

Differentiating Authentic *Adenophorae Radix* from Its Adulterants in Commercially-Processed Samples Using Multiplexed ITS Sequence-Based SCAR Markers

Byeong Cheol Moon ^{1,*}, Wook Jin Kim ¹, Kyeong Suk Han ¹, Sungyu Yang ¹, Young Min Kang ¹, Inkyu Park ¹ and Renzhe Piao ²

Data 1. FASTA file of nrDNA-ITS sequences of plant materials used in this study.

```
>AS-CP_KY829514
TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGACGGGATAAG
GCGACAGCCCCCGTGCATGCAGCC-
CCCTTCCTTGTGGTGCCGGAGCAATCGAGCGAAAGCACGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTCGTGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTGCGGGTACGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCGAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCCTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTGATAATAAGGCCCTCGCGTTCTGTCTGTGCTTGAATCCTTTGCGG
GTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTACGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA
>AS-JS_KY829515
TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTACACGGGACAAG
GCGACAGCTCCCCGTGCATGCAGCC-
CCCTTCCTTGTGGTGCCGGAGCAATCGAGCGAAAGCACGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTGCGGGTGCAGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCGAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCCTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
```

CACGACAAGTGGTGGTTGATAATAAGGCCCTCGCGTTCTGTCTGCTTGAATCCTTTTCGG
GTTTTG-

GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCTTTTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>AS-GA_KY829516

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-

TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCGCGGGACAAG
GCGACAGCCCCCGTACATGCGGCC-CC-

TTCTTGTGGTGCCGGAGCAATCGAGCGAAAGCGCGTGAGCTTTG-GCACCCAAG-

AAACAAACCCCGGCGCAATTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTTCGCGGTGCGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-

CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCAAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCTTCCCGTG
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACA-

CACGACAAGTGGTGGTTTATAATA-

GGCCCTCGCGTTCTGTCTGCTTGAATCCTTTGCGGGTTTTG-

GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCACACCCTAGTAGTGGTTGACG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCACGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>AS-SJ_KY829517

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-

TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGACCGGGACAAG
GCGACAGCCCCCGTGATGCAGCC-

CCCTTCCTTGTGGTGCCGGAGCAATCGAGCGAAAGCACGTGAGCTTCG-GCCCCAAG-

AAACAAACCCCGGCGCAATTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTTCGCGGTGCGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-

CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCGAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCCTCCCGTG
CTCGCAGTTCGGTTGGCTCAAAATGGAGTTCCCTGTGAAGGACG-

CACGACAAGTGGTGGTTGATAATAAGGCCCTCGCGTTCTGTCTGCTTGAATCCTTTTCGG
GTTTTG-

GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCACGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>AT-CC_KY829518

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-

TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGACCGGGACAAG

GCGACAGCCCCCGTGCATGCGGCC-CC-
TTCCTTGTGGTGTCTGGAGCAATCGAGCGAAAGCGCGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTCTGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTGCGGGTGCGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCAAGGGCACGTCTGCATGGGCGTCACGCATCGCATCGCCCCCCCA
AGCATCTTGACCTCCAAGTGCTTGCTTGGTGGGGAGCGTACATTGGCTTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTTATAATA-
GGCCCTCGCGTTCTGTTGTGCTTGAATCCTTTGCGGGTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGATGTGCTTCGAACGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>AT-YS_KY829519

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGACAAG
GCGACAGCCCCCGTGCATGCGGCC-CC-
TTCCTTGTGGTGTCTGGAGCAATCGAGCGAAAGCGCGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTCTGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTGCGGGTGCGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCAAGGGCACGTCTGCATGGGCGTCACGCATCGCATCGCCCCCCCA
AGCATCTTGACCTCCAAGTGCTTGCTTGGTGGGGAGCGTACATTGGCTTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTTATAATA-
GGCCCTCGCGTTCTGTCTGTGCTTGAGTCCTTTGCGGGTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTTGTGGTGGTTGATG
GTGGATACGTGCTTCGAACGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>AT-DG_KY829520

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGACAAG
GCGACAGCCCCCGTGCATGCAGCC-
CCCTTCCTTGTGGTGCCGGAGCAATCGAGCGAAAGCACGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTTGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTGCGGGTGCGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCGAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCCTCCCGTGC

CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTGATAATAAGGCCCTCGCGTTCTGTCTGCTTGAATCCTTTGCGG
GTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCTAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>AT-LJ_KY829521

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGACAAG
GCGACAGCCCCCGTGCATGCAGCC-
CCCTTCCTTGTGGTGCCGGAGCAATCGAGCGAAAGCACGTGAGCTTTG-GCCCCAAG-
AAACAAACCCCGCGCAATTTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGTCTCCTC
ACGTTGCCCGCTTTGCGGGTGCAGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCGAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCCTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTGATAATAAGGCCCTCGCGTTCTGTCTGCTTGAATCCTTTGCGG
GTTTTG-

GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCTAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>ATJ-SC_KY829522

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGACAAG
GCGACAGCCCCCGTGCATGCGGCC-CC-
TTCCTTGTGGTGTCTGGAGCAATCGAGCGAAAGCGCGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGCGCAATTTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGTCTCCTC
ACGTTGCCCGCTTTGCGGGTGCAGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCAAGGGCACGTCTGCATGGGCGTCACGCATCGCATCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCTGCTTGCTTGGTGGGGAGCGTACATTGGCTTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTTATAATA-

GGCCCTCGCGTTCTGTCTGCTTGAAGTCCTTTGCGGGTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTTGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCTAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>ATJ-BC_KY829523

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGACAAG
GCGACAGCCCCCGTGCATGCGGCC-CC-
TTCCTTGTGGTGTCCGAGCAATCGAGCGAAAGCACGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTTCGCGGTACGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCGAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCCCGCTTGCTTGGTGGGGAGCGTACATTGGCCTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTGATAATAAGGCCCTCGCGTTCTGTCTGTGCTTGAATCCTTTGCGG
GTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>ATJ-SJ_KY829524

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGACAAG
GCGACAGCCCCCGTGCATGCGGCC-CC-
TTCCTTGTGGTGTCCGAGCAATCGAGCGAAAGCGCGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTTCGCGGTGCGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG
CCCGAAGCCTTTAGGCCAAGGGCACGTCTGCATGGGCGTCACGCATCGCATCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCTTGCTTGGTGGGGAGCGTACATTGGCTTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTTATAATA-
GGCCCTCGCGTTCTGTCTGTGCTTGAAGTCCTTTGCGGGTTTTG-
GCTCTTCGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTTGTGGTGGTTGATG
GTGGAGACGTGCTTCGAACGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCAT
ATCAATAAGCGGAGGA

>ATJ-GD_KY829525

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCTGAACCCTGCA-
TAGCAGAACAAACCCGCGAACACGTTGAAAAACACATTTGGGGGATGCGTGCACGGGATAAG
GCGACAGCCCCCGTGCATGCGGCC-CC-
TTCCTTGTGGTGTCCGAGCAATCGAGCGAAAGCGCGTGAGCTTCG-GCCCCAAG-
AAACAAACCCCGGCGCAATTTCGCGCCAAGGAAATCTTTAAACTCAAGGGCGTGCTCTCCTC
ACGTTGCCCCCGTTTTCGCGGTGTGCGACTGGGTGTTTGCCCGCTCCTTAGTGAAAA-
CACAAACGACTCTCGGCAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAAT
GCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCG

CCCGAAGCCTTTAGGCCAAGGGCACGTCTGCATGGGCGTCACGCATCGCGTCGCCCCCCCCA
AGCATCTTGACCTCCAAGTGCTTGCTTGGTGGGGAGCGTACATTGGCTTCCCGTGC
CTCGCAGTTCGGTTGGCTCAAAATGGAGTCCCCTGTGAAGGACG-
CACGACAAGTGGTGGTTTATAATA-
GGCCCTCGCGTTCTGTTGTGCTTGAATCCTTTGCGGGTTTTG-
GCTCTTTGATTAATGACCCTGATGACGCGCCTTCACAATCGCACCCCTAGTGGTGGTTGATG
GTGGAGATGTGCTTCGAACGCGACCCCATGTCAG-
CGGGACTACCCGCTGAGTTTAAGCATATCAATAAGCGGAGGA
>CL-SJ_KY829526
TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCGAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGCCCTTGCCGTGCGCGCCCGCCCAACCACTTG
GTGGCAGGG-----AGTGTGCGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACTT-
AACTCAAAGAGCGGCCCGTCCTCCTGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGCGGTTGCTTCTTAGTGAAAAACACAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
CGTCTGCATGGGCGTCACGCATCGCGTCGCTCCCTTAACTTAAT-TGTTACAAA-
ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGTTGGCTCA
AAACGGAGTCCCCCGCGAAGGACG-
CACGACAAGTGGTGGTTGGTAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGCTG
GGTT-G-GCTCTC-----GTGACCCTG---ATGCGTCTA-----
GGCTTAAGCCTAAG--
GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>CL-SN_KY829527
TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCGAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGCCCTTGCCGTGCGCGCCCGCCCAACCACTTG
GTGGCAGGG-----AGTGTGCGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACTT-
AACTCAAAGAGCGGCCCGTCCTCCTGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGCGGTTGCTTCTTAGTGAAAAACACAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
CGTCTGCATGGGCGTCACGCATCGCGTCGCTCCCTTAACTTAAT-TGTTACAAA-
ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGTTGGCTCA
AAACGGAGTCCCCCGCGAAGGACG-
CACGACAAGTGGTGGTTGGTAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGCTG
GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
GGCTTAAGCCTAAG--

GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>CL-GC_KY829528

TCCGTAGGTGAAC-TGCGGAAGGATCATTGTCGAAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGCCCCCTTGCCGTGCGCGCCCCGCCAACCCTTG
GTGGCAGGG-----AGTGTGCGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACCTT-
AACTCAAAGAGCGGCCCGTCCTCCTGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGCGGTTGCTTCTTAGTGAAAAACACAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
CGTCTGTATGGGCGTCACGCATCGCGTCGCCTCCCTTAACTTAAT-TGTTACAAA-
ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGTTGGCTCA
AAACGGAGTCCCCCGCGAAGGACG-
CACGACAAGTGGTGGTTGGTAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGCTG
GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
GGCTTAAGCCTAAG--

GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>CP-YA_KY829529

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCGAAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGCCCCCTTGCCGTGCGCGCATGCACCCGCCAACCCTTG
GTGGAAGGG-----AGCATGTGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACCTT-
AACTCAAAGAGCGCCACGTCCTCCCGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGTGGTTCGCTTCTTAGTGAAAAACACAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
CGTCTGCATGGGCGTCACGCATCGCGTCGCCTCCCTTAACTTAAT-TGTTTACAAA-
ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCCCCGTGCCTTGCGGCGCGGCTGGCTCA
AAACGGAGTCCCCCGCGAAGGACG-
CACGACAAGTGGTGGTTGATAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGATG
GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
GGCTTAAGCCTAAG--

GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>CP-HL_KY829530

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCGAAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGCCCCCTTGCCGTGCGCGCACGCACCCGCCAACCCTTG

GTGGAAGGG-----AGCATGTGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACCTT-
AACTCAAAGAGCGCCACGTCCTCCCGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGCGGTGCTTCTTAGTGAAAAACATAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
CGTCTGCATGGGCGTCACGCATCGCGTCGCTCCCTTAACTTAAT-TGTTTACAAA-
ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGCTGGCTGA
AAACGGAGTCCCCCGCGAAGGACG-
CACGACAAGTGGTGGTTGATAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGATG
GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
GGCTTAAGCCTAAG--
GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>CP-GR_KY829531

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCGAAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGGCCCCTTGCCGTGCGCGCACGCACCCGCCCAACCACTTG
GTGGAAGGG-----AGCATGTGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACCTT-
AACTCAAAGAGCGCCACGTCCTCCCGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGCGGTGCTTCTTAGTGAAAAACATAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
CGTCTGCATGGGCGTCACGCATCGCGTCGCTCCCTTAACTTAAT-TGTTTACAAA-
ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGCTGGCTGA
AAACGGAGTCCCCCGCGAAGGACG-
CACGACAAGTGGTGGTTGATAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGATG
GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
GGCTTAAGCCTAAG--
GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>CP-JB_KY829532

TCCGTAGGTGAACCTGCGGAAGGATCATTGTCGAAACCTGCA-
CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
CGGGGACGCGGGCTTGCCCGTGGCCCCTTGCCGTGCGCGCACGCACCCGCCCAACCACTTG
GTGGAAGGG-----AGCATGTGTGCGTCG-TTCGGCGCC-
AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACCTT-
AACTCAAAGAGCGCCACGTCCTCCCGTCGCCCC-GTTCGCGG-
TGTGCGCACGGTTGGGCGGTGCTTCTTAGTGAAAAACATAAACGACTCTCGGCAACGGAT
ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA

CGTCTGCATGGGCGTCACGCATCGCGTCGCCTCCCTTAACTTAAT-TGTTTACAAA-
 ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGCTGGCTGA
 AAACGGAGTCCCCCGCGAAGGACG-
 CACGACAAGTGGTGGTTGATAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGATG
 GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
 GGCTTAAGCCTAAG--
 GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
 GCGGAGGA
 >CP-WQ_KY829533
 TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCGAAACCTGCA-
 CAGCAGAACGACCCGCGAACACGT-GAACAACAC----
 CGGGGACGCGGGCTTGCCCGTGGCCCCTTGCCGTGCGGCGCACGCACCCGCCCAACCACTTG
 GTGGAAGGG-----AGCATGTGTGCGTCG-TTCGGCGCC-
 AAACGAACCCCGGCGCGATCCGCGCCAAGGAAAACCTT-
 AACTCAAAGAGCGCCACGTCCTCCCGTCGCCCC-GTTCGCGG-
 TGTGCGCACGGTTGGGCGGTGCTTCTTAGTGAAAAACATAAACGACTCTCGGCAACGGAT
 ATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGA
 ATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAAGCCGTTAGGCCGAGGGCA
 CGTCTGCATGGGCGTCACGCATCGCGTCGCCTCCCTTAACTTAAT-TGTTTACAAA-
 ACAAGTCAAGGAAAGGGGGAGCGGATACTGGCCTCCCGTGCCTTGCGGCGCGGCTGGCTGA
 AAACGGAGTCCCCCGCGAAGGACG-
 CACGACAAGTGGTGGTTGATAACAAGGCCCTCGCGTCCCGTCGTGCGCACGTCCTGCGATG
 GGTT-G-GCTCTC-----GTGACCCTG---ACGCGTCTA-----
 GGCTTAAGCCTAAG--
 GCGCTCCGACCGCGACCCCATGTCAGGCGGGACTACCCGCTGAGTTTAAGCATATCAATAA
 GCGGAGGA
 >GL-JJ_KY829534
 TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCAATCCTGCAATAGCAGAATGACCCGCTA
 ACACGTTAACAATTA-----GGGCGAGCAT--
 CGGGGGACCTTGCTCTCCTGTTTGCGAATCC-----CTGGTAGGTGGCCACTC-----
 -----CCGGGTGGCCACTG-GCCTGC----
 AAAATCATTCGGGCGCGGAATGCGCCAAGGA--
 TCTTAAAACTGAATTGTACGTCCGTATCCCGTTAAC-----
 GGGCTCCGGCGTCTT--TCCAAAACACAA-
 CGACTCTCGACAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATA
 CTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAA
 GCCACTAGGCTGAGGGCACGCCTGCCTGGGTGTCACGCATCGTCTTGCCAC--
 AAACCACTCACACCTGAGAA-----
 GTTGTGCCGTTTGGGGCGGAACTGGCCTCCCGTACCTTGTCTTGCGGTTGGCGGAAAAA
 CGAGTCTCCGGCGACGGATGTCGCGGCAT-CGGTGGTTG-TAA-
 AAGACCCTCTTGCTTTGTGTCGCGGAATCCTCGTCATCCTAGCGA-GCTCC-----
 AGGACCCTT---AGGCA-----GCACACACTCTGT--

GCGCTTCGACTGTGACCCAGGTCAGGCGGGATTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>GL-AM_KY829535

TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCAATCCTGCAATAGCAGAATGACCCGCTA
ACACGTTAACAATTA-----GGGCGAGCAT--
CGGGGGACCTTGGTCTCCTGTTTGCGAATCC-----CTGGTAGGTGGCCACTC-----
-----CCGGGTGGCCACTG-GCCTGC----
AAAATCATTCGGGCGCGGAATGCGCCAAGGA--
TCTTAAAACTGAATTGTACGTCCGTATCCCGTTAAC-----
GGGCTCCGGCGTCTT--TCCAAAACACAA-
CGACTCTCGACAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATA
CTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAA
GCCACTAGGCTGAGGGCACGCCTGCCTGGGTGTACGCATCGTCTTGCCAC--
AAACCACTCACACCTGAGAA-----
GTTGTGCCGTTTGGGGCGGAACTGGCCTCCCGTACCTTGTCTTGCGGTTGGCGGAAAAA
CGAGTCTCCGGCGACGGATGTGCGGGCAT-CGGTGGTTG-TAA-
AAGACCCTCTTGTCTTGTGCGCGAATCCTCGTCATCCTAGCGA-GCTCC-----
AGGACCCTT---AGGCA-----GCACACACTCTGT--
GCGCTTCGACTGTGACCCAGGTCAGGCGGGATTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>GL-GJ_KY829536

TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCAATCCTGCAATAGCAGAATGACCCGCTA
ACACGTTAACAATTA-----GGGCGAGCAT--
CGGGGGACCTTGGTCTCCTGTTTGCGAATCC-----CTGGTAGGTGGCCACTC-----
-----CCGTGTGGCCACTG-GCCTGC----
AAAATCATTCGGGCGCGGAATGCGCCAAGGA--
TCTTAAAACTGAATTGTACGTCCGTATCCCGTTAAC-----
GGGCTCCGGCGTCTT--TCCAAAACACAA-
CGACTCTCGACAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATA
CTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAA
GCCACTAGGCTGAGGGCACGCCTGCCTGGGTGTACGCATCGTCTTGCCAC--
AAACCACTCACACCTGAGAA-----
GTTGTGCCGTTTGGGGCGGAACTGGCCTCCCGTACCTTGTCTTGCGGTTGGCGGAAAAA
CGAGTCTCCGGCGACGGATGTGCGGGCAT-CGGTGGTTG-TAA-
AAGACCCTCTTGTCTTGTGCGCGAATCCTCGTCATCCTAGCGA-GCTCC-----
AGGACCCTT---AGGCA-----GCACACACTCTGT--
GCGCTTCGACTGTGACCCAGGTCAGGCGGGATTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA

>GL-JB_KY829537

TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCAATCCTGCAATAGCAGAATGACCCGCTA
ACACGTTAACAATTA-----GGGCGAGCAT--
CGGGGGACCTTGGTCTCCTGTTTGCGAATCC-----CTGGTAGGTGGCCACTC-----

-----CCGGGTGGCCACTG-GCCTGC-----
AAAATCATTCGGGCGCGGAATGCGCCAAGGA--
TCTTAAAACTGAATTGTACGTCCGTATCCCGTTAAC-----
GGGCTCCGGCGTCTT--TCCAAAACACAA-
CGACTCTCGACAACGGATATCTCGGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATA
CTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTCTTTGAACGCAAGTTGCGCCCGAA
GCCACTAGGCTGAGGGCACGCCTGCCTGGGTGTCACGCATCGTCTTGCCAC--
AAACCACTCACACCTGAGAA-----
GTTGTGCCGTTTGGGGCGGAACTGGCCTCCCGTACCTTGTCTTGCGGTTGGCGGAAAAA
CGAGTCTCCGGCGACGGATGTGCGGGCAT-CGGTGGTTG-TAA-
AAGACCCTCTTGTCTTGTGCGCGAATCCTCGTCATCCTAGCGA-GCTCC-----
AGGACCCTT---AGGCA-----GCACACACTCTGT--
GCGCTTCGACTGTGACCCAGGTCAGGCGGGATTACCCGCTGAGTTTAAGCATATCAATAA
GCGGAGGA
>Outgroup_KM051436
TCCGTAGGTGAACCTGCGGAAGGATCATTGTGCAAGCCTGCA-
CAGCAGAACGACCCGTGGACACGT----AATCAC-----
AGCCGGTGTGAGGGGGTTCGGGCGTGAGCCCGGTGCCTGCGATGCCTCGTCGACGTGCGTC
TACGATGCCCCGTTTTGAGGCGTCGTGGATGTTGCGTCGGCACCTAAACAAACCCCGGCAC
GGCATGTGCCAAGGAAAAG---AAAACATAAGAAGGGCGCGTCTCGTGTTGCCCC-
GTTGCGCG- ----TGTGCGCATGGGCCGTGGCCTCTCAAT---
AACCATAAACGACTCTCGGCAACGGATATCTCGGCTCACGCATCGATGAAGAACGTAGCAA
AATGCGATACTTGGTGTGAATTGCAGAATCCCGTGAACCATCGAGTTTTTGAACGCAAGTT
GCGCCCGAAGCCATTTCGGCCGAGGGCACGTCTGCCTGGGCGTCACGCATCGCGTCGCCCCA
--GACCATGCCTCCCCAATGGG-----
GATGCGTTCGTCTGGGGCGGAGAATGGTCTCCCGTGTCGT-
TGCGCGGTTGGCCTAAAAAGGAGTCCCCTTCGACGGACG-
CACGGCTAGTGGTGGTTGTTAA---GGCCTTCGTATCGAGCCGTGCGT-
CGTTAGCCGCAAGGGAAGCGCTCTC---TAAAGACCCA---ACGTG-----

TCGTCTCGTGACGACGCTTCGACCGCGACCCAGGTCAGGCGGGACTACCCGCTGAGTTTA
AGCATATCAATAAGCGGAGGA

	10	20	30	40	50	60	70	80	90	100	
AS-CP	TCCGTAGGTG	AACCTGCGGA	AGGATCATTG	TCGAACCTTG	CA TAGCAGA	ACAACCGCG	AACACGTGA	AAAAACATT	TGGGGGATGC	GTGCACGGGA	99
AS-JS										.A.....	99
AS-GA										.G.....	99
AS-SJ											99
AT-CC											99
AT-YS											99
AT-DG											99
AT-LJ											99
ATJ-SC											99
ATJ-BC											99
ATJ-SJ											99
ATJ-GD											99
CL-SJ				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CL-SN				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CL-GC				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CP-YA				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CP-HL				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CP-GR				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CP-JB				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
CP-WQ				.A.....	.C.....	.G.....		.C.....	---C.....	.G..TT.CCC	94
GL-JJ				.T.....	.A.....	.TG.....	.T.....	.A..C..TT	---GG..	.A..T-CG	88
GL-AM				.T.....	.A.....	.TG.....	.T.....	.A..C..TT	---GG..	.A..T-CG	88
GL-GJ				.T.....	.A.....	.TG.....	.T.....	.A..C..TT	---GG..	.A..T-CG	88
GL-JB				.T.....	.A.....	.TG.....	.T.....	.A..C..TT	---GG..	.A..T-CG	88

