

SUPPLEMENTARY MATERIAL

Tab. S1 – Calculated mean genetic distance (d) values (below the diagonal) between species with the standard errors (above the diagonal) employing CYTB data.

| | FLA | PON | URA | WIT | SYL | ALP | MYS | PEN | GUR | AGR | CHEJ | CHEV | LAT | DRA |
|------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| FLA | | 0,0054 | 0,0118 | 0,0160 | 0,0138 | 0,0133 | 0,0174 | 0,0159 | 0,0188 | 0,0180 | 0,0181 | 0,0173 | 0,0182 | 0,0171 |
| PON | 0,0268 | | 0,0131 | 0,0166 | 0,0147 | 0,0150 | 0,0180 | 0,0160 | 0,0194 | 0,0188 | 0,0189 | 0,0185 | 0,0187 | 0,0174 |
| URA | 0,0871 | 0,0894 | | 0,0151 | 0,0147 | 0,0129 | 0,0163 | 0,0159 | 0,0176 | 0,0168 | 0,0167 | 0,0175 | 0,0174 | 0,0166 |
| WIT | 0,1152 | 0,1088 | 0,1113 | | 0,0165 | 0,0150 | 0,0187 | 0,0188 | 0,0181 | 0,0177 | 0,0177 | 0,0185 | 0,0182 | 0,0172 |
| SYL | 0,0976 | 0,0982 | 0,1123 | 0,1195 | | 0,0162 | 0,0186 | 0,0170 | 0,0188 | 0,0179 | 0,0180 | 0,0177 | 0,0199 | 0,0179 |
| ALP | 0,0810 | 0,0838 | 0,0851 | 0,0886 | 0,1085 | | 0,0176 | 0,0187 | 0,0180 | 0,0176 | 0,0177 | 0,0175 | 0,0182 | 0,0171 |
| MYS | 0,1350 | 0,1339 | 0,1258 | 0,1436 | 0,1530 | 0,1230 | | 0,0190 | 0,0174 | 0,0182 | 0,0183 | 0,0195 | 0,0172 | 0,0172 |
| PEN | 0,1204 | 0,1124 | 0,1266 | 0,1556 | 0,1266 | 0,1347 | 0,1519 | | 0,0188 | 0,0179 | 0,0180 | 0,0173 | 0,0184 | 0,0153 |
| GUR | 0,1601 | 0,1655 | 0,1534 | 0,1461 | 0,1619 | 0,1340 | 0,1369 | 0,1563 | | 0,0183 | 0,0184 | 0,0184 | 0,0192 | 0,0180 |
| AGR | 0,1491 | 0,1519 | 0,1356 | 0,1325 | 0,1392 | 0,1206 | 0,1467 | 0,1345 | 0,1486 | | 0,0051 | 0,0145 | 0,0193 | 0,0173 |
| CHEJ | 0,1479 | 0,1503 | 0,1340 | 0,1311 | 0,1386 | 0,1203 | 0,1439 | 0,1362 | 0,1470 | 0,0173 | | 0,0149 | 0,0191 | 0,0175 |
| CHEV | 0,1412 | 0,1473 | 0,1433 | 0,1489 | 0,1359 | 0,1297 | 0,1629 | 0,1354 | 0,1506 | 0,0808 | 0,0857 | | 0,0193 | 0,0172 |
| LAT | 0,1563 | 0,1506 | 0,1511 | 0,1470 | 0,1823 | 0,1434 | 0,1271 | 0,1416 | 0,1614 | 0,1647 | 0,1599 | 0,1707 | | 0,0141 |
| DRA | 0,1534 | 0,1507 | 0,1429 | 0,1506 | 0,1635 | 0,1427 | 0,1392 | 0,1182 | 0,1542 | 0,1518 | 0,1509 | 0,1511 | 0,1066 | |

*: FLA: *A. flavicollis*, PON: *A. ponticus*, URA: *A. uralensis*, WIT: *A. witherbyi*, SYL: *A. sylvaticus*, ALP: *A. alpicola*, MYS: *A. mystacinus*, PEN: *A. peninsulae*, GUR: *A. gurkha*, AGR: *A. agrarius*, CHEJ: *A. chejuensis*, CHEV: *A. chevrieri*, LAT: *A. latronum*, DRA: *A. draco*

Tab. S2 – Calculated mean genetic distance (d) values (below the diagonal) between species with the standard errors (above the diagonal) employing COI data.

