Title:

Revealing interspecies transmission barriers of avian influenza A viruses

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Abstract

Influenza A virus (IAV) pandemics result from interspecies transmission events within the avian reservoir and further to mammals including humans. Investigating molecular virus–host interactions dictating this process and the adaptations to the new hosts that follow is vital to understand zoonotic IAV spread. Receptor incompatibility has been suggested to limit zoonotic IAV transmission from the wild bird reservoir. Other barriers to interspecies transmission, particularly within the avian system, largely remain elusive. Through assessment of infection dynamics of mallard origin IAV in two different avian hosts, coupled with studies of receptor expression and host response we aimed to reveal the host-pathogen interactions in a cross-species transmission event. We found that shedding patterns and innate immune responses were highly dependent on viral genotypes, host species and inoculation routes, but less dependent on receptor expression. Further, in contrary to the prevailing dogma we demonstrate that birds can produce a wide range of different sialylated structures also found in mammals, e.g. extended *N*- and *O*-linked Neu5Acα2,6 terminated glycans. Overall, receptor incompatibility is not the sole transmission barrier for IAV between birds and to humans, but other host-pathogen factors deserve dedicated studies to achieve proper pandemic preparedness.

Zonotic viruses have the capacity to cause severe pandemics [1]. The three latest influenza A virus (IAV) pandemics (H2N2 1957, H3N2 1968, and H1N1 2009) [2-4] have contained genetic material originating from avian influenza viruses. These events have most likely involved spread from wild to domestic bird species and to pigs. Key barriers for interspecies transmission are molecular interactions between host and virus, including recognition of host receptors by virus surface proteins, adaptation to changes in pH and temperature, as well as avoiding the host´s innate and adaptive immune response to infection [5,6].

One of the biological traits required for interspecies transmissions of IAV is a change in receptor binding specificity. Avian viruses preferentially bind to α2,3-linked sialic acid (SA)-containing receptors, whereas human IAVs prefer α2,6-linked SA-containing receptors [7-11]. Originally it was believed that α2,3-linked SA was exclusive to bird tissues, whereas α2,6-linked SA was exclusive to humans [12-14]. Furthermore, species specific differences in the sialylated glycan structures serving as receptors for IAVs have been proposed as barriers for transmission between bird species [12,13,15]. More recent characterization of the human airway epithelium has revealed that α2,3-linked SA can indeed be found [16,17], and primary screenings with lectins have indicated the presence of α2,6-linked SA in avian tissues as well [18-23]. The most important target organs for IAV replication are poorly defined in most bird species. For mallards (*Anas platyrhynchos*), the central reservoir for IAVs, viruses replicate in the surface epithelium of the intestinal tract and transmission occurs via the fecal–oral route[24]. In contrast, the respiratory tract is known to be important for replication in chickens and indirect evidence suggest that this is the case also in an array of wild bird species, including tufted ducks (*Aythya fuligula*) [23,25-27], particularly in the case of infection with highly pathogenic avian influenza virus (HPAIV).

Considering the barriers that dictate cross species transmission events, we hypothesized that the repertoire of expressed sialylated glycan receptors for IAV differs between birds and mammals, and that differences in the glycan structure were to be found even between distantly related bird species. Furthermore, we hypothesized that the outcome of experimental transmission of low pathogenic avian influenza viruses (LPAIVs) between bird species would differ depending on infection route and site of infection, receptor repertoire, host response and virus subtype. Moreover, successful introduction of an LPAIV into a new host species would likely be accompanied by adaptive viral genetic changes. To test these hypotheses, we undertook two main approaches. First, we comprehensively assessed infection potential and host response to infection of a broad array of mallard-origin LPAIVs in two different avian hosts: chicken - a key link to zoonotic transmission, and tufted duck - a representative of the wild reservoir. To evaluate the outcomes of these experiments we assessed virus shedding and monitored the host response as well as SNPs in viruses after infection. Second, we characterized and compared the IAV glycan receptor repertoire displayed on cell surfaces of presumed target organs of mallards, chickens and tufted ducks using glycoproteomics.

Results

The outcomes of experimental AIV infection differ between virus subtypes, host species and routes of infection.

To interrogate how outcomes of AIV infection can differ depending on host species and route of infection, chickens and tufted ducks were infected with eight different subtypes of mallard-origin LPAIVs (Table S1) using two different routes of virus inoculation: oculonasal or intraesophageal. All birds tested negative for AIV antibodies prior to the infection experiments. All chickens and tufted ducks inoculated intraesophaegally were negative in both oropharyngeal and cloacal swab samples by RT-qPCR for all viruses with only two exceptions: one out of four tufted ducks inoculated with H8N4 showed positive AIV RNA (2.54 10-log EID_{50} equivalent) at 1 day post infection (d.p.i.) and one out of four tufted ducks inoculated with H11N9 (0.79 10-log EID_{50} equivalent) at 2 d.p.i. (data not shown).

In contrast, oculonasal inoculation yielded positive oropharyngeal samples for all viruses in both host species at 1 d.p.i (Figure 1a). In oculonasaly inoculated chickens, virus shedding was detected on all days in all four chickens inoculated with H3N8, H4N6, and H6N2 viruses. In chickens inoculated with H10N1 and H15N5, shedding remained until 3 d.p.i. in a subset of birds whereas the H8N4 virus was detected only at 1 d.p.i. Surprisingly, only one out of four chickens inoculated with the H9N2 virus showed positive AIV RNA (0.58 10-log EID_{50} equivalents), and this was limited to the oropharyngeal sample at 1 d.p.i. Given the high burden of H9N2 in poultry, this is surprising. However, phylogenetically the virus used in this study is located in a distant clade comprising wild bird sequences from Europe, rather than clades dominated by H9N2 viruses in Asian poultry (Figure S1). In chickens, the H6N2 virus showed the most widespread viral replication and AIV RNA was detected in colon in three birds, lungs in two birds, and spleen in a single bird at 3 d.p.i. with virus titre up to 7.27 10-log EID_{50} equivalents. For the other subtypes, viral replication in internal organs were detected to varying extent (Figure S2). In the occulonasally inoculated tufted ducks, all birds shed AIV RNA in oropharyngeal swabs at 1 d.p.i. in all groups except in the H10N1 and H11N9 virus groups, where only two and three birds respectively were positive (Figure 1b). The H6N2 and H9N2 groups showed virus RNA in the oropharyngeal swabs from all tufted ducks until 3 d.p.i. Virus RNA was detected at 3 d.p.i. in the lung (two birds), colon (three birds) and spleen (one bird) of the H6N2 inoculated group (Figure S2). All negative control groups in all experiments demonstrated no signs of disease and no virus was detected in any of the collected swab samples.

Taken together, viral shedding differed depending on AIV subtype, host species and route of inoculation. The intraeosophaegal route produced no virus infections, neither in tufted ducks nor in chickens. This is in contrast to reported results from mallards, where intraeosophaegal inoculation have resulted in cloacal sheding regardless of subtype [24,28-30], and suggests that site of replication might differ between bird species even within the Anatidae family.

A diversity of single nucleotide polymorphisms in progeny viruses following experimental infection.

Putative viral genetic changes during virus infection of chickens and tufted ducks were investigated in swab and tissue samples with virus EID_{50} equivalents high enough to allow for deep sequencing (Table S2). No deletions or insertions were recorded in any of the samples. Previously described amino acid variations associated with host specificity were detected in the NP protein (N319K) of tufted duck/H6 spleen and in the HA protein

(N183H) of the tufted duck/H6 cloacal sample at 3 d.p.i. [31-33]. In addition, a V27L aa substitutional change, previously described in association with amantadine resistance [34], was observed in the virus retrieved from tufted duck/H6 colon. Furthermore, SNPs of unkown significance were recovered in the AIV obtained from oropharyngeal swabs from the H3N8 inoculated chicken group as well as the virus recovered from tufted duck/H8 oropharyngeal swab at 3 d.p.i. (Table S2). Finally, the viruses recovered from H9N2 and H10N1 inoculated groups (Table S2) showed no SNPs in their genomes relative to the inoculum.

Transcriptomics demonstrates differential expression of genes involved in innate immunity and glycosylation in chickens and tufted ducks

In order to understand the host response of chickens and tufted ducks to challenge with mallard-origin LPAIVs, we utilized RNASeq to disentangle gene expression patterns of the hosts. We selected 216 tissue samples comprising lung and colon, as they are important sites of infection, and spleen as it is a primary lymphoid organ. Out of the 216 samples sequenced, 207 were of high quality with an average of 3311801 ± 740763 (mean ± SD) reads per sample. The remaining nine samples were excluded due to low sequencing depth and/or quality.

First, we identified significant differentially expressed genes (DEGs) in each tissue (colon, lung, and spleen) for chickens and tufted ducks for each AIV subtype. In chickens, the number of DEGs ranged from 11–2949 in colon, 34–3225 in lung and 6–3046 in spleen, and in tufted ducks from 49–597 in colon, 7-416 in lung and 92-560 in spleen of birds treated with the different AIV subtypes, see (Figure S3a–b and S4a–b). A marked difference in response to virus challenge in chickens between H3N8 or H4N6 and the other subtypes tested was observed. Fewer DEGs were identified in the tufted duck organs (mean 248 DEGs/organ/virus SD±167), and in contrast to what was observed in chickens, H3N8 was the subtype eliciting the highest number of DEGs. The overlap of DEGs was evaluated between groups infected with the different AIV subtypes within the same species, as well as groups infected with the same subtype between the two species. The proportion of DEGs in response to infection that was unique to each AIV subtype was calculated. In chickens it ranged from 3-32% in colon, 4–24% in lung and 0–31% in spleen across different subtypes (Figure S5a–c). Chickens inoculated with H3N8 had the highest percentage of unique DEGs (32% in colon, 23% in lung, 31% in spleen). The number of unique DEGs detected in a single treatment group in tufted ducks ranged from 6-51% in colon, 0-32% in lung and 10–84% in spleen (Figure S5d–f). As in chickens, H3N8 infected birds displayed the highest percentage of unique DEGs (51% in colon, 31% in lung, 42% in spleen). For all viruses except H3N8 and H4N6, the number of DEGs in response to infection was lower in tufted ducks than in chickens. The overlap of orthologous DEGs between the two species was low to moderate, with H3N8 and H4N6 having a smaller overlap of DEGs between the two species than the remaining virus subtypes (Figure S6-8).

To assess the innate immune response to the LPAIVs used in this study, we specifically studied genes known to be involved in interferone and proinflammatory pathways as well as β-defensins in chickens and ducks at 3 d.p.i [35] [36]. The full list of genes included in this analysis is found in Table S3. In general, up– or down–regulation of such genes was weak or absent in both chickens and tufted ducks. In chickens, a few genes related to interferon signaling were generally affected in response to infection; in colon, *TLR 3* was weakly upregulated for all subtypes except H3N8 and H4N6 (Figure 2, Table S4). However, the adaptor molecule *TICAM1/TRIF* downstream of TLR 3 was generally down–regulated or unaffected in the corresponding colon samples as well as in samples from lung and spleen. The ubiquitine ligase gene, *TRIM25* was weakly up–regulated in response to most IAV subtypes in colon, spleen and lung of chickens. Among the β-defensin genes analyzed, significant changes in response to AIV infection was mainly detected in spleen (and to some extent in lungs) of chickens, where *AvBD1*, *4* and *6* as well as *DEFB4A* were all downregulated at 3 d.p.i. In infected chickens, the H6N2 subtype stood out in evoking the most consistent responses in genes related to IFN signaling (Figure 2, Table S3). From analysis of the tufted duck genome and transcriptome, we could verify for the first time that the RNA sensing protein RIG-I is encoded in this species. However, we could hardly see any transcriptomic response to infection in genes related to IFN signaling or other aspects of innate immunity (data not shown).

Other genes of note, are the *ANP32* family, serving as co-factors for the virus polymerase during transcription. In chickens, *ANP32E* was weakly down–regulated in all tissues in response to infection with all subtypes except H3N8 and H4N6 (Figure 3a, Table S4). The zinc finger protein ZC3H11A has been suggested to affect replication efficiency of several nuclear replicating RNA viruses including IAV[37]. In our experiments in chickens, *ZC3H11B* was weakly up–regulated for several of the IAV subtypes in all tissues, whereas in tufted ducks *ZC3H11A* was slightly down–regulated in colon for some subtypes (Figure 3a–b, Table S4, S5). Glycosyltransferases related to AIV receptor synthesis were differentially expressed in chickens at 3 d.p.i. Of note was that sialyl transferases adding α2,3-linked SA were generally weakly upregulated in response to infection with most viruses (*ST3GAL2* in spleen, *ST3GAL4* in lung, *ST3GAL5* in spleen) whereas *ST6GAL1* encoding a sialyl transferase adding α2,6-linked SA was weakly down–regulated in all tissues for most viruses. Exceptions to this rule were *ST3GAL6* that was down–regulated in lungs and *ST6GAL2* that was largely unaffected but upregulated in lungs from birds infected with H9N2 and H11N9. A similar pattern could not be observed in tufted ducks (Figure 3b, Table S5). The fucosyl transferase gene *FUT8* was generally up–regulated in all chicken tissues for most viruses whereas *FUT11* was down–regulated, predominantly in the chicken spleen. In tufted ducks, these genes were unaffected except for upregulation of *FUT8* in spleen in response to H4N6 and H8N4.

Glycoproteomics reveals similarities in influenza virus receptor repertoirs between bird species.

To study how the repertoires of sialylated glycan receptors for IAV differ across avian species, we performed glycoproteomic analysis on uninfected specimens of mallards (the original host of the IAV isolates used in this study) as well as of the experimental animals; chickens and tufted ducks. Tissue samples were collected from putative AIV target organs comprising trachea, lung, ileum, and colon from healthy individuals of tufted duck, mallard and chicken. In mallards, *N*-glycopeptides terminating with α2,3-linked Neu5Ac were found in membrane proteins from all sampled tissues (Figure 4 and Table S6). Additionally, *N*-glycopeptides terminating with α2,6-linked Neu5Ac were found in secreted serum proteins from all tissues (Figure 5). However, some *N*-glycopeptides terminating with α2,6-linked Neu5Ac were also detected in predicted membrane proteins. Similar numbers of hits of structures terminated with Neu5Acα2,3 and Neu5Acα2,6 were found in the investigated mallard tissues, except for ileum that had a dominance of Neu5Acα2,3 terminated structures. Disialylated glycoforms carrying one Neu5Acα2,3 and one Neu5Acα2,6 were detected in a smaller fraction of the samples, except for colon that lacked these α2,3/α2,6 mixed sialylated *N*-glycans. The *O*-glycopeptides had core 1 structures (Galβ1,3GalNAcα1–*O*–Ser/Thr) with Neu5Acα2,6 on the GalNAc for serum glycoproteins and Neu5Acα2,3 on the Gal, or both on the Gal and on the GalNAc, for membrane glycoproteins (Figure 4C and 4D). Importantly, longer sialylated *N*-glycans and fucosylated sialylated (S-Le) structures were detected in all sampled tissues from mallards, but concentrated towards ileum (Table S6). In general, there was a dominance of sialylated *N*-glycans compared to *O*-glycans in most tissues except the lungs that contained equal amounts of these structures.

In tufted ducks, both transmembrane and secreted glycopeptides terminated with Neu5Acα2,3 or Neu5Acα2,6 were identified (Table S7). Approximately equal ratios of the number of sialylated *N*- vs. *O*-linked glycans were detected in all tissues except for ileum that had dominance of *N*-linked glycans. Fucosylated sialylated glycan structures were detected in all tissues, with the highest amounts in trachea and lowest in ileum. Neu5Acα2,3 was detected in all tissues, with a strong accentuation in trachea (Figure 6a-c). Neu5Acα2,6 was detected in all tissues, but the presence was lower in lung. Disialo glycan structures with both Neu5Acα2,3 and Neu5Acα2,6 were hardly detectable in tufted duck tissues, and only present in trachea and lung at low levels. In chickens, glycopeptides originating from both transmembrane and secreted glycoproteins terminating with Neu5Acα2,3 or Neu5Acα2,6 were identified (Table S8). In trachea, lung, and ileum sialylated *N*-linked glycans dominated and in colon there was a very high dominance of sialylated *N*-linked glycans over sialylated *O*-linked glycans. Fucosylated sialylated glycans were more common in trachea and colon than in lung and ileum. Neu5Acα2,3 was found at similar levels in all sampled tissues, but somewhat concentrated in trachea (Figure 6) and Neu5Acα2,6 was found in similar levels in all sampled tissues.

Comparing expressed glycans terminating with α2,3- or α2,6-linked Neu5Ac in different organs between the three species hence revealed great similarities. One important exception was that the abundance of Neu5Acα2,3 terminated fucosylated (sialyl lewis) glycan structures in ileum varied with the highest abundance in mallards and lowest in tufted ducks. In common for all three species, Neu5Gc could not be detected in any of the tissues. Furthermore, despite previously published *in vitro* data suggesting tropism of chicken origin AIV isolates for sulfated sialylated glycopeptides [12,15], no such structures were identified in any of the samples. However, the recently identified putative AIV receptor structures, phosphorylated high-Man *N*-linked glycopeptides [38,39] were identified in both mallard and chicken samples (not tested in tufted ducks) (Figure 6). These glycopeptides were mainly from predicted lysosomal enzymes, including carboxypeptidase and aminopeptidase.

Discussion

Molecular barriers for transmission of influenza A viruses between birds and to humans can be classified into A) host related factors: e.g. species-specific physiological, biochemical and immunological differences; and B) virus related factors: e.g. subtypes, sublineage specific genetic markers associated with adaptation to a specific host as well as receptor and organ tropism[40]. Mallards are regarded as a key reservoir of AIV, as they carry almost all known AIV subtypes [41,42] and show limited signs of disease even when infected with HPAIV [43], which causes significant morbidity and mortality in other bird species, including closely related ducks, such as tufted ducks [44,45], and in chickens [46]. Through experimental infections together with in-depth molecular characterization of host AIV receptor expression, host response and viral genetic changes during infection, we demonstrate a number of important features central to interspecies transmission.

First, we found that LPAIVs preferentially replicated in the respiratory tract of tufted ducks and chickens. Although this might have been driven by method of inoculation, it is in sharp contrast to LPAIV infection in mallards, where the infection is well-documented in the surface epithelium of the gastrointestinal tract [24,47]. The unsuccessful infection of tufted ducks via the intraesophageal route was unexpected as both mallards and tufted ducks belong to the Anatidae family [48], and it is long assumed that all duck species share mode of IAV transmission. On the other hand, epizootical studies have shown that AIV prevalence differs dramatically between species within the Anatidae family [49]. Additionally, studies using virus histochemistry found more virus staining in trachea, rather than colon for several non-mallard species including tufted duck [23,25] suggesting differences in receptor expression. Taken together, our findings suggest that such differences in AIV prevalence between bird species are due to differences in AIV tropism and infectivity, acting as barriers for interspecies transmission.

Second, we found differences in the outcome of infection across the different AIV subtypes tested. Notably, H6N2 was shed at high loads both in oropharyngeal swabs and in tissue samples from both bird species. This virus subtype is very common in wild mallards [41,50,51] and has been demonstrated to infect gallinaceous birds including pheasants and quails [52] as well as chickens [53]. On the other hand, the unsuccessful infection in chickens with the H9N2 subtype was unexpected as LPAIV H9N2 is endemic in chickens in many countries [54]. The fact that the HA gene of our H9N2 isolate was phylogenetically distinct from chicken endemic H9N2 isolates suggests the importance of sublineages within the same AIV subtype that seem to be adapted to different host species. Furthermore, in some of the viruses used in this study, we identified putative SNPs that may be related to infection of a new host and provide candidates for futher studies on their role in host adaptation.

Thirdly, transcriptomic analysis illuminated that the host response to virus challenge was different in chickens vs. tufted ducks. For instance, LPAIVs H3N8 and H4N6 generated the least number of DEGs in investigated chickens, whereas the same subtypes yielded the greatest number of DEGs in tufted ducks (see Figure S4). The H6N2 subtype gave the most consistent upregulation of IFN related genes in chickens, consistent with its replication to high titres in lungs, spleens and colons. However, a similar response to this subtype was not detected in tufted ducks despite the presence of the *RIG-I* gene in this species. It should be emphasized though, that the samples in our experiments were taken at 3 d.p.i. whereas in other studies, the strongest innate immune responses to IAV infection in chickens and ducks take place 1-2 d.p.i. [26,55,56]. The up–regulation of *ZC3H11B* in chickens is interesting and merits further study as the A ortholog was described to be involved in nuclear export of mRNA in humans and knocking this gene out in HeLa cells resulted in reduced growth of the IAV strain H1N1 A/WSN/33 [37]. Taken together, only minor changes in gene expression were identified in virus challenged birds, well in line with earlier reports of LPAIV only inducing mild response in birds [26,55,56]. Particularly, both in terms of number of significant DEGs identified and particular up-/down–regulated DEGs, clear differences could be observed in host response to virus challenge between chickens vs. tufted ducks suggesting a marked difference in host response to virus challenge between species.

Finally, species specific differences in the glycan structures serving as receptors for AIV have been proposed as important barriers for interspecies transmission, most importantly the receptor tropism for α2,3 vs. α2,6-linked Neu5Ac as a hallmark of AIV vs. human adapted IAV [10,11,57]. The results of our glycoproteomic characterization of the avian sialic acid containing glycoconjugates provide a number of important insights into these aspects: Structures containing Neu5Acα2,6 were detected in all sampled avian tissues. In contrast to earlier studies suggesting that avian glycosylation produce shorter, less complex glycans compared to human glycosylation [58], we demonstrate that longer sialylated glycan structures were present in all analyzed avian tissues as well (Table S6-9, Figure 6, and Figure S9). Sulfated 3'SLN and S-Le^x have been suggested as main receptors for H7 AIVs, H5 AIVs isolated from chickens, and gull-specific H13 and H16 viruses [12,13,59]. However, no sulfated sialylated glycopeptides were identified in any of the investigated avian samples (including chickens), challenging the biological relevance of Sulfated-3'SLN and Sulfated-S-Le^x as major AIV receptors. Instead, phosphorylated high-Man *N*-glycopeptides were identified in both the mallard and chicken samples (not tested in tufted duck). This is of high interest as IAVs (of avian, human, and swine origin) recently were described to bind human lung-derived phosphorylated non-sialylated glycans (particularly Man-6P containing glycans) in a SA-independent manner [38]. We identified these N-glycopeptides on predicted lysosomal enzymes, including carboxypeptidase and aminopeptidase. It can be speculated that IAV binding to phosphorylated glycans takes place during late phase cellular entry, facilitating the virus uncoating process by targeting lysozomal enzymes [60]. Tropism for *N*-glycolyl-neuraminic acid, Neu5Gc, in wild type AIVs is extremely rare and this structure has not been found in birds [61]. Indeed, Neu5Gc was not detected in our glycoproteomic analysis in any of the avian species. Taken together, these results not only indicate great similarities in IAV receptor expression between the three bird species, but also demonstrate that avian glycosylation and the expression of glycan structures in avian tissues is more similar to that seen in mammalian tissues than what was previously anticipated.

In conclusion, the experimental design of this study allowed us to address the role of multiple factors as barriers for successful AIV interspecies transmission. The results suggest that not only are factors related to the physiology of the infected species important, but also route of infection, virus phylogeny (as exemplified by the mallard-derived H9N2 LPAIV in chickens) and host response. Moreover, extensive glycoproteomic analysis of the avian respiratory and intestinal tracts clearly demonstrated that birds can produce longer sialylated Lewis structures, as well as both *N*- and *O*-linked glycans terminated with α2,6-linked Neu5Ac. This is contrary to the current dogma whereby these structures were believed to be mammal specific, suggesting that available receptors in mammals and birds are more closely related than previously thought. Receptor incompatibility has been the major focus of AIV interspecies barrier research for the past decades. However, our results suggest that the importance of the proposed receptor barrier might be limited. Instead, we propose that IAV interspecies transmission depends on several host factors (physiology, host immune response, receptor configuration and expression) and viral factors (route of infection, viral phylogeny and genetic makeup). All these factors need to be considered and studied in order to achieve a thorough understanding of IAV interspecies transmission enabling a prudent pandemic preparedness planning.

Methods

Ethical statement

All procedures of virus screening and propagation were handled in biosecurity level 2 (BSL2) facilities at the Zoonosis Science Center, Uppsala University. All animal experiments were carried out in strict accordance with a protocol legally approved by the regional board of the animal ethics committee, Sweden (permission number 5.8.18-07998/2017). All animal experiments were conducted in BSL2 animal facilities at the Swedish National Veterinary Institute (SVA).

Origin of viruses and virus propagation

Viruses used in the current study were obtained from the Linnaeus University AIV repository (Table 1), and collected and isolated as described in [41]. Briefly, viruses were isolated from mallards captured at a long-term study site at Ottenby bird observatory, Sweden (56º12′ N 16º24′ E). Viruses were propagated in the allantoic cavity of 11-day-old specific pathogen free embryonated chicken eggs and harvested fluid was stored at −70 °C until further use. The egg infectious dose 50 (EID_{50}) of the inoculum was determined by infection in embryonated chicken eggs [62] .

