



**Figure S1.** Neighbor-joining phylogenetic tree based on alignment of CA fragment of *gag* gene. Sequences from this study are labeled by black circles. Subtypes are marked in different colors. Numbers at the branches indicate the percentage of bootstrap values obtained from 1000 replicates. Bootstrap values >70% are shown. In the present study, the SRLV subtypes found by Colitti et al. [23] were renamed from A18 to A19 and from A19 to A20 and subtypes found by Olech et al. [8] were renamed from A23 to A25 and from A24 to A26; goat 2 – blue, goat 3 – black, goat 4 – yellow, goat 5 – green, goat 6 – red, goat 7 – pink.

	V4	HV2
Consensus	TMWGIYKNCTGCANATLDRGTGNGTLGTGTVKNINCSLPHXNESNKWTCAARQNGGKRDSLYIAG-RDFWGRVKAQYS	
Cork B1	.....S..E.....N..E.....G.A.K.....K.....P..RD..T.....GKK..T.I...F.	
1217 B2	.....L..S..E.....A.N.....K.....I...DQ...P.WAK.IS.....GKQ..T....F.	
K1514 A1	...N..Q..SK.N.SS.....NDLK.....R.....RK.SR.....K.	
85/34 A2	..M..LR..S..K.....E.A..N...E..T...K...L...P.RRKRT.....G.Q..T.....	
697 A2/A3	E.MK.....E.N.T.FE.I.Y.....E.....K...T...S..KK.R-.....-	
6221 A4	..Q...G..SQ.V...N.....S.....R.K..Q...TA.K.....-	
5994 A5	..EH.R...N.T.S...E.....P.....K...E...Q..RSKN...V.....N.....	
4819 A12	.....Q...G...G...D.A...A.LS.....K...Q...T...TR...SA-GK..E.I.....	
0016 A13	..ER.Q.....H.....I..N.G.....K...Q...Q..AR.NQ...V.....N.....	
8344 A17	..EY...S..Q.E...E.....E.....P.....I...T...S..TR.E.....-	
1561 A17	..K..R..S..N.E..E...G.....L.....I...T...S..EGQ.....-H..E..	
It38 A19	...F...S..E.E...D...N...E.....R.....P.WGK.GS.....G.Q..T.....	
It009 A20	..KH.Q..SN.G...EV...N.....I..TK...A.DKR...N.....	
4315 A25	..RH.M..S..H...K...I.....G.....K...L...Q..S.KD...V.....N.....	
3201 A26	..ER.E...E.Q..A...E.A...A.K.....R...Q...TSKTRT.....-	
Goat4 L	..T.....C.V...E.T.....V...I..AKR.....KEER.....-	
Goat4 MG	..DT.....V...E.T.....V...I..AK.....KEER.....-	
Goat4 B	..T.....V...E.T.....V...I..AK.....KEE.....-	
Goat4 SM	..ST.T...M...K...E.....E.....V...KR.....DET.....-	
Goat2 SM	..T.....R...E.T.....V...L...KL.....KKKE.....-	
Goat2 PBMC	..T.....V...E.T.....V...L...KL.....K.K.....-	
Goat7 SM	..T.....M...E.T.....EV...I...KQ.....KD.....F.	
Goat6 L	..SK.....T.M...E.....DV...V...KL.K...EKR.....-	
Goat6 MG	..SK...K...M...E.T.....DV...V...GL...K.EKR.....-K..	
Goat6 SM	..SK.....T.M..N.E.S...E.....V...KR.....DET.....-	
Goat5 SM	..EY...E...E.....A.....L.....K..EI.....-	
Goat5 PBMC	..ST.....E.RD.G.....A.....V.....K..ER.....F.	
Goat5 B	..ST.....G...E.....A...V...V...KQ.....EG..R.....-	
Goat5 MG	..ST.....E...E.....AD...V...V...KQ.....ER..R.....F.	
Goat5 CHP	..ST.R...R...E.S.....A..K...V...KQ.....EG...-.....	
<b>Epitope SU5</b>		
Consensus	CESNIGGLDGMHQQXLLQRYQVIRVRAYTYGVVEMPESYXKSQVKRKR--DLKQGRKRK	
Cork B1	.....Q...L...I...K...K.....I...N.A.TRIINRK--KRELSH--	
1217 B2	.....EI...L...I.....ID..TH.G-LRNGNRK--KRELSH--	
K1514 A1	.....L...S...M.....Q...MEA.GENR---SRRNLQ--	
85/34 A2	.....L...I...K...K.....K...ME..KRK---STELQL--	
697 A2/A3	.....L...I.....ID..Q...IE..E.N---S.RSLQ--	
6221 A4	.....L...I.....ID..Q...MQN.E.N---A.R.LQ--	
5994 A5	.....L...V...I.....K.....D...I.T-.GRKR-STGITLR--	
4819 A12	.....L...I.....K.....D..K..ME..RRK---STELQLR--	
0016 A13	.....M.....K.....R...IEK.Q...QR-STELDL--	
8344 A17	.....V.....D..K..MET.-R..KG-STEPQLR--	
1561 A17	.....V.....D..K..LDTH-R...SPARHLE--	
It38 A19	...V.E...L..M...K...K.....DQ.L.TNKR...-STEVI LR--	
It009 A20	...L.....V.....K.....D..N..ME--KN..K--Q.RSLQ--	
4315 A25	.....L.....M.....K.....R..MET...KR-STELEL--	
3201 A26	.....L.....I..K.....Q...IEK.KRKR--STELIH--	
Goat4 L	.....V.....G..K.....-	
Goat4 MG	.....V.....G..KE.....-	
Goat4 B	.....V.....G..RN.....-	
Goat4 SM	.....M.....V...T.....I..EKR..	
Goat2 SM	.....L.....G..N.....-	
Goat2 PBMC	.....L.....G..N.....-	
Goat7 SM	.....L.....V.NK.T...-R...-	
Goat6 L	.....M.....V.NN.....-	
Goat6 MG	.....M.....G..N.....-	
Goat6 SM	.....M.....V...T.....I..EKR..	
Goat5 SM	.....L.....A..N.....-	
Goat5 PBMC	.....L.....V.XN.....-	
Goat5 B	.....V.....A.NN.....-	
Goat5 MG	.....L.....V.NN.....-	
Goat5 CHP	.....V.....I.D...V.T.KR.Q.SAEITLK...-	

**Figure S2.** Alignment of deduced amino acid sequences of immunodominant epitope of ENV protein and variable region V4 of the SRLVs obtained in this study and reference strains representing different subtypes. Deletions are indicated by a dash (-) and identical residues are indicated by dots (.). PBMC- peripheral blood mononuclear cells, L-lung, SM-synovial membrane, B-brain, CHP-choroid plexus, MG-mammary gland.

## References

- 8 Olech, M.; Kuźmak, J. Molecular Characterization of Small Ruminant Lentiviruses in Polish Mixed Flocks Supports Evidence of Cross Species Transmission, Dual Infection, a Recombination Event, and Reveals the Existence of New Subtypes within Group A. *Viruses* **2021**, *13*, 2529.
- 23 Colitti, B.; Coradduzza, E.; Puggioni, G.; Capucchio, M.T.; Reina, R.; Bertolotti, L.; Rosati, S. A new approach for Small Ruminant Lentivirus full genome characterization revealed the circulation of divergent strains. *PLoS ONE* **2019**, *14*, e0212585.