| | FLA | PON | URA | WIT | SYL | ALP | MYS | PEN | AGR | CHEJ | CHEV | LAT | DRA |
|-------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| FLA | | 0,0101 | 0,0106 | 0,0122 | 0,0141 | 0,0103 | 0,0147 | 0,0150 | 0,0162 | 0,0162 | 0,0164 | 0,0162 | 0,0167 |
| PON | 0,0586 | | 0,0117 | 0,0124 | 0,0133 | 0,0107 | 0,0152 | 0,0155 | 0,0164 | 0,0164 | 0,0163 | 0,0159 | 0,0163 |
| URA | 0,0788 | 0,0922 | | 0,0114 | 0,0128 | 0,0109 | 0,0135 | 0,0146 | 0,0163 | 0,0164 | 0,0165 | 0,0153 | 0,0156 |
| WIT | 0,0804 | 0,0895 | 0,0840 | | 0,0129 | 0,0130 | 0,0130 | 0,0149 | 0,0155 | 0,0155 | 0,0159 | 0,0152 | 0,0159 |
| SYL | 0,1155 | 0,1030 | 0,1069 | 0,0901 | | 0,0126 | 0,0151 | 0,0152 | 0,0166 | 0,0168 | 0,0168 | 0,0163 | 0,0163 |
| ALP | 0,0626 | 0,0635 | 0,0759 | 0,0904 | 0,0851 | | 0,0150 | 0,0156 | 0,0166 | 0,0161 | 0,0162 | 0,0163 | 0,0164 |
| MYS | 0,1186 | 0,1325 | 0,1202 | 0,0976 | 0,1318 | 0,1246 | | 0,0154 | 0,0151 | 0,0154 | 0,0164 | 0,0151 | 0,0151 |
| PEN | 0,1322 | 0,1370 | 0,1401 | 0,1317 | 0,1481 | 0,1460 | 0,1419 | | 0,0143 | 0,0149 | 0,0142 | 0,0154 | 0,0149 |
| AGR | 0,1528 | 0,1661 | 0,1618 | 0,1378 | 0,1640 | 0,1605 | 0,1389 | 0,1360 | | 0,0054 | 0,0100 | 0,0144 | 0,0152 |
| CHEJ | 0,1502 | 0,1655 | 0,1622 | 0,1365 | 0,1684 | 0,1574 | 0,1393 | 0,1352 | 0,0201 | | 0,0105 | 0,0145 | 0,0154 |
| CHEV | 0,1528 | 0,1560 | 0,1530 | 0,1404 | 0,1679 | 0,1492 | 0,1583 | 0,1265 | 0,0649 | 0,0640 | | 0,0150 | 0,0155 |
| LAT | 0,1463 | 0,1563 | 0,1580 | 0,1295 | 0,1537 | 0,1581 | 0,1317 | 0,1460 | 0,1332 | 0,1358 | 0,1342 | | 0,0133 |
| DRA | 0,1593 | 0,1570 | 0,1563 | 0,1475 | 0,1600 | 0,1595 | 0,1265 | 0,1388 | 0,1358 | 0,1347 | 0,1368 | 0,1137 | |

*: FLA: *A. flavicollis*, PON: *A. ponticus*, URA: *A. uralensis*, WIT: *A. witherbyi*, SYL: *A. sylvaticus*, ALP: *A. alpicola*, MYS: *A. mystacinus*, PEN: *A. peninsulae*, AGR: *A. agrarius*, CHEJ: *A. chejuensis*, CHEV: *A. chevrieri*, LAT: *A. latronum*, DRA: *A. draco*

