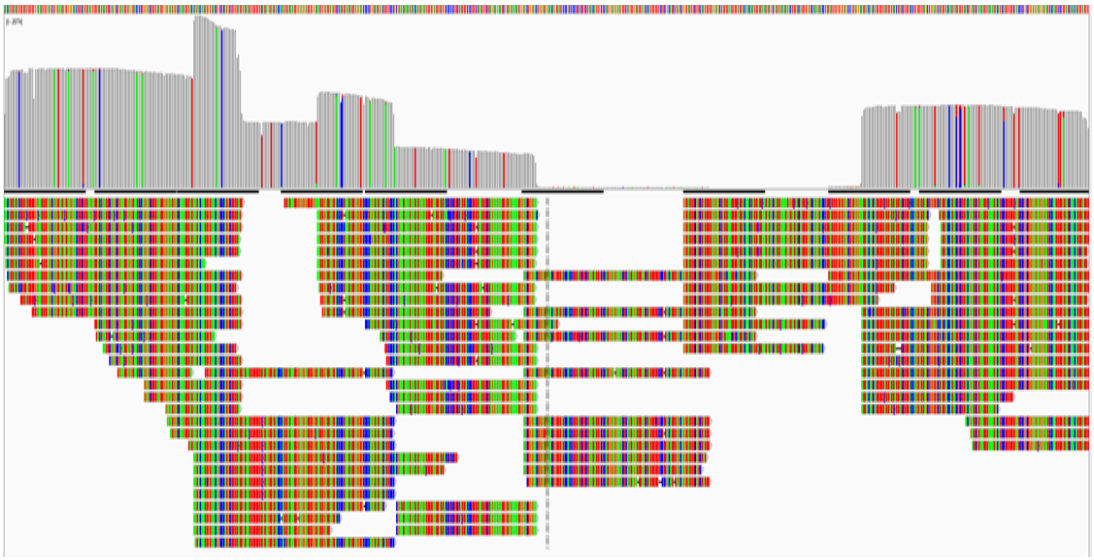
Supporting Information

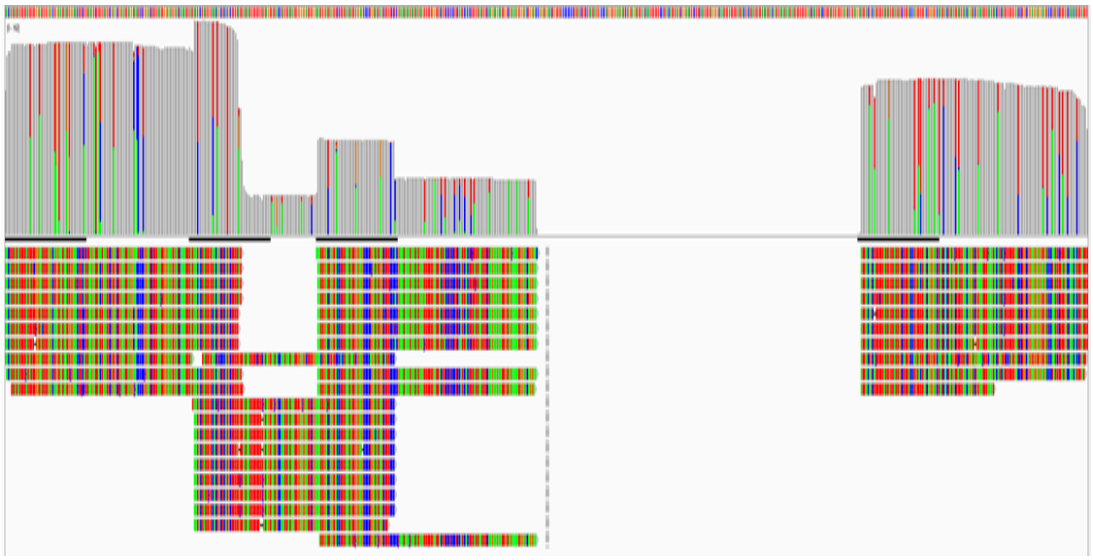
Fig S1. Alignments of sequence records derived from two type specimens of Geometridae, one with high quality DNA (a) and one with low quality DNA (b). The alignments show only a single representative of each distinct sequence. In many cases, there were hundreds or thousands of a particular sequence. High quality reads have high coverage across the entire 658bp barcode region and originate from a single source – indicated by a single nucleotide (color) at each position in the contig. Low quality reads do not span the entire barcode region (i.e. they have regions lacking coverage) and often originate from multiple sources – indicated by multiple nucleotides (colors) at certain positions in the contig.

