGGAGG
          TGGTGAATCACCGTTTCTACTAAAAATACAAAAATTNCC TGCTGGTGGCACGTGCCGTAAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTG
```

```

      810      820      830      840      850      860      870      880      890      900
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_506_[Anan_2.0] cctgaaccaggaggcggaggttgctggtgagccgagatcgcgccattgcactccagcctgggtaacaagagcgaaactccgtctcaaaaaaaaaaaaaa
JW-506-85457-F
JW-506-85457-SIntR-rc CCTGAACCCAGGAGGCAGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACTCCAGCCTGGGTAAACAAGAGCGAAACTCCGCTCCAAAAAAA
JW-506-85457-IntF
JW-506-85457-R-rc
      910      920      930      940      950      960      970      980      990     1000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_506_[Anan_2.0] aaattctatggctTAGGCAAGAAGCAATCCATGCGGGGCTTTATAGGCCATATCAAGAATTCTGTCCCTAAATCCTAAAACCATAGAAAGCCACTTGGGGT
JW-506-85457-F
JW-506-85457-SIntR-rc
JW-506-85457-IntF
JW-506-85457-R-rc AAACCTCTATGGCTTAGGCAAGAAGCAATCCATGCGGGG

```

**Figure S8.** Sequence alignment for *Alu* locus *Aotus\_506\_018511366.1:24422032-24423531* (JW-506). PCR-based genotypes indicate the target *Alu* insertion is present in *A. nancymae* and *A. azarae* while absent in other *Aotus* species. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85457 who shares the target insertion starting at position 604 (grey highlight) with flanking TSDs in yellow highlight. Sequencing confirms the genotypes linking *A. nancymae* and *A. azarae*.

```

      510      520      530      540      550      560      570      580      590      600
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_592_[Anan_2.0] AGGCAACCTAGTTTCATCACTTAGACTGGAATCATGTCTTCTAATTCCTAGTGATTTGCTCTTCTACTGAATCAAAATtattcaattcaaaaaaaaaa
JW-592-85457-R
JW-592-85457-SIntR-rc NNNNAACCTAGTTTCATCACTTAGACTGGAATCATGTCTTNNNNTCTCAGTGATTTGCTCTTCTACTGAATCAAAATTTCAATTCAAA
JW-592-85457-IntF
      610      620      630      640      650      660      670      680      690      700
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_592_[Anan_2.0] actgccgggcgctggtctcaagcctgtaatccagcactttgggaggccgaggcgggtggatcactgaggccaagagatcagagccatcctgggtcaacat
JW-592-85457-R
JW-592-85457-SIntR-rc ACTGCCGGGCGCGGTGGCTCACGCCGTGAATCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAAGAGATCGAGACCATCATGGTCAACAT
JW-592-85457-IntF
      710      720      730      740      750      760      770      780      790      800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_592_[Anan_2.0] ggtgaaacccgctctctactaaaaatacaaaaaattagctgggca-tgggtggcgcgtgccgtgtaatccagctactcaggaggctgaggcaggagaattg
JW-592-85457-R
JW-592-85457-SIntR-rc GGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCA-TGGTGGCGCGTGCCGTAAATCCAGCTACTCAGGAGG
JW-592-85457-IntF
      810      820      830      840      850      860      870      880      890      900
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_592_[Anan_2.0] cctgaaccaggaggcagaggttgctggtgagccgagatcgcgccattgcactccagcctgggtaacaggagcaaaactccgtctcaaaaaaaaaaaaaa
JW-592-85457-R
JW-592-85457-SIntR-rc CCTGAACCCAGGAGGCAGAGGTTGCGGTGAGCCGAGATCGCACCATTTGCACTCCAGCCTGGGTAAACAAGAGCAAAA
JW-592-85457-IntF

```

```

      910      920      930      940      950      960      970      980      990      1000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_592_[Anan_2.0]
JW-592-85457-R
JW-592-85457-SIntR-rc
JW-592-85457-IntF
aaaaaaatacttaggaagaaGCCTGCCACTGTGACAAAGAGAGTGCCATGCTACAGCTCAGCGGTTCCCTCATGAGCAGCTTGTCAAAAAGGACAAGGCC

```

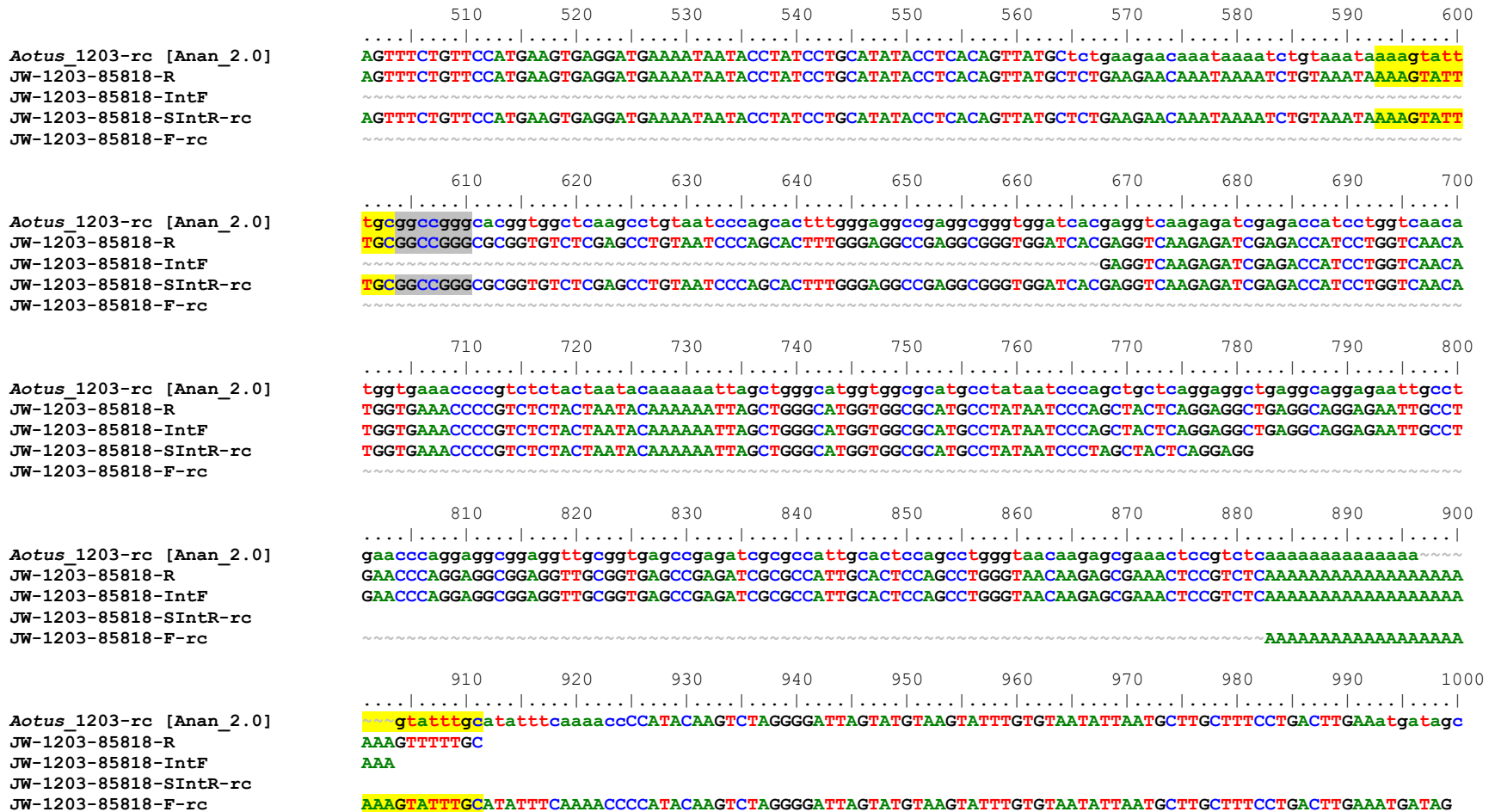
**Figure S9.** Sequence alignment for *Alu* locus *Aotus\_592\_018503629.1:2778893-2780395* (JW-592). PCR-based genotypes indicate the target *Alu* insertion is homozygous present (1/1) in all *A. nancymaae* and *A. azarae* while absent in other *Aotus* species. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85457 who shares the target insertion starting at position 604 (grey highlight) with flanking TSDs in yellow highlight. The internal-*Alu* forward and forward-rc primer sequence traces are relatively poor, however the SIntR-rc sequence trace confirms the *Alu* start position and 5' TSD, confirming the genotypes linking *A. nancymaae* and *A. azarae*.

```

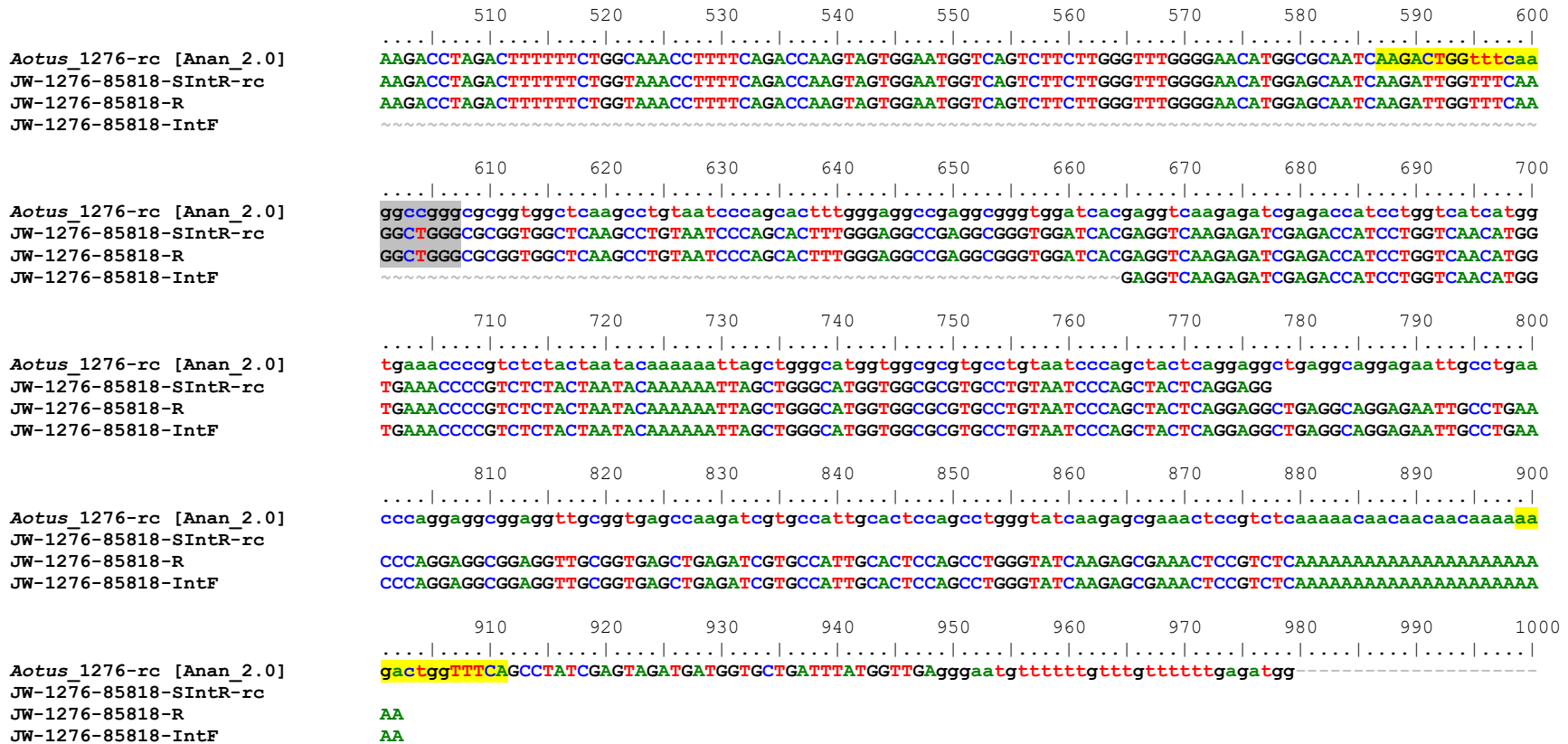
      510      520      530      540      550      560      570      580      590      600
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1202-rc [Anan_2.0]
JW-1202-85818-SIntR-rc
JW-1202-85818-R
TATGTTACTTTATATCATCTTTAGTTTATAGTCAGTCTCTGAAGTAGGTATTACCGTCCTCACCTTATGTTTGAAAACCTGAAGTTAAAAGATgttcag
~~~~~TGA AACCTGAAGTTAAAAGATGTT CAG
      610      620      630      640      650      660      670      680      690      700
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1202-rc [Anan_2.0]
JW-1202-85818-SIntR-rc
JW-1202-85818-R
ggccgggcgcggtggctcaagcctgtaatcccagcactttgggaggccgaggcgggtggatcacgagttcaagagatcgagaccatcctgg tcaacatgg
GGCCGGGCGCGGTGGCTCAAGCCTGTAATCCCAGCAC TTTGGGAGGCCGAGGCCGGTGGATCACGAGTTC AAGAGATCGAGACCATCCTGGTCAACATGG
      710      720      730      740      750      760      770      780      790      800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1202-rc [Anan_2.0]
JW-1202-85818-SIntR-rc
JW-1202-85818-R
tgaaaccccg tcttactaatacaaaaaattagctgggcatgggtggcgcgtgacctgtaatcccagctactcaggaggctgaggcaggagaaattgctgaa
TGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGC
      810      820      830      840      850      860      870      880      890      900
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1202-rc [Anan_2.0]
JW-1202-85818-SIntR-rc
JW-1202-85818-R
cccaggaggcggaggttg cggtgagccgagatcgcgccattgcactccagcctgggtaacaagaa caaaactctgtctcaaaaaaaaaaaaaaaaaaaaa
      910      920      930      940      950      960      970      980      990      1000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1202-rc [Anan_2.0]
JW-1202-85818-SIntR-rc
JW-1202-85818-R
aagatgttcagTAACTAGGCCAAAAATCACAGTCTGGTCTAAGTAG--TCAGATTTGAACAAGGTTGACCTGATTC CAAAATCTATACTGTATTCATT

```

**Figure S10.** Sequence alignment for *Alu* locus *Aotus\_1202\_018500372.1:1331491-1332992* (JW-1202). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals, also homozygous present in all three *A. azarae* individuals, while being absent from other *Aotus* species. DNA sequencing was limited but the SIntR sequence trace from *A. azarae* 85818 shows it shares the target *Alu* insertion in the [Anan\_2.0] reference genome. The target insertion starts at position 601 (grey highlight) and is flanked by TSDs AAAAGATGTTTCAG in yellow highlight.



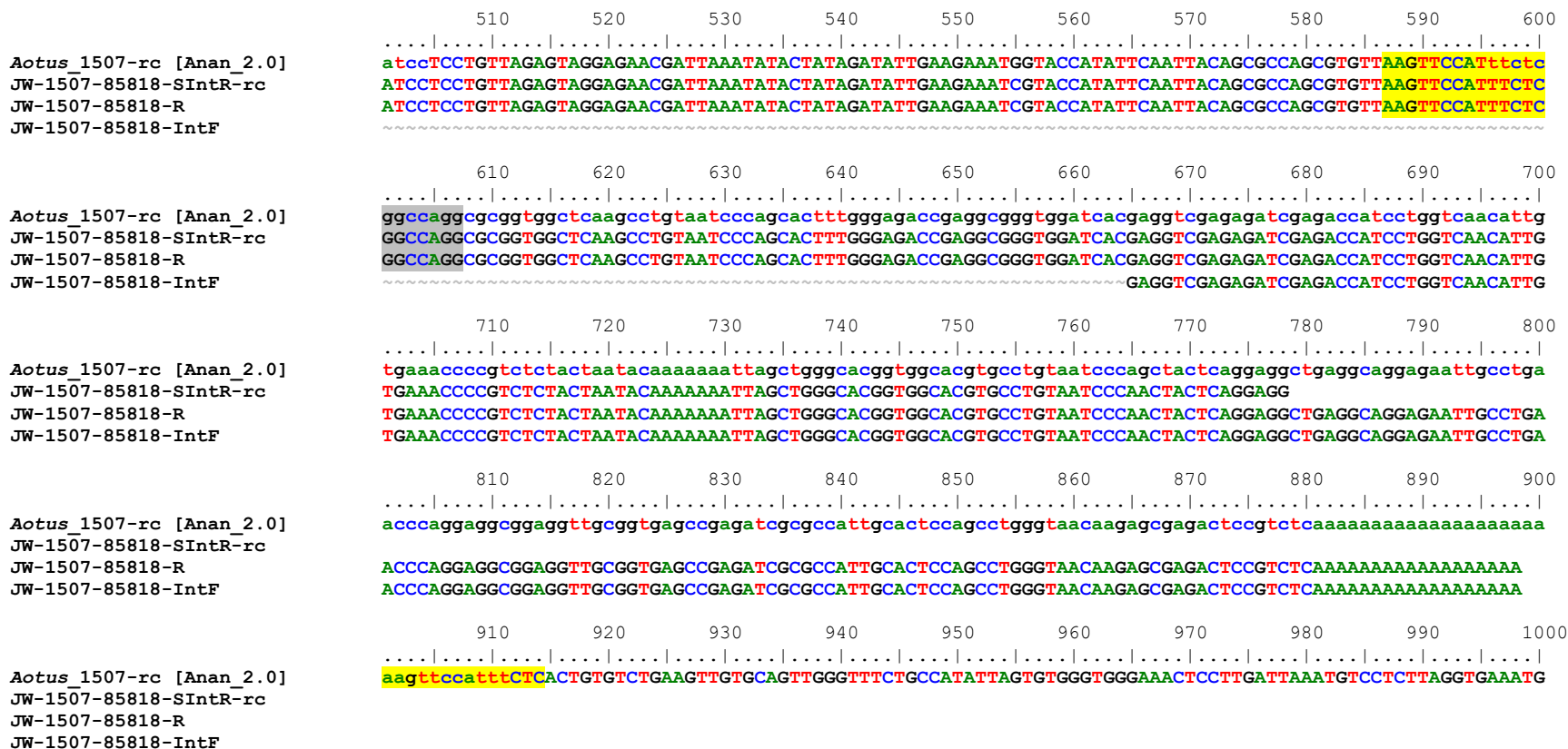
**Figure S11.** Sequence alignment for *Alu* locus *Aotus\_1203\_018500372.1:1581468-1582960* (JW-1203). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals, also present in two of three *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion that starts at position 604 (grey highlight) and flanked by TSDs in yellow highlight.



**Figure S12.** Sequence alignment for *Alu* locus *Aotus\_1276\_018501266.1:1161971-1163470* (JW-1276). PCR-based genotypes indicate the target *Alu* insertion is homozygous present in all *A. nancymae* and *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who appears to share the



target insertion starting at position 601 (grey highlight) and flanked by TSDs in yellow highlight. However, no 3' flanking sequence trace was successfully obtained, therefore it remains a remote possibility that this is a precise parallel insertion based solely on 5' matching flanking sequence. We will consider this sequence as evidence of a shared insertion.



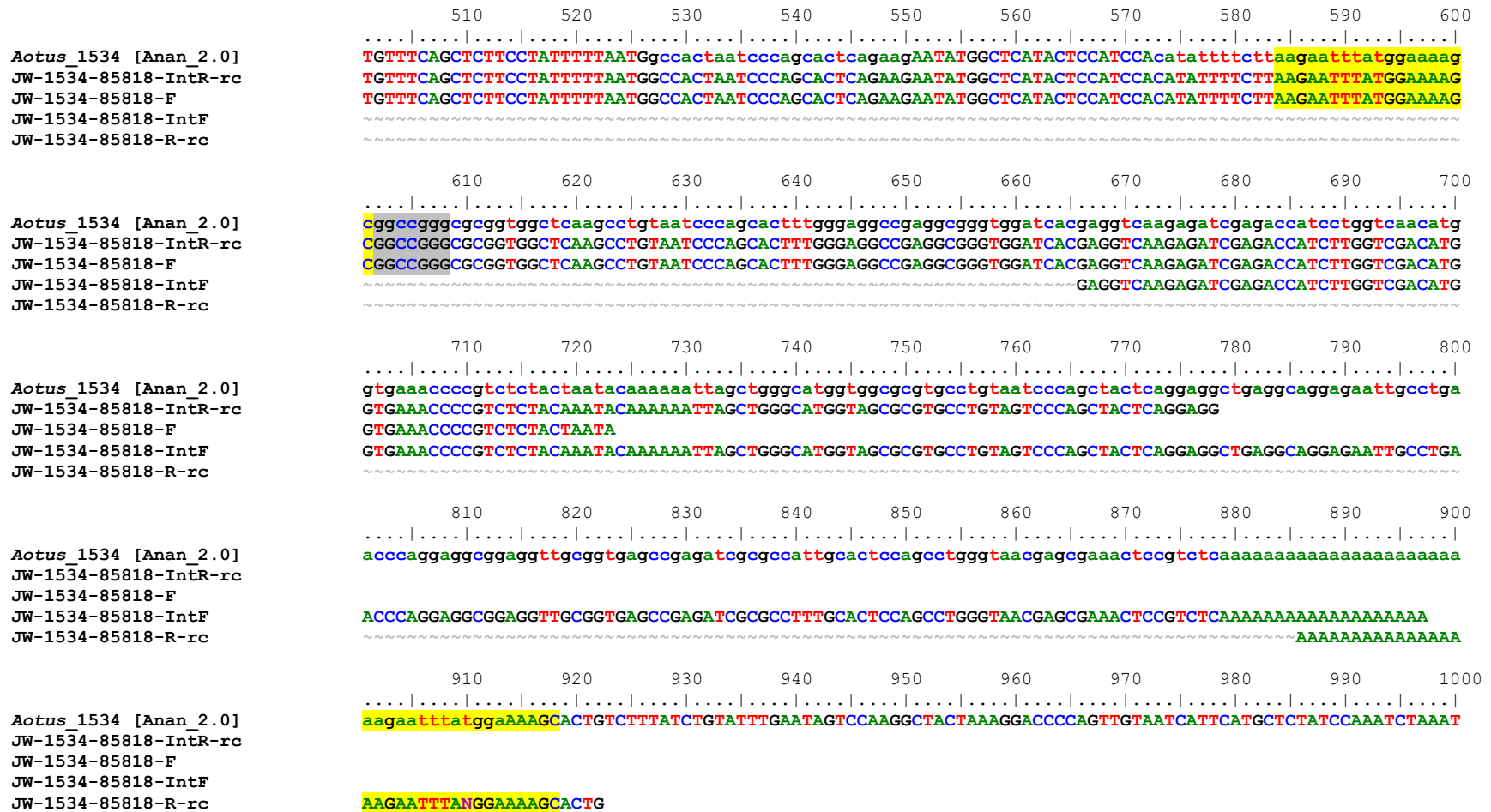
**Figure S13.** Sequence alignment for *Alu* locus *Aotus\_1507\_018505863.1:9051781-9053282* (JW-1507). PCR-based genotypes indicate the target *Alu* insertion is present in all *A. nancymae* and *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who appears to share the target insertion starting at position 601 (grey highlight) and flanked by TSDs in yellow highlight. However, no 3' flanking sequence trace was successfully obtained, therefore it remains a remote possibility that this is a precise parallel insertion based solely on 5' matching flanking sequence. We will consider this sequence as evidence of a shared insertion.

```

      510      520      530      540      550      560      570      580      590      600
Aotus_1528 [Anan_2.0]
JW-1528-85818-F
JW-1528-85818-SIntR-rc
JW-1528-85818-IntF
JW-1528-85818-R-rc
      610      620      630      640      650      660      670      680      690      700
Aotus_1528 [Anan_2.0]
JW-1528-85818-F
JW-1528-85818-SIntR-rc
JW-1528-85818-IntF
JW-1528-85818-R-rc
      710      720      730      740      750      760      770      780      790      800
Aotus_1528 [Anan_2.0]
JW-1528-85818-F
JW-1528-85818-SIntR-rc
JW-1528-85818-IntF
JW-1528-85818-R-rc
      810      820      830      840      850      860      870      880      890      900
Aotus_1528 [Anan_2.0]
JW-1528-85818-F
JW-1528-85818-SIntR-rc
JW-1528-85818-IntF
JW-1528-85818-R-rc
      910      920      930      940      950      960      970      980      990     1000
Aotus_1528 [Anan_2.0]
JW-1528-85818-F
JW-1528-85818-SIntR-rc
JW-1528-85818-IntF
JW-1528-85818-R-rc

```

**Figure S14.** Sequence alignment for *Alu* locus *Aotus\_1528\_018502886.1:12506963-12508462* (JW-1528). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals, homozygous present in all three *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 611 (grey highlight), with matching flanking TSDs in yellow highlight.