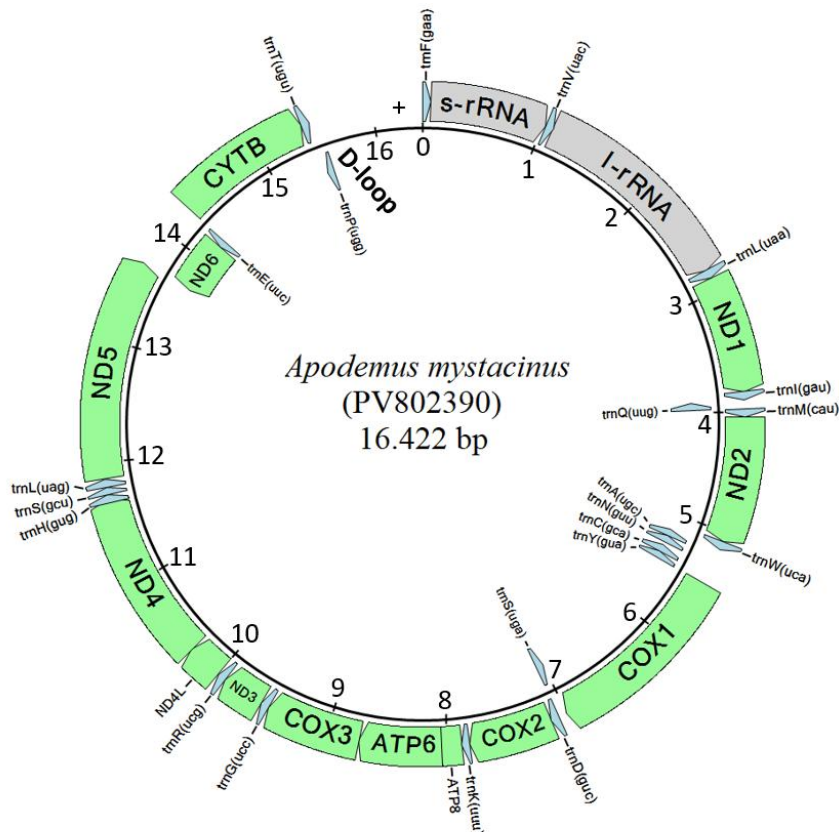
Tab. S3 – Calculated mean genetic distance (d) values (below the diagonal) between subgenera with the standard errors (above the diagonal) employing CYTB data.

| | <i>Sylvaemus</i> | <i>Karstoymys</i> | <i>Apodemus</i> | <i>Alsoymys</i> | <i>M. musculus</i> |
|--------------------|------------------|-------------------|-----------------|-----------------|--------------------|
| <i>Sylvaemus</i> | | 0.016 | 0.015 | 0.015 | 0.016 |
| <i>Karstoymys</i> | 0.136 | | 0.016 | 0.015 | 0.018 |
| <i>Apodemus</i> | 0.140 | 0.151 | | 0.015 | 0.017 |
| <i>Alsoymys</i> | 0.153 | 0.133 | 0.152 | | 0.016 |
| <i>M. musculus</i> | 0.141 | 0.130 | 0.150 | 0.150 | |

Tab. S4 – Calculated mean genetic distance (d) values (below the diagonal) between subgenera with the standard errors (above the diagonal) employing COI data.

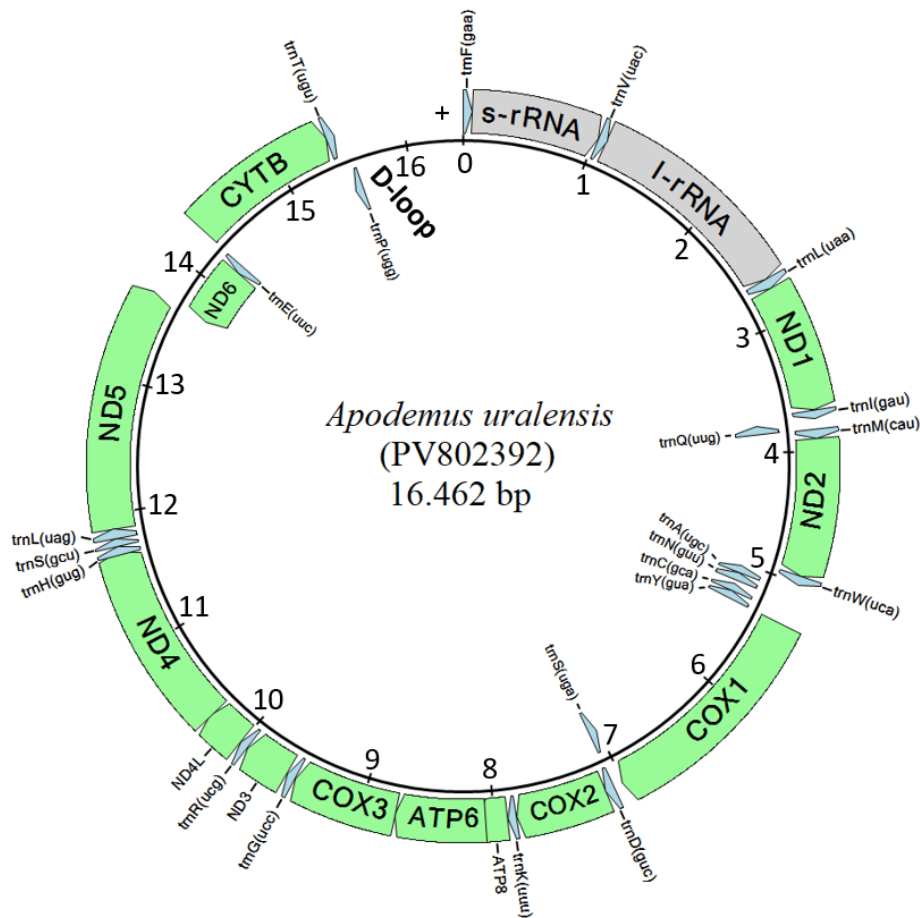
| | <i>Sylvaemus</i> | <i>Karstoymys</i> | <i>Apodemus</i> | <i>Alsoymys</i> | <i>M. musculus</i> |
|--------------------|------------------|-------------------|-----------------|-----------------|--------------------|
| <i>Sylvaemus</i> | | 0.013 | 0.014 | 0.013 | 0.014 |
| <i>Karstoymys</i> | 0.125 | | 0.014 | 0.013 | 0.016 |
| <i>Apodemus</i> | 0.156 | 0.142 | | 0.012 | 0.015 |
| <i>Alsoymys</i> | 0.154 | 0.129 | 0.136 | | 0.014 |
| <i>M. musculus</i> | 0.144 | 0.148 | 0.145 | 0.142 | |

