

**Selective flexible packaging pathways of the segmented genome of Influenza A Virus**

Haralampiev et al.

**Supplementary Information**

1    **Supplementary Method**

2    ***Calculation of all possible combinations of vRNPs***

3    Considering all possible combinations of vRNPs, the random packaging model predicts  
4    that 98% of the MSCs would contain two or more copies of a distinct segment species.

5    This value follows from the equation:

6     $(1 - (\text{Combinations without repetitions}/\text{Combinations with repetitions})) * 100\% \quad (1)$

7    with

8    Combinations with repetition (up to k copies of a segment can occur in an MSC of rank  
9     $k; n$  – number of different segments ( $n = 8$ ))

10    
$$\frac{(n+k-1)!}{(n-1)!k!} = \binom{n+k-1}{k} = \binom{n+k-1}{n-1} = \binom{n}{k} \quad (2)$$

11    and

12    Combinations without repetition (only one copy per segment occur in an MSC of rank  
13     $k; n$  – number of different segments ( $n = 8$ ))

14    
$$\frac{n!}{(n-k)!k!} = \frac{n(n-1)(n-2)\dots(n-k+1)}{k!} = \binom{n}{n-k} = \binom{n}{k} \quad (3)$$

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16    **Supplementary Note 1**

17    ***Imaging of vmRNA***

18    To verify specificity of vRNA probes, we visualized all major vmRNAs (Fig. 1, vmRNA)  
19    except for M2 and NS2 (see Mat. and Meth.). Cytosolic vmRNA spots did not  
20    significantly colocalize with each other or with vRNAs. It is important to note that probes  
21    targeting vmRNA also recognize viral cRNA due to the high similarity of their  
22    sequences. vmRNA copy numbers have been reported to be about 100-fold higher  
23    than cRNA transcripts, which are almost exclusively localized to the nucleus<sup>1, 2</sup>, so the  
24    contribution of the latter RNA species to fluorescent spots was ignored. Our analysis  
25    of the intracellular localization of vmRNA species revealed differences in their  
26    distribution between the nucleus and cytosol (see Fig. 1). vmRNAs of PB2, PB1, PA  
27    and NA appeared to predominantly localize to the nucleus (Supplementary Figure 6),  
28    while the remaining vmRNAs were either rather equally distributed between the  
29    nucleus and cytoplasm (HA, NP, M1) or were largely found in the cytoplasm (NS1).  
30    While here we visualized vmRNAs for the sole purpose of demonstrating the specificity  
31    of our FISH probes, we observed a different distribution of vmRNAs between the

32 nucleus and cytoplasm than found in a previous study on A/PR/8/34-infected 293T  
33 cells<sup>3</sup>. Namely, the vmRNAs of PB2, HA, NP, M1 and NS1 were found predominantly  
34 localized in the cytosol. Further studies are needed to clarify the extent to which  
35 vmRNA distributions are dependent on the strain of IAV and/or target cell line used in  
36 a study.

37

38 **Supplementary Note 2**

39 ***Verification of vRNA spot binning***

40 For an assessment of the colocalization quality, we calculated the center of mass  
41 for each MSC according to (here shown for x coordinate):

42 
$$(\text{Center of Mass})_x = 1/N \sum_k x_k \quad (4)$$

43 The index  $k$  runs over all segments in the MSC.  $N$  is the number of segments in the  
44 MSC. The center of mass for y coordinates were calculated accordingly. Next, the  
45 distance of each spot towards the center could be calculated and plotted in a  
46 histogram (Supplementary Figure 12). Most segments showed a distribution with  
47 a marked peak relatively close to the center of mass (25-60 nm distance), with a  
48 shoulder towards higher distances up to 250 nm. All in all, even though one or more  
49 segments frequently showed signs of sub-optimal registration, distances were still  
50 within the cylinder volume that allowed colocalization to be detected.

51

52 **Supplementary Discussion**

53 ***Potential role of specific vRNPs in MSC assembly***

54 Although we observed this situation only for a few cells, very likely due to the high MOI  
55 used in our experiment, of particular interest for understanding the potential role of  
56 segments in MSC assembly are those cells in which one vRNP species is of low  
57 abundance in comparison to the other vRNPs. In principal, two situations are  
58 interesting. First, if any segment is 'less important' in the packaging of MSCs, and only  
59 becomes relevant in a late step of packaging, such as in the formation of rank 8 MSCs,  
60 we would anticipate a u-shaped MSC frequency distribution with a high occupancy of  
61 rank 7 complexes and a rather low occupancy of rank 8, due to the short supply of that  
62 specific segment. We observed such a u-shaped frequency distribution of MSC ranks  
63 for cells with a low fraction of segment 8 (Fig. 3d and h, 'Cell 29'). This suggests that  
64 at least for A/Panama, this segment is dispensable in the segment packaging pathway

65 and only relevant for the final step of formation of a complete set of segments, that is  
66 MSCs of rank 8.

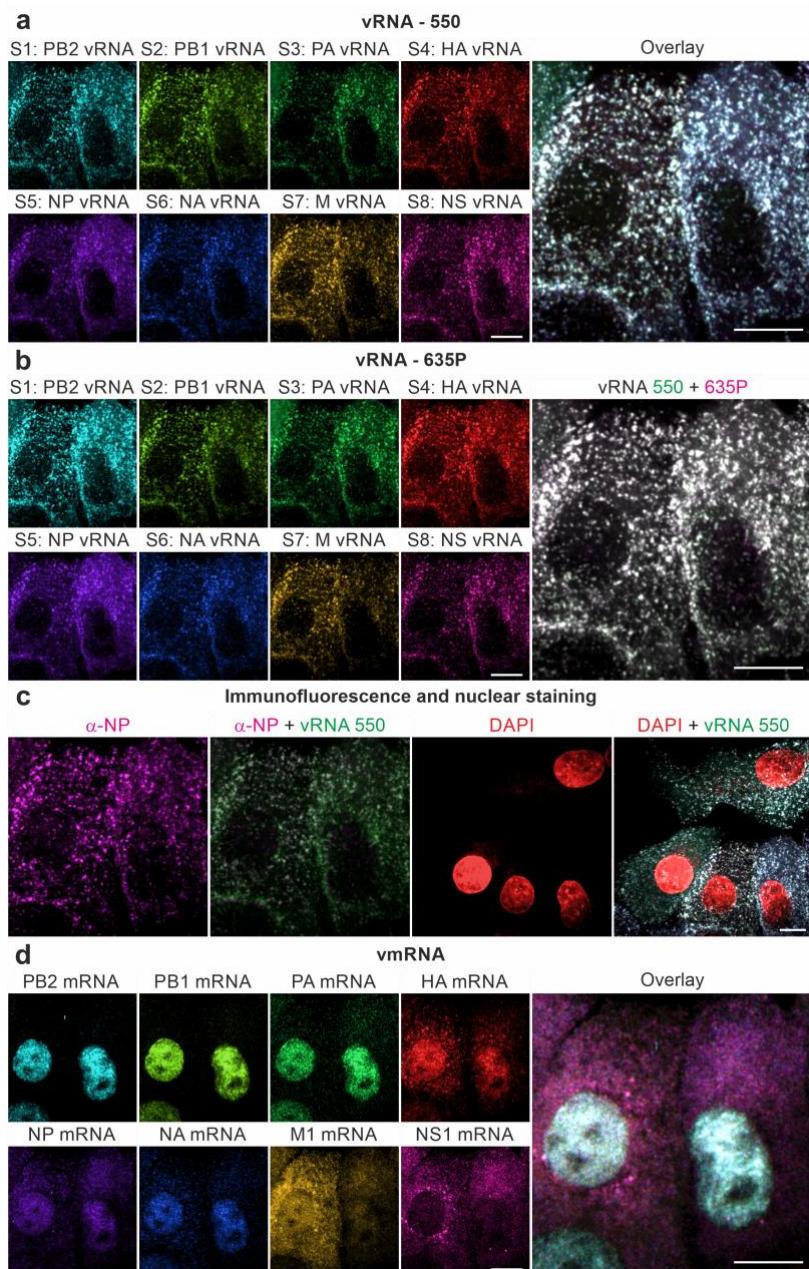
67 A second interesting situation concerns the case where a segment which plays an  
68 important role already in early steps of MSC assembly is of low abundance. In that  
69 case we should expect a left-hand distribution with a frequency maximum for low rank  
70 MSCs and a decreasing frequency towards high rank MSCs. We observed such cells  
71 even more rarely. In addition, these cells exhibited the low abundance of at least two  
72 segments, which does not permit a distinction regarding whether both or only one of  
73 the segments are important for early steps of MSC assembly. An exception is 'Cell 23'  
74 (Fig. 3c,g,k), which exhibited low quantities of both S1 and S8 (Fig. 3g). As S8 seems  
75 to play a decisive role only in the formation of MSCs (see above), the left-hand side  
76 MSC frequency distribution found for 'Cell 23' (Fig. 3c) points towards an important  
77 role of the long vRNP segment S1 in the early and/or intermediate phase of MSC  
78 formation. Of course, this conclusion must be taken with great caution as this is the  
79 only cell we could evaluate. Nevertheless, these examples illustrate that frequency  
80 distribution analysis is a very useful tool to uncover the role of vRNPs in MSC  
81 assembly.

82    **Supplementary References**

- 83    1. Kawakami E, et al. Strand-specific real-time RT-PCR for distinguishing  
84       influenza vRNA, cRNA, and mRNA. *J Virol Methods* **173**, 1-6 (2011).  
85    2. Shapiro GI, Gurney T, Jr., Krug RM. Influenza virus gene expression: control  
86       mechanisms at early and late times of infection and nuclear-cytoplasmic  
87       transport of virus-specific RNAs. *J Virol* **61**, 764-773 (1987).  
88    3. Read EK, Digard P. Individual influenza A virus mRNAs show differential  
89       dependence on cellular NXF1/TAP for their nuclear export. *J Gen Virol* **91**,  
90       1290-1301 (2010).

