

A)

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      10      20      30      40      50      60      70      80      90     100     110     120
M1 - Copy Z TCTGCATCACTAAATCCTTTTATATTTTCTCGAGGGATAGTTCGCGGTCTTCCACGTTTTTTTGGCCGTTTTCTTCTGAGATGGAGTCACATCAGATCCAGAGTATCTTCTGCTCCTA
M1 - Copy W .....A.....T.....G.....T.....CT.....A.....

      130     140     150     160     170     180     190     200     210     220     230     240
M1 - Copy Z CTGCGCCTTCCTTCACTTCCATTAAAGCTGATCTGGAATTCAGAATAAGTAGTTCAAAGCTACATGATTAACAAACATACGTAAAGTTTCACCTAGCCTGTCAAAAT--ATGTGTTCA
M1 - Copy W ...TT.C...T...T.....T.....AG...C...AGC.TT.TAT...CACG.T.T...T...T...TGGG.G.G.GC

      250     260     270     280     290     300     310     320     330     340     350     360
M1 - Copy Z GAAAAGGAAAAGAGAAACAACCCAAAACCCA--ACAACCACCCCAATAAAACAACTAAACCAACAGCAACACAAAAGTACAA-----GTCAGAACCAAGAGACACCTGTTTGCA
M1 - Copy W C.C.C.TG...ACC.CC....A...GTA..AGT...A..A.AG...G..A....-..A....A....A....A.CA..GTTAGTTG...A..T.C...T.....

      370     380
M1 - Copy Z CAGTTTCTCATCCTTGGGAG
M1 - Copy W .....

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B)

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      10      20      30      40      50      60      70      80      90     100     110     120
M2 - Copy Z TCCAGAGTATCTTCTGCTCCTACTGCGCCTTCCCTCACTTCCATTAAAGCTGATCTGGAATTCAGAATAAGTAGTTCAAAGCTACATGATTAACAAACATACGTAAAGTTTCACCTAGC
M2 - Copy W .....A.....TT.C...T.....T.....T.....AG...C...AGC.TT.TAT...CACG.T.T...T

      130     140     150     160     170     180     190     200     210     220     230     240
M2 - Copy Z CTGTCAAAAT--ATGTGTTTCAGAAAAGGAAAAGAGAAACAACCCAAAACCCA--ACAACCACCCCCAATAAAACAACTAAACCAACAGCAACACAAAAGTACAA-----GTCAGA
M2 - Copy W ...T.....TGGG.G.G.GCC.C.C.C.TG...ACC.CC....A...GTA..AGT...A..A.AG...G..A....-..A....A....A....A.CA..GTTAGTTG...A..

      250     260     270
M2 - Copy Z ACCAAGAGACACCTGTTTTGCACAGTTTCTC
M2 - Copy W .T.C...T.....

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C)

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      10      20      30      40      50      60      70      80      90     100     110     120
M3 - Copy Z TAGCAGAAATCAATCCAAGACCACCTCCCTTTAAGGATTGCAAGGT--ATGTAATTTGCAATGGGTTTATAATCAGTTGTACTGGATCTGGATGGGATGGAGTTAAATTTTCTTCATAGC
M3 - Copy W .....T...A.....C.....GAGC.....A.....

      130     140     150     160     170     180     190     200     210     220     230     240
M3 - Copy Z AGCCTGTATGATCCATGTTTTCAGATTGTGAACTGAACAGTGATAACACACTACTTGGCTGTTCAACAGCACCTTGCACAGTGTCAAGGTGTTGTGGTTGGTGCAGCCAGCAACTAAGCA
M3 - Copy W -----

      250     260     270     280     290     300     310     320     330     340     350     360
M3 - Copy Z CCACACAGCTGCTCACTCAACTCCTCTGACCTCTAGTAGGATGGGGAGGAGAAAATACAGTGAAAGGCTCGTGAGTCGAGAGAAGGACAGGGGAGGGATTACTCGCCAATTGTGATCACAG
M3 - Copy W .....G...C....

      370     380     390     400     410     420     430     440     450     460     470     480
M3 - Copy Z GCAAAACAGACTCGGGGAAAAAATCAATTTAATTTGTGTCCTGGTTTTCAGCTGGGACAGTTACCTCTTCTTTTAGCAGCTAGAAAGAGCTCTGTGTTTCGGTTTATAGTCTGAGACTTGT
M3 - Copy W .....