**Figure S15.** Sequence alignment for *Alu* locus *Aotus\_1534\_018505554.1:7580189-7581692* (JW-1534). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals, homozygous present in all three *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 602 (grey highlight), with matching flanking TSDs in yellow highlight.

510 520 530 540 550 560 570 580 590 600  
Aotus\_1559 [Anan\_2.0]  
JW-1559V2-KB10043-SIntR-rc CTATACCCAGCCCCACAGgtacacattcaacacacatatgacacattttAGTTGAGCTACAGGAGATCACTGTTTTTGCAGTAAAAAGTAatttcag  
JW-1559V2-KB10043-F ~~~~~CCCCACAGGTACACATTCACACACATATGCACACATTTTAGTTGAGCTACAGGAGATCACTGTTTTTGCAGTAAAAAGTAATTCAG  
JW-1559V2-KB10043-IntF ~~~~~~TCACTGTTTTTGCAGTAAAAAGTAATTCAG  
JW-1559V2-KB10043-R-rc ~~~~~~  
JW-1559V2-85457-F ~~~~~~GGAGATCACTGTTTTTGCAGTAAAAAGTAATTCAG  
JW-1559V2-85457-IntF ~~~~~~  
JW-1559V2-85457-SIntR-rc ~~~~~~  
JW-1559V2-85457-R-rc ~~~~~~  
JW-1559V2-85818-F ~~~~~~GAGCTACAGGAGANCACTGTTTTTGCAGTAAAAAGTAATTCAG  
JW-1559V2-85818-IntF ~~~~~~  
JW-1559V2-85818-SIntR-rc ~~~~~~  
JW-1559V2-85818-R-rc ~~~~~~

610 620 630 640 650 660 670 680 690 700  
Aotus\_1559 [Anan\_2.0]  
JW-1559V2-KB10043-SIntR-rc ggccgggCGCGgtggctcaagcctgtaatcccagcactttgggagggccgaggggggtggatcacgaggtcaagagatcgagaccatcctggtaacatgg  
JW-1559V2-KB10043-F ~~~~~GGCCGGGCGCGGTGGCTCAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGGCCGGTGGATCACGAGGTC AAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1559V2-KB10043-IntF ~~~~~GAGGTC AAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1559V2-KB10043-R-rc ~~~~~~  
JW-1559V2-85457-F ~~~~~GGCCGGGCGCGGTGNTCAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGGCCGGTGGATCACGAGGTC AAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1559V2-85457-IntF ~~~~~GAGGTC AAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1559V2-85457-SIntR-rc ~~~~~~  
JW-1559V2-85457-R-rc ~~~~~~  
JW-1559V2-85818-F ~~~~~GGCCGGGCGCGGTGGCTCAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGGCCGGTGGATCACGAGGTC AAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1559V2-85818-IntF ~~~~~GAGGTC AAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1559V2-85818-SIntR-rc ~~~~~~  
JW-1559V2-85818-R-rc ~~~~~~

710 720 730 740 750 760 770 780 790 800  
Aotus\_1559 [Anan\_2.0]  
JW-1559V2-KB10043-SIntR-rc tgaaaCCCCgtctctactaatacaaaaaaaaaaacactagctgggcatgggtggcgctgctgtaatcccagctactcaggaggctgaggcaggggaattg  
JW-1559V2-KB10043-F ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA ~ CACTAGCTGGGCATGGTGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGG  
JW-1559V2-KB10043-IntF ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA ~ CACTAGCTGGGCATGGTGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA TTG  
JW-1559V2-KB10043-R-rc ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA ~ CACTAGCTGGGCATGGTGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA TTG  
JW-1559V2-85457-F ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA ~ CTGGGCGGGG TGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGGCTGANGCAGGGGAATTA  
JW-1559V2-85457-IntF ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA ~ CACAANC TGGGCGTGGTGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGAAT TG  
JW-1559V2-85457-SIntR-rc ~~~~~TAAAAA ~ CACTAGCTGGGCATGGTGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA TTG  
JW-1559V2-85457-R-rc ~~~~~~  
JW-1559V2-85818-F ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA ~ ACTAGCTGGGGGGGGGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAA TTG  
JW-1559V2-85818-IntF ~~~~~TGAAA CCCC GTCTCTACTAATACAAAAA  
JW-1559V2-85818-SIntR-rc ~~~~~AAAAA ~ CACTAGCTGGGCATGGTGGCGCGTGCCGTGTAATCCCAGCTACTCAGGAGG  
JW-1559V2-85818-R-rc ~~~~~~



```

          910      920      930      940      950      960      970      980      990      1000
Storer_2020_Aotus-827
JS-827-85818-SIntR-rc
JS-827-85818-F
JS-827-85818-IntF
JS-827-85818-R-rc
TCCcCcaaaaaaacctcaaaaataggcgggcggggtggctcagcctgtaatccaagcactttgggaggccgaggcgggtggatcaagagat
TCCCCCAAAAAACCCTCAAAATAGGCCGGGCGGGTGGCTCACGCCGTAAATCCAAGCACTTTGGGAGGCCGAGGTGGGTGGATCACGAGGTCAAGAGAT
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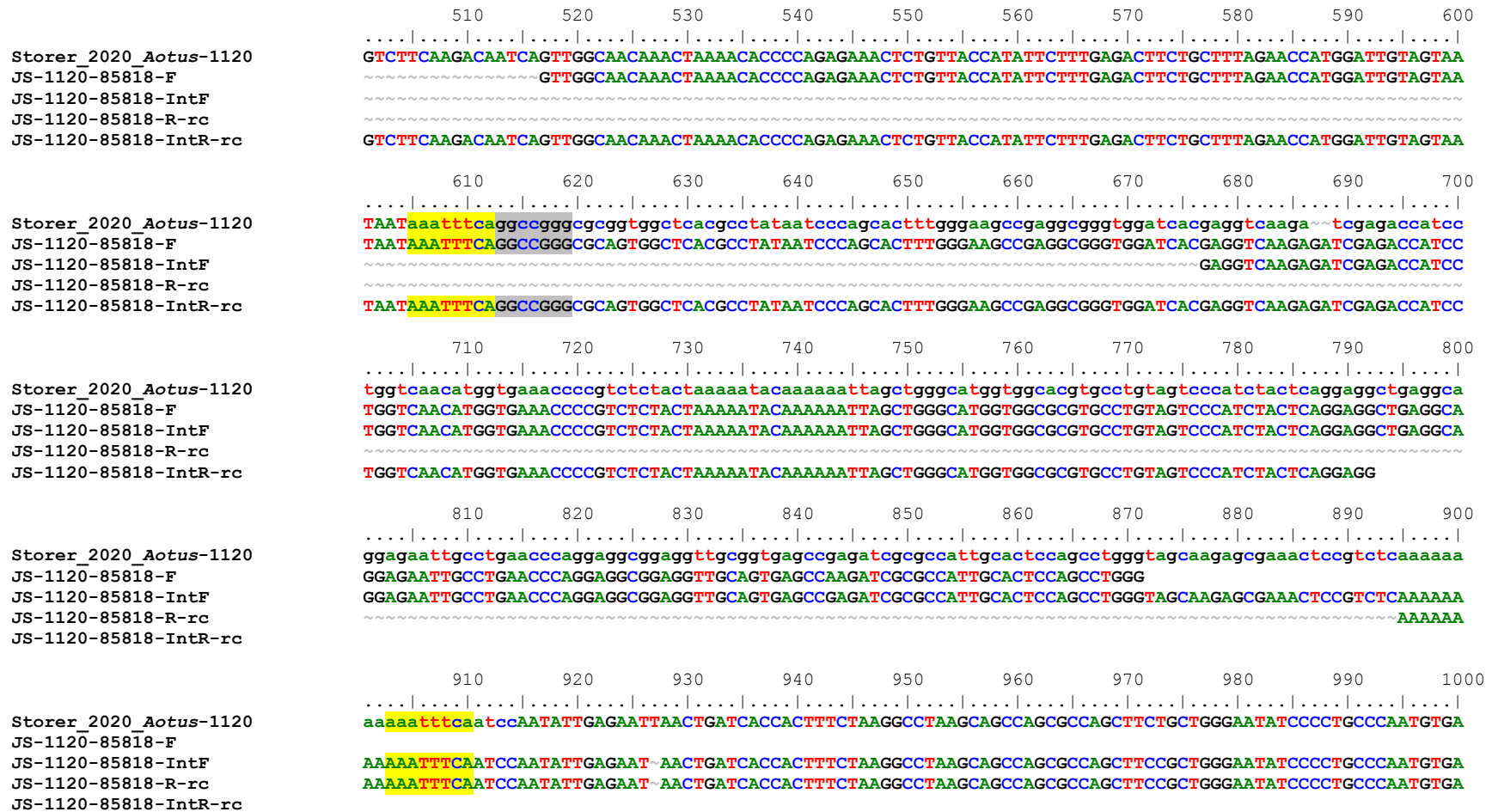
          1010     1020     1030     1040     1050     1060     1070     1080     1090     1100
Storer_2020_Aotus-827
JS-827-85818-SIntR-rc
JS-827-85818-F
JS-827-85818-IntF
JS-827-85818-R-rc
cgagaccatcctgggtcaacaagggtgaaccocgctctactaaaaatacaaaaaattagctgggcatgggtggcgtgcctgtaatcccagctactcagg
CGAGACCATCCTGGTCAACAAGGTGAAACCCCGTCTACTAAAAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCGTAAATCCCAGCTACTCAGG
CGAGACCATCCTGGTCAACAATGGTGAACCCCGTCTACTAAAAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCGTAAATCCCAGCTACTCAGG
CGAGACCATCCTGGTCAACAATGGTGAACCCCGTCTACTAAAAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCGTAAATCCCAGCTACTCAGG

          1110     1120     1130     1140     1150     1160     1170     1180     1190     1200
Storer_2020_Aotus-827
JS-827-85818-SIntR-rc
JS-827-85818-F
JS-827-85818-IntF
JS-827-85818-R-rc
aggctgaggcaggagaattgcctgaaccaggagggtggaggttgtggtgagctgagatcacacattgcaactccagcctgggtaacaagagtgaactcc
AGGCTGAGGCAG
AGGCTGAGGCAGGAGAAATTGCCTGAACCCAGGAGGTGGAGGTTGTGGTGAGCTGAGATCGCGCCATTGCATCCAGCCTGGGTAACAAGAGTGAACTCC
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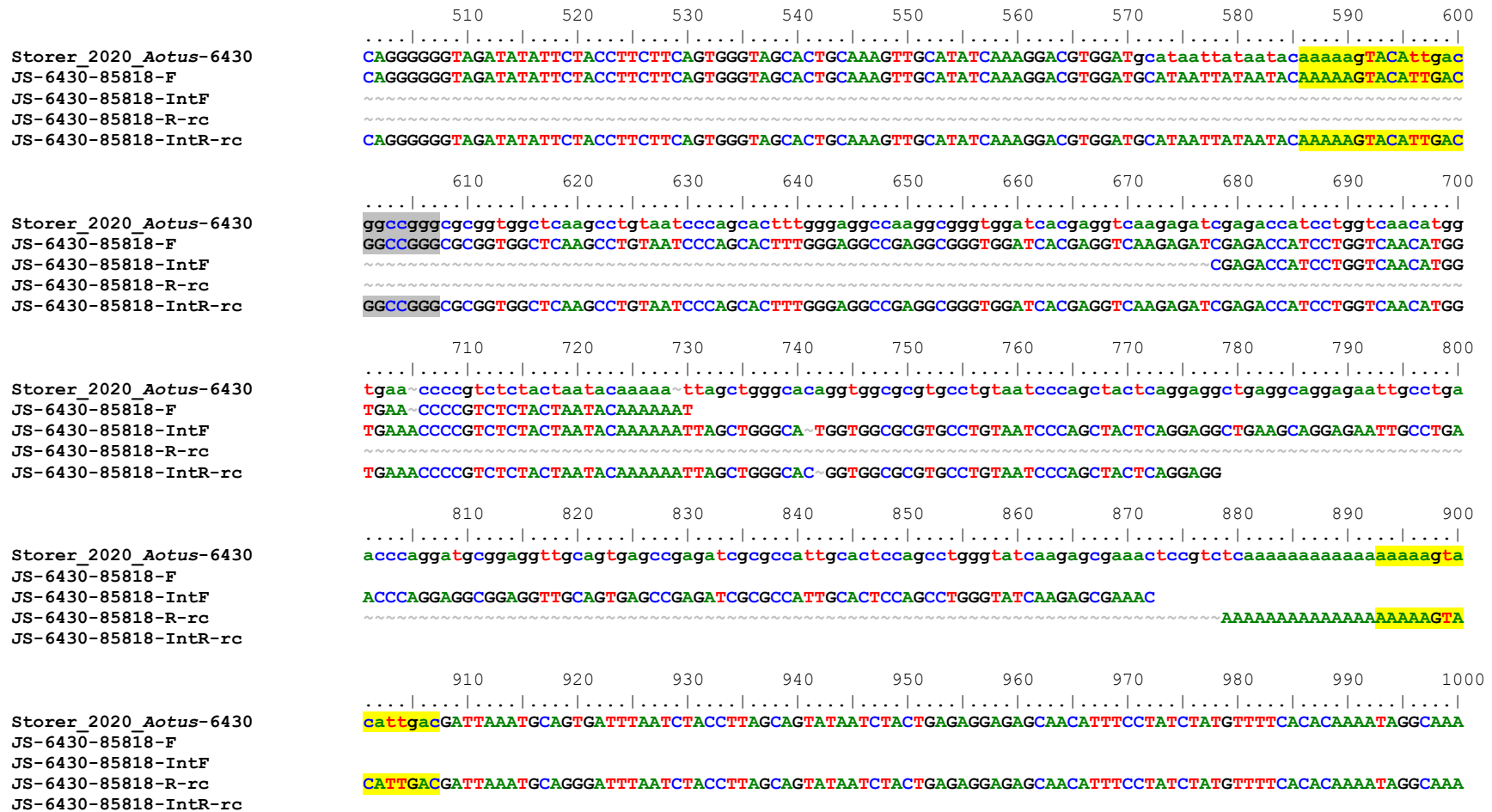
          1210     1220     1230     1240     1250     1260     1270     1280     1290     1300
Storer_2020_Aotus-827
JS-827-85818-SIntR-rc
JS-827-85818-F
JS-827-85818-IntF
JS-827-85818-R-rc
gtctcaaaaaaaaaaaaaaacctcaaaagtaGTAACATCTTTCCAGTcaataaagtgaatgtcaGAGCTAATATTGACTGTTGTCTCTTCATAT
GTTCTCAAAAAAAAAAAAAA
GTTCTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAACCTCAAAATAGTAACATCTTTCCAGTCAATAAATGAAAAATGCAGAGCTAATATTGACTGTTGTCTCTTCATAT

```

**Figure S17.** Sequence alignment for *Alu* locus: Storer, et al. 2020: *Aotus\_827\_018493494\_6605199* (JS-827). PCR-based genotypes indicate that the target *Alu* insertion is homozygous present in *A. nancymae* and *A. azarae* individuals while heterozygous (1/0) in *A. lemurinus griseimembra* KB4883 (filled site amplicons too weak to excise gel fragments). The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target insertion starting at position 924 (grey highlight) and flanked by TSDs shown in yellow highlight.

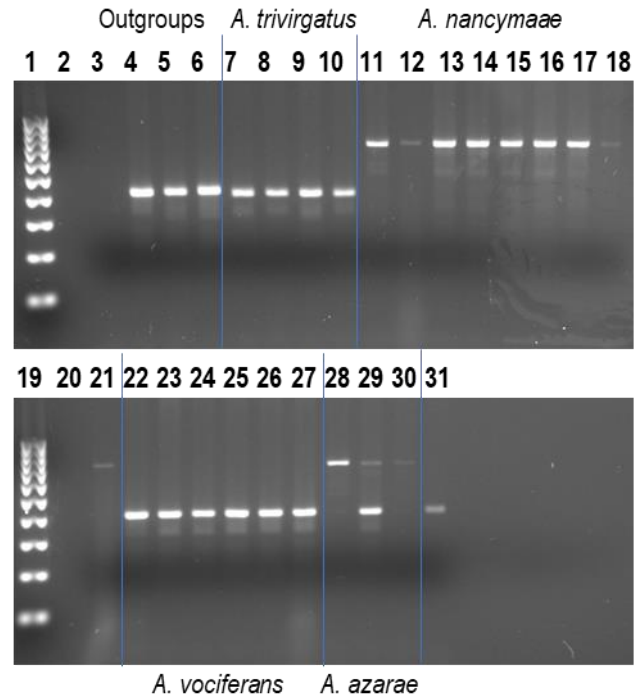


**Figure S18.** Sequence alignment for *Alu* locus: Storer, et al. 2020: *Aotus\_1120\_018497016.1:3680404-3681894* (JS-1120). PCR-based genotypes indicate that all *A. nancymae* and *A. azarae* individuals are homozygous present (1/1) for the target *Alu* insertion, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 613 (grey highlight), with matching flanking TSDs in yellow highlight.



**Figure S19.** Sequence alignment for *Alu* locus: Storer, et al. 2020: *Aotus\_6430\_018507789.1:443811-445305* (JS-6430). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymaae* individuals, homozygous present in all three *A. azarae* individuals, while being absent from other *Aotus* species. The *Aotus* reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* 85818 who shares the target *Alu* insertion starting at position 601 (grey highlight), with matching flanking TSDs in yellow highlight.





**Figure S20a:** *Alu* locus *Aotus\_404\_018513849.1:2616941-2618444* (JW-404): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymaae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. Vertical blue lines superimposed on the gel image visually separate the species groups. The predicted amplicon sizes are 715/411 bp. These PCR genotypes indicate that the target *Alu* insertion is homozygous present in *A. nancymaae* (715 bp fragment) and shared by *A. azarae* individuals, while homozygous absent in grey-necked species. DNA sequencing was performed to determine if *A. azarae* samples share the target insertion (See Figure S20b).

310 320 330 340 350 360 370 380 390 400  
Aotus\_404 [Anan\_2.0] ggagtgagtcctcaaaagaaaaaaaaaaaaaaaaagagaaggaagaccTGAATAATGCTCCCTGCCATAACCATCccagtttctctctttgtttctcCAAGATTAC  
JW-404-85818-R  
JW-404-85818-IntF-rc  
JW-404-85818-F-rc  
JW-404-85818-SIntR  
JW-404-85457-R  
JW-404-85457-IntF-rc  
JW-404-85457-F-rc  
JW-404-85457-SIntR  
JW-404-KB10043-R  
JW-404-KB10043-IntF-rc  
JW-404-KB10043-F-rc  
JW-404-KB10043-Sintr

410 420 430 440 450 460 470 480 490 500  
Aotus\_404 [Anan\_2.0] AGCCACAGTGTGCATGAATCAACTATTACCAACAATCAAGTGGGAAAAATGCCATAATTCGGTCTTTTAGAGACAGGAAACAGGAGCCCGAGTGGGCAAT  
JW-404-85818-R TGCATAAATTCGGTCTTTTAGAGACAGGAAACAGGAGCCCGAGTGGGCAAT  
JW-404-85818-IntF-rc  
JW-404-85818-F-rc  
JW-404-85818-SIntR  
JW-404-85457-R GTGGG AAATGCCATAAATTCGGTCTTTTAGAGACAGGAAACAGGAGCCCGAGTGGGCAAT  
JW-404-85457-IntF-rc  
JW-404-85457-F-rc  
JW-404-85457-SIntR  
JW-404-KB10043-R TGCATAAATTCGGTCTTTTAGAGACAGGAAACAGGAGCCCNNNANGNAAT  
JW-404-KB10043-IntF-rc  
JW-404-KB10043-F-rc  
JW-404-KB10043-Sintr

510 520 530 540 550 560 570 580 590 600  
Aotus\_404 [Anan\_2.0] TAAAGAGGTAGT GAGGTTTCACTTC TTTTTTTTTTT  
JW-404-85818-R TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-85818-IntF-rc TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-85818-F-rc TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-85818-SIntR TAAAGAGGTAGT GAGGTTTCACTTC TTTTTTTTTTT  
JW-404-85457-R TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-85457-IntF-rc TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-85457-F-rc TAAAGAGGTAGT GAGGTTTCACTTC TTTTTTTTTTT  
JW-404-85457-SIntR TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-KB10043-R TAAAGAGGTAGT GAGGTTTCACTTC TTTTTTTTTTT  
JW-404-KB10043-IntF-rc TTTTTTTTTTTTTTTTTTTT GAGACGGAGTTTCGCTCGTTACCCAGGCTGGAGTGCAATGGCGGATCTCGGCTCACCGCAAC  
JW-404-KB10043-F-rc  
JW-404-KB10043-Sintr

610 620 630 640 650 660 670 680 690 700  
Aotus\_404 [Anan\_2.0]  
JW-404-85818-R  
JW-404-85818-IntF-rc  
JW-404-85818-F-rc  
JW-404-85818-SIntR  
JW-404-85457-R  
JW-404-85457-IntF-rc  
JW-404-85457-F-rc  
JW-404-85457-SIntR  
JW-404-KB10043-R  
JW-404-KB10043-IntF-rc  
JW-404-KB10043-F-rc  
JW-404-KB10043-SIntR

710 720 730 740 750 760 770 780 790 800  
Aotus\_404 [Anan\_2.0]  
JW-404-85818-R  
JW-404-85818-IntF-rc  
JW-404-85818-F-rc  
JW-404-85818-SIntR  
JW-404-85457-R  
JW-404-85457-IntF-rc  
JW-404-85457-F-rc  
JW-404-85457-SIntR  
JW-404-KB10043-R  
JW-404-KB10043-IntF-rc  
JW-404-KB10043-F-rc  
JW-404-KB10043-SIntR

810 820 830 840 850 860 870 880 890 900  
Aotus\_404 [Anan\_2.0]  
JW-404-85818-R  
JW-404-85818-IntF-rc  
JW-404-85818-F-rc  
JW-404-85818-SIntR  
JW-404-85457-R  
JW-404-85457-IntF-rc  
JW-404-85457-F-rc  
JW-404-85457-SIntR  
JW-404-KB10043-R  
JW-404-KB10043-IntF-rc  
JW-404-KB10043-F-rc  
JW-404-KB10043-SIntR

```
          910      920      930      940      950      960      970      980      990      1000
Aotus_404 [Anan_2.0] taggcgggcgcggtggctcaagcctgtaatcccagcactttgggaggccgaggcgggtggatcagaggccaagatcgcagaccatcctgggtcaacat
JW-404-85818-R
JW-404-85818-IntF-rc
JW-404-85818-F-rc TA~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
JW-404-85818-SIntR TA~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
JW-404-85457-R
JW-404-85457-IntF-rc
JW-404-85457-F-rc TA~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
JW-404-85457-SIntR TA~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
JW-404-KB10043-R
JW-404-KB10043-IntF-rc
JW-404-KB10043-F-rc TA~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
JW-404-KB10043-SIntR TA~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~::~
```