Strain selection

We selected AIVs comprising eight subtypes of different phylogenetic lineages that have all been detected in the avian reservoir with different frequencies (Table S1). These include those AIVs that are common in mallards at this study site (H4N6 and H6N2) and elsewhere (H3N8), as well as those that are less commonly isolated (H8N4, H9N2, H10N1, H11N9, H15N5). For H15N5 there have only been 14 detections ever defined (https://www.fludb.org/; access 1 July 2020), 6 of which are from this study site. Subtypes seldomly detected in wild bird surveillance (H8N4 and H15N5) may have hosts in undersampled bird species such as diving ducks, although this is still unclear. H9N2 is more common in poultry than in ducks. H10 viruses are isolated from the broadest host range, with infections common in ducks, chickens, seals, and with multiple records of zoonotic infections.

Pathogenicity and transmissibility in chickens and tufted ducks

A total of 72 white leghorn chickens (*Gallus gallus domesticus*) were raised until 3 weeks old at the SVA. Tufted ducks (*Aythya fuligula*) 3-6 weeks old were obtained from Snavelhof, Veeningen, the Netherlands. All animal experiments were carried out in a biosecurity level two animal facility at the SVA. Birds were divided into groups of four and inoculated with one of the eight viruses or a phosphate buffered saline (PBS) mock. Thirty-six individuals of each species were inoculated intraesophageally (IE) and 36 were inoculated oculonasally (ON), using an inoculum of 10^6 EID_{50} per 1 mL per bird. For the mock groups, 1 mL of PBS was used per bird. Birds were monitored daily for clinical signs and mortality until 3 days post infection (d.p.i.), when all birds from each group were euthanized by injection of 1 mL of pentobarbital (100 mg). In order to compare virus shedding patterns via the respiratory and/or digestive tract, oropharyngeal (OP) and cloacal (CL) swabs were taken every day from all birds and placed in Virus Transport Media (Glycerol 10% vol/vol; Hanks 1x; Balanced Polymyxin sulphate B 100U/mL; Nystatin 50u/mL; Lactalbumin 5g/L; Penicillin 200U/mL; Streptomycin 200microl/mL; Gentamycin 250microl/mL; MQ water). Tissue samples were collected from lung, colon, and spleen of euthanized birds to study virus distribution as well as the transcriptomic host response to infection.

Reverse Transcriptase quantitative real-time-PCR

Viral RNA was extracted from the OP and CL swab samples collected from chickens and tufted ducks using Maxwell® 16 Viral Total Nucleic Acid Purification Kit on a Maxwell® 16 System extraction robot (Promega, Madison, WI, USA). RNA was isolated from lung, colon and spleen of all ON inoculated birds using TissueLyser II and RNeasy Mini Kit (Qiagen, Hilden, Germany). Quantification of the viral load (expressed as egg infective dose 50 (EID_{50}) equivalent, as defiend below) from the swab samples was based on Cq values obtained by reverse transcriptase quantitative real-time PCR (RT-qPCR) targeting the matrix (M) gene [63] and using AgPath-ID One-Step RT-PCR reagent kit (Thermo Fisher Scientific, Waltham, MA,USA) on a a BioRad CFX1000 Real-Time PCR System (BioRad, Hercules, CA, USA).

We calculated EID_{50} equivalent by determining the Cq values from a known EID_{50} reference virus inoculum. From this data we generated a standard curve (Figure S10) correlating these measurements and used this curve to predict EID_{50} equivalents from Cq data for all virus experiments.

Whole genome sequencing and variant detection

Total viral RNA was extracted from the virus inocula, all organs with a Cq value < 30, and positive swabs at 3 days post infection (d.p.i.) with a Cq value < 30 (Table 1) using QIAamp viral RNA Mini kit (Qiagen, Hilden, Germany) according to the kit protocol. Virus whole-genome amplification was undertaken as described by Pohlmann, et al. [64]. Sample quality control was assessed using a Qubit 4 Fluorometer (using Qubit™ dsDNA BR assay Kit) and Agilent 2200 TapeStation (using Agilent D5000 ScreenTape assay kit). Library construction and sequencing was undertaken at Novogene (Beijing, China). The genomic DNA was randomly fragmented to size of 350bp, and then DNA fragments were end polished, A-tailed, and ligated with the adapters of Illumina sequencing, and further PCR enriched with primers of P5 and P7 oligos. The PCR products as final construct of the libraries were purified followed by quality control test. 150 bp paired reads were generated with a sequencing depth of 9-12 million reads per sample on the Illumina platform NovaSeq 6000.

For variant detection, generated reads were analysed using Geneious Prime work package (Biomatters, Auckland, New Zealand) through the following pipeline: Initially, the primer sequences were trimmed off from the raw reads using the "Trim Ends" Geneious Prime plugin. Further, the trimmed reads were mapped using bowtie2 implemented in Geneious Prime against the whole genome sequence obtained from the used homologous inoculum, and a consensus sequence was generated for each sample. Finally, SNP (single nucleotide polymorphism) calling was conducted using "variation/SNPs" plugin implemented in Geneious Prime work package on the assembled contigs with a maximum variant p-value of 10^6.

Serology

To confirm that all birds were seronegative prior to infection, blood samples were collected using vacutainer serum plus blood collection tubes (BD, Becton, Dickinson and Company, New Jersey, USA) from all animals 2 days prior to the first animal experiment. Serum was recovered by centrifugation of the tubes at 1000 g for 5 minutes. Samples were examined for AIV-specific antibodies using the Influenza A nucleoprotein (NP) antibody competition ELISA kit (Idexx, Hoofddorp, The Netherlands) according to the manufacturer's instructions.

Transcriptomics

Gene expression was quantified in lung, colon and spleen for all birds three d.p.i using QuantSeq 3' mRNA sequencing [65]. For this purpose, 25 mg of each tissue was homogenized using Qiagen TissueLyser II, and RNA was extracted using RNeasy Mini Kit and DNAse treated using the RNase-Free DNase Set (Qiagen, Hilden, Germany). The quantity and quality of the RNA was assessed using the Qubit (Qubit RNA BR Assay Kit, Invitrogen, CA, USA) and the Agilent 2100 Bioanalyzer system (Agilent RNA 6000 Nano Kit, CA, USA). The library preparation was conducted using the QuantSeq 3‘ mRNA-Seq Library Prep Kit (FWD) (Lexogen Inc., Greenland, USA) according to the manufacturer's instructions. Samples were sequenced (75bp single-end reads) on the Hiseq 4000 platform (Illumina Inc., CA, USA). The raw QuantSeq reads were trimmed using the BBDuk program in the package BBMap (https://sourceforge.net/projects/bbmap/) to remove adapter sequences, poly-A tails, overrepresented sequences, and low-quality bases with the following parameters: k = 13, ktrim = r, useshortkmers = t, mink = 5, qtrim = r, trimq = 10, minlength = 20. Read quality before and after trimming was checked using FASTQC 0.11.5 [66]. The trimmed sequences were aligned to the chicken reference genome (GRCg6a, Ensembl release 99, accession number GCA_000002315.5) and the tufted duck reference genome (bAytFul2.pri, GenBank release 236, accession number GCA_009819795.1) using STAR 2.5.3a [67]. For the STAR indexing step, the tufted duck gff annotation file from NCBI was converted into gtf format using the gffread utility in the Cufflinks software 2.2.1 [68]. Read counts per gene were calculated in STAR 2.5.3a.

Bioconductor DESeq2 v1.24.0 [69] program in R v3.6.1 (RCoreTeam, 2016) was used to calculate statistical differences of the expression levels of genes between the control birds and the infected birds for each species and tissue (four individuals per group). Cut-off values for significant genes were set to an FDR of <0.05 and to genes that were up- or downregulated more than 10%, based on visual inspection of volcanoplots generated in the EnhancedVolcano package [70] in R v3.6.1 [71].

To allow for comparisons of gene expression levels between chicken and tufted duck, a best hit (RBH) analysis was conducted. For this purpose, the DNA sequence information for coding sequences (cds) from chicken (GRCg6a, Ensembl release 99) was downloaded. The gffread utility from the STRINGTIE package [72] was then used to generate a FASTA file with the DNA sequences for the coding sequences in the tufted duck. The coding sequences were reciprocally blasted using blastn [73]. RBHs were identified using the python script reciprocal_blast_hits.py https://scriptomika.wordpress.com/2014/01/28/extract-best-reciprocal-blast-matches/.

To compare the response between treatment groups the overlap of differentially expressed genes between groups treated with different virus subtypes within one species, and between groups treated with the same virus subtypes between the two species were visualised using the UpSetR package v 1.4.0 [74] in R v3.6.1 [75].

Transcriptomic response and gene onthology

Gene expression levels for genes associated with innate immune response, transcription, glycosylation, and inflammation were visualized in heatmaps. Significantly differentially expressed genes associated with these functions were identified by filtering the DESeq2 output files for gene names identical to the list disclosed in supplementary Table S1 or gene names including any of the search terms disclosed in supplementary Table S2 and S3 or gene descriptions including “defensin” or “gallinacin” (for β-defensins/gallinacins). A threshold for significant DEGs was set at ≥ 10% fold change relative to control birds and an adjusted p-value ≤ 0.05. Gene ontology and pathway analysis were undertaken for differentially expressed genes (adjusted p-value ≤0.05) for each virus/bird species/organ. Gene set analysis/overrepresentation analysis was conducted using the Webgestalt web interface (http://webgestalt.org/) searching the gene ontology database for “molecular function”, “cellular component”, and “biological process”. Additionally, pathway analysis was conducted searching KEGG using the Webgestalt web interface as well. Ontology terms/pathways with a FDR≤0.05 were visualised in heatmaps.

Epithelial cell isolation for glycoproteomic analysis

Tissue samples were collected from trachea, lung, ileum, and colon of captive healthy uninfected mallards, chickens and tufted ducks (5 individuals per species). The biopsies were rinsed in chilled (~8 °C) PBS (Sigma-Aldrich AB, Stockholm, Sweden) upon collection to remove any debris. Adipose tissue, blood vessels, etc. was removed and the intestinal specimens were cut open and intestinal content and mucus was carefully removed. Cleaned tissue samples were incubated at 37 °C for 1 h in 10 mL DPBS with 1 mM DTT and 3 mM EDTA (Sigma-Aldrich). After incubation, the liquid was carefully aspirated and replaced with PBS (Sigma-Aldrich). The samples were vortexed for 5×20 s and the tissue was then removed. The remaining cell slurry was spun at 1000 g for 5 min at 4 °C and the supernatant was discarded. The pellets were snap-frozen in liquid nitrogen and stored at −80 °C.

Protein digestion, enrichment and fractionation

The samples were homogenized using the lysis matrix D on FastPrep®-24 instrument (MP Biomedicals, OH) in lysis buffer (50 mM triethylammonium bicarbonate (TEAB), 2% sodium dodecyl sulfate (SDS)) and 5 cycles 40 s each. The samples were centrifuged at maximum speed for 15 min, and supernatants harvested. The protein concentration was determined using Pierce™ BCA Protein Assay (Thermo Fisher Scientific) and the Benchmark Plus microplate reader (BIO-RAD) with BSA solutions as standards.

Sample aliquots (500–1000 µg) were digested with trypsin using the filter-aided sample preparation (FASP) method [76], with small modifications. Briefly, samples were reduced with 100 mM dithiothreitol at 60°C for 30 min, spin-filtered (30 kDa MWCO Pall Nanosep centrifugation filters, Sigma-Aldrich), washed repeatedly with 8 M urea and followed by digestion buffer (1% sodium deoxycholate (SDC) in 50 mM TEAB) prior to alkylation with 10 mM methyl methanethiosulfonate in digestion buffer for 20 min. Protein digestion was performed in digestion buffer by addition of 5 µg Pierce MS grade Trypsin (Thermo Fisher Scientific) at 37°C overnight, followed by an additional 2 h incubation with new trypsin added the consecutive day. Peptides were isolated by centrifugation and SDC was removed by acidification with 10% trifluoroacetic acid. Glycopeptides were enriched with hydrophilic interaction liquid chromatography **(**HILIC) according to [77], with slight modifications. In short, peptides were loaded onto an in-house zwitterionic Zic-HILIC SPE cartridge containing 20 mg of Zic-HILIC particles (10 µm, 200 Å; Sequant/Merck). The flow-through was collected and re-circulated through the column an additional three times. The column was washed with totally 1.2 mL of 80 % (v/v) acetonitrile and 1 % (v/v) trifluoroacetic acid. Enriched glycopeptides were eluted with 4 times 50 µL 0.1 % (v/v) trifluoroacetic acid followed by 50 µL of 25 mM NH_4HCO_3 and finally 50 µL of 50 % (v/v) acetonitrile and dried by vacuum centrifugation. The samples were fractionated into six fractions (5.0-17.5 % acetonitrile in 0.1% trimethylamine), using Pierce high pH reversedphase peptide fractionation kit (Thermo Fisher Scientific) according to the manufacturer's protocol and pooled into 3 samples. Pooled samples were dried in a vacuum centrifuge and reconstituted in 15 µL of 3 % acetonitrile, 0.1 % formic acid for LC-MS/MS analysis.

NanoLC MS analysis

Peptide samples were analyzed on an Orbitrap Fusion Tribrid mass spectrometer interfaced with Easy-nLC1200 liquid chromatography system (Thermo Fisher Scientific). Peptides were trapped on an Acclaim Pepmap 100 C18 trap column (100 µm x 2 cm, particle size 5 µm, Thermo Fischer Scientific) and separated on an in-house packed analytical column (75 µm x 30 cm, particle size 3 µm, Reprosil-Pur C18, Dr. Maisch) using a linear gradient (solvent A; 0.2 % formic acid in water and solvent B; 80 % acetonitrile, 0.2 % formic acid in water) from 7 % to 35 % of solvent B over 45 min followed by an increase to 100% solvent B in 5 min, and finally 100% solvent B for 10 min at a flow rate of 300 nL/min. MS^1 scans were performed at 120 000 resolution, *m/z* range 600-2000, the most abundant double or multiply charged precursors from the MS^1 scans were selected with a duty cycle of 3 s, isolated with a 3 Da window, fragmented with higher-energy collision induced dissociation (HCD) at 30% normalized collision energy (NCE), *m/z* range 100-2000, and then two times at 40% NCE, *m/z* range 100-2000 and *m/z* 300-2000. The maximum injection time was 118 ms and MS^2 spectra were detected in the Orbitrap at 30 000 resolution. Dynamic exclusion was enabled with 10 ppm tolerance and 10 s duration. For selected samples, MS^3 was performed on the *m/z* 657.23 ion $[\text{Neu5AcHexHexNAc}]^+$ using HCD 20% NCE at both the MS^2 and the MS^3 steps, and with detection in the ion trap.

Glycoproteomic data analysis

The LC-MS/MS raw files were analyzed with the Byonic software (Protein metrics) using a modified list of the glycan modifications "182 human N-glycans" and "6 most common O-glycans", such that e.g. glycoforms with a $Hex_4HexNAc_5$ core structure, differing from the normal $Hex_5HexNAc_4$ complex biantennary core, were added. Further Byonic search criteria: the FASTA database was *Anas platyrhynchos* (Organism ID 8840; 27089 sequences) and *Gallus gallus* (Organism ID 9031); C-terminal cleavage allowed after Lys and Arg; accuracy for MS^1 was 10 ppm and for MS^2 it was 20 ppm; static modification was methylthio on Cys (+45.9877 u) and variable modification, apart from glycans, was Met oxidation (+15.9949 u). Tufted duck glycopeptides were identified using the mallard genome as template, due to non-available tufted duck genome at the time of analysis. A Byonic score cut off >300 was used for glycopeptide hits and Neu5Ac containing hits were manually verified with the following inclusion criteria 1) presence of the correct peptide+HexNAc ion with respect to the precursor mass and identified glycan mass; 2) presence of the Neu5Ac oxonium ions *m/z* 274 and *m/z* 292; and 3) for hits including fucose (dHex), presence of peptide+HexNAc+dHex ion for the identification of a core fucose, and/or presence of *m/z* 512 ion (HexHexNAcdHex) for identification of Fuc on the antennae. Extracted ion chromatograms were traced at diagnostic MS^2 ions including peptide+HexNAc ions, chosen to identify additional glycoforms sharing the same peptide, and saccharide oxonium ions, for instance *m/z* 274.09 for tracing Neu5Ac; *m/z* 290.09 for tracing Neu5Gc and *m/z* 495.18 for tracing Neu5AcHexNAc.

The Neu5Acα2,3/Neu5Acα2,6 isomeric structures of glycopeptide hits were determined according to [78].. Briefly, the relative LacNAc to Neu5Ac (L/N) oxonium ion ratio (*m/z* 204 + *m/z* 366) / (*m/z* 274 + *m/z* 292) were calculated at an NCE of 40% for *N*-glycopeptide hits carrying $Hex5HexNAc4NeuAc_2(dHex)_{0\text{-}1}$ complex biantennary structures; and for *O*-glycopeptide hits carrying $HexHexNAc(Neu5Ac)_{1\text{-}2}$ structures. The ratio was then multiplied with the stoichiometric compensation factor *n*(NeuAc) / *n*(HexNAc) to obtain the normalized ratio Ln/Nn. For the MS^3 based methodology, the MS^3 spectrum of the MS^2 generated *m/z* 657.23 ion was manually inspected. When the (*m/z* 204 + *m/z* 366) ion intensities were larger than the (*m/z* 274 + *m/z* 292) intensities, the linkage structure was considered as Neu5Acα2,6 and when smaller the linkage structure was considered as Neu5Acα2,3. For the MS^3 experiments, Byonic hits with scores <300 were also considered, provided that the same hit was present with a score >300 in the corresponding MS^2 experiment.

Data and Code Availability

The authors declare that all data supporting the findings of this study are available within the article, its supplementary information files, or are available from the authors upon request. The nucleotide sequences generated for variant detection and transcriptomic analyses (RNAseq) reported in this paper have been deposited into public databases, Sequence Read Archives, under project number PRJNA664709.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [79] partner repository with the dataset identifier PXD021392.

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Conflict of interest

We declare no conflict of interest for any of the authors.

Author contributions

Conceptualization: PEl, JJ, BO, AL, MW, MN, PEr

Animal experiment: MN, PEr, PEl, JJ, CL, CB

Transcriptomic analysis: EJ, PEr, RHSK, MN

Glycoproteomic analysis: JN, PEr, CS, BMO, GL

Writing — original draft: MN, PEr, PEl, EJ

Writing — review & editing: MN, PEr, PEl, JJ, AL, BO, JN, GL, MW, EJ, CL

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Figures

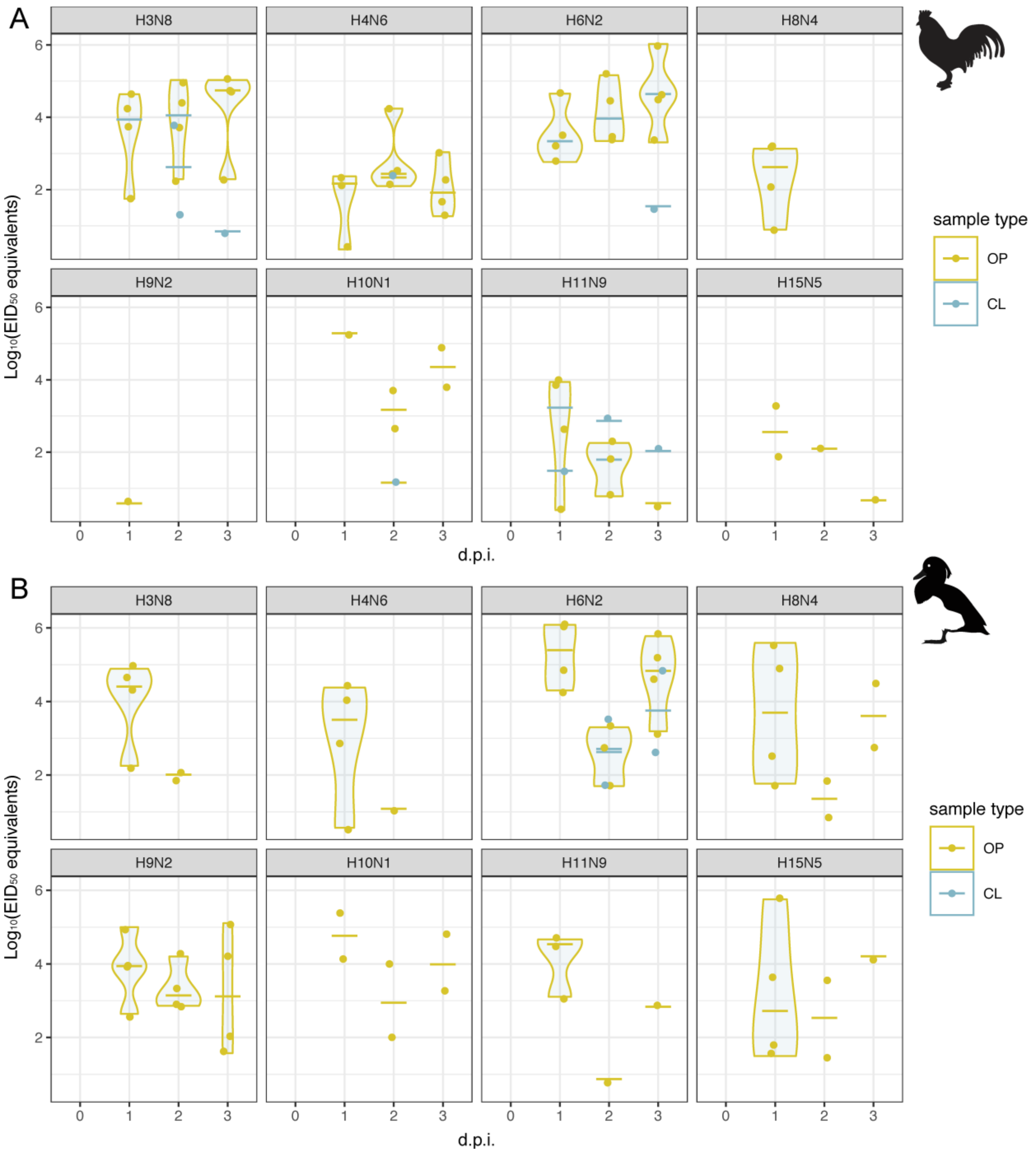

Figure 1. Viral load of mallard origin AIV subtypes in occulonasally inoculated A) chickens and B) tufted ducks. Four birds were inoculated with each virus respectively. Points represent positive samples and horizontal bars their respective median values, and are coloured by sample type; yellow — oropharyngeal (OP) and blue — cloacal (CL) swabs. Violins correspond to kernel density distributions of only positive samples. Negative samples are not shown. Y axis corresponds to $\log_{10}$ egg infectious dose 50

equivalents, which are inferred from Cq values based on the relationship reported in Figure S1

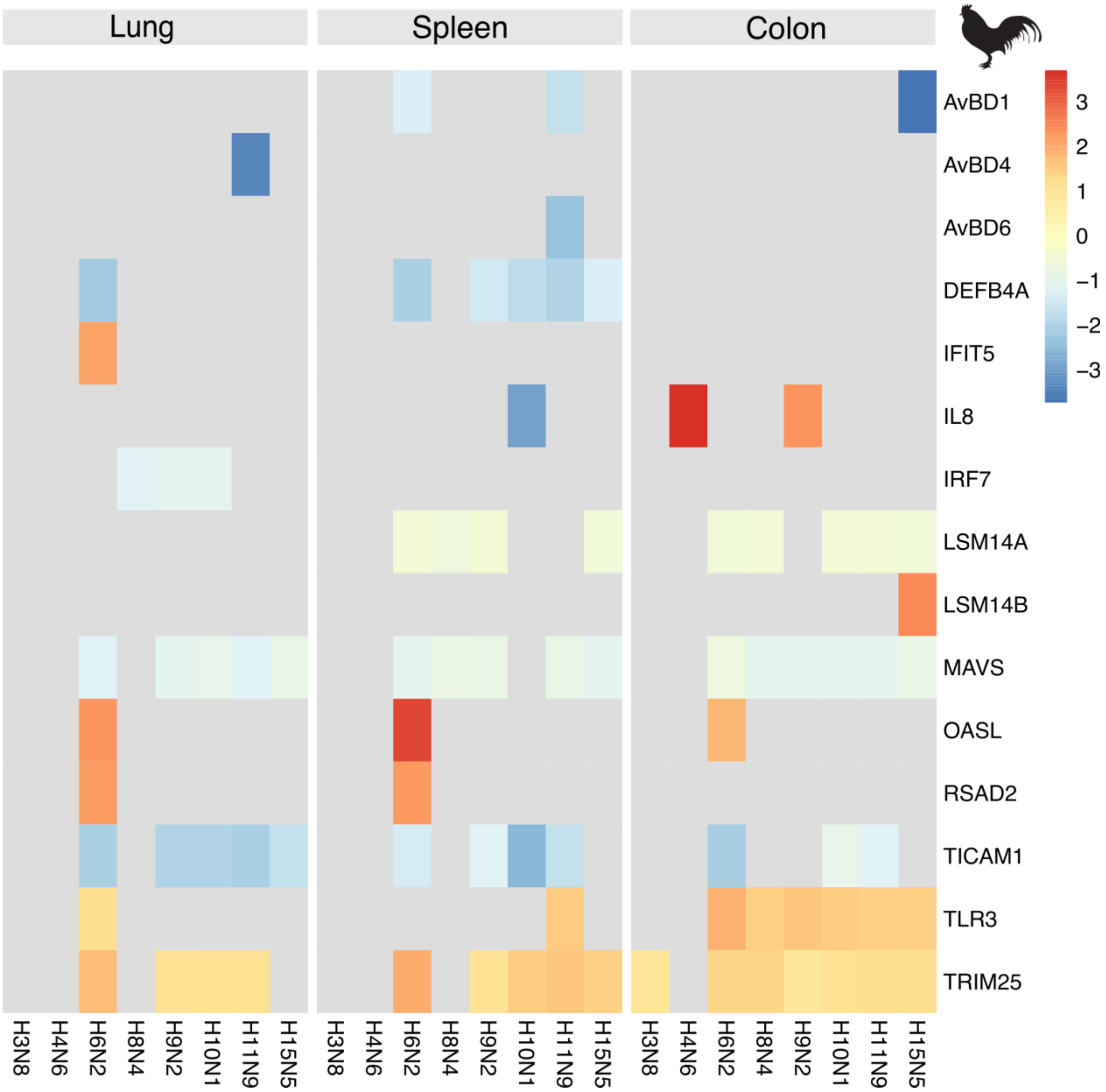

Figure 2. Selected significant DEGs associated with innate immunity in chickens. Genes in the proinflammatory- or RLR signaling pathways as well as β-defensin genes with described functions in birds were selected (Table S1) based on current literature. The color indicates the $\log_2$ fold change of significant (adjusted p value <0.05 and a threshold of ≥ 10% fold change) DEG's relative to control birds. Grey indicates non-significant DEGs. Data from lung samples is shown to the left, spleen in the center and colon on the right.