FIGURE S1



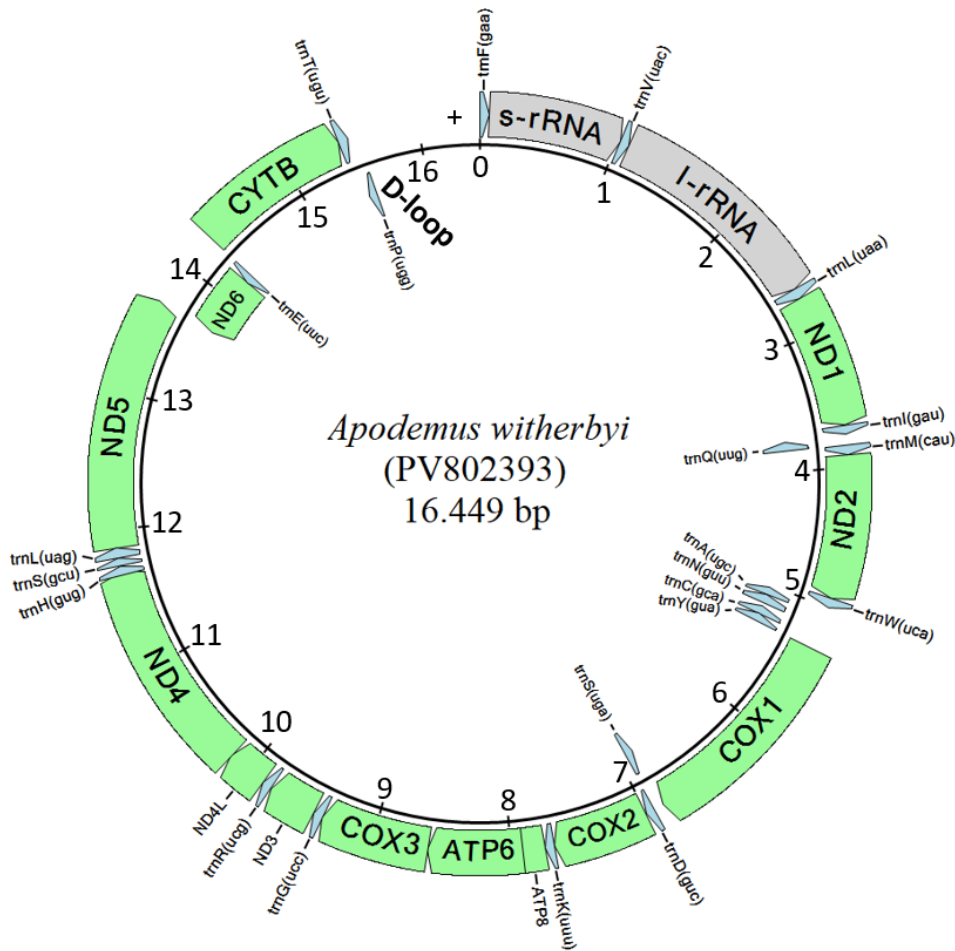
| Start | End | Length(bp) | Direction | Type | Gene_name | Gene_product | Total_freq_occurred |
|-------|-------|------------|-----------|------|-----------|----------------------------------|---------------------|
| 1 | 70 | 70 | + | tRNA | trnF(gaa) | tRNA-Phe | 1 |
| 70 | 1024 | 955 | + | rRNA | s-rRNA | 12S ribosomal RNA | 1 |
| 1024 | 1092 | 69 | + | tRNA | trnV(uac) | tRNA-Val | 1 |
| 1090 | 2805 | 1716 | + | rRNA | l-rRNA | 16S ribosomal RNA | 1 |
| 2803 | 2879 | 77 | + | tRNA | trnL(uaa) | tRNA-Leu | 2 |
| 2879 | 3836 | 958 | + | CDS | ND1 | NADH dehydrogenase subunit 1 | 1 |
| 3834 | 3903 | 70 | + | tRNA | trnI(gau) | tRNA-Ile | 1 |
| 3900 | 3971 | 72 | - | tRNA | trnQ(uug) | tRNA-Gln | 1 |
| 3976 | 4045 | 70 | + | tRNA | trnM(cau) | tRNA-Met | 1 |
| 4045 | 5083 | 1039 | + | CDS | ND2 | NADH dehydrogenase subunit 2 | 1 |
| 5081 | 5150 | 70 | + | tRNA | trnW(uca) | tRNA-Trp | 1 |
| 5151 | 5220 | 70 | - | tRNA | trnA(ugc) | tRNA-Ala | 1 |
| 5221 | 5292 | 72 | - | tRNA | trnN(guu) | tRNA-Asn | 1 |
| 5323 | 5389 | 67 | - | tRNA | trnC(gca) | tRNA-Cys | 1 |
| 5389 | 5456 | 68 | - | tRNA | trnY(gua) | tRNA-Tyr | 1 |
| 5457 | 7002 | 1546 | + | CDS | COX1 | cytochrome c oxidase subunit I | 1 |
| 6999 | 7068 | 70 | - | tRNA | trnS(uga) | tRNA-Ser | 2 |
| 7071 | 7139 | 69 | + | tRNA | trnD(guc) | tRNA-Asp | 1 |