	110	120	130	140	150	160	170	180	190	200	
AS-CP	TAAGGCGACA	GCCCCCGTG	CATGCAGCC	CCCTTCCTTG	TGGTGCCGGA	GCAATCGAGC	GAAAGCACGT	GAGCTTCGGC	CCCCAAGAAA	CAAAACCCGG	198
AS-JS	C.....	.T.....									198
AS-GA	C.....		.A.....	.G.....			.G.....		.T.....	.A.....	197
AS-SJ	C.....										198
AT-CC	C.....		.G.....		.T.....		.G.....				197
AT-YS	C.....		.G.....		.T.....		.G.....				197
AT-DG	C.....										198
AT-LJ	C.....							.T.....			198
ATJ-SC	C.....		.G.....		.T.....		.G.....				197
ATJ-BC	C.....		.G.....								197
ATJ-SJ	C.....		.G.....		.T.....		.G.....				197
ATJ-GD			.G.....		.T.....		.G.....				197
CL-SJ	GTG.C.CCTT	...GT.GAC	TGC...GC..G	...AA..ACT	...G.A.G	-----	...TGT.C	.T..G...TT	GG.GCC...	.G.....	182
CL-SN	GTG.C.CCTT	...GT.GAC	TGC...GC..G	...AA..ACT	...G.A.G	-----	...TGT.C	.T..G...TT	GG.GCC...	.G.....	182
CL-GC	GTG.C.CCTT	...GT.GAC	TGC...GC..G	...AA..ACT	...G.A.G	-----	...TGT.C	.T..G...TT	GG.GCC...	.G.....	182
CP-YA	GTG.C.CCTT	...GT.G.C.	...C...C..G	...AA..ACT	...GAA.G	-----	...T...T..G...TT	GG.GCC...	.G.....	182	
CP-HL	GTG.C.CCTT	...GT.G.C.	...C...C..G	...AA..ACT	...GAA.G	-----	...T...T..G...TT	GG.GCC...	.G.....	182	
CP-GR	GTG.C.CCTT	...GT.G.C.	...C...C..G	...AA..ACT	...GAA.G	-----	...T...T..G...TT	GG.GCC...	.G.....	182	
CP-JB	GTG.C.CCTT	...GT.G.C.	...C...C..G	...AA..ACT	...GAA.G	-----	...T...T..G...TT	GG.GCC...	.G.....	182	
CP-WQ	GTG.C.CCTT	...GT.G.C.	...C...C..G	...AA..ACT	...GAA.G	-----	...T...T..G...TT	GG.GCC...	.G.....	182	
GL-JJ	GGG.A.CTTG	.T.T..T..T	TGC.A.T..	-----	TGGT A...G.CAC T	-----	C.GG...GC.ACT...	.TG.....	ATC.TT.G..	167	
GL-AM	GGG.A.CTTG	.T.T..T..T	TGC.A.T..	-----	TGGT A...G.CAC T	-----	C.GG...GC.ACT...	.TG.....	ATC.TT.G..	167	
GL-GJ	GGG.A.CTTG	.T.T..T..T	TGC.A.T..	-----	TGGT A...G.CAC T	-----	C.GT...GC.ACT...	.TG.....	ATC.TT.G..	167	
GL-JB	GGG.A.CTTG	.T.T..T..T	TGC.A.T..	-----	TGGT A...G.CAC T	-----	C.GG...GC.ACT...	.TG.....	ATC.TT.G..	167	

[illegible]

	410	420	430	440	450	460	470	480	490	500	
AS-CP	CCATCGAGTC	TTTGAACGCA	AGTTGCGCCC	GAAGCCTTTA	GGCCGAGGGC	ACGCTCTGCAT	GGGCGTCACG	CATCGCGTCG	CCCCCCCAG	CATCTTGAC	497
AS-JS											497
AS-GA					A						496
AS-SJ											497
AT-CC				A				A			496
AT-YS				A				A			496
AT-DG											497
AT-LJ											497
ATJ-SC				A				A			496
ATJ-BC											496
ATJ-SJ				A				A			496
ATJ-GD				A							496
CL-SJ				G					TTA	TAA	TGT
CL-SN				G					TTA	TAA	TGT
CL-GC				G					TTA	TAA	TGT
CP-YA				G					TTA	TAA	TGT
CP-HL				G					TTA	TAA	TGT
CP-GR				G					TTA	TAA	TGT
CP-JB				G					TTA	TAA	TGT
CP-WQ				G					TTA	TAA	TGT
GL-JJ				AC	T	C	T	TC	T	A	CA
GL-AM				AC	T	C	T	TC	T	A	CA
GL-GJ				AC	T	C	T	TC	T	A	CA
GL-JB				AC	T	C	T	TC	T	A	CA