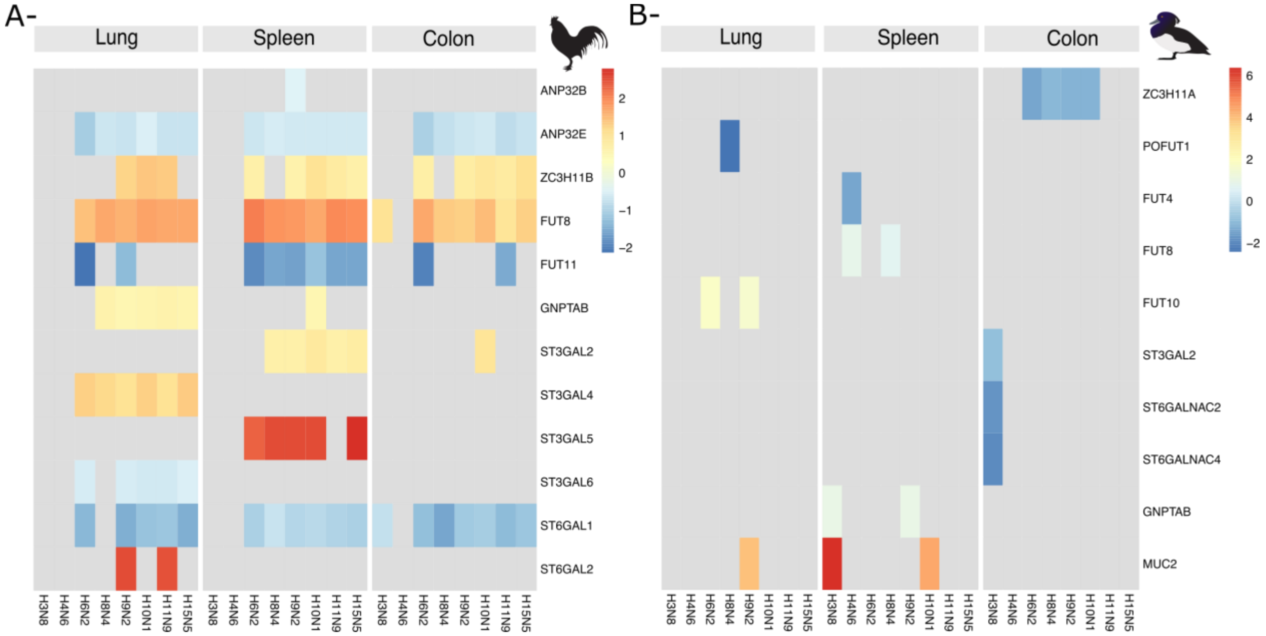

Figure 3. Selected significant DEGs associated with glycosylation and transcription in chickens and tufted ducks. Genes with described association to glycosylation or transcription in birds (Table S2) were selected based on current literature. The color indicates the $\log_2$ fold change of significant (adjusted p value <0.05 and a threshold of $\geq$ 10% fold change) DEG's relative to control birds. Grey indicates non-significant DEGs. Data from chicken (A) and tufted duck (B) lung samples are shown in the left panels, spleen in the center and colon in the right panels.

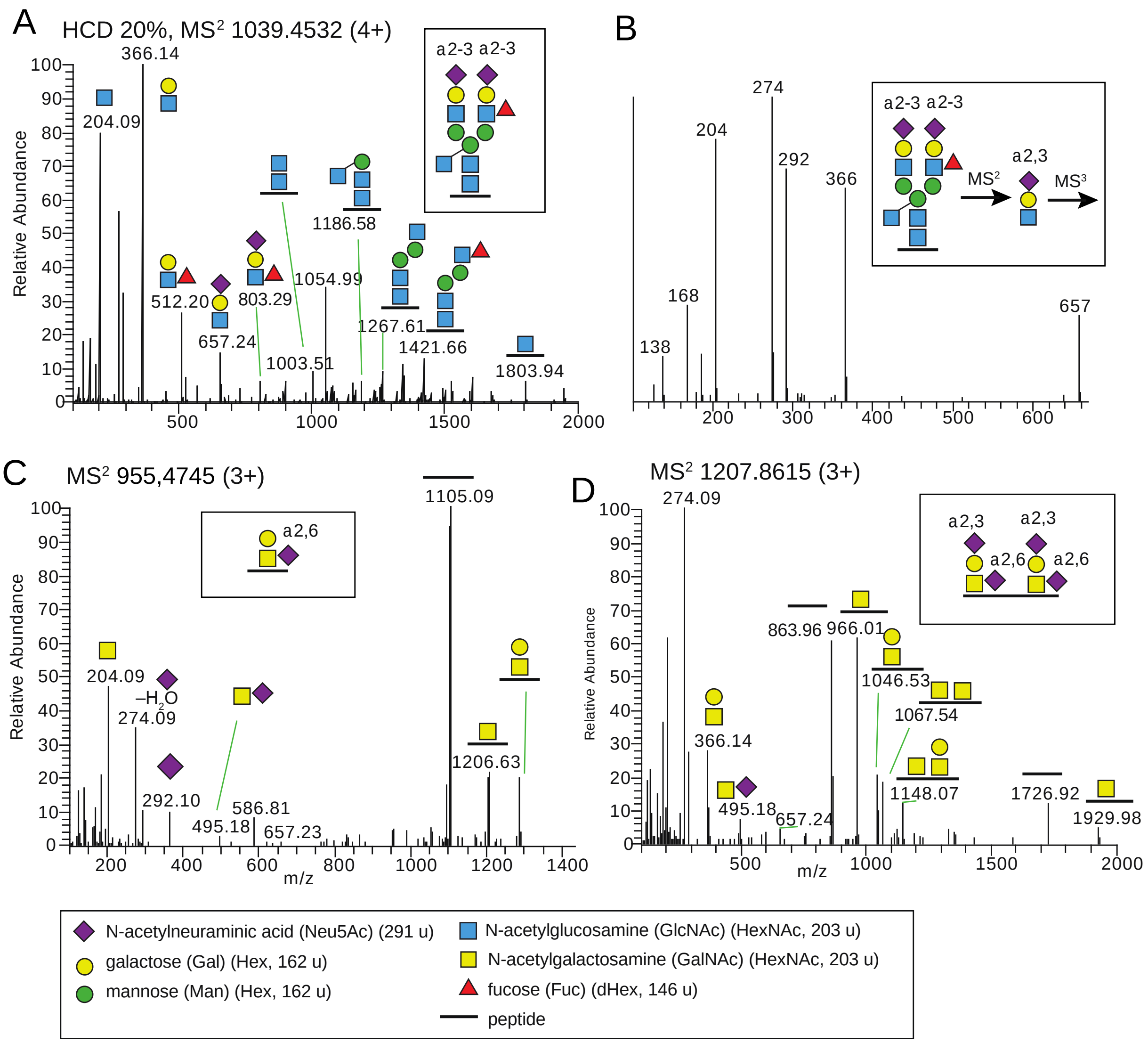

Figure 4. An example of a longer complex disialylated and monofucosylated *N*-glycan and a α2,3/α2,6 core 1 *O*-glycan found in mallards. These glycan epitope structures were also detected in chickens and tufted ducks. (**A**) HCD-MS^2 of a disialylated complex biantennary N-glycopeptide including a bisecting GlcNAc and a Lewis x fucose (boxed structure) from Epithelial cell adhesion molecule (U3J672_ANAPL) with the sequence R.LNVSIDNEVVQLEK.A. (**B**) MS^3 of the *m/z* 657 ion provided identification of the Neu5Acα2,3 linkages on both antennas. (**C**) HCD-MS^2 of a Neu5Acα2,6 sialylated core 1 *O*-glycopeptide from fibrinogen (U3I9E6_ANAPL) with the R.ETAPTLRPVAPPISGTGYQPR.P sequence. (**D**) HCD-MS^2 of two Neu5Acα2,3 and Neu5Acαα2,6 disialylated core 1 *O*-linked glycans of a glycopeptide from dystroglycan 1 (U3IBQ2_ANAPL) with the R.VISEATPTLAAGKDPEK.S sequence. Glycan symbols are according to the SNFG format [80].

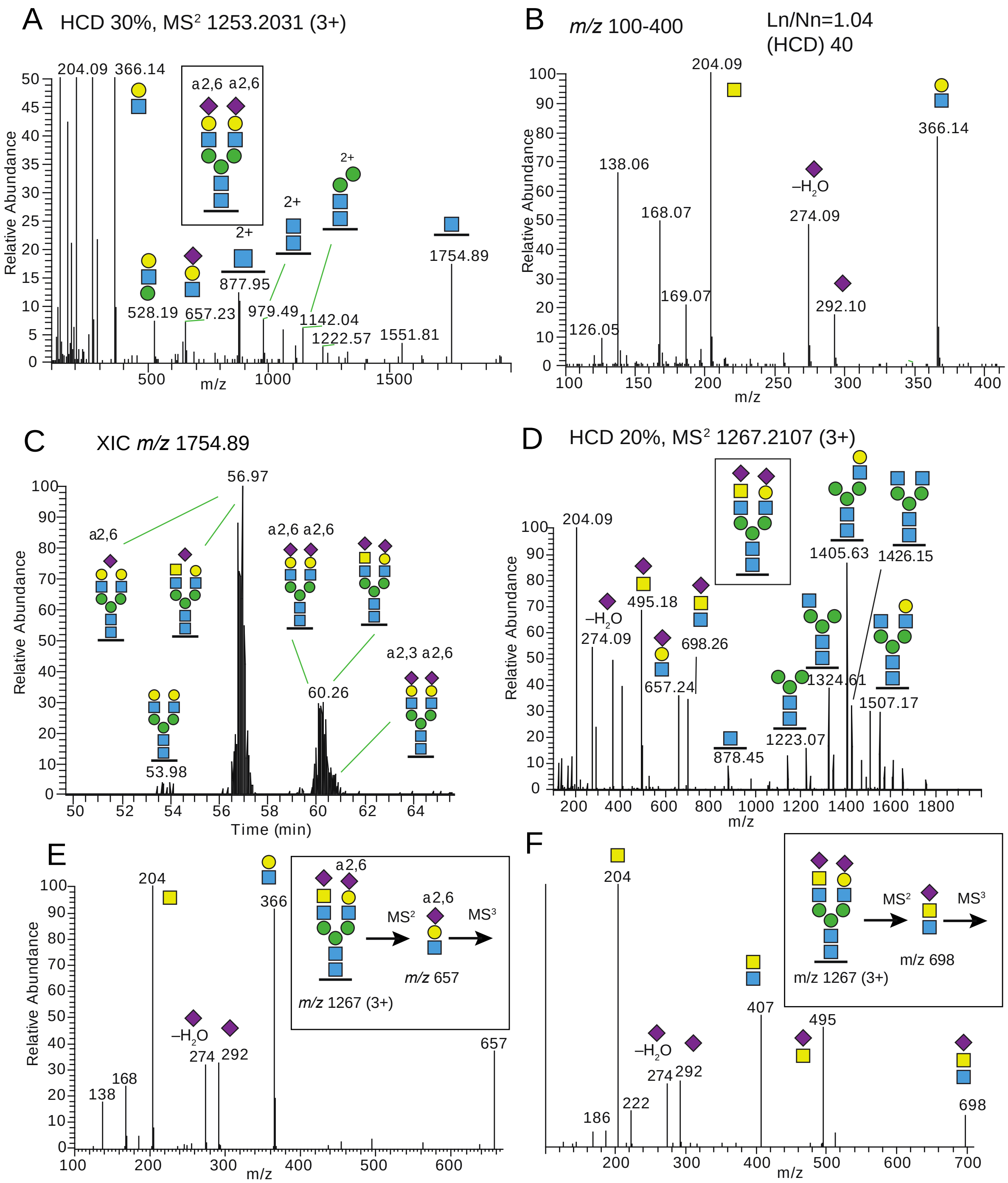

Figure 5. Examples from LC-MS/MS of various Neu5Acα2,6 sialylated *N*-glycopeptides from mallard tissues. These glycan epitope structures were also detected in chickens and tufted ducks. (**A**) HCD-MS^2 spectrum of a disialylated complex biantennary *N*-glycopeptide (boxed structure) from ovotransferrin (U3J851_ANAPL). (**B**) The *m/z* 100-400 region of the expanded MS^2 spectrum shows the presence of several oxonium ions used to identify the Neu5Acα2,6 linkage of the sialic acids. (**C**) Extracted ion chromatogram (XIC) of the peptide+HexNAc ion (*m/z* 1754.89) reveals several

additional glycoforms of this glycopeptide, e.g. a mixed Neu5Acα2,3; Neu5Acα2,6 glycoform eluting slightly after the major disialylated glycoform at ~60 min. (**D**) HCD-MS^2 spectrum of the Neu5Ac$_2$Hex$_4$HexNAc$_5$ glycoform of panel (C) reveals two different antennas. (**E**) MS^3 of the *m/z* 657.24 ion in panel (D) provides identification of a Neu5Acα2,6 linkage of the HexHexNAc terminated antenna; and (**F**) MS^3 of the *m/z* 698.26 ion provides identification of Neu5Acα2,6 linkage the HexNAcHexNAc antenna. Glycan symbols are according to the SNFG format [80].

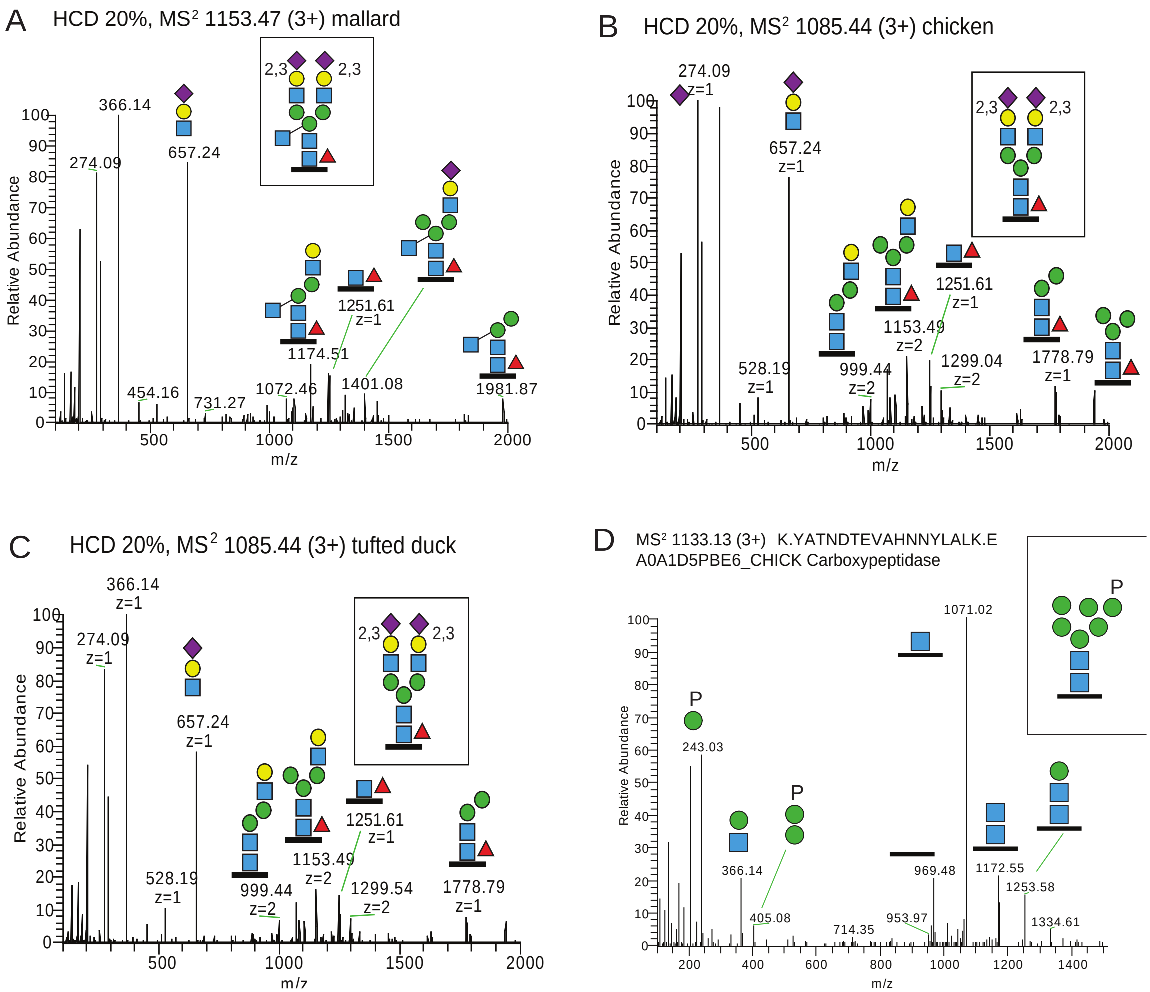

Figure 6. LC-MS/MS of a lumican *N*-glycopeptide and a phosphorylated high mannose glycan detected in bird tissues. The lumican *N*-glycopeptide was found in the trachea of all three species (**A**) mallard, (**B**) chicken and (**C**) tufted duck. The sialic acids are Neu5Acα2,3 linked and the peptide sequence is R.LDGNNLTR.A. (**D**) The phosphorylated high-Man glycopeptide, originated from carboxypeptidase in chicken colon, with the K.YAT<u>N</u>DTEVAHNNYLALK.E sequence. This glycan structure was also detected in mallards (not tested in tufted ducks). Glycan symbols are according to the SNFG format [80].

Supplementary Materials

Supplementary figures

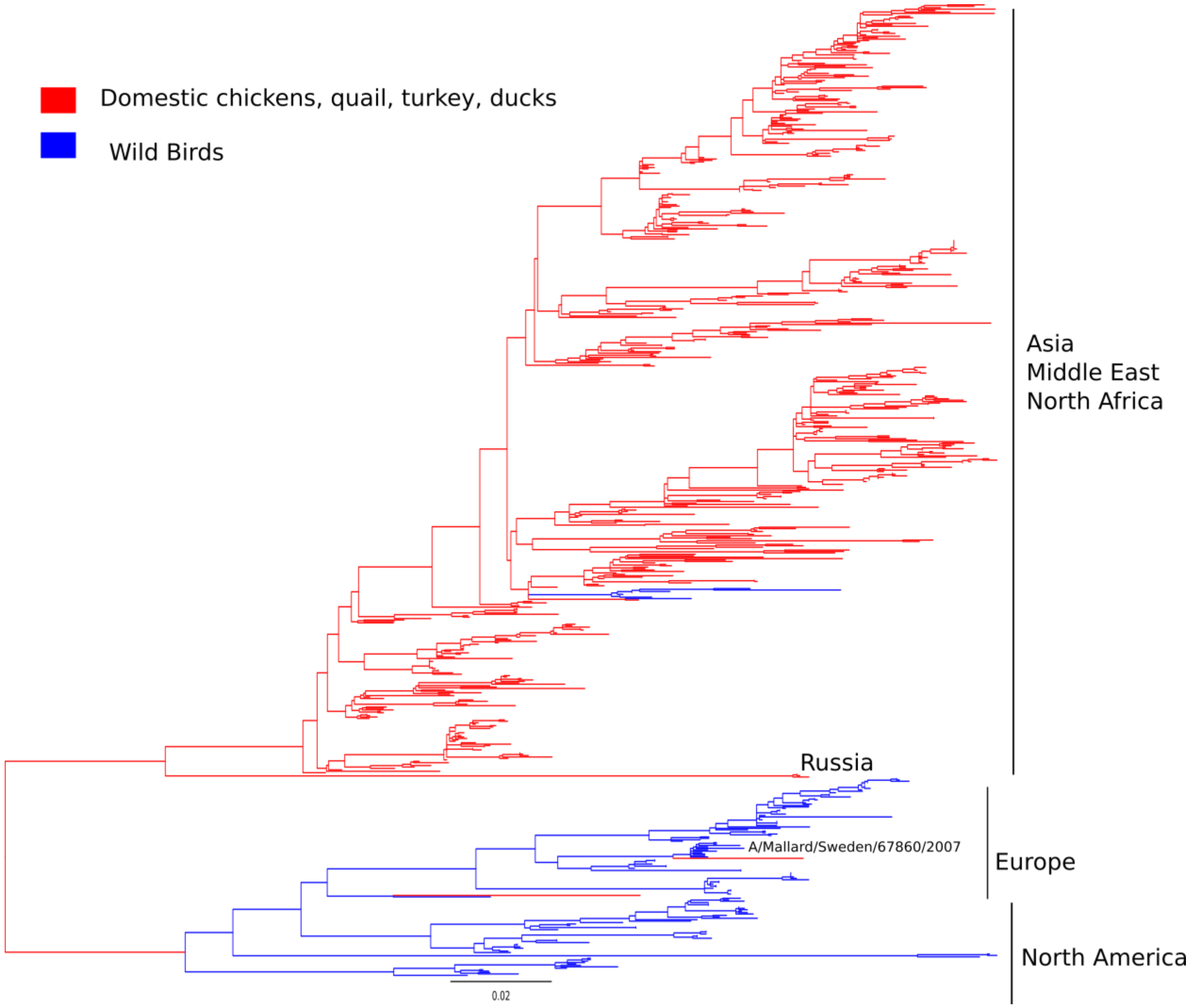

Figure S1. LPAIV H9 Phylogeny. Maximum likelihood tree of the HA gene segment of influenza A(H9N2) virus. Sequences obtained from domestic chickens, quail, turkeys, and ducks are coloured in red. Sequences obtained from wild birds are coloured in blue. Geographic location is provided to the right of the tree. Scale bar indicates number of nucleotide substitutions per site. Tree is midpoint rooted, reflecting the long branch length between the poultry-associated clade and those viruses from Europe and North America.

