SUPPLEMENTARY MATERIAL FOR:

5′-Tailed sequencing primers improve sequencing quality of PCR products

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Supplementary Table S1. Sample Details

Sample Type and No.	C14 Age	Location
Musk Ox (IEM 199-007)	Late Pleistocene	Taymir Peninsula
Musk Ox (IEM 202-0860)	Late Pleistocene	New Siberian Islands
Musk Ox (GIN 367/117)	Late Pleistocene	Aldan
Woolly Rhino (5-18438)	Pleistocene	Not Applicable
Woolly Rhino (9-10693)	Pleistocene	Nizhnyi Novgorod District, Irset River

Primer Details

The primers were designed to the desired length by adding a by adding a neutral 40-bp sequence (5′-AACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA-3′) and a poly(C) tail to the 5′ end of the PCR primer (1,2). The neutral sequence is a randomly generated sequence not matching any sequence when a simple Basic Local Alignment Search Tool (BLAST) search is done in GenBank®. Primers for woolly rhino (WR15500F and WR15600R) were designed for this study, the musk ox dloop L1 and H1 primers are from MacPhee et al (3).
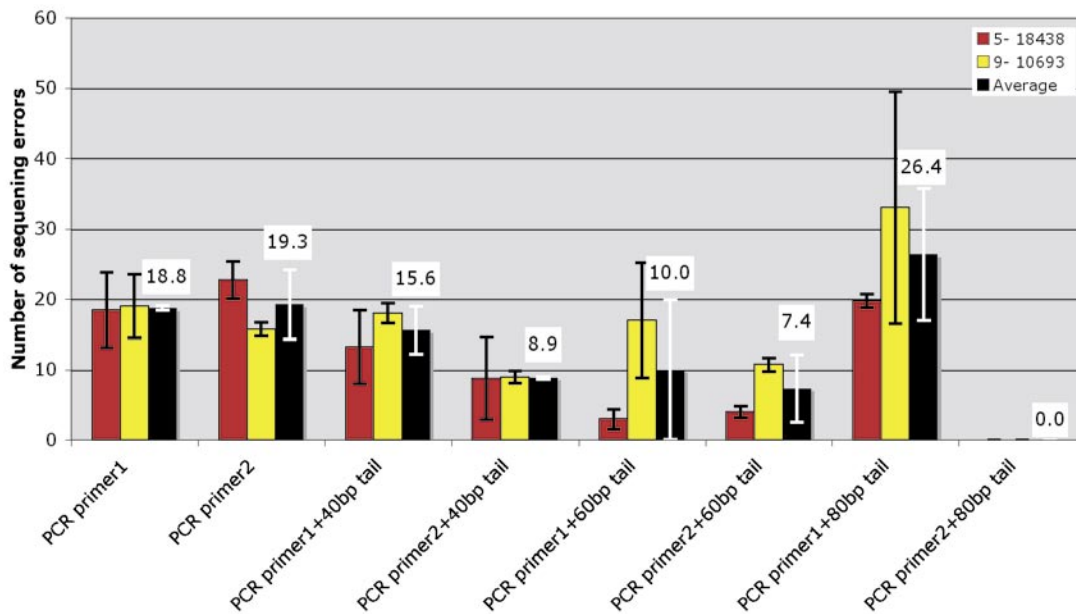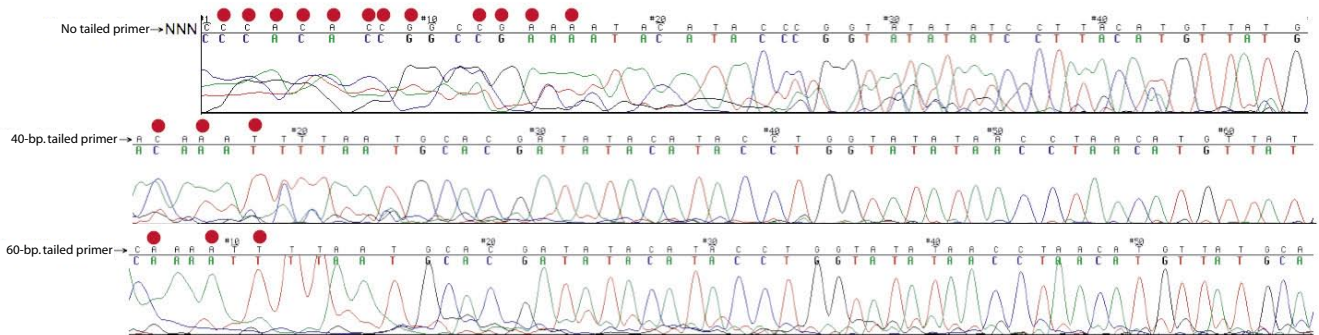
Benchmarks

