

1 **Table S1.** Primers used for genome sequencing of DcNDV.

| Primer pairs | Primers name | Location | Primers (5' – 3') |
|--------------|------------------------|------------------|---|
| 1 | LPW 38283 LPW 38284 | 1 -800 | ATGTCATCCGTCTTGAC AATGCAGTTAACCCGGTG |
| 2 | LPW 38285 LPW 38286 | 700 – 1,500 | GAGCTTAAGAGGGGACGC GCCCGGTGGGGCGGGCT |
| 3 | LPW 38287 LPW 38288 | 1,396 – 2,293 | CAGAGCACTACTCATCTGG GCTTCCAGGGGGCGGCTT |
| 4 | LPW 38289 LPW 38290 | 2,192 – 2,950 | GAAAACCACCATCAACCC CAGCGCAAGGC GTT GAT |
| 5 | LPW 38291 LPW 38292 | 2,854 – 3,674 | ACGCCCGATGCATCCAAA CCGCTCCCAGGGATCTTC |
| 6 | LPW 38293 LPW 38294 | 3,558 – 4,377 | CTTCTCAGTAATGCAGGC TTCTAATTAGATAGACAG |
| 7 | LPW 36838 LPW 36839 | 4,681 – 5,762 | CGGCAGTGTAGCTCTGGGG CCGCTAACCTATCCAGGGCA |
| 8 | LPW 38295 LPW 38296 | 4,261 – 5,085 | AAGAAAGTAAGCTGCACCC CGTAGTCAATTCAAGTTAG |
| 9 | LPW 38297 LPW 38298 | 4,969 – 5,806 | AAGATGCAGCAGTTGTT TGCCCGTCACGATGACTT |
| 10 | LPW 38299 LPW 38300 | 5,699 – 6,507 | GATA GATAGACATTCATG TAATCTTCTCCTCCGCCT |
| 11 | LPW 37470 LPW 37471 | 6,368 – 7,216 | AGAACACATGGCGTTGGTT AAGGATCCCGTTCCACT |
| 12 | LPW 38301 LPW 38302 | 6,389 – 7,222 | TCTAGTAGTAATGACTTT TCAATAAAGGATCCGCTT |
| 13 | LPW 37466 LPW 37467 | 6,430 – 6,977 | TGCATAGCATGAGGGCCAG GATGGAACGCAGAGTCGAG |
| 14 | LPW 38303 LPW 38304 | 7,103 – 7,937 | AATGGTGCACGGAAGGTT TTCTCGAATGCTAAGACA |
| 15 | LPW 38305 LPW 38306 | 7,817 – 8,657 | CAACATATCCCGCAGTCG AACTT GCGAACAGGTCT |
| 16 | LPW 38307 LPW 38308 | 8,535 – 9,369 | CCATCCCAGGTGTTAGA GCGAGACTCAAGCAGTGG |
| 17 | LPW 38309 LPW 38310 | 9,138 – 10,072 | ATATAGCAGAATCAGTAA ATAGTTGACTCATCGCTA |
| 18 | LPW 38311 LPW 38312 | 9,953 – 10,780 | ACTGCCAAGTAATGGCAG TAAGATCGCCTGATATTAA |
| 19 | LPW 38313 LPW 38314 | 10,661 – 11,506 | GTGAAACCACATCAGGT CAG TCCGTGTCAGCCTTGA |
| 20 | LPW 38315 LPW 38316 | 11,370 – 12,190 | ACGTGTCGCGCATGCTAT CCTCTTGACTCCTCTT |
| 21 | LPW 38317 LPW 38318 | 12,074 – 12,901 | TAGATGATGGCATAACAC CAGACAATTGATAAAAT |
| 22 | LPW 38319 LPW 38320 | 12,777 – 13,602 | TCTACTCTCTAATATTGC TTCCGCCAAGTATAAGGA |
| 23 | LPW 38321 LPW 38322 | 13, 478 – 14,290 | ACCTAGTACGGTATTGT CTATTACACGATGCTGTT |
| 24 | LPW 38323 LPW 38324 | 14,172 – 14,880 | TGTGCACGAGGTGGTGAG TTAAGAGTCATTGTCACA |

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11 **Figure S1.** Alignment of deduced amino acid sequence of complete F gene of DcNDV. The residue profile of
 12 DcNDV is compared with the three closest pigeon NDV strains from Egypt. Structurally and functionally
 13 important domains are indicated. Amino acid changes are highlighted in yellow. Cleavage site motif is bolded
 14 in red font, fusion peptide is shaded in grey, heptad repeats are in orange font, cysteine residues are shown
 15 with arrows and transmembrane domain is in purple font.

