

Supplementary Materials for

***In vivo* profiling of individual multi-ciliated cells during acute influenza A virus infection**

Authors: Cait E. Hamele, Alistair B. Russell, and Nicholas S. Heaton*

*To whom correspondence should be addressed:
Nicholas S. Heaton, PhD
Email: nicholas.heaton@duke.edu

This file includes:

Table S1. Internal deletions in influenza segments by timepoint.

Table S1

cell barcode	segment	fiveprime	threeprime	count	dpi	final length
AACAAAGTCCTTCTTC-1	PB1	262	2133	16	one	469
ACCTGAAAGAGCCGTA-1	PB1	135	2144	145	one	331
ACTTTCACATCGTTCC-1	PB1	283	1896	42	one	727
CGTCAAATCGGTGTAT-1	PB1	239	1978	15	one	601
CTCCTTTTCATTATCC-1	PB1	135	2144	144	one	331
CTTCGGTCAATAGAGT-1	PB1	143	2147	388	one	336
GCATGATAGATCCCGC-1	PB1	283	1896	31	one	727
GGAAGTGGTGCCAGT-1	PB1	213	2139	235	one	414
GTTAGACAGTTCCATG-1	PB1	262	2133	15	one	469
TACACCCGTAGGACTG-1	PB1	203	2087	58	one	456
TCCGATCGTGTTTCGAT-1	PB1	262	2130	23	one	472
TCCGATCGTGTTTCGAT-1	PB1	262	2133	49	one	469
TCGCAGGAGCTTTCCC-1	PB1	262	2133	17	one	469
TGATCTTGTAATCAAG-1	PB1	262	2133	20	one	469
TTGTTGTTGCAATGT-1	PB1	262	2133	19	one	469
AACAAAGTCGACCACG-1	NA	62	1271	172	one	248
AACACACTCGTTATCT-1	NA	97	1212	41	one	342
AACCTGAAGGTCGTAG-1	NA	205	1311	603	one	351
AATTCCTGTACTAACC-1	NA	143	1308	279	one	292
ACTTCGCCAGAGACTG-1	NA	120	1270	683	one	307
AGAAATGCATTGGGAG-1	NA	120	1270	158	one	307
AGATAGAGTGTATACC-1	NA	97	1212	29	one	342
AGCTACAGTATACCCA-1	NA	120	1270	432	one	307
AGTTCCCAAGTTTGC-1	NA	148	1303	280	one	302
ATGAGTCTCTACGCAA-1	NA	371	947	33	one	881
ATTTCTGTCCGTCAAA-1	NA	143	1308	370	one	292
CAACAACAGCCATTTG-1	NA	148	1303	347	one	302
CTGTGAAGTGCGGATA-1	NA	120	1270	183	one	307
GATGACTGTACAAGTA-1	NA	120	1270	110	one	307
GGGCTCAAGACGATAT-1	NA	143	1308	50	one	292
GTAACACGTCCAGGTC-1	NA	188	1250	1998	one	395
GTCTACCCATGGCACC-1	NA	400	1176	22	one	681
TATCCTAAGCTCATAC-1	NA	205	1311	569	one	351
TCGCTTGAGAGCAACC-1	NA	143	1308	1636	one	292
TCGTCCATCGTTGTAG-1	NA	143	1308	1032	one	292
TCTGGCTCAAATTGCC-1	NA	120	1270	591	one	307
TGATCTTGATCCTCC-1	NA	120	1270	79	one	307
TGGATGTAGCGAATGC-1	NA	143	1308	48	one	292

