Figure S1. Recombination analysis of the nucleotide sequences of Polish IBDV strain 75/01-Poland-2001. For the recombination analysis the software package RDP v4.97 was used. For simplification purposes only the Bootscan analysis is shown as a method detecting the recombination event. A) Visualization of the recombination event detected by Bootscan analysis, the recombinant strain is denoted and the major parent-recombinant the minor parent-recombinant were denoted in blue and red, respectively. B) Neighbour Joining phylogenetic tree showing the topology organization using the minor parental segment (left) and the major parental segment (right). Minor parental strain is denoted in blue, major parental strain is denoted in green and the recombinant strains denoted by an arrow and highlighted in red.

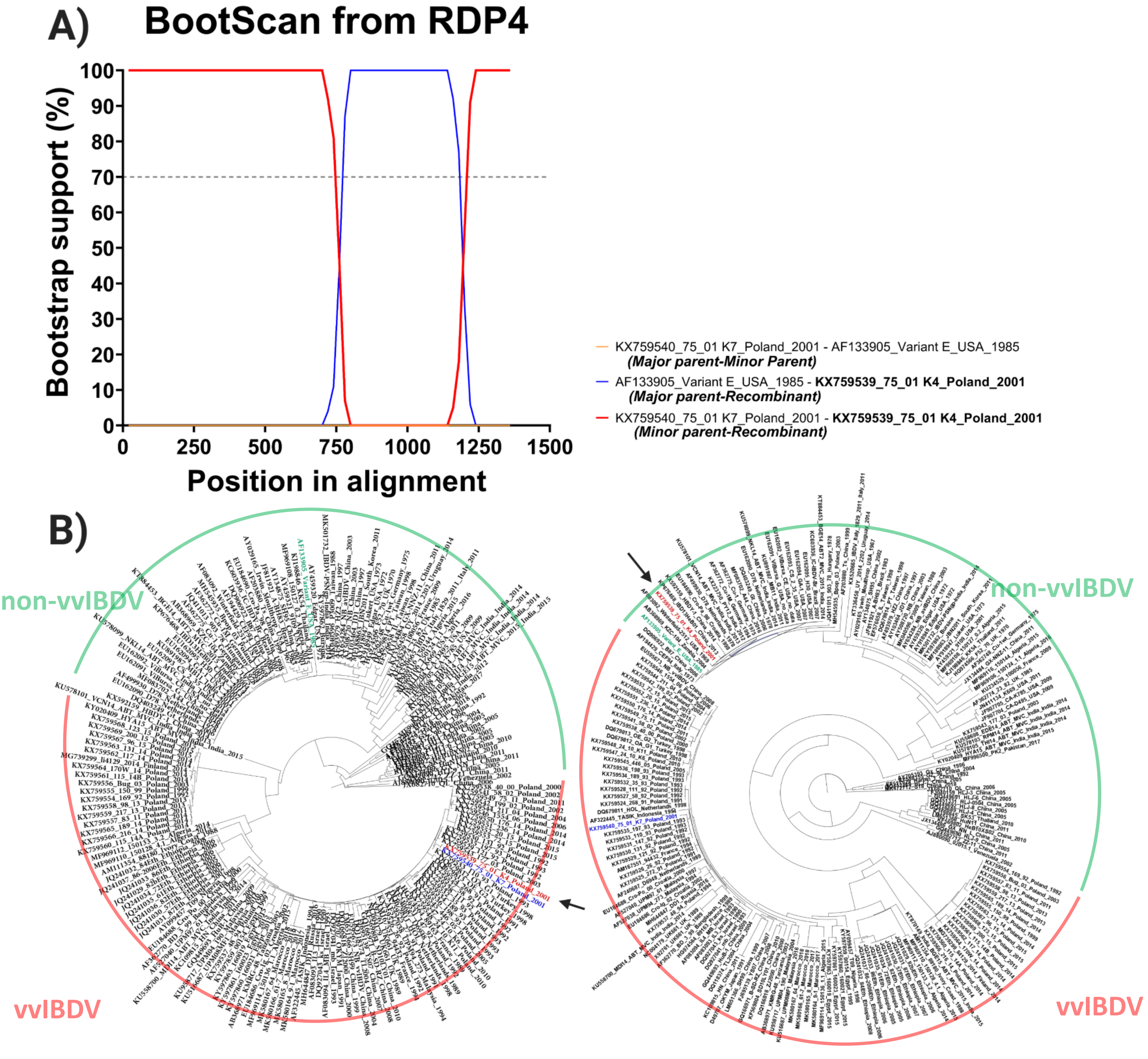

Figure S2. Sequence alignment of ORF2 of Segment A of IBDV. Sequences from the strains used in the experimental infection were used, the strain D78 representative of the attenuate IBDV strain was used for comparison purposes, the location of coding regions for VP2, VP4 and VP3 immature proteins are denoted in rectangle colours (red:VP2, green:VP4 and yellow:VP3), mature protein sequences were denoted in dark coloured rectangle (red:VP2, green:VP4 and yellow:VP3).