Supplementary Table S2. Primer Details

Name	Full Sequence[a]	Performance[b]
Wr15500F	5′-CACTCCCTTCTTAAACCA(C/G)AAG-3′	1
Wr15600R	5′-CATGCTTATATGCATGGGGC-3′	1
Wr15500F + 40-bp tail	5′-AACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**CACTCCCTTCTTAAACCA(C/G)AAG**-3′	1.2
Wr15600R + 40-bp tail	5′-AACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**CATGCTTATATGCATGGGGC-**3′	2.2
Wr15500F + 60-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**CACTCCCTTCTTAAACCA(C/G)AAG**-3′	1.9
Wr15600R + 60-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**CATGCTTATATGCATGGGGC**-3′	2.6
Wr15500F + 80-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**CACTCCCTTCTTAAACCA(C/G)AAG**-3′	0.7
Wr15600R + 80-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**CATGCTTATATGCATGGGGC**-3′	N.A.
dloop L1	5′-AAAGGATCCTAAACTACTCCCTGAATT-3′	1
dloop H1	5′-AAAGGATCCATCATGCGTTGTTGCGT-3′	1
dloop L1 + 40-bp tail	5′-AACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**AAAGGATCCTAAACTACTCCCTGAATT-**3′	2.4
dloop H1 + 40-bp tail	5′-AACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**AAAGGATCCATCATGCGTTGTTGCGT**-3′	4.6
dloop L1 + 60-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**AAAGGATCCTAAACTACTCCCTGAATT**-3′	2.4
dloop H1 + 60-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**AAAGGATCCATCATGCGTTGTTGCGT**-3′	2.6
dloop L1 + 80-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**AAAGGATCCTAAACTACTCCCTGAATT**-3′	1.9
dloop H1 + 80-bp tail	5′-CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCAACTGACTAAACTAGGTGCCACGTCGTGAAAGTCTGACAA**AAAGGATCCATCATGCGTTGTTGCGT**-3′	0.5

[a]The specific part of the tailed primers is written in bold.
[b]Performance is calculated by dividing the average sequencing errors of nontailed PCR primer with the average sequencing errors of the tailed sequencing primer. N.A., not available due to very divergent sequence produced, that could not be aligned in Sequencher™ 3.1.1 using default settings.

Woolly Rhino Data

Supplementary Figure S1. Number of sequencing errors in a 113-bp region of the D-loop of two woolly rhino (*Coelodonta antiquitatis*) samples (5-18438 and 9-10693). Black columns and numbers are the average number of sequencing errors for each sequencing primer for the two samples with 3–4 sequence runs for each sample. Error bars indicate standard deviation. One primer (PCR primer2 + 80-bp tail) performed poorly and did not produce a sequences that could be aligned in Sequencher 3.1.1, thus no data is available for this primer.

Supplementary Figure S2. Examples of electropherograms showing the beginning of sequencing runs with nontailed primer and 40- and 60-bp tailed primers, respectively. The electropherograms are shown from the first position after the primer, except for the nontailed primer electropherogram in which the three first nucleotides where not detected (indicated by NNN). Red circles show where Sequencher 3.1.1 misreads the electropherograms compared to the known sequence (only for the first 20 nucleotides). The examples are from woolly rhino sample 5-18438 using WR15600R primers.