See associated image file "Figure S1.svg"

(a)



(b)



17

18 **S1 Table. Type specimens analyzed, including sequencing results and accession numbers.**

Process ID (Sanger/NGS)	Age (Yrs)	Identification	Status	Sanger Group	No. NGS Reads	Min. Cov.	Max. Cov.	Avg. Cov.	Recovered bp by NGS	NGS Contig GenBank Acc.	Sequence Read Archive Acc.
PNGTY381-13 / PNGTY1837-15	104	*Myrioblephara mixticolor*	Syntype	HQ	143804	7	115751	29924	658	KR070780	SRR1867808
PNGTY404-13 / PNGTY1827-15	112	*Cassephyra plenimargo*	Holotype	HQ	213007	72	146189	42992	658	KR070771	SRR1867811
PNGTY417-13 / PNGTY1843-15	109	*Psilalcis auropurpurea*	Syntype	HQ	106286	0	74012	20477	448	KR070767	SRR1867812
PNGTY466-13 / PNGTY1839-15	110	*Paralcidia marginata*	Syntype	HQ	221885	5	168474	44541	657	KR070779	SRR1867813
PNGTY473-13 / PNGTY1823-15	110	*Atmoceras plumosa*	Syntype	HQ	143340	30	76376	28215	658	KR070768	SRR1867814
PNGTY1047-14 / PNGTY1845-15	110	*Tripteridia viridisecta*	Syntype	HQ	188107	1	101191	37855	570	KR070783	SRR1867815
PNGTY1070-14 / PNGTY1834-15	111	*Gymnoscelis ochriplaga*	Holotype	HQ	186897	1	103399	38169	657	KR070772	SRR1867816
PNGTY1098-14 / PNGTY1824-15	110	*Axinoptera fasciata*	Holotype	HQ	166116	0	83389	31838	474	KR070785	SRR1867817
PNGTY1106-14 / PNGTY1826-15	112	*Calluga semirasata*	Holotype	HQ	215946	1	154302	43408	658	KR070769	SRR1867818
PNGTY1124-14 / PNGTY1833-15	123	*Eois semirubra*	Holotype	HQ	232024	106	143908	46803	658	KR070773	SRR1867819
PNGTY142-12 / PNGTY1831-15	112	*Collix ghosha dichobathra*	N/A	MQ	11665	0	11082	2142	459	KR070778	SRR1945335
PNGTY158-12 / PNGTY1838-15	111	*Papuarisme brunneata*	Holotype	MQ	6479	0	5747	1165	569	KR070787	SRR1945382
PNGTY189-12 / PNGTY1835-15	109	*Hyposidra apicifulva*	N/A	MQ	62208	0	45441	12301	570	KR070781	SRR1945383
PNGTY801-13 / PNGTY1836-15	101	*Milionia knowlei*	Syntype	MQ	44190	1	43301	9153	658	KR070777	SRR1945384
PNGTY587-13 / PNGTY1846-15	118	*Ctimene basistraga obsoleta*	Syntype	MQ	546	0	105	31	323	KR070784	SRR1946575
PNGTY639-13 / PNGTY1842-15	102	*Pseudeusemia bursadoides dignitosa*	Syntype	MQ	134542	37	82031	27382	658	KR070774	SRR1945385
PNGTY917-13 / PNGTY1840-15	108	*Pingasa nobilis furvifrons*	Holotype	MQ	46793	6	24276	9516	658	KR070782	SRR1945386
PNGTY923-13 / PNGTY1821-15	121	*Aeolochroma caesia*	Holotype	MQ	68837	3	43442	14002	658	KR070764	SRR1945387
PNGTY957-13 / PNGTY1844-15	106	*Sarcinodes subvirgata*	Holotype	MQ	99655	86	42405	20379	658	KR070762	SRR1945388
PNGTY971-13 / PNGTY1828-15	105	*Celerena lerne amplimargo*	Holotype	MQ	113363	1	42333	21657	569	KR070763	SRR1945389
PNGTY475-13 / PNGTY1832-15	104	*Dyscheralcis retroflexa*	Syntype	LQ	2681	0	1278	424	514	KR070766	SRR1867935
PNGTY1146-14 / PNGTY1822-15	110	*Alcis irrufata*	Holotype	LQ	49944	2	37401	8881	657	KR070770	SRR1867936