	510	520	530	540	550	560	570	580	590	600	
AS-CP	CTCCAAGTGC	CCGCTTGCTT	GGTGGGAGC	GTACATTGGC	CTCCCGTGCC	TCGCAGTTCG	GTTGGCTCAA	AATGGAGTCC	CCTGTGAAGG	ACG CACGAC	596
AS-JS											596
AS-GA					T					A	595
AS-SJ									T		596
AT-CC	T			T							595
AT-YS	T			T							595
AT-DG											596
AT-LJ											596
ATJ-SC		T		T							595
ATJ-BC											595
ATJ-SJ		T		T							595
ATJ-GD		T		T							595
CL-SJ	TCA	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CL-SN	TCA	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CL-GC	TCA	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CP-YA	T.A	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CP-HL	T.A	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CP-GR	T.A	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CP-JB	T.A	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
CP-WQ	T.A	A A	AA.TCAAGGA	AAG	G.T.C		T.G.CG		C	C.C	576
GL-JJ	GAG.A		T.GTGCC	TT	G	G.A.C		A	T.TCT	G	530
GL-AM	GAG.A		T.GTGCC	TT	G	G.A.C		A	T.TCT	G	530
GL-GJ	GAG.A		T.GTGCC	TT	G	G.A.C		A	T.TCT	G	530
GL-JB	GAG.A		T.GTGCC	TT	G	G.A.C		A	T.TCT	G	530