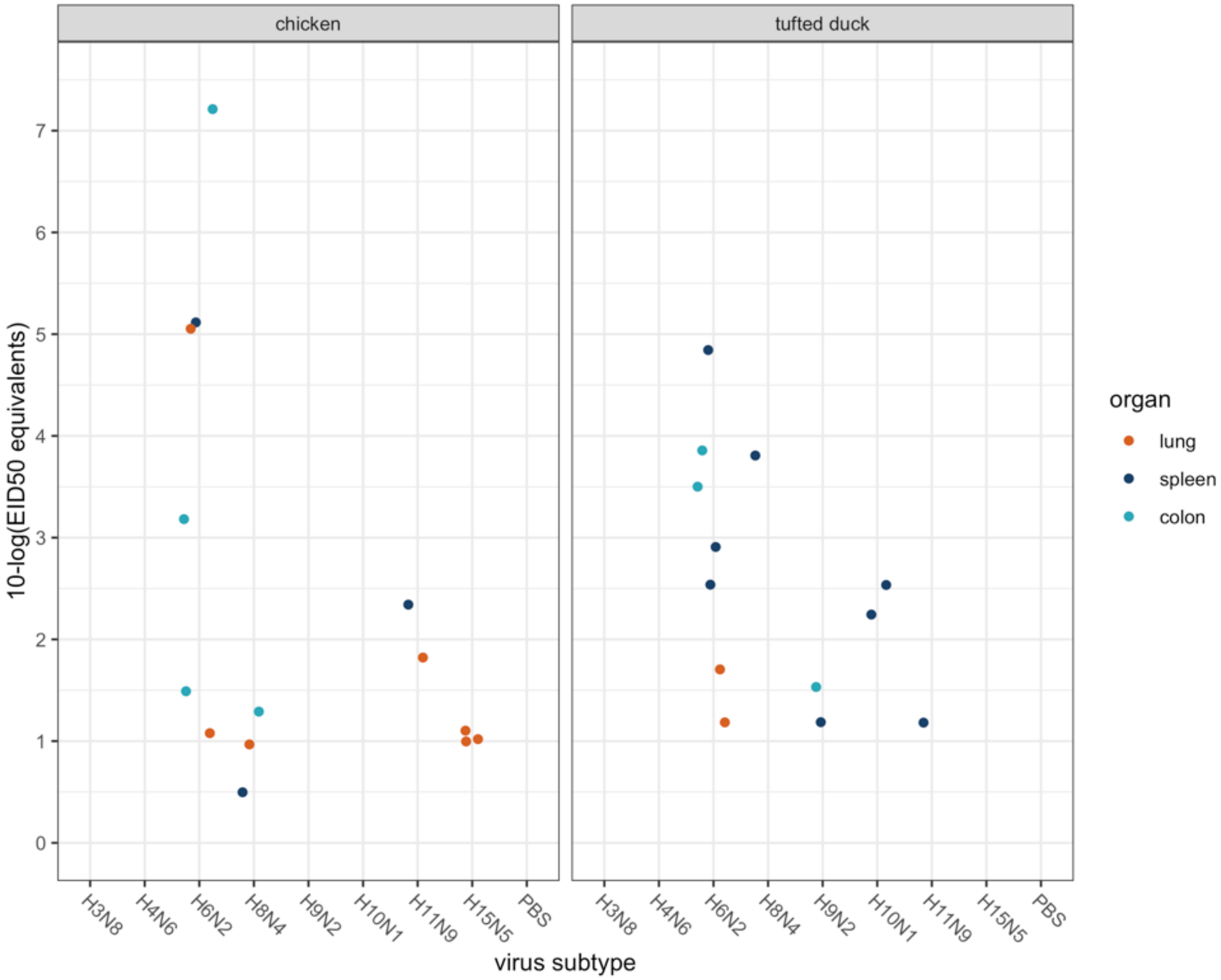

Figure S2. Strain specific AIV positive organ samples. Scatter plot of obtained positive organ samples at 3 days post infection from ON inoculated chickens and tufted ducks. Each point illustrates one positive sample from one individual. Four individuals were inoculated with each virus respectively. The points are coloured based on organ type; orange — lung, dark blue — spleen, and light blue — colon. Log_{10} egg infectious dose 50 equivalents vs. inoculum.

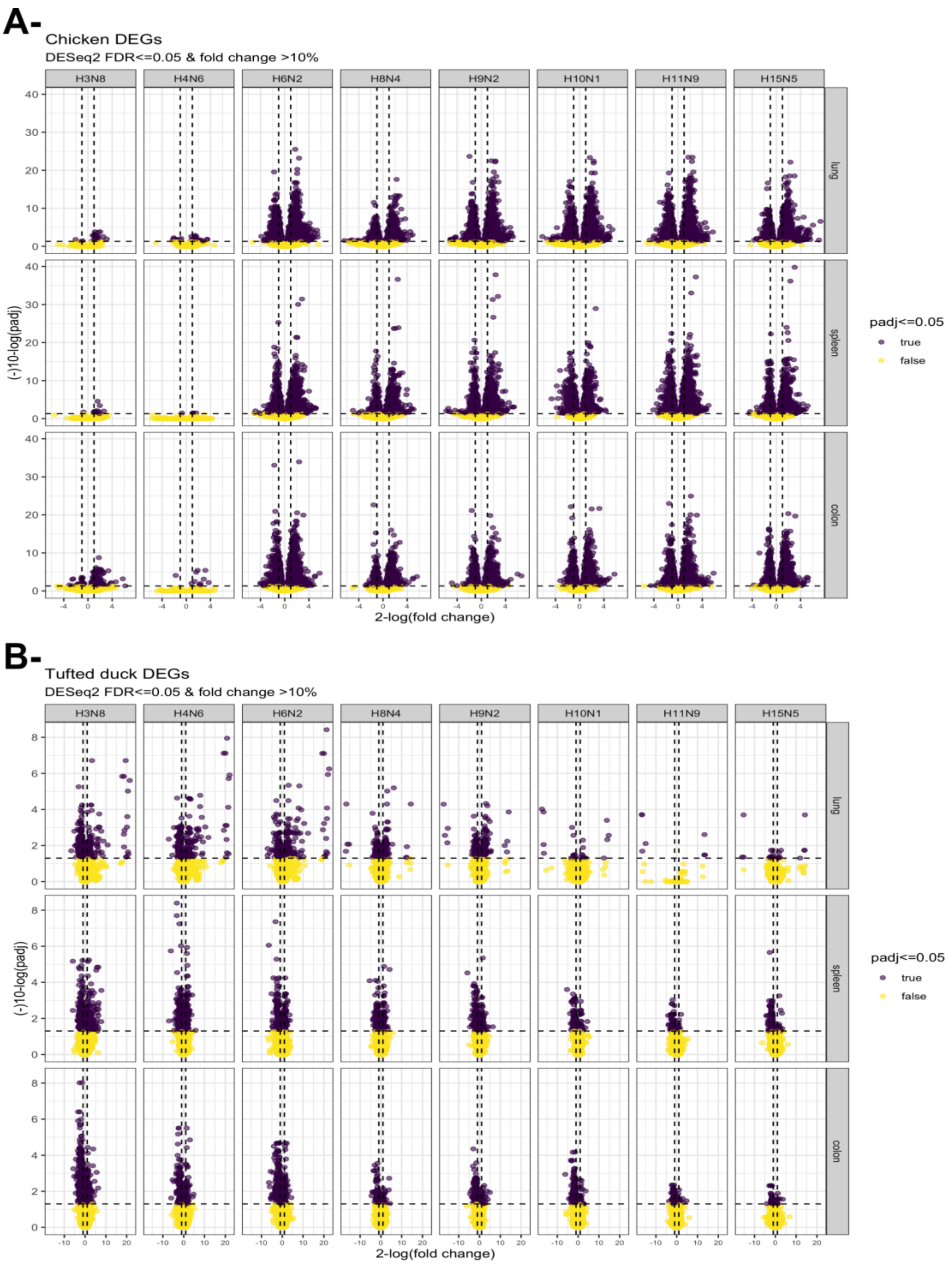

Figure S3. Volcano plots obtained from chickens (a) and tufted ducks (b) infection experiments. Volcano plot showing DEGs for H3N8, H4N6, H6N2, H8N4, H9N2, H10N1, H11N9, and H15N5. The x-axis represents the log2 values of the fold change observed for each mRNA transcript, and the y-axis represents the log10 values of the adjusted p-values <=0.05.

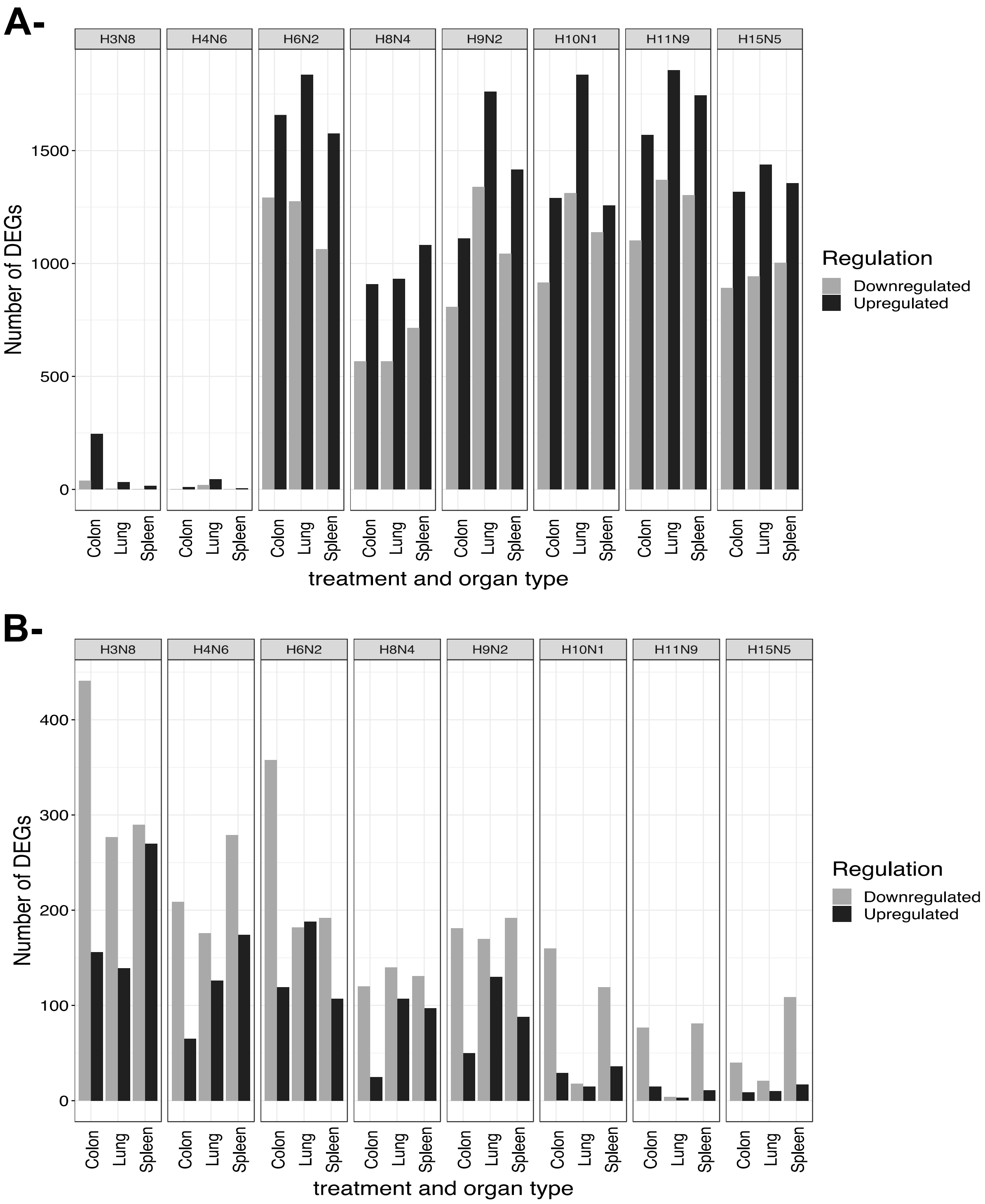

Figure S4. Differentially expressed genes in infected chickens (a) and tufted ducks (b). Number of differentially expressed genes (DEGs) in each tissue type for each virus subtype in chicken (a) and tufted ducks (b). Genes with an adjusted p-value (FDR) of ≤ 0.05 that were up- or down regulated at least 10% were considered differentially expressed.

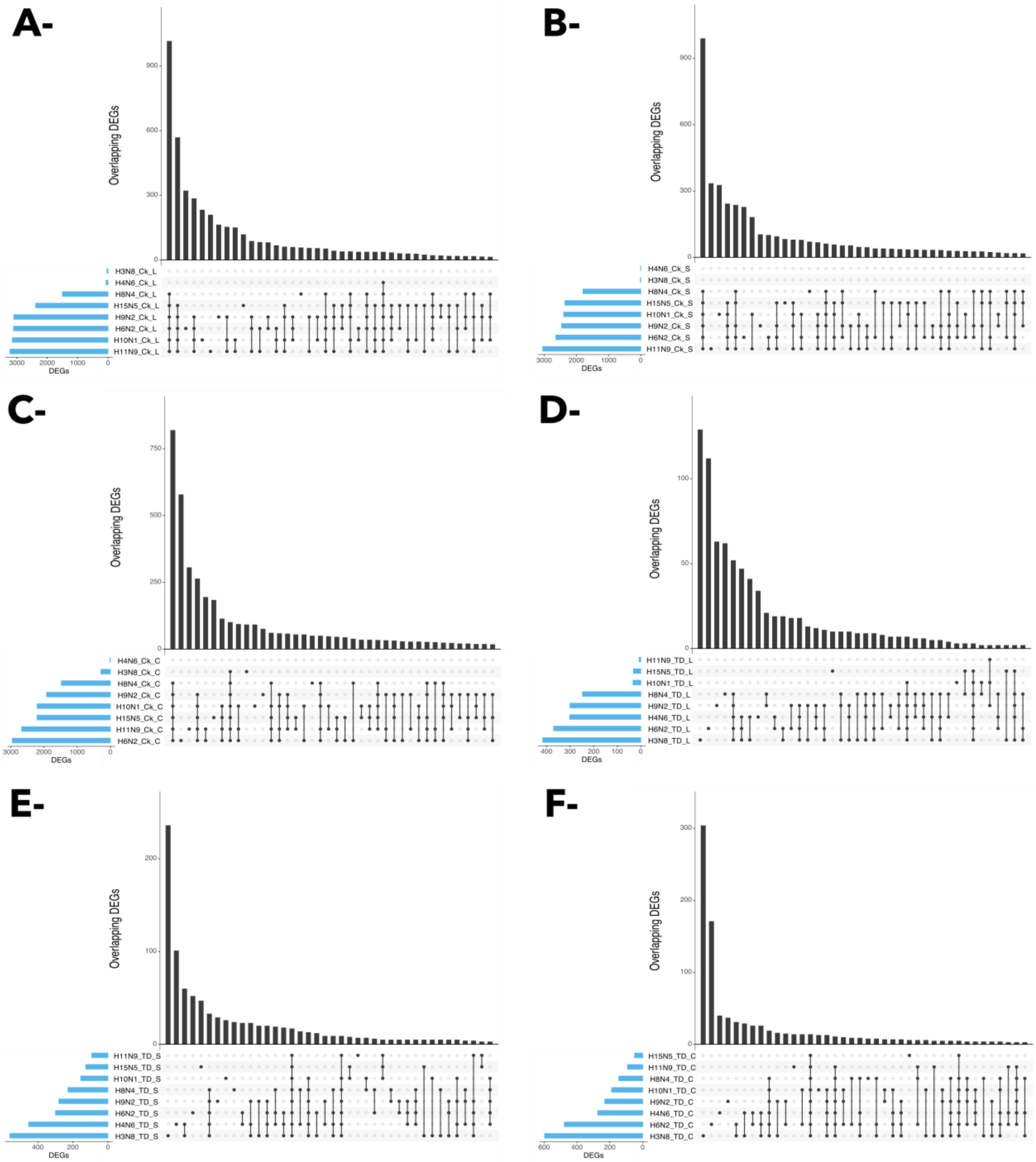

Figure S5. UpSet plot of the intersection of differentially expressed genes in chickens (a-c) and tufted ducks (d-e) tissues displayed for each virus subtype. Ck = chickens, TD= tufted ducks, L = lung, S = spleen C = colon. The nature of a given intersection is indicated by the dots below the bar plot. For instance, the genes in the 9th column in A are differentially expressed in chicken lung following treatment with H10N1 and H11N9, whereas the genes in the 3rd column in A were differentially expressed in chicken lung in response to H6N2 only.

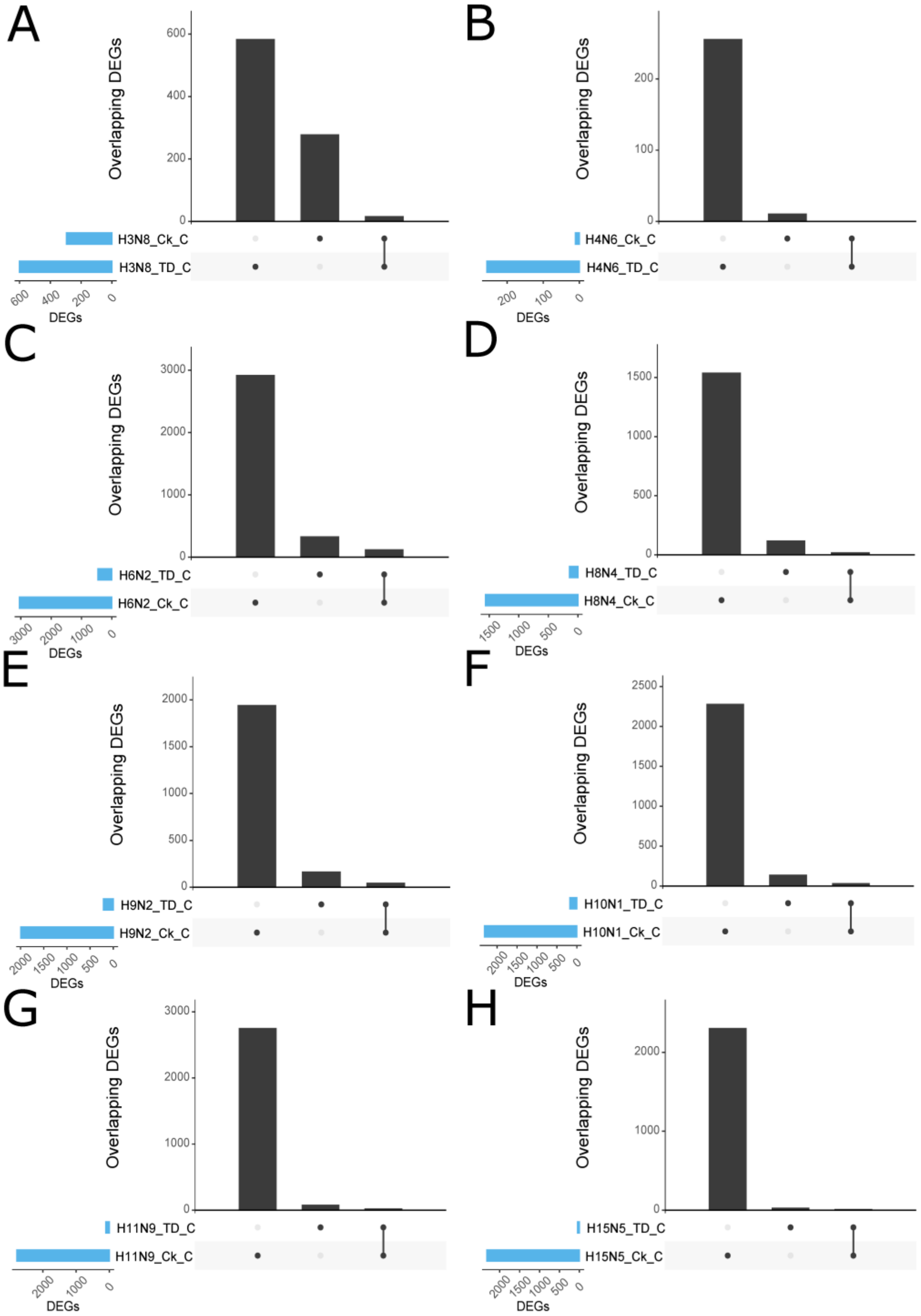

Figure S6. UpSet plot of the intersection of differentially expressed orthologous genes in tufted duck and chicken colon tissue, dispalyed for each virus subtype. A) H3N8, B) H4N6, C) H6N2, D) H8N4, E) H9N2, F) H10N1, G) H11N9, and H) H15N5. Ck = chickens, TD= tufted ducks. The nature of a given intersection is indicated by the dots below the bar plot. For instance, the genes in the first column in A are differentially expressed in tufted duck (TD) but not in chicken (Ck). Orthologs represent reciprocal best blast hits between the two species.

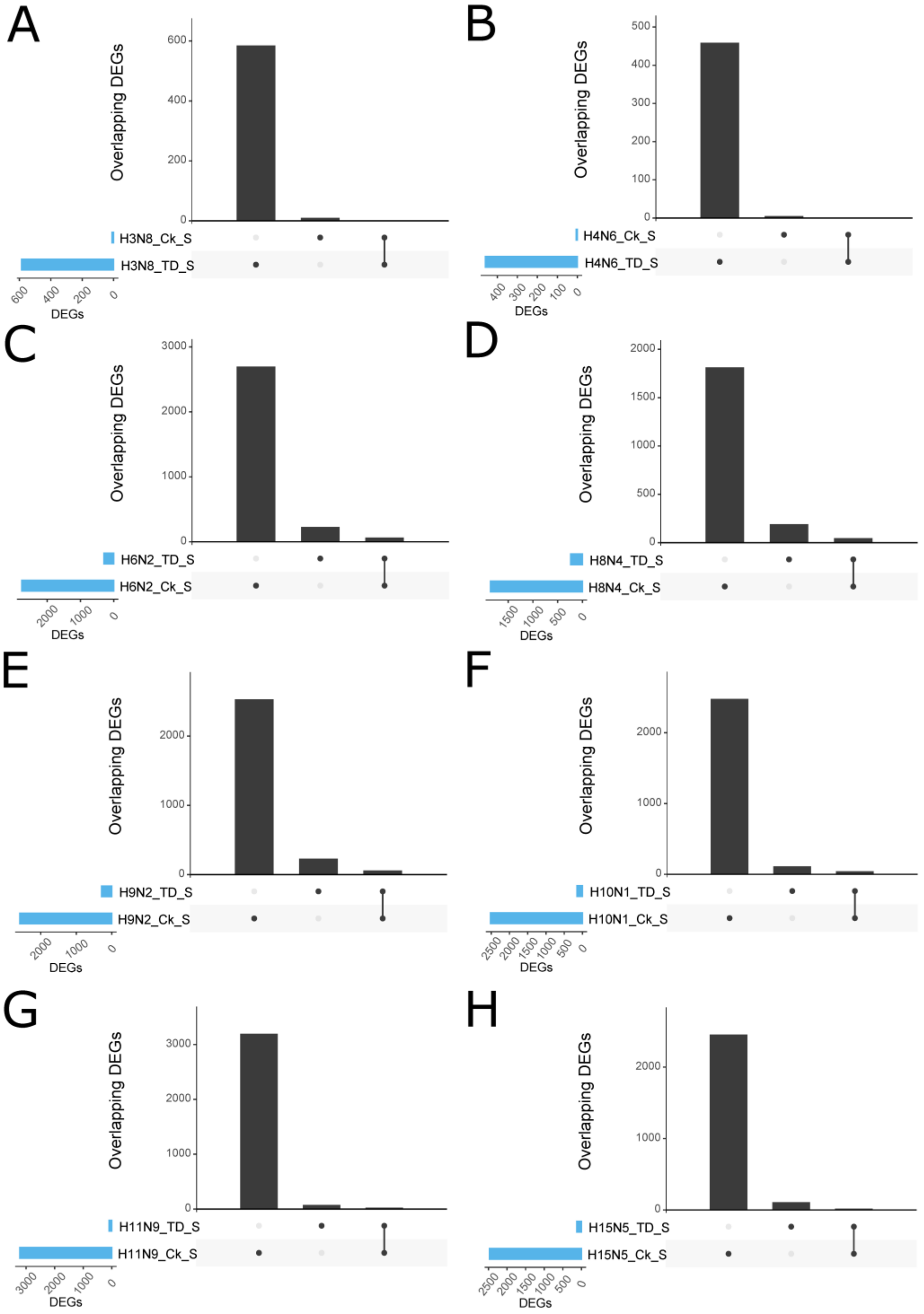

Figure S7. UpSet plot of the intersection of differentially expressed orthologous genes in tufted duck and chicken spleen tissue, displayed for each virus subtype. A) H3N8, B) H4N6, C) H6N2, D) H8N4, E) H9N2, F) H10N1, G) H11N9, and H) H15N5. Ck = chickens, TD= tufted ducks. The nature of a given intersection is indicated by the dots below the bar plot. For instance, the genes in the first column in A are differentially expressed in tufted duck (TD) but not in chicken (Ck). Orthologs represent reciprocal best blast hits between the two species.