ATGTCCCAACAGTGG-1	NP	668	880	26	one	1352
CCGGGTATCGCAATTG-1	NP	199	1281	53	one	482
GACATCAAGCGGGTTA-1	NP	266	1303	160	one	527
GATTCTTCACCATAAC-1	NP	930	1430	15	one	1064
GCCCGAACAGCGTAGA-1	NP	416	1081	105	one	899
GGATGTTACGAGGTA-1	NP	266	1303	306	one	527
GTAGTACAGTGCACAG-1	NP	663	1420	15	one	807
GTGCTGGCAAATTGCC-1	NP	99	1433	15	one	230
TACGTCCAGGGATCGT-1	NP	416	1081	71	one	899
TGCTCGTGTATAGGGC-1	NP	270	1277	512	one	557
TTGAACGTCCAAGCTA-1	NP	199	1281	522	one	482
AGATCCACACGGTGAA-1	HA	23	510	18	one	1289
AGGTTGTAGCGCCGTT-1	HA	455	1344	23	one	887
AGTACTGGTTATTCCT-1	HA	318	1296	113	one	798
CGTGTCTCAGTTTGGT-1	HA	120	1563	67	one	333
CTAGACAAGAGGACTC-1	HA	239	1475	230	one	540
CTCCCTCGTGAATATC-1	HA	106	1569	1001	one	313
GCCCGAACAGCGTAGA-1	HA	126	1539	518	one	363
GGACGTCCAACAGAGC-1	HA	83	1570	434	one	289
GGTTGTACAGAGCTAG-1	HA	345	1333	771	one	788
GTAACACGTCCAGGTC-1	HA	270	1509	1288	one	537
GTGGAAGTCCGGCTTT-1	HA	239	1475	444	one	540
TATCCTAAGCTCATAC-1	HA	455	1344	18	one	887
TCCGTGTTCAATTGCTT-1	HA	243	1419	618	one	600
TGCTTGCAGTGTGTTT-1	HA	117	1544	221	one	349
TTACAGGCATGGCTGC-1	HA	94	1537	77	one	333
TTCCTAATCTAGCATG-1	HA	79	1531	27	one	324
TTGGGTACAACACAAA-1	HA	561	1224	17	one	1113
ACATCGATCCGTAGTA-1	PB2	244	1995	27	one	589
ACGGGTCCATCGAGCC-1	PB2	216	2140	82	one	416
ACTGTGAGTGCCTACG-1	PB2	159	2127	82	one	372
AGAACCTGTCGTGTTA-1	PB2	256	2086	93	one	510
ATCTCTATCTCTGACC-1	PB2	320	1936	23	one	724
CGCGTGACAATGTCTG-1	PB2	224	2157	16	one	407
CTTCGGTCAATAGAGT-1	PB2	191	2159	282	one	372
GAGTCATTCAAGGAGC-1	PB2	152	2038	45	one	454
GCATTAGTCGAACGGA-1	PB2	152	2038	15	one	454
GCCATTCTCCTACCAC-1	PB2	307	1909	20	one	738
GTCTCACGTATGCAAA-1	PB2	318	1929	29	one	729
TCCGGGATCCATCCGT-1	PB2	320	1936	17	one	724
TCGTCCATCGTTGTAG-1	PB2	199	2096	127	one	443

TGGGAAGAGGAAGTGA-1	PB2	114	2125	1120	one	329
TGGTAGTTCCCTTTGG-1	PB2	152	2038	39	one	454
TTATTGCGTGTTTCGTA-1	PB2	318	1929	16	one	729
TTCAGGAAGGTTTGAA-1	PB2	210	2119	77	one	431
ACGATCAGTGAAAGTT-1	NS	352	1548	83	one	739
AGAACCTGTCGTGTTA-1	NS	1389	1795	132	one	1529
AGGACGATCAGGAAAT-1	NS	1734	1809	20	one	1860
AGGCCACAGCGCCTAC-1	NS	110	1707	684	one	338
AGTACTGGTTATTCCT-1	NS	474	1571	42	one	838
ATTTCTGTCCGTCAAA-1	NS	169	1713	27	one	391
CACGTTCCAGTGCCTG-1	NS	283	1313	20	one	905
CATACAGAGGATTTCC-1	NS	280	1832	86	one	383
CCGGTGAGTAGTCACT-1	NS	210	1726	64	one	419
CGTCCATAGCGTACAG-1	NS	478	1800	1290	one	613
CGTGATACAAGTTCCA-1	NS	523	1417	33	one	1041
CGTGTCTCAGTTTGGT-1	NS	478	1800	518	one	613
CTTCGGTCAATAGAGT-1	NS	236	1661	106	one	510
GAGGGTAAGACCGTTT-1	NS	523	1417	15	one	1041
GCCCGAACAGCGTAGA-1	NS	478	1800	133	one	613
GTAATGCTCCCATACC-1	NS	185	1804	85	one	316
GTGTGGCGTCCACATA-1	NS	444	1419	101	one	960
GTTCTATCAGGAGACT-1	NS	280	1832	75	one	383
TACACCCGTAGGACTG-1	NS	216	1662	20	one	489
TACTGCCGTTGGCCGT-1	NS	523	1417	26	one	1041
TCGTCCATCGTTGTAG-1	NS	169	1713	1973	one	391
TGATCTTTCACGGTCG-1	NS	523	1417	16	one	1041
TTCTTCCAGGCATTTTC-1	NS	899	1628	211	one	1206
TTGAACGTCCAAGCTA-1	NS	701	1838	4674	one	798
TTGCATTCAGTCACGC-1	NS	701	1838	5440	one	798
AGTACTGGTTATTCCT-1	PA	528	1692	18	one	1068
CCCTCTCAGGGACCAT-1	PA	174	1952	19	one	454
GTTTGGGAAGCTAGAAT-1	PA	410	1724	17	one	918
TAGGTTGCAACGACAG-1	M	822	919	15	one	929
TCCGTGTTCAATTGCTT-1	M	321	763	95	one	584
TTCTTCCCATGAAGCG-1	M	662	837	17	one	851
AAGGAATAGTCTTGGT-1	PB1	262	2130	15	two	472
AAGGAATAGTCTTGGT-1	PB1	262	2133	16	two	469
AATTTCCCACCCTCTA-1	PB1	262	2130	27	two	472
AATTTCCCACCCTCTA-1	PB1	262	2133	61	two	469
ACCTACCAGCCTCAAT-1	PB1	262	2133	42	two	469
AGCATCAGTCACTTCC-1	PB1	262	2133	36	two	469