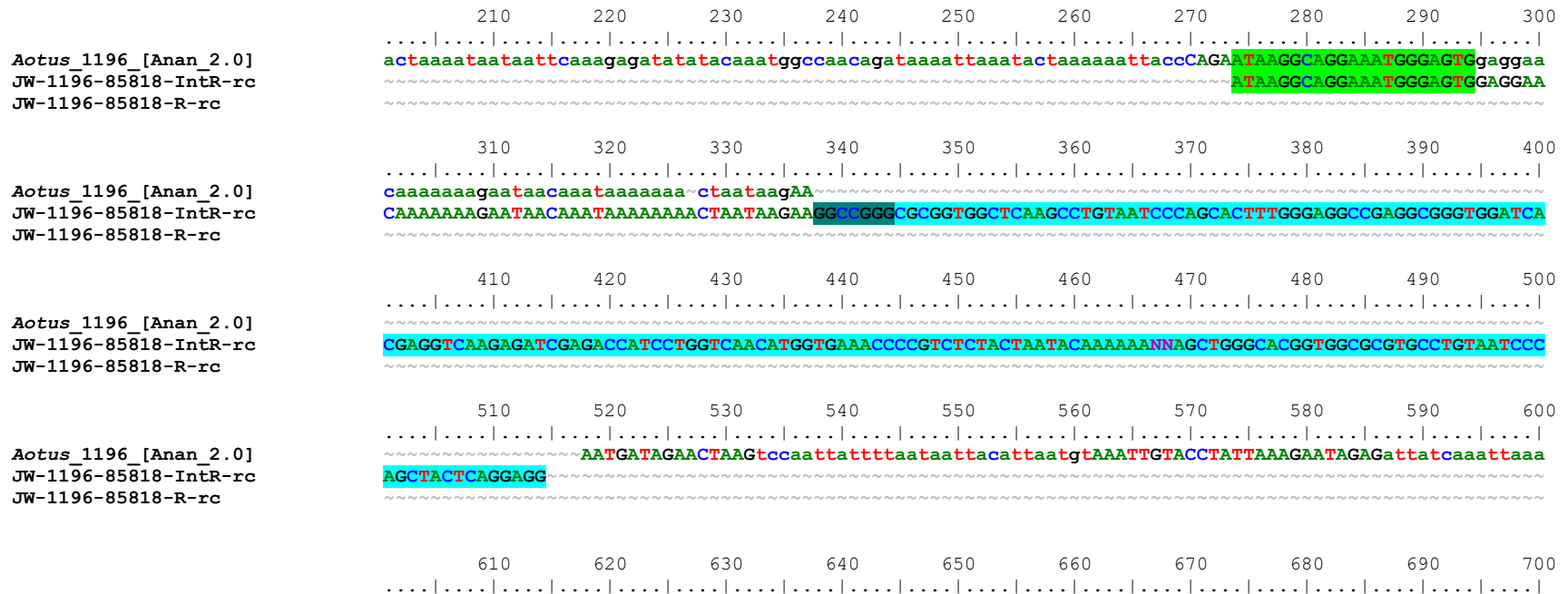
```
          1010     1020     1030     1040     1050     1060     1070     1080     1090     1100
Aotus_404 [Anan_2.0] tgtgaaaccccgctctactaatacaaaaaattagctgggcatgggtggcgcgtgcctgtaatcccagctcaggaagctgaggcaggagaatgctgaa
JW-404-85818-R
JW-404-85818-IntF-rc
JW-404-85818-F-rc
JW-404-85818-SIntR
JW-404-85457-R
JW-404-85457-IntF-rc
JW-404-85457-F-rc
JW-404-85457-SIntR
JW-404-KB10043-R
JW-404-KB10043-IntF-rc
JW-404-KB10043-F-rc
JW-404-KB10043-SIntR
```

```
          1110     1120     1130     1140     1150     1160     1170     1180     1190     1200
Aotus_404 [Anan_2.0] cccaggaggcggagggttgtagtgagcagagatcgcgcattgcactccagcctgggtaccgagagcgaactccgtctcaaaaaaaaaaaaaaaaaaaaaa
JW-404-85818-R
JW-404-85818-IntF-rc
JW-404-85818-F-rc
JW-404-85818-SIntR
JW-404-85457-R
JW-404-85457-IntF-rc
JW-404-85457-F-rc
JW-404-85457-SIntR
JW-404-KB10043-R
JW-404-KB10043-IntF-rc
JW-404-KB10043-F-rc
JW-404-KB10043-SIntR
```



**Figure S20b.** Sequence alignment for *Alu* locus *Aotus\_404\_018513849.1:2616941-2618444* (JW-404). PCR-based genotypes indicate the target *Alu* insertion is homozygous present (1/1) in *A. nancymae* individuals and two of three *A. azarae* individuals while being

heterozygous present (1/0) in the third *A. azarae* sample and homozygous absent (0/0) in other *Aotus* species. DNA sequencing was performed to determine if the target insertion is shared by *A. azarae*. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* samples 85818, 85457 and KB10043. This alignment has been expanded to accommodate the sequence trace data. Oligonucleotide primers for PCR are highlighted in bright green at positions 389 and 1385. The target *Alu* starts at position 903 (grey highlight) and has TSDs (AAAGAAACCCACAATA) in yellow highlight. All three *A. azarae* samples lack the target insertion as sequence traces span the pre-integration site. Instead, the *A. azarae* individuals all share a different *Alu*, a near parallel insertion, starting at position 815 (teal highlight) and running in the reverse orientation back to the T-tail (reverse complement of an A-tail) at position 527. TSDs (GAGGTTTCACTTCT) are shown in aqua highlight before sequence traces once again align with the reference genome. This is the only confirmed case in which all three *A. azarae* samples on our panel appeared to share the target insertion but did not. Locus *Aotus\_1196* had only one of three *A. azarae* sample, 85818, who appeared to share the target insertion but had a near parallel insertion instead. An alternative forward PCR primer has been designed, *Aotus\_404\_azarae*-F: AGTGCTGCAGCTACCCTCAT (purple highlight) that could be used in conjunction with the existing reverse primer shown at position 389 (CTCCAAGATTACAGCCACAGTG) to potentially genotype this *A. azarae* derived *Alu* element separately. We did not attempt this PCR as the locus is not parsimony informative within our sample set.



```

Aotus_1196_[Anan_2.0]      ttttaaaaataagatccaactatatagttattctcaaaaaaaattcactttaaataatgttgaataaagttaaaagtaaaaagacGAAAAAAGATATAACATGC
JW-1196-85818-IntR-rc    ~~~~~
JW-1196-85818-R-rc      ~~~~~
                          ~~~~~A AAAAATTCACCTTTAAATATGTTGATAAAGTTAAAAGTAAAAGACGAAAAAAGATATAACATGC
                          ~~~~~

                          710      720      730      740      750      760      770      780      790      800
. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
Aotus_1196_[Anan_2.0]    AAAtactaaccaaaagaagctggagaagctatgctaatacoagacaagcagactttggaacaagaaaaataactgccagccgggocggtggctcaag
JW-1196-85818-IntR-rc    ~~~~~
JW-1196-85818-R-rc      ~~~~~
                          ~~~~~A AATACTAACCAAAAAGCTGGAGAAGCTNNNAANNNTATCAGACAAAGCAGACTTTGGAACAGAAAA
                          ~~~~~

                          810      820      830      840      850      860      870      880      890      900
. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
Aotus_1196_[Anan_2.0]    cctgtaatcccagcactttgggaggccgagacgggtggatcacgaggtcaagagatcgagaccgttctggtcaacatggtgaaaccccgctcctactaat
JW-1196-85818-IntR-rc    ~~~~~
JW-1196-85818-R-rc      ~~~~~

                          910      920      930      940      950      960      970      980      990     1000
. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
Aotus_1196_[Anan_2.0]    acaaaaattagctgggcatgggtggcgcctgtaatcccagcactcaggaggtgaggcagagaaattgacctgaaccaggaggcgagggttcggg
JW-1196-85818-IntR-rc    ~~~~~
JW-1196-85818-R-rc      ~~~~~

                          1010     1020     1030     1040     1050     1060     1070     1080     1090     1100
. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
Aotus_1196_[Anan_2.0]    tgagccgtgatcgccattgcactccagcctgggtaacgagcgaaacttcgacctcaaaaaaaaaaaaaaaaaaaaaaaaaaagaaaaaataactgcctAG
JW-1196-85818-IntR-rc    ~~~~~
JW-1196-85818-R-rc      ~~~~~
                          ~~~~~N NNNNNNNCCNAG
                          ~~~~~

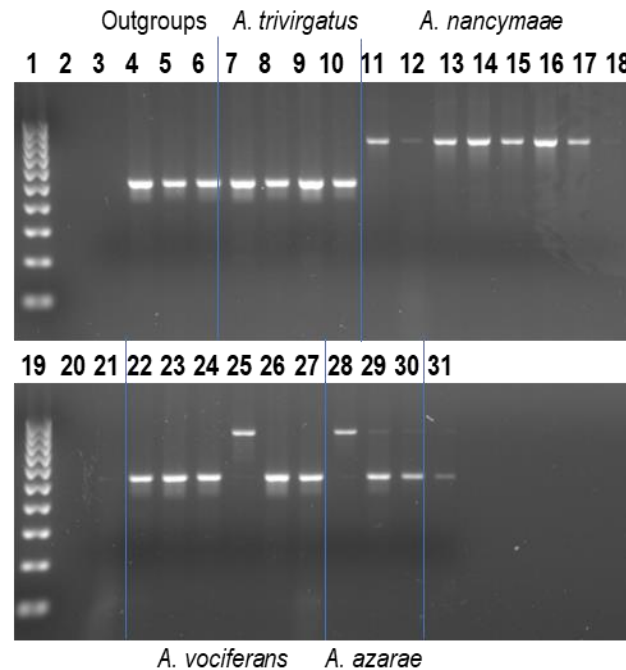
                          1110     1120     1130     1140     1150     1160     1170     1180     1190     1200
. . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . | . . . |
Aotus_1196_[Anan_2.0]    GAAGAAGAACATTTTATAGTGGTAAAGGATCAATTACCAAGATACACAGCATTTCCAACGTGCATGTACTTTTAAAGGGTGCTGCTCCAAAATA
JW-1196-85818-IntR-rc    ~~~~~
JW-1196-85818-R-rc      ~~~~~
                          ~~~~~A AAGAAGAACATTTTATAGTGGTAAAGGATCAATTACCAAGATACA
                          ~~~~~

```

**Figure S21.** Sequence alignment for *Alu* locus *Aotus\_1196\_018495318.1:3327241-3328746* (JW-1196). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals, also present in one of three *A. azarae* individuals, 85818, while being absent from other *Aotus* species. DNA sequencing was performed to determine if the target insertion is shared by *A. azarae* 85818. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* sample 85818. Oligonucleotide primers for PCR are highlighted in bright green at positions 274 and 1178. The target *Alu* starts at position 780 (grey highlight) and has TSDs (aagaaaaataactgcc) in yellow highlight. *A. azarae* sample 85818 lacks the target insertion as the R-rc sequence trace spans the pre-integration site. Instead, the *A. azarae* individual has a different *Alu*, a near parallel insertion, starting at position 338 (teal highlight) and running to position 514 shown in aqua highlight. Unfortunately, sequencing failed using the forward primer so only part of this novel *A. azarae Alu* element is detected. An alternative reverse PCR primer has been designed, *Aotus\_1196\_azarae-R*:

ccagctttcttttggttagtaTT (purple highlight) that could be used in conjunction with the existing forward primer (ATAAGGCAGGAAATGGGAGTG) shown at position 274 to potentially genotype this novel *A. azarae* derived *Alu* element separately, one that is polymorphic among *A. azarae* individuals. We did not attempt this PCR.

OLIGO	<u>start</u>	<u>len</u>	<u>tm</u>	<u>gc%</u>	<u>any th</u>	<u>3' th</u>	<u>hairpin</u>	<u>seq</u>
LEFT PRIMER	29	21	57.70	47.62	0.00	0.00	0.00	ATAAGGCAGGAAATGGGAGTG
RIGHT PRIMER	528	23	55.14	34.78	0.00	0.00	0.00	ccagctttcttttggttagtaTT



**Figure S22a:** *Alu* locus *Aotus\_364\_018513626.1:9585827-9587338* (JW-364): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3-TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. Vertical blue lines superimposed on the gel image visually separate the species groups. The predicted amplicon sizes are 846/521 bp. These PCR genotypes indicate that the target *Alu* insertion is present in *A. nancymae*, *A. azarae* as well as one *A. vociferans* individual



86218, while homozygous absent in *A. trivirgatus*. Perform DNA sequencing to confirm that *A. azarae* and *A. vociferans* share the target *Alu* insertion.

```

      110      120      130      140      150      160      170      180      190      200
...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
Aotus_364_[Anan_2.0]  CTGTAGGTAGAGAGCCCGGATTTTCCTAAACAGCTTTGATATTAGTTCCGTGAGAAATGTGTTTGCTTGGTCCCTGCCGGCTCATCTGCCAACACTGGAGCA
JW-364-85457-SIntR-rc  ~~~~~~
JW-364-85457-F       ~~~~~~
JW-364-85457-IntF    ~~~~~~
JW-364-85457-R-rc   ~~~~~~
JW-364-86218-F      ~~~~~~
JW-364-86218-R-rc   ~~~~~~
JW-364-86218-SIntR  ~~~~~~
JW-364-86218-IntF-rc ~~~~~~

      210      220      230      240      250      260      270      280      290      300
...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
Aotus_364_[Anan_2.0]  ATCCCTATGTCAGGGGTGAGGTATTCCTGATTGGCCAGATTGGATCTCATGATCAGATGTGTGACAAGCCAGGGACATTTTCATGTTTGACAGTCCCCCAGG
JW-364-85457-SIntR-rc  ~~~~~~
JW-364-85457-F       ~~~~~~
JW-364-85457-IntF    ~~~~~~
JW-364-85457-R-rc   ~~~~~~
JW-364-86218-F      ~~~~~~
JW-364-86218-R-rc   ~~~~~~
JW-364-86218-SIntR  ~~~~~~
JW-364-86218-IntF-rc ~~~~~~
                        GATTGGCCAGATTGGATCTCATGATCAGATGTGTGACAAGCAAGGGACATTTTCATGTTTGACAGTCCCCCAGG

      310      320      330      340      350      360      370      380      390      400
...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
Aotus_364_[Anan_2.0]  AGCTAGAAGGAGAGGTTCCCTAAAAGAGAATAGAAGAAATGATTGctcgaagaaaaaggaagggataTTAAAGGCTGTTCACAGGTTTAAGAGGCAGAGA
JW-364-85457-SIntR-rc  ~~~~~~
JW-364-85457-F       ~~~~~~
JW-364-85457-IntF    ~~~~~~
JW-364-85457-R-rc   ~~~~~~
JW-364-86218-F      ~~~~~~
JW-364-86218-R-rc   ~~~~~~
JW-364-86218-SIntR  ~~~~~~
JW-364-86218-IntF-rc ~~~~~~
                        AGCTAGAAGGAGAGGTTCCCTAAAAGAGAATAGAAGAAATGATTGCTGAAGAAAAAGGAAGGGATATTAAGGCTGTTCACAGGTTTAGGAGGCAGAGA

      410      420      430      440      450      460      470      480      490      500
...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
Aotus_364_[Anan_2.0]  CGTTGGCTTGGGGCAGAAAGAAATATTGATTTGGGAAATAGGGGATCACACTAGAAAAGCAAGCTTCATGACGCCAAAGTTTTTATTTATTCACTACTTCT~
JW-364-85457-SIntR-rc  ~~~~~~
JW-364-85457-F       ~~~~~~
JW-364-85457-IntF    ~~~~~~
JW-364-85457-R-rc   ~~~~~~
JW-364-86218-F      ~~~~~~
JW-364-86218-R-rc   ~~~~~~
JW-364-86218-SIntR  ~~~~~~
JW-364-86218-IntF-rc ~~~~~~
                        CATTGGCTTGGGGCAGAAAGAAATATTGATTTGGGAAATAGGGGATCACACTAGAAAAGCAAGCTTCATGACGCCGAAAGTTTTTATTTATTCACTACTTCTTT

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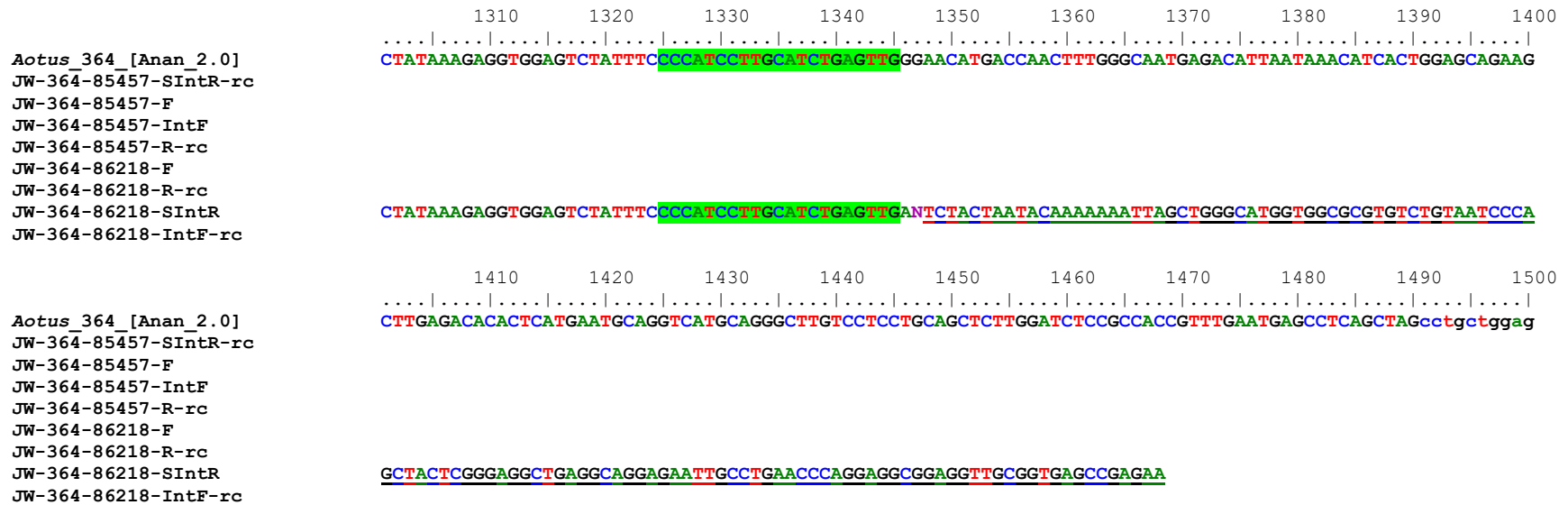


910 920 930 940 950 960 970 980 990 1000  
Aotus\_364\_[Anan\_2.0]  
JW-364-85457-SIntR-rc  
JW-364-85457-F  
JW-364-85457-IntF  
JW-364-85457-R-rc  
JW-364-86218-F  
JW-364-86218-R-rc  
JW-364-86218-SIntR  
JW-364-86218-IntF-rc  
ATTTACTTGAAAATATCATgaataggccgggcggtggctcacgcctgtaatcccagcactttgggagccgagggggtggatcacgaggtcaagaga  
ATTTACTTGAAAATATCATGAATAGGCCGGCCTGGCTCACGCCTGTAAATCCCAAGCATTGGGAGGCCGAGGCCGGTGGAATCACGAGGTCGAAGAG  
ATTTACTT  
GAGGTCA-GAGA  
ATTTACTTGAAAATATCATGAATA  
ATTTACTTGAAAATATCATGAATA

1010 1020 1030 1040 1050 1060 1070 1080 1090 1100  
Aotus\_364\_[Anan\_2.0]  
JW-364-85457-SIntR-rc  
JW-364-85457-F  
JW-364-85457-IntF  
JW-364-85457-R-rc  
JW-364-86218-F  
JW-364-86218-R-rc  
JW-364-86218-SIntR  
JW-364-86218-IntF-rc  
tcgagaccatcctggcaacaagggtgaaaccccgctctactaaaaatacaaaaaattagctgggcatggtggcgcgtgctgtaatcccagctactcag  
TCGAGACCATCCTGGTCAACAAGGTGAAACCTCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCGCGTGCCGTAAATCCCACTACTCAG  
TCGAGACCATCCTGGTCAACAAGGTGAAACCTCGTCTCTACTAAAAATACAAAAATAACCTGGGCATGGTGGCGCGTGCCGTAAATCCCACTACTCAG

1110 1120 1130 1140 1150 1160 1170 1180 1190 1200  
Aotus\_364\_[Anan\_2.0]  
JW-364-85457-SIntR-rc  
JW-364-85457-F  
JW-364-85457-IntF  
JW-364-85457-R-rc  
JW-364-86218-F  
JW-364-86218-R-rc  
JW-364-86218-SIntR  
JW-364-86218-IntF-rc  
gaggctgaggcaggagaattgctgaaacccaggaggcggaggttgccggtgagccgagatcgccattgcactccagcctgggtaacaagagcgaactc  
GAGGCTGAGGC  
GAGGCTGAGGCAGGAGAATTGCTGAACCCAGGAGGCAGGTTGCGGTGAGCCGAGATCGCGCCATTGCCTCCAGCCTGGGTAACAAGAGCGAACTC

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300  
Aotus\_364\_[Anan\_2.0]  
JW-364-85457-SIntR-rc  
JW-364-85457-F  
JW-364-85457-IntF  
JW-364-85457-R-rc  
JW-364-86218-F  
JW-364-86218-R-rc  
JW-364-86218-SIntR  
JW-364-86218-IntF-rc  
cgtctcaaaaaaaaaaaaaaaaaagaaagaaaaagaaaataatcatgaaTATCCTGGGGATGATATGGTAGATTATAAAATGCTCACAAATTGTCACCCCTTT  
CGTCTCAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAGAAAATATCATGAATATCCTGGGGATGATATGGTAGATTATAAAATGCTCACAA  
TCCCTGGGGATGATATGGTAGATTATAAAATGCCACAAATTGTCACCC  
TCCCTGGGGATGATATGGTAGATTATAAAATGCCACAAATTGTCACCCCTTT



**Figure S22b.** Sequence alignment for *Alu* locus *Aotus\_364\_018513626.1:9585827-9587338* (JW-364). PCR-based genotypes indicate the target *Alu* insertion is present in *A. nancymaae*, *A. azarae* as well as one *A. vociferans* individual 86218, while homozygous absent in *A. trivirgatus*. The reference genome [Anan\_2.0] is shown at the top followed by *A. azarae* sample 85457 and *A. vociferans* sample 86218. Oligonucleotide primers for PCR are highlighted in bright green at positions 175 and 1325. The target *Alu* starts at position 925 (grey highlight) and has TSDs (**GAAAATATCAtgaata**) in yellow highlight and is shared by *A. azarae* sample 85457. However, the *A. vociferans* 86218 filled site amplicon lacks the target insertion as sequence traces span the pre-integration site. Instead, *A. vociferans* has a different *Alu*, a near parallel insertion, starting at position 810 (teal highlight) and running in the reverse orientation back to the T-tail (reverse complement of an A-tail) at position 499. TSDs (**TTATTCACTACTTCT**) are shown in aqua highlight before sequence traces once again align with the reference genome. An alternative reverse PCR primer has been designed, *Aotus\_364\_vociferans*-R: GAGTGTTTACTTTGTGCCAAGC (purple highlight) that could be used in conjunction with the existing forward primer shown at position 175 (AGGTCATCTGTCCAACACTG) to potentially genotype this novel *A. vociferans* derived *Alu* element separately. We did not attempt this PCR as the locus is not parsimony informative within our sample set. In addition, the *A. vociferans* 86218 sequence trace has the 2<sup>nd</sup> half of another *Alu* element (confirmed by RepeatMasker) starting at the mid-A-rich region at about position 1350 where the trace no longer matches the [Anan\_2.0] reference genome, marked in underline text until the trace terminates.

310 320 330 340 350 360 370 380 390 400  
Owl\_2LS\_120\_[Anan\_2.0]  
LR-120-85962-SIntR-rc  
LR-120-85962-F  
LR-120-85962-IntF  
LR-120-85962-R-rc

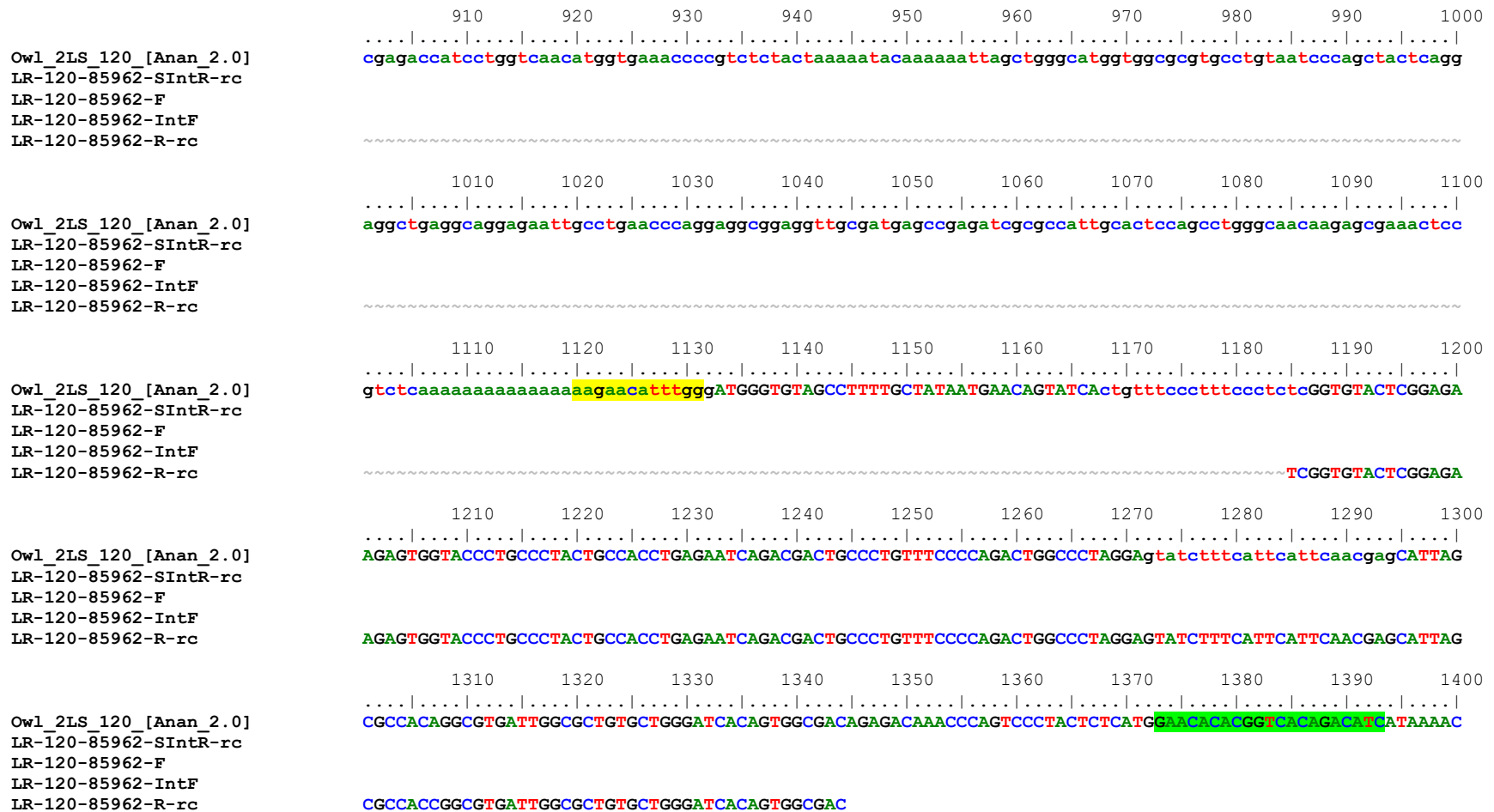
410 420 430 440 450 460 470 480 490 500  
Owl\_2LS\_120\_[Anan\_2.0]  
LR-120-85962-SIntR-rc  
LR-120-85962-F  
LR-120-85962-IntF  
LR-120-85962-R-rc

510 520 530 540 550 560 570 580 590 600  
Owl\_2LS\_120\_[Anan\_2.0]  
LR-120-85962-SIntR-rc  
LR-120-85962-F  
LR-120-85962-IntF  
LR-120-85962-R-rc

610 620 630 640 650 660 670 680 690 700  
Owl\_2LS\_120\_[Anan\_2.0]  
LR-120-85962-SIntR-rc  
LR-120-85962-F  
LR-120-85962-IntF  
LR-120-85962-R-rc

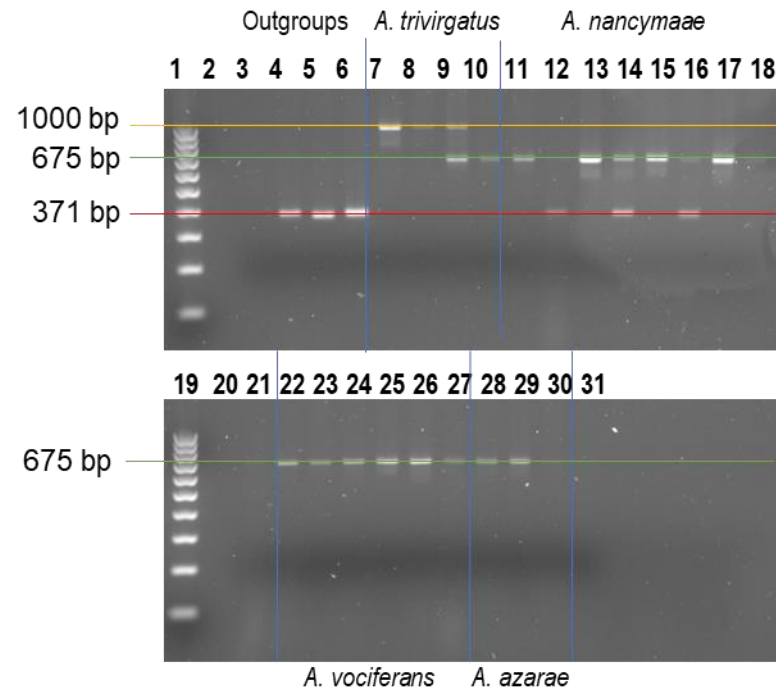
710 720 730 740 750 760 770 780 790 800  
Owl\_2LS\_120\_[Anan\_2.0]  
LR-120-85962-SIntR-rc  
LR-120-85962-F  
LR-120-85962-IntF  
LR-120-85962-R-rc

810 820 830 840 850 860 870 880 890 900  
Owl\_2LS\_120\_[Anan\_2.0]  
LR-120-85962-SIntR-rc  
LR-120-85962-F  
LR-120-85962-IntF  
LR-120-85962-R-rc

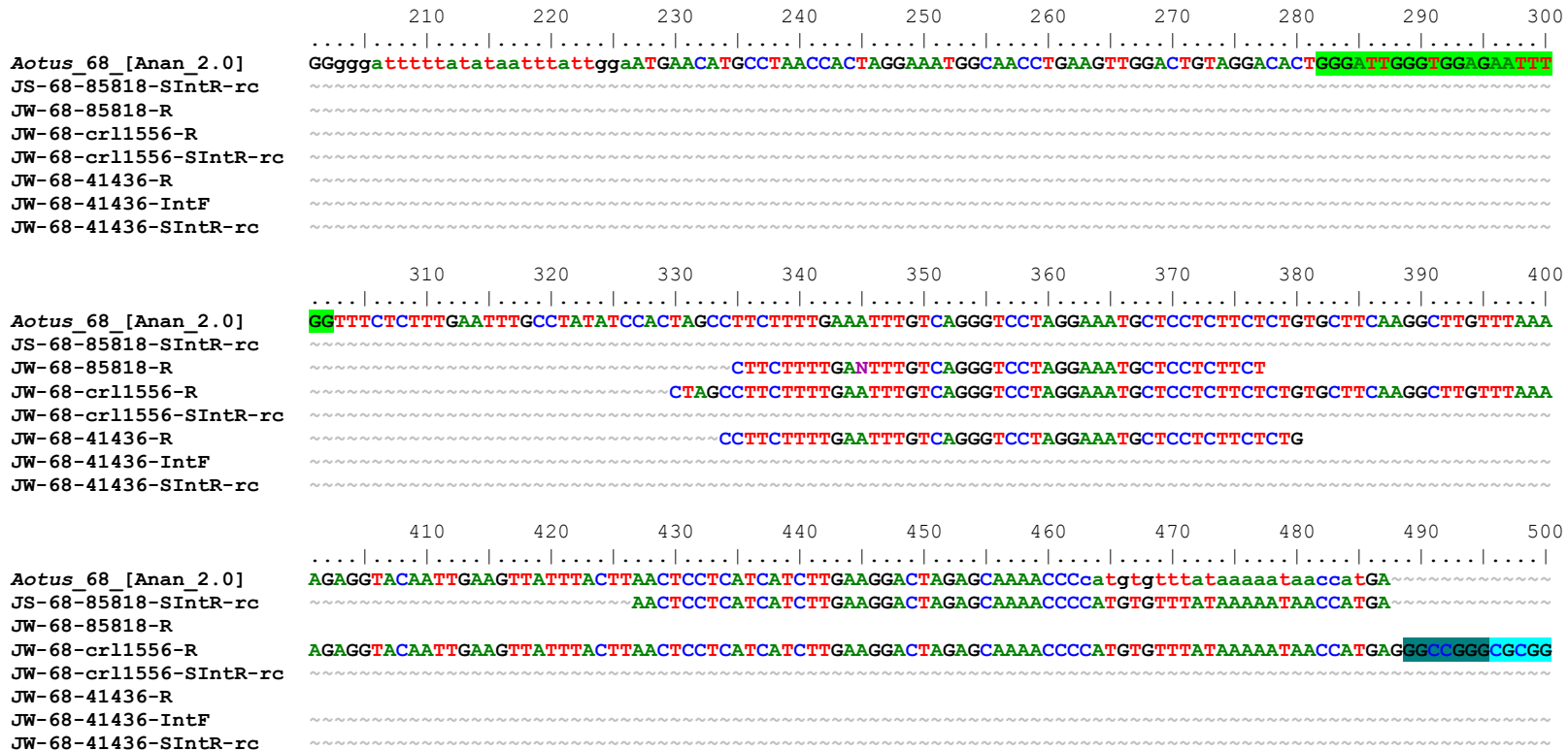


**Figure S23.** Sequence alignment for *Alu* locus Owl\_2LS\_120\_018512055.1:2444349-2445849 (LR-120). PCR based genotypes indicate the target *Alu* is restricted to *A. nancymae*, with the exception of *A. vociferans* sample 85962 who appears heterozygous for the insertion (1/0). The reference genome [Anan\_2.0] is shown at the top, the target *Alu* starts at position 824 (grey highlight) and is flanked by TSDs AAGAACATTTGG in yellow highlight. Sequencing reveals that *A. vociferans* 85962 has a different *Alu*, a near parallel insertion, starting at position 405 (teal highlight) and extending about 178 bp into the *Alu* sequence before terminating. Oligonucleotide primers for PCR are shown in bright green highlight. The SIntR-rc sequence that provides 5' flanking sequence. The

reverse primer sequence does not reach the A-tail. The target *Alu* insertion is likely restricted to *A. nancymae*, however, this genomic region is very repeat dense so we recommend not using this locus for *Aotus* phylogeny due to the potential for confusing PCR amplicons. We have designed an alternative reverse primer, Owl\_2LS\_120-A.voc.-R:CAAGTGAAGTGGAGGTTAGTGT, in purple highlight to use in conjunction with the existing forward primer to potentially genotype this novel *A. vociferans* *Alu* element separately. These primers were confirmed to have only one match within this repeat dense genomic landscape.



**Figure S24a:** *Alu* locus *Aotus\_68\_018491627.1:7167631-7169129* (JW-68): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. The predicted PCR amplicon sizes are 675 bp (green line) for *Alu* present and 371 bp (red line) for *Alu* absent. *A. nancymae* individuals appear polymorphic for presence / absence of the target insertion while homozygous present in other *Aotus* species. *A. trivirgatus* appears to harbor a possible 2<sup>nd</sup> *Alu* insertion (~1000 bp; yellow line) that is not present in other *Aotus* species. Perform DNA sequencing to identify this amplicon (See Figure S24b).







