

JVDI: Supplementary material

Mitchell PK, et al. Method comparison of targeted influenza A virus typing and whole-genome sequencing from respiratory specimens of companion animals

Supplementary Table 1. List of strain names, NCBI accessions, and U.S. state.

Strain	State	PB2	PB1	PA	HA	NP	NA	M	NS
A/Canis lupus familiaris/USA/000915/2018(H3N2)	KY	MK690062	MK690061	MK690060	MK690059	MK690058	MK690057	MK690056	MK690055
A/Canis lupus familiaris/USA/006974/2018(H3N2)	CA	MK690070	MK690069	MK690068	MK690067	MK690066	MK690065	MK690064	MK690063
A/Canis lupus familiaris/USA/007780/2018(H3N2)	KY	MK690078	MK690077	MK690076	MK690075	MK690074	MK690073	MK690072	MK690071
A/Canis lupus familiaris/USA/007781/2018(H3N2)	CA	MK690086	MK690085	MK690084	MK690083	MK690082	MK690081	MK690080	MK690079
A/Felis catus/USA/047732/2018(H1N1)	CT	MK690094	NA*	MK690092	MK690091	MK690090	MK690089	MK690088	MK690087

Influenza A virus whole-genome sequencing

A/Equus caballus/USA/149632/2018(H3N8)	NY	MK690102	MK690101	MK690100	MK690099	MK690098	MK690097	MK690096	MK690095
A/Canis lupus familiaris/USA/150620/2018(H3N2)	MI	MK690110	MK690109	MK690108	MK690107	MK690106	MK690105	MK690104	MK690103
A/Canis lupus familiaris/USA/152386/2018(H3N2)	MI	MK690118	MK690117	MK690116	MK690115	MK690114	MK690113	MK690112	MK690111
A/Equus caballus/USA/154390/2018(H3N8)	VT	MK690126	MK690125	MK690124	MK690123	MK690122	MK690121	MK690120	MK690119
A/Canis lupus familiaris/USA/188191/2017(H3N2)	OH	MK690134	MK690133	MK690132	MK690131	MK690130	MK690129	MK690128	MK690127
A/Canis lupus familiaris/USA/188203/2017(H3N2)	OH	MK690142	MK690141	MK690140	MK690139	MK690138	MK690137	MK690136	MK690135
A/Canis lupus familiaris/USA/188226/2017(H3N2)	OH	MK690150	MK690149	MK690148	MK690147	MK690146	MK690145	MK690144	MK690143
A/Canis lupus familiaris/USA/188297/2017(H3N2)	OH	MK690158	MK690157	MK690156	MK690155	MK690154	MK690153	MK690152	MK690151