| 7140 | 7824 | 685 | + | CDS | COX2 | cytochrome c oxidase subunit II | 1 |
| 7827 | 7891 | 65 | + | tRNA | trnK(uuu) | tRNA-Lys | 1 |
| 7892 | 8096 | 205 | + | CDS | ATP8 | ATP synthase F0 subunit 8 | 1 |
| 8053 | 8734 | 682 | + | CDS | ATP6 | ATP synthase F0 subunit 6 | 1 |
| 8733 | 9518 | 786 | + | CDS | COX3 | cytochrome c oxidase subunit III | 1 |
| 9517 | 9585 | 69 | + | tRNA | trnG(ucc) | tRNA-Gly | 1 |
| 9585 | 9933 | 349 | + | CDS | ND3 | NADH dehydrogenase subunit 3 | 1 |
| 9934 | 10002 | 69 | + | tRNA | trnR(ucg) | tRNA-Arg | 1 |
| 10005 | 10302 | 298 | + | CDS | ND4L | NADH dehydrogenase subunit 4L | 1 |
| 10295 | 11699 | 1405 | + | CDS | ND4 | NADH dehydrogenase subunit 4 | 1 |
| 11673 | 11740 | 68 | + | tRNA | trnH(gug) | tRNA-His | 1 |
| 11740 | 11799 | 60 | + | tRNA | trnS(gcu) | tRNA-Ser | 2 |
| 11798 | 11869 | 72 | + | tRNA | trnL(uag) | tRNA-Leu | 2 |
| 11869 | 13690 | 1822 | + | CDS | ND5 | NADH dehydrogenase subunit 5 | 1 |
| 13676 | 14195 | 520 | - | CDS | ND6 | NADH dehydrogenase subunit 6 | 1 |
| 14195 | 14264 | 70 | - | tRNA | trnE(uuc) | tRNA-Glu | 1 |
| 14267 | 15411 | 1145 | + | CDS | CYTB | cytochrome b | 1 |
| 15411 | 15478 | 68 | + | tRNA | trnT(ugu) | tRNA-Thr | 1 |
| 15478 | 15544 | 67 | - | tRNA | trnP(ugg) | tRNA-Pro | 1 |
| 15545 | 16422 | 878 | - | NCR | D-loop | - | 1 |

