

**Figure S4.** Alignment of protein coding sequences of the *Rhizopertha dominica* mitochondrial genome from this paper (top sequence) and that predicted by Ouyang et al. [15] (lower sequence). a), *nad2*; b), *cox1*; c), *cox2*; d), *atp8*; e), *atp6*; f), *cox3*; g), *nad3*; h), *nad5*; i), *nad4*; j), *cytB*; k), *nad1*. Amino acid differences due to SNVs are notated with turquoise shading.

**a. *nad2***

Seq4	MIKLSKISFTITMMIGSMITISSYTWGMWVGLEINLLSIPLLTTKKNIYSTEAAIKYF 60	
QCI56356.1	MIKLSKISFTITMMIGSMITISSYTWGMWVGLEINLLSIPLLTTKKNIYSTEAAIKYF 60	
	*****	
Seq4	ITQALSSILLMSILILSTNLINQKSAMMILYSSLMTKMGTAFFHFPEIEGLDWMNC 120	
QCI56356.1	ITQALSSILLMSILILSTNLINQKSAMMILYSSLMTKMGTAFFHFPEIEGLDWMNC 120	
	*****	
Seq4	LIMMTWQKIAPAMILSSMNMTFIYITITSSMLISGIMGVNQTSRLKIMAYSSINHMAW 180	
QCI56356.1	LIMMTWQKIAPAMILSSMNMTFIYITITSSMLISGIMGVNQTSRLKIMAYSSINHMAW 180	
	*****	
Seq4	MMASMNEKIFYIYLSIYITMSSIFITLKSNNSLYIYQMNTSNQSPIIKKTFIINLLSM 240	
QCI56356.1	MMASMNEKIFYIYLSIYITMSSIFITLKSNNSLYIYQMNTSNQSPIIKKTFIINLLSM 240	
	*****	
Seq4	GGLPPLLGGFFPKWMVINSMIQSNLILSTFMVMTLLTLYFYMQISMPILTMKMKMKWS 300	
QCI56356.1	GGLPPLLGGFFPKWMVINSMIQSNLILSTFMVMTLLTLYFYMQISMPILTMKMKMKWS 300	
	*****	
Seq4	KKNPQQFFMNKMNMINLLSIPVCTIWFNFY 330	
QCI56356.1	KKNPQQFFMNKMNMINLLSIPVCTIWFNFY 330	
	*****	

**b. *cox1***

Seq8	NKWLYSTNHKDIGTLYFIFGIWSGMVGTALESMLIRSELGNPGALIGDDQIYNVIVTAHAF	36
YP_009655010.1	NKWLYSTNHKDIGTLYFIFGIWSGMVGTALESMLIRSELGNPGALIGDDQIYNVIVTAHAF	60
	*****	
Seq8	IMIFFVMVPMIMIGGFGNWLVPLMIGAPDMAFFRMNNSFWLLPPLTLTLLTSSIVETGAG	96
YP_009655010.1	IMIFFVMVPMIMIGGFGNWLVPLMIGAPDMAFFRMNNSFWLLPPLTLTLLTSSIVETGAG	120
	*****	
Seq8	TGWTVPPLSNNTAHSGASVDLAIFSLHLAGISSILGAVNFITTIINMRPKGMPERIPPL	156
YP_009655010.1	TGWTVPPLSNNTAHSGASVDLAIFSLHLAGISSILGAVNFITTIINMRPKGMPERIPPL	180
	*****	
Seq8	FVWSVGITALLLLSLPVLAGAITMLLTDRNLNTSFFDPAGGGDPILYQHLFWFFGHPEV	216
YP_009655010.1	FVWSVGITALLLLSLPVLAGAITMLLTDRNLNTSFFDPAGGGDPILYQHLFWFFGHPEV	240
	*****	
Seq8	YILILPGFGMISHIISHESGKKETFGSLGMIYAMMAIGLLGFIVWAHMFVGMVDVTRA	276
YP_009655010.1	YILILPGFGMISHIISHESGKKETFGSLGMIYAMMAIGLLGFIVWAHMFVGMVDVTRA	300
	*****	
Seq8	YFTSATMIIAVPTGIKVFVSWLATLHGTQMNYSPPMMWSLGFVFLFTVGGLTGVVLANSI	336
YP_009655010.1	YFTSATMIIAVPTGIKVFVSWLATLHGTQMNYSPPMMWSLGFVFLFTVGGLTGVVLANSI	360
	*****	
Seq8	DIILHDTYYVVAHFHYVLSMGAVFAIMAGIIQWFPPLFTGLTLNEKMLKIQFLIMFMGVNI	396
YP_009655010.1	DIILHDTYYVVAHFHYVLSMGAVFAIMAGIIQWFPPLFTGLTLNEKMLKIQFLIMFMGVNI	420
	*****	
Seq8	TFFPQHFLGLSGMPRRYSYDPAYLTWNIISISGSMSTVSIIFMSFIMWESLSSKRKNI	456
YP_009655010.1	TFFPQHFLGLSGMPRRYSYDPAYLTWNIISISGSMSTVSIIFMSFIMWESLSSKRKNI	480
	*****	
Seq8	SNNQLSSAIEWLQNSPPEEHSYSELPILAKF 487	
YP_009655010.1	SNNQLSSAIEWLQNSPPEEHSYSELPILAK- 510	
	*****	

