



Figure S1. Neighbor-joining phylogenetic tree based on alignment of CA fragment of *gag* gene. Sequences from this study are labeled by black circles and their names are preceded by the flock origin and the animal species (s-sheep; g-goat). Numbers at the branches indicate the percentage of bootstrap values obtained from 1000 replicates. Bootstrap values >70% are shown.



Figure S2. Bayesian phylogenetic tree based on alignment of CA fragment of *gag* gene. The name of sequences from this study are preceded by the flock origin and the animal species (s-sheep; g-goat). Posterior probability of each node is showed above branches.

		Epitope 2										GG
Cork (B1)	LQTVMQHGLVSEDFERQLAYATTWTSKDILEVLAMPFGNRAQKELIC	GLNEEAERWRNRNFFPA	GG	GG	GG	GG	GG	GG	GG	GG	GG	GG
K1514 (A1)												Q.S.
13g9692 (A5)		M										HQ.S.A.
13g1318 (A5)												HQ.S.A.
13g8039 (A5)		M										HQ.S.A.
13g8008 (A5)		M										HQ.S.A.
13g8046 (A5)		M										HQ.S.A.
16s6 (A12)	N	M										Q.S.
16s40 (A12)	N	M										Q.S.
16s33 (A12)	N	M										Q.S.
16s16 (A12)	N	M										Q.S.
16s14' (A12)	CKN											Q.S.
16s13 (A12)	N	M										Q.S.
16s12 (A12)	N	M										Q.S.
16s1 (A12)	N	M										Q.S.
16s4 (A12)	N	M										Q.S.
16s3 (A12)	N	M										Q.S.
10g7134 (A12)												P.
10g7102 (A12)												Q.S.
10g8891 (A12)												Q.S.
10g7219 (A12)												Q.S.
10g6808 (A12)		R										Q.?
16g3535 (A12)	N	V										Q.S.
10g7096 (A12)		I										Q.S.
16g8699 (A12)		I										Q.S.
16g3533 (A12)	N	V										Q.S.
16g9509 (A12)	N	I	M									Q.S.
17g1580 (A17)		M										Q.S.
17g1485 (A17)		M										Q.S.
17g5686 (A17)		M										Q.S.
17g8172 (A17)												Q.S.
17g5621 (A17)		R										Q.S.
17g6909 (A17)		R										Q.S.
17g5654 (A17)		M										Q.S.
13s2590' (A23)												Q.S.
13s1622 (A23)												Q.S.
13s4315' (A23)												Q.S.
13s4018 (A23)												Q.S.
12s3201 (A24)												Q.S.
12s3188 (A24)												Q.S.
12s3225 (A24)												Q.S.
12s3249 (A24)												Q.S.
2s5023 (A24)												Q.S.
10s0334 (B2)												Q.S.
16g0788 (B2)												Q.S.
16g0599 (B2)												Q.S.
16g9510 (B2)												Q.S.
16g3535' (B2)												Q.S.
16g3540 (B2)												Q.S.
16g0580 (B2)												Q.S.
16s14 (B2)												Q.S.
16s20 (B2)												Q.S.
16s21 (B2)												Q.S.
16s29 (B2)												Q.S.
13s4315 (B2)												Q.S.
13s2590 (B2)												Q.S.
13s3275 (B2)												Q.S.
13s3691 (B2)												Q.S.
14s9855 (B2)												Q.S.

		MHR										Epitope 3									
Cork (B1)	QICLQWINALRAVRHMAHRPG	PMLV	QRTNE	PYEDFA	ARILEA	DAEP	VTQ	PKDY	LKLT	SYTN	ASAD	QQK	MDRT	LGH	QV	QQA	SV	EE	RM	QA	Q
K1514 (A1)		R	T	S	S																
13g9692 (A5)		T	S	S		I	N	S	E	I											
13g1318 (A5)		T	S	S		N	S	E	I												
13g8039 (A5)		T	S	S		N	S	E	I												
13g8008 (A5)		T	S	S		N	S	E	I												
10g8046 (A5)		T	S	S		N	S	E	I												
16s6 (A12)		T	S	S		N	S	E	I												
16s40 (A12)		T	S	S		N	S	E	I												
16s33 (A12)		T	S	S		N	S	E	I												
16s16 (A12)		T	S	S		N	S	E	I												
16s14' (A12)		LT	S	S		NS	S														
16s13 (A12)		T	S	S		N	S	E	I												
16s12 (A12)		T	S	S		N	S	E	I												
16s1 (A12)		T	S	S		N	S	E	I												
16s4 (A12)		T	S	S		N	S	E	I												
16s3 (A12)		I	S	S		N	S	E	I												
10g7134 (A12)						N	S														
10g7102 (A12)						N	S														
10g8891 (A12)		T	S	S		NS	S														
10g7219 (A12)		T	S	S		NS	S														
10g6808 (A12)						R	S														
16g3535 (A12)						RNS	S	E	I												
10g7096 (A12)		M				N	S	E	I												
16g8699 (A12)						NS	S														
16g3533 (A12)						NS	S														
16g9509 (A12)						RN	S	E	I												
17g1580 (A17)		V	S			R	N	S	E	I											
17g1485 (A17)		V	S			R	N	S	E	I											
17g5686 (A17)		V	S			R	N	S	E	I											
17g8172 (A17)						R	N	S	E	I											
17g5621 (A17)						R	N	S	E	I											
17g6909 (A17)						R	N	S	E	I											
17g5654 (A17)		V	S			R	N	S	E	I											
13s2590' (A23)		T	S	S		N	S	E	I												
13s1622 (A23)		A	S	S		N	S	E	I												
13s4315' (A23)		T	S	S		N	S	E	I												
13s4018 (A23)		T	S	S		N	S	E	I												
12s3201 (A24)		T	S	S		N	S	E	I												
12s3188 (A24)		T	S	S		N	S	E	I												
12s3225 (A24)		T	S	S		N	S	E	I												
12s3249 (A24)		T	S	S		N	S	E	I												
2s5023 (A24)		T	S	S		N	S	E	I												
10s0334 (B2)		L	S			SS	S														
16g0788 (B2)		S				G															
16g0599 (B2)		S				S															
16g9510 (B2)		S				S															
16g3535' (B2)		S				S															
16g3540 (B2)		S				S															
16g0580 (B2)		S				S															
16s14 (B2)		T	S			S															
16s20 (B2)		S				S															
16s21 (B2)		S				S															
16s29 (B2)		S				S															
13s4315 (B2)		S				S															
13s2590 (B2)		S				S															
13s3275 (B2)		S				S															
13s3691 (B2)		S				S															
14s9855 (B2)		S				S															

Figure S3. Alignment of deduced amino acid sequences of immunodominant epitopes of capsid protein and major homology region (MHR) of the SRLVs obtained in this study and reference strains. Identical residues are indicated by dots (.).