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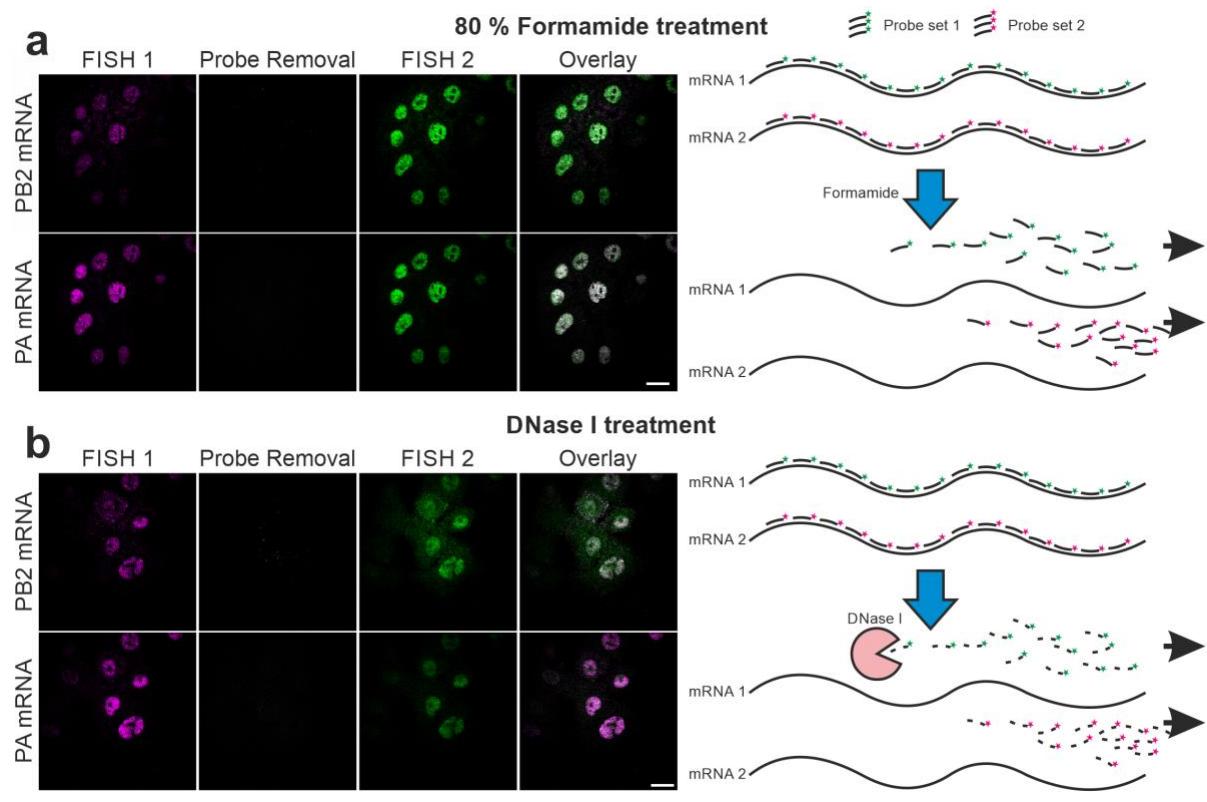
93 **Supplementary Figures**

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95 **Supplementary Figure 1: Localization of vRNA and vmRNA in A/Panama-infected**  
 96 **A549 cells identified by MuSeq-FISH.** (a, b) Viral genomic RNAs were stained by  
 97 FISH 10 h p.i. (MOI 5). To cover all vRNAs and major vmRNAs 12 cycles of FISH  
 98 labelling were performed. Along these cycles each vRNA was targeted twice, once with  
 99 with Atto550 (a) (see also Fig. 1) and once with STAR635P (635P) (b) labelled probe  
 100 sets (for details see text). (c) Immunofluorescence staining of NP. DAPI labelling was  
 101 performed to exclude nuclear vRNA spots for further colocalization analysis. (d) All  
 102 major unspliced vmRNAs were stained. Images represent max-z-projections. The  
 103 intensities of images were scaled according to corresponding images taken after probe  
 104 removal by formamide. Scale bars correspond to 10  $\mu$ m. Representative images of  
 105 four independent experiments are shown.

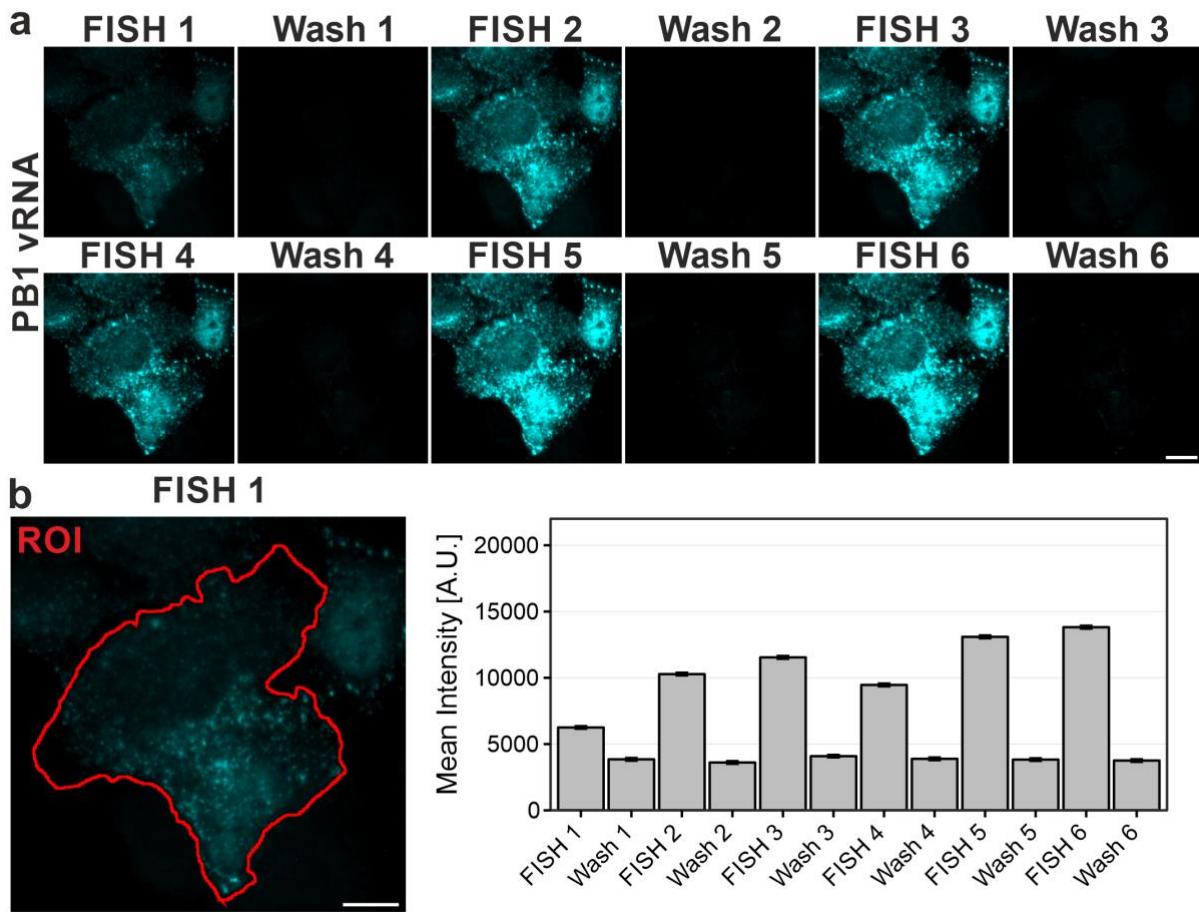
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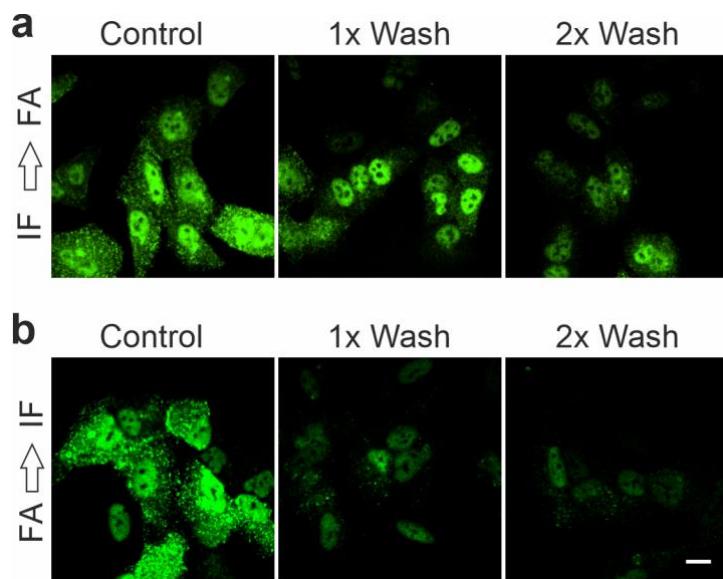


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**109 Supplementary Figure 2: Comparison of FISH probe removal by formamide and**  
**110 by DNase I probe digestion.** A549 cells were infected with A/Panama for 10 h, fixed  
 111 and stained by FISH targeting mRNAs of PB2 (Atto550-coupled probes) and PA  
 112 (STAR635P-coupled probes). DNA-Probes were removed either by washing with 80 %  
 113 formamide for 10 min at 37 °C (a) or by cleavage with DNase I for 3 h at 37 °C (b).  
 114 FISH 1 corresponds to the first staining cycle. After treatment with formamide, the  
 115 signal intensity of the following labelling cycle (FISH 2) was significantly increased  
 116 using the same probe sets and fluorophores as in the first FISH cycle. This was not  
 117 observed for probe removal by DNase I. Here, we found partially decreased signal  
 118 intensity for FISH 2 in comparison to FISH 1. Note, for improved visual distinction FISH  
 119 1 and FISH 2 are shown in different colours (magenta, green) although the same  
 120 fluorescent probe sets were used. Scale bars 10 µm. Experiment was performed once  
 121 as proof of principle.

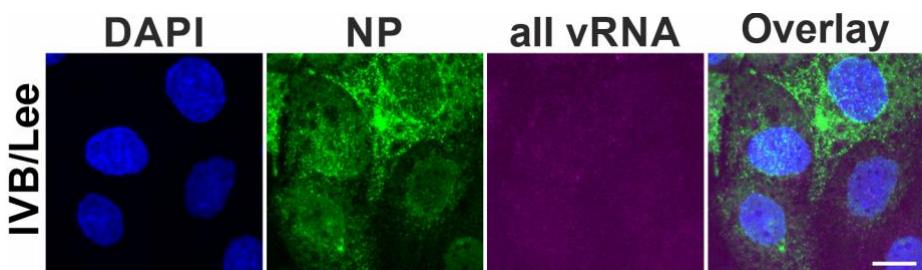


123 **Supplementary Figure 3: Mean fluorescence intensity of PB1 vRNA in six runs**  
124 **of MuSeq-FISH.** A549 cells were infected with A/Panama and fixated 10 h p.i. (a) FISH  
125 was performed to visualize PB1 vRNA using Atto550 probes in six sequential cycles.  
126 After each staining probes were removed by formamide washes. (b) A ROI was defined  
127 to measure the mean fluorescence intensity before and after removal of probes by  
128 ImageJ. The data documents successful PB1 vRNA staining and probe removal in  
129 each cycle. Moreover, formamide treatment enhanced FISH signal intensity of  
130 subsequent FISH staining - with the strongest increase after the first cycle. Specific  
131 FISH signal was significantly higher than the signal remaining after washing with  
132 formamide. For images, fluorescence intensity was scaled equally for all cycles  
133 according to that of images after formamide washing. Mean and s.e.m. of all pixels  
134 within the ROI are shown. Experiment was performed once as proof of principle. Scale  
135 bars correspond to 10 µm. Source data are provided as a Source Data file.