**c. *cox2***

Seq10	MATWKMTSMSNSNSPAMEQLTFFHDTMTVLIMITILVGylMSTLFTNKLTYRFLLEGQT	60
YP_009655011.1	MATWKMTSMSNSNSPAMEQLTFFHDTMTVLIMITILVGylMSTLFTNKLTYRFLLEGQT	60
*****		
Seq10	IEMIWTILPAITLIFIALPSLQILYTLDEIINPSMSVKSIGHQWWSYEYSDFKKTEFDS	120
YP_009655011.1	IEMIWTILPAITLIFIALPSLQILYTLDEIINPSMSVKSIGHQWWSYEYSDFKKTEFDS	120
*****		
Seq10	YMKSPNEIKNQEFRLDVDNRMTLPMKTKIRLLVSSTDVIHSWTIPSLGVKIDATPGRLN	180
YP_009655011.1	YMKSPNEIKNQEFRLDVDNRMTLPMKTKIRLLVSSTDVIHSWTIPSLGVKIDATPGRLN	180
*****		
Seq10	QASMFIIINPGLMYGQCSEICGANHSFMPIVVESITPNKFIEWIKNS 229	
YP_009655011.1	QASMFIIINPGLMYGQCSEICGANHSFMPIVVESITPNKFIEWIKN- 225	
*****		

**d. *atp8***

Seq13	---MSPLNWMTLFIFFTITLVMSTMNFYNYKPEPLKGEKTISMSKKNWKW	48
YP_009655012.1	MPQMSPLNWMTLFIFFTITLVMSTMNFYNYKPEPLKGEKTISMSKKNWKW	51
*****		

**e. *atp6***

Seq14	MMSNLFSSFDpstQILSLNWLSSLIILMIMPMNFWLIPSRMSLLWMKISKKLHNEFKILI	60
YP_009655013.1	MMSNLFSSFDpstQILSLNWLSSLIILMIMPMNFWLIPSRMSLLWMKISKKLHNEFKILI	60
*****		
Seq14	GKNNGSSLMFTSLLLLIMINNFMGLFPYIFTSTSHLTMTLTALPLWTSFMIYGWFNNTI	120
YP_009655013.1	GKNNGSSLMFTSLLLLIMINNFMGLFPYIFTSTSHLTMTLTALPLWTSFMIYGWFNNTI	120
*****		
Seq14	SMLAHLVPQGTppILMPFMVCIETISNIIRPGTLAIRLTANMIAGHLLLTLLGNTGAGIS	180
YP_009655013.1	SMLAHLVPQGTppILMPFMVCIETISNIIRPGALAIRLTANMIAGHLLLTLLGNTGAGIS	180
*****		
Seq14	SILVSILILTQILLLVLESavaIIQSYVFAILSTLYSSEVN 221	
YP_009655013.1	SILVSILILTQILLLVLESavaIIQSYVFAILSTLYSSEVN 221	
*****		