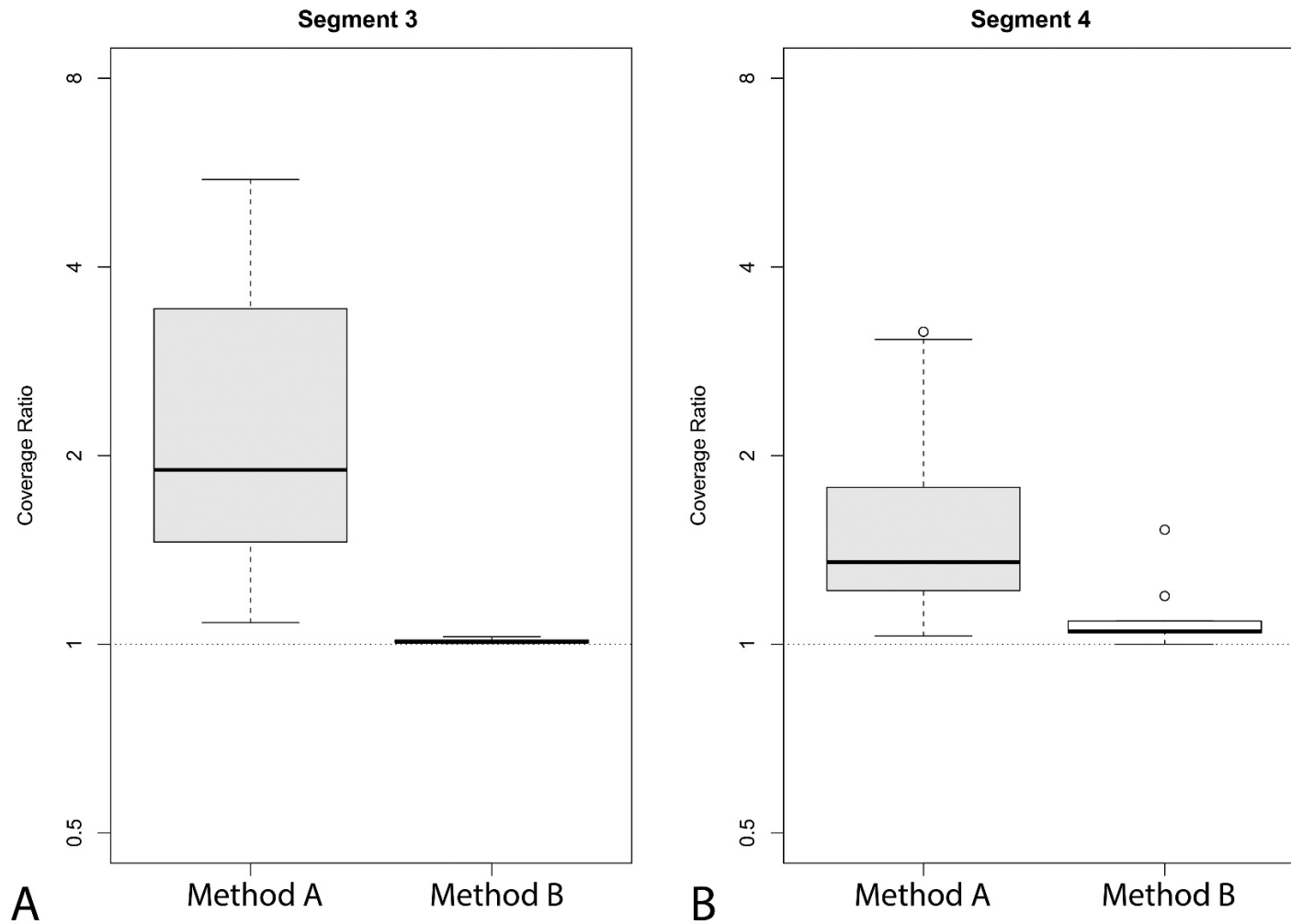
Influenza A virus whole-genome sequencing

A/Canis lupus familiaris/USA /188305/ 2017(H3N2)	KY	MK690166	MK690165	MK690164	MK690163	MK690162	MK690161	MK690160	MK690159
A/Canis lupus familiaris/USA /218592/ 2017(H3N2)	CA	MK690174	MK690173	MK690172	MK690171	MK690170	MK690169	MK690168	MK690167
A/equine/NC /048519/ 2019(H3N8)	NC	MT212114	MT212115	MT212116	MT212117	MT212118	MT212119	MT212120	MT212121
A/equine/AL /051053/ 2019(H3N8)	AL	MT212122	MT212123	MT212124	MT212125	MT212126	MT212127	MT212128	MT212129
A/equine/NY /053954/ 2019(H3N8)	NY	MT212130	MT212131	MT212132	MT212133	MT212134	MT212135	MT212136	MT212137
A/equine/PA /072778/ 2019(H3N8)	PA	MT212138	MT212139	MT212140	MT212141	MT212142	MT212143	MT212144	MT212145
A/equine/ME /082889/ 2019(H3N8)	ME	MT212146	MT212147	MT212148	MT212149	MT212150	MT212151	MT212152	MT212153
A/equine/GA /168830/ 2019(H3N8)	GA	MT212084	NA*	MT212085	MT212086	MT212087	MT212088	MT212089	MT212090
A/equine/NH /176576/ 2019(H3N8)	NH	MT212098	MT212099	MT212100	MT212101	MT212102	MT212103	MT212104	MT212105
A/equine/OH /218776/ 2018(H3N8)	OH	MT212106	MT212107	MT212108	MT212109	MT212110	MT212111	MT212112	MT212113