```

          910          920          930          940          950          960          970          980          990          1000
Aotus_68_[Anan_2.0]  ggtggctcagcctgtaatcccagcactttgggagggcagagggcgggaggatcagcaggtcaagagatcgagaccatcctgggtcaacatggtgaaaccccg
JS-68-85818-SIntR-rc GGTGGCTCACGCCGTAAATCCCAGCACTTTGGGAGGCAGAGGC GGGTGGATCAGAGGTC AAGAGATCGAGACCATCC TNNTCAACATGGTGA AACCCCG
JW-68-85818-R
JW-68-cr11556-R
JW-68-cr11556-SIntR-rc
JW-68-41436-R
JW-68-41436-IntF
JW-68-41436-SIntR-rc

          1010          1020          1030          1040          1050          1060          1070          1080          1090          1100
Aotus_68_[Anan_2.0]  tctctactaaaaatacaaaaaattagctgggcatgggtggcgcgtgcctgtaatcccagctactcaggaggctgaggcaggagaaattgcctgaaccaggga
JS-68-85818-SIntR-rc TCTCTACTAAAAATACAAAAAATTNGCTGGGCATGGTGGCCGCTGCCGTAAATCCCAGCTACTCAGGAGGCTGAGG
JW-68-85818-R
JW-68-cr11556-R
JW-68-cr11556-SIntR-rc
JW-68-41436-R
JW-68-41436-IntF
JW-68-41436-SIntR-rc

          1110          1120          1130          1140          1150          1160          1170          1180          1190          1200
Aotus_68_[Anan_2.0]  ggcggaggttgcggtgagccgagatcgcgccattgcagcctgggtaacaagagcgaactccgtctccaaaaaaaaaaaaaaaaaaaaaagggttatcaCCG
JS-68-85818-SIntR-rc
JW-68-85818-R
JW-68-cr11556-R
JW-68-cr11556-SIntR-rc
JW-68-41436-R
JW-68-41436-IntF
JW-68-41436-SIntR-rc

          1210          1220          1230          1240          1250          1260          1270          1280          1290          1300
Aotus_68_[Anan_2.0]  AAAAAATCGCATTTTGTAGTTTACAGAGGACACTGAAAGCTCTTTGTGTTTCagcattttcaaaaagattttctACAGTATTTGGTCAAATTACCATGCTT
JS-68-85818-SIntR-rc
JW-68-85818-R
JW-68-cr11556-R
JW-68-cr11556-SIntR-rc
JW-68-41436-R
JW-68-41436-IntF
JW-68-41436-SIntR-rc

```

**Figure S24b.** Sequence alignment for *Alu* locus *Aotus\_68\_018491627.1:7167631-7169129* (JW-68). PCR-based genotypes indicate the target *Alu* insertion is polymorphic among *A. nancymae* individuals while homozygous present in other *Aotus* samples. *A. trivirgatus* appears to harbor a 2<sup>nd</sup> *Alu* insertion that is not present in other *Aotus* species (See Figure S24a). DNA sequencing was performed to confirm this prediction. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. azarae* 85818 and

*A. trivirgatus* crl-1556 and MSB-41436. Oligonucleotide primers for PCR are highlighted in bright green at positions 282 and 1225. *A. azarae* 85818 shares the target *Alu* which starts at position 891 (grey highlight) and is flanked by TSDs in yellow highlight. The PCR primer at position 1225-1246 is the reverse complement of the forward primer shown in Supplemental File 1. It is located very close to the 3' end of the target insertion and therefore did not generate sequence traces. *A. trivirgatus* crl-1556 has a 2<sup>nd</sup> *Alu* insertion that starts at position 488 (teal highlight) and extends to the A-tail at position 777 (*Alu* in aqua highlight) that is not present in [Anan\_2.0] or *A. azarae* 85818. We have designed an alternative forward PCR primer, (*Aotus\_68\_A.triv-F:ACTTGCTTTGTCATGGCTTCATC*) shown in purple highlight at position 845 that could be used in conjunction with the existing reverse primer listed and shown in this alignment at position 282 (GGGATTGGGTGGAGAATTTGG) to potentially genotype this newly discovered *A. trivirgatus* derived *Alu* element separately from the [Anan\_2.0] ascertained target insertion. We did not attempt this alternative PCR as the locus is not parsimony informative among our sample set.

```

                    510      520      530      540      550      560      570      580      590      600
Owl_2LS_78_[Anan_2.0]      TCTGTAGATGGGTGGTAGAGGAACCTGTTTTACCCACTTTACAGGTTTGTTTCAATCGcagataaaagactatacatgcaagtgtgttataaaaataaag
LR-78-cr11556-F           ~~~~~~
LR-78-cr11556-SIntR-rc    ~~~~~~TTTACCCACTTTACAGGTTTGTTTCAATCACAGATAAAAGACTATACATGCAAGTGTGTATAAAAAGAAG
LR-78-cr11556-IntF       ~~~~~~
LR-78-cr11556-R-rc       ~~~~~~
LR-78-85818-F           ~~~~~~TATACATGCAAGTGTGTATAAAAATAAG
LS-78-85818-SIntR-rc    ~~~~~~TTACCCACTTTACAGGTTTGTTTCAATCGCAGATAAAAGACTATACATGCAAGTGTGTATAAAAATAAG
LR-78-85818-IntF       ~~~~~~
LS-78-85818-R-rc       ~~~~~~
LR_78-KB4883-R-rc       ~~~~~~
LR-78-86230-E-F         ~~~~~~ATCGCAGATAAAAGACTATACATGCAAGTGTGTATAAAAATAAG
LR-78-86230-E-R-rc     ~~~~~~TGGGTGGTAGAGGAACCTGTTTTACCCACTTTACAGGTTTGTTTCGATCGCAGATAAAAGACTATACATGCAAGTGTGTATAAAAATAAG

                    610      620      630      640      650      660      670      680      690      700
Owl_2LS_78_[Anan_2.0]      atactcggccgggcgcggtggctcaagcctgtaatcccagcactttgggaggccgaggcgggtggatcacgaggtcaagagatcgagaccatcctggtca
LR-78-cr11556-F           ~~~~~~
LR-78-cr11556-SIntR-rc    ~~~~~~ATACTCGGCCGGGCGCGGTGGCTCAAGCCTGTAATCCTAGCACCTTTGGGAGGCCGAGGCCGGGTGGATCATGAGGTCAGGAGATCGAGACCATCTGGTCA
LR-78-cr11556-IntF       ~~~~~~
LR-78-cr11556-R-rc       ~~~~~~GAGACCATCTGGTCA
LR-78-85818-F           ~~~~~~
LS-78-85818-SIntR-rc    ~~~~~~ATACTCN~GGGCGCGGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGANGCCGAGGCCGGGTGGATCACGAGGTCAGAGATCGAGACCATCTGGTCA
LR-78-85818-IntF       ~~~~~~
LS-78-85818-R-rc       ~~~~~~ATACTCGGCCGGGCGCGGTGGCTCAAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGGTGGATCACGAGGTCAGAGATCGAGACCATCTGGTCA
LR_78-KB4883-R-rc       ~~~~~~
LR-78-86230-E-F         ~~~~~~GAGGTCAGAGATCGAGACCATCTGGTCA
LR-78-86230-E-R-rc     ~~~~~~
ATACT~
ATACT~

```

```

      710      720      730      740      750      760      770      780      790      800
Owl_2LS_78_[Anan_2.0] acgtggtgaaaccctgtctctactaaaaatacaaaaaattagctgggcacgggtggcgcgtgctgtaatcccagctactcaggaggctgaggcaggagaa
LR-78-cr11556-F ACATGGTGAAACCCCTGCTCTACTAAAAATACAAAAAATTAGCTGGGTGTGGCGGTGGGCACCTGTTATCCCAGCTACTCGTGAGGCTGAGGCAGGAGAA
LR-78-cr11556-SIntR-rc ACATGGTGAAACCCCTGCTCTACTAAAAATACAATAAATTAGCTGGGTGTGGCGGTGGGCACCTGTTATCCCAGCTACTC
LR-78-cr11556-IntF ACATGGTGAAACCCCTGCTCTACTAAAAATACAAAAAATTAGCTGGGTGTGGCGGTGGGCACCTGTTATCCCAGCTACTCGTGAGGCTGAGGCAGGAGAA
LR-78-cr11556-R-rc
LR-78-85818-F ACGTGGTGAAACCCC
LR-78-85818-SIntR-rc ACGTGGTGAAACCCCTGCTCTACTAAAAATACAAAAAATTAGCTGGGCACGGTGGCAGGTGCCTGTAATCCCAGCTACTCAGGAGG
LR-78-85818-IntF ACGTGGTGAAACCCCTGCTCTACTAAAAATACAAAAA
LR-78-85818-R-rc
LR_78-KB4883-R-rc
LR-78-86230-E-F
LR-78-86230-E-R-rc

      810      820      830      840      850      860      870      880      890      900
Owl_2LS_78_[Anan_2.0] ttgacctgaaccaggaggcggagggttgccgtgagccgagatagcgcattgcaactccagcctgggttaacaagagcgaactccgtctcaaaaaaaaaaaat
LR-78-cr11556-F TTGCCTGAAACC
LR-78-cr11556-SIntR-rc
LR-78-cr11556-IntF TTGCCTGAAACCAGGAGGCAGAGGTTGCGGTGAGCCGAGATTGCACCATTTGCACTCCAGCCTGGGTAACAAGAGCGAAACTCCGTCTCAAAAA
LR-78-cr11556-R-rc
LR-78-85818-F
LR-78-85818-SIntR-rc
LR-78-85818-IntF
LR-78-85818-R-rc
LR_78-KB4883-R-rc
LR-78-86230-E-F
LR-78-86230-E-R-rc