**f. *cox3***

Seq15	MTKKNHPPHFLVDVSPWPILGALSAMSTMVGLIKWFHMYQVNLFLVGLLSTSLIMYQWWRD	60
YP_009655014.1	MTKKNHPPHFLVDVSPWPILGALSAMSTMVGLIKWFHMYQVNLFLVGLLSTSLIMYQWWRD	60
*****		
Seq15	ITREGSFQGHHTFIVTMGLRWGMILFITSEVFFFISFFWGFHSSLSPSIEIGMNWPPLG	120
YP_009655014.1	ITREGSFQGHHTFIVTMGLRWGMILFITSEVFFFISFFWGFHSSLSPSIEIGMNWPPLG	120
*****		
Seq15	ILTFNPLSIPLLNTLILLTSGLTVTWAHHSIMENNWKQANQGLTLTIILGLYFTILQAYE	180
YP_009655014.1	ILTFNPLSIPLLNTLILLTSGLTVTWAHHSIMENNWKQANQGLTLTIILGLYFTILQAYE	180
*****		
Seq15	YIEAPFTISDSVYGSSFFMATGFHGLHVIIGTTFLSVCLLRHLMNHFSMIHHFGFEAAAW	240
YP_009655014.1	YIEAPFTISDSVYGSSFFMATGFHGLHVIIGTTFLSVCLLRHLMNHFSMIHHFGFEAAAW	240
*****		
Seq15	YWHFVDVVWLFlyLSIYWwGK 280	
YP_009655014.1	YWHFVDVVWLFlyLSIYWwGS 261	
*****		

**g. nad3**

Seq17	MKIILISSMIIFSISLILMMMNQVISKKTFKDREKMSPYECGFDPKSHARIPLSIRFFLI	60
YP_009655015.1	MKIILISSMIIFSISLILMMMNQVISKKTFKDREKMSPYECGFDPKSHARIPLSIRFFLI	60
	*****	
Seq17	TMIFLIFDVEITLLLPAINNLTNNPLEFLITFIFFISILTGTIHEWKQGALNWK	117
YP_009655015.1	TVIFLIFDVEITLLLPAINNLTNNPLEFLITFIFFISILTGTIHEWKQGALNWK	117
	*.*****	

**h. nad5**

Seq24	MSLTFVFFSLFLFCSEFFFFFLSLYFMILDFSLFVEYELFSLNSSLINFSLYFDFMSLIFM	60
YP_009655016.1	MSLTFVFFSLFLFCSEFFFFFLSLYFMILDFSLFVEYELFSLNSSLINFSLYFDFMSLIFM	60
	*****	
Seq24	SFVFFISSMVVFYSEDYMHGDLMLNRFILLVVLVFLSMMMILSPNIISILLGWDGLGLV	120
YP_009655016.1	SFVFFISSMVVFYSEDYMHGDLMLNRFILLVVLVFLSMMMILSPNIISILLGWDGLGLV	120
	*****	
Seq24	SYSLVIYYQNFKSFSAGMLTALSNRIGDVALLMISIAWMLNYGSWNYLFYVFFIDNLYFI	180
YP_009655016.1	SYSLVIYYQNFKSFSAGMLTALSNRIGDVALLMISIAWMLNYGSWNYLFYVFFIDNLYFI	180
	*****	
Seq24	ISLFIMLAFTKSAQIPFSAWLPAAMAAPTVPSSLVHSSTLVTAGVYLMIRFSYCFCDKV	240
YP_009655016.1	ISLFIMLAFTKSAQIPFSAWLPAAMAAPTVPSSLVHSSTLVTAGVYLMIRFSYCFCDKV	240
	*****	
Seq24	LILGLLLSCLTMFMAGLGANFEFDLKKIIALSTLSQLGLMMSILFSGGEYLAFFHLLSHA	300
YP_009655016.1	LILGLLLSCLTMFMAGLGANFEFDLKKIIALSTLSQLGLMMSILFSGGEYLAFFHLLSHA	300
	*****	
Seq24	LFKALLFMCAGSFIHSFMNFQDIRFMGSALNFMPLTSCFFIICNFSLCGLPFLSGFYSKD	360
YP_009655016.1	LFKALLFMCAGSFIHSFMNFQDIRFMGSALNFMPLTSCFFIICNFSLCGLPFLSGFYSKD	360
	*****	
Seq24	LILEFYSMKFVNMFSYILFFVSTGLTVSYTVRLMYLFFGYLNFSPLFLISEGGNFMLFG	420
YP_009655016.1	LILEFYSMKFVNMFSYILFFVSTGLTVSYTVRLMYLFFGYLNFSPLFLISEGGNFMLFG	420
	** *****	
Seq24	MLGLIFPVIVAGSVLSWLMFSTPYIICLPLYMKFMTLFVIFSGLLIGVEVSRFSLNYHSK	480
YP_009655016.1	MLGLIFPVIVAGSVLSWLMFSTPYIICLPLYMKFMTLFVIFSGLLIGVEVSRFSLNYHSK	480
	*****	
Seq24	SLNFMNFSWFSSLMWGLPLISSLGMSIFPLTLGRLFISSFDQGWLEHLGAQGFMNLIK	540
YP_009655016.1	SLNFMNFSWFSSLMWGLPLISSLGMSIFPLTLGRLFISSFDQGWLEHLGAQGFMNLIK	540
	*****	
Seq24	TRSLHLIFSNQLKLFLIMLIFWVSFLILFYLNSL	577
YP_009655016.1	TRSLHLIFSNQLKLFLIMLIFWVSFLILF-----	569
	*****	