Positions and Types of Sequencing Errors

		1	11	21	31	41	51	61	71	81	91	101	111	
IEM 202-0860 CONSENSUS		GTGGAGTA-G	GA-AATTA-G	T-GTTATATT	ATTGAAA-GT	TTT-GGT-AG	ATTTGATACT	GGGAAGGC-T	CT-TAATGTT	TTTAGTGGTA	TA-TT-AATA	GA-A-G-GTG	TTA-GTGGT	
IEM 202-0860 H1-no tail		.C.TGCG...	.G.T.:....	....	C..CCCCC..	.......G	GGG...GG..	.......A	.......A	....	..A.A.	....	....	19
IEM 202-0860 H2-no tail		A.....A...	.G......A.	....	.T..	....	.......T	....	....	....	....	....	....	07
IEM 202-0860 H3-no tail		.....AT..	.G...A....	....	.G GGG...:..	....	....	....	....	...A.AA.	....	....	....	12
IEM 202-0860 H1-40bp tail	AG....	....	....	....	....	.C..	....	....	....	....	....	....	04
IEM 202-0860 H2-40bp tail	.AA....	....	....	....	....	....	....	....	....	....	....	....	03
IEM 202-0860 H3-40bp tail	.A....	....	....	.A AAAA..A.	....	....	....	....	....	....	....	....	07
IEM 202-0860 H1-60bp tail	T.CTT.GG.T	TC.CCC.G.T	......C..C	...T..	....	....	....	....	....	....	....	....	17
IEM 202-0860 H2-60bp tail	.GTA..G..A	:.....A..	AA..A.A..	....	....	....	....	....	....	.......G.	....	....	12
IEM 202-0860 H3-60bp tail	TCA.T..C..	AG.......	A..C..:..	.CTTTC.:	.......T.	....	....	....	....	....	....	....	18
IEM 202-0860 H1-80bp tail	..AT...G.	.......T..	....	:::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	78
IEM 202-0860 H2-80bp tail	T..T.:::..	.TT...T.	....	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	::::::::::	79
IEM 202-0860 H3-80bp tail	...:.G.A	.......T.T	....	....	..G..A	.......A..	....	....	.G..A. A..	....A....	......G.	....	14

		1	11	21	31	41	51	61	71	81	91	101	111	
IEM 202-0860 CONSENSUS		GTGGAGTA-G	GA-AATTA-G	T-GTTATATT	ATTGAAA-GT	TTT-GGT-AG	ATTTGATACT	GGGAAGGC-T	CT-TAATGTT	TTTAGTGGTA	TA-TT-AATA	GA-A-G-GTG	TTA-GTGGT	
IEM 202-0860 L1-no tail		....	....	.T.T..	C.CCCC...	....	....	:C.TTT..	T..CTC...	....	....AT	.G.G.T.T.T AGG....T:	32
IEM 202-0860 L2-no tail		.......T	....	.T..	C.CTC....	....	....	CCATTTT.T.	..TT...	....	...C.:.	.TG....T	.T.AC...	28
IEM 202-0860 L3-no tail		....	....	....	....	....	....	....	.CCCC...	....	...C.T	.T.AC...	11
IEM 202-0860 L1-40bp tail		....	....	....	....	....	....	....	..T..	....	....	...TGT.	04
IEM 202-0860 L2-40bp tail		....	....	....	....	....	....	.C.C..C.C.	T..TT.CCC	....	....A.C.	...CGT.	16
IEM 202-0860 L3-40bp tail		.A......	....	....	.T.......	.......G.G	.......C..	.:T......	.C..CCCCCC	.CC..v..	...TA.A.C	..CC.C..	24
IEM 202-0860 L1-60bp tail		....	....	....	....	....	....	....	....	....	....	..A.GT.	03
IEM 202-0860 L2-60bp tail		....	....	....	....	....	....	....	..T.	....	A.T.G.T.	..G.A..G.	.G.TAA.C	13
IEM 202-0860 L3-60bp tail		....	....	....	....	....	....	....	....	....	....	...:A....	02
IEM 202-0860 L3-80bp tail		...G.G.	....	T.A......	....	.......C.	....	.C.......	....	A......G.	..C.AT..	11