AGGAATATCTGCATGA-1	PB1	137	2045	260	two	432
ATCACTTTTCGATGGAG-1	PB1	262	2133	49	two	469
ATGGGAGTCCTGTAAG-1	PB1	197	2110	522	two	427
CCAATGATCACGTAGT-1	PB1	233	2183	2160	two	390
CGCATGGGTTATAGAG-1	PB1	262	2133	22	two	469
CTCACTGGTCCTACAA-1	PB1	1573	2173	15	two	1740
CTGAATGCAGTCCCGA-1	PB1	262	2133	26	two	469
CTGTAGATCCGCACGA-1	PB1	262	2130	37	two	472
CTGTAGATCCGCACGA-1	PB1	262	2133	70	two	469
CTGTAGATCCGCACGA-1	PB1	266	2130	17	two	476
CTTACCGGTTTGTCT-1	PB1	262	2133	22	two	469
GACCTTCTCGGTCTAA-1	PB1	262	2133	30	two	469
GCTGCAGGTACCATAC-1	PB1	169	2152	991	two	357
GGAGATGGTTCTCACC-1	PB1	262	2130	37	two	472
GGAGATGGTTCTCACC-1	PB1	262	2133	93	two	469
GTAACCACACGCTGCA-1	PB1	312	2068	69	two	584
GTTGTCCCAAGTCCCG-1	PB1	262	2130	39	two	472
GTTGTCCCAAGTCCCG-1	PB1	262	2133	116	two	469
GTTGTCCCAAGTCCCG-1	PB1	266	2130	39	two	476
GTTGTCCCAAGTCCCG-1	PB1	266	2133	31	two	473
TCACAAGAGGTTCGAGT-1	PB1	262	2133	18	two	469
TTCTAACAGCCTCAAT-1	PB1	262	2130	62	two	472
TTCTAACAGCCTCAAT-1	PB1	262	2133	204	two	469
TTCTAACAGCCTCAAT-1	PB1	266	2130	52	two	476
TTCTAACAGCCTCAAT-1	PB1	266	2133	44	two	473
AGACAGGTCTCTGACC-1	NA	243	1188	89	two	512
AGATAGACATGGCCAC-1	NA	78	1341	7573	two	194
CCACGTTAGCAATAAC-1	NA	120	1270	4700	two	307
CTATAGGAGAAGTCAT-1	NA	128	1188	563	two	397
GGTGTTCGGTTTAGAGA-1	NA	303	1213	598	two	547
TCATGCCGTATGTGTC-1	NA	110	1164	17	two	403
TCATGCCGTTAGGGAC-1	NA	303	1213	1173	two	547
TCCAGAACACGGGCTT-1	NA	110	1164	23	two	403
TCGTGCTGTACGATGG-1	NA	600	1253	32	two	804
TCTACCGTCGAGTTGT-1	NA	78	1341	4588	two	194
TGTGTGACACATACTG-1	NA	303	1213	1191	two	547
TTACAGGCATAATCGC-1	NA	303	1213	896	two	547
TTACGTTAGCTTTGTG-1	NA	74	1333	2138	two	198
GTTATGGCAGTGTGGA-1	NP	441	1043	22	two	962
TACCTGCCAGGACTTT-1	NP	631	778	15	two	1417
AAAGTGAGTAGTCTTG-1	HA	396	1149	2142	two	1023