**i. nad4**

Seq26	MMKFILFVFFMIPLSFLDFYLVFLFLGLMMFIFLKIAPVSTILLGLGFGCDLFSGPLILL	60
YP_009655017.1	MMKFILFVFFMIPLSFLDFYLVFLFLGLMMFIFLKIAPVSTILLGLGFGCDLFSGPLILL	60
	*****	
Seq26	SFFICLLMFIASSKIYMDNNFHFYFSLNVIMLLFFLICAFSSLNFLFYVFFESSLIPTL	120
YP_009655017.1	SFFICLLMFIASSKIYMDNNFHFYFSLNVIMLLFFLICAFSSLNFLFYVFFESSLIPTL	120
	*****	
Seq26	FLILGWGYQPERIQAGFYLLFYTLFASLPMFLGLMHYYLSFGSLSMFLMFQVNSMIFNFM	180
YP_009655017.1	FLILGWGYQPERIQAGFYLLFYTLFASLPMFLGLMHYYLSFGSLSMFLMFQVNSMIFNFM	180
	*****	
Seq26	MIFVFLVKIPMFVVLWLPAKAVEAPVSGSMILAGVMLKLGGYGLLRVFLPKAEVSFFS	240
YP_009655017.1	MIFVFLVKIPMFVVLWLPAKAVEAPVSGSMILAGVMLKLGGYGLLRVFLPKAEVSFFS	240
	*****	
Seq26	TFFVSIISVFGGLIVSLICLRQSDIKSLIAYSSVAHMSMVISGCFTLTTWGVIGSLIMMIS	300
YP_009655017.1	TFFVSIISVFGGLIVSLICLRQSDIKSLIAYSSVAHMSMVISGCFTLTTWGVIGSLIMMIS	300
	*****	
Seq26	HGICSSGLFCLANITYERSLSRSLYLNKGYINILPNLSLWWFLLCSSNMAAPPSSLNVSE	360
YP_009655017.1	HGICSSGLFCLANITYERSLSRSLYLNKGYINILPNLSLWWFLLCSSNMAAPPSSLNVSE	360
	*****	
Seq26	ILILSSLVSWSSLMILILSFLSFLSAAYSFLYSFTQHGMVSSGLFSFWSVNVREYLLLF	420
YP_009655017.1	ILILSSLVSWSSLMILILSFLSFLSAAYSFLYSFTQHGMVSSGLFSFWSVNVREYLLLF	420
	*****	
Seq26	FHWIPLNLIFLFMDNLFSL	451
YP_009655017.1	CHWIPLNLIFLFMHNLFSL	439
	*****.	