PNGTY1155-14 / PNGTY1830-15	120	*Cleora repetita* ab. *suffusa*	Holotype	LQ	7632	1	5708	731	454	KR070765	SRR1867937
PNGTY008-12* / N/A	109	*Spectrobasis differens*	Syntype	LQ	1468	0	1157	280	237	N/A	SRR1867938
PNGTY073-12* / N/A	104	*Desmoclystia unipuncta*	Syntype	LQ	320	0	116	40	357	N/A	SRR1867939
PNGTY102-12* / N/A	120	*Sterrhochaeta minuta*	Syntype	LQ	3081	0	215	91	324	N/A	SRR1867940
PNGTY120-12* / N/A	118	*Propithex alternata*	Holotype	LQ	14863	0	1554	163	323	N/A	SRR1867941
PNGTY756-13 / PNGTY1825-15	105	*Bursadopsis plenifascia*	Syntype	LQ	133263	4	71444	20742	634	KR070786	SRR1867942
PNGTY1080-14 / PNGTY1829-15	117	*Chloroclystis rufofasciata*	Syntype	LQ	4411	0	1685	647	419	KR070775	SRR1867943
PNGTY1128-14 / PNGTY1841-15	112	*Polyacme straminea* ab. *brunneata*	Holotype	LQ	141402	23	71197	28117	658	KR070776	SRR1867944

The four Process ID's marked with an asterisk (*) represent specimens where NGS analysis generated sequence reads from multiple species. HQ – high quality; MQ – medium quality; LQ – low quality; N/A – not applicable.

Table S2. Primers used in the first (PCR1) and second (PCR2) reactions to allow the analysis of 10 specimens in an Ion Torrent PGM run.

PCR	Code	Primer Name	Sequence (5'-3')	MID	Adapter
PCR1	F1	**ARTH-NGS-F1.1-ion1**	CTAAGGTAACATTCAACCAATCATAAAGATATTGG	None	None
	F2	**ARTH-NGS-F2.1-ion1**	CTAAGGTAACATTRRWRATGATCAARTWTATAAT	None	None
	F3	**ARTH-NGS-F3.1-ion1**	CTAAGGTAACTTATAATTGGDGGRTTTGGWAATTG	None	None
	F4	**ARTH-NGS-F4.1-ion1**	CTAAGGTAACAGWAGWATWRTWRAWAVWGG	None	None
	F5	**ARTH-NGS-F5.1-ion1**	CTAAGGTAACATTTTTWSWCTWCATWTDGCWGG	None	None
	F6	**ARTH-NGS-F6.1-ion1**	CTAAGGTAACTATTTGTWTGAKCWRTWKKWATTAC	None	None
PCR1	R1	**ARTH-NGS-R1.1-ion1**	CTAAGGTAACWGGTATWACTATRAARAAAATTAT	None	None
	R2	**ARTH-NGS-R2.1-ion2**	TAAGGAGAACTCARAAWCTWATRTTRTTTADWCG	None	None
	R3	**ARTH-NGS-R3.1-ion3**	AAGAGGATTCARDGGDGGRTAWACWGTTCAWCC	None	None
	R4	**ARTH-NGS-R4.1-ion4**	TACCAAGATCGTWGWAATRAARTTDATWGCWCC	None	None
	R5	**ARTH-NGS-R5.1-ion5**	CAGAAGGAACGTTARWARTATDGTRATDGCWCC	None	None

