

[illegible]

	130	140	150	160	170	180	190	200	210	220	230	240
Consensus	NL	GKAVQAKKRILPEPLGLVEDPVNTAPAKKNTKGLTDHYPVVKPKLT	EVSAGGGSSAVDQGGAETEGTPVAASEMAEGGGGAMGDSSGGADGVGNASGHWHNCDSQMNGHTVTIKTT									
NC_001701 GPV virulent B	.	.	.	.	.	.	.	.	.	.	.	.
EU583392 GPV strain VG32/1	.	.	I.	.	.	.	.	.	.	.	.	.
BDDU22967 BDGP strain FM	L..E..M.....SS.....DI.....S.N.PSPSN.GGEASA.AT..S....PN...S....A.....LD..											
KU684472.1 GPV strain GPV GER	.	.	E.I.....T.....V.....									
Z68272 MDPV 89384/France	.L.E.....SS.....I.....S.N.PSPSN.GGEASA.AT..S....PN...S....A.....LD..											
KR075690 DPV strain FJM3	.	L..E.....SS.....I.....S.N.PSPSN.GGEASA.AT..S....PN...S....A.....LD..										
EU088102 GPV strain DB3	.	.	I.	.	.	E						
KR091959 GPV strain WX	.	.	.	.	.	.	.	.	.	.	.	.
MT646164 GPV isolate AHAUJ30	.	.	.	.	.	V.	.	.	L.A.	.	.	.
MK736656 GPV strain HuN18	.	.	.	.	.	T.V.	.	.	L.A.	.	.	.
MN549533 GPV isolate GDQY1802	.	.	.	.	.	V.	.	.	L.A.	.	.	.
MN549532 GPV isolate GDSG1901	.	.	.	.	.	V.	.	.	L.A.	.	.	.
Mw386077 GPV strain Corum/19	.	.	I.	.	.	S.	.	.	.	.	.	.
MW386078 GPV strain Konya/19	.	.	I.	.	.	S.	.	.	.	.	.	.
MW386079 GPV strain Yozgat/19	.	.	I.	Yozgat/19	.	S.	.	.	.	.	.	.

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	730	
Consensus	RLIGTRYLTQNLX	733
NC_001701 GPV virulent B		733
EU583392 GPV strain VG32/1		733
BDU22967 BDPV strain FM		733
KU684472.1 GPV strain GPV GER		733
Z68272 MDPV 89384/France		733
KR075690 DPV strain FJM3		733
EU088102 GPV strain DB3		733
KR091959 GPV strain WX		733
MT646164 GPV isolate AHAU30		732
MK736656 GPV strain HuN18		733
MN549533 GPV isolate GDQY1802		733
MN549532 GPV isolate GDSG1901		733
MW386077 GPV strain Corum/19		733
MW386078 GPV strain Konya/19		733
MW386079 GPV strain Yozgat/19		733

Supplementary Figure 3: The multiple comparison analysis of the Minor Asian strains with some of the GPV and MDPV strains based on 732 aa VP1 protein sequence (BDPV, Barbarie duck parvovirus; DPV, duck parvovirus). Residues were highlighted by comparing them with the consensus. Non-highlighted residues were represented as dots.