Erratum to: Improving non-invasive genotyping in capercaillie (*Tetrao urogallus*): redesigning sexing and microsatellite primers to increase efficiency on faeces samples

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Published online: 3 July 2012
© Springer Science+Business Media B.V. 2012

**Erratum to: Conservation Genet Resour (2011)
3:483–487
DOI 10.1007/s12686-011-9385-8**

are incorrectly placed. The author apologizes for this error.
The correct Table 1 is provided below.

Unfortunately, in the original publication of the article, the
sequences of most of the internal primers listed in Table 1

The online version of the original article can be found under
doi:[10.1007/s12686-011-9385-8](https://doi.org/10.1007/s12686-011-9385-8).

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Table 1 Primers used (#F and R: forward and reverse external primers, FI and RI: forward and reverse internal primers)

Locus (i, j) ^a	Fluorescence	Primer sequence (5' → 3') [#]	Tpa. annealing (°C)	Allele size range (bp)	ADO	FA	GeneBank accession no.	Reference
TUD4 (1,1)	–	F: TTAGCAACCGCAGTGATGTG	60	93–125	0.08	0.00	AF254647	Segelbacher et al. (2000)
	–	R: GGGAGGACTGTGTAGGAGAGC						Segelbacher et al. (2000)
	HEX	FI: TCCCAAGGAGAGACAAAAGG						This work
TUT3 (1,1)	–	F: CAGGAGGCTCAACTAATCACC	60	103–111	0.02	0.00	AF254655	Segelbacher et al. (2000)
	–	R: CGATGCTGGACAGAAAGTGAC						Segelbacher et al. (2000)
	FAM	RI: TGAGGGATTTATGCAITGCTGC						This work
TUD3 (1,2)	–	F: TCCAAAGGGGAAAAATATGTGTG	60	120–122	0.09	0.04	AF254646	Segelbacher et al. (2000)
	–	R: TTCTCCAGCCCTAGCTTTG						Segelbacher et al. (2000)
	FAM	RI: TGGCTCTATTAAAGCTGCTG						This work
TUT1 (1,2)	–	F: GGTCTACATTTGGCTCTGACC	60	147–171	0.10	0.00	AF254653	Segelbacher et al. (2000)
	–	R: ATATGGCATCCAGCTATGG						Segelbacher et al. (2000)
	HEX	FI: GTATATCTGTCTGTCTGCCCC						This work
TUD1 (2,1)	–	F: ATTTGCCAGGAACTTGCTC	59	165–173	0.03	0.00	AF254644	Segelbacher et al. (2000)
	–	R: AACTACCTGCTGTGTGCTTGG						Segelbacher et al. (2000)
	FAM	RI: TGAACATAAACCTTTGCCCTCC						This work
TUD2 (2,1)	–	F: GTGACAACTCAGCCCTGTC	59	152–168	0.00	0.00	AF254645	Segelbacher et al. (2000)
	–	R: AATAAGGTGGGCATACACC						Segelbacher et al. (2000)
	HEX	FI: GGTCTTCTAACGCTGTGTCAC						This work
TUD5 (2,2)	–	F: CCTTGCTGCACATTTTCTCC	59	101–117	0.02	0.00	AF254648	Segelbacher et al. (2000)
	–	R: GGTGCTGAGCATGTACTAGGG						Segelbacher et al. (2000)
	NED	FI: CTGTACACAGCACTGAGCC						This work
TUD7 (2,2)	–	F: TGACACTGGGTCTATTAGGC	59	157–161	0.02	0.00	AF254650	Segelbacher et al. (2000)
	–	R: AACATGGGCAGGAGGAGAC						Segelbacher et al. (2000)
	HEX	RI: CCTCTGGTGAAAGGGGAATGG						This work
BG10 (3,1)	–	F: ATGTTTCATGTCTTCTGGAATAG	57	175–199	0.09	0.00	AF381546	Piertney and Höglund (2001)
	–	R: ATTTGGTTAGTAACGCATAAGC						Piertney and Höglund (2001)
	HEX	RI: GCATACTATACTGTCTATGCAG						This work
BG15 (3,1)	–	F: AAATATGTTTGTAGGGCTTAC	57	110–126	0.33	0.03	AF381549	Piertney and Höglund (2001)
	–	R: TACATTTTTCATTGTGGACTTC						Piertney and Höglund (2001)
	FAM	RI: GCTCCCTGTAAAGGTAAATAGA						This work
BG16 (3,2)	–	F: GTCATTAGTGTCTGTCTATCT	57	133–145	0.14	0.06	AF381550	Piertney and Höglund (2001)
	–	R: TGCTAGGTAGGTAAAAATGG						Piertney and Höglund (2001)
	HEX	RI: CGGATGAATGGATGGAGGGG						This work
BG18 (3,2)	–	F: CCATAACTTAACCTTGCACTTTC	57	153–169	0.00	0.00	AF381551	Piertney and Höglund (2001)
	–	R: CTGATACAAAGATGCCTACAA						Piertney and Höglund (2001)

Table 1 continued

Locus (i, j) ^a	Fluorescence	Primer sequence (5' → 3') [#]	Tpa. annealing (°C)	Allele size range (bp)	ADO	FA	GeneBank accession no.	Reference
BG12(3,3)	FAM	FI: CAGAATTAATGTTTGGCTCTAAC	57	139–147	0.11	0.04	AF381547	This work
	–	F: TCTCCTTCTAAACCAGTCATTG						Piertney and Höglund (2001)
	–	R: TAGTTTCCACAGAGCACATTG						Piertney and Höglund (2001)
TUD6(3,3)	FAM	RI: CAATGTCGTGGCCCACTGAG	57	151–155	0.08	0.02	AF254649	This work
	–	F: GGTGAGCAAGCCACAAAATAAC						Segelbacher et al. (2000)
	–	R: GAGGACTGCAGAACCCACTG						Segelbacher et al. (2000)
	NED	FI: GCCTTTACTGCACTACTGC						This work

Alelic dropout (ADO) and false alleles (FA) values for each locus are included

New primers designed for this work are in bold

^a Identifier number of preamplification (i) and amplification (j) PCR