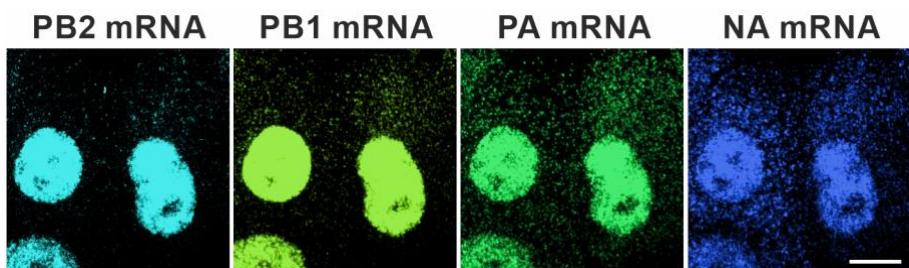
138 **Supplementary Figure 4: Influence of formamide (FA) treatment on**  
 139 **immunofluorescence (IF).** A549 cells were infected with A/Panama and fixated 10 h  
 140 p.i. IF for influenza NP was either conducted before (a: IF → FA) or after (b: FA → IF)  
 141 washing with 80% formamide. As a respective intensity scaling control, antibody  
 142 staining was conducted without formamide treatment. Irrespective of the particular  
 143 order, in general, any formamide wash decreased IF signal intensity significantly. But  
 144 the overall signal was still significantly higher when immunofluorescence was carried  
 145 out first (upper row) rather than after a formamide wash (lower row). For this reason,  
 146 immunofluorescence labelling is strongly recommended to be performed before the  
 147 MuSeq-FISH cycles. Scale bar corresponds to 10 µm. Images are from one experiment  
 148 as proof of principle.

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**Supplementary Figure 5: Detection of vRNA in IVB/Lee infected A549 cells.** Cells were stained by a mixture of all Atto550-coupled viral genomic RNA probe sets of A/Panama 10 h p.i. (MOI 5). Using the same conditions of image acquisition as for A/Panama, no signal of vRNA probes could be detected (see 'all vRNA'). NP was stained by immunofluorescence using first an unlabelled primary mouse antibody (MCA403, Bio-Rad, Hercules, Germany) targeting IVB NP and second an Alexa Fluor 488-labelled goat anti mouse antibody (ab150117, Abcam, Cambridge, UK) . DAPI was used as counterstaining for nuclei. Scale bar corresponds to 10  $\mu$ m. Images are from one experiment.

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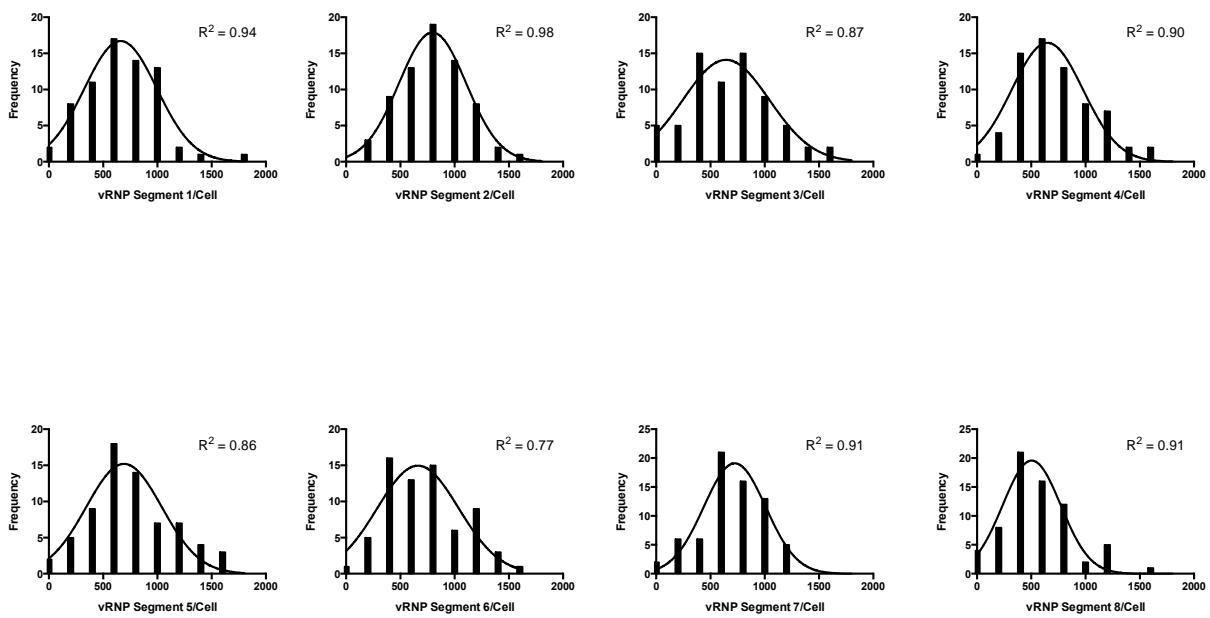


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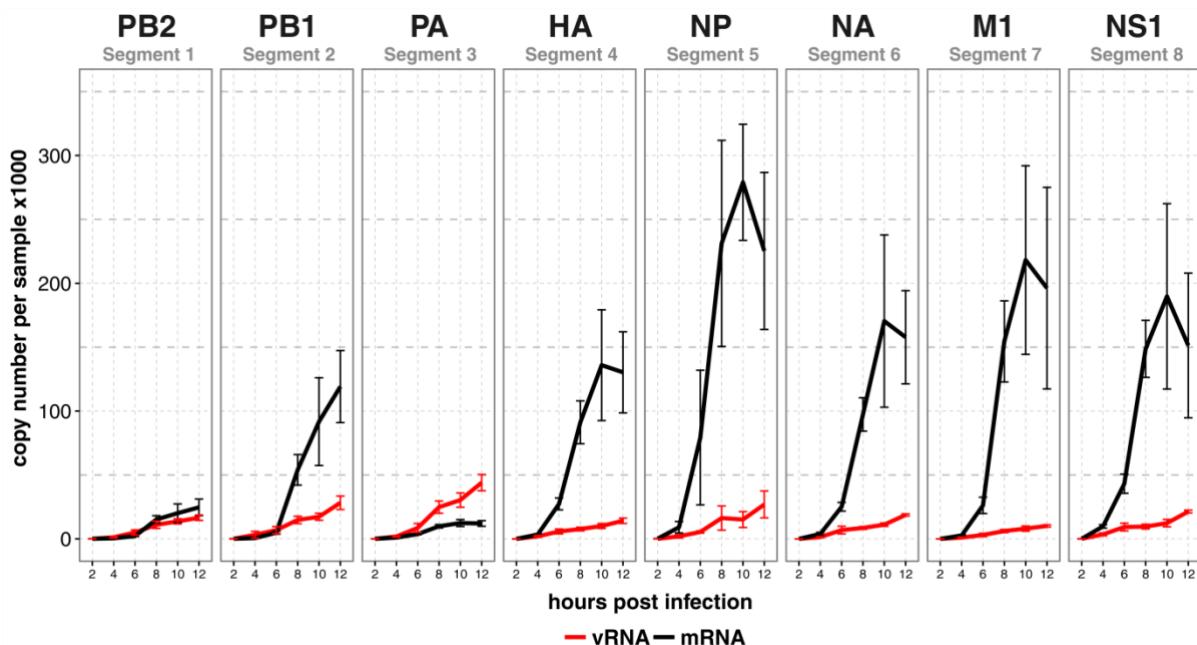
173 **Supplementary Figure 6: High nuclear density of polymerase and NA mRNA**  
174 **species.** Images correspond to mRNA data of Fig. 1. Signal intensity contrast was  
175 increased to demonstrate the occurrence of spot-like vmRNA signals in the cytosol.  
176 Scale bar corresponds to 10  $\mu\text{m}$ .

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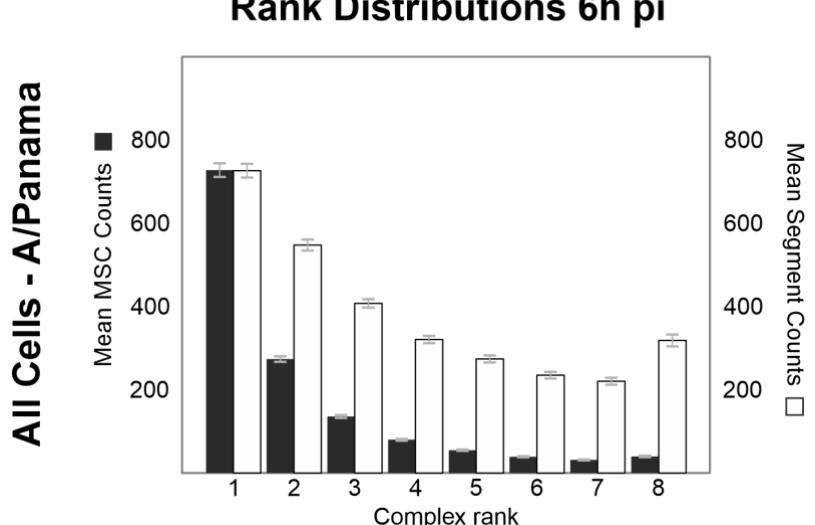


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179 **Supplementary Figure 7: Frequency distribution of the number of vRNP**  
 180 **segments per cell for all eight vRNP segments.** Data are taken from 69 cells (see  
 181 Fig. 2). Distributions were fitted by a Gaussian function (straight line) using PRISM  
 182 (version 6.0d, GRAPHPAD Software, Inc.). All fits passed normality test by D'Agostino-  
 183 Pearson with  $p=0.05$  (one-sided).  $R^2$  is the correlation coefficient. Source data are  
 184 provided as a Source Data file (see page Segment Distribution (data of Fig. 2)).



187 **Supplementary Figure 8: qRT-PCR measurements of vRNAs and vmRNAs in**  
188 **A/Panama-infected A549 cells.** A549 cells were infected with A/Panama at MOI of 5  
189 for 2, 4, 6, 8, 10, and 12 h. Afterwards, RNA was extracted with an RNeasy extraction  
190 Kit (Qiagen, Hilden, Germany). The extracted mRNA was specifically transcribed with  
191 an anchored poly-dT-primer (Life Technologies, Henningsdorf, Germany) and the  
192 vRNA with an UNI12-primer (AGCAAAAGCAGG) recognizing the highly conserved  
193 5'end of the viral segments into DNA by SuperScript IV polymerase (Life Technologies,  
194 Henningsdorf, Germany). Subsequently, remaining RNA molecules were cleaved by  
195 RNase H (Life Technologies, Henningsdorf, Germany) and qRT-PCR measurements  
196 were performed with SYBRgreen (KAPA Biosystems, Wilmington, MA, USA) and  
197 segment-specific primers. Three biological and three technical replicates were  
198 measured. The results show a strong increase over time for vmRNAs except for PB2  
199 and PA mRNAs. This increase of vmRNAs is stronger compared to the raise of vRNAs.  
200 At 10 h p.i. the maximum values for HA, NP, NA, M1 and NS1 mRNAs were reached.  
201 Note, mRNA for M2 and NS2 were not measured (see Material and Methods).  
202 Genomic vRNAs increased continuously without reaching a plateau phase within the  
203 time frame of the experiments. Time dependence of expression levels were similar for  
204 all vRNAs. Mean and s.e.m. of  $n=3$  independent experiments are shown. Source data  
205 are provided as a Source Data file.