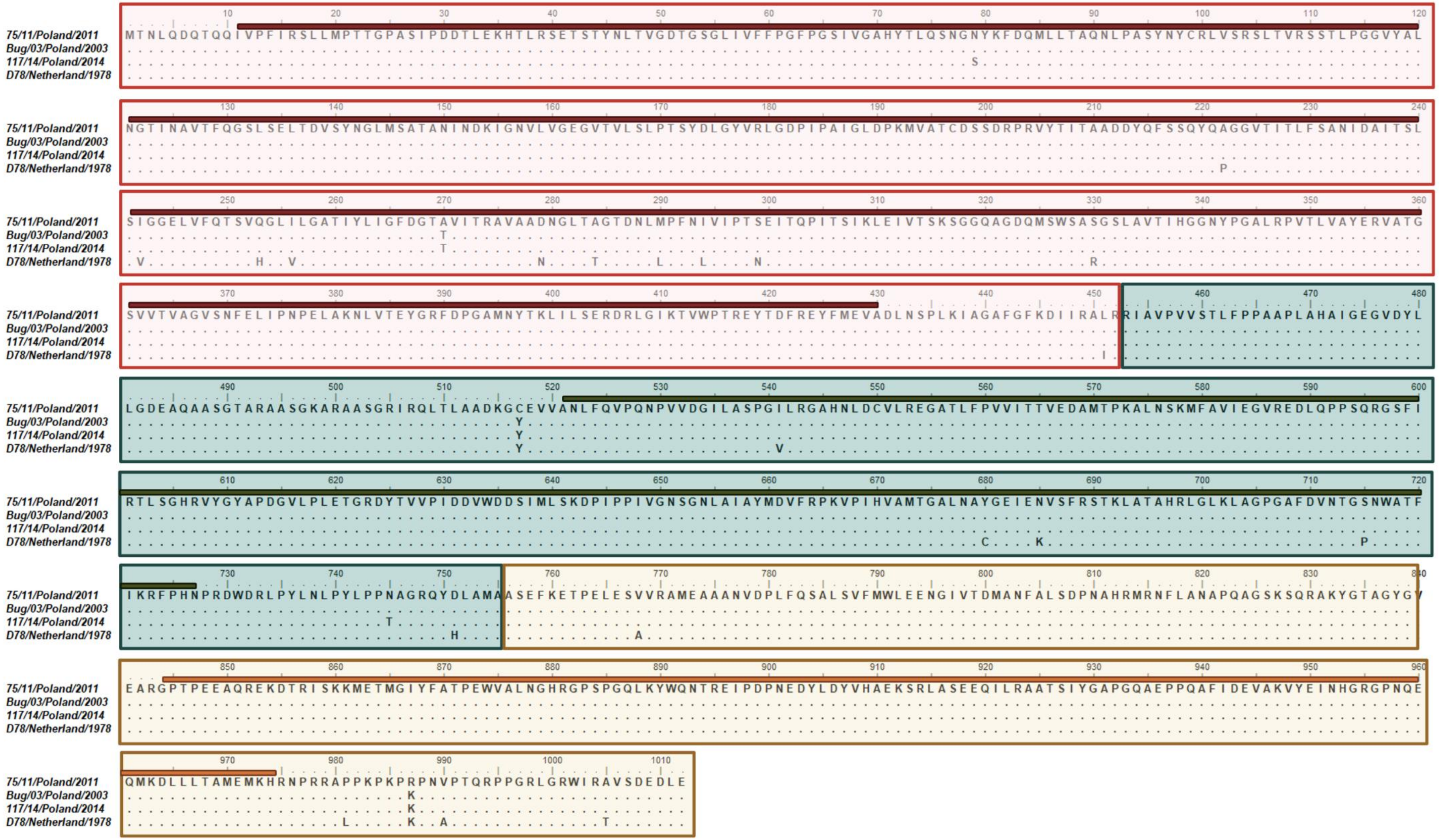

Table S1. PAML branch-site model A analysis to identify branches under episodic positive selection in Polish IBDV strains.