	R6	**ARTH-NGS-R6.1-ion6**	CTGCAAGTTCTAAACTTCTGGATGTCCAAAAAATCA	None	None
PCR2	F1	**ARTH-NGS-F1.2-ion1**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTAAGGTAACATTCAACCAATCATAAAGAT ATTGG	IonXpress1	A
	F2	**ARTH-NGS-F2.2-ion1**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTAAGGTAACATTRRWRATGATCAARTWTA TAAT	IonXpress1	A
	F3	**ARTH-NGS-F3.2-ion1**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTAAGGTAACTTATAATTGGDGGRTTTGGW AATTG	IonXpress1	A
	F4	**ARTH-NGS-F4.2-ion1**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTAAGGTAACAGWAGWATWRTWRAWAVW GG	IonXpress1	A
	F5	**ARTH-NGS-F5.2-ion1**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTAAGGTAACATTTTTWSWCTWCATWTDG CWGG	IonXpress1	A
	F6	**ARTH-NGS-F6.2-ion1**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTAAGGTAACTATTTGTWTGAKCWRTWKK WATTAC	IonXpress1	A
PCR2	F1	**ARTH-NGS-F1.2-ion2**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTAAGGAGAACATTCAACCAATCATAAAGAT ATTGG	IonXpress2	A
	F2	**ARTH-NGS-F2.2-ion2**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTAAGGAGAACATTRRWRATGATCAARTWT ATAAT	IonXpress2	A
	F3	**ARTH-NGS-F3.2-ion2**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTAAGGAGAACTTATAATTGGDGGRTTTGGW AATTG	IonXpress2	A
	F4	**ARTH-NGS-F4.2-ion2**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTAAGGAGAACAGWAGWATWRTWRAWAVW GG	IonXpress2	A
	F5	**ARTH-NGS-F5.2-ion2**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTAAGGAGAACATTTTTWSWCTWCATWTDG CWGG	IonXpress2	A
	F6	**ARTH-NGS-F6.2-ion2**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTAAGGAGAACTATTTGTWTGAKCWRTWKK WATTAC	IonXpress2	A
PCR2	F1	**ARTH-NGS-F1.2-ion3**	CCATCTCATCCCTGCGTGTCTCCGACTCAGAAGAGGATTCATTCAACCAATCATAAAGAT ATTGG	IonXpress3	A
	F2	**ARTH-NGS-F2.2-ion3**	CCATCTCATCCCTGCGTGTCTCCGACTCAGAAGAGGATTCATTRRWRATGATCAARTWTA TAAT	IonXpress3	A
	F3	**ARTH-NGS-F3.2-ion3**	CCATCTCATCCCTGCGTGTCTCCGACTCAGAAGAGGATTCTTATAATTGGDGGRTTTGGW AATTG	IonXpress3	A
	F4	**ARTH-NGS-F4.2-ion3**	CCATCTCATCCCTGCGTGTCTCCGACTCAGAAGAGGATTCAGWAGWATWRTWRAWAVW GG	IonXpress3	A
	F5	**ARTH-NGS-F5.2-ion3**	CCATCTCATCCCTGCGTGTCTCCGACTCAGAAGAGGATTCATTTTTWSWCTWCATWTDG CWGG	IonXpress3	A
	F6	**ARTH-NGS-F6.2-ion3**	CCATCTCATCCCTGCGTGTCTCCGACTCAGAAGAGGATTCTATTTGTWTGAKCWRTWKK WATTAC	IonXpress3	A
PCR2	F1	**ARTH-NGS-F1.2-ion4**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTACCAAGATCATTCAACCAATCATAAAGAT ATTGG	IonXpress4	A
	F2	**ARTH-NGS-F2.2-ion4**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTACCAAGATCATTRRWRATGATCAARTWTA TAAT	IonXpress4	A
	F3	**ARTH-NGS-F3.2-ion4**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTACCAAGATCTTATAATTGGDGGRTTTGGW AATTG	IonXpress4	A
	F4	**ARTH-NGS-F4.2-ion4**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTACCAAGATCAGWAGWATWRTWRAWAVW GG	IonXpress4	A
	F5	**ARTH-NGS-F5.2-ion4**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTACCAAGATCATTTTTWSWCTWCATWTDGC WGG	IonXpress4	A
	F6	**ARTH-NGS-F6.2-ion4**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTACCAAGATCTATTTGTWTGAKCWRTWKK WATTAC	IonXpress4	A
PCR2	F1	**ARTH-NGS-F1.2-ion5**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCAGAAGGAACATTCAACCAATCATAAAGAT ATTGG	IonXpress5	A
	F2	**ARTH-NGS-F2.2-ion5**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCAGAAGGAACATTRRWRATGATCAARTWT ATAAT	IonXpress5	A
	F3	**ARTH-NGS-F3.2-ion5**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCAGAAGGAACTTATAATTGGDGGRTTTGGW AATTG	IonXpress5	A
	F4	**ARTH-NGS-F4.2-ion5**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCAGAAGGAACAGWAGWATWRTWRAWAV WGG	IonXpress5	A
	F5	**ARTH-NGS-F5.2-ion5**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCAGAAGGAACATTTTTWSWCTWCATWTDG CWGG	IonXpress5	A
	F6	**ARTH-NGS-F6.2-ion5**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCAGAAGGAACTATTTGTWTGAKCWRTWKK WATTAC	IonXpress5	A
PCR2	F1	**ARTH-NGS-F1.2-ion6**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGCAAGTTCATTCAACCAATCATAAAGAT ATTGG	IonXpress6	A