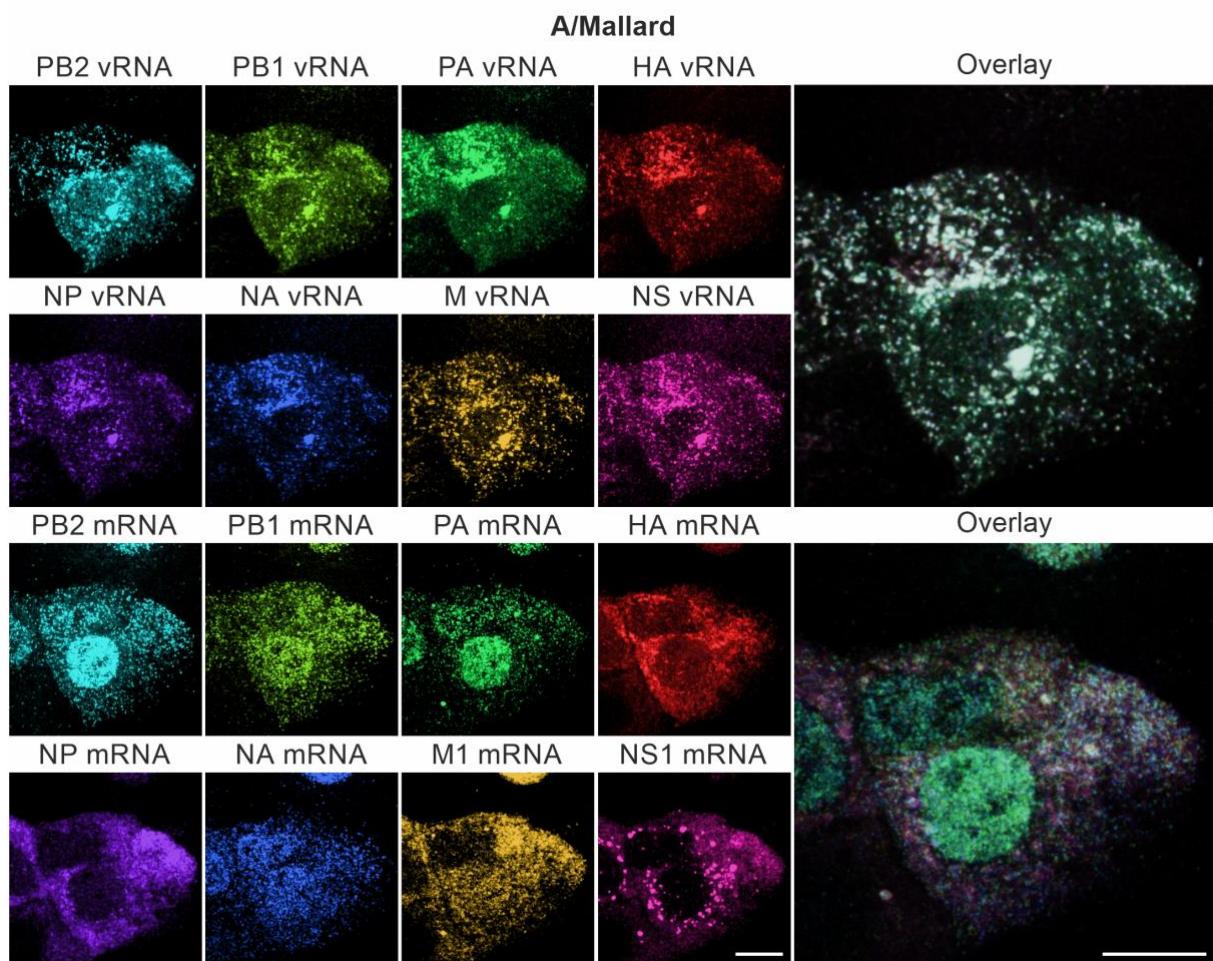
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209 **Supplementary Figure 9: Frequency distribution of MSC ranks after 6 h p.i. (MOI  
210 5).** A total of  $2.6 \times 10^5$  distinct segment spots were detected in  $n = 84$  A/Panama-infected  
211 A549 cells of three independent experiments and binned into  $2.1 \times 10^4$  MSCs. Mean  $\pm$   
212 s.e.m. are shown. Source data are provided as a Source Data file.

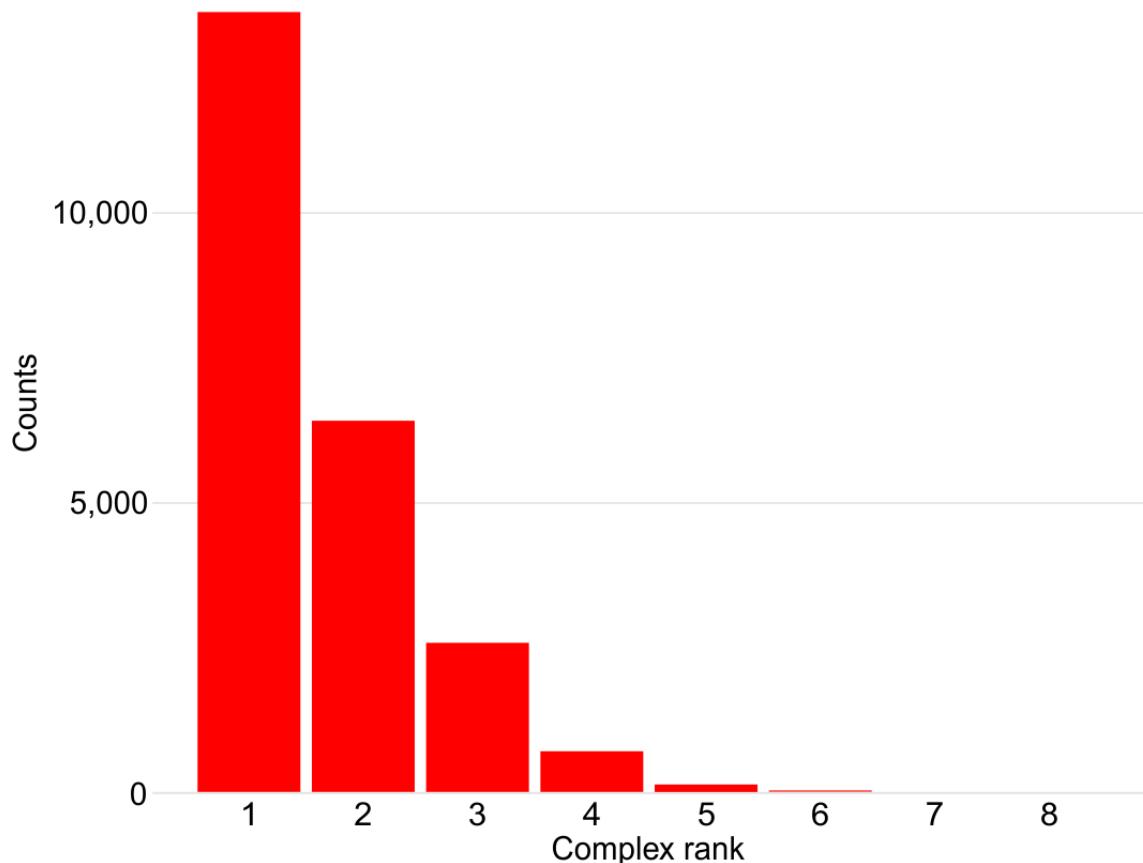
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217 **Supplementary Figure 10: Localization of vRNA and vmRNA in A/Mallard-**  
 218 **infected A549 cells identified by MuSeq-FISH.** Viral genomic RNAs were stained by  
 219 FISH 10 h p.i. (MOI 5). To cover all vRNAs and major vmRNAs, 12 cycles of FISH  
 220 labelling were performed. Along these cycles each vRNA was targeted twice, once with  
 221 Atto550 (shown here) and once with STAR635P (Supplementary Figure 1) labelled  
 222 probe sets (for details see text). High degree of colocalization was observed for all  
 223 vRNA segments (white colouring in vRNA overlay). IAV NP stained by  
 224 immunofluorescence displayed the same spot pattern as the vRNA spots. DAPI  
 225 labelling was performed to exclude nuclear vRNA spots for further colocalization  
 226 analysis. All major unspliced vmRNAs were stained. Images represent max-z-  
 227 projections. The intensities of images were scaled according to corresponding images  
 228 taken after probe removal by formamide. Scale bars correspond to 10  $\mu$ m.  
 229 Representative images of  $n = 3$  independent experiments are shown.

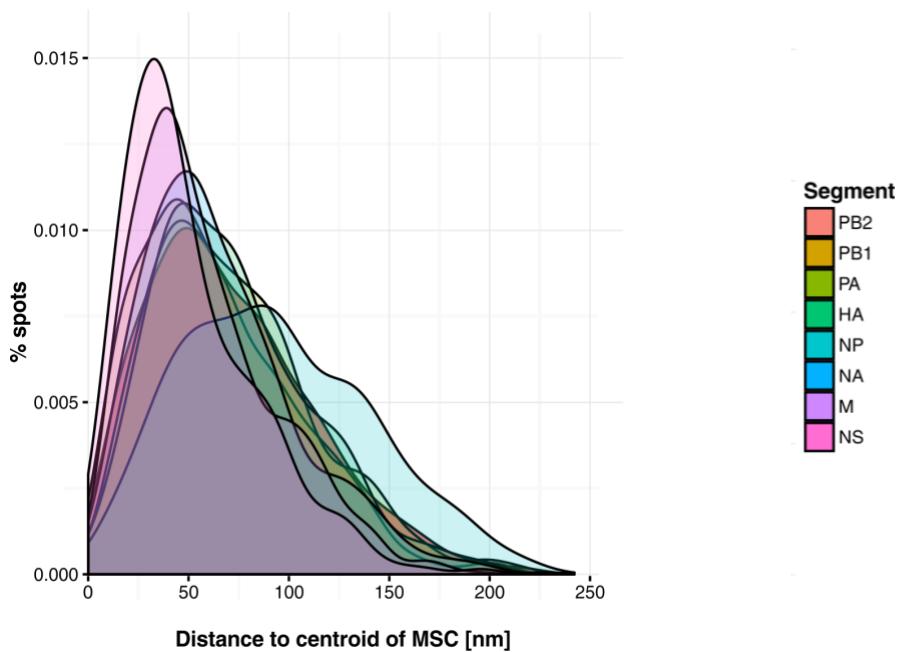
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232 **Supplementary Figure 11: Colocalization of the different A/Panama vmRNA**  
233 **species of a representative microscopy position.** All vmRNAs were analysed with  
234 the same settings for identification of colocalization that were applied to vRNA. Source  
235 data are provided as a Source Data file. A representative position from data of Fig. 1  
236 was used to analyze vmRNA colocalization.