Supplementary Figure S3. Alignment showing the types and positions of the sequencing errors for each sequencing run. Primer sequences have been removed. The number following each sequence is the total number of sequencing errors. ".''s are insertions added when comparing each sequence with consensus sequence in Sequencher version 3.1.1, these are counted as sequencing errors. "-''s are used to align all sequences together and are not counted as sequencing errors.

Supplementary Figure S4. Alignment showing the types and positions of the sequencing errors for each sequencing run. Primer sequences have been removed. The number following each sequence is the total number of sequencing errors. "."s are sequencing errors. ":"s are insertions added when comparing each sequence with consensus sequence in Sequencher version 3.1.1, these are counted as sequencing errors "-"s are used to align all sequences together and are not counted as sequencing errors.

```
                            1          11         21         31         41         51         61         71         81         91         101        111
                            |          |          |          |          |          |          |          |          |          |          |          |
IEM 199-007 CONSENSUS       ATGGA-G-T- A-GG-AAATT AG-TGTTATA TTATTGAAAG TTTTGGTAGA TTTGAT-ACT GGGAAGGCT- C-T-TAATGT TTTTAGTGGT ATATTAATAG AA-GG-TGTT A-G-TGCT 00
IEM 199-007H1-no tail       .G......GC ..T..GT.:  .......... .GG......  ..........  .........  ..........  .........  ..........  ......A..A  .......... 15
IEM 199-007H2-no tail       GA......G. G.AT..GG.A .......... .GGG.....  ..........  ....A....  ..........  .........  ...A......  .......... .......... 15
IEM 199-007H3-no tail       .G......G. C..A.T.GGC .TA......  .......... AGG:..A.:  .........T: G.........  .........  ..G..G.AA  .......... 25
IEM 199-007H1-40bp tail     GG........ .......... .......... ..........  .........  .........  ..........  .........  ..........  .......... .......... 02
IEM 199-007H2-40bp tail     .GT....... .......... .......... ..........  .........  .........  ..........  .........  ..........  .......... .......... 02
IEM 199-007H3-40bp tail     GA........ .......... .......... ..........  .........  .........  ..........  .........  ..........  .......... .......... 02
IEM 199-007H1-60bp tail     T...G..... ....G..... .......... ..........  .........  .........  ..........  .........  ..........  .......... .......... 03
IEM 199-007H2-60bp tail     T...G..... ....G..... T...T..... ..........  .........  .........  ..........  .........  ..........  .......... .......... 05
IEM 199-007H3-60bp tail     T......G.. .A........ .......... ..........  .........  .........  ..........  .........  ..........  .......... .......... 03
IEM 199-007H1-80bp tail     .G..A..G.. ...A...... T......... .......C.  .......G.  .........  ...T......  .........  G..G.A..A.A .C..G....  .......... 16
IEM 199-007H2-80bp tail     T......G.. ....G..... T....T.T   .........  .........  .........  ....T.....  .........  ...A...A   ...G......  .......... 12
IEM 199-007H3-80bp tail     CCCCC.C.C. G...CCCCA  C.C.CC.A. AC........T: .......A.  .........  ..........  .........  ..........  .......... .......... 22


IEM 199-007 CONSENSUS       ATGGA-G-T- A-GG-AAATT AG-TGTTATA TTATTGAAAG TTTTGGTAGA TTTGAT-ACT GGGAAGGCT- C-T-TAATGT TTTTAGTGGT ATATTAATAG AA-GG-TGTT A-G-TGCT 00
IEM 199-007L1-no tail       .......... .......... .......... ..........  .........  ....GG...  ..........  .........  .G..G..... ...G..G... .....T.C 08
IEM 199-007L2-no tail       .......... .......... .......... ..........  .........  ....C...A  ..C.C.....  .........  GA .G...G.CC T.A.A.GG 17
IEM 199-007L3-no tail       .......... .......... T.:T.T.... .........  .........  .........  C.C.CC....  .........  .G...G...  .G...G... TT.:G.:: 15
IEM 199-007L1-40bp tail     .......... .......... .......... ..........  .........  .........  ..........  .........  .G...G...  ..C...C 04
IEM 199-007L2-40bp tail     .......... .......... .......... ..........  .........  .........  ..........  .........  ...A.....  .......C 02
IEM 199-007L3-40bp tail     .......... .......... .......... ..........  .........  .........  ..........  .........  ..........  .....A 01
IEM 199-007L1-60bp tail     .......... .......... .......... ..........  .........  .........  ..........  .........  ..........  .T...... 01
IEM 199-007L3-60bp tail     .......... .......... ..A...... ..........  .........  .........  ..........  .........  ..........  .T..... 02
IEM 199-007L1-80bp tail     .......... .......... .......... ..........  .........  .........  ..........  .........  ...A......  .......... 02
IEM 199-007L2-80bp tail     .......... .......... ..A...... ..........  .........  .........  ..........  ...G...... ...A.....G ..A.G.G. 06
IEM 199-007L3-80bp tail     .......... .......... .......... ..........  .........  .........  ..........  .........  T.T....A  ..T....TC 07
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Supplementary Figure S5. Alignment showing the types and positions of the sequencing errors for each sequencing run. Primer sequences have been removed. The number following each sequence is the total number of sequencing errors. ":"s are insertions added when comparing each sequence with consensus sequence in Sequencher version 3.1.1, these are counted as sequencing errors. "."s are used to align all sequences together and are not counted as sequencing errors.