	F2	**ARTH-NGS-F2.2-ion6**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGCAAGTTCATTRRWRATGATCAARTWTATAAT	IonXpress6	A
	F3	**ARTH-NGS-F3.2-ion6**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGCAAGTTCTTATAATTGGDGGRTTTGGWAATTG	IonXpress6	A
	F4	**ARTH-NGS-F4.2-ion6**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGCAAGTTCAGWAGWATWRTWRAWAVWGG	IonXpress6	A
	F5	**ARTH-NGS-F5.2-ion6**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGCAAGTTCATTTTTWSWCTWCATWTDGCWGG	IonXpress6	A
	F6	**ARTH-NGS-F6.2-ion6**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGCAAGTTCTATTTGTWTGAKCWRTWKKWATTAC	IonXpress6	A
PCR2	F1	**ARTH-NGS-F1.2-ion7**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCGTGATTCATTCAACCAATCATAAAGATATTGG	IonXpress7	A
	F2	**ARTH-NGS-F2.2-ion7**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCGTGATTCATTRRWRATGATCAARTWTATAAT	IonXpress7	A
	F3	**ARTH-NGS-F3.2-ion7**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCGTGATTCTTATAATTGGDGGRTTTGGWAATTG	IonXpress7	A
	F4	**ARTH-NGS-F4.2-ion7**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCGTGATTCAGWAGWATWRTWRAWAVWGG	IonXpress7	A
	F5	**ARTH-NGS-F5.2-ion7**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCGTGATTCATTTTTWSWCTWCATWTDGCWGG	IonXpress7	A
	F6	**ARTH-NGS-F6.2-ion7**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCGTGATTCTATTTGTWTGAKCWRTWKKWATTAC	IonXpress7	A
PCR2	F1	**ARTH-NGS-F1.2-ion8**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCCGATAACATTCAACCAATCATAAAGATATTGG	IonXpress8	A
	F2	**ARTH-NGS-F2.2-ion8**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCCGATAACATTRRWRATGATCAARTWTATAAT	IonXpress8	A
	F3	**ARTH-NGS-F3.2-ion8**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCCGATAACTTATAATTGGDGGRTTTGGWAATTG	IonXpress8	A
	F4	**ARTH-NGS-F4.2-ion8**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCCGATAACAGWAGWATWRTWRAWAVWGG	IonXpress8	A
	F5	**ARTH-NGS-F5.2-ion8**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCCGATAACATTTTTWSWCTWCATWTDGCWGG	IonXpress8	A
	F6	**ARTH-NGS-F6.2-ion8**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTTCCGATAACTATTTGTWTGAKCWRTWKKWATTAC	IonXpress8	A
PCR2	F1	**ARTH-NGS-F1.2-ion9**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTGAGCGGAACATTCAACCAATCATAAAGATATTGG	IonXpress9	A
	F2	**ARTH-NGS-F2.2-ion9**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTGAGCGGAACATTRRWRATGATCAARTWTATAAT	IonXpress9	A
	F3	**ARTH-NGS-F3.2-ion9**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTGAGCGGAACTTATAATTGGDGGRTTTGGWAATTG	IonXpress9	A
	F4	**ARTH-NGS-F4.2-ion9**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTGAGCGGAACAGWAGWATWRTWRAWAVWGG	IonXpress9	A
	F5	**ARTH-NGS-F5.2-ion9**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTGAGCGGAACATTTTTWSWCTWCATWTDGCWGG	IonXpress9	A
	F6	**ARTH-NGS-F6.2-ion9**	CCATCTCATCCCTGCGTGTCTCCGACTCAGTGAGCGGAACTATTTGTWTGAKCWRTWKKWATTAC	IonXpress9	A
PCR2	F1	**ARTH-NGS-F1.2-ion10**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGACCGAACATTCAACCAATCATAAAGATATTGG	IonXpress10	A
	F2	**ARTH-NGS-F2.2-ion10**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGACCGAACATTRRWRATGATCAARTWTATAAT	IonXpress10	A
	F3	**ARTH-NGS-F3.2-ion10**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGACCGAACTTATAATTGGDGGRTTTGGWAATTG	IonXpress10	A
	F4	**ARTH-NGS-F4.2-ion10**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGACCGAACAGWAGWATWRTWRAWAVWGG	IonXpress10	A
	F5	**ARTH-NGS-F5.2-ion10**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGACCGAACATTTTTWSWCTWCATWTDGCWGG	IonXpress10	A
	F6	**ARTH-NGS-F6.2-ion10**	CCATCTCATCCCTGCGTGTCTCCGACTCAGCTGACCGAACTATTTGTWTGAKCWRTWKKWATTAC	IonXpress10	A
PCR2	R1	**ARTH-NGS-R1.2-ion1-trP1**	CCTCTCTATGGGCAGTCGGTGATCTAAGGTAACWGGTATWACTATRAARAAAATTAT	IonXpress1	trP1
	R2	**ARTH-NGS-R2.2-ion2-trP1**	CCTCTCTATGGGCAGTCGGTGATTAAGGAGAACTCARAAWCTWATRTTRTTTADWCG	IonXpress2	trP1
	R3	**ARTH-NGS-R3.2-ion3-trP1**	CCTCTCTATGGGCAGTCGGTGATAAGAGGATTCARDGGDGGRTAWACWGTTCAWCC	IonXpress3	trP1