Influenza A virus whole-genome sequencing

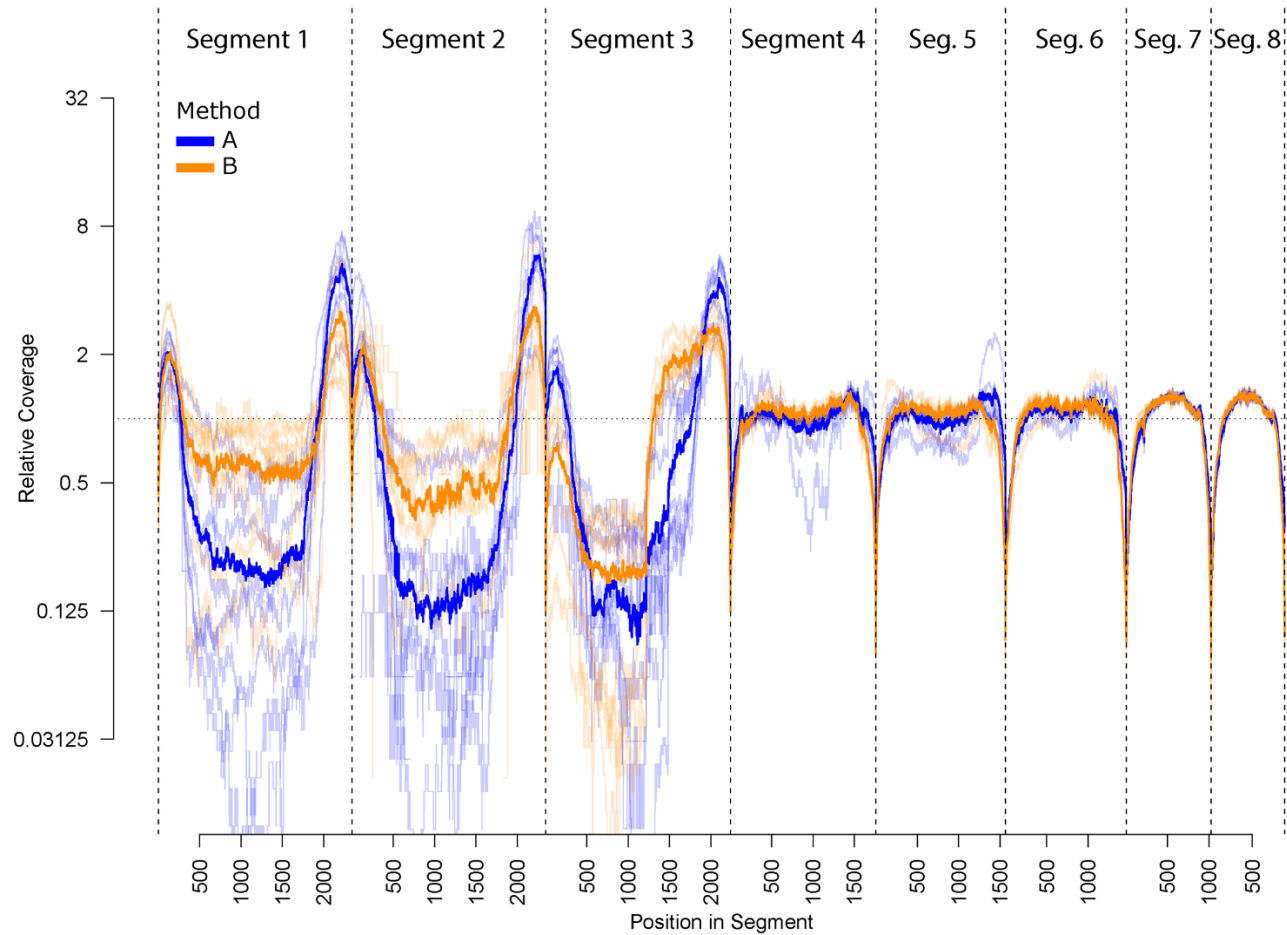
A/equine/NY/2 20792/ 2018(H3N8)	NY	MT212091	NA*	MT212092	MT212093	MT212094	MT212095	MT212096	MT212097
---------------------------------------	----	----------	-----	----------	----------	----------	----------	----------	----------

* Segment not uploaded because of poor coverage by both methods.



Supplementary Figure 1. Boxplot of ratio of coverage depth between **A.** bases 1,482 and 1,481 of segment 3 and **B.** bases 1,076 and 1,075 of segment 4 for set 1 H3N2 samples.

Influenza A virus whole-genome sequencing



Supplementary Figure 2. Relative coverage across each segment for set 2 H3N8 samples, with data for method A shown in blue and method B in orange. Each sample is represented by a light line, and the mean value for the method is shown as a dark line. The relative coverage for each base position is the number of reads at the base divided by the average coverage depth of the segment for a given sample.