```
                      1          11         21         31         41         51         61         71         81         91        101        111        121

5-18438 CONSENSUS             AAACAATTTA A-TG-CACG- A-TATACATA CCTGGTATAT AACCTAACAT GTTATGCACG ATATACA-TA AGCGGGTGAC AGATATTATT GATAC-TG-- AGG-T-GT-C A-CA-TGGT- GGGATGT

5-18438-15500F1-no tail       ...G....   ..........  .A.......  ..........  ..........  ..........  ..G......  ..........  G..A....   TT.....TA  ..........  ..C..:::   ::::::::   24
5-18438-15500F2-no tail       ..........  ..........  .A.......  ..........  ..........  ..........  ...G.....  ..........  .C...T..   .G...T.   ..........  ..........  ::::::::   22
5-18438-15500F3-no tail       ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ....T.   ..T......  .....TAG.  .::::::::  13
5-18438-15500F4-no tail       ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  .C......   ..G...T.  ..........  ..AC.CT.   TAT..:::   15
5-18438-15500F1-40bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ....T.   ...T.....  ...CCC..  T..T..G   10
5-18438-15500F2-40bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..A....   ...A.   ..T.T..   ....CCT.   .T.G.A   11
5-18438-15500F3-40bp tail     .........A  ..........  ..........  ..........  .A.......  ..........  ..........  ..........  .G...AT.A  T...CT.C.  C..C....  .........  TACGA..   21
5-18438-15500F4-40bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ..T......  ..........  ....AT..   ..........  ..T....CCC.  T..T..A   11
5-18438-15500F1-60bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  .G....A  .....C.   03
5-18438-15500F2-60bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ...T.....  ..........  ..........  ..........  ..........  .G....T  ....CG   05
5-18438-15500F3-60bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ...CT.   02
5-18438-15500F4-60bp tail     ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ...CT.   02
5-18438-15500F1-80bp tail     ..........  ..........  ..C...   .A.A.A.A.   ..........  ..T.T..C.  ..A......  ..A..G.G.  ..A..A..T.  T........  ..........  .C......  .GGCG   20
5-18438-15500F2-80bp tail     ..........  ..........  ..C...   .A.A.A.A.   ..........  ..T.T..C.  ..A.....   ..A..G.C.  ..A..A..T.  T.A......  ..........  ..........  .GG.G   21
5-18438-15500F3-80bp tail     ..........  ..........  ..C...   .A.A.A.A.   ..........  ..T.T..C.  ..A.....   ..A..G.C.  ..A..A..T.  T........  ..........  .C......  .......   19
5-18438-15500F4-80bp tail     ..........  ..........  ..........  .A.A.A.A.   ..........  ..T.T..C.  ..A.....   ..A..G.G.  ..A..A..T.  T........  ..........  .A......  ...G...   19
```