AGCGATTTCAAGCCAT-1	HA	306	1447	1250	two	635
AGGGTTTAGGAAGAAC-1	HA	94	1537	2128	two	333
CCAATTTTCGAAGTGG-1	HA	1006	1595	15	two	1187
CTCAGTCCAGCGGATA-1	HA	232	1489	425	two	519
GACCTTCGTCGTA-1	HA	164	1501	440	two	439
GGTGATTAGCCGTCGT-1	HA	284	1442	597	two	618
TCATCCGGTAGGTACG-1	HA	191	1591	884	two	376
TCTTAGTCATTCTTCA-1	HA	787	1129	169	two	1434
TGCAGGCGTTGGCCTG-1	HA	434	1343	734	two	867
TGCTTGCAGCTTCTAG-1	HA	1371	1589	976	two	1558
TGCTTGCAGCTTCTAG-1	HA	321	1537	102	two	560
TGGGCTGCACCTTCCA-1	HA	254	1396	17	two	634
TGGGCTGGTCTTACAG-1	HA	205	1507	151	two	474
TTGGGATAGGAGACCT-1	HA	1371	1589	907	two	1558
TTGGGATAGGAGACCT-1	HA	321	1537	76	two	560
AATCACGTCCGCAGTG-1	PB2	160	2069	24	two	431
AGAGAATCATAGTCGT-1	PB2	210	2119	119	two	431
AGATCGTGTCTGGGT-1	PB2	105	2113	179	two	332
AGCGATTCACTAGTAC-1	PB2	196	2104	19	two	432
AGGAATAGTTAAGTCC-1	PB2	196	2104	240	two	432
AGGAATATCTGCATGA-1	PB2	152	2038	44	two	454
ATGGGAGCAGAACTAA-1	PB2	199	2096	191	two	443
ATGGGAGCAGAACTAA-1	PB2	244	2099	258	two	485
CTATAGGCACGTTGGC-1	PB2	199	2096	65	two	443
CTCAGTCGTCATCGGC-1	PB2	199	2096	56	two	443
GATGATCAGGAGATAG-1	PB2	216	2140	1160	two	416
GCATCGGGTCCGCAGT-1	PB2	152	2038	50	two	454
GCGATCGCAGGAAGTC-1	PB2	400	2166	214	two	574
GGGATCCGTAACAGGC-1	PB2	207	2104	660	two	443
GTAATCGGTACGGATG-1	PB2	282	2247	50	two	375
TACAGGTTCCGTATGA-1	PB2	199	2096	24	two	443
TGAGGAGCATCCAACA-1	PB2	196	2104	1482	two	432
TTACCATCACTCACTC-1	PB2	199	2096	148	two	443
AAAGTGAGTAGTCTTG-1	NS	184	1735	840	two	384
AATGGCTGTGGTAATA-1	NS	168	1801	3627	two	302
AGCCAATTCTCCCATG-1	NS	330	1750	23	two	515
AGCGATTTCAAGCCAT-1	NS	99	1628	269	two	406
CACGGGTCAACTGATC-1	NS	103	244	17	two	1794
CACGGGTCAACTGATC-1	NS	640	1791	822	two	784
CAGCAGCGTCTGTAGT-1	NS	64	1752	2537	two	247
CATCGGGGTGCGGTAA-1	NS	305	1797	5058	two	443