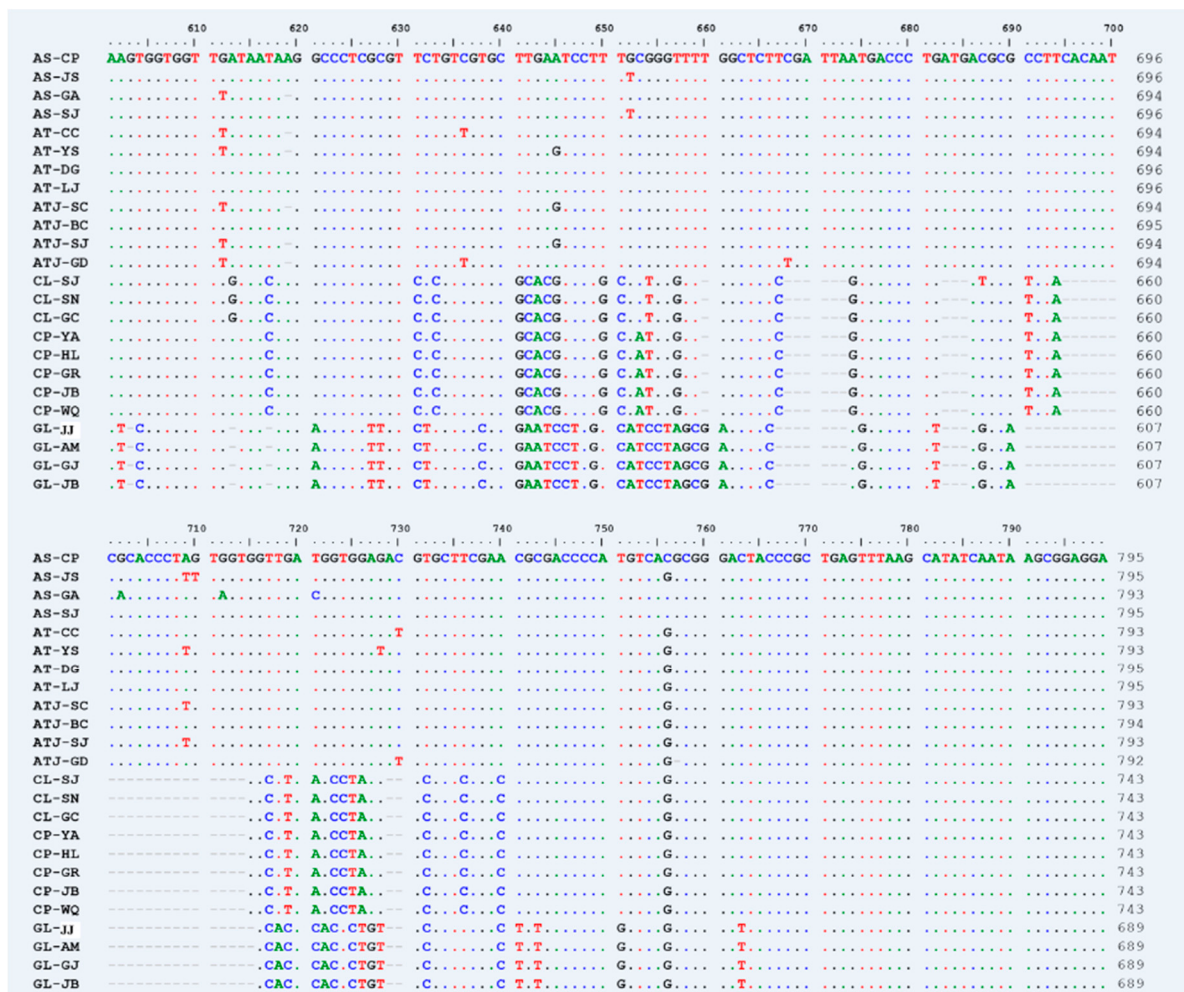


Figure S1. Comparison of nrDNA-ITS sequences of six plant species related to *Adenophorae Radix* and adulterants. Sequences were aligned using ClustalW alignment tool of BioEdit program (version 7.2.6). Dots (.) indicate sequences identical with *A. stricta* AS-CP sample, and dashes (-) represent gaps introduced to maximize alignment.

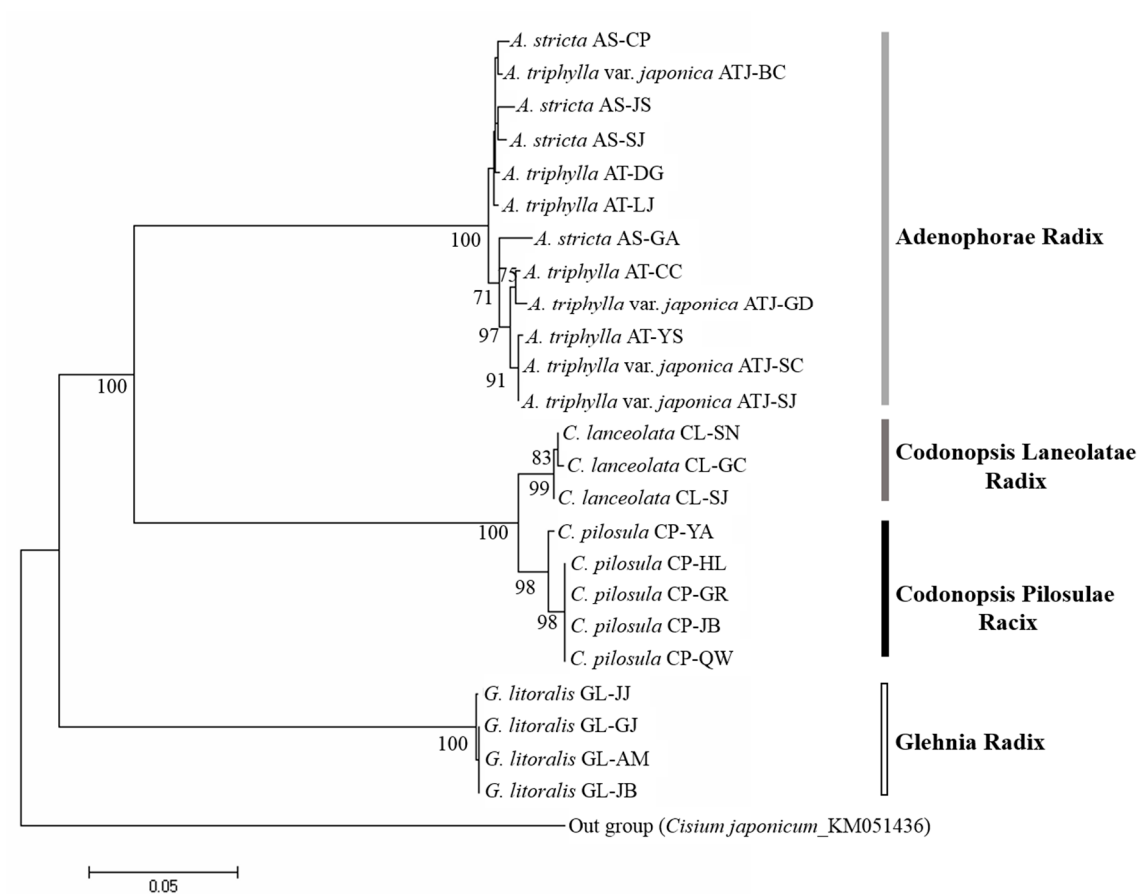


Figure S2. Neighbor-joining (NJ) phylogenetic tree with 1000 bootstrap replicates based on nrDNA-ITS sequences from six plant species related to *Adenophorae Radix* and adulterants. NJ tree was constructed using MEGA6 (Version 6.06) and bootstrap values greater than 70% are shown below the relevant branches.