

Table S2. Single base extension primers

Name	Forward SNUPE primer (5'-3')	Reverse SNUPE primer (5'-3')
Blut1-1f+2r	GGG GTA TAG TTG TTT AGT AAT AGG	CTA AAA AAT ACA AAC TTA AAA AAT ACA AAA C
Blut1-1f+2r	GTA GTT TTG GTA AGA ATT AAA GGA A	CCA TAT ACC CTA AAA TTC TAC CAC
Mens1-F3m	<u>GGC</u> GTT TGT TGT TGG <u>TTC</u>	---
Mens1-F3nm	<u>GIG</u> TTT GTT GTT GGT <u>TIG</u> G	---
Spei1-Fm	CTT TCA CAA <u>CGC</u> TCA <u>CG</u>	---
Spei1-Fnm	CTT CTT TCA CAA <u>CAC</u> TCA <u>CAT</u>	---
Spei2-3r	---	GAG TAG GTA TAT TGT TTT TTG TTT TTT T
Vag1-1r	---	TAA TTA AAA AAA AAA TCA TCA ACA TAA AC
Vag2-1f	ATA TTT GGG TAG AGT TAT TTT TTT GTT	---
Sperm1-4r	---	TTT TTT TTA TAT GTG AGG AAA GAG
Sperm2-3r	---	GTG GGG AGT TGG GTT TT

SNUPE primer sequences are specific for the first bisulfite converted DNA strand (Blut1, Blut2, Mens1, Vag1 and Vag2) or the second one (Spei1, Spei2, Sperm1 and Sperm2). In methylaton specific primers (Mens1 and Spei1) the discriminating bases are underlined.