

Table B. Mitochondrial transcripts

<i>RNA</i> ^a	<i>Gene product</i>	<i>RefSeq</i> ^b	<i>Frequencies</i> ^c	
			HM3	HM3/S ³
12S	ribosomal RNA, small subunit	648 - 1601	0.3	0.0
16S	ribosomal RNA, large subunit	1671 - 3229	4.2	0.3
RNA 13	NADH dehydrogenase, subunit 1	3305 - 4262	3.0	0.0
RNA 12	NADH dehydrogenase, subunit 2	4470 - 5511	n.d.	0.0
RNA 9	cytochrome c oxidase, subunit 1	5901 - 7517	1.0	0.1
RNA 16	cytochrome c oxidase, subunit 2	7586 - 8294	n.d.	0.0
RNA 14	ATPase, subunits 6-8	8365 - 9206	n.d.	0.1
RNA 15	cytochrome c oxidase, subunit 3	9207 - 9990	n.d.	0.0
RNA 17	NADH dehydrogenase, subunit 3	10059 - 10404	n.d.	0.0
RNA 7	NADH dehydrogenase, subunits 4L-4	10470 - 12137	3.2	0.0
RNA 5	NADH dehydrogenase, subunit 5	12337 - 14148 ^d	0.1	0.0
RNA 11	cytochrome b	14747 - 15887	1.5	0.2

^aRNA molecules, nomenclature after GenBank sequence J01415. ^bPosition in the mitochondrial genome, RefSeq accession no. NC_001807. ^cFrequencies of cDNA clones identifying mitochondrial genes respectively in the HM3 library (not subtracted) and in the subtracted HM3/S³ library. n.d. = Not determined in the HM3 library; the frequencies in the HM1 library are reported elsewhere (Ref. 13). Note that the ESTs of five transcripts were systematically excluded from DNA sequencing through semi-multiplexed interference PCR (Ref. 23). ^dThe most 3' terminal ESTs showed in Figure 3 end instead at position 14746.