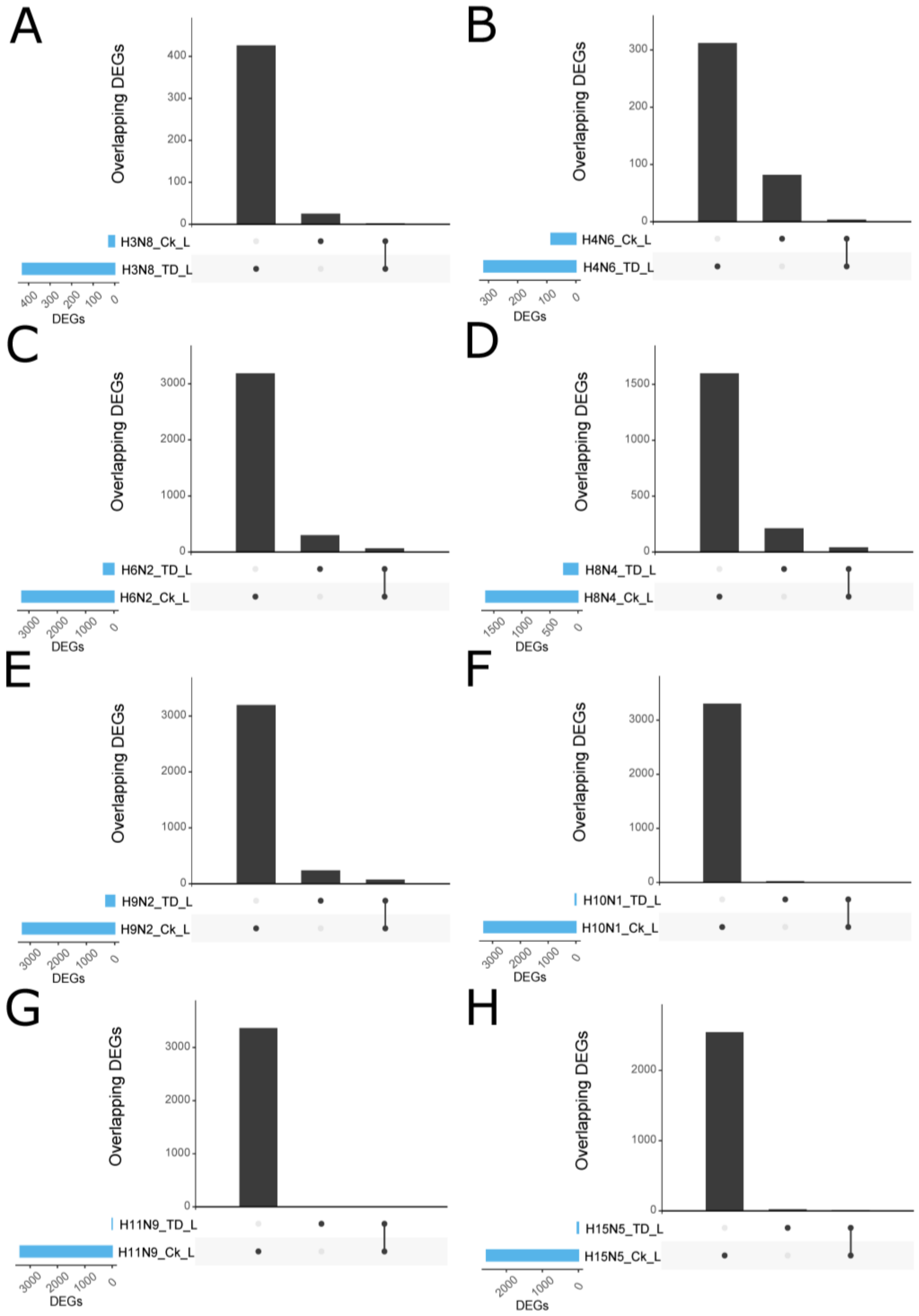

Figure S8. UpSet plot of the intersection of differentially expressed orthologous genes in tufted duck and chicken lung tissue, displayed for each virus subtype. A) H3N8, B) H4N6, C) H6N2, D) H8N4, E) H9N2, F) H10N1, G) H11N9, and H) H15N5. Ck = chickens, TD= tufted ducks. The nature of a given intersection is indicated by the dots below the bar plot. For instance, the genes in the first column in A are differentially expressed in tufted duck (TD) but not in chicken (Ck). Orthologs represent reciprocal best blast hits between the two species.

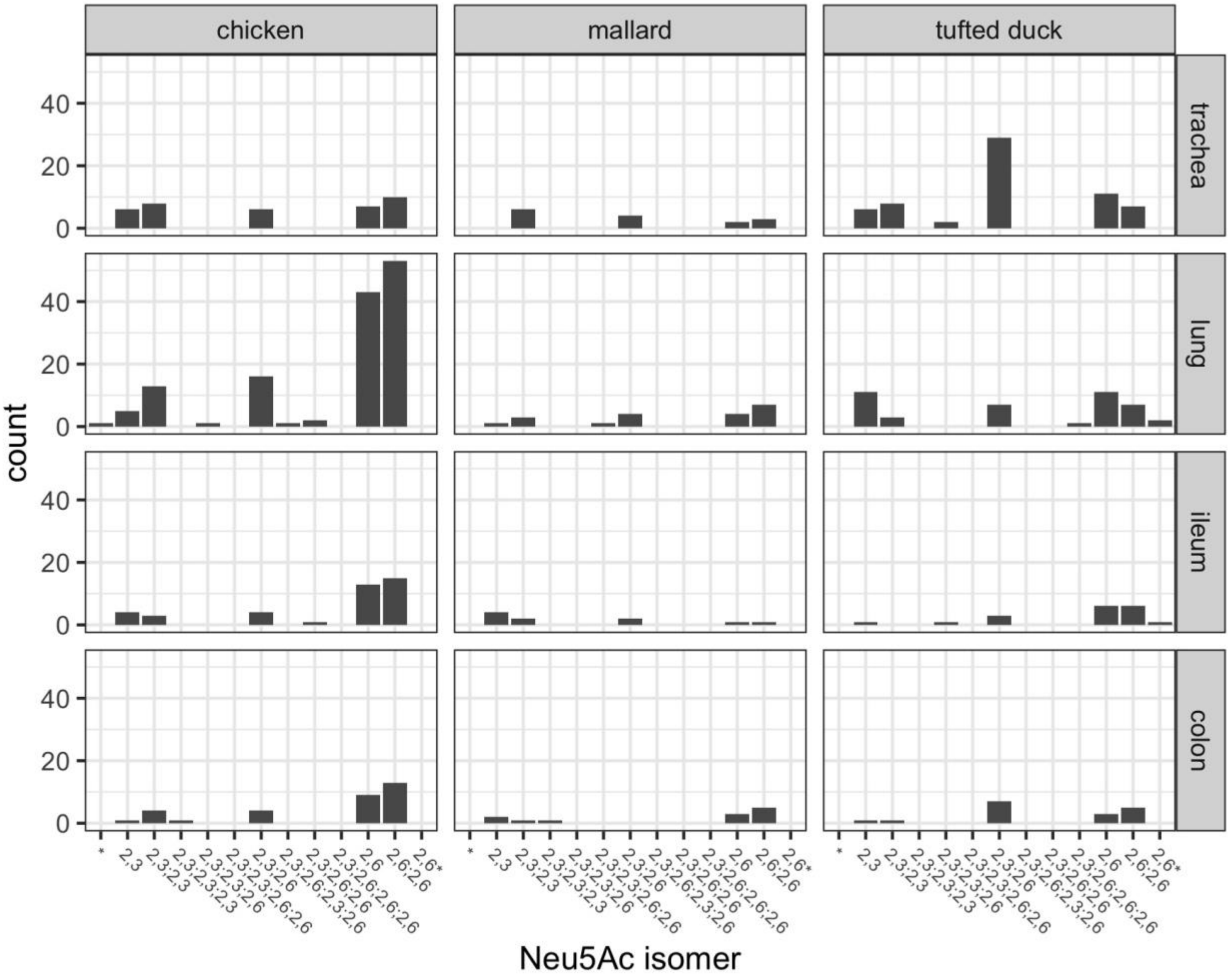

Figure S9. Distribution of sialylated glycoforms in chicken, mallard, and tufted duck. The figure illustrates the frequency of the different sialylated glycoforms (mono- to polysialylated glycoforms) identified in chicken, mallard, and tufted duck trachea, lung, ileum, and colon. 2,3 indicates α2,3-linked Neu5Ac and 2,6 indicates α2,6-linked Neu5Ac. A separation with ; indicates that the glycan carries multiple Neu5Acs with different linkages. * indicates undetermined.

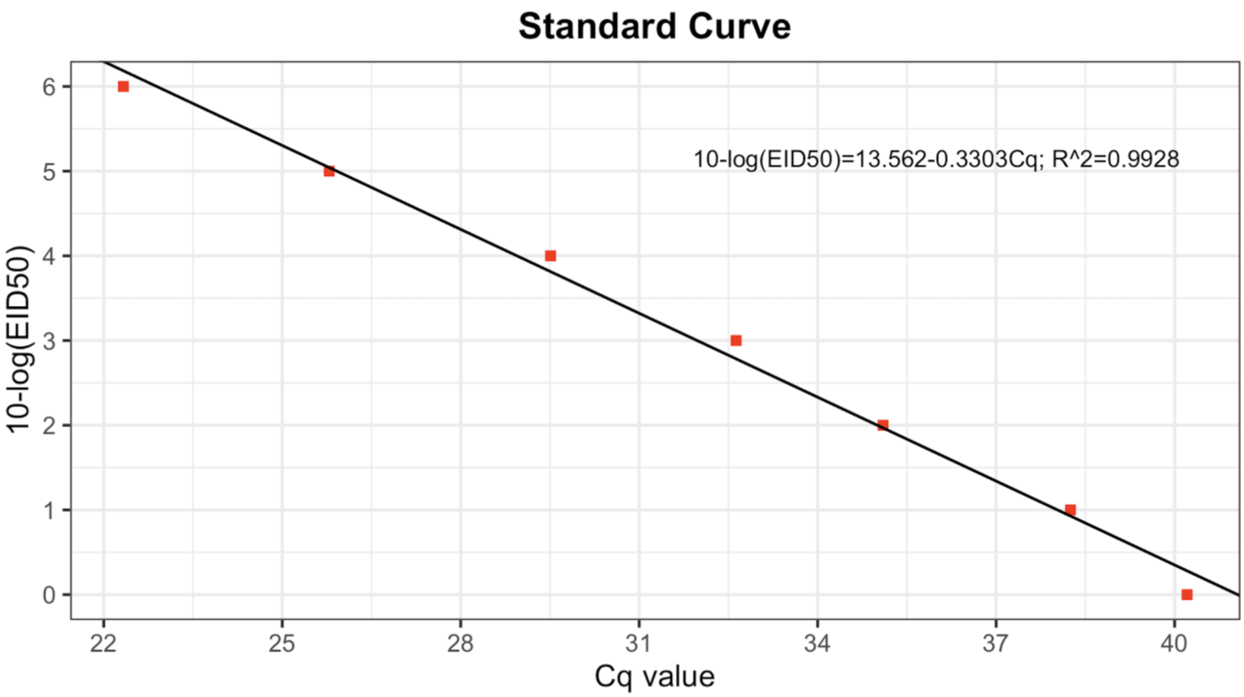

Figure S10. Rt-qPCR standard curve for the titeration of the inoculum. Standard curve was obtained from three 10-fold dilutions of the inoculum. Red squares showing the Cq values. Correlation coefficient R^2 (0.998)

Supplementary tables

Table S1. Investigated virus isolates.

Subtype	Virus Designation
H3N8	A/Mallard/Sweden/101487/2009
H4N6	A/Mallard/Sweden/80148/2008
H6N2	A/Mallard/Sweden/99825/2009
H8N4	A/Mallard/Sweden/58256/2006
H9N2	A/Mallard/Sweden/67860/2007
H10N1	A/Mallard/Sweden/102087/2009
H11N9	A/Mallard/Sweden/102103/2009
H15N5	A/Mallard/Sweden/139647/2012

Table S2. Variant detection after influenza A virus infection using virus inoculum as a reference.

Virus	Sample ID	Gene segment	Position	Change	Polymorphism type	Variant Frequency	Reference frequency	AA
H3	Ck/H3/2OP 3d.p.i.	PB2	47	C -> A	SNP	85.6%	14.2%	T 16 N
		NA	612	T -> C	SNP	99.9%	0.01%	Silent
	Ck/H3/4OP 3d.p.i.	PA	960	C -> A	SNP	99.4%	0.6%	Silent
H6	Ck/H6/colon	PA	187	G -> T	SNP	99.7%	0.03%	V 63 L
	Ck/H6/spleen	PB2	252	G -> A	SNP	42.2%	57.8%	Silent
		PA	187	G -> T	SNP	93.0%	7.0%	V 63 L
		M	726	G -> A	SNP	83.1%	16.9%	M2; S 13 N
			815	C -> T	SNP	84.9%	14.8%	M2; L 43 F
			910	A -> G	SNP	79.8%	20.0%	Silent
			913	G -> A	SNP	79.8%	20.0%	Silent
	Ck/H6/lung	PA	187	G -> T	SNP	99.4%	0.06%	V 63 L
	Ck/ H6/3OP 3d.p.i.	PA	1404	C -> T	SNP	99.8%	0.02%	Silent
		HA	1300	G -> A	SNP	100%	0%	D 434 N
	TD/H6/colon	PB2	1,753	C -> G	SNP	85.7%	14.3%	P 585 A
		PB1	84	C -> T	SNP	92.9%	7.1%	Silent
		M	726	G -> A	SNP	92.4%	7.6%	M2; S 13 N
			767	G -> A	SNP	51.8%	48.2%	M2; V 27 I
			815	C -> T	SNP	34.9%	64.3%	M2; L 43 F
			910	A -> G	SNP	36.6%	63.4%	Silent
			913	G -> A	SNP	84.0%	16.0%	Silent
	TD/H6/ Spleen	PB2	683	A -> G	SNP	99.9%	0.03%	Y 228 C
		NP	198	G -> A	SNP	99.8%	0.1%	M 66 I
			495	T -> C	SNP	99.9%	0.02%	Silent
			957	T -> A	SNP	99.7%	0.04%	N 319 K
		M	726	G -> A	SNP	99.7%	0.3%	M2; S 13 N
			763	T -> C	SNP	99.8%	0.03%	Silent
			815	C -> T	SNP	99.6%	0.1%	M2; L 43 F
			910	A -> G	SNP	99.8%	0.02%	Silent
			913	G -> A	SNP	98.3%	1.6%	Silent
	TD/H6/ OP 3d.p.i.	HA	374	A -> G	SNP	99.9%	0.01%	E 125 G
			547	A -> C	SNP	99.9%	0.01%	N 183 H
	TD/H6/CL 3d.p.i.	PA	187	G -> T	SNP	99.8%	0.02%	V 63 L
		HA	547	A -> C	SNP	99.9%	0.01%	N 183 H
H8	TD/H8/Spleen	PB1	1170	G -> A	SNP	99.9%	0.01%	Silent
	TD/H8/3OP 3d.p.i.	PB2	1402	G -> A	SNP	67.2%	32.7%	A 468 T
			1932	G -> A	SNP	67.0%	32.9%	Silent
			2153	A -> G	SNP	66.6%	33.3%	K 718 R
		PB1	1915	T -> C	SNP	68.5%	31.4%	S 639 P
		PA	1997	A -> G	SNP	58.7%	41.2%	E 666 G
		HA	366	C -> A	SNP	80.1%	19.8%	F 122 L
			997	A -> G	SNP	76.3%	23.3%	I 333 V
H9	TD/H9/4OP 3d.p.i.		None					
H10	Ck/H10/2OP 3d.p.i.		None					
	TD/H10/3OP 3d.p.i.		None					

Table S3. Genes used for construction of heat map showing significant DEGs related to innate immunity (Figure 7)

Gene Name[a]	Lung								Spleen								Colon							
	H3	H4	H6	H8	H9	H10	H11	H15	H3	H4	H6	H8	H9	H10	H11	H15	H3	H4	H6	H8	H9	H10	H11	H15
AvBD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,34	NA	NA	NA	-1,72	NA	NA	NA	NA	NA	NA	NA	NA	-3,74
AvBD4	NA	NA	NA	NA	NA	NA	-3,41	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AvBD6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-2,34	NA	NA	NA	NA	NA	NA	NA	NA	NA
DEFB4A	NA	NA	-2,18	NA	NA	NA	NA	NA	NA	NA	-2,05	NA	-1,46	-1,77	-1,96	-1,35	NA	NA	NA	NA	NA	NA	NA	NA
IFIT5	NA	NA	2,11	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL8	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-2,95	NA	NA	NA	3,70	NA	NA	2,34	NA	NA	NA
IRF7	NA	NA	NA	-1,16	-1,10	-1,05	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LSM14A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,48	-0,64	-0,53	NA	NA	-0,59	NA	NA	-0,56	-0,53	NA	-0,48	-0,52	-0,54
LSM14B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	2,50
MAVS	NA	NA	-1,28	NA	-1,11	-0,92	-1,25	-0,85	NA	NA	-1,03	-0,79	-0,85	NA	-0,91	-1,13	NA	NA	-0,76	-1,05	-1,06	-1,08	-1,10	-0,88
OASL	NA	NA	2,33	NA	NA	NA	NA	NA	NA	NA	3,37	NA	NA	NA	NA	NA	NA	NA	1,80	NA	NA	NA	NA	NA
RSAD2	NA	NA	2,18	NA	NA	NA	NA	NA	NA	NA	2,22	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TICAM1	NA	NA	-2,04	NA	-2,01	-1,98	-2,08	-1,69	NA	NA	-1,42	NA	-1,16	-2,60	-1,72	NA	NA	NA	-2,12	NA	NA	-0,97	-1,22	NA
TLR3	NA	NA	1,21	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1,52	NA	NA	NA	1,88	1,45	1,61	1,50	1,46	1,43
TRIM25	NA	NA	1,75	NA	1,06	1,14	1,10	NA	NA	NA	1,95	NA	1,07	1,53	1,56	1,41	1,01	NA	1,39	1,33	0,91	1,14	1,18	1,19
CCL19	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL21	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDX58	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EIF2AK2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IFITM3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IFNA1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IFNA2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IFNA3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IFNB	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IFNG	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL1B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL6	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IRF3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LGP2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MDA5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MX1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NFKB1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NFKB2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NOS2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STING1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TLR7	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TNFA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIM27.1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIM27.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIM27-L	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZC3HAV1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

[a]Significantly differentially expressed genes (DEGs) were identified by filtering the DESeq2 output files for gene names identical to the genes listed in the table or gene descriptions including “defensin” or “gallinacin” (for β-defensins/gallinacins) using a threshold of ≥ 10% fold change relative to control birds and an adjusted p value <0.05. NA indicates values below this threshold.

Table S4. Differentially expressed genes identified by filtering DESeq2 output files from infected chickens using search terms[a] related to glycosylation and transcription (Figure 8a)

Gene Name[a]	Lung								Spleen								Colon							
	H3	H4	H6	H8	H9	H10	H11	H15	H3	H4	H6	H8	H9	H10	H11	H15	H3	H4	H6	H8	H9	H10	H11	H15
ANP32B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,50	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANP32E	NA	NA	-1,07	-0,67	-0,72	-0,54	-0,72	-0,75	NA	NA	-0,71	-0,59	-0,62	-0,63	-0,63	-0,61	NA	NA	-1,05	-0,79	-0,69	-0,65	-0,84	-0,72
ZC3H11B	NA	NA	NA	NA	1,27	1,38	1,34	NA	NA	NA	0,70	NA	0,67	1,04	0,87	0,69	NA	NA	0,74	NA	0,81	0,94	0,87	1,10
FUT8	NA	NA	1,45	1,68	1,57	1,75	1,71	1,69	NA	NA	2,10	1,89	1,86	1,71	1,99	1,93	1,04	NA	1,70	1,32	1,27	1,49	0,97	1,29
FUT11	NA	NA	-2,14	NA	-1,34	NA	NA	NA	NA	NA	-1,87	-1,59	-1,64	-1,24	-1,56	-1,56	NA	NA	-1,98	NA	NA	NA	-1,53	NA
GNPTAB	NA	NA	NA	0,67	0,53	0,60	0,64	0,60	NA	NA	NA	NA	NA	0,57	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ST3GAL2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,71	0,68	0,92	0,69	0,80	NA	NA	NA	NA	NA	0,98	NA	NA
ST3GAL4	NA	NA	1,30	1,21	1,03	1,27	1,05	1,34	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ST3GAL5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	2,34	2,54	2,51	2,51	NA	2,80	NA	NA	NA	NA	NA	NA	NA	NA
ST3GAL6	NA	NA	-0,57	NA	-0,61	-0,61	-0,61	-0,54	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ST6GAL1	NA	NA	-1,37	NA	-1,46	-1,22	-1,19	-1,48	NA	NA	-1,03	-0,74	-0,92	-0,87	-0,99	-1,01	-0,78	NA	-1,26	-1,56	-1,12	-1,07	-1,32	-1,18
ST6GAL2	NA	NA	NA	NA	2,52	NA	2,45	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

[a] Significantly differentially expressed genes (DEGs) were identified by filtering the DESeq2 output files for gene names including any of the search terms: “ANP32”, ”ZC3H11”, “ST3GAL”, “ST6GAL”, “FUT”, “GNPT”, “NAGPA”, “MUC” or “CGT” using a threshold of ≥ 10% fold change relative to control birds and an adjusted p value <0.05. NA indicates values below this threshold.

Table S5. Differentially expressed genes identified by filtering DESeq2 output files from infected tufted ducks using search terms[a] related to glycosylation and transcription (Figure 4b)

Gene Name[a]	Lung								Spleen								Colon							
	H3	H4	H6	H8	H9	H10	H11	H15	H3	H4	H6	H8	H9	H10	H11	H15	H3	H4	H6	H8	H9	H10	H11	H15
ZC3H11A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,42	-1,10	-1,13	-1,12	NA	NA
POFUT1	NA	NA	NA	-2,42	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FUT4	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,42	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FUT8	NA	NA	NA	NA	NA	NA	NA	NA	NA	0,92	NA	0,68	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FUT10	NA	NA	1.72	NA	1,62	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ST3GAL2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-0,91	NA	NA	NA	NA	NA	NA	NA
ST6GALNAC2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,73	NA	NA	NA	NA	NA	NA	NA
ST6GALNAC4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-1,91	NA	NA	NA	NA	NA	NA	NA
GNPTAB	NA	NA	NA	NA	NA	NA	NA	NA	0,94	NA	NA	NA	0,96	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MUC2	NA	NA	NA	NA	3,96	NA	NA	NA	6,37	NA	NA	NA	NA	4,42	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

[a] Significantly differentially expressed genes (DEGs) were identified by filtering the DESeq2 output files for gene names including any of the search terms: “ANP32”, ”ZC3H11”, “ST3GAL”, “ST6GAL”, “FUT”, “GNPT”, “NAGPA”, “MUC” or “CGT” using a threshold of ≥ 10% fold change relative to control birds and an adjusted p value <0.05. NA indicates values below this threshold.

Table S6. Annotated list of sialylated *N*- and *O*-linked glycans detected in mallard tissues. *m/z* — mass to charge ratio, z — charge, UID — Uniprot ID, and Ln/Nn — number of LacNAc/number of Neu5Ac ratio, 0.4–0.6 for Neu5Acα2,3 and 0.8–1.5 for Neu5Acα2,6 terminated glycopeptides.