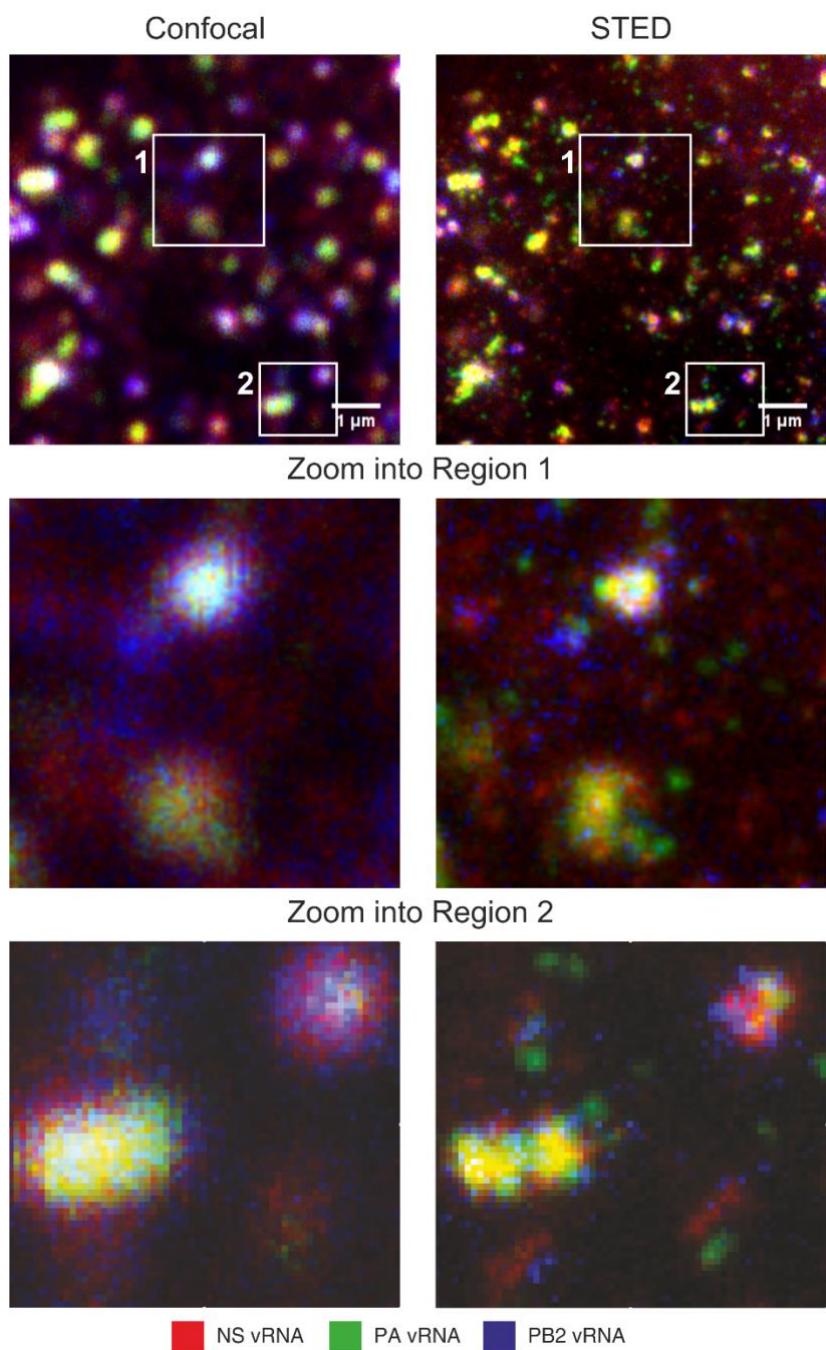
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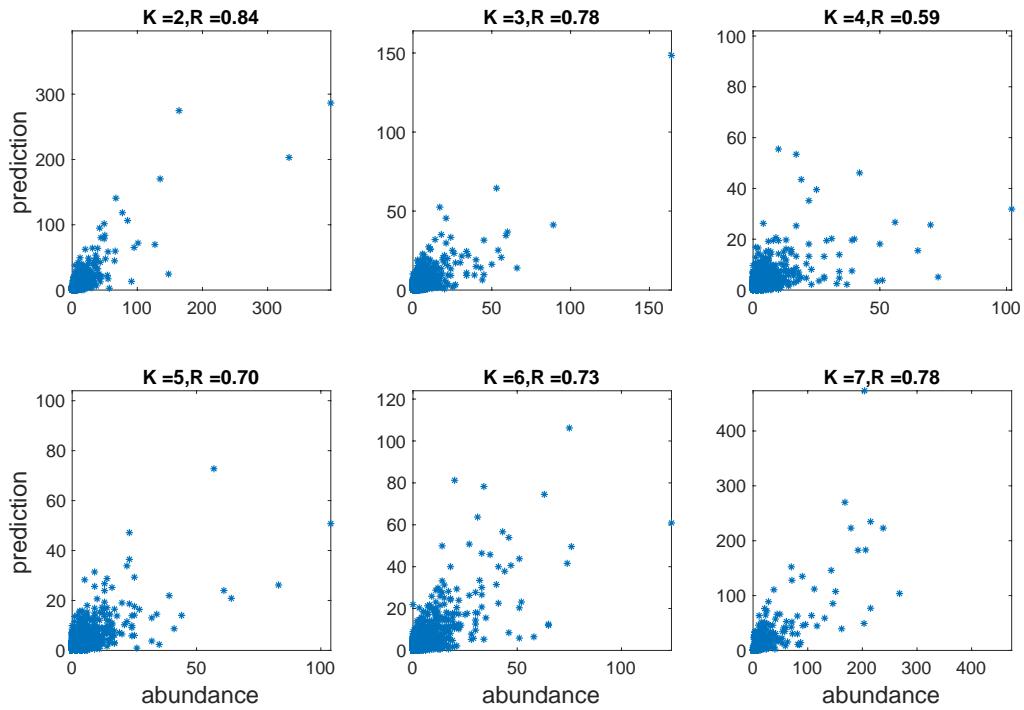
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240 **Supplementary Figure 12: Distance of vRNP spots to Center of Mass in MSCs.**  
 241 vRNA spots colocalising within a cylinder of radius 300 nm and height 1000 nm were  
 242 binned into one MSC. For MSCs, the Center of Mass (centroid) in x and y directions  
 243 were calculated. Then, distributions of distances of spots to centroids were  
 244 calculated for each segment. High distances indicate sub-optimal image  
 245 registration and a bias towards a shift of spots of this segment in comparison to  
 246 the other segments. Here, segment 5 (NP) showed the least optimal registration  
 247 as its distribution was shifted towards higher distances. However, all spots and  
 248 their peaks are well localized within the colocalization radius of 300 nm.



251 **Supplementary Figure 13: STED vs. confocal microscopy.** A549 cells were fixated  
 252 at 10 h p.i. and FISH staining was performed with three colours: NS vRNA (red,  
 253 STAR635P), PA vRNA (green, Atto594), PB2 vRNA (blue, Atto655). Images were  
 254 taken in confocal as well as in STED mode. Lateral resolutions were calculated to be  
 255 310 nm (confocal) and 79 nm (STED), respectively. Images show high degree of  
 256 colocalization for all three colours. Most of confocal single spots were also classified  
 257 as single spots by STED (Region 1). In a few cases multiple spots identified by STED  
 258 appear as a single spot in the confocal image (Region 2). Scale bars correspond to 1  
 259 μm. Representative images of  $n = 3$  independent experiments are shown (for details,  
 260 see Methods).



261

262 **Supplementary Figure 14: Predicted vs measured abundances for individual**  
 263 **MSC ranks 2 to 7.** Prediction is based on the mathematical model described in the  
 264 Method Mat. and Meth. section. The plot shows predicted vs. measured abundance of  
 265 an MSC of specific rank and specific composition. The Pearson correlation coefficient  
 266 (R) is shown for each plot. For an exemplary illustration see Supplementary Table 2.  
 267 Source data are provided as a Source Data file.