Foreground branches	**Parameters$^{n.m}$**	**-lnL$^{n.m}$**	**Parameters$^{a.m}$**	**-lnL$^{a.m}$**	**-2ΔlnL**	**Positively selected sites**
VP2 Clade A1	P_0= 0.0191 P_1= 0.9809 P_{2a}= 0.0000 P_{2b}= 0.0000 ω_0= 0.0000 ω_1= 1.0000 ω_2=1.0000	2512.644628	P_0= 0.0000 P_1= 0.0000 P_{2a}= 0.9998 P_{2b}= 0.0002 ω_0= 1.0000 ω_1=1.0000 ω_2=**217.4730**	2506.148819	**12.5794****	**206, 207, 210, 215, 221, 222, 230, 234, 237, 246, 254, 261, 282, 286, 302, 304, 312**
VP2 Clade A2	P_0= 0.5245 P_1= 0.2737 P_{2a}= 0.1326 P_{2b}= 0.0692 ω_0= 1.0000 ω_1= 1.0000 ω_2= 1.000	2512.850945	P_0= 0.0000 P_1= 0.0000 P_{2a}= 0.7266 P_{2b}= 0.2734 ω_0= 1.0000 ω_1= 1.0000 ω_2= **1.6607**	2518.690369	**11.678848****	0
VP2 Clade A3	P_0= 0.8814 P_1= 0.0311 P_{2a}= 0.0846 P_{2b}= 0.0030 ω_0= 1.0000 ω_1= 1.0000 ω_2= 1.0000	2512.850753	P_0= 0.8730 P_1= 0.1190 P_{2a}= 0.0001 P_{2b}= 0.0001 ω_0= 0.0000 ω_1= 1.0000 ω_2= **216.4132**	2518.728187	**11.754868****	0
VP1 non-vvIBDV	P_0= 0.9580 P_1= 0.0178 P_{2a}= 0.0238 P_{2b}= 0.0004 ω_0= 0.0382 ω_1= 1.0000 ω_2= 1.0000	13348.604162	P_0= 0.9581 P_1= 0.0177 P_{2a}= 0.0238 P_{2b}= 0.0004 ω_0= 0.0352 ω_1=1.0000 ω_2= 1.0000	13348.60416	0.00004	0
VP1 vvIBDV	P_0= 0.9745 P_1= 0.0168 P_{2a}= 0.0086 P_{2b}= 0.0002 ω_0= 0.0375 ω_1= 1.0000 ω_2= 1.0000	13332.88523	P_0= 0.9745 P_1= 0.0168 P_{2a}= 0.0086 P_{2b}= 0.0002 ω_0= 0.0375 ω_1= 1.0000 ω_2= 1.0000	13340.3787	14.98694	0
VP1 transIBDV	P_0= 0.9795 P_1= 0.0105 P_{2a}= 0.0063 P_{2b}= 0.0037 ω_0= 0.0382 ω_1= 1.0000 ω_2= 1.0000	13348.604162	P_0= 0.9795 P_1= 0.0105 P_{2a}= 0.0063 P_{2b}= 0.0037 ω_0= 0.0382 ω_1= 1.0000 **ω_2= 16.3423**	13338.8682	**19.471922****	**396, 466**

lnL: log-likelihood scores; n.m: null model; a.m: alternative model; *$p<0.05$, χ^2= 3.84; **$p<0.01$, χ^2= 5.99.

Table S2. Positively selected sites and parameters estimated by the CODEML program implemented in the PAML package.

Gene	Model	log-likelihood score						Positive site
VP2	**M1**	-10080.290	p0=0.93345	p1=0.06655				
	M2	-10068.144	ω=2.00672	p0=0.93380	p1=0.06399	p2=0.00222		217, 248, 249, 315
	M7	-10079.394	p=0.27465	q=1.97108				
	M8	-10061.359	ω=1.29072	p0=0.97370	p=0.46792	q=5.09210	p1=0.02630	217, 248, 249, 315

codons selected with a posterior probability greater than 0.99 belonging to the positively selected class ($\omega > 1$).

Table S3. Statistical analysis to avoid false estimations of sites under positive pressure selection.

Gene	Models compared	$-2\Delta l$	d.f	dN/dS
VP2	M1 vs. M2	24.29**	2	2.01
	M7 vs. M8	36.07**	2	1.29

Neutral models (M1 and M7) were compared to selection models (M2 and M8); *, $P < 0.05$ **, $P < 0.01$ ($\chi^2_{0.05,2}$= 5.99, $\chi^2_{0.01,2}$= 9.21). Δl: likelihood-ratio statistic; d.f., degrees of freedom between nested models.

Table S4. Maximum Likelihood estimates of the coefficient of Type-II functional divergence (θ_{II}) from pairwise comparison among VP1 IBDV Polish lineages.

IBDV Polish lineage VP1	**θ_{II}ML**	**θ_{II}SE**	**θLTR**	**Qk**	**p**
vvIBDV/transIBDV	0.00744	0.00887	3.15581	115, 116, 117, 189, 212	**$p<0.01$**