```
                      1          11         21         31         41         51         61         71         81         91        101        111        121

5-18438 CONSENSUS             AAACAATTTA A-TG-CACG- A-TATACATA CCTGGTATAT AACCTAACAT GTTATGCACG ATATACA-TA AGCGGGTGAC AGATATTATT GATAC-TG-- AGG-T-GT-C A-CA-TGGT- GGGATGT

5-18438-15600R1-no tail       :::.GTCC.C  G.G......   .C..A.A...  .C..A.G.   .G..T.:.C  ..........  ..........  ..........  ..........  T.......   ..........  ..........  ........   23
5-18438-15600R2-no tail       :::.GC..T  G.AA...:.G  .CA.A.AT..  .C...TG.   TG.:.....  ..........  ..........  ..........  ..........  T.......   ..........  .T......  ........   25
5-18438-15600R3-no tail       :::::.A..   ....GCG..  AA...A...  TC.A.G.:   ..........  ..........  ..........  ..........  ..........  T.......   ..........  ..........  ........   24
5-18438-15600R4-no tail       :::.CCACAC  C.G...CGA.  .A.......  ...C.....  .T..T.:   ..........  ..........  ..........  ..........  T.......   ..........  ..........  ........   19
5-18438-15600R1-40bp tail     C.TATC..A.  C...G....A  .....T....  ..........  ..T......  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   11
5-18438-15600R2-40bp tail     .C.T.T...   .A.......  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   04
5-18438-15600R3-40bp tail     C.G.GGC...  G.G.G.T.A.  .A.A......  ..........  ..A..:....  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   16
5-18438-15600R4-40bp tail     .C.A.T....  ..........  ..........  ..........  ..A...:T.T  ..........  T........  ..........  ..........  ..........  ..........  ..........  .A......   04
5-18438-15600R1-60bp tail     ..ATTC....  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   04
5-18438-15600R2-60bp tail     ..ATTC....  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   04
5-18438-15600R3-60bp tail     C..ATTC...  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   05
5-18438-15600R4-60bp tail     C..A.T....  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ..........  ........   03
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Supplementary Figure S6. Alignment showing the types and positions of the sequencing errors for each sequencing run. Primer sequences have been removed. The number following each sequence is the total number of sequencing errors. ":"s are insertions added when comparing each sequence with consensus sequence in Sequencher version 3.1.1, these are counted as sequencing errors. "-"s are used to align all sequences together and are not counted as sequencing errors.

```
                    1          11         21         31         41         51         61         71         81         91         101        111        121
                    |          |          |          |          |          |          |          |          |          |          |          |          |
9-10693_CONSENSUS            AAACAATTTA -AT-GCACGA -TATACATAC CTGGTATATA ATCTAGCATG TTATGTA-CG A-CGTACATA A-GCGGGTGA CAGATATTAC -TGATAC-TG AG-GT-G--T C-AC-ATGG- -TGAGATGT

9-10693_15500F1-no tail      ..........                                                                                                          .A.CTA.GC TT..C..... C A.GG..C::.   .:::::::::: 25
9-10693_15500F2-no tail      ..........                                                                                                          .......:.: C A.T......              .GCCCC:::   14
9-10693_15500F3-no tail      ..........                                                                                                          .......... .CA.     ...G.GCCC.   .:::::::::: 19
9-10693_15500F4-no tail      ..........                                                                                                          .......:.: .A.....C A.T.....C CC:::::::   18
9-10693_15500F1-40bp tail    ..........                                                                              A.T...A.   .:.G..:A C.TC... .G G..A...T .AC..TG.G 19