      490     500     510     520     530     540     550     560     570     580     590     600
M3 - Copy Z TCTGAGAAATGCTGACAGTGTAAGTGTGTTGTAAGTTGGCACTGAGGTCCTCAAGCACCTTTTCAGCTTCTGCTGTTCTTGCAGTGTGCAGGAGCAGTCTTGCCAGTGTGCAGGAGCA
M3 - Copy W -----

      610     620     630     640     650     660     670     680     690     700     710     720
M3 - Copy Z TAACAGGATAGGGGGAGCATAGCTGGGACGGAGGATCCATGACTCTCCTTATCGTTTGTACTTAGGATTGAGGGCCAATTTGGCCAATTAGTATTTCCATATCATGCAGCGTCATGCCCC
M3 - Copy W -----

      730     740     750     760     770     780     790     800     810     820     830     840
M3 - Copy Z AGTATAAAATGAAGGTCAGCTGGAAGAAAGGGCTTTTGTCTTCCCGGACTCTCACTTCAGCACTCTCAGAGTGCTCTCTCTGTTTCTCTCTCTATTTTCGGGCCTCTCACTTGTCCAG
M3 - Copy W -----

      850     860     870     880     890     900     910     920     930     940     950     960
M3 - Copy Z AATTGCAGTGTGCGGAGGTACCTGTTTTGGGATTGTTAGTCTGTGACAGGACAGGCCGTGGTCAAGGGGTGGTGAGAAATTACCTGTGCATCAGTTTGTGTATATATTTATCATTTGTG
M3 - Copy W -----

      970     980     990     1000    1010    1020    1030    1040    1050    1060    1070    1080
M3 - Copy Z CACATATATATTCATATATTAGTAGTAGTAGTGTAAATTGTTCTGTATCAACCCACGCGTCTCTTTCCCTTTTCCCTTTAGTTCTCTTACCATCCCTCGCCGTGGGGGAAGGTAA
M3 - Copy W -----

      1090    1100    1110    1120    1130    1140    1150    1160    1170    1180    1190    1200
M3 - Copy Z GCGAGCGGCTCATGTGCAGTTTAGTTCCTGGCCAGCCTAAACCATAAACAATTTTGTACCAATCAAACTCAGAGTAAGATAATAAGAAATAAACCAAAATCTTAAGAACACCTTCCCCCAG
M3 - Copy W -----

      1210    1220    1230    1240    1250    1260    1270    1280    1290    1300    1310    1320
M3 - Copy Z CCTTCCTTCTCCCCAGGTTCAACTTTTTCTCTGATTTCTCTAACTCTTCCCTCGAGTGGCACAGGGGGACAGAGGAATGGGAGTTTGGTCAGTTCATCACATGTTTCTGCTGTTTCT
M3 - Copy W -----

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1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440

M3 - Copy Z TCCTCCTCAGGGGCACCTCTTCCTCACACTCTTGCCCTGCTCCAGCATGGGATCCCTCCCATTTGGAGATAGTCTCTCCATGAACCTTACCTGACATGAATCCCTTCCCACAGGCTGCAGTTCTT

M3 - Copy W

1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560

M3 - Copy Z CACGAACCTGCTGCAGTGTGGGTCCCACCCATGGGGTGAGTCTCTTACCCAAAAGACTGCTCCAGTGCAGGTTTCCACAGAGTACGGTCACCTTCAGGCACAGCCATCTACTCCAGCAT

M3 - Copy W

1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680

M3 - Copy Z GGGATTGTCCACAGGCTGCAGGTGGATCTCTACTCCACTGTTAACTCCATGGGCTGCAGGGGACATCTTGTCTCACCACAGGCTGCAGGGGAATCTCAGCTCCAGCACTCCTCCTCCC

M3 - Copy W

1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800

M3 - Copy Z TCTCCTTCCTGACTTTAGTGTCTTCGTAGTTGTTTCTCCAACATCCCACTCCTCTCTCCTCATTGCTGTGCCAGGCTGACCAGCCTGACGAAGCTTGCTGGCCCCAGTCACAGACAGC

M3 - Copy W

1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920

M3 - Copy Z TGCCTACATGGGCACCTGGGGTGATGCCTTTGCCCTCCACTGCAGGTTTGTCCAGCAGTGGGTTTTTTTTTTCTTCCCTTAAATGTATCACATCACACAGGTGATACCACCTGTTGCTG

M3 - Copy W

1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040

M3 - Copy Z AATTGCTCAGCCTTGGCCAGAGCTGAGTTAGACTTGGAGCCAGGGAAAGCTTCTAGCAGCTTCTCATAGGAGCCACCCCTGTAAACCCCTCCCTCATTACCAAAACACTACTACACAAACCC

M3 - Copy W

2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160

M3 - Copy Z AATACTCAGGGCTGCCCTTGTTTCTTGCTGTGCTGTGCCCAACCATGAGTAGACTGGGACTTTGGCAAGGGCTGGGAGGGAACACAGCCAGTATAGCTGACCAAGTCACCAAGAAGTA

