Supplementary Table I.- Primer sequences used for identification and amplification of Fusion (F) and Hemagglutinin (HN) Genes of Avian Paramyxovirus Serotype I from Peacocks in Pakistan

<table>
<thead>
<tr>
<th>No.</th>
<th>Primer sequences (5’ - 3’)</th>
<th>Position on viral genome (bp)</th>
<th>Product size (bp)</th>
<th>Reference</th>
</tr>
</thead>
</table>
| 1   | Sense: GTGAAAYTTTGTTCCTCCTTGAC  
     Anti-sense: GAGGCAATGTGACRAAAGC | 3833-3852 to 4814-4798 | 965 bp | Munir et al., 2012 |
| 2   | Sense: TTGAYGGGAGGGGCTCCTTG  
     Anti-sense: GTGATAGAAGARCTTGACACCTC | 4673-4690 to 5585-5563 | 890 bp |          |
| 3   | Sense: ATATATGCGTGCCACCTA  
     Anti-sense: ATAYACGGGTAGAACGGT | 5465-5483 to 6370-6353 | 888 bp |          |
| 4   | Sense: TGGCTTGGGAAYAATAACCTC  
     Antisense: TGCAGTGTGAGTGCAACT | 6190-6209 to 7176-7159 | 969 bp |          |
| 5   | Sense: GGGAGGCCATAACACAGGACA  
     Antisense: TGGTTCGCAATTGCTC | 289-308 to 512-530 | 242 bp | Ling et al., 1997 |

Primer 1 to 4, used for amplification of F and HN gene of study isolate; Primer 5, used for the identification of NDV isolate.
Supplementary Fig. 1: Phylogenetic consensus tree for the pigeon-originated NDV isolate for fusion gene (A), hemagglutinin gene (B) and hyper-variable region of F gene (C). The nucleotide sequences of study isolate for each gene were compared with corresponding genes of representative strains reported previously to public database, the GenBank. The evolutionary history was inferred using the Neighbor-Joining method with 1000 bootstrap value in MEGA version 6.0.
Supplementary Fig. 2. Alignment of deduced amino acid sequence of complete F gene of peacock isolate. The residue profile of study isolate is compared with strains of NDVs representing different genotypes including the vaccine strains. Structurally and functionally important residues are boxed and highlighted.

--- Glycosylation Site ▼= Cysteine Residue
Supplementary Fig. 3. Alignment of deduced amino acid sequence of complete HN gene of pigeon isolate. The residue profile of study isolate is compared with strains of NDVs representing different genotypes including the vaccine strains. Structurally and functionally important residues are boxed and highlighted.