CCTCACACATGAAGCG-1	NS	217	1814	20	two	338
CGGCAGTGTCTAACTG-1	NS	478	1800	20	two	613
CGGGTCAGTATTGAGA-1	NS	371	1451	30	two	855
CTCCTCCAGACCGCCT-1	NS	189	1794	1501	two	330
CTGCCTATCTGGCCGA-1	NS	721	1517	41	two	1139
GAGTGAGAGGAACGAA-1	NS	264	1754	1562	two	445
GATTCTTTCCGATAGT-1	NS	281	1601	343	two	615
GCACTAACATTCTTCA-1	NS	378	1536	141	two	777
GGAGGATCAGCTGTTA-1	NS	280	1459	20	two	756
GTCGTAATCACATTGG-1	NS	217	1814	230	two	338
GTGTTAGGTCCGGTGT-1	NS	721	1517	24	two	1139
TACAGGTTCCGTATGA-1	NS	478	1800	377	two	613
TCTTAGTCATTCTTCA-1	NS	105	1628	529	two	412
TGTCCCACAAACAGGC-1	NS	203	1675	1575	two	463
TGTCCTGCATTGAAGA-1	NS	595	1726	1320	two	804
TTACCATCACTCACTC-1	NS	97	1728	94	two	304
TTAGGCACACAGCCTG-1	NS	261	1695	1101	two	501
ACTGTCCGTTACACTG-1	PA	134	1980	31	two	386
ATGGGAGCAGAATAA-1	PA	241	1940	31	two	533
GGATGTTTCCATTTCA-1	PA	129	2000	252	two	361
GGTCACGAGCTAATGA-1	PA	517	1709	33	two	1040
TATGTTTCAGAGATGCC-1	PA	593	1491	25	two	1334
TTTATGCAGACGTCTGA-1	M	264	351	23	two	939
ATACTTCTCCGTAGTA-1	PB1	317	2148	1494	three	509
CATACCCAGCGAGTA-1	PB1	262	2133	18	three	469
CATCGGGGTAATTAGG-1	PB1	145	2183	21	three	302
CGCCAGACACGGATCC-1	PB1	262	2130	31	three	472
CGCCAGACACGGATCC-1	PB1	262	2133	49	three	469
CGCCAGACACGGATCC-1	PB1	266	2133	35	three	473
GTAGAAAGTCAACGCC-1	PB1	136	2047	181	three	429
GTCTCACCACCAACAT-1	PB1	262	2130	27	three	472
GTCTCACCACCAACAT-1	PB1	262	2133	103	three	469
GTCTCACCACCAACAT-1	PB1	266	2130	17	three	476
GTCTCACCACCAACAT-1	PB1	266	2133	33	three	473
TAGACTGGTGTGTCCG-1	PB1	262	2133	46	three	469
TCCACGTCACCCAATA-1	PB1	97	2239	2038	three	198
AACAAAGCACTGTGAT-1	NA	59	1341	306	three	175
ACCAAAGTCGCTGCA-1	NA	87	1349	89	three	195
AGGTTACCATAGCACT-1	NA	309	1079	17	three	687
AGGTTACCATAGCACT-1	NA	54	1252	916	three	259
CGCATAACAGACCTAT-1	NA	153	1287	6363	three	323

