

		NLS/NoLS	NES	
CAEV	M63105.1	46 LPAGSHHGK SR - <u>RRRQSGFWRWLRGI</u> -RRQDKPKGDSEK LGSCV GALAE LT LEA 104		
	P33460.1	46 IPTGHSHHGK SR -RRRKSGFWRWLRGI-RRQNRKRKSDSTESLEPCLGALAE LT LEGA 104		
	KT749880.1	43 IPTGHSHHGK SR -RRRKSGFWRWLRGI-RRQNRPKSDSTESLGPC LG ALAE LT LEGA 100		
	KT749879.1	43 IPTGHSHHGK SR -RRRKSGFWRWLRGI-RRQNRPKSDSTESLGPC LG ALAE LT LEGA 100		
	KT749878.1	43 IPTGHSHHGK SR -RRRKSGFWRWLRGI-RRQNRPKSDSTESLEPCLGALAE LT LEGA 100		
	KT214469.1	43 IPTGHSHHGK SR -RRRKSGFWRWLRGI-RRQNRPKSDSTESLEPCLGALAE LT LEGA 100		
	FJ195346.1	46 IPKSYSDNGK SR RGRRKRAGFWKWLRGI-RRQRAAKSNNQESMEQCVGALGN LT LEGA 105		
	JF502417.1	48 IPKGDHNGSKTKR-RKRNKGWWRRLRGVIRAGTTIQETNPDRSLED CR EPMER LT LEH 107		
	JF502416.1	48 LPKGDNNGDKT RRRRRR NRGWKQLREIMQ TR RANTTNDYSR SL EQCCG AM E Q LT ME KH 108		
	AF322109.1	20 QLGDGDPGATRRR RRRR KGWWRWLR EMQ SRQQRN---Y EE LEES LG DLE KL TL AE H 75		
Visna	GQ381130.1	55 -----MR GR R-RRRGFWRWLRKL-RARR FTEP ---D PL ED PV PGMET LT LE DP 101		
	EU293537.2	40 -----LR GR R-RRR-RGWYRWLRKL-RARR FTEP ---D PL ED PI PDVE AL TL LD R 85		
	M23048.1	60 NSGDRTTGGIG KT -KKK-RGWYKWLRKL-RAREKNIP SQ FYP ME SNMVG ME N LT LE TQ 117		
	L06906.1	60 NSGDRSTGGIG KT -KKK-RGWYKWLRKL-RAREKNIP SQ FYP ME SNMVG ME N LT LE TQ 117		
	M31646.1	60 NSSDRSTRGP GKT -KRR-KGWFWWRKL-RAREKNIP SQ FYP ME GN CAG LEN LT LE G 117		
	HQ848062.1	60 NSGDRSTGSG GKS -KKR-RGWYKWLRRL-KAREKNIP QA FYP ME GINDGMEN LN LE HG 117		
	AF479638.1	57 NHSDRRTSGPR GKP -KRR-HGWFWWRKL-KAREKTIP AE FYP LE GN IA GLEEL CL CK G 114		
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Supplementary File S1. Multiple amino acid sequence alignment of Rev proteins from SRLVs strains. Multiple sequence alignments using MFFAT (Multiple Alignment using Fast Fourier Transform, v7.429) were done using several CAEV and Visna strains. NLS key-residues are indicated in bold while those composing the NoLS are underlined. Hydrophobic residues composing the NES are shown in bold. This study was carried out with M63105.1 CAEV Cork strain as the reference sequence. The letters/numbers in the left column correspond to the accession numbers found in GenBank.