M3 - Copy W

2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280

M3 - Copy Z TTTCTGCTATGTAATGTATGCTCAGCAATAAAACTGGGTGGGCTGAGCAGGGAGTATAAAGGTGGCTGTTGCTTGGAGACTTGCTGGTGAGTTAATATGTGACTCTCTTTCAGTCACT

M3 - Copy W

2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400

M3 - Copy Z TGTGGGTTTTTTTTTGGTTGAGGTTTGTCTTTGGTTGTTTTTTTCCCTTACCAGTGAATTCCTTATTTTGAACCCACAGTTTTCTCTACTTTCACCCCTTTCAGTTCTCTCCCTTGTCTC

M3 - Copy W

2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520

M3 - Copy Z CTGCTAGTGTGGTAGTGAGTAAGGAACCTAGTGGCAGCTTAGCGGCTGGCCAGGTTCAAACCAACCATCAGTTGTGATATTAAAAATCTGTATGAATCCAGAGATAAGGTAGATATAA

M3 - Copy W

2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640

M3 - Copy Z TGAATAATTTTGAAGGTTTTTTCAGAAATAATAATGATA-TATAGTAATATATGGAATAATCACTACTAAG-TAACTTTTGTAGATACCAGTCCCTGTGT-TTTTACTGAT

M3 - Copy W

2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760

M3 - Copy Z GTTCAAGAATAGGCTTGCTTAGTTTCTAGTTTATTTTAAAGTAAGACTT-TGAGTGGGTAAATATCACCTCCCATTGTGAAATTTAGAGTAGCAATCAAACTAAATTTTCAGCTTCAAAAT

M3 - Copy W

2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880

M3 - Copy Z TGCTTGATCTTTT-TGGCCTAGTTTTATCAATGGAATAAGACTAGACTTGGTGACCCAGTAGATCCCTACT-TGCTTTTTTCTAGAGGAAGACATTTTCGTAACTTCAGTCAG

M3 - Copy W

2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000

M3 - Copy Z TAGTAGGACTGATGAGTGAATTTGCTTTTACAGGTTCTAAACACAGAGGCCAAGGTTGTGTGCACATAAAGAAGCAACCATCTATATTTGGAGGACACGAAAGTTTAGAGTTAAGAGATTAT

M3 - Copy W

3010

M3 - Copy Z CAGTTAAATGGACTG

M3 - Copy W

D)

10 20 30 40 50 60 70 80 90 100 110 120

M4 - Copy Z GCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTCCTAATTTTCTCACAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGTCAGTTTCCCTTTCAGGTAAAGAA

M4 - Copy W

130 140 150 160 170 180 190 200 210 220 230 240

M4 - Copy Z CTTGGTGGTAGTAGCAAGAACTTTGATCTTGAAATAAGGAAGTCGTTTTCTTAACTCAACTGTTTTGTGTTTATGTGATCTTATGCTTTTGCTTAAGAAAAGATACAGAA

M4 - Copy W

250 260 270 280 290 300 310 320 330 340 350 360

M4 - Copy Z AAGTGTTCTTTTTCTAG-AAAGACTGGCAATTGCTATGTACCTAATAGTATTTTG-AATTAACCTGATAAATTAATAACTATGTAAAGTGTGCATTAATTTTTATTTCCCTTCACAT

M4 - Copy W

370 380 390 400 410 420 430 440 450 460 470 480

M4 - Copy Z AACAGTTTTGGCAGTTAGGAATTCAGTAGCTCTGATTTTGAATATAGTATAAGAATTACTTTTTAACGTAGTTTTCTCAATCTCTTAGAGACTTGTATGGATCAATAAAGGGGAATTG

M4 - Copy W

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          490      500
M4 - Copy Z   AGGAAACAAGCCTGGATCATTTTAAT
M4 - Copy W   .....C.....

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E)

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          10      20      30      40      50      60      70      80      90     100     110     120
M5 - Copy Z   GTCCTAATTTCTCACAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGTCAGTTTCCCTTCAGGTAAGAACTCTGGTGGTAGTAGCCAGAACTTTGATCTTGA
M5 - Copy W   ..A..G.....T.....A.....A.....T.....T.....C.....A.....G..C.....G.....T.....

          130     140     150     160     170     180     190     200     210     220     230     240
M5 - Copy Z   AAAAAGGAAAGTCGTTTCTTATAACCTCAACTGTTTGTGTTTATGTGATCTTTACTGCTTTCCTTAAGAAAAGATACAAGAAAAGGTTCCTTTTCTTCTAG-AAAGACTGGCAATT
M5 - Copy W   .....C.AC.....A.CT.....A.....TC.....GTAG.....TT.T.....GTT.AA.T..A.G.A.AG.A.....A.G...

