

Supplementary Table S2. Splicing profile and viral protein details of AMDV and SKAV strains sequenced in this study and compared to the reference sequence AMDV-G

Splicing sites were determined following what was experimentally demonstrated. Scores were assigned to donor and acceptor sites using the splicing prediction algorithm NNSPLICE from fruitfly.org.

Strain	Protein	Size (aa)	Exon position*	Donor score [§]	Exon position* [§]	Acceptor score [§]
AMDV						
G	NS1	641	206-1961	1.00	2042-2211	0.94
	NS2	114	206-384	0.95	2042-2207	0.94
	NS3	87	206-384	0.95	1737-1821	/
	VP1	681	2204-2213	0.84	2287-4322	0.95
	VP2	638	2406-4322	/	/	/
BCM-1	NS1	641	69-1824	1.00	1906-2075	0.93
	NS2	114	69-247	0.93	1906-2071	0.93
	NS3	92	69-247	0.93	1600-1699	/
BCM-3	NS1	641	69-1824	1.00	1906-2075	0.93
	NS2	114	69-247	0.93	1906-2071	0.93
	NS3	92	69-247	0.93	1600-1699	/
BCM-12	NS1	641	44-1799	1.00	1880-2049	0.95
	NS2	114	44-222	0.94	1880-2045	0.95
	NS3	87	44-222	0.94	1575-1659	/
BCM-13	NS1	641	45-1800	1.00	1881-2050	0.93
	NS2	114	45-223	0.90	1881-2046	0.93
	NS3	92	45-223	0.90	1576-1675	/
BCM-21	NS1	641	69-1824	1.00	1905-2074	0.95
	NS2	114	69-247	0.93	1905-2070	0.95
	NS3	87	69-247	0.93	1600-1684	/
BCM-22	NS1	641	69-1824	1.00	1906-2075	0.93
	NS2	114	69-247	0.93	1906-2071	0.93
	NS3	92	69-247	0.93	1600-1699	/
BCM-31	NS1	641	2-1757	1.00	1838-2007	0.93
	NS2	114	2-180	0.93	1838-2003	0.93
	NS3	92	2-180	0.93	1533-1632	/
BCM-32	NS1	641	69-1824	1.00	1905-2074	0.94
	NS2	114	69-247	0.94	1905-2070	0.94
	NS3	87	69-247	0.94	1600-1684	/
BCM-41	NS1	641	69-1824	1.00	1905-2074	0.93
	NS2	114	69-247	0.93	1905-2070	0.93
	NS3	92	69-247	0.93	1600-1699	/
BCM-43	NS1	641	51-1806	1.00	1887-2056	0.95
	NS2	114	51-229	0.95	1887-2052	0.95
	NS3	87	51-229	0.95	1582-1666	/

SKAV						
SK-1	NS1	641	69-1824	1.00	1907-2076	0.93
	NS2	114	69-247	0.94	1907-2072	0.93
	NS3	71	69-247	0.94	1600-1636	/
	VP1	677	2069-2078	0.99	2152-4175	0.95
	VP2	634	2271-4175	/	/	/
SK-12	NS1	641	68-1823	1.00	1906-2075	0.94
	NS2	114	68-246	0.94	1906-2071	0.94
	NS3	71	68-246	0.94	1599-1635	/
	VP1	677	2068-2077	0.99	2151-4174	0.88
	VP2	634	2270-4174	/	/	/
SK-16	NS1	641	69-1824	1.00	1907-2076	0.94
	NS2	114	69-247	0.94	1907-2072	0.94
	NS3	71	69-247	0.94	1600-1636	/
	VP1	677	2069-2078	0.99	2152-4175	0.90
	VP2	634	2271-4175	/	/	/
SK-23	NS1	641	69-1824	1.00	1907-2076	0.94
	NS2	114	69-247	0.94	1907-2072	0.94
	NS3	71	69-247	0.94	1600-1636	/
	VP1	677	2069-2078	0.99	2152-4175	0.95
	VP2	634	2271-4175	/	/	/
SK-24	NS1	641	69-1824	1.00	1907-2076	0.97
	NS2	114	69-247	0.94	1907-2072	0.97
	NS3	71	69-247	0.94	1600-1636	/
	VP1	677	2069-2078	0.99	2152-4175	0.90
	VP2	634	2271-4175	/	/	/
SK-36	NS1	641	69-1824	1.00	1907-2076	0.94
	NS2	114	69-247	0.94	1907-2072	0.94
	NS3	71	69-247	0.94	1600-1636	/
SK-39	NS1	641	69-1824	1.00	1907-2076	0.94
	NS2	114	69-247	0.94	1907-2072	0.94
	NS3	71	69-247	0.94	1600-1636	/
	VP1	677	2069-2078	0.99	2152-4175	0.9
	VP2	634	2271-4175	/	/	/
SK-47	NS1	641	69-1824	1.00	1907-2076	0.93
	NS2	114	69-247	0.94	1907-2072	0.93
	NS3	71	69-247	0.94	1600-1636	/
	VP1	677	2069-2078	0.99	2152-4175	0.90
	VP2	634	2271-4175	/	/	/

* Positions refer to each sequence as published in GenBank with accession numbers listed in Supplementary Table S1.

§ A / indicates that the site was absent (for VP2) or not detected using the splicing prediction algorithm (for NS3).