	R4	ARTH-NGS-R4.2-ion4-trP1	CCTCTCTATGGGCAGTCGGTGATTACCAAGATCGTWGWAATRAARTTDATWGCWCC	IonXpress4	trP1
	R5	ARTH-NGS-R5.2-ion5-trP1	CCTCTCTATGGGCAGTCGGTGATCAGAAGGAACGTTARWARTATDGTRATDGCWCC	IonXpress5	trP1
	R6	ARTH-NGS-R6.2-ion6-trP1	CCTCTCTATGGGCAGTCGGTGATCTGCAAGTTCTAAACTTCTGGATGTCCAAAAAATCA	IonXpress6	trP1

The "Code" column refers to primer labels in Fig. 1. The COI binding region within each primer sequence is shown in black, while the 10bp tail (PCR1) or MID tag (PCR2) is shown in blue. The "key sequence" (required for Ion Torrent sequencing) is shown in green and the sequencing adapters are shown in red. The 10bp tails on the PCR1 primers are technically IonXpress MID tags, but they serve only to block short amplicons from acting as primers during PCR1. They were chosen over random decamer tails to maximize primer-template matching in PCR2. The same forward and reverse PCR1 primers are used for all ten samples in the first round of PCR. In the second round of PCR, samples are discriminated by using ten different sets of MID-tagged forward PCR2 primers (the same set of PCR2 reverse primers is used for all ten samples).

Table S3. **Components of PCR reactions in the NGS protocol**.

	PCR 1.1	PCR 1.2	PCR 2.1, 2.2, 2.3, 2.4	PCR 2.5	PCR 2.6
10% Trehalose	5.125 µL	5.25 µL	5.75 µL	5.875 µL	6.0 µL
H_2O	0.13 µL	0.13 µL	0.13 µL	0.13 µL	0.13 µL
5X Buffer	2.5 µL	2.5 µL	2.5 µL	2.5 µL	2.5 µL
25 mM $MgCl_2$	1.25 µL	1.25 µL	1.25 µL	1.25 µL	1.25 µL
10 µM primers	0.125 µL each	0.125 µL each	0.125 µL each	0.125 µL each	0.125 µL each
10 µM dNTP	0.0625 µL	0.0625 µL	0.0625 µL	0.0625 µL	0.0625 µL
Taq (5U/ µL)	0.06 µL	0.06 µL	0.06 µL	0.06 µL	0.06 µL
Template	2 µL	2 µL	2 µL	2 µL	2 µL
TOTAL	12.5 µL	12.5 µL	12.5 µL	12.5 µL	12.5 µL

Reactions differ only in the number of primers and the amount of trehalose. Trehalose sourced from Fluka Analytical; Hyclone ultra-pure water from Thermo Fisher Scientific; Buffer (- $MgCl_2$), $MgCl_2$, and Taq polymerase from KAPA Biosystems (while standard CCDB protocols utilize Platinum Taq, KAPA Taq was found to be less prone to co-amplifying trace amounts of residual DNA - derived from the Taq manufacturing process - and is therefore more amenable to high cycle PCR); primers from Integrated DNA Technologies.