**Supplementary Table 1**

A/Panama PB2 vRNA	A/Panama PB1 vRNA	A/Panama PA vRNA	A/Panama HA vRNA
AACGGGACTCTAGCATCTT	CGAGCTGGACGGATTAAAGA	CAATCGCTTGGGTCACCT	TTGCTGGGTTCATCATGTG
TGTGCTAATGGCAAGGGAG	CGGATTGATGCCAGAATTGA	CTTGATCTTGGGGCTAT	CGAACGCATTAACAAACCGGT
CAGAAGATAACGGACCAGCAT	GGAGACGGTTGGAATTCT	TCTTAGGGACAACCTCGAAC	CTGCATAGGGTCAATCAGAA
AAAGCACATCCGGAGTGGAG	GTGCTGCAACTTGTGAGA	AAGGATTTCAGCGGAGTC	TGCTGAGGATATGGCAATG
CACTTAAATTGAAAGACCCAG	GCCATAAAGAGATTGAGTCT	GGCTAAGTCGGTGTCAATA	AGATCTCTGGTGTACACG
CAATTCTCGAAAAGATGCC	TGGATGAGGATTATCGGGGA	CCAAGGGAGTGGAAAGGT	CCAAATCAACGGGAAACTGA
TCAACTACAACAAGACCACT	ACATTCCCAGTCTGCTTA	ATAAACATCGAAGCATGGCCC	AAAGCACTCAAGCAGCAATC
CTTGGGACATTGATACACAC	CCCAATCAAAGGCAGGACTA	TTGTATGTGAGGACAAACGG	CACAGGACAAGCAGCAGATC
TCTCAGAACTCTGCAATGTT	CTAAAGAAGCTGTGGATCA	CCAAATTCAAGGCCTATGT	GTACGGTTTCAAGGCATCAA
GATTAACGGTCTGAGTCGG	TCAGACGAGAAGATCATTG	TAATGTGTCCTTGAGATAGG	TTGGGAGGGAATGGTGACG
ACACAGGGAACAGAGAGACT	AATGACCTGGACCAGCAAC	AGAGGGAGGCAGAAAACCA	TCGCGGGTTTCAAGAAAAT
TGGTTAGCATTGATCGGTTT	CAGTTTGAGTGTCTGGAA	CATTAATACTGCCTGCTCA	AACTAGAGGCATATTCCGCG
GTCAGCAAATGGGTGTGGA	GGATAGATTCTACAGGACCT	GACATAAGCGATTGAAAGCA	GATGCGGAATGTACCAAGAGA
GACAGTGTGATGGGAATGGT	TTTGCCCTCATAGTGAATG	AGTAGACTTGTACAATGCA	ACACTCTGAAATTGGCAACA
TGCACTCAGCTTAAAGGCAT	AGTACGGTTTAGGAGTCTC	TCAGAGTTGCAGGACATTGA	TGTCCCAGATATGTTAAGCA
TTTCGTCAACAGGGCAAACC	GCATCGACCTGAAGTATTC	ATTACCTGCTGTATGGAAG	AGATGCACCCATTGGCAAAT
GTTTCACAAGAGGATTGCA	GAGAATGAAGCTCCGAACAC	CAAACACACGAAAAGGGGA	CTCCTCGGGTTACTTCAA
AGCCGAAGCAATAATCGTGG	AAGGATACATGTCGAGAGT	CAAATTCTCCTGATGGATG	GTAAAACCGGGAGACATACT
AGATTGGTTCACTCATAGT	GCATCGCACCAATAATGTT	GAATGGACCTCCTGTTATC	CTCCAGCAGAATAAGCATCT
CCGACTGAAGAACAGCTGT	GGTTCGTGACTTCGTTGAA	AGGAACATATGCGCAGGCTTG	CCAACAAACTGTAATCCGA
GGTGGACATTCTAGGCAGA	AACACCCGGGATGCAAATT	TCAGTCCGAAAGAGGCCAG	GAGTACGGACAGTGACCAA
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GTCAGAGATACGCCAAGAGT	ACCTGAGGATAATGAGCCAA	CAACACTACTGGACCTGAGA	GGAAATGGGACCTTTGTTG
ATGGACCTGTGACAAGTACG	AATACAGAAACTGGGGCACC	GGCATGAGACAGTAGTAAACA	GAATATGCGACAGTCCTCAC
GCTGTGACATGGTGGAAATAG	CAGAAAAGGGGAAGTGGACG	TAGAGGGAGAGACAGAACAA	GTTCAGAGTTCTCAACAGG
CAGAAATGGTCCGGAGAGA	TTTCCTAAAGGTTCCAGCG	CAAGGCGAATCAATAGTGGT	TTTCGCTCAAAACTTCCCG
A/Panama NP vRNA	A/Panama NA vRNA	A/Panama M vRNA	A/Panama NS vRNA
GAAGGCACCGAACCCGATCG	ATTGTTGTGTTTGTCGGCAC	GAGTACCTGAGTCTATGAGG	TTCATGCAAGCATTACAGCT
GAGTTTCGAGCTCTCAGAC	AAGTCTGGTGGACCTCAAAC	GAAAAGAGGGCCTCTACGG	AATGGCGAGAACAGCTAGGT
TCACTGGAAATACGGAGGG	GTGCTTTATGTTGGAGTTGA	ATCGACTCTTCAAACACGGC	TCCACTTACTCCAAAACAGA
CCAAATCAGTGTGCAACCTA	GAAAGAGGTAATATGTCGGG	CTTGCACTTGATATTGTTGA	TCTACAGAGATTGCTGTTGGA
TACTAATCAACAGAGGGCCT	GCAGATAAATAGGCAAGTC	TGTTGCTGCGAGTATCATTG	ACACAGTTGAGTCTCTAAA
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GTTAAGCTTCATCAGAGGG	TGGGCTTGTATGATGGAAA	AACCGTTGGACTCATCCTA	AGGGAGCAGTTGTTGGC
TCAGACCGAACGAGAACCA	AGGGGGTATGGAGTGAAG	AGGCAAATGGTCAGGCAAT	TTACTAAGGGCTTCACCGA
AATAGCCAAGTATACAGCCT	GCCTGGATCTAACATGAA	CATGGAGATTGCTAGTCAGG	TGGCGACTAGAGACCATAG
TGTGTATGGACCTGAGTAT	TATGTTGCTCAGGACTGT	CACTACAGCTAAGGCTATGG	CGAATTTCAGTGTGATCTT
CACAAATCTGCTACCTGC	GGATTATAGCATTGTTCCA	GTCTCATAGGCAAATGGTGG	TCAGAATGGACCAGGAATC
TGAGAGAAAGTCGGAACCCA	CTCCTGTTATCCTGATATC	CTGGTATGTGCAACATGTGA	AACTGGTTATGCTAATGCC
GCACAAAGAGCAATGGTGG	CGTTCATACTAGCAAATTGT	TAACCACCGAAGTGGCATT	CTGCTTCGCGATACTAACT
GGCCGGAAAACAAGAAGTGC	ACTTTTATTGAGGAGGGGA	GGGCCTCATATACAATAGGA	TAAAATGACCATGGCCTCCA
CGAAATTCTGGAGAGGTGA	TCGGAATGCGTTGTATCAA	ATTTGGGGTTTGTTAC	AAACACTCTGGTCTAGACAT
TCAGAATGGTCAAACGGGG	ATAGTATTGGTCTATGGTC	CTTGAGGCTCTCATGGAATG	CGAGATCAGAGGTCCCTAAG
GAATGTGCTCTGATGCA	ATTACGATGGGAGACTGT	AAAGCCGAAATCGCCAGAG	AACTGAGTGTGATGCCCATTC
CGACAGCTGGTTAACTCAC	TGAAAATGCAACTGCTAGCT	CGTATGTTCTCTATCGTT	TCCGGAAGCAAGTTGAGAC
CCCATATACAGGAGAGTAGA	CACGATGGAAAAGCATGGCT	AAGATGAGCCTCTAACCGA	GGATTCCAACACTGTGTC
GATATCTGGAAAGAACCCCC	TAGCATGGTCCAGCTCAAGT		AGCAGGGTGACAAAGACATA
AGAAAATGGTCTCTCGCT	CTTATCGAACCCATTGATG		
TGATCCAAAACAGCTTGACA	TGGACAGGGAAACAACACTAA		
CTCAGTGTGCACTGAACCTA	ACAAGTGTATCAATTG		
CCAAATGTGCACTGAACCTA	AACCTTATGTGTCATGCGAT		
GCCAGAATGCAACTGAGATT	AGGATTGACCTTCTATG		
AGGCACCAACGGCTTATG	ACAACCAAGTAATGCTGT		
ACATCAAATCATGGCGTCC	CTACTGTAACATTGCAATT		
GCAGGGTTAATAATCACTCA	CTTATGCAAATAGCCATCCT		

A/Panama PB2 mRNA	A/Panama PB1 mRNA	A/Panama PA mRNA	A/Panama HA mRNA
ATTCTCTCCCGAACCATTT	TGTGTTCTGTTGACTGTGTC	GATCATCAAGTCTACCACT	GTGATTGTTTCACTAGCGT
CTCCATAGAGTTGTCCTTG	CAGTTCTGATTTGTCGTC	TACTACTGTCATGCCATTG	CGCATATTCTACCTGTTGAG
TGGACCGTACTTGTACAGG	TGGGATTCTCAAGGAAGGC	TCCAGTAGTGTGAGATAC	TCAAGGATTGGTGGAGGACT
ATGAACAGGGCAAAGGTTC	GGCATGAGCTCTAAAGATC	GTCACTCCAATTTCGATGAA	TCCTTATTGGAAAGCCATC
GGCGTATCTTGTACTGATT	TGTTTGTGAAACGACTTCCA	TAGCCTGGTCTTAATCCTAG	CGCTTCAACAAAAAGGTC
TGTATGCAACCATAAGGG	CTTAGAGTTAGTTGTCACC	GTTCGAATCCATCCACATAG	AACAGTTGCTGTAGGCTTG
TCGGACAAGTCTCTCTCA	GTCCAATCATAGTCTGGCG	AAGGAGGTCCATTGGAGT	TAATCCGGCACATCATAAGG
GCAACTGGGAGAAATTTGT	TGCCGGTTGATTCTGTTA	AGGAATTGGACCGCTGATA	ATGAGGCAACTAGTGAACCA
TCAACATCGTCTTCTCAC	TAATTGTCATCCCCGGTGT	GATCGCATCATATACTGGGA	TTGTTAAACTCCAGTGTGCC
GGCTGCAATAATTAGGCTT	TCAACGAAGTACAGAACCC	CTTGGGAATCTCTCCTCATT	AGAGCTTGTCCATTCTGAG
CGGCTCTTCTACTATGTT	TTTGGCCTTCTTCATTAC	AGAGCCCACTTAGTGTACT	TTTCATTGGTCAGTGTCCGTA
ACAGCTGTTCTCAGTCGG	TCTTCTCACAAACATTGCC	TGCACTGTCAAAGTCTACT	TGAGGCAACTAGTGAACCA
CTCTCTTGTACTGATGACC	GCTCTGTCTTGTGAATTA	TGCTCAAATCGCTATGTC	CCTGATGCTTGTGAGCATATAT
TGTTTGGAGATTGCTGTAA	TCCCCAGTGTGAAAGA	TTCAAGGTTGTCACTATCAT	TCGGGATTACAGTTGTGG
ACCATTGTGAACCTCTATA	TCATCGCCAAGAACATTGA	GCTCTATCCAGATTGAATCA	CCGGTTTACTATTGTCCA
TATGAGCTGAACCAATCTCC	ATTATTGGTGCATGCTCAG	GACACCTCTGCTGTGAATA	TAACCCCGAGGAGCAATTAG
TATTGACTGTTCGTCCCTC	TCGAACATGTATCCTTCC	GTACTCAGTGGCTCTACAA	GCATCTGACCTCATTATTGA
GTCACCTCTAAGTCTTTA	TTCGGAGCTTCATTCTCTTA	GTTGAAAATCGTCATTGCT	TGTTGCAATTTCAGAGTGT
CACTTCGCATCTTCTGAA	TAGCATTCTGCGGGTATT	AAATTGGTTTCGCGCTTCC	TCTCTGGTACATTCCGCATC
GTCATATCTGGAATACTCC	AATACTCAGGTCATGCTT	CTTCCTTTATGATGAATCC	CCGAATATGCCTCTAGTTG
CATTGACATCTGTGCTTG	GAGACTCTAAACCGTACT	CCTATCTCAAGGACACAGTA	CATTTTCTATGAAACCCGCG
CGATCAATGCTAACACCAC	GACTCTTTGCTCATGTT	CATAGGCCCTGAAATTGGC	CTGAAACCGTACCAACCGTC
GTTAATCTCCACATCATTG	CCACAAATCCATAGCGATAA	CGTTGTCCTCACATACAAG	TGTGCCCTCAGAATTGAT
TGACCAAAACCGACTCAGGA	TCATTATTCCAGACACTCC	TCTCTATCTGCTGGAGTGC	ATTGGTTGATTGCTGCTTG
GGATTCTGAGACCATTGGAT	GGTCCAAGGTCATTGTTAT	GAGGACTCGGCTTCAATCAT	GGAATTCTCGTTCGTTTC
AGTGGTCTTGTGTAGTTGA	TCTGATAACCATAGTCTGC	ACAGGCTATTGAACACCGAC	ATTTCCTGAGGTCTGAATT
AATCCTCTCAAGACAGCGGA	GTTGATAAGTTGGTCCTC	CCTTCTAATTGTGGAGATGC	GATCTATTTAGTGTCTCA
AGGTTACTCAGTTCATTGAT	GCAGACTTCGGGAATGTGAA	TTTCTGACTCCGCTGAAA	TCAGCATTTCCTCAGTTG
TTGCCCAATTAGCACATTAG	AGACTCAATCTCTTATGCC	GAGCCTGAACAACAAGGAGC	AGTCCATTCTGATTGACC
TTCTGTTCTTACCAACACC	TTCTGGTACATGTGTCATC	AAGATCAAAGGCCAGGTT	TCAGCTCAACACCTTGTAC
A/Panama NP mRNA	A/Panama NA mRNA	A/Panama M mRNA	A/Panama NS mRNA
TCAGTTCCATCTGTCATA	ATGTTACAGTACTTACAGG	AAGTCTCTGCGCGATTTCGG	TCTTGGTCTACAACCTGCTT
CCTAATCTCAGTTCGATTCT	GTTGATTCTATGCTGTA	TTTCCCAGCAAAGACATCT	GAAGCCGATCAAGGAATGGG
CATCAATCATCTCCCGACG	CTATTATTGTTGGTCACAC	ATGAGAGCCTCAAGATCTGT	CTTAGGGACCTCTGATCTCG
TGGATGTAGAATGCCAAAT	TATGGTGGTGTGGTCAGAT	CCTTAGTCAGAGGTGACAGG	TGATGTCTAGACCGAGAGT
CTGAGTTAAAGTTCAGTGC	CAGCGGAAAGCCGAATTGAA	GGCTGAACACAAACCCAAA	CTTCCCTCAGAATCTTTCT
AAGCTTTGGATCAACCG	TCAGGATCGCATGACACATA	CTCCCTTAAAGTTTCTAT	GTCATTAAAGTGCCTCATC
TGGGGTGTCTCCAGATAT	AATGCCCTGTTAGTGT	AAATGCCACTTCGGGGTTA	TATCGCGAAGCAGGTGTGGA
ATCTACTCTCTGTATATGG	CATTCAATAGGTTGCGA	TCACATGTTGCACATACCG	CCTCAATAGTCATGTCAGTT
TAAGGACGAGTCCCTCAT	CCAAATGAAATGGAACACC	CACCATTTGCATGAGACC	ATGAACCAGTTCTTGACAA
TGAGTTAAACAGCTGTCG	TGCTATACACACTGCTTG	TAATGGATTGGTTGGCCA	CACTTTTGCTTGGGATTA
CGGTTGAACAAAGAGCTTT	ATCGTGACAACCTGAGCTGG	AGCTGTAGTGTGGCCAAA	ATACTATGGTCTAGTCGG
CCTCTCCAGAAATTTCGATC	CGTAAATGAAGCTAGCAGTT	CTGACTAGCAATCTCCATGG	TCTTCGGTGAAAGCCCTAG
TAAGCACTCTGTTTCCG	ATACTATCTACAAGTCTCCC	TAGGATGAGTCCCAACGGTT	GTGAGATTTCGCCAACAACT
CGACTTCTCTCACTTGATC	CTGAGGATTTTTGGACCA	TCATCTCTAGACCACTACT	
GATCTCGATCTCAGCATTT	CAAACGCATTCCGACTCCTG	CATTGTTCTGATAGGTCT	
TATTAATGCAGATCTGCCA	TACTGTACAAGTCCATTGA		
AGATTGTGAGCAACTGACC	TGAGCACTTCCCTGACAATT		
CATACACACAGGCAGGTAGG	ATAACAGGAGCACTCCTCGA		
TTCCGTCTGATTAGGCTGA	ATCTGACACCAGGATATCGA		
TCCCTCTGATGAAGCTTAA	TTATATCTACGATGGGCTA		
CGCTTCTCAGTCAAGAGTA	AAACAGTCCCTGAGCACACAT		
AACGTAGGTTGACACTGAT	AATGGCTACTGCTGGAGCTG		
CCATGACAGTGTGACTTTCA	CTTCTTCTGTTAGGATCC		
CTCCGTATTCCAGTGAATG	TTTGGAGTTAGGTTGGACC		
TCTCGTCTGAGAGCTCGAA	TGACTTGCCTATTATCTGC		
AAAAGAGGGCACGATCGGGT	CGGACATATTACCTCTTCA		
AATTGTCGTACTCTTGCA	ACTCACATAAAAGCACCAGA		
	AATACTGTTGAGGTCCACC		
	CTGAGGTGCCACAAACACA		
	CATGAGCCTGTTCCATATGT		

