

Table S1. Organization of the *Scarites subterraneus* mitogenome. A. *Scarites subterraneus* ssp. *nebraskensis*. B. *Scarites subterraneus* ssp. *arkansensis*. Mitogenomes were annotated using MitoS2.

| <i>Scarites. sp nebraskensis</i> | | | | | <i>Scarites sp. arkansensis</i> | | | | |
|---|--------------|-------------|---------------|---------------|--|--------------|-------------|---------------|---------------|
| Name | Start | Stop | Strand | Length | Name | Start | Stop | Strand | Length |
| OH_0 | 550 | 764 | + | 215 | nad1 | 10 | 951 | - | 942 |
| trnI(gat) | 1371 | 1436 | + | 66 | trnL1(tag) | 961 | 1025 | - | 65 |
| trnQ(ttg) | 1439 | 1507 | - | 69 | rrnL | 1003 | 2326 | - | 1324 |
| trnM(cat) | 1517 | 1585 | + | 69 | trnV(tac) | 2351 | 2422 | - | 72 |
| nad2 | 1607 | 2614 | + | 1008 | rrnS | 2423 | 3211 | - | 789 |
| trnW(tca) | 2617 | 2680 | + | 64 | OH_0 | 3626 | 3854 | + | 229 |
| trnC(gca) | 2710 | 2777 | - | 68 | trnI(gat) | 4470 | 4535 | + | 66 |
| OH_1-a | 2748 | 2804 | + | 57 | trnQ(ttg) | 4538 | 4606 | - | 69 |
| trnY(gta) | 2783 | 2850 | - | 68 | trnM(cat) | 4616 | 4684 | + | 69 |
| cox1 | 2856 | 4391 | + | 1536 | nad2 | 4706 | 5713 | + | 1008 |
| trnL2(taa) | 4401 | 4466 | + | 66 | trnW(tca) | 5716 | 5779 | + | 64 |
| cox2 | 4468 | 5175 | + | 708 | trnC(gca) | 5809 | 5876 | - | 68 |
| trnK(ctt) | 5156 | 5226 | + | 71 | OH_1-a | 5847 | 5903 | + | 57 |
| trnD(gtc) | 5227 | 5293 | + | 67 | trnY(gta) | 5882 | 5949 | - | 68 |
| atp8_0 | 5294 | 5455 | + | 162 | cox1 | 5955 | 7490 | + | 1536 |
| atp6 | 5449 | 6126 | + | 678 | trnL2(taa) | 7500 | 7565 | + | 66 |
| cox3 | 6136 | 6924 | + | 789 | cox2 | 7567 | 8274 | + | 708 |
| trnG(tcc) | 6924 | 6989 | + | 66 | trnK(ctt) | 8255 | 8325 | + | 71 |
| OH_1-b | 6971 | 7036 | + | 66 | trnD(gtc) | 8326 | 8392 | + | 67 |
| nad3 | 6990 | 7343 | + | 354 | atp8_0 | 8393 | 8554 | + | 162 |
| trnA(tgc) | 7342 | 7406 | + | 65 | atp6 | 8548 | 9225 | + | 678 |
| trnR(tcg) | 7415 | 7481 | + | 67 | cox3 | 9235 | 10023 | + | 789 |
| trnN(gtt) | 7486 | 7551 | + | 66 | trnG(tcc) | 10023 | 10088 | + | 66 |
| trnS1(gct) | 7552 | 7618 | + | 67 | OH_1-b | 10070 | 10135 | + | 66 |
| trnE(ttc) | 7619 | 7686 | + | 68 | nad3 | 10089 | 10442 | + | 354 |
| trnF(gaa) | 7685 | 7751 | - | 67 | trnA(tgc) | 10441 | 10505 | + | 65 |
| nad5 | 7762 | 9480 | - | 1719 | trnR(tcg) | 10514 | 10580 | + | 67 |
| trnH(gtg) | 9512 | 9563 | - | 52 | trnN(gtt) | 10585 | 10650 | + | 66 |
| nad4 | 9563 | 10903 | - | 1341 | trnS1(gct) | 10651 | 10717 | + | 67 |
| nad4l | 10897 | 11190 | - | 294 | trnE(ttc) | 10718 | 10785 | + | 68 |
| trnT(tgt) | 11193 | 11257 | + | 65 | trnF(gaa) | 10784 | 10850 | - | 67 |
| trnP(tgg) | 11258 | 11322 | - | 65 | nad5 | 10861 | 12579 | - | 1719 |
| nad6 | 11343 | 11849 | + | 507 | trnH(gtg) | 12611 | 12662 | - | 52 |
| cob | 11849 | 12985 | + | 1137 | nad4 | 12662 | 14002 | - | 1341 |
| trnS2(tga) | 12985 | 13052 | + | 68 | nad4l | 13996 | 14289 | - | 294 |
| nad1 | 13074 | 14015 | - | 942 | trnT(tgt) | 14292 | 14356 | + | 65 |
| trnL1(tag) | 14025 | 14089 | - | 65 | trnP(tgg) | 14357 | 14421 | - | 65 |
| rrnL | 14067 | 15390 | - | 1324 | nad6 | 14442 | 14948 | + | 507 |
| trnV(tac) | 15416 | 15487 | - | 72 | cob | 14948 | 16084 | + | 1137 |
| rrnS | 15488 | 16241 | - | 754 | trnS2(tga) | 16084 | 16151 | + | 68 |