Sub-strands classification, according to their nucleotide-skew, for 15 LDV genomes.

LDV	Class I segments		CDS*	Class II segments		CDS*	Fisher's test *p*-value
	Position			Position			
Mycobacteriophage Bxzl	0..156102		143 (27)	complement(0..156102)		4 (0)	1
***Pseudomonas* phage phiKZ**	0..280334		229 (22)	complement(0..280334)		49 (5)	0.99
Tupaiid herpesvirus 1	0..13000, complement(13000..108000), 180000..195859		83 (34)	complement(0..13000), 13000..108000, complement(180000..195859)		61 (25)	1
Human herpesvirus 5 strain AD169	complement(0..93000), 93000..190000, complement(190000..230287)		73 (19)	0..93000, complement(93000..190000), 190000..230287		72 (34)	0.0098
Human herpesvirus 5 strain merlin	complement(0..93000), 93000..200000, complement(200000..235645)		71 (17)	0..93000, complement(93000..200000), 200000..235645		82 (39)	0.002
Human herpesvirus 6(A)	complement(0..68000), 68000..135000, complement(135000..159321)		61 (4)	0..68000, complement(68000..135000), 135000..159321		46 (7)	0.2
Human herpesvirus 6B	complement(0..68000), 68000..1400000, complement(140000..162114)		54 (4)	0..68000, complement(68000..140000), 140000..162114		37 (2)	1
Human herpesvirus 7	complement(0..62000), 62000..140000, complement(140000..153080)		43 (2)	0..62000, complement(62000..140000), 140000..143080		35 (6)	0.13
Fowlpox virus	0..125000, complement(125000..288539)		71 (7)	complement(0..125000), 125000..288539		159 (5)	0.05
Canarypox virus	0..175000, complement(175000..359853)		93 (8)	complement(0..175000), 175000..359853		198 (6)	0.072
***A.moorei* entomopoxvirus**	0..232392		94 (7)	complement(0..232392)		124 (9)	0.99
Invertebrate iridescent virus 6	0..45000, complement(45000..113000), 113000..212482		74 (7)	complement(0..45000), 45000..113000, complement(113000..212482)		104 (8)	0.78
Shrimp white spot syndrome virus	0..305107		133 (47)	complement(0..305107)		112 (49)	0.19
African swine fever virus	complement(0..74000), 74000..161000, complement(161000..170101)		56 (9)	0..74000, complement(74000..161000), 161000..170101		73 (13)	0.81
***A.polyphaga* mimivirus**	0..380000, complement(380000..1181404)		333 (28)	complement(0..380000), 380000..1181404		577 (55)	0.633

* Number of CDS analysed in this study (*i.e.* length ≥ 100 amino-acids). Numbers of identified cA genes are shown in parentheses.