GAGACTTGTACCGTCG-1	NA	153	1287	885	three	323
GGGAGATGTGGCAACA-1	NA	59	1341	325	three	175
GGTGAAGAGCTTCTAG-1	NA	202	1188	167	three	471
GTATTCGTCTGTAAC-1	NA	120	1270	2359	three	307
GTGCACGTCGTGGCGT-1	NA	203	1210	174	three	450
TAGGTTGGTGTGAATA-1	NA	101	1327	1203	three	231
TAGGTTGGTGTGAATA-1	NA	701	1327	17	three	831
TCCTCTGTAGTGATA-1	NA	120	1270	3165	three	307
TGTTGAGCAGTTTCGA-1	NA	288	1153	378	three	592
CATTGTTGTGGAACAC-1	NP	124	1525	90	three	163
CGTCAAACAGTGTGGA-1	NP	24	114	15	three	1474
GCAGTTAGTCTGCAAT-1	NP	416	1093	104	three	887
GCCAGCACAGGCCTGT-1	NP	216	1524	15	three	256
TTACCATAGCAAATCA-1	NP	305	1529	123	three	340
AATGCCAGTAGACTGG-1	HA	650	1148	208	three	1278
ACCTGAAAGTCAGAGC-1	HA	754	1342	15	three	1188
AGTCACAGTGGCCACT-1	HA	117	1544	1834	three	349
AGTTAGCTCCCTCTTT-1	HA	216	1415	222	three	577
CCCTCAACATGTGACT-1	HA	117	1544	4128	three	349
CGAATTGTCTCTGCCA-1	HA	196	1570	28	three	402
CGAGGCTTCGCAAGAG-1	HA	196	1570	36002	three	402
GACCCTTCATCGGTTA-1	HA	117	1544	179	three	349
GACCCTTGTTATGACC-1	HA	1281	1618	19	three	1439
GTAATCGGTTTGCAGT-1	HA	196	1570	1362	three	402
GTTCCGTAGCACACCC-1	HA	117	1544	255	three	349
TATTCCACATAACGGG-1	HA	117	1544	2971	three	349
TCACGCTGTATGAGAT-1	HA	117	1544	3572	three	349
TCCCAGTCATCTAGAC-1	HA	117	1544	3764	three	349
TGCAGTAGTACTGCGC-1	HA	31	1643	47	three	164
TTGGTTTCAATCGCGC-1	HA	92	1589	19	three	279
TTGGTTTCAATCGCGC-1	HA	96	1593	15782	three	279
TTGGTTTCACTCTAGA-1	HA	233	1411	86	three	598
AACCCAACATTCCTAT-1	PB2	189	2054	77	three	475
AGTACTGTCCGGTAGGA-1	PB2	215	2085	1112	three	470
AGTTAGCTCCCTCTTT-1	PB2	233	2127	1772	three	446
CAGGGCTAGTTCATCG-1	PB2	252	2164	2780	three	428
CATACTTAGTCGCTAT-1	PB2	152	2038	75	three	454
CTATCTAGTACCGTCG-1	PB2	215	2085	140	three	470
GAGTCTAGTTCTTCAT-1	PB2	233	2127	6207	three	446
GGCAGTCCATCGTTCC-1	PB2	276	2151	1603	three	465
GTGCTTCGTTTCGATG-1	PB2	313	2148	24	three	505

TATTCCACATAACGGG-1	PB2	313	2148	674	three	505
TCACAAGGTGGGCTCT-1	PB2	294	2142	1790	three	492
TCGCTCACACGGTGCT-1	PB2	215	2085	51	three	470
TTGACCCTCTTTGATC-1	PB2	233	2127	15	three	446
TTTATGCAGACAACTA-1	PB2	252	2164	2426	three	428
AGACCCGCAAGAGTAT-1	NS	257	1626	30	three	566
AGGTTGTCAATTGCAC-1	NS	391	1798	19	three	528
CAAGACTTCCGAGCTG-1	NS	721	1517	35	three	1139
CACTAAGGTCCGAAAC-1	NS	280	1900	22	three	315
CATGCCTTCAGAGCAG-1	NS	306	1482	30	three	759
CGGACACTCAGACCGC-1	NS	250	1569	677	three	616
GACCTTCGTATTAAGG-1	NS	156	1783	418	three	308
GAGTCTAGTTCTTCAT-1	NS	152	1669	2101	three	418
GCGTGCAAGGCTTTCA-1	NS	125	1852	3776	three	208
GTAGAAAGTCAACGCC-1	NS	238	1716	241	three	457
GTGGGAAGTATTGACC-1	NS	346	1798	39	three	483
GTTAGACGTTACCCTC-1	NS	335	1627	1013	three	643
TAACACGAGTCTTCGA-1	NS	227	1740	16	three	422
TAGGTTGGTGTGAATA-1	NS	250	1569	22	three	616
TATTCCACATAACGGG-1	NS	152	1669	79	three	418
TCAAGTGTCCCATAAG-1	NS	250	1569	33	three	616
TTGACCCTCTTTGATC-1	NS	152	1669	34	three	418
GAGTCTAGTTCTTCAT-1	PA	223	1995	833	three	460
GGTGAAGAGCTTCTAG-1	PA	207	1978	75	three	461
TATTCCACATAACGGG-1	PA	223	1995	17	three	460
ATGTTGGTATAGGAT-1	M	394	598	16	three	822
CCCACTCAAGACTGG-1	M	414	903	16	three	537
GGCTTTCGTTCAAACC-1	M	157	846	23	three	337