Sequence	Glycan	Glycan type	Observed m/z	z	Mass error (ppm)	Starting position	Protein Name	UID	Species	Tissue	Neu5Ac linkages	Ln/Nn Ratio
K.KGQNETIK.I	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1090.1182	3	1.4	444	Integrin beta	U3IPD4	mallard	trachea	2.3;2.3	0.46
K.LHLNVTK.D	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	913.3977	3	0.9	212	Ig-like domain-containing protein (CD80)	U3IIG5	mallard	colon	2.6;2.6	MS3
K.LVDGIDAPIANETIR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1267.883	3	0.8	372	Uncharacterized protein (alpha 2 macroglobulin)	U3IGH7	mallard	colon	2.6;2.6	MS3
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	926.6451	4	0.0	376	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	lung	2.6;2.6	0.97
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1235.1913	3	0.3	376	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	trachea	2.6;2.6	0.99
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1138.1599	3	0.7	376	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	trachea	2.6	MS3
K.MGTDEDPSGSNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1162.7643	3	1.4	1521	Complement C3	U3J6P0	mallard	lung	2.6;2.6	0.97
K.NTVSGIDAQLLFDNVTSKPEEGK.N	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1556.345	3	1.5	467	Solute carrier family 15 member 1	U3I719	mallard	ileum	2.3;2.6	0.67
K.NTVSGIDAQLLFDNVTSKPEEGK.N	HexNAc(3)Hex(5)NeuAc(1)	N-glycan	1043.9659	4	0.7	467	Solute carrier family 15 member 1	U3I719	mallard	ileum	2.3	MS3
K.SDNGTYTCEVK.S	HexNAc(5)Hex(4)NeuAc(1)	N-glycan	1073.0735	3	-0.1	187	Transmembrane and immunoglobulin domain containing 1	U3IRQ4	mallard	lung	2.3	MS3
K.TNNTCLSTEDACLQMR.F	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1061.4024	4	2.3	39	CD59 molecule (CD59 blood group)	U3IGH4	mallard	trachea	2.3;2.6	0.7
K.TNNTCLSTEDACLQMR.F	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1420.1981	3	1.6	39	CD59 molecule (CD59 blood group)	U3IGH4	mallard	lung	2.6;2.6	0.94
K.TNNTCLSTEDACLQMR.F	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1112.1703	4	0.5	39	CD59 molecule (CD59 blood group)	U3IGH4	mallard	colon	2.6;2.6	MS3
K.VECNVTYGLICK.N	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1329.8538	3	1.9	1359	Uncharacterized protein (Mucin 2)	U3IKI8	mallard	lung	2.3;2.6	MS3
K.VNCSEGQPMSTLLR.R	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	1276.18	3	0.9	367	Kininogen 1	U3IFX9	mallard	colon	2.6	MS3
K.VNGTYAHLSPK.H	HexNAc(5)Hex(4)Fuc(2)NeuAc(1)	N-glycan	1145.1525	3	0.6	720	Cadherin 17	U3J5I2	mallard	colon	2.3	MS3
K.VVKSDNGTYTCEVK.S	HexNAc(5)Hex(6)Fuc(1)NeuAc(2)	N-glycan	1076.9252	4	-4.2	184	Transmembrane and immunoglobulin domain containing 1	U3IRQ4	mallard	ileum	2.3;2.3	MS3
R.ENSLLFDGNYSSVGNK.E	HexNAc(6)Hex(7)NeuAc(3)	N-glycan	1243.2448	4	1.3	350	Aminopeptidase	U3ID57	mallard	colon	2.3;2.3;2.3	MS3
R.HVKPGNISYYK.D	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	1184.5052	3	2,0	157	Apolipoprotein H	U3IRY3	mallard	trachea	2.6;2.6	0.91
R.ILQQVTNATGK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1126.4848	3	1.2	70	Fibrinogen gamma chain	U3IA23	mallard	lung	2.6;2.6	1.17
R.ILQQVTNATGK.A	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	1140.1593	3	0.3	70	Fibrinogen gamma chain	U3IA23	mallard	colon	2.6	MS3
R.ITSNATSDLNIK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1161.1561	3	2,0	210	Sarcoglycan beta	U3I6K4	mallard	trachea	2.3;2.3	0.45
R.IVDVNLTSEGK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1030.1071	3	-0.5	137	Transmembrane 9 superfamily member	U3ISZ6	mallard	colon	2.3	MS3
R.IVDVNLTSEGK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1030.1089	3	1.2	137	Transmembrane 9 superfamily member	U3ISZ6	mallard	ileum	2.3	MS3
R.IVDVNLTSEGK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1127.1416	3	1.9	137	Transmembrane 9 superfamily member	U3ISZ6	mallard	trachea	2.3;2.3	MS3
R.LDGNNLTR.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1152.798	3	0.2	317	Lumican	U3J2R5	mallard	trachea	2.3;2.3	MS3
R.LNVSIDNEVVQLEK.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1039.453	4	4.4	230	Epithelial cell adhesion molecule	U3J672	mallard	colon	2.3;2.3	MS3

R.LNVSIDNEVVQLEK.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1039.4532	4	4.6	230	Epithelial cell adhesion molecule	U3J672	mallard	ileum	2.3;2.3	MS3
R.LNVSIDNEVVQLEK.A	HexNAc(5)Hex(6)Fuc(2)NeuAc(2)	N-glycan	1116.2299	4	4.2	230	Epithelial cell adhesion molecule	U3J672	mallard	lung	2.3;2.3	MS3
R.NISIQQEK.F	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1104.1215	3	1.2	630	Leucyl and cystinyl aminopeptidase	U3J380	mallard	trachea	2.3;2.3	0.5
R.NQTIK.F	HexNAc(5)Hex(4)Fuc(1)NeuAc(1)	N-glycan	902.042	3	1.4	118	Tetraspanin	R0KL21	mallard	lung	2.3;2.3	MS3
R.NSTVEWWK.R	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1104.7783	3	0.3	1303	P-type domain-containing protein	U3I472	mallard	ileum	2.3	MS3
R.NVSNMVIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1146.8137	3	1,0	1389	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	trachea	2.6;2.6	1.09
R.NVSNMVIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1146.8144	3	1.6	1389	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	lung	2.6;2.6	1.17
R.NVSNMVIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1141.4809	3	-0.1	1389	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	ileum	2.6;2.6	1.69
R.NVSNMVIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1141.4817	3	0.7	1389	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	colon	2.6;2.6	MS3
R.NVSNMVIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1146.8134	3	0.7	1389	Uncharacterized protein (alpha 2 macroglobulin)	U3I742	mallard	lung	2.6;2.6	MS3
R.NVTVNILNEK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1116.8096	3	1.5	55	Sarcoglycan delta	U3IA81	mallard	trachea	2.3;2.3	0.54
R.TAGWNIPMGLIHNK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	939.9012	4	0.2	469	Ovotransferrin	U3J851	mallard	colon	2.6;2.6	MS3
R.TAGWNIPMGLIHNK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1252.869	3	2.6	469	Ovotransferrin	U3J851	mallard	lung	2.6;2.6	MS3
R.VENMSMR.L	HexNAc(5)Hex(4)Fuc(2)NeuAc(1)	N-glycan	1038.4073	3	0.6	1200	Transient receptor potential cation channel subfamily M member 1	U3ID69	mallard	ileum	2.3	MS3
R.VENMSMR.L	HexNAc(5)Hex(6)Fuc(1)NeuAc(2)	N-glycan	1194.7892	3	1.3	1200	Transient receptor potential cation channel subfamily M member 1	U3ID69	mallard	lung	2.3;2.3 and 2.6;2.6	MS3
K.APVRQTKVPGER.H	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	762.3679	3	0.6	83	Polypeptide N-acetylgalactosaminyltransferase	U3J257	mallard	lung	2.3;2.6	0.47
K.EIESLAPDLVFTSPSPAGVK.R	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1002.1405	3	1.3	1218	Collagen type VI alpha 3 chain	U3ID88	mallard	trachea	2.3;2.6	MS3
K.IQASKDTEVNPNSDDQAISK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1036.4617	3	1.9	167	Cancer susceptibility 4	U3IJL7	mallard	ileum	2.3;2.6	1.6
K.MPAQTKSPEEIDKEERPEVDTK.K	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	808.1232	4	1.1	99	Syndecan	U3IZZ0	mallard	lung	2.6	1.1
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955.4749	3	1.9	12	Fibrinogen beta chain	U3I9E6	mallard	lung	2.6	0.8
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955.4755	3	2.5	12	Fibrinogen beta chain	U3I9E6	mallard	trachea	2.6	1
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955.4749	3	1.9	12	Fibrinogen beta chain	U3I9E6	mallard	ileum	2.6	1.1
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955.4745	3	1.5	12	Fibrinogen beta chain	U3I9E6	mallard	colon	2.6	1.3
R.KPVPPTAVGSTSSLPAPDGEK.T	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	897.7728	3	2.1	336	Fetuin B	U3IFE7	mallard	lung	2.6	1
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730.3507	4	2.5	2102	Fibronectin 1	U3IZ83	mallard	lung	2.3;2.3	0.5
R.SVSTARPSTGK.R	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	679.9768	3	3.8	139	Cochlin	U3J879	mallard	trachea	2.3;2.6	0.46
R.VISEATPTLAAGKDPEK.S	2*HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1207.8607	3	-0.2	731	Dystroglycan 1	U3IBQ2	mallard	trachea	2.3;2.6	0.48
R.VISEATPTLAAGKDPEK.S	2*HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1207.8615	3	0.5	731	Dystroglycan 1	U3IBQ2	mallard	lung	2.3;2.6	0.7
R.VNDTLR.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	832.8605	2	1,0	2030	Laminin subunit alpha 1	U3ISC0	mallard	lung	2.3;2.6	0.48
R.VTTTAPVQACEPER.G	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	735.3218	3	1.8	198	Prothrombin	U3J210	mallard	lung	2.6	0.8

Table S7. Annotated list of sialylated *N*- and *O*-linked glycans detected in sampled tufted duck tissues. *m/z* — mass to charge ratio, z — charge, UID — Uniprot ID, and Ln/Nn — number of LacNAc/number of Neu5Ac ratio, 0.4–0.6 for Neu5Acα2,3 and 0.8–1.5 for Neu5Acα2,6 terminated glycopeptides. ND= not determined. Disialo core 1 glycopeptides were assumed to be 2,3;2,6. * One NeuAc is on Gal and the second is on GalNAc.

Sequence	Glycan	Glycan type	Observed m/z	z	Mass error (ppm)	Starting position	Protein Name	UID	Species	Tissue	Neu5Ac isomer	Ln/Nn
R.LNESNTCK.Q	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1102,416	3	0,7	58	Uncharacterized protein	U3I0T7	tufted duck	lung	2,3;2,6/ 2,6;2,6	0,79
R.ILQQVTNATGK.A	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1029,453	3	1,1	70	Fibrinogen gamma chain	U3IA23	tufted duck	ileum	2,6	MS3
R.ILQQVTNATGK.A	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1029,452	3	0,8	70	Fibrinogen gamma chain	U3IA23	tufted duck	trachea	2,6	MS3
R.ILQQVTNATGK.A	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1029,453	3	1,1	70	Fibrinogen gamma chain	U3IA23	tufted duck	lung	2,6	MS3
R.ILQQVTNATGK.A	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	1140,160	3	0,7	70	Fibrinogen gamma chain	U3IA23	tufted duck	lung	2,6*	MS3
R.ILQQVTNATGK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1126,484	3	0,3	70	Fibrinogen gamma chain	U3IA23	tufted duck	ileum	2,6;2,6	1,32
R.ILQQVTNATGK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1126,485	3	1,0	70	Fibrinogen gamma chain	U3IA23	tufted duck	colon	2,6;2,6	1,91
K.VLKDNGTEDEIR.S	HexNAc(3)Hex(4)Fuc(1)NeuAc(1)	N-glycan	1028,440	3	0,2	73	Uncharacterized protein	U3IT26	tufted duck	trachea	2,6	MS3
K.IVNITLPK.I	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1054,135	3	0,2	93	BPI fold containing family B member 3	U3I5S1	tufted duck	trachea	2,6	MS3
K.IVNITLPK.I	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1151,169	3	2,0	93	BPI fold containing family B member 3	U3I5S1	tufted duck	trachea	2,3;2,6	MS3
K.NITVIK.D	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	984,090	3	0,2	119	Thy-1 cell surface antigen (Fragment)	R0KPM 3	tufted duck	trachea	2,3	MS3
K.NITVIK.D	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1013,431	3	2,5	119	Thy-1 cell surface antigen (Fragment)	R0KPM 3	tufted duck	trachea	2,3;2,3	0,59
R.TPNVSK.E	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	964,388	3	-2,0	131	Uncharacterized protein	U3I466	tufted duck	ileum	2,6 *	MS3
R.TPNVSK.E	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	950,715	3	0,7	131	Uncharacterized protein	U3I466	tufted duck	trachea	2,6;2,6	0,96
R.TPNVSK.E	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	950,717	3	2,5	131	Uncharacterized protein	U3I466	tufted duck	colon	2,6;2,6	0,95
R.TPN[+2204.772]VSK.E	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	950,714	3	-0,8	131	Uncharacterized protein	U3I466	tufted duck	lung	2,6;2,6	1,65
K.ANVTHYAEYDIFR.V	HexNAc(4)Hex(6)NeuAc(1)	N-glycan	1225,503	3	1,4	137	Uncharacterized protein	U3ID90	tufted duck	lung	2,3	MS3
K.ANVTHYAEYDIFR.V	HexNAc(5)Hex(6)NeuAc(1)	N-glycan	1293,196	3	1,0	137	Uncharacterized protein	U3ID90	tufted duck	lung	2,3	MS3
R.IVDVNLTSEGK.V	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1146,488	3	0,7	137	Transmembrane 9 superfamily member	U3ISZ6	tufted duck	colon	2,6	MS3
R.IVDVNLTSEGK.V	HexNAc(5)Hex(6)Fuc(2)NeuAc(1)	N-glycan	1249,192	3	1,0	137	Transmembrane 9 superfamily member	U3ISZ6	tufted duck	colon	2,6	MS3
R.IVDVNLTSEGK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1127,141	3	1,7	137	Transmembrane 9 superfamily member	U3ISZ6	tufted duck	trachea	2,3;2,3	0,50
R.IVDVNLTSEGK.V	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1175,827	3	1,1	137	Transmembrane 9 superfamily member	U3ISZ6	tufted duck	trachea	2,3;2,6	0,67
K.NGSLYAFR.G	HexNAc(3)Hex(5)NeuAc(1)	N-glycan	880,027	3	-0,1	164	Vitronectin	U3J2R0	tufted duck	ileum	2,6	MS3
K.NGSLYAFR.G	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	934,046	3	1,7	164	Vitronectin	U3J2R0	tufted duck	ileum	2,6	MS3
K.NGSLYAFR.G	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	1058,427	3	-0,1	164	Vitronectin	U3J2R0	tufted duck	ileum	2,6	MS3
K.ETNCSK.A	HexNAc(5)Hex(4)NeuAc(1)	N-glycan	894,665	3	1,1	203	Kininogen 1	U3IFX9	tufted duck	lung	2,6	MS3
K.IINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1097,795	3	1,4	223	Serpin family C member 1	U3IB67	tufted duck	ileum	2,6;2,6	1,35
K.IINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1097,794	3	0,1	223	Serpin family C member 1	U3IB67	tufted duck	trachea	2,6;2,6	1,03
R.LANLSR.G	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	979,409	3	0,1	317	Clusterin	U3ISS8	tufted duck	lung	2,3	MS3
R.LANLSR.G	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1076,442	3	1,2	317	Clusterin	U3ISS8	tufted duck	lung	2,3;2,3	MS3
R.LDGNNLTR.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1055,766	3	0,2	317	Lumican	U3J2R5	tufted duck	ileum	2,3	MS3
R.LDGNNLTR.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1055,765	3	-0,8	317	Lumican	U3J2R5	tufted duck	trachea	2,3	MS3
R.LDGNNLTR.A	HexNAc(5)Hex(6)Fuc(1)NeuAc(1)	N-glycan	1109,783	3	-0,3	317	Lumican	U3J2R5	tufted duck	trachea	2,3	MS3
R.LDGNNLTR.A	HexNAc(6)Hex(6)Fuc(1)NeuAc(1)	N-glycan	1177,477	3	0,5	317	Lumican	U3J2R5	tufted duck	trachea	2,3	MS3
R.LDGNNLTR.A	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1085,105	3	-0,1	317	Lumican	U3J2R5	tufted duck	trachea	2,3;2,3	MS3
R.LDGNNLTR.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1152,798	3	0,6	317	Lumican	U3J2R5	tufted duck	trachea	2,3;2,3	MS3
R.LDGNNLTR.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1152,799	3	0,9	317	Lumican	U3J2R5	tufted duck	colon	2,3;2,3	MS3
R.LDGNNLTR.A	HexNAc(6)Hex(6)Fuc(1)NeuAc(2)	N-glycan	1274,510	3	1,2	317	Lumican	U3J2R5	tufted duck	trachea	2,3;2,3	MS3

R.LDGNNLTR.A	HexNAc(6)Hex(6)Fuc(1)NeuAc(2)	N-glycan	1274,511	3	1,9	317	Lumican	U3J2R5	tufted duck	lung	2,3;2,3	MS3
K.ASLVEEGTGLEM(ox)NNTK.S	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1208,167	3	1,0	325	Uncharacterized protein	U3ITB1	tufted duck	lung	2,6	MS3
K.ASLVEEGTGLEM(ox)NNTK.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1305,200	3	1,8	325	Uncharacterized protein	U3ITB1	tufted duck	lung	2,6;2,6	1,10
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1138,161	3	1,8	376	Uncharacterized protein	U3I742	tufted duck	trachea	2,6	MS3
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1138,160	3	0,3	376	Uncharacterized protein	U3I742	tufted duck	lung	2,6	MS3
K.LVDGSGAPIANETVR.I	HexNAc(5)Hex(6)NeuAc(1)	N-glycan	1259,872	3	1,7	376	Uncharacterized protein	U3I742	tufted duck	lung	2,6	MS3
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1235,193	3	1,3	376	Uncharacterized protein	U3I742	tufted duck	lung	2,6;2,6	MS3
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1235,193	3	1,4	376	Uncharacterized protein	U3I742	tufted duck	ileum	2,6;2,6	2,76
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1235,193	3	1,4	376	Uncharacterized protein	U3I742	tufted duck	trachea	2,6;2,6	1,00
K.LVDGSGAPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1235,191	3	-0,2	376	Uncharacterized protein	U3I742	tufted duck	colon	2,6;2,6	1,89
R.LASSQIGPINASR.L	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1192,850	3	1,3	412	BPI fold containing family B member 3	U3I5S1	tufted duck	trachea	2,6	MS3
R.TAATGEEKENLTAEVLDLSLK.Y	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1109,737	4	-0,6	533	Uncharacterized protein	U3I976	tufted duck	lung	2,6;2,6	MS3
R.TAATGEEKENLTAEVLDLSLK.Y	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1109,990	4	1,4	533	Uncharacterized protein	U3I976	tufted duck	ileum	2,6;2,6	1,00
R.TAATGEEKENLTAEVLDLSLK.Y	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1109,989	4	0,4	533	Uncharacterized protein	U3I976	tufted duck	colon	2,6;2,6	1,09
K.KQAEEWLNK.S	HexNAc(5)Hex(6)Fuc(2)NeuAc(1)	N-glycan	1239,513	3	0,8	603	Serine/threonine kinase 31	U3J355	tufted duck	trachea	2,6	MS3
K.KQAEEWLNK.S	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	925,633	4	0,9	603	Serine/threonine kinase 31	U3J355	tufted duck	trachea	2,3;2,6	MS3
K.KHNTTTVIK.H	HexNAc(6)Hex(6)Fuc(1)NeuAc(1)	N-glycan	918,144	4	0,5	755	Uncharacterized protein	U3IL89	tufted duck	trachea	2,6	MS3
K.SGTVNGTFR.V	HexNAc(6)Hex(6)Fuc(1)NeuAc(3)	N-glycan	1383,542	3	1,4	861	Uncharacterized protein	U3IMB2	tufted duck	trachea	2,3;2,3;2,6	MS3
K.SGTVNGTFR.V	HexNAc(5)Hex(6)Fuc(1)NeuAc(2)	N-glycan	1218,817	3	1,3	861	Uncharacterized protein	U3IMB2	tufted duck	trachea	2,6;2,6	MS3
K.VTAANITDIVPNTESETK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1272,888	3	2,1	913	Complement C3	U3J6P0	tufted duck	ileum	2,6	MS3
K.VTAANITDIVPNTESETK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	954,917	4	1,0	913	Complement C3	U3J6P0	tufted duck	trachea	2,6	MS3
K.VTAANITDIVPNTESETK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1272,887	3	1,3	913	Complement C3	U3J6P0	tufted duck	lung	2,6	MS3
K.VTAANITDIVPNTESETK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1369,585	3	1,1	913	Complement C3	U3J6P0	tufted duck	lung	2,6;2,6	MS3
K.VTAANITDIVPNTESETK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1369,921	3	2,5	913	Complement C3	U3J6P0	tufted duck	trachea	2,6;2,6	1,12
K.NLTK.L	HexNAc(5)Hex(4)NeuAc(2)	N-glycan	907,701	3	1,1	1030	Myosin heavy chain 11	U3IFD3	tufted duck	lung	2,6*	MS3
R.NLTVK.S	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	878,704	3	2,5	1254	Uncharacterized protein	U3IG09	tufted duck	lung	2,3	MS3
R.NLTVK.S	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	946,395	3	-0,2	1254	Uncharacterized protein	U3IG09	tufted duck	lung	2,3	MS3
R.TIAEANNK.T	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1041,759	3	0,2	1332	Laminin subunit gamma 1	U3I6H8	tufted duck	lung	2,3	MS3
R.NVSNM(ox)VIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1146,813	3	0,2	1389	Uncharacterized protein	U3I742	tufted duck	trachea	2,6;2,6	MS3
R.NVSNM(ox)VIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1146,813	3	0,3	1389	Uncharacterized protein	U3I742	tufted duck	lung	2,6;2,6	MS3
R.NVSNM(ox)VIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1146,814	3	1,1	1389	Uncharacterized protein	U3I742	tufted duck	colon	2,6;2,6	1,73
R.NVSNMVIVDVK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1141,483	3	1,3	1389	Uncharacterized protein	U3I742	tufted duck	ileum	2,6;2,6	1,65
K.M(ox)GTDEDPSGSNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1162,764	3	0,7	1521	Complement C3	U3J6P0	tufted duck	lung	2,6;2,6	1,01
K.EAGNITTDGYEILGK.L	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1214,178	3	1,0	2687	Collagen type XII alpha 1 chain	U3J0G6	tufted duck	trachea	2,3	MS3
K.EAGNITTDGYEILGK.L	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1311,213	3	3,1	2687	Collagen type XII alpha 1 chain	U3J0G6	tufted duck	trachea	2,3;2,3	0,53
K.VNFSQELSGNTK.S	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1079,782	3	0,1	3429	Apolipoprotein B	U3IWA4	tufted duck	trachea	2,6	MS3
K.ADVSHHSTM(ox)ESAHSFVTAASHQK.Q	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	857,866	4	-0,2	158	LysM and putative peptidoglycan-binding domain-containing protein 3 (Fragment)	R0LLV4	tufted duck	colon	2,3,2,6	ND
K.APVRQTKVPGER.H	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	762,369	3	1,8	83	Polypeptide N-acetylgalactosaminyltransferase	U3J257	tufted duck	ileum	2,3,2,6	ND
K.APVRQTKVPGER.H	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	762,368	3	0,6	83	Polypeptide N-acetylgalactosaminyltransferase	U3J257	tufted duck	colon	2,3,2,6	ND
K.APVRQTKVPGER.H	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	762,368	3	0,6	83	Polypeptide N-acetylgalactosaminyltransferase	U3J257	tufted duck	trachea	2,3,2,6	ND

K.AQSVETLPPGK.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1037,470	2	0,0	35	Polypeptide N-acetylgalactosaminyltransferase	U3I3A3	tufted duck	trachea	2,3,2,6	ND
K.EHENRKPVPPTAVGSTSSLPAPDGEK.T	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	839,903	4	1,1	331	Fetuin B	U3IFE7	tufted duck	lung	2,6	1,38
K.EPTKSR.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	832,860	2	0,9	1103	Regulator of G protein signaling 12	U3IMK7	tufted duck	lung	2,3,2,6	ND
K.ESEKPSSLEAEGQKEPVPINER.Q	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	850,889	4	-1,0	158	alpha-1,2-Mannosidase (Fragment)	R0K4C7	tufted duck	trachea	2,3,2,6	ND
K.EVTQVPAAASEPGK.Q	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	777,684	3	1,4	171	Fibroblast growth factor-binding protein 1 (Fragment)	R0LS14	tufted duck	trachea	2,3,2,6	ND
K.GGLPATLSPEEEEK.A	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	802,018	3	0,0	97	Putative polypeptide N-acetylgalactosaminyltransferase-like protein 3 (Fragment)	R0JYD9	tufted duck	colon	2,3,2,6	ND
K.GSSPVAPVHLVSEESPDK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	928,085	3	0,1	4	Transmembrane protein 165	U3IHR5	tufted duck	trachea	2,3,2,6	ND
K.GSSPVAPVHLVSEESPDK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	928,088	3	2,7	4	Transmembrane protein 165	U3IHR5	tufted duck	colon	2,3,2,6	ND
K.IQASKDTEVNPNSDDQAISK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1036,462	3	2,2	167	Cancer susceptibility 4	U3IJL7	tufted duck	trachea	2,3,2,6	ND
K.IQASKDTEVNPNSDDQAISK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1036,461	3	1,5	167	Cancer susceptibility 4	U3IJL7	tufted duck	lung	2,3,2,6	ND
K.KHPEPLPTVTPEK.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	807,383	3	0,0	537	Fibulin 2	U3J315	tufted duck	trachea	2,3,2,6	ND
K.LQIGAPVQPEEPPRSAR.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	931,447	3	2,1	76	Polypeptide N-acetylgalactosaminyltransferase	U3J1S2	tufted duck	colon	2,3,2,6	ND
K.LQIGAPVQPEEPPRSAR.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	931,447	3	1,8	76	Polypeptide N-acetylgalactosaminyltransferase	U3J1S2	tufted duck	ileum	2,3,2,6	ND
K.M(ox)PAQTKSPEEIDKEERPEVDTK.K	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	808,123	4	0,3	99	Syndecan	U3IZZ0	tufted duck	lung	2,6	1,09
K.M(ox)PAQTKSPEEIDKEERPEVDTK.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	880,896	4	0,2	99	Syndecan	U3IZZ0	tufted duck	trachea	2,3,2,6	ND
K.NRLSQQAR.Y	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	640,623	3	-1,6	472	Golgi integral membrane protein 4	U3J030	tufted duck	trachea	2,3,2,6	ND
K.PAEVSSR.-	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	701,310	2	0,7	66	Uncharacterized protein	U3I2W3	tufted duck	lung	2,3	0,16
K.SRDEIQAEIQTEKNK.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	684,814	4	0,7	131	alpha-1,2-Mannosidase	U3INZ0	tufted duck	lung	2,3,2,6	ND
K.SRDEIQAEIQTEKNK.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	684,812	4	-1,5	131	alpha-1,2-Mannosidase	U3INZ0	tufted duck	trachea	2,3,2,6	ND
K.TVAWLVTPR.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	663,980	3	-1,0	876	Uncharacterized protein	U3I742	tufted duck	trachea	2,3,2,6	ND
K.TVAWLVTPR.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	663,979	3	-2,5	876	Uncharacterized protein	U3I742	tufted duck	trachea	2,3,2,6	ND
K.TYTKIIDGRPVEVTEK.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	699,838	4	-0,3	708	Periostin	U3IFM7	tufted duck	trachea	2,3,2,6	ND
R.APSPHSSLPVHHEAVAEEPKEDEKPK.E	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	948,818	5	0,3	264	Golgi integral membrane protein 4	U3J030	tufted duck	trachea	2,3,2,6	ND
R.APSSNEASGVTQLLPTAVER.R	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	1307,904	3	2,9	41	ST3 beta-galactoside alpha-2,3-sialyltransferase 6 (Fragment)	R0M6H0	tufted duck	trachea	2,3,2,6	ND
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955,475	3	1,8	12	Fibrinogen beta chain	U3I9E6	tufted duck	ileum	2,6	0,84
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955,474	3	1,4	12	Fibrinogen beta chain	U3I9E6	tufted duck	lung	2,6	0,82
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	716,856	4	-0,7	12	Fibrinogen beta chain	U3I9E6	tufted duck	lung	2,6	0,94
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955,471	3	-2,3	12	Fibrinogen beta chain	U3I9E6	tufted duck	colon	2,6	1,02
R.ETAPTLRPVAPPISGTGYQPR.P	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	955,474	3	1,0	12	Fibrinogen beta chain	U3I9E6	tufted duck	trachea	2,6	1,04
R.KPVPPTAVGSTSSLPAPDGEK.T	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	897,772	3	1,5	336	Fetuin B	U3IFE7	tufted duck	trachea	2,6	1,33
R.KPVPPTAVGSTSSLPAPDGEK.T	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	897,772	3	1,7	336	Fetuin B	U3IFE7	tufted duck	lung	2,6	1,29