FIGURE S2



| Start | End | Length(bp) | Direction | Type | Gene_name | Gene_product | Total_freq_occurred |
|-------|-------|------------|-----------|------|-----------|----------------------------------|---------------------|
| 1 | 69 | 69 | + | tRNA | trnF(gaa) | tRNA-Phe | 1 |
| 69 | 1026 | 958 | + | rRNA | s-rRNA | 12S ribosomal RNA | 1 |
| 1026 | 1094 | 69 | + | tRNA | trnV(uac) | tRNA-Val | 1 |
| 1092 | 2667 | 1576 | + | rRNA | l-rRNA | 16S ribosomal RNA | 1 |
| 2665 | 2740 | 76 | + | tRNA | trnL(uaa) | tRNA-Leu | 2 |
| 2740 | 3697 | 958 | + | CDS | ND1 | NADH dehydrogenase subunit 1 | 1 |
| 3695 | 3764 | 70 | + | tRNA | trnI(gau) | tRNA-Ile | 1 |
| 3761 | 3832 | 72 | - | tRNA | trnQ(uug) | tRNA-Gln | 1 |
| 3839 | 3908 | 70 | + | tRNA | trnM(cau) | tRNA-Met | 1 |
| 3908 | 4946 | 1039 | + | CDS | ND2 | NADH dehydrogenase subunit 2 | 1 |
| 4944 | 5013 | 70 | + | tRNA | trnW(uca) | tRNA-Trp | 1 |
| 5014 | 5083 | 70 | - | tRNA | trnA(ugc) | tRNA-Ala | 1 |
| 5084 | 5155 | 72 | - | tRNA | trnN(guu) | tRNA-Asn | 1 |
| 5187 | 5256 | 70 | - | tRNA | trnC(gca) | tRNA-Cys | 1 |
| 5256 | 5324 | 69 | - | tRNA | trnY(gua) | tRNA-Tyr | 1 |
| 5325 | 7011 | 1687 | + | CDS | COX1 | cytochrome c oxidase subunit I | 1 |
| 7008 | 7077 | 70 | - | tRNA | trnS(uga) | tRNA-Ser | 2 |
| 7080 | 7148 | 69 | + | tRNA | trnD(guc) | tRNA-Asp | 1 |
| 7149 | 7833 | 685 | + | CDS | COX2 | cytochrome c oxidase subunit II | 1 |
| 7836 | 7900 | 65 | + | tRNA | trnK(uuu) | tRNA-Lys | 1 |
| 7901 | 8105 | 205 | + | CDS | ATP8 | ATP synthase F0 subunit 8 | 1 |
| 8062 | 8743 | 682 | + | CDS | ATP6 | ATP synthase F0 subunit 6 | 1 |
| 8742 | 9527 | 786 | + | CDS | COX3 | cytochrome c oxidase subunit III | 1 |
| 9526 | 9595 | 70 | + | tRNA | trnG(ucc) | tRNA-Gly | 1 |
| 9595 | 9943 | 349 | + | CDS | ND3 | NADH dehydrogenase subunit 3 | 1 |
| 9944 | 10012 | 69 | + | tRNA | trnR(ucg) | tRNA-Arg | 1 |
| 10013 | 10310 | 298 | + | CDS | ND4L | NADH dehydrogenase subunit 4L | 1 |
| 10303 | 11707 | 1405 | + | CDS | ND4 | NADH dehydrogenase subunit 4 | 1 |
| 11681 | 11748 | 68 | + | tRNA | trnH(gug) | tRNA-His | 1 |
| 11748 | 11807 | 60 | + | tRNA | trnS(gcu) | tRNA-Ser | 2 |
| 11806 | 11877 | 72 | + | tRNA | trnL(uag) | tRNA-Leu | 2 |
| 11877 | 13701 | 1825 | + | CDS | ND5 | NADH dehydrogenase subunit 5 | 1 |
| 13687 | 14206 | 520 | - | CDS | ND6 | NADH dehydrogenase subunit 6 | 1 |
| 14206 | 14275 | 70 | - | tRNA | trnE(uuc) | tRNA-Glu | 1 |
| 14278 | 15422 | 1145 | + | CDS | CYTB | cytochrome b | 1 |
| 15422 | 15489 | 68 | + | tRNA | trnT(ugu) | tRNA-Thr | 1 |
| 15489 | 15556 | 68 | - | tRNA | trnP(ugg) | tRNA-Pro | 1 |
| 15557 | 16462 | 906 | - | NCR | D-loop | - | 1 |