      910      920      930      940      950      960      970      980      990      1000
Owl_2LS_78_[Anan_2.0] aaataaaaataaaagatactatGCAAACTTAGTTATTATTATGGCTTACGATTACTGCATGAGCGTAGTACAGGAAGAACTGTTTTGCAGTGGATTTTTG
LR-78-cr11556-F
LR-78-cr11556-SIntR-rc
LR-78-cr11556-IntF
LR-78-cr11556-R-rc
LR-78-85818-F
LR-78-85818-SIntR-rc
LR-78-85818-IntF
LR-78-85818-R-rc
LR_78-KB4883-R-rc
LR-78-86230-E-F
LR-78-86230-E-R-rc

```

**Figure S25.** Sequence alignment for *Alu* locus Owl\_2LS\_078\_018494005.1:2492157-2493663 (LR-78). PCR-based genotypes indicate that *A. vociferans* is homozygous absent (0/0) for the target *Alu* insertion, while other *Aotus* species are homozygous present (1/1), suggesting that *A. vociferans* is basal among the *Aotus* species on our panel. DNA sequencing was performed to confirm this

pattern. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. trivirgatus* crl-1556, *A. azarae* 85818 and *A. l. griseimembra* KB4883 (signal very weak, but has TSD, in yellow highlight). Sequencing confirms that *A. trivirgatus* crl-1556 and *A. azarae* 85818 share target *Alu* insertion starting at position 607 (grey highlight), while *A. vociferans* 86230 empty site amplicon displays a precise pre-integration site with both forward and reverse sequences spanning the target region.

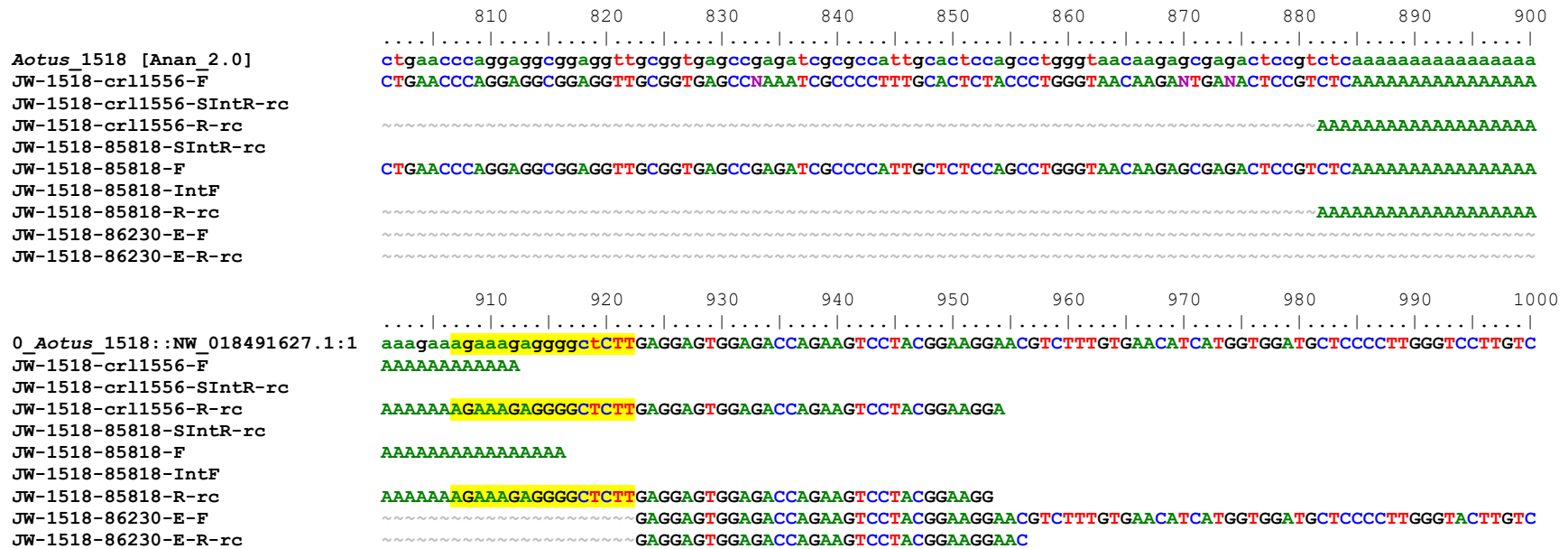
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Aotus_1518 [Anan_2.0] TGGCCATGGGTGCCAGTGACAAAGTAACAGCTCTGTCAAGCCCCAAACTAAGTACCTAGTTAGTCACCTGTTGTGCAGCCGGTTAGAAAGAGGGGctcttg
JW-1518-crl1556-F ~~~~~~CTAAGTACCTAGTTAGTCACCTGTTGTGCAGCCGGTTAGAAAGAGGGGCTCTTG
JW-1518-crl1556-SIntR-rc ~~~~~~
JW-1518-crl1556-R-rc ~~~~~~
JW-1518-85818-SIntR-rc TGGCCATGGGTGCCAGTGACAAAGTAACAGCTTTGTCAAGCCCCAAACTAAGTACCTAGTTAGTCACCTGTTGTGCAGCTGGTTAGAAAGAGGGGCTTTTG
JW-1518-85818-F ~~~~~~CTAAGTACCTAGTTAGTCACCTGTTGTGCAGCTGGTTAGAAAGAGGGGCTCTTG
JW-1518-85818-IntF ~~~~~~
JW-1518-85818-R-rc ~~~~~~
JW-1518-86230-E-F ~~~~~~CTGTC~AGCCCCAAACTAAGTACCTAGTTAGTCACCTGTTGTGCAGCCGGTTAGAAAGAGGGGCTCTT~
JW-1518-86230-E-R-rc ~~~~~~TGGCCATGGGTGCCAGTGACAAAGTAACAGCTCTGTCAAGCCCCAAACTAAGTACCTAGTTAGTCACCTGTTGTGCAGCCGGTTAGAAAGAGGGGCTCTT~

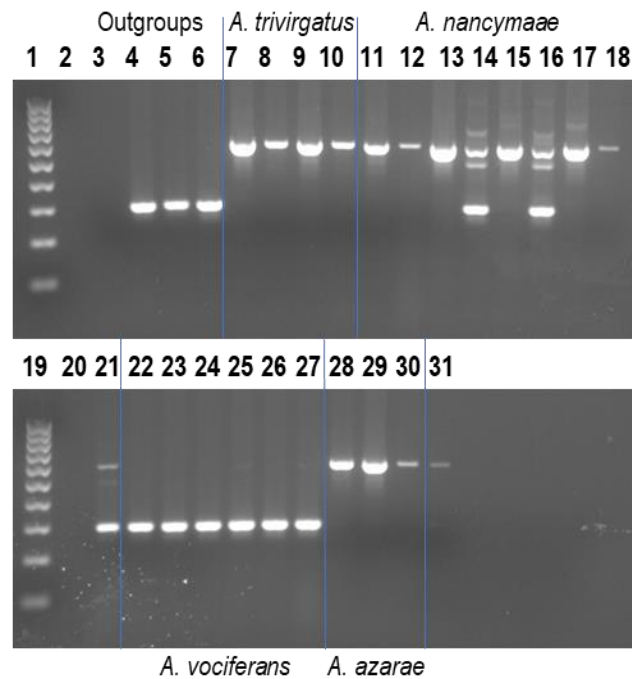
      610      620      630      640      650      660      670      680      690      700
Aotus_1518 [Anan_2.0] gccgggcacggtggctcaagcctgtaatcccagcactttgggaggccgaggcgggtggatcacgaggtcgagagatcgagaccatcctggttaacattg
JW-1518-crl1556-F ~~~~~~GCCAGGCGCGGTGGCTCAAGCCTGTAAATCCAGCAGCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCGAGAGATCGAGACCATCCTGGTCAACATTGT
JW-1518-crl1556-SIntR-rc ~~~~~~
JW-1518-crl1556-R-rc ~~~~~~
JW-1518-85818-SIntR-rc ~~~~~~GCCGGGGCGGTGACTCAAGCCTGTAAATCCAGCAGCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCGAGAGATCGAGACCATCCTGGTCAACATTGT
JW-1518-85818-F ~~~~~~GCCGGGCGCGGTGACTCAAGCCTGTAAATCCAGCAGCTTTGGGAGTCCGAGGCGGGTGGATCACGAGGTCGAGAGATCGAGACCATCCTGGTCAACATTGT
JW-1518-85818-IntF ~~~~~~
JW-1518-85818-R-rc ~~~~~~
JW-1518-86230-E-F ~~~~~~
JW-1518-86230-E-R-rc ~~~~~~

      710      720      730      740      750      760      770      780      790      800
Aotus_1518 [Anan_2.0] gaaacccggtcttactaatacaaaaaaaaaa~ttagctgggcgcggtggcgcatgcctgtaatcccagctactcaggaggctgaggcaggagaaattgc
JW-1518-crl1556-F ~~~~~~GAAACCCCGTCTCTACTAATAACAAAAAATAACT- GGGCACGGGGGCCGTCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAAAAATTGC
JW-1518-crl1556-SIntR-rc ~~~~~~TACAAAAAATAAATAAGCTGGGCACGGTGGCGCGTGCCTG
JW-1518-crl1556-R-rc ~~~~~~
JW-1518-85818-SIntR-rc ~~~~~~GAAACCCCGTTTTTAATAATAACAAAAAATAA~TTAGCTGGGCACGGTGGCGCATGCCTGTAATCCCAGCTACTCAGGAGG
JW-1518-85818-F ~~~~~~GAAACCCCGTCTCTACTAATAACAAAAAATAA~TTANCTGGGCACGGTGGCGCATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAAAAATTGC
JW-1518-85818-IntF ~~~~~~GAAACCCCGTCTCTACTAATAACAAAAAATAA
JW-1518-85818-R-rc ~~~~~~
JW-1518-86230-E-F ~~~~~~
JW-1518-86230-E-R-rc ~~~~~~

```



**Figure S26.** Sequence alignment for *Alu* locus *Aotus\_1518\_018491627.1:11015550-11017060* (JW-1518). The gel image is shown in the main text as Figure 1d. PCR based genotypes indicate that all *A. trivirgatus*, *A. nancymae* and *A. azarae* individuals are homozygous present (1/1) for the target *Alu* while all *A. vociferans* individuals are homozygous absent (0/0) for the insertion. DNA sequencing was performed to confirm this pattern. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. trivirgatus* crl-1556 and *A. azarae* 85818, both of whom share the target *Alu* insertion that starts at position 600 (gray highlight), TSDs are in yellow highlight. Sequence for the empty site amplicon fragment for *A. vociferans* 86230 flanks the target region as a precise pre-integration site, confirming the genotypes. This *Alu* presence/absence pattern suggests *A. vociferans* is basal among the *Aotus* species on our panel.



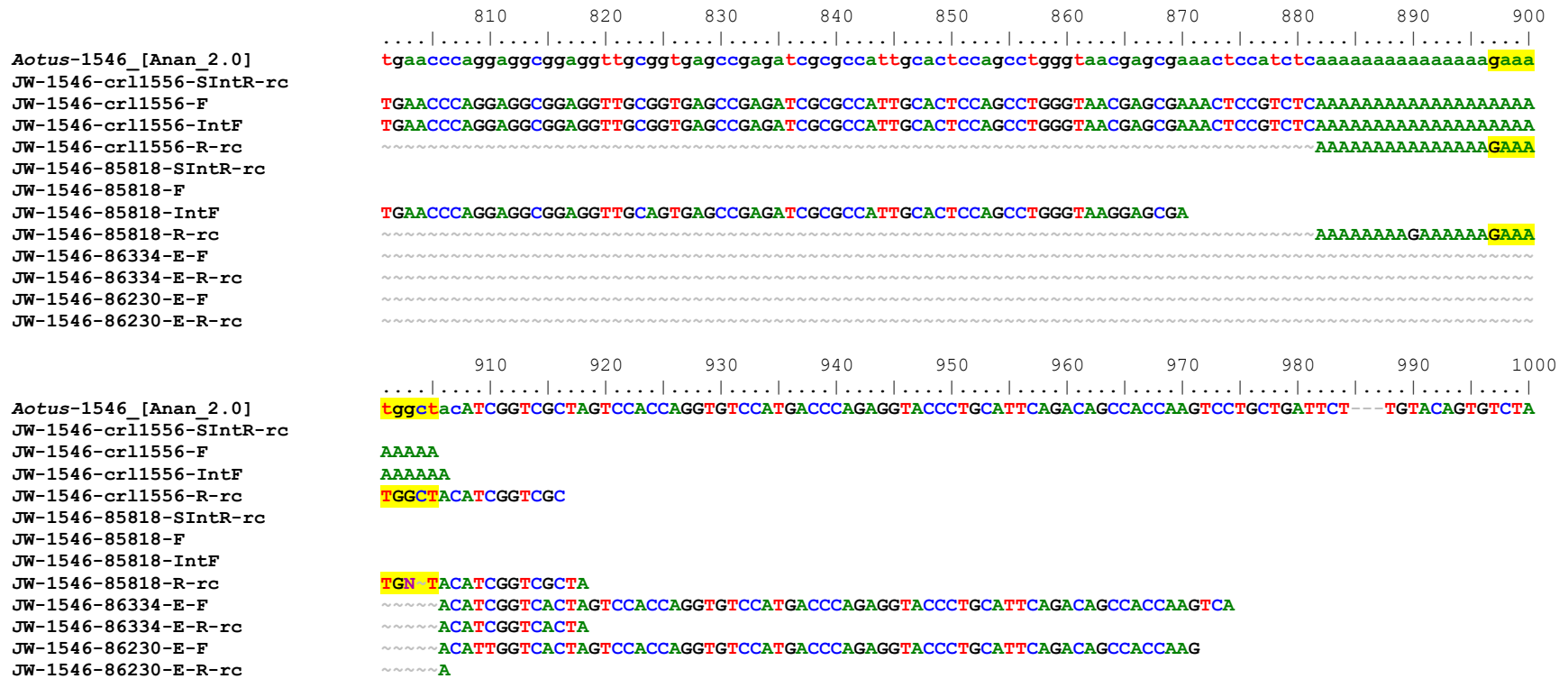
**Figure S27a:** *Alu* locus *Aotus\_1546\_018502359.1:170192-171687* (JW-1546): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. *Alu* is homozygous present in *A. trivirgatus*, *A. azarae* and *A. lemurinus griseimembra* (~595 bp fragment) while homozygous absent (~298 bp fragment) in *A. vociferans* and showing heterozygosity in three of nine *A. nancymae* individuals. DNA sequencing is required to confirm this insertion pattern (see alignment Figure S27b) Sequencing confirms that both *A. trivirgatus* and *A. azarae* share the target *Alu* insertion while *A. nancymae* 86334 and *A. vociferans* 86230 empty site amplicons (~298 bp) represent precise pre-integration sites. This *Alu* pattern suggests *A. vociferans* is basal while *A. nancymae* is more closely related to grey-neck species than *A. azarae* is.

510 520 530 540 550 560 570 580 590 600  
Aotus-1546\_[Anan\_2.0] GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAAGGCAGAATAAGAAATggct  
JW-1546-crl1556-SIntR-rc GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-crl1556-F GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-crl1556-IntF  
JW-1546-crl1556-R-rc  
JW-1546-85818-SIntR-rc GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-85818-F GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-85818-IntF  
JW-1546-85818-R-rc  
JW-1546-86334-E-F GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTAAAGTTATAGGTTCTGAATGGTAAAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-86334-E-R-rc GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTAAAGTTATAGGTTCTGAATGGTAAAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-86230-E-F GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT  
JW-1546-86230-E-R-rc GACCTGGCCCTTGCAAATATTTGACTTTGCAACACTTGCCCTGAAGTTATAGGTTCTGAATGGTAGAGAAGCAGGGCTAAATGCAGAATAAGAAATGGCT

610 620 630 640 650 660 670 680 690 700  
Aotus-1546\_[Anan\_2.0] ggccgggacacggtggctcaagcctgtaatcccagcactttgggagccgagggcgggtgg ~ ~ ~ atcacgaggtcaagagatcgagaccatcctggtcaac  
JW-1546-crl1556-SIntR-rc GGCCGGGCACGGTGGCTCAAGCCTGTAATCCCAGCAGCTTTGGGAGGCCAGGGCGGTTGG ~ ~ ~ ATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAAC  
JW-1546-crl1556-F GGCCGGGCACGGTGGCTCAAGCCTGTAATCCCAGCAGCTTTGGGAGGCCAGGGCGGTTGG ~ ~ ~ ATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAAC  
JW-1546-crl1556-IntF GAGGTCAAGAGATCGAGACCATCCTGGTCAAC  
JW-1546-crl1556-R-rc  
JW-1546-85818-SIntR-rc GGCCGGGCACGGTGGCTCAAGCCTGTAATCCCAGCAGCTTTGGGAGGCCAGGGCGGTTGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAAC  
JW-1546-85818-F GGCCGGGCACGGTGGCTCAAGCCTGTAATCCCAGCAGCTTTGGGAGGCCAGGGCGGTTGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAAC  
JW-1546-85818-IntF GAGGTCAAGAGATCGAGACCATCCTGGTCAAC  
JW-1546-85818-R-rc  
JW-1546-86334-E-F  
JW-1546-86334-E-R-rc  
JW-1546-86230-E-F  
JW-1546-86230-E-R-rc

710 720 730 740 750 760 770 780 790 800  
Aotus-1546\_[Anan\_2.0] atggtgaaaccccgctctactaatacaaaaaattagctgggcatggtggcgcgctgcctgtaatcccagctactcaggaggctgaggcaggagaaattgcc  
JW-1546-crl1556-SIntR-rc ATGGTGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCATGCCTGTAATCCCAGCTACTCAGGAGG  
JW-1546-crl1556-F ATGGTGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCC  
JW-1546-crl1556-IntF ATGGTGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCC  
JW-1546-crl1556-R-rc  
JW-1546-85818-SIntR-rc ATGGTGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGG  
JW-1546-85818-F ATGGTGAA  
JW-1546-85818-IntF ATGGTGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCC  
JW-1546-85818-R-rc  
JW-1546-86334-E-F  
JW-1546-86334-E-R-rc  
JW-1546-86230-E-F  
JW-1546-86230-E-R-rc





**Figure S27b.** Sequence alignment for *Alu* locus *Aotus\_1546\_018502359.1:170192-171687*. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. trivirgatus* crl-1556, *A. azarae* 85818, both of whom share the target *Alu* insertion that starts at position 601 (gray highlight), TSDs are in yellow highlight. Empty site amplicon fragments for *A. nancymae* 86334 and *A. vociferans* 86230 flank the target region and are precise pre-integration sites. This *Alu* pattern suggests *A. vociferans* is basal while *A. nancymae* (86334 heterozygous for the target insertion) is more closely related to grey-neck species than *A. azarae* is.

410 420 430 440 450 460 470 480 490 500  
Aotus\_1288 [Anan\_2.0] .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-F atatgaGGGGTAGTCAACTTCCACAAGTGAGGTGCAGAGAGTTTGC AAACAGATTGTAATCAAACAGATCATAATCAaacaaatgctattttttaacagc  
JW-1288V2-crl1556-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-F .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-F .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86100-E-F .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86100-E-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86230-E-F .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86230-E-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

510 520 530 540 550 560 570 580 590 600  
Aotus\_1288 [Anan\_2.0] .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-F tttactaAAGTTTCTGTATATAATGAAAACCTTgcatttaatacataattttgataaGTTTGACATATGCATATACTCATAATAATATCaccacag  
JW-1288V2-crl1556-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-F TTTACTAAAGTTTCTGTATATAATGAAAACCTTGCATTTAATACATACATTTTGATAAGTTTGACATATGCATATACTCATAATAATATCACCACAG  
JW-1288V2-86218-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-F TTTACTAAAGTTTCTGTATATAATGAAAACCTTGCATTTAATACATACATTTTGATAAGTTTGACATATGCATATACTCATAATAATATCACCACAG  
JW-1288V2-85818-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-85818-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86100-E-F TTTACTAAAGTTTCTGTATATAATGAAAACCTTGCATTTAATACATACATTTTGATAAGTTTGACATATGCATATACTCATAATAATATCACCACA~  
JW-1288V2-86100-E-R-rc TTTACTAAAGTTTCTGTATATAATGAAAACCTTGCATTTAATACATACATTTTGATAAGTTTGACATATGCATATACTCATAATAA  
JW-1288V2-86230-E-F TTTACTAAAGTTTCTGTATATAATGAAAACCTTGCATTTAATACATACATTTTGATAAGTTTGACATATGCATATACTCATAATAATATCACCACA~  
JW-1288V2-86230-E-R-rc TTTACTAAAGTTTCTGTATATAATGAAAACCTTGCATTTAATACATACATTTTGATAAGTTTGACATATGCATATACTCATAATAATATCACCACA~

610 620 630 640 650 660 670 680 690 700  
Aotus\_1288 [Anan\_2.0] .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-F ccgggCGCGGTGGCTCACGCCGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACGAGGTCAAGAGATTGAGACCATCCTGGTCAACATGGTG  
JW-1288V2-crl1556-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-crl1556-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-F CCGGGCGCGGTGGCTCACGCCGTAATCCTAGCACTTTGGGAGGCCGAGGCAGGTGGATCACGAGGTCAAGAGATTGAGACCATCCTGGTCAACATGGTG  
JW-1288V2-86218-IntF .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-SIntR-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|  
JW-1288V2-86218-R-rc .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

JW-1288V2-85818-F  
JW-1288V2-85818-IntF  
JW-1288V2-85818-SIntR-rc  
JW-1288V2-85818-R-rc  
JW-1288V2-86100-E-F  
JW-1288V2-86100-E-R-rc  
JW-1288V2-86230-E-F  
JW-1288V2-86230-E-R-rc

```
CCGGGCGGGTGACTCAGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACGAGGTCAAGAGATTGAGACCATCCTGGTCAACATGGTG  
GAGGTCAAGAGATTGAGACCATCCTGGTCAACATGGTG
```

710 720 730 740 750 760 770 780 790 800

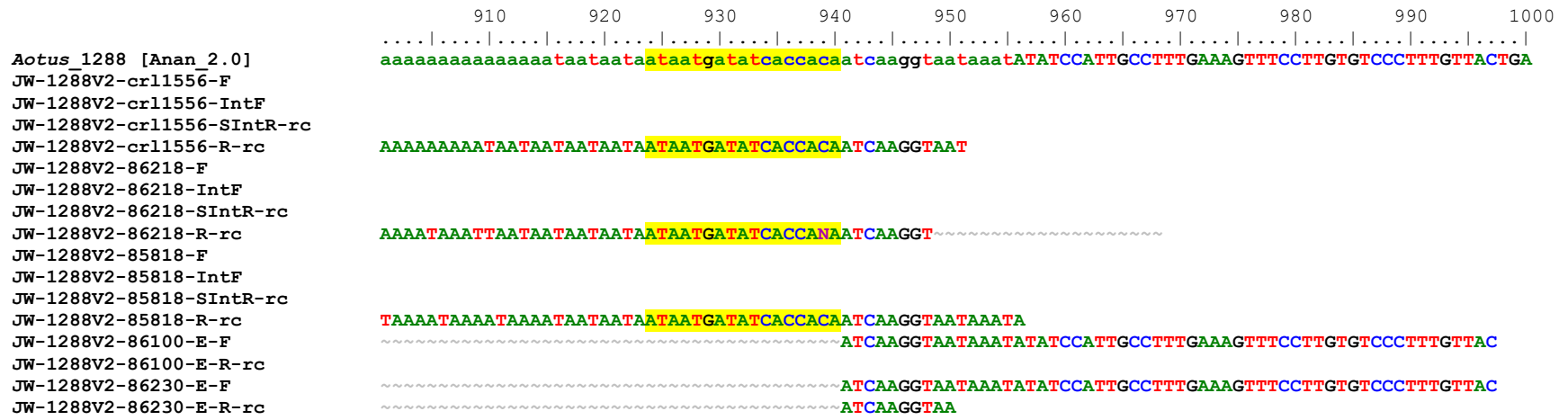
Aotus\_1288 [Anan 2.0]  
JW-1288V2-cr11556-F  
JW-1288V2-cr11556-IntF  
JW-1288V2-cr11556-SIntR-rc  
JW-1288V2-cr11556-R-rc  
JW-1288V2-86218-F  
JW-1288V2-86218-IntF  
JW-1288V2-86218-SIntR-rc  
JW-1288V2-86218-R-rc  
JW-1288V2-85818-F  
JW-1288V2-85818-IntF  
JW-1288V2-85818-SIntR-rc  
JW-1288V2-85818-R-rc  
JW-1288V2-86100-E-F  
JW-1288V2-86100-E-R-rc  
JW-1288V2-86230-E-F  
JW-1288V2-86230-E-R-rc

```
aaaccccgctctactaaaaatacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaatagctgggcatgggtggcgctgtaatacccagctactcaggaggctgagac  
AAACCCCGTCTCTACTAAAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAACCCCGTCTCTACTAAAAATCAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAATAGCTGGGCATGGTGGCGCATGCCGTGTAATCCCAGCTACTCAGGA  
AAACCCCGTCTCTACTAAAAATCAAAAAAAAAAAAAAAAAAAAA  
AAACCCCGTCTCTACTAAAAATCAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAATAGCTGGGCATGGTGGCGCATGCCGTGTAATCCCAGCTACTCAGGAGGC  
AAAAAAAAAAAAAAAAAAAAAAAAAATAGCTGGGCATGGTGGCGCATGCCGTGTAATCCCAGCTACTCAGGAGG
```

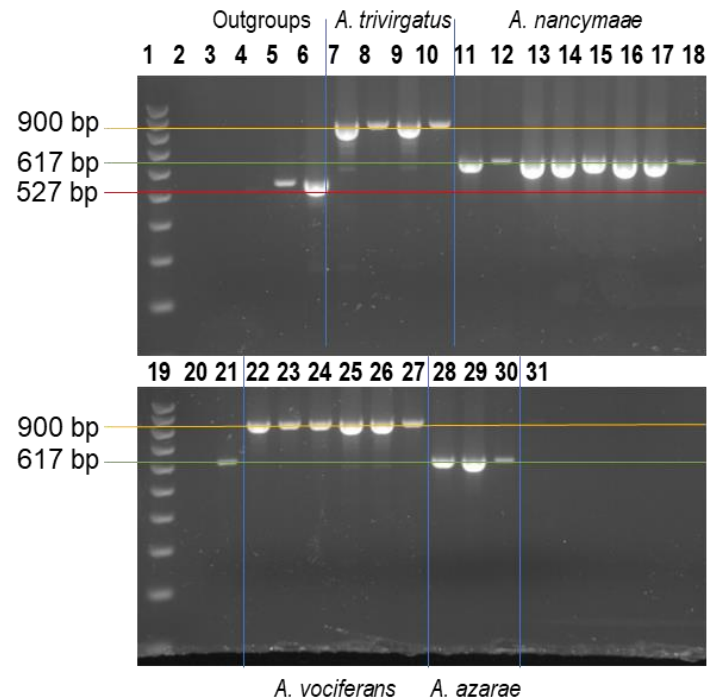
810 820 830 840 850 860 870 880 890 900

Aotus\_1288 [Anan 2.0]  
JW-1288V2-cr11556-F  
JW-1288V2-cr11556-IntF  
JW-1288V2-cr11556-SIntR-rc  
JW-1288V2-cr11556-R-rc  
JW-1288V2-86218-F  
JW-1288V2-86218-IntF  
JW-1288V2-86218-SIntR-rc  
JW-1288V2-86218-R-rc  
JW-1288V2-85818-F  
JW-1288V2-85818-IntF  
JW-1288V2-85818-SIntR-rc  
JW-1288V2-85818-R-rc  
JW-1288V2-86100-E-F  
JW-1288V2-86100-E-R-rc  
JW-1288V2-86230-E-F  
JW-1288V2-86230-E-R-rc

```
aggagaaattgcctgaacccaggaggcagaggttgcggtgagccgagatcgcgccattgcactccagcctgggtaacaagagcgaactccgctctcaaaaa  
AAAAA  
AG  
AAAAAA
```



**Figure S28.** Sequence alignment for *Alu* locus *Aotus\_1288\_V2* 018488858.1:16800884-16802399. PCR-based genotypes indicate the target *Alu* insertion is homozygous present (1/1) in all *Aotus* samples with the exception of two *A. vociferans*, 86100 and 86230 who displayed only the empty site (0/0) or homozygous absent for the target insertion (See main text Figure 2a). DNA sequencing was performed to confirm this pattern. The reference genome [Anan\_2.0] is shown at the top followed by *A. trivirgatus* crl-1556, *A. vociferans* 86218 and *A. azarae* 85818 all of whom share the target *Alu* insertion starting at position 600 (grey highlight) and flanked by TSDs in yellow highlight. This *Alu* element has a particularly long middle A-rich region that was difficult to sequence through, but the internal-*Alu* primer sequences complete the entire element. Empty site amplicons for *A. vociferans* 86100 and 86230 display precise pre-integration sites with sequence traces spanning the target region, confirming the genotypes. This pattern suggests that *A. vociferans* is basal among the *Aotus* species on our DNA panel. However, individuals 86100 and 86230 are known to be full siblings (sister and brother, respectively) having the same Dam and Sire. Therefore, this locus should be applied to wild *Aotus* populations for evaluation.



