



**Supplementary Figure S1.** Geographic distribution of ASFV variants in Europe and Asia based on the partial sequencing of CVR (B602L gene)—(A), and the Intergenic region I73R/I329L (IGR)—(B). Number and size of dots do not reflect the number of outbreaks.

**Supplementary Table S1.** List of 24 ASFV isolates used in the phylogenetic analysis to confirm the respective genotypes.

Accession number	Isolate name	Country	Genotype
DQ250114	SPEC-205	Namibia	I
FR682468.2	Georgia 2007/1	Georgia	II
DQ250120	SPEC/257	South Africa	III
AF449477	RSA 1/1999	Thabazimbi/South Africa	IV
AF270708	Tete	Mozambique	V
AF270710	SPEC-265	Mozambique	VI
AF302818	RSA 1/1998	South Africa	VII
AF270705	Tete-1	Mozambique	VIII
MH025916	R8	Uganda	IX
AF449463	BUR-1	Burundi	X
AY351522	KAB	Zambia	XI

AY351543	MZI-921	Malawi	XII
AY351542	SUM-1441	Zambia	XIII
AY351555	NYA	Zambia	XIV
AY494552	Tan-1	Tanzania	XV
AY494551	Tan-2	Tanzania	XVI
DQ250119	Zim-1	Zimbabwe	XVII
DQ250122	NAM 1/1995	Windhoek, Namibia	XVIII
DQ250127	3-Pienaars	South Africa	XIX
DQ250109	Lillie	South Africa	XX
DQ250125	1-Gravelotte	South Africa	XXI
DQ250117	SPEC-245	South Africa	XXII
KT795360	ETH-3	Ethiopia	XXIII
KY353989	Moz10	Mozambique	XXIV

**Supplementary Table S2. Primer sequences previously described for the amplification and sequencing of ASFV genotype II markers.**

Marker	Primer	Sequence (5'–3')	Position	Fragment length (bp)	Reference
B646L (genotyping)	P72-F	GGCACAAGTTCGGACATGT	104,581–104,599	478	[4]
	P72-R	GTACTGTAACGCAGCACAG	105,040–105,058		
CVR of B602L gene	CVR-Fwd	AAGCTCATTAGGCACATTTAATGTTTTT GC	102,591–102,621	459	[30]
	CVR-Rvs	CTGCAGGAATGGATGCCTTC	103,030–103,049		
Intergenic region I73R/I329L (IGR)	ECO1A	CCATTTATCCCCGCTTTGG	172,272–172,291	356	[30]
	ECO1B	TCGTCATCCTGAGACAGCAG	172,608–172,627		
	IGR-F	CTC AGA ACT TTT TGA GAA GAT TG	172,236–172,258	349	[36]

	IGR-R	CAG CAA ACA GTC CTA TTG TT	172,585– 172,566		
Intergenic region MGF- 505 9R/10R	MGF- Fwd	AGAAACCGCAGATGAATGTA	45,079– 45,098	552	[38]
	MGF- Rvs	TACAGCCCTAGTTGTTGAAG	45,611– 45,630		
Intergenic region A179L/A137R	Forward	CCATAGCGGCACCCTATATT	55,295– 55,314	270	[39]
	Reverse	CCTCCTGGTCGAGTTTGTA	55,545– 55,564		
K145R	K145R- Fwd	TTTCAGGCTGAAAACCTTTTAT	66,015– 66,036	283	This study
	K145R- Rvs	AAAGTTTTCAATGGTTGTTAGC	66,276– 66,297		
O174L	O174L- Fwd	TGGCTCAGACGATATTTCAACTC	129,152– 129,174	673	[36]
	O174L- Rvs	GCCTCCACCACTTGAACCAT	129,805– 129,824		
MGF-505-5R	MGF- 505-5R-F	TACGCTTCTTTTCAATCATCAT	38,942– 38,963	641	[36]
	MGF- 505-5R- R	AAATTAACAGTTGTTTGCCTTC	39,561– 39,582		
I267L	I267L- Fwd	TTGGACAAATTGCGTTGCGA	170,704– 170,723	337	This study
	I267L- Rvs	AAATGCGACCGTCCAGAACT	171,021– 171,040		