FIGURE S3



| Start | End | Length(bp) | Direction | Type | Gene_name | Gene_product | Total_freq_occurred |
|-------|-------|------------|-----------|------|-----------|----------------------------------|---------------------|
| 1 | 69 | 69 | + | tRNA | trnF(gaa) | tRNA-Phe | 1 |
| 69 | 1024 | 956 | + | rRNA | s-rRNA | 12S ribosomal RNA | 1 |
| 1024 | 1092 | 69 | + | tRNA | trnV(uac) | tRNA-Val | 1 |
| 1090 | 2664 | 1575 | + | rRNA | l-rRNA | 16S ribosomal RNA | 1 |
| 2662 | 2737 | 76 | + | tRNA | trnL(uaa) | tRNA-Leu | 2 |
| 2737 | 3694 | 958 | + | CDS | ND1 | NADH dehydrogenase subunit 1 | 1 |
| 3692 | 3761 | 70 | + | tRNA | trnI(gau) | tRNA-Ile | 1 |
| 3758 | 3829 | 72 | - | tRNA | trnQ(uug) | tRNA-Gln | 1 |
| 3836 | 3905 | 70 | + | tRNA | trnM(cau) | tRNA-Met | 1 |
| 3905 | 4943 | 1039 | + | CDS | ND2 | NADH dehydrogenase subunit 2 | 1 |
| 4941 | 5010 | 70 | + | tRNA | trnW(uca) | tRNA-Trp | 1 |
| 5011 | 5080 | 70 | - | tRNA | trnA(ugc) | tRNA-Ala | 1 |
| 5081 | 5152 | 72 | - | tRNA | trnN(guu) | tRNA-Asn | 1 |
| 5184 | 5253 | 70 | - | tRNA | trnC(gca) | tRNA-Cys | 1 |
| 5253 | 5321 | 69 | - | tRNA | trnY(gua) | tRNA-Tyr | 1 |
| 5322 | 6867 | 1546 | + | CDS | COX1 | cytochrome c oxidase subunit I | 1 |
| 6864 | 6933 | 70 | - | tRNA | trnS(uga) | tRNA-Ser | 2 |
| 6936 | 7004 | 69 | + | tRNA | trnD(guc) | tRNA-Asp | 1 |
| 7005 | 7689 | 685 | + | CDS | COX2 | cytochrome c oxidase subunit II | 1 |
| 7692 | 7757 | 66 | + | tRNA | trnK(uuu) | tRNA-Lys | 1 |
| 7758 | 7962 | 205 | + | CDS | ATP8 | ATP synthase F0 subunit 8 | 1 |
| 7919 | 8600 | 682 | + | CDS | ATP6 | ATP synthase F0 subunit 6 | 1 |
| 8599 | 9384 | 786 | + | CDS | COX3 | cytochrome c oxidase subunit III | 1 |
| 9383 | 9452 | 70 | + | tRNA | trnG(ucc) | tRNA-Gly | 1 |
| 9452 | 9800 | 349 | + | CDS | ND3 | NADH dehydrogenase subunit 3 | 1 |
| 9801 | 9870 | 70 | + | tRNA | trnR(ucg) | tRNA-Arg | 1 |
| 9871 | 10168 | 298 | + | CDS | ND4L | NADH dehydrogenase subunit 4L | 1 |
| 10161 | 11706 | 1546 | + | CDS | ND4 | NADH dehydrogenase subunit 4 | 1 |
| 11680 | 11747 | 68 | + | tRNA | trnH(gug) | tRNA-His | 1 |
| 11747 | 11806 | 60 | + | tRNA | trnS(gcu) | tRNA-Ser | 2 |
| 11805 | 11876 | 72 | + | tRNA | trnL(uag) | tRNA-Leu | 2 |
| 11876 | 13697 | 1822 | + | CDS | ND5 | NADH dehydrogenase subunit 5 | 1 |
| 13683 | 14202 | 520 | - | CDS | ND6 | NADH dehydrogenase subunit 6 | 1 |
| 14202 | 14271 | 70 | - | tRNA | trnE(uuc) | tRNA-Glu | 1 |
| 14274 | 15418 | 1145 | + | CDS | CYTB | cytochrome b | 1 |
| 15418 | 15486 | 69 | + | tRNA | trnT(ugu) | tRNA-Thr | 1 |
| 15486 | 15553 | 68 | - | tRNA | trnP(ugg) | tRNA-Pro | 1 |
| 15554 | 16449 | 896 | - | NCR | D-loop | - | 1 |

