

Table S2. Sequence correction record

Done in the alignments whose both ends were already trimmed.

Gene	Sequence	Diagnosis and treatment
atp6	Megaloblatta_sp_ECMD1_MG882218_1_Ectobiidae	Beginning with 60 missing cells; question-marked
atp6	Schultesia_lampyridiformis_MG882163_1_Blaberidae	Beginning with 36 missing cells; question-marked
atp8	Aposthonia_borneensis_KX965988_1_Oligotomidae	Near end are 12 missing cells; question-marked
atp8	Asiablatta_kyotensis_MG882166_1_Ectobiidae	Ending with 21 missing cells; question-marked
atp8	Ectoneura_hanitschi_MG882219_1_Ectobiidae	Near end are 36 missing cells; question-marked
atp8	Galiblatia_cribrosa_MG882232_1_Blaberidae	Beginning with 48 missing cells; question-marked
atp8	Megaloblatta_sp_ECMD1_MG882218_1_Ectobiidae	Beginning with 72 missing cells; question-marked
cox1	Megaloblatta_sp_ECMD1_MG882218_1_Ectobiidae	33 out of 36 Ns are redundant (as inserts) and deleted
cox3	Aposthonia_borneensis_KX965988_1_Oligotomidae	Beginning with 24 missing cells; question-marked
cox3	Cryptocercus_punctulatus_MG882217_1_Cryptocercidae	Beginning with 15 missing cells; question-marked
cox3	Ergaula_capucina_MG882188_1_Corydiidae	Beginning with 18 missing cells; question-marked
cox3	Tryonicus_parvus_MG882230_1_Tryonicidae	Beginning with 15 missing cells; question-marked
cytb	Eublaberus_distanti_MG882147_1_Blaberidae	Poorly-sequenced tail beginning with 8 Ns; question-marked for 55 bases
cytb	Rhabdoblatta_sp_RHA_MG882228_1_Blaberidae	(1) 12 different codons (36 bases) and an indel (3 bases) and a stop codon (1 base) in conserved region; question-marked, 40 in total (2) Poorly-sequenced tail; question-marked for 39 bases
nad1	Anallacta_methanoides_MG882165_1_Ectobiidae	Many indels and differences in conserved region; whole sequence discarded!
nad1	Beybienkoa_kurandanensis_MG882208_1_Ectobiidae	45 out of 52 Ns redundant (as inserts) and deleted
nad2	Galiblatia_cribrosa_MG882232_1_Blaberidae	Ending with 204 missing cells; question-marked
nad2	Megaloblatta_sp_ECMD1_MG882218_1_Ectobiidae	Ending with 94 Ns in alignment; kept
nad2	Metallyticus_sp_JZ_2017_KY689122_1_Metallyticidae	Many indels and stop codons throughout; whole sequence discarded!
nad3	Epilampra_maya_MG882194_1_Blaberidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad4	Allacta_bimaculata_MG882128_1_Ectobiidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad4	Beybienkoa_kurandanensis_MG882208_1_Ectobiidae	Poorly-sequenced tail beginning with 44 Ns; question-marked for 111 cells
nad4	Ergaula_capucina_MG882188_1_Corydiidae	Ending with missing 72 cells; question-marked
nad4	Eublaberus_distanti_MG882147_1_Blaberidae	Missing and not aligned in conserved region in the middle; question-marked for 231 cells
nad4	Euphyllodromia_sp_Z257_MG882238_1_Ectobiidae	Ending with 54 missing cells; question-marked
nad4	Epilampra_maya_MG882194_1_Blaberidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad4	Galiblatia_cribrosa_MG882232_1_Blaberidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad4	Nocticola_sp_JW1_9_1_MG882221_1_Nocticolidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad4	Paranauphoeta_circumdata_MG882225_1_Blaberidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad4	Platyzoetia_sp_AUS3_MG882132_1_Blattidae	Beginning with a certain number of missing bases but the region is not very conserved; question-marked for 147 that are relatively conserved
nad4L	Galiblatia_cribrosa_MG882232_1_Blaberidae	Many differences in conserved region at the end of the sequence; question-marked for 48
nad4L	Leptomantella_albella_KJ463364_1_Tarachodidae	Many differences in conserved region at the end of the sequence (almost the latter half); question-marked for 147
nad4L	Megaloblatta_sp_ECMD1_MG882218_1_Ectobiidae	Ending with 96 missing cells; question-marked
nad5	Anaplecta_calosoma_MG882215_1_Ectobiidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad5	Anaplecta_omei_MG882129_1_Ectobiidae	Beginning with a certain number of missing bases but the region is not very conserved; not question-marked
nad5	Aposthonia_borneensis_KX965988_1_Oligotomidae	Many differences at the beginning; the whole poor beginning containing bad cells was deleted and most of them (156 cells) were question-marked
nad5	Balta_sp_Cairns_Australia_MG882206_1_Ectobiidae	69 out of 71 Ns redundant (as inserts) and 93 bases duplicated (also as inserts while these positions are gaps in other sequences); deleted
nad5	Galiblatia_cribrosa_MG882232_1_Blaberidae	Beginning with 159 missing cells; question-marked
nad5	Lamproblatta_albipalpus_MG882233_1_Lamproblattidae	27 out of 48 Ns redundant (as inserts); deleted
nad5	Megaloblatta_sp_ECMD1_MG882218_1_Ectobiidae	Poorly-sequenced tail beginning with 118 Ns; question-marked for 134 cells
nad5	Platyzoetia_sp_AUS3_MG882132_1_Blattidae	Middle portion with 24 Ns and also 48 missing cells; the latter question-marked
nad6	Galiblatia_cribrosa_MG882232_1_Blaberidae	Latter half missing; question-marked for 294 cells
nad6	Platyzoetia_sp_AUS3_MG882132_1_Blattidae	Poorly-sequenced latter half (59 Ns followed by many differences and stop codons); question-marked for 223 cells