9-10693_15500F2-40bp tail    ..........                                                                              A.......   T.T.C...T C....... .A A..T.G.AC .A.T.G.CA 18
9-10693_15500F3-40bp tail    ..........                                                                              .A......   .A..C.T.C G.......  G.TA.C..T. G.TC.A.A 16
9-10693_15500F4-40bp tail    ..........                                                                       .CA.....   A.GC.A.CT TC....... .A..A....T .AC..TG.. 19
9-10693_15500F1-60bp tail    ..........                                                   .C.C .C.  .C.......    .A..C..GT C...C.A.. G.T..:.AC  ...TCG.CA 21
9-10693_15500F2-60bp tail    ..........                                                   .C..C.C .C.  .C.......   .A..C..GT C...C.A.A G.T..:.AC  ...TCG.CA 23
9-10693_15500F3-60bp tail    ..........                                              .C...........   .C.......    .::.G..CA .C..C...C.  .T.G.CT. .ACT.TC.G 19
9-10693_15500F4-60bp tail    ..........                                                                              .T..T.....   .T.T...   ..:..:.A 05
9-10693_15500F2-80bp tail    .....C....     A.A.A.A.          .C.C.T .T.T....C C..CCC.... .C...G.    .AA.A ....C... G.CAA...... .T.A...C.. .AACA.C... 33

9-10693_CONSENSUS            AAACAATTTA -AT-GCACGA -TATACATAC CTGGTATATA ATCTAGCATG TTATGTA-CG A-CGTACATA A-GCGGGTGA CAGATATTAC -TGATAC-TG AG-GT-G--T C-AC-ATGG- -TGAGATGT

9-10693_15600R1-no tail      TT.TG.GCA. .T...:.T.G ....G.......            .G. CA....     ..........                                                  .......... 15
9-10693_15600R2-no tail      .TT.GG...T G.C.T.T.T. .GC.G:....            .T......     ..........                                                  .......... 15
9-10693_15600R3-no tail      .CCTTGG.A. .G..TT.TC .TGG.......            .T......     ..........                                                  .......... 16
9-10693_15600R4-no tail      CCT.GG.A:. .G..AG.TC .TGG.......            ..T...T      ..........                                                  .......... 17
9-10693_15600R1-40bp tail    CG.AGG..A. ........G .G...........                     ..........                                                  .......... 08
9-10693_15600R2-40bp tail    CG.AGG..A. .......G.G .G.............                  ..........                                                  .......... 09
9-10693_15600R3-40bp tail    CGTTGG..A. ........G .G.............                   ..........                                                  .......... 09
9-10693_15600R4-40bp tail    TCGTTG.... ..T.T..G .G............                     ..........                                                  .......... 10
9-10693_15600R1-60bp tail    G..GGT.A.. ..:...G.G .AG..........                     ..........                                                  .......... 10
9-10693_15600R2-60bp tail    CG.AGG...T TG....G.G .G............                    ..........                                                  .......... 11
9-10693_15600R3-60bp tail    G..GTT...T ......G.G .AG..........                     ..........                                                  .......... 10
9-10693_15600R4-60bp tail    CG.AGG..A. .T..G.A.G G.G..........                     ..........                                                  .......... 12
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Supplementary Figure S7. Alignment showing the types and positions of the sequencing errors for each sequencing run. Primer sequences have been removed. The number following each sequence is the total number of sequencing errors. "."s are insertions added when comparing each sequence with consensus sequence in Sequencher version 3.1.1, these are counted as sequencing errors. "-"s are used to align all sequences together and are not counted as sequencing errors.

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