

Table 1 Primers for the amplification and identification of whole genome

primers	Sequences (5'–3')	Positions	Size(bp)
F (1-623)	TTTGAAATGGGGGGCTGGG	1-623	623
R(1-623)	CTATCAGGCAGTATCCAAAGCACGC	1-623	
(498-1352)M13+	CGACCCAGGACTTCTTTTGAAT	498-1352	855
(498-1352)M13-	GAGAAGGTTTTTACAGCT	498-1352	
(1336-1662)M13+	GCTGTAAAAACCTTCTC	1336-1662	327
(1336-1662)M13-	ATAGTATGTGCCAAGAG	1336-1662	
(1612-2748)M13+	GATTACCGGACCGGAAAAACAT	1612-2748	1137
(1612-2748)M13-	ACCAGAGAAATCGGTGTCAGT	1612-2748	
(2996-4041)M13+	CTTCACTGGACTTCAATTTTTATA	2996-4041	1046
(2996-4041)M13-	CTCCAAC TGGTACTGGAGGACAG	2996-4041	
(4004-4995)M13+	AAGAGAAAGCCAGCCCTGTCCTCC	4004-4995	991
(4004-4995)M13-	ACCTAGCTTGGCAAGAATAGCCAAACG	4004-4995	
(4929-5949)M13+	GGCGCTTGTCGACCTCACTCCAGA	4929-5949	1021
(4929-5949)M13-	ATCAAATTTTGACAACACAGCA	4929-5949	
(5879-6908)M13+	AATTGAGAAAGACGACCGCACA	5879-6908	1030
(5879-6908)M13-	GTCATCTTATACCCCAACTT	5879-6908	
(6881-7297)M13+	GCGCTGCCAAGTTGGGGTATAA	6881-7297	417
(6881-7297)M13-	CCTTTTCTGTTCCGACTGAGTT	6881-7297	
SVV-F	AACCGGCTGTGTTTGCTAGAG	59–79	
SVV-R	GAAC TCGCAGACCACACCAA	205–186	147
SVV-P	6/FAM-TCGAGAAGCTGCAATCTG/MGB-	143–167	