FIGURE S5

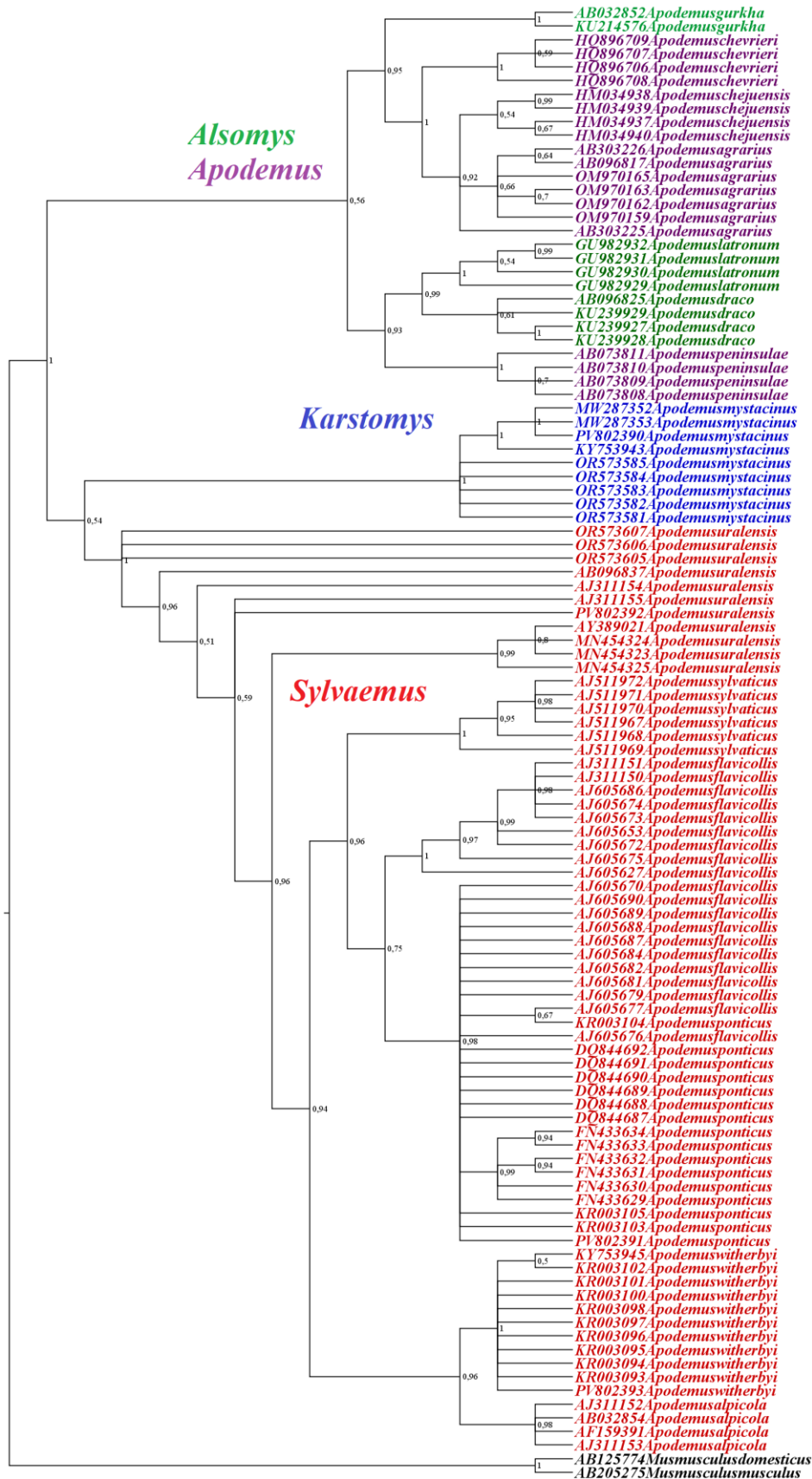


FIGURE S6