R.QKSPQEPR.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	639,616	3	-0,4	175	Synaptotagmin like 4	U3IJD8	tufted duck	trachea	2,3,2,6	ND
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730,349	4	0,5	2102	Fibronectin 1	U3IZ83	tufted duck	lung	2,3,2,3	0,52
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730,349	4	0,3	2102	Fibronectin 1	U3IZ83	tufted duck	trachea	2,3,2,3	0,49
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(3)	O-glycan	803,123	4	0,2	2102	Fibronectin 1	U3IZ83	tufted duck	ileum	2,3,2,3,2,6	0,52
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	875,896	4	-0,2	2102	Fibronectin 1	U3IZ83	tufted duck	colon	2,3,2,6	ND
R.SVSTARPSTGK.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	801,686	3	0,8	139	Cochlin	U3J879	tufted duck	trachea	2,6,2,6	0,97
R.SLPQLLSQANVR.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	758,364	3	0,8	24	N-sulfoglucosamine sulfohydrolase	U3I4F8	tufted duck	trachea	2,3,2,6	ND
R.SVSTARPSTGK.R	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	995,749	3	0,4	139	Cochlin	U3J879	tufted duck	trachea	2,3,2,6	ND
R.SALDAAARSTKPPR.Y	HexNAc(2)Hex(1)NeuAc(2)	O-glycan	864,405	3	2,5	39	Family with sequence similarity 3 member C	U3J9G8	tufted duck	ileum	2,6,2,6	2,93
R.SQSEITPTKAVTKR.Y	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	860,882	4	0,4	392	Golgi integral membrane protein 4	U3J030	tufted duck	trachea	2,3,2,6	ND
R.STTTSQSIIEQQHHVR.N	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	933,754	3	-2,1	160	G protein-coupled receptor 107	U3IQ48	tufted duck	lung	2,3,2,6	ND
R.STTTSQSIIEQQHHVR.N	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	700,570	4	0,9	160	G protein-coupled receptor 107	U3IQ48	tufted duck	ileum	2,3,2,6	ND
R.STTTSQSIIEQQHHVR.N	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	700,568	4	-1,3	160	G protein-coupled receptor 107	U3IQ48	tufted duck	trachea	2,3,2,6	ND
R.STTTSQSIIEQQHHVR.N	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	700,569	4	0,4	160	G protein-coupled receptor 107	U3IQ48	tufted duck	colon	2,3,2,6	ND
R.SVSTARPSTGK.R	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	679,974	3	0,2	139	Cochlin	U3J879	tufted duck	trachea	2,3,2,6	ND
R.TEIMSEILQK.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	713,654	3	-2,9	107	Uncharacterized protein	U3J732	tufted duck	lung	2,3,2,6	ND
R.TEIMSEILQK.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	713,654	3	-2,9	107	Uncharacterized protein	U3J732	tufted duck	trachea	2,3,2,6	ND
R.TNNQLK.L	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	832,860	2	0,9	1362	RP1, axonemal microtubule associated	U3I6P0	tufted duck	lung	2,3,2,6	ND
R.TKPESR.K	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	687,312	2	0,7	243	G protein-coupled receptor 182	U3HYX6	tufted duck	lung	2,3	0,43
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	887,431	3	-0,9	1751	Collagen type XII alpha 1 chain	U3J0G6	tufted duck	trachea	2,3,2,3	0,65
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(3)	O-glycan	984,462	3	-1,0	1751	Collagen type XII alpha 1 chain	U3J0G6	tufted duck	trachea	2,3,2,3,2,6	0,81
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	1081,496	3	0,9	1751	Collagen type XII alpha 1 chain	U3J0G6	tufted duck	trachea	2,3,2,6	ND
R.VHGDTVTQISNM(ox)R.A	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	807,684	3	0,8	65	Mannosidase endo-alpha	U3IBN6	tufted duck	trachea	2,3,2,6	ND
R.VISEATPTLAAGKDPEK.S	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	1207,864	3	2,4	731	Dystroglycan 1	U3IBQ2	tufted duck	lung	2,3,2,6	ND
R.VISEATPTLAAGKDPEK.S	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	1207,864	3	2,7	731	Dystroglycan 1	U3IBQ2	tufted duck	trachea	2,3,2,6	ND
R.VNDTLR.K	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	687,313	2	0,9	2030	Laminin subunit alpha 1	U3ISC0	tufted duck	lung	2,3	0,40
R.VSDGEDKAQSVETLPPGK.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	935,421	3	0,2	28	Polypeptide N-acetylgalactosaminyltransferase	U3I3A3	tufted duck	trachea	2,3,2,6	ND
R.VTTTAPVQACEPER.G	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	735,321	3	0,8	198	Prothrombin	U3J210	tufted duck	lung	2,3	0,65
R.VTTTAPVQACEPER.G	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	735,322	3	1,4	198	Prothrombin	U3J210	tufted duck	trachea	2,3	0,69
R.VTTTAPVQACEPER.G	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	735,320	3	-0,6	198	Prothrombin	U3J210	tufted duck	colon	2,3	0,70
S.GPTGAVPTSR.C	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	799,868	2	1,0	2	Uncharacterized protein	U3IJ28	tufted duck	lung	2,3	0,53

Table S8. Annotated list of sialylated *N*- and *O*-linked glycans detected in sampled chicken tissues. *m/z* — mass to charge ratio, z — charge, UID — Uniprot ID, and Ln/Nn — number of LacNAc/number of Neu5Ac ratio, 0.4–0.6 for Neu5Acα2,3 and 0.8–1.5 for Neu5Acα2,6 terminated glycopeptides.

Sequence	Glycan	Glycan type	Observed m/z	z	Mass error (ppm)	Starting position	Protein Name	UID	Species	Tissue	Neu5Ac isomer	Ln/Nn
R.M(ox)VSVEFAVAATNCTSQQAK.D	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1063,681	4	0,4	194	Alpha 2-HS glycoprotein	E1BZE1	chicken	lung	2,6;2,6	1,06
R.LNETCVVK.N	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	955,719	3	0,0	89	Alpha-1-acid glycoprotein	Q8JIG5	chicken	lung	2,6	MS3
R.LNETCVVK.N	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1052,752	3	1,6	89	Alpha-1-acid glycoprotein	Q8JIG5	chicken	lung	2,6;2,6	MS3
R.LNETCVVK.N	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1052,751	3	0,5	89	Alpha-1-acid glycoprotein	Q8JIG5	chicken	colon	2,6;2,6	1,09
R.LNETCVVK.N	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1052,750	3	-0,1	89	Alpha-1-acid glycoprotein	Q8JIG5	chicken	colon	2,6;2,6	1,19
R.LNETCVVK.N	HexNAc(5)Hex(6)NeuAc(2)	N-glycan	1174,461	3	-0,3	89	Alpha-1-acid glycoprotein	Q8JIG5	chicken	ileum	2,6	MS3
R.ENEAAFPLNASLPR.Y	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	1134,480	3	-0,3	562	Amine oxidase	A0A1D5PTV1	chicken	lung	2,3	MS3
K.IINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1097,795	3	1,2	174	Antithrombin-III	A0A1L1S0N7	chicken	lung	2,6;2,6	0,99
R.KIINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1140,488	3	-3,5	173	Antithrombin-III	A0A1L1S0N7	chicken	lung	2,6;2,6	1,05
K.IINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1097,795	3	0,9	174	Antithrombin-III	A0A1L1S0N7	chicken	ileum	2,6;2,6	MS3
K.IINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1097,798	3	3,9	174	Antithrombin-III	A0A1L1S0N7	chicken	trachea	2,6;2,6	1,18
R.KIINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1140,493	3	1,0	173	Antithrombin-III	A0A1L1S0N7	chicken	ileum	2,6;2,6	1,31
K.IINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1097,795	3	0,8	174	Antithrombin-III	A0A1L1S0N7	chicken	colon	2,6;2,6	1,02
R.KIINEWVANK.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1140,493	3	0,8	173	Antithrombin-III	A0A1L1S0N7	chicken	colon	2,6;2,6	1,05
K.M(ox)NFSQELSGNTK.S	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1095,773	3	2,2	3431	Apolipoprotein B	F1NV02	chicken	lung	2,6	MS3
K.M(ox)NFSQELSGNTK.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1192,805	3	2,1	3431	Apolipoprotein B	F1NV02	chicken	lung	2,6;2,6	2,17
R.GLEVTNGTAR.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1074,772	3	-0,9	648	Band 3 anion transport protein	B3AT	chicken	lung	2,3;2,3	MS3
R.GLEVTNGTAR.G	HexNAc(5)Hex(6)NeuAc(2)	N-glycan	1196,485	3	0,8	648	Band 3 anion transport protein	B3AT	chicken	lung	2,3;2,3	MS3
R.GLEVTNGTAR.G	HexNAc(5)Hex(6)NeuAc(2)	N-glycan	1196,485	3	1,1	648	Band 3 anion transport protein	B3AT	chicken	trachea	2,3;2,3	MS3
K.GNVSIEVEPQVVAYK.K	HexNAc(6)Hex(6)Fuc(1)NeuAc(1)	N-glycan	1065,962	4	3,1	221	Basigin	BASI	chicken	colon	2,6	MS3
K.QTLNDTANPR.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1112,116	3	0,6	11	Carboxypeptidase B2	F1NXB6	chicken	lung	2,6;2,6	1,07
R.NYTLHPHGVK.Y	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1124,135	3	1,7	118	Ceruloplasmin	A0A1D5PBP6	chicken	lung	2,6;2,6	1,21
K.EAGNITTDGYEILGK.L	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1214,177	3	0,6	2680	Collagen alpha-1(XII) chain	COCA1	chicken	trachea	2,3	MS3
R.SNYTITPK.D	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	995,079	3	1,2	214	Collagen alpha-2(VI) chain	CO6A2	chicken	trachea	2,3	MS3
R.NNVSLDELAK.D	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1103,120	3	-0,3	508	Complement C1r	F1NAB7	chicken	lung	2,6;2,6	0,96
K.NFTEYTAK.N	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1060,085	3	1,4	292	Complement C8 alpha chain	F1NJU5	chicken	lung	2,6;2,6	1
K.QNSSDKTPGDVDITDVAYYFEK.D	HexNAc(5)Hex(4)Fuc(1)NeuAc(2)	N-glycan	1221,757	4	0,9	192	Epithelial cell adhesion molecule	EPCAM	chicken	colon	2,6;2,6	MS3
R.M(ox)QGIIDDTDQNYSQR.I	HexNAc(3)Hex(5)NeuAc(1)	N-glycan	1170,801	3	1,2	70	Fibrinogen alpha chain	FIBA	chicken	lung	2,6	MS3
R.M(ox)QGIIDDTDQNYSQR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1238,495	3	1,6	70	Fibrinogen alpha chain	FIBA	chicken	lung	2,6	MS3
K.GNAGNALM(ox)EGASQLYGENR.T	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	971,146	4	-0,6	350	Fibrinogen beta chain (Fragment)	FIBB	chicken	colon	2,6	MS3
K.GNAGNALM(ox)EGASQLYGENR.T	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	971,146	4	-0,5	350	Fibrinogen beta chain (Fragment)	FIBB	chicken	lung	2,6	MS3

K.GNAGNALM(ox)EGASQLYGENR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1391,560	3	1,4	350	Fibrinogen beta chain (Fragment)	FIBB	chicken	lung	2,6;2,6	1,26
K.GNAGNALMEGASQLYGENR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1039,923	4	1,2	350	Fibrinogen beta chain (Fragment)	FIBB	chicken	ileum	2,6;2,6	1,03
K.LNLTTDPK.F	HexNAc(3)Hex(6)Fuc(1)NeuAc(1)	N-glycan	974,075	3	1,0	127	Golgi apparatus protein 1	GSLG1	chicken	trachea	2,6	MS3
R.HGNTSWGNAGDR.C	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1159,446	3	0,0	188	Hemopexin	H9L385	chicken	lung	2,6;2,6	MS3
R.HGNTSWGNAGDR.C	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1159,446	3	0,0	188	Hemopexin	H9L385	chicken	trachea	2,6;2,6	1,31
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1105,432	3	2,4	172	Histidine rich glycoprotein	F1NL38	chicken	colon	2,6;2,6	0,97
K.ETNCSR.G	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	890,325	3	1,3	205	Histidine rich glycoprotein	F1NL38	chicken	lung	2,6	MS3
K.ETNCSR.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	987,356	3	0,4	205	Histidine rich glycoprotein	F1NL38	chicken	lung	2,6;2,6	MS3
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1008,397	3	-0,7	172	Histidine rich glycoprotein	F1NL38	chicken	lung	2,6	MS3
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1105,431	3	1,9	172	Histidine rich glycoprotein	F1NL38	chicken	lung	2,6;2,6	0,88
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1008,398	3	0,1	172	Histidine rich glycoprotein	F1NL38	chicken	ileum	2,6	MS3
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1008,397	3	-0,5	172	Histidine rich glycoprotein	F1NL38	chicken	trachea	2,6	MS3
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1105,430	3	0,3	172	Histidine rich glycoprotein	F1NL38	chicken	trachea	2,6;2,6	MS3
R.EGNHTNYFK.V	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1105,431	3	1,3	172	Histidine rich glycoprotein	F1NL38	chicken	ileum	2,6;2,6	1,08
R.VTHNGTSITK.T	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1107,465	3	0,7	87	Ig lambda chain C region	LAC	chicken	colon	2,6	MS3
R.VTHNGTSITK.T	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1039,771	3	0,2	87	Ig lambda chain C region	LAC	chicken	lung	2,6	MS3
R.VTHNGTSITK.T	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	830,851	4	0,9	87	Ig lambda chain C region	LAC	chicken	lung	2,6	MS3
R.VTHNGTSITK.T	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1107,465	3	0,4	87	Ig lambda chain C region	LAC	chicken	ileum	2,6	MS3
R.NASILCQTR.G	HexNAc(5)Hex(5)NeuAc(1)	N-glycan	1056,758	3	-0,1	130	Ig mu chain C region	IGHM	chicken	lung	2,6	MS3
K.KGQNETIK.I	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1090,118	3	0,9	442	Integrin beta-1	ITB1	chicken	lung	2,3;2,3	0,53
R.IAATGEEKENFTAK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1238,518	3	1,7	570	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	colon	2,6;2,6	1,28
K.ENFTAK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	972,046	3	0,2	578	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	lung	2,6;2,6	MS3
R.IAATGEEKENFTAK.A	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1141,484	3	0,4	570	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	lung	2,6	MS3
R.IAATGEEKENFTAK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	929,138	4	-0,8	570	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	lung	2,6;2,6	MS3
R.IAATGEEKENFTAK.A	HexNAc(5)Hex(6)NeuAc(2)	N-glycan	1360,229	3	2,1	570	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	lung	2,6;2,6	MS3
K.RIAATGEEKENFTAK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	968,164	4	0,6	569	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	lung	2,6;2,6	0,97
K.ENFTAK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	972,046	3	0,1	578	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	ileum	2,6;2,6	1,19
R.IAATGEEKENFTAK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1238,518	3	2,1	570	Inter-alpha-trypsin inhibitor heavy chain 3	A0A1D5P4L6	chicken	trachea	2,6;2,6	0,99
K.IKYEIEETNCSK.D	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1236,493	3	1,5	197	Kininogen 1	A0A1L1RNR4	chicken	lung	2,6;2,6	MS3
K.TNCSK.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	935,008	3	1,6	325	Kininogen 1	A0A1L1RNR4	chicken	lung	2,6;2,6	MS3
K.TSNVSQDCK.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1078,069	3	0,6	119	Kininogen 1	A0A1L1RNR4	chicken	lung	2,6;2,6	MS3
R.SFAVLSQVDETSPSNATEGESQR.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1161,731	4	0,2	390	Kininogen 1	A0A1L1RNR4	chicken	lung	2,6;2,6	MS3
K.TSNVSQDCK.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1078,068	3	-0,4	119	Kininogen 1	A0A1L1RNR4	chicken	ileum	2,6;2,6	0,99
K.TSNVSQDCK.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1078,069	3	0,1	119	Kininogen 1	A0A1L1RNR4	chicken	colon	2,6;2,6	0,92
K.APANNISSSIQR.I	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1106,468	3	0,1	810	Laminin subunit alpha 4	F1NSZ5	chicken	lung	2,3	MS3
K.GLNYTIR.L	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1063,104	3	1,0	172	Laminin subunit beta-1	F1NJ23	chicken	lung	2,3;2,6	0,65
R.GSKDNATESVSLR.T	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1238,843	3	1,1	2119	Low-density lipoprotein receptor-related protein 1	LRP1	chicken	lung	2,3;2,3	0,6

R.LDGNNLTR.A	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1085,105	3	0,5	316	Lumican	LUM	chicken	lung	2,3;2,3	MS3
R.LDGNNLTR.A	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1085,105	3	-0,1	316	Lumican	LUM	chicken	trachea	2,3;2,3	MS3
K.APTFEASNDSMSELRATVGNSYK.C	HexNAc(4)Hex(7)NeuAc(1)	N-glycan	1179,239	4	0,6	311	Lysosome-associated membrane glycoprotein 1	A0A1D5PG23	chicken	ileum	2,3	MS3
R.PANTSLDR.G	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1075,430	3	0,3	304	Mannose receptor C type 2	F1NP60	chicken	lung	2,3;2,3	MS3
R.NPDGEQM(ox)PWCYTTNATAR.W	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1081,163	4	1,1	326	Plasminogen	F1NWX6	chicken	lung	2,6;2,6	MS3
K.VLKDNGTEDEIR.S	HexNAc(3)Hex(4)Fuc(1)NeuAc(1)	N-glycan	1028,441	3	0,9	77	Prosaposin	SAP	chicken	lung	2,3	MS3
K.VLKDNGTEDEIR.S	HexNAc(3)Hex(4)Fuc(1)NeuAc(1)	N-glycan	1028,441	3	0,9	77	Prosaposin	SAP	chicken	trachea	2,3	MS3
R.GTINYTK.S	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	904,038	3	0,9	119	Prothrombin	A0A1L1RV31	chicken	lung	2,6	MS3
R.GTINYTK.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1001,069	3	0,4	119	Prothrombin	A0A1L1RV31	chicken	lung	2,6;2,6	MS3
R.NPDNNSEGPWCYTR.D	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1301,819	3	1,6	158	Prothrombin	A0A1L1RV31	chicken	lung	2,6;2,6	1,43
R.GTINYTK.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1001,070	3	0,9	119	Prothrombin	A0A1L1RV31	chicken	colon	2,6;2,6	0,93
R.GTINYTK.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1001,069	3	-0,1	119	Prothrombin	A0A1L1RV31	chicken	trachea	2,6;2,6	MS3
K.DAHTHENGTYNM(ox)PDLPLEFHR.E	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	943,786	5	2,2	33	Serpin family D member 1	A0A1D5PLZ2	chicken	trachea	2,6;2,6	0,79
K.DAHTHENGTYNM(ox)PDLPLEFHR.E	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1179,481	4	2,7	33	Serpin family D member 1	A0A1D5PLZ2	chicken	lung	2,6;2,6	1,03
R.ELSGNESLDLQR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1189,154	3	1,6	286	Serpin family G member 1	F1NA58	chicken	lung	2,6;2,6	1,03
R.KQETTPINDNVSQCCSSSYANR.R	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1186,212	4	0,5	491	Serum albumin	A0A1D5NW68	chicken	lung	2,6;2,6	MS3
K.NITVIK.D	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1013,429	3	0,9	118	Thy-1 membrane glycoprotein	THY1	chicken	trachea	2,3;2,3	0,50
K.NITVIK.D	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	984,090	3	0,3	118	Thy-1 membrane glycoprotein	THY1	chicken	lung	2,3	MS3
K.NITVIK.D	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1519,641	2	1,6	118	Thy-1 membrane glycoprotein	THY1	chicken	lung	2,3;2,3	0,58
K.NITVIK.D	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	984,090	3	0,1	118	Thy-1 membrane glycoprotein	THY1	chicken	trachea	2,6	MS3
R.IVDVNLTSEGK.V	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1146,488	3	0,7	171	Transmembrane 9 superfamily member	F1NRG5	chicken	trachea	2,3	MS3
R.NNSIYVVANIGDK.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1204,506	3	0,7	130	Uncharacterized protein	A0A1D5PJX9	chicken	lung	2,6;2,6	1,16
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1143,491	3	0,4	371	Uncharacterized protein	A0A1D5PCD2	chicken	colon	2,6	MS3
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	978,066	3	0,5	893	Uncharacterized protein	A0A1D5PCD2	chicken	colon	2,6	MS3
K.VYGNETK.F	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1025,076	3	-0,2	397	Uncharacterized protein	A0A1D5PRW6	chicken	colon	2,6	MS3
K.DYPNISLEELGQK.V	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1015,925	4	4,3	1569	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3;2,3	MS3
K.INNSSFVCVK.A	HexNAc(1)Fuc(1),HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1286,178	3	0,9	1550	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3;2,6	MS3
R.AKDYPNISLEELGQK.V	HexNAc(5)Hex(5)NeuAc(2)	N-glycan	1029,194	4	4,6	1567	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,6;2,6	MS3
R.AKDYPNISLEELGQK.V	HexNAc(5)Hex(6)Fuc(2)NeuAc(2)	N-glycan	1142,485	4	3,4	1567	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3;2,3	MS3
R.AKDYPNISLEELGQK.V	HexNAc(6)Hex(6)Fuc(1)NeuAc(3)	N-glycan	1229,766	4	4,6	1567	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3;2,3;2,3	MS3
R.SDVNSGDYETIDKINNSSFVCVK.A	HexNAc(7)Hex(7)NeuAc(1)	N-glycan	1357,304	4	2,8	1537	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3	MS3
R.SDVNSGDYETIDKINNSSFVCVK.A	HexNAc(5)Hex(5)NeuAc(2)	N-glycan	1248,015	4	4,5	1537	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,6;2,6	MS3
R.SDVNSGDYETIDKINNSSFVCVK.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1284,529	4	4,6	1537	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3;2,3	MS3
R.SDVNSGDYETIDKINNSSFVCVK.A	HexNAc(5)Hex(5)Fuc(2)NeuAc(2)	N-glycan	1320,789	4	1,0	1537	Uncharacterized protein	A0A1D5PSC1	chicken	colon	2,3;2,6	MS3
K.NGSIYAFR.G	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	934,044	3	-0,1	167	Uncharacterized protein	A0A1L1RY57	chicken	colon	2,6	MS3
M.GLIHNR.T	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	875,035	3	0,9	2	Uncharacterized protein	A0A1L1S118	chicken	colon	2,6	MS3