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| Camel/Dubai/DcNDV_F/2015 KY042133/Pigeon/Egypt/ElFayom/79/112/2015 KY042131/Pigeon/Egypt/Qena/56/1107/2015 KY042129/Pigeon/Egypt/Giza/11/1088/2015 | MSSKSSSRTPAPLMLITRIMLILSCICLTSSLDRPLAAAGIVVTGDKAVNIYTSSQTGS MSSKSSTRIPAPLMLITRIMLILSCICLTSSLDRPLAAAGIVVTGDKAVNIYTSSQTGS MSSKSSTRIPAPLMLITRIMLILSCICLTSSLDRPLAAAGIVVTGDKAVNIYTSSQTGS MSSKSSTRIPAPLMLITRIMLILSCICLTSSLDRPLAAAGIVVTGDKAVNIYTSSQTGS *****:*****:*****:*****:*****:*****:*****:*****:*****:*****: IIKLLPNMPKDKEACARAPLEAYNRTLTALLNLPGDSIRRIQGSVSTSGG KRQKRFIGA IIKLLPNMPKDKEACARAPLEAYNRTLTALLNLPGDSIRRIQGSVSTSGG KRQKRFIGA IIKLLPNMPKDKEACARAPLEAYNRTLTALLNLPGDSIRRIQGSVSTSGG KRQKRFIGA IIKLLPNMPKDKEACARAPLEAYNRTLTALLNLPGDSIRRIQGSVSTSGG KRQKRFIGA *****:*****:*****:*****:*****:*****:*****:*****:*****: IIGSVALGVATSAQITAAAALI QANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAVG IIGSVALGVATSAQITAAAALI QANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAVG IIGSVALGVATSAQITAAAALI QANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAVG IIGSVALGVATSAQITAAAALI QANQNAANILRLKESIAATNEAVHEVTDGLSQLAVAVG *****:*****:*****:*****:*****:*****:*****:*****: KMQQFVNDQFNNTARELDCIKITQQVGIELNLYTELTTVFGQPITSPALTRLTIQALYN KMQQFVNDQFNNTARELDCIKVTQQVGIELNLYTELTTVFGQPITSPALTRLTIQALYN KMQQFVNDQFNNTARELDCIKVTQQVGIELNLYTELTTVFGQPITSPALTRLTIQALYN KMQQFVNDQFNNTARELDCIKVTQQVGIELNLYTELTTVFGQPITSPALTRLTIQALYN *****:*****:*****:*****:*****:*****:*****: LAGGNMDYLLTKLGIGNNQLSSLI GSLITGHPILYDSQTQLLGIQVNLP SVGNLNMMRA LAGGNMDYLLTKLGIGNNQLSSLI GSLITGHPILYDSQTQLLGIQVNLP SVGNLNMMRA LAGGNMDYLLTKLGIGNNQLSSLI GSLITGHPILYDSQTQLLGIQVNLP SVGNLNMMRA LAGGNMDYLLTKLGIGNNQLSSLI GSLITGHPILYDSQTQLLGIQVNLP SVGNLNMMRA *****:*****:*****:*****: TYLGLTLSVSTTKGFA SLAVPKVVTQVG SVIEELDTSHCIESDLDDLYCTRIVTFPMSPSIY TYLGLTLSVSTTKGFA SLAVPKVVTQVG SVIEELDTSHCIESDLDDLYCTRIVTFPMSPGIY TYLGLTLSVSTTKGFA SLAVPKVVTQVG SVIEELDTSHCIESDLDDLYCTRIVTFPMSPGIY TYLGLTLSVSTTKGFA SLAVPKVVTQVG SVIEELDTSHCIESDLDDLYCTRIVTFPMSPGIY *****:*****:*****: SCLSGNTSACMYSKTEGALTTPY MALKGSVIANCKITTCRCV DPPGIISQNYGEAVSLID SCLSGNTSACMYSKTEGALTTPY MALKGSVIANCKITTCRCV DPPGIISQNYGEAVSLID SCLSGNTSACMYSKTEGALTTPY MALKGSVIANCKITTCRCV DPPGIISQNYGEAVSLID SCLSGNTSACMYSKTEGALTTPY MALKGSVIANCKITTCRCV DPPGIISQNYGEAVSMID *****:*****:*****:*****:*****: RHSCNV I SLDGITLRLSGEFDTYQKNISILD SQIVTGNLDISTELGNV NNISNALDR RHSCNV I SLDGITLRLSGEFDTYQKNISILD SQIVTGNLDISTELGNV NNISNALDR RHSCNV I SLDGITLRLSGEFDTYQKNISILD SQIVTGNLDISTELGNV NNISNALDR RHSCNV I SLDGITLRLSGEFDTYQKNISILD SQIVTGNLDISTELGNV NNISNALDR *****:*****:*****: LAESNSKLDKVNV KLTSALITYI VLTVISL IFGALS LILACYL MYKQKAQKTLI GLG LAESNSKLDKVNV KLTSALITYI VLTVISL IFGALS LILACYL MYKQKAQKTLI WLG LAESNSKLDKVNV KLTSALITYI VLTVISL IFGALS LILACYL MYKQKAQKTLI WLG LAESNSKLDKVNV KLTSALITYI VLTVISL IFGALS LILACYL MYKQKAQKTLI WLG *****:*****:*****: NNTLDQM RAT TRT 553 NNTLDQM RAT TRT 553 NNTLDQM RAT ART 553 NNTLDQM RAT TRT 553 *****:*****: | 60 60 60 60 120 120 120 120 180 180 180 180 240 240 240 240 300 300 300 300 360 360 360 360 420 420 420 420 480 480 480 480 540 540 540 540 |
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