A. NDV Fusion (F) protein: 81.4% coverage (95% confidence) and 48 unique peptides

LDGRPLAAAGIVVTGDKAVNIYTSSQTGSIIVKLLPNMPKDKEACARAPLEAYNRTLTTLLTPLGDSIRKIQGSV
STSGGRRRKRFIGAIIGSVALGVATAAQITAAAALIQANQNAANILRLKESIAATNEAVHEVTNGLSQLSVAVGK
MQQFVNDQFNNTARELDCIKITQQVGVELNLYLTELTTVFGPQITSPALTQLTIQALYNLAGGNMDYLLTKLGVG
NNQLSSLIGSGLITGYPILYDSQTQLLGIQVNLPSVGNLNNMRATYLETLSVSTTKGFASALVPKVVTQVGSVIE
ELDTSYCIESDLDLYCTRIVTFPMSPGIYSCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKITTCRCADPPG
IISQNYGEAVSLIDRRSCNVLSLDGITLRLSGEFDATYQKNISILDSQVIVTGNLDISTELGNVNNSISNALDKL
AESNNKLDKVNVRLTSTSALITYIVLTVISLVFGALSLILACYLMYKQKAQQKTLLWLGNNTLDQMRATTRA

B. NDV Hemagglutinin-neuraminidase (HN) protein: 72.7% coverage (95% confidence) and 51 unique peptides

MDRVVNRVVLENERREAKNTWRLVFRITVLLLMVMILAISAAALAHSMGACTPRDLAGISTGISKTEDRVTSLLS
SSQDVIDRIYKQVALESPLALLNTESIIMNAITSLSYQINGAANSSGCGAPVHDPDYIGGIGKELIVDDTSDVTS
FYPSAYQEHLNFIPAPTTGSGCTRIPSFDMSTTHYCYTHNVILSGCRDHSHSHQYLALGVLRTSATGRIFFSTLR
SINLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYRSVTPTSMVHGRLGFDGQYHEKDLDTTVLFKDWVANYP
GVGGGSFINDRVWFPVYGGLKPNSPSDTAQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPQRFGGKRVQQAILS
IEVSTSLGKDPVLTIPPNTITLMGAEGRILTVGTSHFLYQRGSSYFSPALLYPMIVHNKTATLHNPYTFNAFTRP
GSVPCQASARCPNSCITGVYTDPYPLIFHRNHTLRGVFGTMLDDGQARLNPTSAVFDNISRSRVTRVSSSSTKAA
YTTSTCFKVVKTNKTYCLSIAEISNTLFGEFRIVPLLIEILKDDRV

C. NDV Matrix (M): 21.4% coverage (95% confidence) and 9 unique peptides

MDSSRTIGLYFDSALPSSSLLAFPIVLQDTGDGKKQITPQYRIQRLDSWTDSKEDSVFITTYGFIFQIGNEEVTV
GVINNNPRHELLSSAMLCLGSVPNDRDLVELARACLTMVVTCKKSATNTERIVFSVVQAPQVLQSCMVVANRYSS
VNAVKHVKAPEKIPGSGTLEYKVNFVSLTVVPRRDVYRIPTAVLKVSGSSLYNLALNVTIDVDVDPKSPLVKSLS
RSDSGYYANLFLHIGLMSTVDKKGKKVTFDKIEEKIRRLNLSVGLSDVLGPSVLVKARGVRTKLLAPFFSSSGTA
CYPIANASPQVAKILWSQTAHLRSVKVIIQAGTQRAVAVTADHEVTSTKIEKKHTIAKYNPFKK

Supplementary Figure 1: LC-MS/MS-based peptide sequencing analysis for SDS-PAGE bands of approximately 56 kDa (A), 62 kDa (B) and 40 kDa (C), mapped against the Fusion (F), Hemagglutinin-neuraminidase (HN) and matrix (M) protein sequences, respectively, of Newcastle disease virus (NDV) turkey/South Africa/N2057/2013. Peptides identified with >95% confidence are highlighted in green, with 50-95% confidence are highlighted in yellow, and with <50% confidence are highlighted in red. Peptides were not identified for the non-highlighted regions (grey) of the respective sequences.