**Figure S29a:** *Alu* locus Owl\_2LS\_042\_018498342.1:691757-693258 (LR-42): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymaae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. At first glance, this gel image seems to indicate that *A. trivirgatus* and *A. vociferans* contain the *Alu* insertion while *A. nancymaae* and *A. azarae* do not. However, the predicted amplicon sizes are 617 bp (green line) for the *A. nancymaae* reference genome containing a full length *Alu* insertion and 527 bp (red line) for the squirrel monkey outgroup. The amplicon sizes are not 300 bp smaller in the outgroups due to extra sequence that is not present in *Aotus*. *A. trivirgatus* and *A. vociferans* have a larger amplicon (900-1000 bp, yellow line) that was suspected to be a 2<sup>nd</sup> *Alu* element, in addition to the target, based on the size difference. However, DNA sequencing revealed that these larger amplicons do not contain a 2<sup>nd</sup> *Alu*, but rather include ~225 bp of extra non-repeat sequence about 80 bp 5' of the reverse primer and about 100 bp downstream of the target (see alignment Figure S29b.) The target *Alu* is likely fixed present in *Aotus*. Evidence of shared extra sequence in both *A. trivirgatus* and *A. vociferans* implies a close relationship but it does not represent an additional homoplasy free element. Vertical blue lines superimposed on the gel image visually separate the species groups. Gel electrophoresis for this image consisted of 175V for 90 minutes.

410 420 430 440 450 460 470 480 490 500  
Owl\_2LS\_042 [Anan\_2.0]  
LR-42-cr11556-R-rc TAAGAGGAAGCTGAGGAGAGTGCCTCAGGATAGATAGACATTGGGCCAATTTTCATCATGTTTTTATAATGCTACACAGTCTTGTATTAGAGGGTAACAGG  
LR-42-86218-R-rc  
LR-42-cr11556-F  
LR-42-cr11556-IntF  
LR-42-cr11556-SIntR-rc GGGTAACAGG  
LR-42-86218-F  
LR-42-86218-IntF  
LR-42-86218-SIntR-rc GGGTAACAGG

510 520 530 540 550 560 570 580 590 600  
Owl\_2LS\_042 [Anan\_2.0]  
LR-42-cr11556-R-rc CTTTGACAGTTTCTAATTCACATTCCTAAGCATCACTAATTCAGGCTATAATAATGGCTCTGGGATCTGTATCTAAACTTAGTATAAGATTTCAAGatcg  
LR-42-86218-R-rc  
LR-42-cr11556-F GGCTCTGGGATCTGTATCTAAACTTAGTATAAGATTTCAAGATCG  
LR-42-cr11556-IntF  
LR-42-cr11556-SIntR-rc CTTTGACAGTTTCTAATTCACATTCCTAAGCATCACTAATTCAGGCTATAATAATGGCTCTGGGATCTGTATCTAAACTTAGTATAAGATTTCAAGATCG  
LR-42-86218-F TATAATAATGGCTCTGGGATCTGTATCTAAACTTAGTATAAGATTTCAAGATCG  
LR-42-86218-IntF  
LR-42-86218-SIntR-rc CTTTGACAGTTTCTAATTCACATTCCTAAGCATCACTAATTCAGGCTATAATAATGGCTCTGGGATCTGTATCTAAACTTAGTATAAGATTTCAAGATCG

610 620 630 640 650 660 670 680 690 700  
Owl\_2LS\_042 [Anan\_2.0]  
LR-42-cr11556-R-rc gctgggCGCGTGGCTCAAGCCTGTAATCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATGGT  
LR-42-86218-R-rc  
LR-42-cr11556-F GCTGGGCGCGTGGCTCAAGCCTGTAATCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATGGT  
LR-42-cr11556-IntF GAGGTCNAGAGATCGAGACCATCCTGGTCAACATGGT  
LR-42-cr11556-SIntR-rc GCTGGGCGCGTGGCTCAAGCCTGTAATCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATGGT  
LR-42-86218-F GCTGGGCGCGTGGCTCAAGCCTGTAATCCAGCACCTTTGGGAGGCCGAGGCGGGTGAATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATGGT  
LR-42-86218-IntF CGAGACCATCCTGGTCAACATGGT  
LR-42-86218-SIntR-rc GCTGGGCGCGTGGCTCAAGCCTGTAATCCAGCACCTTTGGGAGGCCGAGGCGGGTGAATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATGGT

710 720 730 740 750 760 770 780 790 800  
Owl\_2LS\_042 [Anan\_2.0]  
LR-42-cr11556-R-rc gaaaccccgtccctactaaaaaatacaaaaaattagctgggcatggtggcgcgtgctgtaatccagctactcaggaggctgaggcaggagaattgcct  
LR-42-86218-R-rc  
LR-42-cr11556-F GAAACCCCGTCCCTACTAAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCT  
LR-42-cr11556-IntF GAAACCCCGTCCCTACTAAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCT  
LR-42-cr11556-SIntR-rc GAAACCCCGTCCCTACTAAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCT  
LR-42-86218-F GAAACCCCGTCCCTACTAAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCT  
LR-42-86218-IntF GAAACCCCGTCCCTACTAAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCT  
LR-42-86218-SIntR-rc GAAACCCCGTCCCTACTAAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCAGCTACTCAGGAGG

```

      810      820      830      840      850      860      870      880      890      900
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Owl_2LS_042_[Anan_2.0]
LR-42-cr11556-R-rc
LR-42-86218-R-rc
LR-42-cr11556-F
LR-42-cr11556-IntF
LR-42-cr11556-SIntR-rc
LR-42-86218-F
LR-42-86218-IntF
LR-42-86218-SIntR-rc

```

```

gaaccccaggaggcgagggttgcggtgagtcgagatcgcgccattgcactccagcctgggtaacaagagcgaaactccgtctcaaaaaaaaaaaaaaaaa
AAAAAAAAAAAAAAAA
GAACCCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAAACAAGAGCGAAACTCCGTCTCAAAAAAAAAAAAAAA
GAACCCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAAACAAGAGCGAAACTCCGTCTCAAAAAAAAAAAAAAA
GAACCCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAAACAAGAGCGAAACTCCGTCTCAAAAAAAAAAAAAAA
GAACCCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAAACAAGAGCGAAACTCCATCTCAAAAAAAAAAAAAAA

```

```

Owl_2LS_042_[Anan_2.0]
LR-42-cr11556-R-rc
LR-42-86218-R-rc
LR-42-cr11556-F
LR-42-cr11556-IntF
LR-42-cr11556-SIntR-rc
LR-42-86218-F
LR-42-86218-IntF
LR-42-86218-SIntR-rc

```

```

      910      920      930      940      950      960      970      980      990      1000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
aggtttcaagaTTATGGTATATTGAGATTCAGGCTGAACAGATGAAAGGTTTTGGCAAAAAGGACCCAAGGACGGGAAagataattctgctttttatta
AGGTTTCAAGATTAATGGTATATTGAGATTCAGGCTGAACAGATGAAAGGTTTTGGCAAAAAGGACCCAAGGACGGGAAAGATAATTCTGCTTTTTATTA

```

```

Owl_2LS_042_[Anan_2.0]
LR-42-cr11556-R-rc
LR-42-86218-R-rc
LR-42-cr11556-F
LR-42-cr11556-IntF
LR-42-cr11556-SIntR-rc
LR-42-86218-F
LR-42-86218-IntF
LR-42-86218-SIntR-rc

```

```

      1010      1020      1030      1040      1050      1060      1070      1080      1090      1100
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
a
ATGTTTACTTGAAGTATCTTTTGGTTGCTTTTACTTTTCAAAGTAAATTTCAAATTATCAAGCTATCTTTGGCTTGATAATTGAAGATTTAATTA
AAAGTAAATTTCAAATTATCAAGCTATCTTTGCTTGATAATTGAAGATTTAATTA

```

```

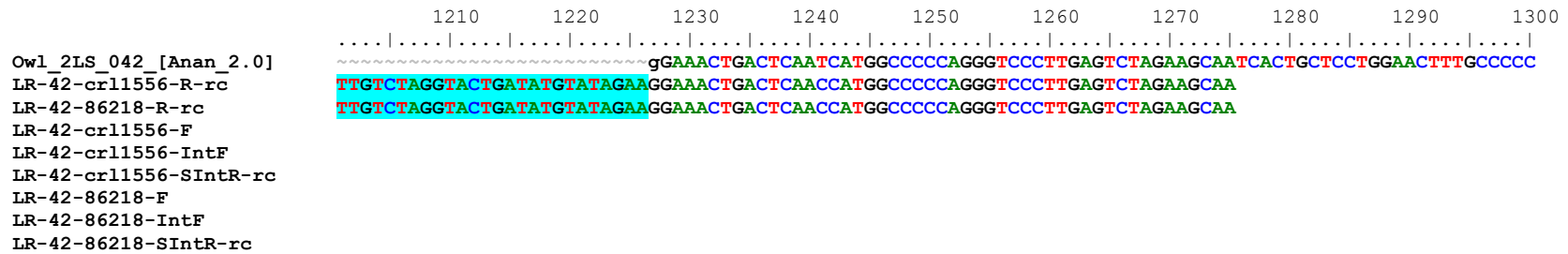
Owl_2LS_042_[Anan_2.0]
LR-42-cr11556-R-rc
LR-42-86218-R-rc
LR-42-cr11556-F
LR-42-cr11556-IntF
LR-42-cr11556-SIntR-rc
LR-42-86218-F
LR-42-86218-IntF
LR-42-86218-SIntR-rc

```

```

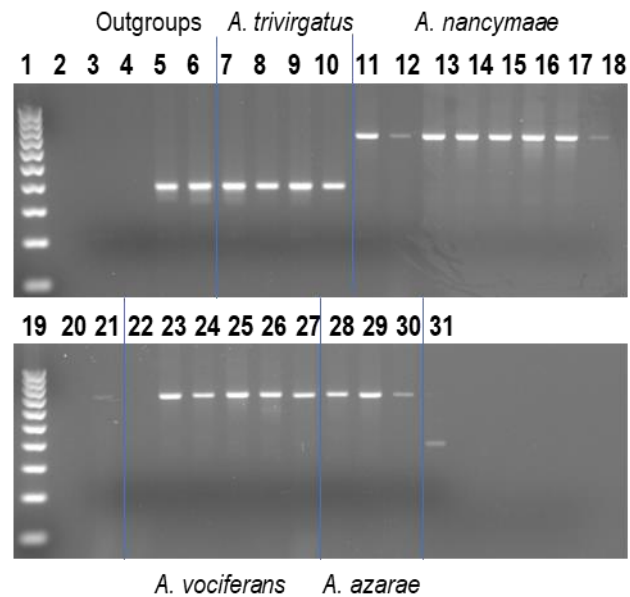
      1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
ATTATTATACACTGAACATATGTGTGCATTTGTGAGCACACATAAAGGAATGTTAAAGTGCCCTCATAGGAATTTCTCCTCTATCAACTCAAGAATCGTATG
ATTATTATACACTGAACATATGTGTGCATTTGTGAGCACACATAAAGGAATGTTAAAGTGCCCTCATAGGAATTTCTCCTCTATCAACTCAAGAATCGTATG

```



**Figure S29b.** Sequence alignment for *Alu* locus Owl\_2LS\_042\_018498342.1:691757-693258 (LR-42). The reference genome [Anan\_2.0] is shown at the top followed by samples *A. trivirgatus* crl-1556 and *A. vociferans* 86218. The target *Alu* insertion starts at position 600 (grey highlight) and ends in an A-tail at ~900 and is flanked by matching sequence indicating that these samples share the target insertion. The TSDs are in yellow highlight (AAGG/ATTTCAAGATC/T). However, beginning at position ~1002, *A. trivirgatus* crl-1556 and *A. vociferans* 86218 have a ~225 bp insertion of extra non-repeat (based on RepeatMasker) sequence (aqua highlight) that is about 80 bp 5' of the reverse primer (not shown). The target *Alu* is likely homozygous present within *Aotus*. Evidence of shared extra sequence in both *A. trivirgatus* and *A. vociferans* hints at a close relationship but it does not represent an additional homoplasmy free element. DNA sequencing using internal *Alu* primers easily detects if multiple *Alus* are present versus having a single signal. There is only one *Alu* at this locus, the target insertion.





**Figure S30a:** *Alu* locus *Aotus\_127\_018503376.1:406405-407905* (JW-127): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymaae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. Vertical blue lines superimposed on the gel image visually separate the species groups. The predicted amplicon sizes are 690/380 bp. These PCR genotypes indicate that the target *Alu* insertion is homozygous present in *A. nancymaae*, *A. vociferans* and *A. azarae* while homozygous absent in *A. trivirgatus* and *A. lemurinus griseimembra*. Similar to locus *Aotus\_1602*, this suggests that *A. trivirgatus* is basal to *A. vociferans*. Perform DNA sequencing to confirm this pattern.

```

      510      520      530      540      550      560      570      580      590      600
Aotus_127_[Anan_2.0]  ATATCTATTAGTTGGTGTGAAAGtgcaaaaacc-gcaattacttttgcaccaacctcatagcaaaataaaattgaaatcatttctaaaaataaagatatttc
JW-127-cr11556-E-R    ATATCTATTAGTTGGTGTGAAAGTGCAAAAACC-GCAATTACTTCTGCACCAACCTCATATCAAAATAAAATTGAAATCATTTCATAAAATAAAGATATTTTC
JW-127-cr11556-E-F-rc ATATCTATTAGTTGGTGTGAAAGTGCAAAAACC-GCAATTACTTCTGCACCAACCTCATATCAAAATAAAATTGAAATCATTTCATAAAATAAAGATATTTTC
JW-127-155159-SIntR-rc ATATCTATTAGTTGGTGTGAAAGTGCAAAAACC-GCAATTACTTCTGCACCAACCTCATAGCAAAATAAAATTGAAATCATTTCATAAAATAAAGATATTTTC
JW-127-155159-R      ATATCTATTAGTTGGTGTGAAAGTGCAAAAACC
JW-127-155159-IntF   ~~~~~
JW-127-155159-F-rc   ~~~~~
JW-127-85818-SIntR-rc ATATCTATTAGTTGGTGTGAAAGTGCAAAAACCCGCAATTACTTTTGCACCAACCTCATAGCAAAATAAAATTGAAATCATTTCATAAAATAAAGATATTTTC
JW-127-85818-R      ATATCTATTAGTTGGTGTGAAAGTGCAAAAACCCGCAATTACTTTTGCACCAACCTCATAGCAAAATAAAATTG
JW-127-85818-IntF   ~~~~~
JW-127-85818-F-rc   ~~~~~

```

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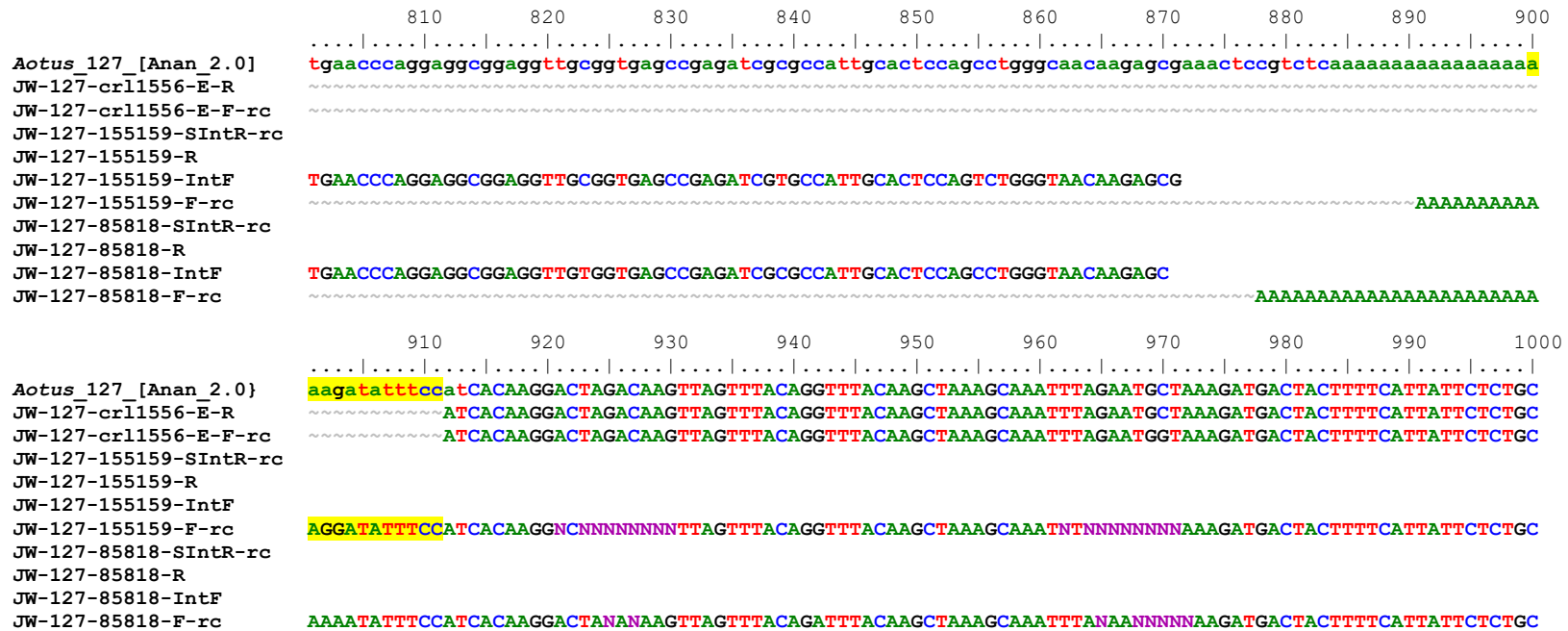
      610      620      630      640      650      660      670      680      690      700
Aotus_127_[Anan_2.0]  cggccgggcgcggtggctcagcctgtaatcccagcactttgggaggccgaggcggtggatcacgaggtcgcagagatcgcagaccatcctggccaacatg
JW-127-cr11556-E-R    cggccgggcgcggtggctcagcctgtaatcccagcactttgggaggccgaggcggtggatcacgaggtcgcagagatcgcagaccatcctggccaacatg
JW-127-cr11556-E-F-rc C
JW-127-155159-SIntR-rc CggccgggCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGC GGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATG
JW-127-155159-R      ~~~~~
JW-127-155159-IntF   ~~~~~
JW-127-155159-F-rc   ~~~~~
JW-127-85818-SIntR-rc CggccaggCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGC GGGTGGATCACGAGGTCAAGAGATCGAGACCATCCTGGTCAACATG
JW-127-85818-R      ~~~~~
JW-127-85818-IntF   ~~~~~
JW-127-85818-F-rc   ~~~~~

```