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A/Mallard PB2 vRNA	A/Mallard PB1 vRNA	A/Mallard PA vRNA	A/Mallard HA vRNA
GTGTTGATAGGGCAAGGAGA	ACAGAACGCCAGTTGAAATT	GGGGTTTTCAGCTGAATCAA	CGTCCTATTACGAATTCCAG
TGCGAAAGGGGAGAAGGCTA	TACAGATGCCACAGAGGTGA	CCCTCAACAAATTGAGAGC	TAGGAACGGGACTTATGACC
GAGTGGAATCTCGGGTATT	GCTCTTCAGCTATTCAAA	AAATGAGGGCATGCCTTCTT	GTCTTATAATGCGGAACCTCC
AAGATGCAGGTGCTTGACA	CTGGGATTAACGAATCGGCT	CTCCTACGGACTGCAATAGG	GGAGGATTCAAGAACCTTGAG
CAACCAAGAGGCTCACAGTC	GGATTGAGGCAACTTCAG	GTGTTCTCGAGATAGGAGAC	TATGTGAAGCAGAACACCCCT
GGGGTTCAGGAATGAGGATA	TGGTGGGATCAATATGAGC	CGGAAGACTAATCTGTATGG	GATCACATACGGAGCATGTC
TCTTCTGACTGTGAACT	ATGAGAATCAGAATCCTCGG	GGAGTGTACATAAACACAGC	CACCTATTGACACCTGTATT
CACCGGAACAGAGTAGGATG	CCGTGGAGGGAAATGAGAAA	TTGCAGGGCTACTGAATAAC	GGACGTACTGGTATGAAATA
ATAAAGCTCTTACATTGCA	ATTAGCGAGGACATCTGTG	ATTTCACAGCGGAAGTATCC	GCAGACTATAATCCCTAACAA
AGGCCAGTATAGTGGATTG	AAAGTGAAGAGGGGGCAAT	GCACATTGCGAGTATGAGAA	ATGTTCAAGCCTCAGGAAGA
AAGATGGAGTTGAGCCCTT	CATTGAATAGGAACCAGCCG	GGGAAGACATTGCTCCAATT	TATACATCTGGGAGTTCAC
CTGTGAAGATTCACTGGTCC	GGATAAACTGACCCAAGGTC	AGTTGGATTGAGCTGATGA	GTTTCACTGGGAGGAGTG
AAATGGTCGGAATCAGTGC	ACCATTGCGTGGAGGATAACG	GGCATGTGAATTGACAGATT	ACATTGGAGTTCATCACTGA
CATCGTCTATGATGTGGGAG	AGCATGGATATGATGCTGT	CTGGATCCAGAGTGAATTCA	TACCAGACTATGCATCCCTT
GGGAACAGAGAACGCTGACGA	GTCAAAGGCAGGACTGTTG	CAGACTCTAGATCGTAGCA	GACCATTACAGATGATCAGA
CAGAGGGGAAACGTGCTCTT	AAGAACGCTGTGGAGCAGAC	AGACAGTATGACAGTGTGATGA	CAGTGCCTAATGGGACAATA
ACTGAGAGAGTGGTCGTGAG	AACGATCTTGGACCAGCAAC	GGACTGCAAAGATGTTAGCG	CCTTTAGGGAGCGACAATA
GAGGAGTGAGAGTCAGTAAA	CCCCGATAATGTTCTAACAC	AGGGCATAAACCCCCAATTAC	GACCATTATCGCTTAAGCT
GATCGGAATATTGCTGACA	ACCAACCTGAATGGTTAGA	GAAGACATTTCGCGCTGGA	AGAATTGCCCTTAAGTTGG
GACAAGCAGCGTGTATATCG	ACTGGGAGACAACACCAAGT	GTATACCGCTATATGATGCA	CTGAAGACATGGCAATGGT
GAGCATCAACGAATTGAGCA	GGTCTGTACTTTGTCGAA	TGCTCTCAACGGTCAAGTT	AGACCAGAAGGCAACTGAGG
GATGTGTTGGGACATTGAA	GAGCACTGACACTGAACACA	CTCTCAAGCTACCTGATGGG	AAGGAATTCTCGAGGTAGA
AGACCCCTACAATGTTATACA	TCTTCAGATCGAACGGTCTA	CCATTCTGAAGACAAACACC	ACCTTAAAGACACTCAGGCA
CCCAGTACAGAGATGTCACT	TGCTTGGCCAACACTATAG	AGAAGTGAACGCCGAATTG	ACAGTCTTACCAAGGAGAAAG
AGACGAGCAGTCAATCGCTG	CCGAGCGGATATGCACAAAC	TGAGGGCAAGCTTCTCAA	CCAGTGTGAACTGACTAT
GTGTTGCATTGACTCAAGG	ACAAACACCGAGACTGGAGC	GTGGATGGATTGCAACCGAA	AGGTGACTAATGCTACCGAG
CGGGACTCTAGCATACTTAC	CTCAGAGAAAGGGAAGTGG	GCCTTAAAACCTTAGAGCC	TTTGCTGGGGTCATTATG
CCCTGTGTTCAACTATAACA	CAGCCATGGAACAGGAACAG	AAAGTCTCCACCGAACCTC	ATATGCAACAATCCTCACAG
AGAACGCTATTCAGCAGAT	ACTACATTCCCTTACTGG	AAATCACAGGAACCATGCGC	GGAGCAAAGCAGGGATAT
CTCCTGAAGAGGTTAGTGA	AAAGTGCCAGCGAAATGCA	CGAGAGAGGCGAAGAGACAA	
A/Mallard NP vRNA	A/Mallard NA vRNA	A/Mallard M vRNA	A/Mallard NS vRNA
GGATGATGGAAAGTGCAGA	GTATCGTCGTATTTGTTG	TGTCAACATAGAGCTGGAGT	AGAACTTTCTCGTTTCACT
GCAGAACATCTGACATGAGG	TAAGAGGAAGGCCACAGGAG	TGGATGTTGACGATGGTCAT	CTATTGCTGAAAGTAGAGCA
GCATTACAGGGAACTGTA	CCATGGCTATTCCAATCA	TATCGGCAGGAACAGCAGAG	TACGTTTATGCAAGCCTTAC
CGAAAGGGCACCATTATGG	TTCAAGGTCTATTGTTG	GCCTGAGTCTATGGGGAAAG	ACAGAGAACAGCTCGAACAA
CAGTACAGAGAAATCTTCCC	GCCTTGACTATGGAGATGA	AAAGAGGGCCTCTACGGAA	ATGGCTGATTGAAGAGGGTC
AGAGCATCTGCAAGGACAAAT	TGATAGCTCTAGAACAGCA	CGTCGCCTTAAATACGGTT	TGGCGAGAACAAATTGAGTC
TGGAGGAAACACCAACCAGC	GTATGGCAGACTATAGCATT	TTGTGGATTCTTGTACGCT	CCTCCAAGCAGAACGGAA
ATTGGGCTATAAGAACCAAGG	ATCCAGACGTTAGATGTGTT	AGTATCATTGGGATCTGCA	GTAAATGAGGATGGGAGACCT
AACTATCCACCAAGAGGAGTC	TTGTTCATGTCAGCCATTG	GGATGGGAGTGCAAATGCA	TCTACAGAGATTGCTTGG
GACAAGAGTGGTCCAAAGAG	ACTATTCTAGAGAGGGGA	TGAAAATTGCAAGGCCATT	AAACACAGTTGAGCTCTGA
GAGTATCAAGTTTCATCAGA	CTCAGAACTCAGGAATCAGA	TGCCGGTCTGAAGATGATC	AAAATGCAATTGGGTCCTC
CATTCTGCAGCGTTGAAGA	TATGATGGGATGCTTGTG	CAATTGAACTCACCTAGC	TCCAGGACATACTGATGAGG
GAGCCAATTGGTATGGATGG	ACGAATTAGGCGTTCCATT	CAGATGGTCAGGGCATGAG	AAATCTCACCGTTACCTTCT
AAAACAGCCAGGTCTCAGT	TCCTCATCGAACTCTTGT	CATGGAGGTTGCTAGTCAGG	GAAGAAGGAGCAATTGGGG
ATAGATCCTTCTGCTTCT	CACTGAATGGCACAATACA	TACCAACCAACCCACTAATT	CCCTAATACTACTTAGAGCT
AGAAGGATACTCTGGTCG	AGGAACCACGCTGGATAAC	GATTGCTGATTACAGCATC	TCAGTGTGATTGGACCGGG
GCCAGTGGATATGACTTGA	GCCCCGATAAAATGTTATCA	GAACGGTGCACACAGAAAGT	CTTTCATCAGAACATGGACCA
GAGGATCAGTGGCCATAAG	GTTTGCCAAAATGGTAGA	AGAAGTGGCTTGGCCTAG	GTCAAAATGCAATTGGGGT
AATCCTGGGAATGCTGAAAT	TGCCATGTGAAACCAATCATA	AAACAGGATGGGAACGGTGAC	ATCAGAATGGACCAAGGCAAT
GGATCAAGTACGAGAAAGCA	AAAATGAGTGCAATACCCCC	ACAGGGCAGTCAAACGTAC	ATGTCAAGGGACTGGTCAT
TCGGATGATAAGCGAGGG	TTGCAACAGTATGTTCTC	TGGGAATGGAGACCCAAACA	GCTACCTAACTGACATGACT
CGGGACGATGGTATGGAAC	TAGAGTATGGTGGACCTCA	TTAGGATTGTTGTCACGCT	AATGACTATTGCTTCACTG
CTCTGATGCAAGGATCAACC	GGGATCTTAAATGAGAGA	CTGTCACCTCTGACTAAGGG	GGAAAGATCTGATGAGGCAC
ACTGGTATGGACCCAAGAAT	GAATGTTCTGTTATCCTCG	CTCATGGAATGGCTAAAGAC	GCAAATAGTGGAGCGGATT
CAACCTGAATGATGCCACAT	TGTCAGATTACAGGGTTGC	GAAGAACACCGATCTCGAGG	GACATCGAGACAGCTACTCG
GTCTCACTCATCTGATGATC	CAGGAATTGGTCAAACACCGC	GACTTGAGATGTCCTTGCA	AAGAGGTAGCACTTGGTC
GCGAACACGGAGAAGACGC	TTGTTGGTACACACCAAGA	GAGGTGCAAACCGTACGTTCT	CGTGATCAGAACGTCCTAAG
GAGATCAGGAAGATCTGGCG	AGGAAGTGGCCACATATAG	GATGGAAAGGCGATGGCTACA	ATTCCAACACTGTCAGCAGC
GGATGAGGGAGTTGATTCTG	GTATTGGTTCATGGTCTAA		
ATCTACCGAAGGAGAGACGG	GATGGAAAGGCGATGGCTACA		

