

**Table S1.** Overrepresented sequences reported in FastQC during quality control. These sequences were used to collect raw read sequences for *CO1* sequence analysis.

Species	Overrepresented sequence
<i>M. rubra</i>	CTCCATT TAAAAGACA AACTGATTATGCTACCTTAGCACAGTCAATTTACT CTCCCAACTAAATATAAATTCATAAGTTAAAAAATCTAATTAAATCTTAT CTTAATCACAATTAAGATTTTAACTTAATAACAAAATTCAAATTTTAAT CTTTCGTACAAATATATTTATTTTATTAAAGATAGAAACCGATCTGGCT GTCCAATCTAGTAGTGCTGAGCCCAAGTTTTTCGTCGATGGAATGACTTT GTCCTTTCGTACAAATATATTTATTTTATTAAAGATAGAAACCGATCTG
<i>M. ruginodis</i>	CTCCATT TAAAAGACA AACTGATTATGCTACCTTAGCACAGTCAATTTACT CTCCATT TAAATTTTATCTTAATTCACATCGAGGTCGCAATCATTTTAA CTCCCAACTAAATATAAATTTATAAGTTATAAAAATCTAATTAAATCTTA CTTTCGTACAAATATATTTATTTTATTAAAGATAGAAACCGATCTGGCT GTCCAATCTAGTAGTGCTGAGCCCAAGTTTTTCGTCGATGGAATGACTTT GTCCTTTCGTACAAATATATTTATTTTATTAAAGATAGAAACCGATCTG

**Table S2.** Results of *CO1* sequence analysis. We used overrepresented sequences to extract all corresponding raw reads with their mates, dereplicated them and ran a BLAST search against BOLD. Only hits with 100% identity and query coverage were kept. One read could match more than one record in BOLD.

	<i>Myrmica rubra</i>	<i>Myrmica ruginodis</i>
Reads	634,472	1,328,614
Unique reads	40,978	98,119
Unique reads after BLAST search and filtering	1,045	28,119
Matching BOLD records	21 Formicidae 160 <i>Myrmica</i> 2,343 <i>Myrmica rubra</i>	13 Formicidae 43 <i>Myrmica</i> 858 <i>Myrmica ruginodis</i>