```

      710      720      730      740      750      760      770      780      790      800
Aotus_127_[Anan_2.0]  gtgaaaccccgctctactaaaaatacaaaaaattagctgggctgggtggcgctgcctgtaattccagctactcaggaggctgaggcaggagaattgcc
JW-127-cr11556-E-R    ~~~~~
JW-127-cr11556-E-F-rc ~~~~~
JW-127-155159-SIntR-rc GTGAAACCCGCTCTACTAAAAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCGTAATCCCAGCTACTCAAGAGGCTGAGGCAGG
JW-127-155159-R      ~~~~~
JW-127-155159-IntF   GTGAAACCCGCTCTACTAAAAATACAAAAAATTACCTGGGCATGGTGGCGCGTGCCGTAATCCCAGCTACTCAAGAGGCTGAGGCAGGAGAAATTGCC
JW-127-155159-F-rc   ~~~~~
JW-127-85818-SIntR-rc GTGAAACCTCGTCTCTACTAAAAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCGTAATCCCAGCTACTCAGGAGGCTGAGGCAGG
JW-127-85818-R      ~~~~~
JW-127-85818-IntF   GTGAAACCTCGTCTCTACTAAAAATACAAAAAATAACCTGGGCATGGTGGCGCGTGCCGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCC
JW-127-85818-F-rc   ~~~~~

```



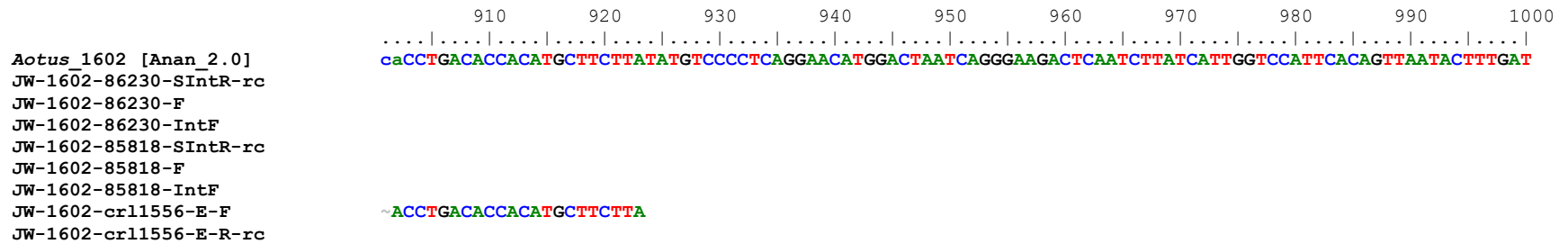
**Figure S30b.** Sequence alignment for *Alu* locus *Aotus\_127\_018503376.1:406405-407905* (JW-127). PCR based genotypes indicate the target *Alu* is homozygous present (1/1) in all *A. nancymae*, *A. vociferans* and *A. azarae* individuals while homozygous absent (0/0) in all *A. trivirgatus* individuals and the *A. l. griseimembra* sample. DNA sequencing was performed to confirm this pattern. The reference genome [Anan\_2.0] is shown at the top followed by the empty site sequence for *A. trivirgatus* cr1-1556 and filled site amplicons for *A. vociferans* MVZ-155159 and *A. azarae* 85818 both of whom share the target *Alu* starting at position at 602 (grey highlight) and flanked by TSDs in yellow highlight. Sequencing of the empty site amplicon in *A. trivirgatus* cr1-1556 has a precise pre-integration site spanning the target region, confirming the genotypes. This *Alu* insertion/absence pattern supports *A. trivirgatus* as basal to *A. vociferans* rather than the other way around, evidence of incomplete lineage sorting among grey-necked species.

510 520 530 540 550 560 570 580 590 600  
Aotus\_1602 [Anan\_2.0] TCTATTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTgattaaggtcacacagccagtaagtggcaagGCTCAGATAAAAAGTCACAtgcg  
JW-1602-86230-SIntR-rc TCTATTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTGATTAAGGTCACACAGCCAGTAAGTGGCAAGGCTCAGATAAAAAGTCACATGCG  
JW-1602-86230-F TCTATTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTGATTAAGGTCACACAGCCAGTAAGTGGCAAGGCTCAGATAAAAAGTCACATGCG  
JW-1602-86230-IntF  
JW-1602-85818-SIntR-rc TCTATTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTGATTAAGGTCACACAGCCAGTAAGTGGCAAGGCTCAGATAAAAAGTCACATGCG  
JW-1602-85818-F TCTATTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTGATTAAGANACACACAGCCAGTAAGTGGCAAGGCTCAGATAAAAAGTCACATGCG  
JW-1602-85818-IntF  
JW-1602-cr11556-E-F TCTAGTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTGATTAAGGTCACACAGCCAGTAAGTGGCAAGGCTCAGATAAAAAGTCACATGC~  
JW-1602-cr11556-E-R-rc TCTAGTACTATTTTCCAATTGAGACAGTCAGAGAGTTGAAGTAACTTGATTAAGGTCACACAGCCAG

610 620 630 640 650 660 670 680 690 700  
Aotus\_1602 [Anan\_2.0] ggccgggCGCGGTGGCTTAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGACGGGTGGAATCACGAGGTCAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1602-86230-SIntR-rc GGCCGGGCGCGGTGGCTTAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGACGGGTGGAATCACGAGGTCAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1602-86230-F GGCCGGGCGCGGTGGCTTAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGACGGGTGGAATCACGAGGTCAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1602-86230-IntF  
JW-1602-85818-SIntR-rc GGCCGGGCGCGGTGGCTTAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGACGGGTGGAATCACGAGGTCAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1602-85818-F GGCCGGGCGCGGTGGCTTAAGCCTGTAATCCCAGCCTTTGGGAGGCCGAGACGGGTGGAATCACGAGGTCAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1602-85818-IntF GAGGTCAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1602-cr11556-E-F  
JW-1602-cr11556-E-R-rc

710 720 730 740 750 760 770 780 790 800  
Aotus\_1602 [Anan\_2.0] tgaaaCCCCGtctttactaaTACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGG  
JW-1602-86230-SIntR-rc TGAAAACCCCGTCTTTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGG  
JW-1602-86230-F TGAAAACCCCGTCTTTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCTGAA  
JW-1602-86230-IntF ~AAAACCCCGTCTTTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCTGAA  
JW-1602-85818-SIntR-rc TGAAAACCCCGTCTTTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCTGAA  
JW-1602-85818-F TGAAAACCCCGTCTTTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCTGAA  
JW-1602-85818-IntF TGAAAACCCCGTCTTTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATTGCCTGAA  
JW-1602-cr11556-E-F  
JW-1602-cr11556-E-R-rc

810 820 830 840 850 860 870 880 890 900  
Aotus\_1602 [Anan\_2.0] CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-86230-SIntR-rc CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-86230-F CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-86230-IntF CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-85818-SIntR-rc CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-85818-F CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-85818-IntF CCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCACCTCCAGCCTGGGTAACGAGCGAAACTCCGTCTCAAAAAAAAAAAAAA  
JW-1602-cr11556-E-F  
JW-1602-cr11556-E-R-rc



**Figure S31.** Sequence alignment for *Alu* locus *Aotus\_1602\_018513626.1:10501295-10502786* (JW-1602). PCR based genotypes indicate the target *Alu* is homozygous present (1/1) in all *A. nancymaae*, *A. vociferans* and *A. azarae* individuals while homozygous absent (0/0) in all *A. trivirgatus* individuals and the *A. l. griseimembra* sample. The gel image is shown in the main text as Figure 2b. DNA sequencing was performed to confirm this pattern. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. vociferans* 86230 and *A. azarae* 85818 both of whom share the target *Alu* based on 5' flanking sequence and the *Alu* start position at 601 (grey highlight). Sequencing of the empty site amplicon in *A. trivirgatus* crl-1556 has a precise pre-integration site spanning the target region, confirming the genotypes. This *Alu* insertion/absence pattern supports *A. trivirgatus* as basal to *A. vociferans* rather than the other way around.

510 520 530 540 550 560 570 580 590 600  
Storer\_2020\_Aotus-622 TCCTCCGCCCCAGTGCTCCCTCAGTTAAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGctgaaaagaaaag  
JS-622-155159-SIntR-rc TCCTCCGCCCCAGTGCTCCCTCAGTTAAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-155159-F ~~~~~ CCCTCCAGTTAAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-155159-R-rc ~~~~~  
JS-622-85818-SIntR-rc TCCTCCGCCCCAGTGCTCCCTCAGTTAAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-85818-F ~~~~~ TTAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-85818-IntF ~~~~~  
JS-622-85818-R-rc ~~~~~  
JS-622-86230-E-F ~~~~~ AACGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-86230-E-R-rc TCCTCCGCCCCAGTGCTCCCTCAGTTAAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-cr11556-E-F ~~~~~ AACGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG  
JS-622-cr11556-E-R-rc TCCTCCGCCCCAGTGCTCCCTCAGTTAAAGATTAAAGTGATCCGTTAGCGATGCTGTTTTGTGAATCCAGGGCAGTCAGCACTGCTGAAAAGAAAAG

610 620 630 640 650 660 670 680 690 700  
Storer\_2020\_Aotus-622 agcatttcgcccgggcgggcgggtggctcagccctgtaatcccaggactttgggagggcaggcgggtggatcatgaggtcaagagatcaagaccatcctgggtc  
JS-622-155159-SIntR-rc AGCATTTGCGCCGGGCGCGGTGGCTCAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCATGAGATCAAGAGATCGAGACCATCCTGGTC  
JS-622-155159-F ~~~~~ NCGATTTGCGCCGGGCGCGGTGGCTCAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGG  
JS-622-155159-R-rc ~~~~~  
JS-622-85818-SIntR-rc AGCATTTGCGCCGGGCGCGGTGGCTCAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAAGAGATCAAGACCATCCTGGTC  
JS-622-85818-F ~~~~~ AGCATTTGCGCCGGGCGCGGTGGCTCAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCGGGTGGATCATGAGGTCAAGAGATCAAGACCATCCTGGTC  
JS-622-85818-IntF ~~~~~ GAGGTCAAGAGATCAAGACCATCCTGGTC  
JS-622-85818-R-rc ~~~~~  
JS-622-86230-E-F AGCATTT  
JS-622-86230-E-R-rc AGCATTT  
JS-622-cr11556-E-F AGCATTT  
JS-622-cr11556-E-R-rc AGCATTT

710 720 730 740 750 760 770 780 790 800  
Storer\_2020\_Aotus-622 aacatggtgaaaaccctgctctactataaatacaaaaaattagctgggcatgggtggcagctgacctgtaatcccagctactcaggaggctgaggcaggaga  
JS-622-155159-SIntR-rc AACATGGTGAAAACCCCGTCTACTATAAATACAAAAAANTAGCTGGGCATGGTGGCACGTGCCGTAATCCCAGCTACTCAGGAGG  
JS-622-155159-F ~~~~~  
JS-622-155159-R-rc ~~~~~  
JS-622-85818-SIntR-rc AACATGGTGAAAACCCCGTCCCTACTATAAATACAAAAAATTAGCTGGGCATGGTGGCACGTGCCGTAATCCCAGCTACTCAGGAGG  
JS-622-85818-F AACATGGTGAAAACCCCGTCCCTACTATAAATACAAAAAATTAGCTGGGCATGGTGGCACGTGCCGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGA  
JS-622-85818-IntF AACATGGTGAAAACCCCGTCCCTACTATAAATACAAAAAATTAGCTGGGCATGGTGGCACGTGCCGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGA  
JS-622-85818-R-rc ~~~~~  
JS-622-86230-E-F ~~~~~  
JS-622-86230-E-R-rc ~~~~~  
JS-622-cr11556-E-F ~~~~~  
JS-622-cr11556-E-R-rc ~~~~~



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510 520 530 540 550 560 570 580 590 600
Owl_2LS_018_[Anan_2.0]
LR-18-cr11556-F TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-cr11556-SIntR-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-cr11556-IntF TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-cr11556-R-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-86230-F GGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-86230-IntF TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-86230-SIntR-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-86230-R-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-KB4883-F GAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGNAGAAGAGTCTGcatga
LR-18-KB4883-IntF TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-KB4883-SIntR-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-KB4883-R-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-85464-E-F GAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-85464-E-R-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-85818-E-F TTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-85818-E-R-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
LR-18-86100-E-F TTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGANTCTGcatga
LR-18-86100-E-R-rc TGGAGGGAGTGGTGGCAAAGCTTAAGCAGACAGAGTTCTAGAGAGAAGGGGAAAACCTGAAAGCAGCAAGTAGGAATAACTTGTAGAAGAGTCTGcatga
```

```
610 620 630 640 650 660 670 680 690 700
Owl_2LS_018_[Anan_2.0]
LR-18-cr11556-F ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-cr11556-SIntR-rc ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-cr11556-IntF ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-cr11556-R-rc ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-86230-F ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-86230-IntF ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-86230-SIntR-rc ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-86230-R-rc ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-KB4883-F ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-KB4883-IntF ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-KB4883-SIntR-rc ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-KB4883-R-rc ggccgggcgcggtggctcaagcctgtaatcccagcactttgggagcggagggggtggaacacgagtgaaacagatcgcagaccatcctggatcaacatgg
LR-18-85464-E-F
LR-18-85464-E-R-rc
LR-18-85818-E-F
LR-18-85818-E-R-rc
LR-18-86100-E-F
LR-18-86100-E-R-rc
```

```
710 720 730 740 750 760 770 780 790 800
Owl_2LS_018_[Anan_2.0]
LR-18-cr11556-F tgaaaccccgctctactaatacaaaaaacttagctgggcatggctggcgctgctgtaatcccagctactcaggaggctgaggcagggaaattgacctgaac
LR-18-cr11556-SIntR-rc tgaaaccccgctctactaatacaaaaaacttagctgggcatggctggcgctgactgtaatcccagctactcaggaggctgaggcagggaaattgacctgaac
LR-18-cr11556-IntF tgaaaccccgctctactaatacaaaaaacttagctgggcatggctggcgctgactgtaatcccagctactcaggaggctgaggcagggaaattgacctgaac
LR-18-cr11556-R-rc tgaaaccccgctctactaatacaaaaaacttagctgggcatggctggcgctgactgtaatcccagctactcaggaggctgaggcagggaaattgacctgaac
```



LR-18-86230-F  
LR-18-86230-IntF  
LR-18-86230-SIntR-rc  
LR-18-86230-R-rc  
LR-18-KB4883-F  
LR-18-KB4883-IntF  
LR-18-KB4883-SIntR-rc  
LR-18-KB4883-R-rc  
LR-18-85464-E-F  
LR-18-85464-E-R-rc  
LR-18-85818-E-F  
LR-18-85818-E-R-rc  
LR-18-86100-E-F  
LR-18-86100-E-R-rc

TGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGAAATTGCC TGAAC  
TGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGAAATTGCC TGAAC  
TGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGAAATTGCC TGAAC  
TGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGAAATTGCC TGAAC  
TGAAACCCCGTCTCTACTAATACAAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGGAAATTGCC TGAAC

810 820 830 840 850 860 870 880 890 900

Owl\_2LS\_018 [Anan\_2.0]  
LR-18-cr11556-F  
LR-18-cr11556-SIntR-rc  
LR-18-cr11556-IntF  
LR-18-cr11556-R-rc  
LR-18-86230-F  
LR-18-86230-IntF  
LR-18-86230-SIntR-rc  
LR-18-86230-R-rc  
LR-18-KB4883-F  
LR-18-KB4883-IntF  
LR-18-KB4883-SIntR-rc  
LR-18-KB4883-R-rc  
LR-18-85464-E-F  
LR-18-85464-E-R-rc  
LR-18-85818-E-F  
LR-18-85818-E-R-rc  
LR-18-86100-E-F  
LR-18-86100-E-R-rc

ccaggaggcgaagttgCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT  
CCAGGAGGCGGAAGTTGCGGTGAGCCGAGATCGCGCCATTGCAC TCCAGCCTGGGTAACGAGCGAAACTCCGTCCCAAAAAAAAAAAAAAAAAAAGAGT

910 920 930 940 950 960 970 980 990 1000

Owl\_2LS\_018 [Anan\_2.0]  
LR-18-cr11556-F  
LR-18-cr11556-SIntR-rc  
LR-18-cr11556-IntF  
LR-18-cr11556-R-rc  
LR-18-86230-F  
LR-18-86230-IntF  
LR-18-86230-SIntR-rc  
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LR-18-KB4883-F  
LR-18-KB4883-IntF  
LR-18-KB4883-SIntR-rc

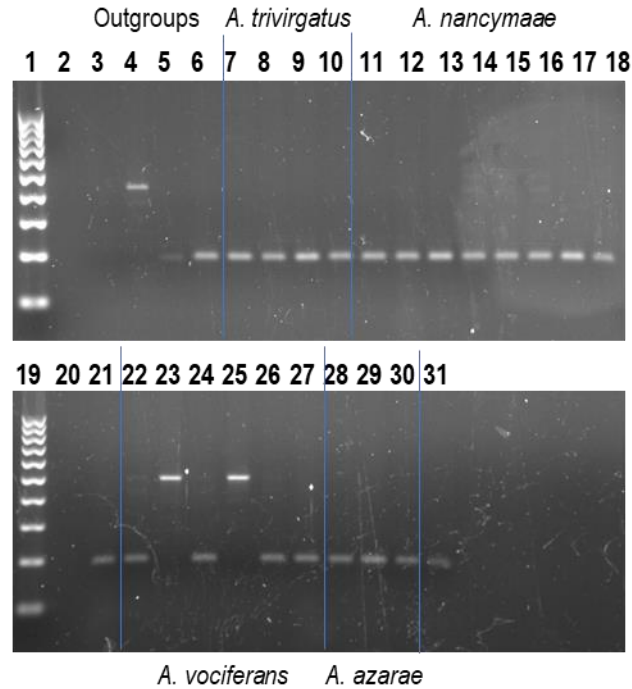
ctgcatgaaaaaggaggtaaaaaaaaggagaggattGGGGTCAcaagagttgtttttgttttagatggcaGATAGTAGCTTGTATATGCTGATGGGA  
CTGCATGAAAAGGAGGTAAA GAAAAGGAGGGGATTAGGGTC  
CTGCATGAAAAGGAGATAAA GAAAAGGAGGGGATTGGGGTCACAAGA

```

LR-18-KB4883-R-rc      NTGCANGAAAAGGAGGTAAAGAAAAGGAGGGGATTGGGGTCAACAAGAG
LR-18-85464-E-F       ~~~~~~AAAGGAGGTCAAGAAAAGGAGGGGATTGGGGTCAACAAGAGTTGTTTTGTTTTTCAGATGGCAGATAATAGCTTGTTATATGCTGATGGGAAG
LR-18-85464-E-R-rc   ~~~~~~AAAGGAGGTCAAGAAAAGGAGGGGATTGGGGTCAACAAGAGTTGT
LR-18-85818-E-F      ~~~~~~AAAGGAGGTCAAGAAAAGGAGGGGATTGGGGTCAACAAGAGTTGTTTTGTTTTTCAGATGGCAGATAATAGCTTGTTATATGCTGATGGGAAG
LR-18-85818-E-R-rc   ~~~~~~AAAGGAGGTCAAGAAAAGGAGGGGATTGGGGTCAACAAGAG
LR-18-86100-E-F      ~~~~~~AAAGGAGGTAAAGAAAAGGAGGGGATTGGGGTCAACAAGAGTTGTTTTGTTTTTCAGATGGCAGATAATAGCTTGTTATATGCTGATGGGAAG
LR-18-86100-E-R-rc   ~~~~~~AAAGGAGGTAAAGAAAAGGAGGGGA

```

**Figure S33.** Sequence alignment for *Alu* locus Owl\_2LS\_018\_018514491.1:3469855-3471351 (LR-18). PCR analyses produced a strange pattern of insertion presence/absence in which the target *Alu* is polymorphic among *A. nancymae* and *A. vociferans*; homozygous present in all four *A. trivirgatus* individuals and the *A. l. griseimembra* sample KB4883 (1/1), while homozygous absent (0/0) in all three *A. azarae* samples. DNA sequencing was performed to confirm these genotypes. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. trivirgatus* crl-1556, *A. vociferans* 86230 and *A. l. griseimembra* sample KB4883, all of whom share the target *Alu* insertion starting at position 601 (grey highlight). The TSDs are highlighted in yellow. Sequence of empty site amplicons in *A. nancymae* 85464, *A. azarae* 85818 and *A. vociferans* 86100 all reveal precise pre-integration sites with both forward and reverse sequences spanning the target region, confirming the genotypes. This pattern suggests extensive incomplete lineage sorting (ILS) of the target *Alu* insertion. **NOTE: *A. voc.* 86230 (with *Alu*) and 86100 (*Alu* absent) are siblings, same Dam and Sire.**



**Figure S34a:** *Alu* locus *Aotus*\_1582\_018497893.1:1531600-1533091 (JW-1582): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa-has a different *Alu* in this region), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymaae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. Vertical blue lines superimposed on the gel image visually separate the species groups. The predicted amplicon sizes are 483/192 bp. PCR-based genotypes indicate that all *Aotus* individuals are homozygous absent (~192 bp fragment) except for these two *A. vociferans* individuals who have a homozygous present (~483 bp fragment) shown in lanes 23 and 25. DNA sequencing was performed to determine if *A. vociferans* MVZ-155159 and 86218 share the target *Alu* or perhaps have a near parallel insertion unique to *A. vociferans*. See alignment Figure S34b.

510 520 530 540 550 560 570 580 590 600  
Aotus-1582-rc\_[Anan\_2.0] GAGTCAGCCATTTCTTTAAGAAGCCTTGGTTTGGTTGGAGAATGGTCTTTAGAAGCCAAAGAAGGGATGGGATTAAGCACTTCCCCAACTGAAAA  
JW-1582-155159-SIntR-rc GAGTCAGCCATTTCTTTAAGAAGCCTTGGTTTGGTTGGAGAATGGTCTTTAGAAGCCAAAGAAGGGATGGGATTAAGCACTTCCCCAACTGAAAA  
JW-1582-155159-R ~~~~~GTTTGGTTGGAGAATGGTCTTTAGAAGCCAAAGAAGGGATGGGATTAAGCACTTCCCCAACTGAAAA  
JW-1582-155159-IntF1 ~~~~~  
JW-1582-155159-F-rc ~~~~~  
JW-1582-86218-SIntR-rc GAGTCAGCCATTTCTTTAAGAAGCCTTGGTTTGGTTGGAGAATGGTCTTTAGAAGCCAAAGAAGGGATGGGATTAAGCACTTCCCCAACTGAAAA  
JW-1582-86218-R ~~~~~TTTGGTTGGAGAATGGTCTTTAGAAGCCAAAGAAGGGATGGGATTAAGCACTTCCCCAACTGAAAA  
JW-1582-86218-IntF ~~~~~  
JW-1582-86218-F-rc ~~~~~

610 620 630 640 650 660 670 680 690 700  
Aotus-1582-rc\_[Anan\_2.0] gaaacattaatagtagcaggccgggCGCGGTGGTCTAAGCCTGTAATCCAGCCTTTGGAGGCCGAGCCGGTGGATCACAAGGTC AAGAGATCGAG  
JW-1582-155159-SIntR-rc GAAACATTAATTAGTAGCAGGCCGGGCGCGGTGGTCTAAGCCTGTAATCCAGCCTTTGGAGGCCGAGCCGGTGGATCACAAGGTC AAGAGATCGAG  
JW-1582-155159-R ~~~~~CGAG  
JW-1582-155159-IntF1 ~~~~~  
JW-1582-155159-F-rc ~~~~~  
JW-1582-86218-SIntR-rc GAAACATTAATTAGTAGCAGGCCGGGCGCGGTGGTCTAAGCCTGTAATCCAGCCTTTGGAGGCCAAGCCGGTGGATCACAAGGTC AAGAGATCGAG  
JW-1582-86218-R ~~~~~CGAG  
JW-1582-86218-IntF ~~~~~  
JW-1582-86218-F-rc ~~~~~

710 720 730 740 750 760 770 780 790 800  
Aotus-1582-rc\_[Anan\_2.0] accatcctgggtcaacatgggtgaaacccccgtctctactaacaacacaaaaattagctgggcatggtggcaagtgcctctaattcccagctactcaggaggctga  
JW-1582-155159-SIntR-rc ACCATCCTGGTCAACATGGTGAACCCCGTCTCTACTAACACAAAAATTAGCTGGGCATGGTGGCCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGA  
JW-1582-155159-R ~~~~~  
JW-1582-155159-IntF1 ~~~~~  
JW-1582-155159-F-rc ~~~~~  
JW-1582-86218-SIntR-rc ACCATCCTGGTCAACATGGTGAACCCCGTCTCTACTAACACAAAAATTAGCTGGGCATGGTGGCCGTGCCTGTAATCCCAGCTACTCAGGAGG  
JW-1582-86218-R ~~~~~  
JW-1582-86218-IntF ~~~~~  
JW-1582-86218-F-rc ~~~~~

