

Supplementary Figure S1a-b-c:

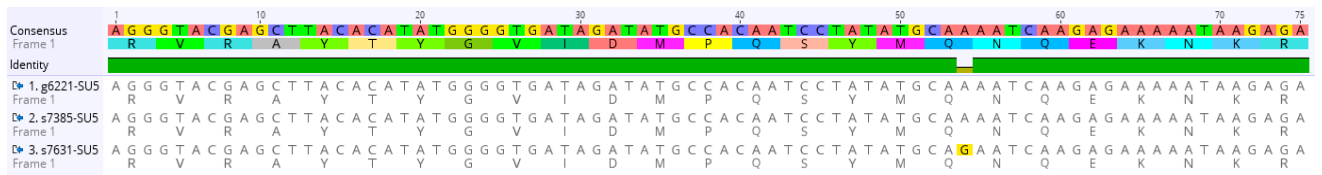


Figure S1a. Alignment of the SU5 region of viruses isolated from two sheep and one goat of the same farm: The sequence alignment shows a single synonymous mutation in the s7631-SU5 sequence (yellow G).

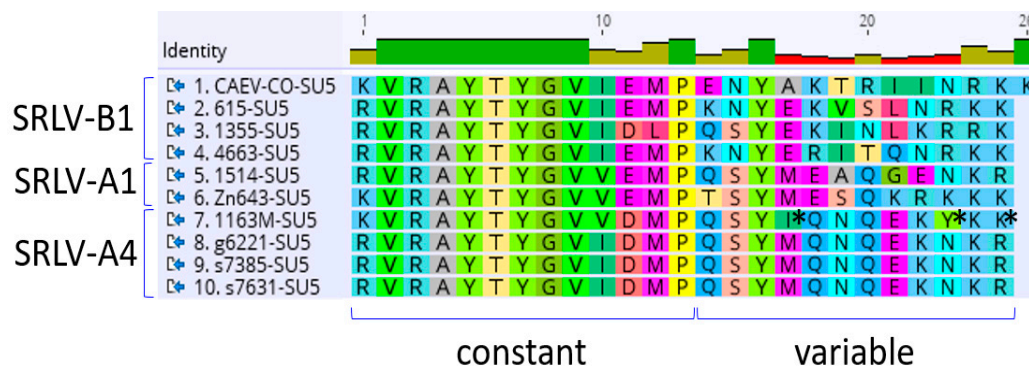


Figure S1b. Alignment of the SU5 region of different SRLV isolates: The SU5 amino acid sequences of the two prototypic SRLV sequences CAEV-CO (B1) and 1514 (A1) were aligned to different Swiss field isolate sequences. The constant and variable portions of SU5 are marked. Asterisk (*) point to the amino acid mutations in the 1163M SRLV-A4 isolate compared to the constant goat and sheep field isolates obtained from the same epidemiological unit (see Figure S1a).

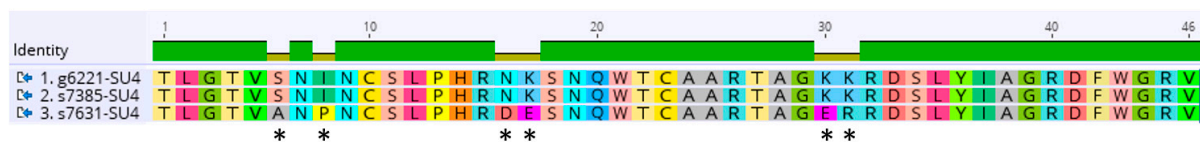


Figure S1c. Alignment of the SU4 region of goat g6221 and sheep s7385 and s7631: The SU4 amino acid sequences obtained from sheep s7631 shows 6 mutations (*) out of 46 amino acids, representing potential escape mutations from neutralizing antibody directed to this particular epitope [29]. In contrast, the variable portion of the SU5 region of these animals did not show mutations (see Figure S1a).