M.GLIHNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	972,066	3	0,2	2	Uncharacterized protein	A0A1L1S118	chicken	colon	2,6;2,6	MS3
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1240,527	3	3,3	371	Uncharacterized protein	A0A1D5PCD2	chicken	trachea	2,6;2,6	1,26
R.VNISAWR.T	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1066,105	3	2,6	1722	Uncharacterized protein	A0A1D5P6F4	chicken	lung	2,3;2,3	0,53
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1143,494	3	2,5	371	Uncharacterized protein	A0A1D5PCD2	chicken	lung	2,6	MS3
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	930,644	4	0,6	371	Uncharacterized protein	A0A1D5PCD2	chicken	lung	2,6;2,6	MS3
R.ISLQGGQEM(ox)NYTTNEEGR.A	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	1305,861	3	2,1	386	Uncharacterized protein	A0A1D5PCD2	chicken	lung	2,6	MS3
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1466,598	2	2,4	893	Uncharacterized protein	A0A1D5PCD2	chicken	lung	2,6	MS3
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1075,099	3	1,7	893	Uncharacterized protein	A0A1D5PCD2	chicken	lung	2,6;2,6	MS3
R.NTTVETPEK.G	HexNAc(5)Hex(6)NeuAc(1)	N-glycan	1099,777	3	0,4	893	Uncharacterized protein	A0A1D5PCD2	chicken	lung	2,6	MS3
K.TNSTCLSNEDTCLQM(ox)R.F	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1425,530	3	1,9	39	Uncharacterized protein	A0A1D5PFW6	chicken	lung	2,6;2,6	0,88
K.KPCNSSDPK.C	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1076,078	3	0,9	143	Uncharacterized protein	A0A1D5PJX9	chicken	lung	2,6;2,6	1,27
K.IGECHYLNGTER.V	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1234,152	3	0,7	38	Uncharacterized protein	A0A1D5PM07	chicken	lung	*	MS3
K.AANLSDIVPNTESETK.V	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	1187,833	3	-0,1	955	Uncharacterized protein	A0A1D5PQ85	chicken	lung	2,6	MS3
K.AANLSDIVPNTESETK.V	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1201,509	3	0,2	955	Uncharacterized protein	A0A1D5PQ85	chicken	lung	2,6	MS3
K.TLSTVPTNLTVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1072,477	3	-1,3	1273	Uncharacterized protein	A0A1D5PU94	chicken	lung	2,6	MS3
R.DPNVIPVPGNHTK.G	HexNAc(5)Hex(4)Fuc(1)NeuAc(1)	N-glycan	1163,504	3	0,6	171	Uncharacterized protein	A0A1D5PZU5	chicken	lung	2,6	MS3
R.LNESHTCK.H	HexNAc(4)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1013,055	3	-1,0	214	Uncharacterized protein	E1BUT3	chicken	lung	2,3	MS3
R.LNESHTCK.H	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1110,088	3	0,5	214	Uncharacterized protein	E1BUT3	chicken	lung	2,3;2,3	MS3
K.GNVSALFILPNEGK.L	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1221,863	3	2,0	298	Uncharacterized protein	E1C206	chicken	lung	2,6;2,6	1,07
K.NGSIYAFR.G	HexNAc(3)Hex(5)NeuAc(1)	N-glycan	880,027	3	0,3	167	Uncharacterized protein	E1C7A7	chicken	lung	2,6	MS3
R.LVNQSLK.M	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	905,726	3	0,8	883	Uncharacterized protein	E1C7P4	chicken	lung	2,6	MS3
R.LVNQSLK.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1002,757	3	0,4	883	Uncharacterized protein	E1C7P4	chicken	lung	2,6;2,6	MS3
R.LLQLLNDSQR.D	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1135,488	3	0,8	125	Uncharacterized protein	E1C7T1	chicken	lung	2,6;2,6	MS3
K.NVTFDETSLYVK.A	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1207,498	3	0,7	936	Uncharacterized protein	F1NEQ4	chicken	lung	2,6;2,6	MS3
K.NVTFDETSLYVK.A	HexNAc(5)Hex(6)NeuAc(3)	N-glycan	1069,933	4	0,9	936	Uncharacterized protein	F1NEQ4	chicken	lung	2,3;2,6;2,6	MS3
K.NVTFDETSLYVK.A	HexNAc(5)Hex(6)Fuc(2)NeuAc(2)	N-glycan	1426,243	3	-1,8	936	Uncharacterized protein	F1NEQ4	chicken	lung	2,3;2,6	MS3
R.NNSFHCR.S	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1043,383	3	0,5	277	Uncharacterized protein	F1NF64	chicken	lung	2,6;2,6	0,93
K.ASLVEEGTGLEM(ox)NNTK.T	HexNAc(3)Hex(5)NeuAc(1)	N-glycan	1140,473	3	0,7	318	Uncharacterized protein	F1NK40	chicken	lung	2,6	MS3
K.ASLVEEGTGLEM(ox)NNTK.T	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1208,166	3	0,2	318	Uncharacterized protein	F1NK40	chicken	lung	2,6	MS3
K.GKEEIAQLSVSIEGESLNTTR.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1117,240	4	0,6	95	Uncharacterized protein	F1NK40	chicken	lung	2,6;2,6	1,02
R.ADGAGNITLLER.K	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1572,168	2	1,1	63	Uncharacterized protein	F1NK40	chicken	lung	2,6	MS3
R.ADGAGNITLLER.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1145,479	3	0,7	63	Uncharacterized protein	F1NK40	chicken	lung	2,6;2,6	MS3
R.ADGAGNITLLER.K	HexNAc(5)Hex(6)NeuAc(1)	N-glycan	1170,158	3	0,6	63	Uncharacterized protein	F1NK40	chicken	lung	2,6	MS3
R.KVEEPQLLLNVTFPAPAPSK.G	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1023,731	4	1,6	75	Uncharacterized protein	F1NK40	chicken	lung	2,6	MS3
K.ACHEVNNTNLR.D	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1174,459	3	1,8	25	Uncharacterized protein	F1NPN5	chicken	lung	2,6;2,6	1,00
K.EGYLHNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1031,740	3	0,3	48	Uncharacterized protein	F1P2M6	chicken	lung	2,6;2,6	MS3
K.NAEAPDGNYSCEVTELNR.E	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1411,547	3	2,5	103	Uncharacterized protein	F7BCL1	chicken	lung	2,3;2,3	0,6
K.TGNWSTK.P	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1000,057	3	0,0	275	Uncharacterized protein	A0A1D5PNU2	chicken	lung	2,6;2,6	0,93
K.TLSTVPTNLTVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1169,511	3	1,3	1273	Uncharacterized protein	A0A1D5PU94	chicken	lung	2,6;2,6	1,22
M.GLIHNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	972,068	3	1,8	2	Uncharacterized protein	A0A1L1S118	chicken	lung	2,6;2,6	0,58
R.LHYNGSATAFLILPAK.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1307,581	3	2,0	267	Uncharacterized protein	E1BS56	chicken	lung	2,6;2,6	1,44
K.GEIISSNFQNSTEAK.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1277,190	3	0,6	192	Uncharacterized protein	E1C206	chicken	lung	2,6;2,6	1,11
K.NGSIYAFR.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1044,755	3	3,4	167	Uncharacterized protein	E1C7A7	chicken	lung	2,6;2,6	1,03
R.CSQGSENATR.M	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1101,740	3	1,1	722	Uncharacterized protein	E1C7P4	chicken	lung	2,6;2,6	0,89
R.VQCINGTFK.Y	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1087,431	3	1,2	1224	Uncharacterized protein	E1C7P4	chicken	lung	2,6;2,6	1,15
K.NGTSVCSTTGK.N	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1102,421	3	1,5	94	Uncharacterized protein	F1NF64	chicken	lung	2,6;2,6	1,19
K.FNEESEQTHYFSVLNVTR.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1468,943	3	2,3	175	Uncharacterized protein	F1NHT5	chicken	lung	2,6;2,6	1,14

K.NCTVR.P	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	948,356	3	2,4	102	Uncharacterized protein	F1NHT5	chicken	lung	2,6;2,6	0,9
R.KVEEPQLLLNVTFPAPAPSK.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1096,504	4	1,1	75	Uncharacterized protein	F1NK40	chicken	lung	2,6;2,6	0,91
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1143,491	3	0,5	371	Uncharacterized protein	A0A1D5PCD2	chicken	ileum	2,6	MS3
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1240,524	3	1,3	371	Uncharacterized protein	A0A1D5PCD2	chicken	ileum	2,6;2,6	1,18
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	978,065	3	-0,3	893	Uncharacterized protein	A0A1D5PCD2	chicken	ileum	2,6	MS3
K.EVNITTDYDAPK.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1210,162	3	0,7	267	Uncharacterized protein	A0A1D5PRW6	chicken	ileum	2,6	MS3
K.SIGNDNATLR.L	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	978,398	3	-3,5	183	Uncharacterized protein	A0A1D5PRW6	chicken	ileum	2,6	MS3
K.VYGNETK.F	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1025,074	3	-1,8	397	Uncharacterized protein	A0A1D5PRW6	chicken	ileum	2,6	MS3
K.AENISCR.A	HexNAc(5)Hex(5)Fuc(1)NeuAc(1)	N-glycan	1034,396	3	1,4	1560	Uncharacterized protein	A0A1D5PSC1	chicken	ileum	2,3	MS3
K.AENISCR.A	HexNAc(6)Hex(6)Fuc(1)NeuAc(1)	N-glycan	1156,105	3	-0,1	1560	Uncharacterized protein	A0A1D5PSC1	chicken	ileum	2,3	MS3
K.VENVSCR.A	HexNAc(6)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1203,792	3	0,8	1846	Uncharacterized protein	A0A1D5PSC1	chicken	ileum	2,3;2,3	MS3
M.GLIHNR.T	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	875,034	3	0,3	2	Uncharacterized protein	A0A1L1S118	chicken	ileum	2,6	MS3
M.GLIHNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	972,066	3	0,5	2	Uncharacterized protein	A0A1L1S118	chicken	ileum	2,6;2,6	MS3
R.AQNQELNSTIK.D	HexNAc(3)Hex(5)NeuAc(1)	N-glycan	986,086	3	1,0	276	Uncharacterized protein	E1C703	chicken	ileum	2,3	MS3
K.NGSIYAFR.G	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	934,045	3	0,5	167	Uncharacterized protein	E1C7A7	chicken	ileum	2,6	MS3
R.DENVNSTLHVHYR.M	HexNAc(6)Hex(6)NeuAc(1)	N-glycan	1017,166	4	-0,8	85	Uncharacterized protein	F1N9E2	chicken	ileum	2,6	MS3
R.DENVNSTLHVHYR.M	HexNAc(6)Hex(6)NeuAc(2)	N-glycan	1089,941	4	0,3	85	Uncharacterized protein	F1N9E2	chicken	ileum	2,6;2,6	MS3
K.NCTVR.P	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	851,323	3	1,4	102	Uncharacterized protein	F1NHT5	chicken	ileum	2,6	MS3
K.NCTVR.P	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	948,358	3	4,3	102	Uncharacterized protein	F1NHT5	chicken	ileum	2,6;2,6	0,96
R.ADGAGNITLLER.K	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1048,447	3	0,5	63	Uncharacterized protein	F1NK40	chicken	ileum	2,6	MS3
K.GNESSLFK.C	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1078,095	3	1,2	128	Uncharacterized protein	A0A1D5P246	chicken	trachea	2,3;2,6	0,65
K.GNESSLFK.C	HexNAc(5)Hex(5)NeuAc(2)	N-glycan	1097,106	3	4,5	128	Uncharacterized protein	A0A1D5P246	chicken	trachea	2,3;2,3	MS3
K.LVDGSGSPIANETVR.I	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1143,491	3	0,3	371	Uncharacterized protein	A0A1D5PCD2	chicken	trachea	2,6	MS3
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	978,066	3	0,0	893	Uncharacterized protein	A0A1D5PCD2	chicken	trachea	2,6	MS3
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1075,097	3	-0,6	893	Uncharacterized protein	A0A1D5PCD2	chicken	trachea	2,6;2,6	1,15
K.AANLSDIVPNTESETK.V	HexNAc(3)Hex(6)NeuAc(1)	N-glycan	1187,832	3	-0,9	955	Uncharacterized protein	A0A1D5PQ85	chicken	trachea	2,6	MS3
K.LNATQR.V	HexNAc(5)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1086,104	3	-0,8	1013	Uncharacterized protein	A0A1D5PWQ4	chicken	trachea	2,3	MS3
M.GLIHNR.T	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	972,066	3	0,4	2	Uncharacterized protein	A0A1L1S118	chicken	trachea	2,6;2,6	MS3
R.ADGAGNITLLER.K	HexNAc(4)Hex(5)NeuAc(1)	N-glycan	1048,447	3	0,7	63	Uncharacterized protein	F1NK40	chicken	trachea	2,6	MS3
R.ADGAGNITLLER.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1145,479	3	0,8	63	Uncharacterized protein	F1NK40	chicken	trachea	2,6;2,6	MS3
R.IVNITLPK.I	HexNAc(4)Hex(5)Fuc(1)NeuAc(2)	N-glycan	1083,476	3	1,6	255	Uncharacterized protein	F1NPN6	chicken	trachea	2,3;2,3	0,59
K.TLSTVPTNLTVR.I	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1169,512	3	1,7	1273	Uncharacterized protein	A0A1D5PU94	chicken	ileum	2,6;2,6	1,44
R.ADGAGNITLLER.K	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1145,480	3	1,2	63	Uncharacterized protein	F1NK40	chicken	ileum	2,6;2,6	1,04
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1075,098	3	0,6	863	Uncharacterized protein (alpha 2 macroglobulin)	A0A1D5PVX4	chicken	colon	2,6;2,6	1,03
R.NTTVETPEK.G	HexNAc(4)Hex(5)NeuAc(2)	N-glycan	1075,095	3	-2,2	863	Uncharacterized protein (alpha 2 macroglobulin)	A0A1D5PVX4	chicken	ileum	2,6;2,6	1,06
R.YNCSR.G	HexNAc(5)Hex(5)NeuAc(1)	N-glycan	935,675	3	0,4	120	Uncharacterized protein (CD55)	A0A1D5PU53	chicken	lung	2,6	MS3
K.LECVVAPASGK.P	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	689,631	3	0,7	103	Adenosine deaminase domain containing 1	A0A1L1RSV5	chicken	lung	2,3;2,6	0,8
K.DACPAAGEETGEGSAATAEPQLG.-	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	945,379	3	-0,8	181	Alpha-1-acid glycoprotein	Q8JIG5	chicken	lung	2,6	1,15
K.DACPAAGEETGEGSAATAEPQLG.-	HexNAc(2)Hex(2)NeuAc(1)	O-glycan	1067,092	3	1,7	181	Alpha-1-acid glycoprotein	Q8JIG5	chicken	lung	2,6	0,81
K.SRDEIQAEIQTEKNK.V	HexNAc(2)Hex(1)NeuAc(2)	O-glycan	735,584	4	1,3	131	alpha-1,2-Mannosidase	A0A1D5PZT0	chicken	ileum	2,6;2,6	0,95
K.SSDEHGTEPDAPGLR.L	HexNAc(2)Hex(1)NeuAc(2)	O-glycan	906,705	3	-0,5	89	alpha-1,2-Mannosidase	A0A1D5PBZ7	chicken	ileum	2,6;2,6	1,03
K.SRDEIQAEIQTEKNK.V	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	684,814	4	0,9	131	alpha-1,2-Mannosidase	A0A1D5PZT0	chicken	ileum	2,3;2,6	1,02

K.SSDEHGTEPDAPGLR.L	HexNAc(2)Hex(1)NeuAc(2)	O-glycan	906,705	3	0,0	89	alpha-1,2-Mannosidase	A0A1D5PBZ7	chicken	colon	2,3;2,6	2,59
K.SSDEHGTEPDAPGLR.L	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	839,012	3	0,1	89	alpha-1,2-Mannosidase	A0A1D5PBZ7	chicken	ileum	2,3;2,6	0,74
K.SVPSQEKRK.I	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	669,312	3	1,5	533	Anion exchange protein	E1BVW9	chicken	trachea	2,3;2,6	1,07
R.QRPEEEQPTASLAELAAQK.T	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	918,102	3	1,0	122	Chromogranin A	F1NLZ2	chicken	colon	2,6	0,97
R.SVATARPATGK.R	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	669,312	3	0,9	134	Cochlin	COCH	chicken	trachea	2,3;2,6	0,95
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	887,433	3	1,8	1745	Collagen alpha-1(XII) chain	COCA1	chicken	ileum	2,3;2,3	0,7
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(3)	O-glycan	984,466	3	3,1	1745	Collagen alpha-1(XII) chain	COCA1	chicken	ileum	2,3;2,6; 2,6	3,05
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(1)	O-glycan	790,402	3	2,7	1745	Collagen alpha-1(XII) chain	COCA1	chicken	trachea	2,3	0,29
R.TLPLVPITTPAPK.S	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	887,433	3	1,4	1745	Collagen alpha-1(XII) chain	COCA1	chicken	trachea	2,3;2,3	0,47
K.GLDAEPTEVPEPPPHEK.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	930,411	3	1,6	140	Elastin microfibril interfacer 2	A0A1D5P4I7	chicken	lung	2,3;2,6	0,93
R.HSIGSSTSSHVTGAGSSHLGTGGK.D	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	717,077	4	-0,5	386	Fibrinogen alpha chain	FIBA	chicken	lung	2,6	1,73
R.QEAAPTLRPVAPPISGTGYQPRPPK.Q	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	821,919	4	0,0	26	Fibrinogen beta chain (Fragment)	FIBB	chicken	lung	2,6	1,76
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730,349	4	0,2	2156	Fibronectin	F1NJT3	chicken	lung	2,3;2,3	0,47
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(3)	O-glycan	803,123	4	0,5	2156	Fibronectin	F1NJT3	chicken	lung	2,3;2,3, 2,6	0,35
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730,349	4	0,6	1030	Fibronectin (Fragments)	FINC	chicken	ileum	2,3;2,3	0,51
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730,349	4	0,4	1030	Fibronectin (Fragments)	FINC	chicken	trachea	2,3;2,3	0,54
R.RPVPTTATPLRPGSR.R	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	730,349	4	-0,4	1030	Fibronectin (Fragments)	FINC	chicken	colon	2,3;2,3	0,5
K.GPSPVAPVHLVNEESTDK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	941,761	3	0,5	69	GDT1 family protein	R4GIM6	chicken	ileum	2,3;2,6	1,86
K.GPSPVAPVHLVNEESTDK.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	941,762	3	0,9	69	GDT1 family protein	R4GIM6	chicken	colon	2,3;2,6	1,1
R.GLPTVK.P	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	781,362	2	4,5	189	Glypican 6	F1P027	chicken	lung	2,3;2,6	0,34
K.AVPTVK.R	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	781,362	2	4,5	221	Golgi membrane protein 1	E1C3N9	chicken	lung	2,3;2,6	0,34
K.ETLPSSTAETALELVNPDVVR.T	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	966,468	3	0,6	498	Kininogen 1	A0A1L1RNR4	chicken	lung	2,6	1,02
R.TETGTPTEPVNSPDISSFNGLLDHTESPLPK.C	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	1312,944	3	1,4	519	Kininogen 1	A0A1L1RNR4	chicken	lung	2,6	3,73
K.ETLPSSTAETALELVNPDVVR.T	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1063,501	3	1,7	498	Kininogen 1	A0A1L1RNR4	chicken	lung	2,3;2,6	0,82
K.GTDVKEPEITTQGSK.E	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	846,380	3	0,5	975	Mannose receptor C type 2	F1NP60	chicken	lung	2,3;2,6	1,56
R.GVLPPPPSPVDAEQLR.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	873,749	3	0,7	50	Polypeptide N-acetylgalactosaminyltransferase	F1NMD3	chicken	ileum	2,3;2,6	0,35
R.VKPSTTGQPCESEK.G	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	731,649	3	0,9	198	Prothrombin	A0A1L1RV31	chicken	lung	2,6	0,76
K.M(ox)PAQTKSPEEIDKEERPEVDSK.K	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	804,619	4	1,1	97	Syndecan	Q8JIY0	chicken	lung	2,6	1,13
K.MPAQTKSPEEIDKEERPEVDSK.K	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	877,393	4	1,2	97	Syndecan	Q8JIY0	chicken	lung	2,3;2,6	0,81
R.GSLGGADMER.E	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	970,388	2	-0,5	4	Testis associated actin remodelling kinase 1	R4GJB8	chicken	lung	2,3;2,6	1,86
K.AVPSVKPEVTEPK.C	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	776,704	3	0,7	678	Uncharacterized protein	E1C6U2	chicken	lung	2,3;2,6	0,72
K.CLASPSVSDTTAVTDSTTHLEEK.A	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1129,148	3	0,4	212	Uncharacterized protein	A0A1D5PU53	chicken	lung	2,3;2,3	2,13
K.DSDNPRPATPVKPR.E	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	736,016	3	-0,7	58	Uncharacterized protein	E1BRC1	chicken	lung	2,6	0,86
K.DSDNPRPATPVKPR.E	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	833,049	3	0,2	58	Uncharacterized protein	E1BRC1	chicken	lung	2,3;2,6	1,76
K.DSDNPRPATPVKPR.E	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	736,018	3	1,2	58	Uncharacterized protein	E1BRC1	chicken	lung	2,6	1,55
K.DSDNPRPATPVKPR.E	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	625,039	4	1,6	58	Uncharacterized protein	E1BRC1	chicken	lung	2,3;2,6	0,68
K.EALNTITLR.A	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	781,687	3	0,7	43	Uncharacterized protein	A0A1L1RV71	chicken	lung	2,3;2,3	0,6
K.EALNTITLR.A	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	843,913	2	0,6	43	Uncharacterized protein	A0A1L1RV71	chicken	lung	2,6	0,96
K.KHPEPSPTATPEK.I	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	789,355	3	0,3	572	Uncharacterized protein	F1NWN4	chicken	lung	2,3;2,6	0,82
K.YMSVTFGR.K	HexNAc(2)Hex(2)NeuAc(1)	O-glycan	991,413	2	-1,4	79	Uncharacterized protein	E1C4E6	chicken	lung	2,6	2,12

R.VISEATPTLAAGKDPEK.S	HexNAc(2)Hex(2)NeuAc(3)	O-glycan	1110,830	3	0,8	728	Uncharacterized protein	A0A1D5PFK3	chicken	lung	2,3,2,6; 2,6	1,57
R.VISEATPTLAAGKDPEK.S	HexNAc(2)Hex(2)NeuAc(4)	O-glycan	1207,863	3	1,7	728	Uncharacterized protein	A0A1D5PFK3	chicken	lung	2,3;2,6; 2,3;2,6	1,23
K.IPAPTESSCQGVGEGHQCPTATSG TCVVTGDR.S	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1058,428	4	1,1	636	Uncharacterized protein	A0A1D5P6F4	chicken	lung	2,3;2,6	2,5
R.GPCLQSPTK.P	HexNAc(2)Hex(2)NeuAc(1)	O-glycan	999,411	2	-1,8	1196	Uncharacterized protein	E1BR07	chicken	lung	2,6	2,65
R.GTEASATAATPK.I	HexNAc(2)Hex(2)NeuAc(1)	O-glycan	1063,463	2	2,7	369	Uncharacterized protein	E1BS56	chicken	lung	2,6	0,77
R.GTEASATAATPK.I	HexNAc(1)Hex(1)NeuAc(1)	O-glycan	880,895	2	0,7	369	Uncharacterized protein	E1BS56	chicken	lung	2,6	0,84
K.DSDNPRPATPVKPR.E	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	833,048	3	-0,5	58	Uncharacterized protein	E1BRC1	chicken	trachea	2,3;2,6	1,15
K.KHPEPSPTATPEK.I	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	789,355	3	-0,1	572	Uncharacterized protein	F1NWN4	chicken	trachea	2,3;2,6	0,73
K.TGEEVETGTTEPSHTGHEDL.-	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	1025,084	3	-0,6	205	Uncharacterized protein	A0A1L1RLI6	chicken	trachea	2,3;2,6	1,27
R.VIPSRESNR.E	HexNAc(2)Hex(2)NeuAc(2)	O-glycan	790,682	3	0,2	390	Uncharacterized protein	A0A1D5PVD2	chicken	trachea	2,3;2,3	0,5
K.QWEESWK.Q	HexNAc(1)Hex(1)NeuAc(2)	O-glycan	647,262	3	-0,1	678	Unkempt family zinc finger	F1P3C2	chicken	lung	2,3;2,6	0,72