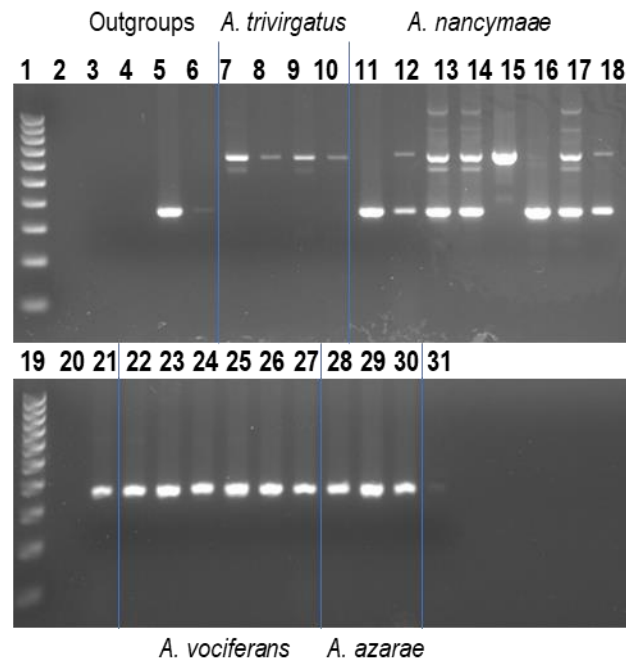
810 820 830 840 850 860 870 880 890 900  
Aotus-1582-rc\_[Anan\_2.0] ggcaggagaattgcctgaaacccaggaggcggagggttgcggtgagccgagatcgccattgcaactccagcctgggtaacgagcgaaactccgttgccaaa  
JW-1582-155159-SIntR-rc GGCAGGAGAATTGCCTGAACCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCCTCCAGCCTGGGTAAACGAGCGAAACTCCGTCACAAAA  
JW-1582-155159-R ~~~~~AAAA  
JW-1582-155159-IntF1 ~~~~~  
JW-1582-155159-F-rc ~~~~~  
JW-1582-86218-SIntR-rc GGCAGGAGAATTGCCTGAACCCAGGAGGCGGAGGTTGCGGTGAGCCGAGATCGCGCCATTGCCTCCAGCCTGGGTAAACGAGCGAAACTCCGTCGAAAA  
JW-1582-86218-R ~~~~~AAAA  
JW-1582-86218-IntF ~~~~~  
JW-1582-86218-F-rc ~~~~~

```

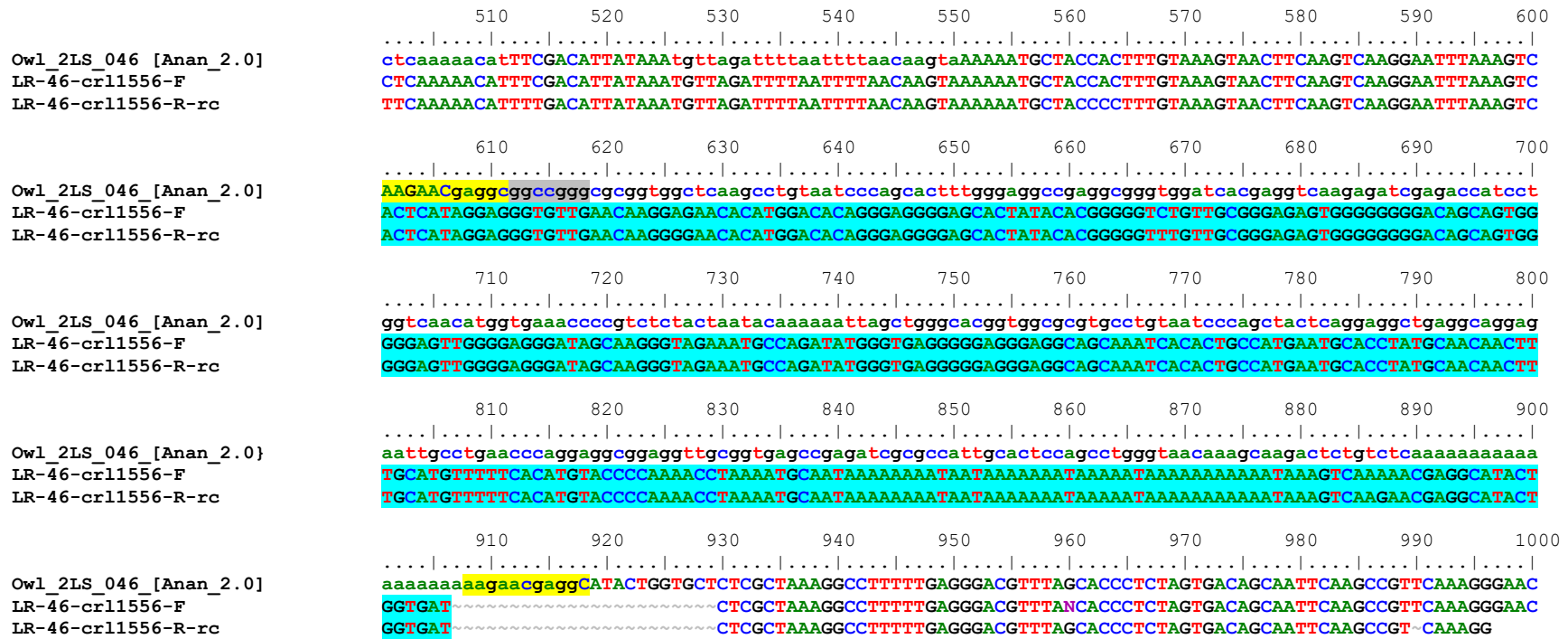
          910      920      930      940      950      960      970      980      990      1000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus-1582-rc_[Anan_2.0] aaaaaaaaaattagtagcaaCAGCTAAAAGCCGGGTGCCAACAGCTGAACAAAGTGACAggacaggaaggagaagaggaaatagTGCTCTGGGGCTAGA
JW-1582-155159-SIntR-rc
JW-1582-155159-R      AAAAAAAAAAAAAA
JW-1582-155159-IntF1  AAAAAAAAAAAAAA
JW-1582-155159-F-rc  AAAAAAAAAAATTAGTAGCAACAGC
JW-1582-86218-SIntR-rc
JW-1582-86218-R      AAAAAAAAAAAAAA
JW-1582-86218-IntF   AAAAAAAAAAAAAA
JW-1582-86218-F-rc  AAAAAAAAAAATTAGTAGCAACAGC

```

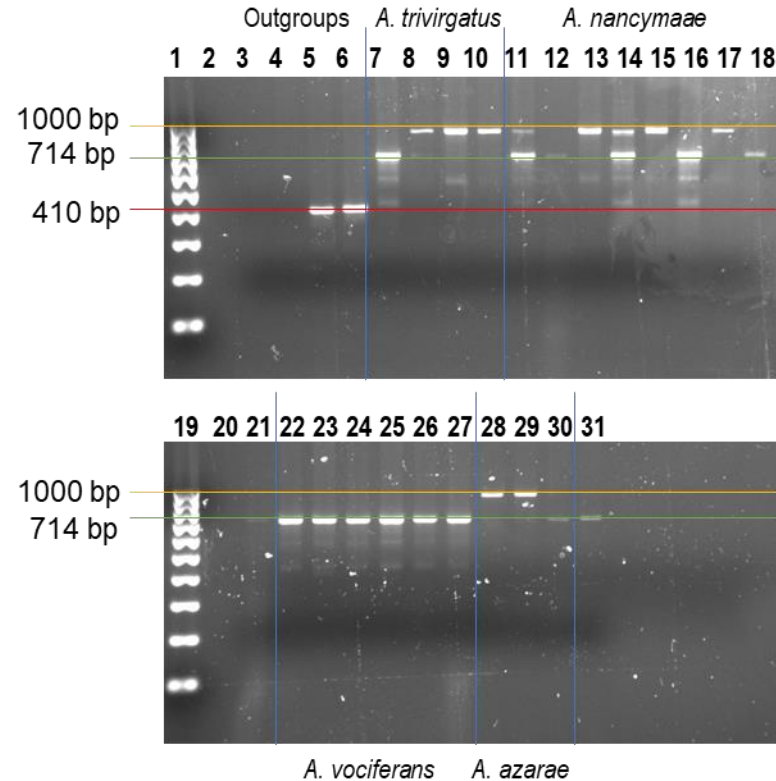
**Figure S34b.** Sequence alignment for *Alu* locus *Aotus*\_1582 018497893.1:1531600-1533091. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. vociferans* MVZ155159 and 86218. PCR-based genotypes indicate that all *Aotus* individuals are homozygous absent (0/0) except for these two *A. vociferans* individuals who have a homozygous present (1/1) insertion pattern. DNA sequencing was performed to determine if they share the target *Alu* or perhaps have a near parallel insertion unique to *A. vociferans*. This alignment confirms that both *A. vociferans* samples share the target *Alu* with the reference *A. nancymae* genome. The *Alu* starts at position 620 (grey highlight), TSDs are in yellow highlight. This locus illustrates an interesting case of incomplete lineage sorting (ILS), especially given that none of our *A. nancymae* samples have the target reference genome insertion.



**Figure S35a:** *Alu* locus Owl\_2LS\_046\_018514732.1:7169258-7170758 (LR-46): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. The predicted amplicon sizes are 668/363 bp. PCR based genotypes indicate that the target *Alu* is polymorphic among *A. nancymae* individuals, homozygous absent (363 bp fragment) in *A. vociferans* and *A. azarae*, while homozygous present in all four *A. trivirgatus* individuals. This pattern suggests that *A. trivirgatus* is most related to *A. nancymae*. Perform DNA sequencing to confirm. See alignment Figure S35b.



**Figure S35b.** Sequence alignment for *Alu* locus Owl\_2LS\_046\_018514732.1:7169258-7170758 (LR-46). PCR based genotypes indicate that the target *Alu* is polymorphic among *A. nancymae* individuals, homozygous absent in *A. vociferans* and *A. azarae*, while homozygous present in all four *A. trivirgatus* individuals. This pattern suggests that *A. trivirgatus* is most related to *A. nancymae*. Perform DNA sequencing to confirm. The reference genome [Anan\_2.0] is shown at the top, the target *Alu* starts at position 612 (grey highlight) and TSDs are shown in yellow highlight. While sequencing *A. trivirgatus* crl-1556 the internal-*Alu* primer sequences failed, meaning the *A. trivirgatus* filled site amplicon does not contain an *Alu* element. Instead, *A. trivirgatus* contains 306 bp of non-*Alu* sequence (aqua highlight), some of which is an L1, before matching flanking sequence resumes. *A. trivirgatus* is 0/0 for the target *Alu* based on this sequence alignment. However, we recommend not using this *Alu* locus for *Aotus* phylogeny due to the potential for confusing amplicons.



**Figure S36a:** *Alu* locus *Aotus*\_1153 018486804.1:1542204-1543700 (JW-1153): Lanes: 1, 19- 100 bp DNA ladder, 2, 20-blank, 3- TLE (negative control), 4- Human (HeLa), 5- *Callithrix jacchus* (Common marmoset), 6- *Saimiri s. sciureus* (Common squirrel monkey), 7-10 *A. trivirgatus*, 11-18, 21 *A. nancymae*, 22-27 *A. vociferans*, 28-30 *A. azarae*, 31-*A. lemurinus griseimembra*. Vertical blue lines superimposed on the gel image visually separate the species groups. The predicted amplicon sizes are 714 bp (green line) for the *A. nancymae* reference genome containing a full length *Alu* insertion and 410 bp (red line) for the outgroups. There is a larger than predicted amplicon (~1000 bp, yellow line) in some *Aotus* individuals of *A. trivirgatus*, *A. nancymae* and *A. azarae* but not in *A. vociferans*. DNA sequencing was performed to determine if this larger amplicon was a 2<sup>nd</sup> *Alu* insertion, in addition to the target insertion, that could perhaps be genotyped separately, as a surreptitious finding not ascertained from the reference genome (see alignment Figure S36b). This larger amplicon is not a 2<sup>nd</sup> *Alu* that can be genotyped separately. The target *Alu* is likely homozygous present in *Aotus*.



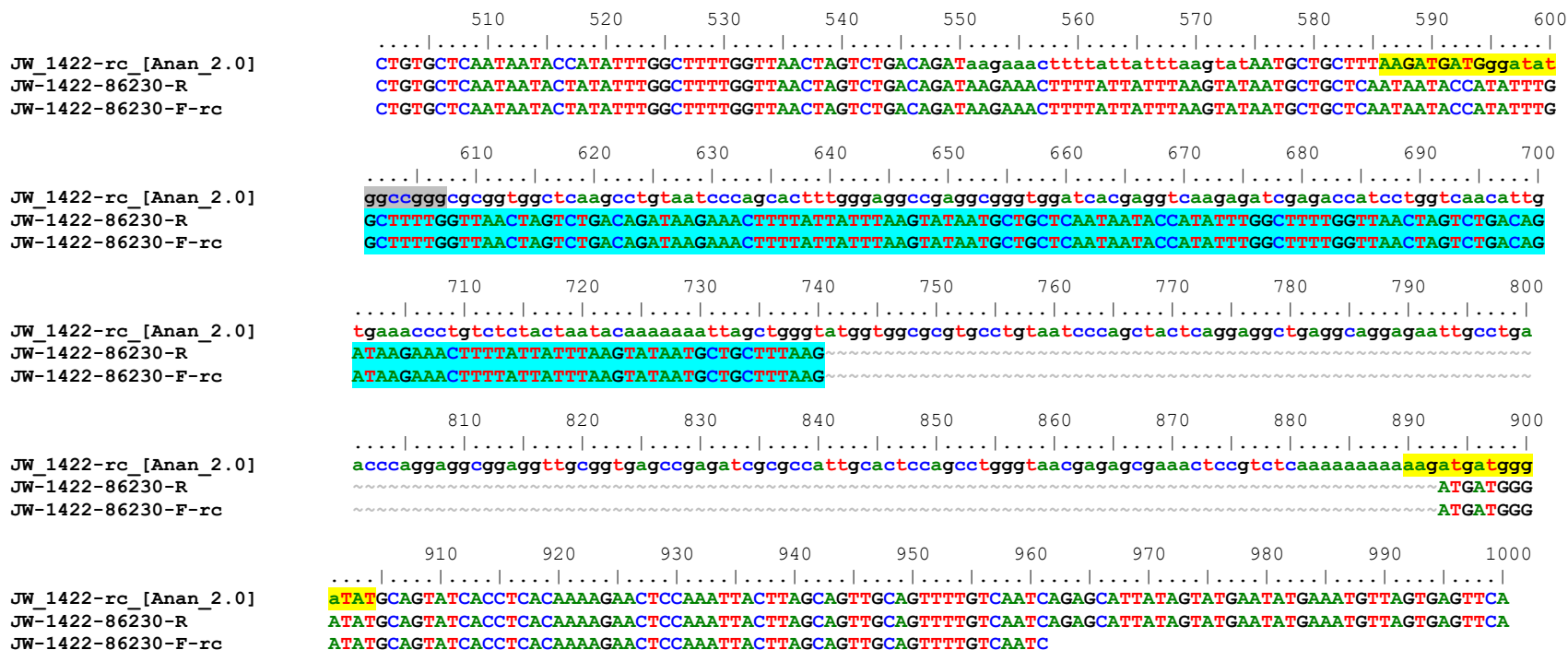
510 520 530 540 550 560 570 580 590 600  
Aotus\_1153\_RC [Anan\_2.0] ggtaaaaaaaaaatagaagaataagaacctactatgttagtagcacagtagggtagctatattcaataacaattgtacattttaaagtaacctaaagggtt  
JW-1153-41436-SInR-rc GGTAACAAAAAATAGAAAGAATAAGACCTACTATTTGATAGCACAGTAGGGTACTATATTCAATAACAATTGTACATTTTAAAGTAACCTAAAGGTT  
JW-1153-41436-F-rc ~~~~~  
JW-1153-41436-IntF ~~~~~  
JW-1153-85457-SIntR-rc GGTAACAAAAAATAGAAAGAATAAGACCTACTATTTGATAGCACAGTCGGGTACTATATTCAATAACAATTGTACATTTTAAAGTAACCTAAAGGTT  
JW-1153-85457-F-rc ~~~~~  
JW-1153-85457-R ~~~~~  
JW-1153-86116-SIntR-rc ~~~~~  
JW-1153-86116-F-rc ~~~~~  
JW-1153-86116-IntF ~~~~~

610 620 630 640 650 660 670 680 690 700  
Aotus\_1153\_RC [Anan\_2.0] ggccgggtgcggtggctcaagcctgtaatcccagcactttggaggccgagggcggtggatcagaggtcaagagatcgagaccatcctgggtcaacatgg  
JW-1153-41436-SInR-rc GGCCGGGCGCGGTGGCTCAAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGAAAAAAAAAAAAAAAAAGAGATCGAGACCATCCCGGTCAACATGG  
JW-1153-41436-F-rc ~~~~~  
JW-1153-41436-IntF ~~~~~  
JW-1153-85457-SIntR-rc GGCCGGGCGCGNTGGCTCAAGCCTGTAATCCCAGCAGTGTGGGAGGCCGAGAAGGAAGGATCAAAAAAAAAAAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1153-85457-F-rc ~~~~~  
JW-1153-85457-R ~~~~~  
JW-1153-86116-SIntR-rc GGCCGGGCGCGGTGGCTCAAGCCTGTAATCCCAGCACCTTTGGGAGGCCGAGGCCGGTGGATCAGAGGTCAAGAGATCGAGACCATCCTGGTCAACATGG  
JW-1153-86116-F-rc ~~~~~  
JW-1153-86116-IntF ~~~~~

710 720 730 740 750 760 770 780 790 800  
Aotus\_1153\_RC [Anan\_2.0] tgaaacccgtctctactaaaaatacaaaaaattagctgggctggtggcgctgacctgaatcccagctactcaggaggctgagggcaggaaattgcct  
JW-1153-41436-SInR-rc TGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAG  
JW-1153-41436-F-rc ~~~~~  
JW-1153-41436-IntF ~~~~~  
JW-1153-85457-SIntR-rc TGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCGCGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAG  
JW-1153-85457-F-rc ~~~~~  
JW-1153-85457-R ~~~~~  
JW-1153-86116-SIntR-rc TGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCACGGTGGCGCGTGCCTATAATCCCAGCTACTCAGGAGGCTGAGGCAGGAAATTGCCT  
JW-1153-86116-F-rc ~~~~~  
JW-1153-86116-IntF ~~~~~

810 820 830 840 850 860 870 880 890 900  
Aotus\_1153\_RC [Anan\_2.0] gaaacccaggaggcgagggttgccgtgagccgagatcgcgccattgcactccagcctgggtaacaagagcgaacctccaactcaaaaaaaaaaaaaaagta  
JW-1153-41436-SInR-rc ~~~~~  
JW-1153-41436-F-rc ~~~~~  
JW-1153-41436-IntF ~~~~~  
JW-1153-85457-SIntR-rc ~~~~~  
JW-1153-85457-F-rc ~~~~~  
JW-1153-85457-R ~~~~~  
JW-1153-85457-R ~~~~~

**Figure S36b.** Sequence alignment for *Alu* locus *Aotus\_1153* 018486804.1:1542204-1543700 (JW-1153). PCR analyses revealed a larger than predicted amplicon in some *Aotus* samples but not in *A. vociferans* (see Figure S36a). DNA sequencing was performed to determine if this larger amplicon was a 2<sup>nd</sup> *Alu* insertion, in addition to the target insertion, that could perhaps be genotyped separately, as a surreptitious finding not ascertained from the reference genome. The reference genome [Anan\_2.0] is shown at the top followed by samples *A. trivirgatus* 41436, *A. azarae* 85457, and *A. nancymae* 86116. The target *Alu* starts at position 601 (grey highlight) and is shared by the sequenced individuals. The SIntR signal gets messy going out the 5' end of the target *Alu* suggesting that the 5' flanking has extra sequence; the reverse primer entering the 5' *Alu* fails or is very messy. The target *Alu* is likely homozygous present in *Aotus*. A 2nd *Alu* is unlikely or perhaps inserted within the target (A-stretch in aqua highlight) unable to be genotyped independently. RepeatMasker indicates that the target *Alu* is inside an L1. Therefore, we recommend not using this locus for *Aotus* phylogeny.



**Figure S37.** Sequence alignment for *Alu* locus *Aotus\_1422* 018505596.1:1353282-1354772 (JW-1422). The predicted PCR fragment

sizes are 565/256 bp. PCR based genotypes indicate the target *Alu* is restricted to *A. nancymae*, however the *A. vociferans* individuals have amplicon that is a different size, about 400 bp. DNA sequencing was performed to determine if this fragment contained the target *Alu* with some missing sequence or is an artifact. The reference genome [Anan\_2.0] is shown at the top followed by *A. vociferans* 86230. The target *Alu* starts at position 601 (grey highlight) and the TSDs are shown in yellow highlight. During sequencing of *A. vociferans* 86230 the internal-*Alu* primers failed, meaning no *Alu* element is present. Instead, *A. vociferans* has ~140 bp of extra non-repetitive sequence (aqua highlight) in this region resulting in the observed ~400 bp amplicon. Therefore, *A. vociferans* are 0/0 for the target insertion.

```

      510      520      530      540      550      560      570      580      590      600
Owl_2LS_110_[Anan_2.0]
LR-110-41436-SIntR-rc
LR-110-41436-IntF
LR-110-41436-R-rc
LR-110-41436-E-F
LR-110-41436-E-R-rc
      610      620      630      640      650      660      670      680      690      700
Owl_2LS_110_[Anan_2.0]
LR-110-41436-SIntR-rc
LR-110-41436-IntF
LR-110-41436-R-rc
LR-110-41436-E-F
LR-110-41436-E-R-rc
      710      720      730      740      750      760      770      780      790      800
Owl_2LS_110_[Anan_2.0]
LR-110-41436-SIntR-rc
LR-110-41436-IntF
LR-110-41436-R-rc
LR-110-41436-E-F
LR-110-41436-E-R-rc
      810      820      830      840      850      860      870      880      890      900
Owl_2LS_110_[Anan_2.0]
LR-110-41436-SIntR-rc
LR-110-41436-IntF
LR-110-41436-R-rc
LR-110-41436-E-F
LR-110-41436-E-R-rc

```

```

          910      920      930      940      950      960      970      980      990      1000
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Owl_2LS_110_[Anan_2.0]
LR-110-41436-SIntR-rc
LR-110-41436-IntF
LR-110-41436-R-rc
LR-110-41436-E-F
LR-110-41436-E-R-rc

```

**Figure S38.** Sequence alignment for *Alu* locus Owl\_2LS\_110\_018501792.1:6759460-6760958 (LR-110): PCR-based genotypes indicate that *A. trivirgatus* MSB-41436 is the only *Aotus* sample that is not homozygous present (1/1) for the target insertion. DNA sequencing was performed for both the filled and empty amplicon fragments to confirm the heterozygous genotype. The reference genome [Anan\_2.0] is shown at the top followed by *A. trivirgatus* MSB-41436 who shares the target *Alu* insertion starting at position 602 (grey highlight) and flanked by TSDs in yellow highlight, while the empty site sequence displays a precise pre-integration site spanning the target region, confirming the genotype.

```

          510      520      530      540      550      560      570      580      590      600
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1765 [Anan_2.0]
JW-1765-85464-E-F
JW-1765-85464-E-R-rc
JW-1765-85464-R-rc
JW-1765-85464-SIntR-rc
JW-1765-85464-IntF

```

```

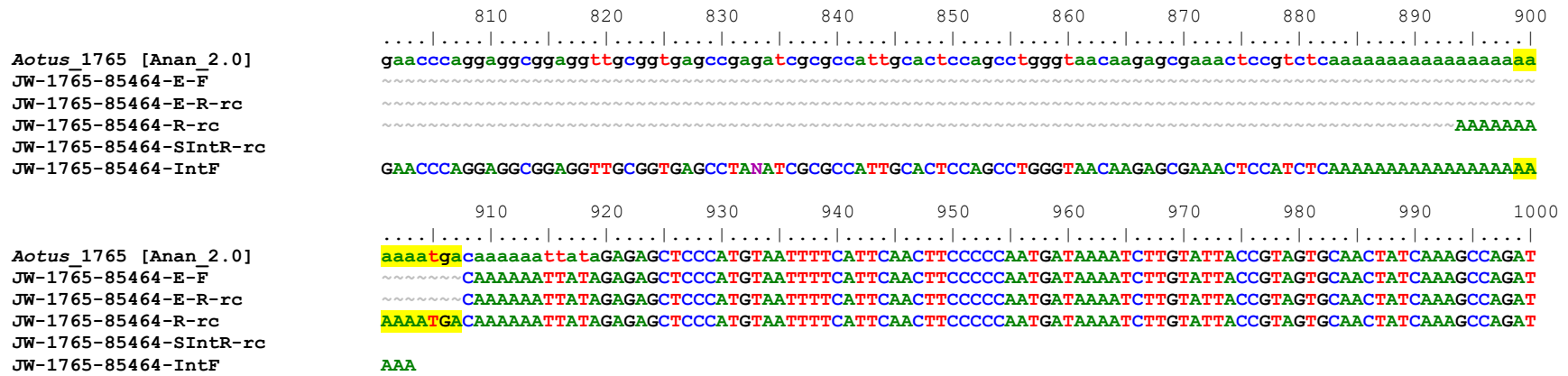
          610      620      630      640      650      660      670      680      690      700
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1765 [Anan_2.0]0
JW-1765-85464-E-F
JW-1765-85464-E-R-rc
JW-1765-85464-R-rc
JW-1765-85464-SIntR-rc
JW-1765-85464-IntF

```

```

          710      720      730      740      750      760      770      780      790      800
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Aotus_1765 [Anan_2.0]
JW-1765-85464-E-F
JW-1765-85464-E-R-rc
JW-1765-85464-R-rc
JW-1765-85464-SIntR-rc
JW-1765-85464-IntF

```



**Figure S39.** Sequence alignment for *Alu* locus *Aotus\_1765\_018493376.1:4506820-4508322* (JW-1765). PCR-based genotypes indicate the target *Alu* insertion is homozygous present (1/1) in all *Aotus* samples except for *A. nancymae* 85464 who appears heterozygous (1/0) for the insertion. The reference genome [Anan\_2.0] is shown at the top followed by sequence traces for the empty site amplicon in *A. nancymae* 85464 followed by filled site traces, The target *Alu* elements starts at position 602 (grey highlight) and flanked by TSDs in yellow highlight. The filled site amplicon shares the target *Alu* while the empty site displays a precise pre-integration site spanning the target region, confirming the genotype.