          250     260     270     280     290     300     310     320     330     340     350     360
M5 - Copy Z   GCTATGTACCTAATAGTATTTTG-AAATAAAGCTGATAAAATAAAAACTATGTAAAGTGTTCATTAAATTTTTTATTTCCCTTCACAT-AAAGTTTGGCAGTTAGGAATTCAAGTAGCTC
M5 - Copy W   A.....A.G.TA.....G.....A.....G.....C..G.....G.....GA.G.....A.....C.C.C..C.....C.CCA..TT.....A..A..GA.....T.....

          370     380     390     400     410     420     430     440     450     460
M5 - Copy Z   TGATTGTGAATATAGTATAAGAAATTAATTTTAACTGTTAGTTTCAATCTCTTTAGAGACTTGATGGATCAATAAAAGGGGAATTGAGGAAACAAGCACCTGGATCAT
M5 - Copy W   .....A.....G..G..C.....T.A..A.....C.....C.....C.....

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F)

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          10      20      30      40      50      60      70      80      90     100     110     120
M7 - Copy Z   TTGTGAGAGTTGCTAGAGATACAGCTTCTTACTGATACAACTATCCTTCAGGTAAGTTTATCAGAAGAATTTCGTCCAAGAATGTTGGTTTTCTTTCCAGAGAGAATATAAAGTA
M7 - Copy W   .....T.....G.....TG.....T.....C.G.....G

          130     140     150     160     170     180     190     200     210     220     230     240
M7 - Copy Z   TCATCATCGCAGTGACATGAAGCATGAAGTCAGTACAACTTACGAATTATTAACATCGAAGTAAGTAGTTTGTGTGTAGTAGGTAACTCTGCAGGAGAAGAGCATTGATGTTCAAATC
M7 - Copy W   .G..TG..T..A.....AT.....TT.....G.....G..A..A.....T.....A..G.....A.....C...

          250     260     270     280     290     300     310     320     330     340     350     360
M7 - Copy Z   TTTAATGGCTCTCTCTGTATACCTTAAGAAAGCTTTAACCTGATTGCATTCAAATGTAGTCAGAGAATCAATTTAGATTGGAAGAGCCCTTAAAGTCGTCAGTCCAACCTAAACCTAAC
M7 - Copy W   .....T..A.G..C.....C..A.....T.....

          370     380     390     400     410     420     430     440     450     460     470     480
M7 - Copy Z   GCTGCCAAGTCCACCCTAAACCATTTCTGCAAGTGCTACACATCTTTTAAAGTACTTCCAGGGATGGTAACCAAGCACTTCCCTGGGCAGCCTGTTCCAGTGCTTGACAAACCTTTTG
M7 - Copy W   .....

          490     500     510     520     530     540     550     560     570     580     590     600
M7 - Copy Z   GTGAAGAAATTTTTCACAAATATCCGATCTAAACCTTCCATGTCAAGTTGAGGCGTTTCTTCTTGTCTCTATCGCTTGTATCTGGGAAATGAGATTGACACCCACCTCACTACAGCCT
M7 - Copy W   .....

          610     620     630     640     650     660     670     680     690     700     710     720
M7 - Copy Z   CCTTTCAGGTAGCTGCAGAGAGCAGTAAGGTCTCCCTCAGCCTCTTTTCTCTAGCCTAAACAATGCCCGTTTCTCAGCCACTCCTCAGGACTTGTTCCTCAATATCCTTCAATAA
M7 - Copy W   .....T.....

          730     740     750     760     770     780     790     800     810     820     830     840
M7 - Copy Z   CTTTATTGCGCATAATATAAAGTAATGCATCTTGTGAATACCTTACCTGCTGAATGAATA-ACCTATGAAATCGCATAAATATAAGTTCATTAGTCAAAATATACTTAGAATAAT
M7 - Copy W   A.....AA.....G.....A..G.....C.....ACCT...G.....GT.....C.....TG.....C.C.....C

          850     860     870     880     890     900     910     920
M7 - Copy Z   TTATTTCATTGATAGGTATCCTCTATGGGAATAACACCTTCTTTGTAGAAAATGTCAGTGAACATACAGTTATGTGCCATCAAGTT
M7 - Copy W   ..C.....G.....A.....C.....C.....A..

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Figure S1. Two-copy (Z and X-specific) sequence comparison of six markers (M1-M5 and M7) tested in this study. The alignments are shown for *Tauraco erythrolophus*. Dots indicate residues identical in both copies. The sequences were aligned with MUSCLE [37] in MEGA [36].