**j. cytB**

Seq31	MKKQLMKISPVTKIINNALIDLPTPSNISIWWMGSILGLCLIIQIITGMFLTMHYTPNT	60
YP_009655020.1	MKKQLMKISPVTKIINNALIDLPTPSNISIWWMGSILGLCLIIQIITGLFLTMHYTPNT	60
	*****.	
Seq31	EMAFNSVVHICRDVNYGWMIRTIHANGASMEFFICIYMHIGRGLYYGSYKLIHTWMVGVII	120
YP_009655020.1	EMAFNSVVHICRDVNYGWMIRTIHANGASMEFFICIYMHIGRGLYYGSYKLIHTWMVGVII	120
	*****	
Seq31	LFLVMATAFLGYVLPWGQMSFWGATVITNLLSAIPYVGKMIVEWLWGGFAVDNATLNRFF	180
YP_009655020.1	LFLVMATAFLGYVLPWGQMSFWGATVITNLLSAIPYVGKMIVEWLWGGFAVDNATLNRFF	180
	***.*****	
Seq31	AFHFLLPFIVSAMVMIHLLFLHQTGSNPLGTNSNIDKIPFHPYFSTKDMGFIIVTMML	240
YP_009655020.1	AFHFLLPFIVSAMVMIHLLFLHQTGSNPLGTNSNIDKIPFHPYFSTKDMGFIIVTMML	240
	*****.	
Seq31	MTISLWNPYLLGDPDNFIPANPLVTPVHIQPEWYFLFAYAILRSIPNKLGGVIALIMSIA	300
YP_009655020.1	MTISLWNPYLLGDPDNFIPANPLVTPVHIQPEWYFLFAYAILRSIPNKLGGVIALIMSIA	300
	*****	
Seq31	ILFIIPLTNKSKFQSMNFYPMNKFLFWSMVSTVILLTWIGARPVQDPYITTGQVLTIIYF	360
YP_009655020.1	ILFIIPLTNKSKFQSMNFYPMNKFLFWSMVSTVILLTWIGARPVQDPYITTGQVLTIIYF	360
	*****.	
Seq31	LYYMITPLTLKIWDKILIK	379
YP_009655020.1	LYYMITPLTLKIWDKILIK	379
	*****	

***k. nad1***

Seq33	MFIFDFILVFFSLLVLIIGVLVGVAFLTLMERKVLGYIQLRKGPKNKVGFMGLLQPFSDA	60
YP_009655021.1	-MFIFDFILVFFSLLVLIIGVLVGVAFLTLMERKVLGYIQLRKGPKNKVGFMGLLQPFSDA	59
	:*****	
Seq33	IKLFSKEQCLPLVSNYVFYYFSPVMNFFISLMMWLSFPFFSYFLSFNLGMLFFLCFSSLS	120
YP_009655021.1	IKLFSKEQCLPLVSNYVFYYFSPVMNFFISLMMWLSFPFFSYFLSFNLGMLFFLCFSSLS	119
	*****	
Seq33	VYAVMISGWSSNSNYSMIGSLRSMAQTISYEVSLVIIISFLVMTSSLCFYDFFKYQKYL	180
YP_009655021.1	VYAVMISGWSSNSNYSMIGSLRSMAQTISYEVSLVIIISFLVMTSSLCFYDFFKYQKYL	179
	*****	
Seq33	WFVFLMFPLSLILFVSMLAETNRTPFDFAEGESELVSGFNVEYSSGGFALIFLAEYSSIL	240
YP_009655021.1	WFVFLMFPLSLILFVSMLAETNRTPFDFAEGESELVSGFNVEYSSGGFALIFLAEYSSIL	239
	*****	
Seq33	FMSMICSLMFFGGDYMNLFYFFIKIVFFSFLWVWVRGTLPRYRYDKLMYLAWKIYLPVSLC	300
YP_009655021.1	FMSMICSLMFFGGDLYKFIFFFIKIVFFSFLWVWVRGTLPRYRYDKLMYLAWKIYLPVSLC	299
	***** : : *****	
Seq33	FLLFYLGKTLWCWFII 317	
YP_009655021.1	FLLFYLGKTLWCWFII 316	
	*****	