A/Mallard PB2 mRNA	A/Mallard PB1 mRNA	A/Mallard PA mRNA	A/Mallard HA mRNA
AGGTTTTGTAGACCTTGGAA	TGTTCCATGGCTATGGAG	GTCGTTTCGATTTCGGAT	TGAACTAGCTCGGTAGCATT
GTTTTAATCTTCGACCTTT	GATGTGTTCTATTGACTGTG	TAAGTGTGTGCATATCGCGG	GCATATTTCCCTGTTGAAG
AAGTGAACGGGACCGAAGGT	CACTCCCTTCTGAGTA	CCGAATACATGAAACAGACC	CTTCCATCAAGAACCTGTG
CGGCATTTAACCTGATT	TCCAGTCTCGGTGTTGTTG	CCCCGTTCATCAATAAAGTG	GTAGGGCATCTATTAGTGTG
AGCACTGAGATCTGAATGGC	CAATTGGATTGAGTTGGGGT	TCGGTGTTCATAATGCAT	AGACATCGCAATGAGGATCC
TGATGACATCTGTGCTTCT	CTCGTTATCCTCAGGCAATG	TCTCTCCCTCAATTATTTC	CAAAGAGATCCCATGTC
TCGTTGGGAAACGACCTC	AATCTGTTGTGACATATCGG	GTTGAGATACTATTGCCA	CTGAAAGCATTGCTTCGCTC
CTCTGATGTCAATATCCTGG	ACTTCATTGTTCAAGACA	AATTAGGCTTATCGACTCC	GGTACATCGTAAGGATGCA
CCACCATCAAAGGAGCAATC	TCAGTTTATCCACTTGTG	CGGTTCTTGTAGTCATA	GGATCGAAGGGATGCATAGT
AGTTCTCTCCAACATGTA	TTCAATGTCCAGTCAGGT	GTGTCACTCCAATTTCATG	CAATGTGCTGTGATGCAA
TGGTAGGAATCTGGTTTGC	TCTATAGTGTGGCCAAAGC	TAGTATATGAACTTCCCT	CCAAGTAAACCTTCAGTGA
CTCGATATAACGCTGCTTG	GTTAGACCCTGATCTGAA	TTTCCTCCAGTGAATGAA	TGAAGAAACCGCTAGCAGG
TCCCTTAGTCAATGCAAC	TATTAGTCTCCCTGATTCA	TTCATCAAGAGTGTAGTCG	TCACGTTAACACTGGTAT
GTTGTACATTGTTCCACAG	CTTACTCTCTTGTGTTG	TTTCCTGCTTATAGTGAAC	CCCAGATGTATAATTGTC
ACATCATCATTCTCACCTC	CCATTTCCTGGTCATGTG	CTCTGGACTGACGAAAGGA	TTTGTGCTGGGTGGTGAAC
ATTCTGGCAGCAATAATCA	TTCTCCATTGTTCTTGTG	TTCTCAATTGTCCTTCGC	TCCTGAGGCTTGAACATACA
TGATACTGTGCTCTCTAA	CATTGTGTTCAAGTGTCA	CATGGTTCTGTGATTCAA	TCCTGGTAGAGACTGTGACT
TCTCCAAAAGCGAAGCCAAC	CATTCCGGGTGTTGCAATTG	AAGTCGGTGGGAGACTTGG	GGGATTATACTGCTGGCT
CGCCAATTGTGTAATATGG	AGTACACGAACCCCTGATT	TCTAAAGTTTCAAGGCTGG	CCAGGGCTAGATCCAATG
AAGGATGTCCACCATCCTA	CTCCTCGCTAATGTTGAC	GTTGAATCCATCCACATAG	ATGCTTATTCTGCCAGACTG
TGCTCTCTGTGGGTTTG	ACTGCTCAAGTTCTCACAG	GAGAAAGCTTGCCTCAATG	CAGGTTGACTATTGTCAG
TGCTTGCATATATCCACAG	TTTTCTCATCCCTCAAC	GCGTTCACTCTTTGACAT	CTATTGATACCACTGAC
TGAAGTATTCTTAGACCCA	CACGACATTGCGAGTTAG	GTTGTCTCAGAAATGGCTC	AGGAGCATTAGGTTCCAT
AGTGAACCTCCAAAGCTGA	GTGAGTTAGTCATCATCTT	CATCAGTAGCTGAGAGGG	CACTGCGCATCTGAAGTAG
TTTCAATGTTGGAGGTTGC	GTAAAGGAGAGCTCTGTG	GGAACCTCGACCGTTGAGAG	GACCTCATTATCGAGCTTT
TATTAGTGGATCAGCCTTC	CTTGGTGTGTCAGTAA	AATTAAAGGCATCCATCAG	ACAGGTGTCATAGGTGCA
CGATTGACTGCTGCTCTC	ATCCGAGGATTCTGATTCTC	CATGACTCGGTCTCGATG	TTGGGTGATGCATTCAAGA
AACCATTGCCACTATGATCG	TATATGTTATCATTGCCAGA	TGATTGCATCATAGCGGT	CTTGTCAATTGGGATGCTTC
TTATCATGCAATCCTTGT	CATTCAAGGTTGGTTCTGT	CCAGCGAAAAATGCTTCA	GTGATCTGTTCACATTG
TTCAAATCACCTCGTACTGC	GCGACTACTCAGGACATTCT		CATATTGGGACATGCTCCG
			AACTTCAGGGTGTCTGCTT
			TACATTCCGCATTCTGTG
			AA TAGG CCTCTGGTTGCT
			CTATAAAGCCCTGCTATTG
			ATCTATCATTCTCCCTCATC
			GATGCCTGAAGCCATACAA
			TG C CT GT ACCTT CG GA ATT
			AGTGCTTTAAGGTCTGCTG
			TTGATCTGGTCAATGGCTGC
			AATCACTCTGTCATTTCC
			GGAACCTCTCATCGTCTT
			CTCGGAGAATTCCCTTCA
			TTCTCAAGGTTCTGAATCCT
			GAGTTCCGCATTATAAGACC
			TGTATGCTGATTCTCTAGGG
			GTTCAATTCTGAACTAGTC
			CCTCTGGTCTTTCAAAACA
			CATGCTTCAGCATTTCCC
			CTATGCAAGCATTGTCACAC
A/Mallard NP mRNA	A/Mallard NA mRNA	A/Mallard M mRNA	A/Mallard NS mRNA
TTCTCCAACAGATGCTCTG	GGGGTATTGCACTCATTG	CTGACGGGACGATAGAGAGA	AGTGCCTTTAAGGTCTGCTG
AACCTTCCAATCCACCAAC	ATGGCACCACTTGATTGTC	CCCTGCAAAGACATCTCAA	TTGATCTGGTCAATGGCTGC
TTCACTGACATCTGTATGT	TCTGACATTGCGTTTGC	TGAGAGCCTCGAGATCGGT	AATCACTCTGTCATTTCC
CTTCATAGTCGCTGAGTTG	GCTGCATGACACATAAGTT	GGTCTTGCTTGTGCAATT	GGAACCTCTCATCGTCTT
TTATGCTGTCGATCAGC	TTTGTATCAGCGTGGTC	CTTAGTCAGAGGTGACAGGA	CTCGGAGAATTCCCTTCA
TGGGATGTTCTCCAGATAT	CTGGACCATGCTATGCAC	AGCGTGAACACAACTCTAA	TTCTCAAGGTTCTGAATCCT
TAGATTGGACCTCCAGTTT	TAGCAGTCGCTTCTATCA	ATGTTGTTGGGTCTCCATT	GAGTTCCGCATTATAAGACC
ATCAGATGAGTGGAGACCA	TCTGATTCTGAGTTCTGAG	CTTCCGTACAGTTGACTG	TGTATGCTGATTCTCTAGGG
ATCATTCAAGGTTGGAATGCC	AGTCCATTGATGCAAACGC	CATACAACGGCAAGTGCAC	GTTCAATTCTGAACTAGTC
CTCTCGTCTCTGGTATGTG	CTTCCCCTCTCTAAATGAA	CCATCCTGTTGATATGAGA	CCTCTGGTCTTTCAAAACA
CATTCTGGGCCATACCAAG	CTGACAATGGGCTGACATG	AAAAGCCACTCTGTTGTC	CATGCTTCAGCATTTCCC
TTGATCCTTGACAGAGAG	CAATGCTATAGTGTGCA	ATGTTGTTGGGTCTCCATT	CTATGCAAGCATTGTCACAC
AATTAGTCCATCACCATCG	GATAGTTCTCCCATCCAAA	CTTCCTGTACAGTTGACTG	
AAGTCCGTACACACAAGCAG	CATAACCTGAGCGTGAATCC	CATACAACGGCAAGTGCAC	
AAGTCATATCCACTGGCCAC	CCTCTTATCAACTCCACATA	CCATCCTGTTGATATGAGA	
CAGAGAGTATCCTCTCTC	CATACTCTAGTCTCTGTGG	AAAAGCCACTCTGTTGTC	
GACGAAAAGGATCTTCCG	TAGGATGGCAACCTGCA	CTGTGAATCAGCAACTGCT	
GAAGACCTGGCTTTGAA	TCCTTCTATTATGATTGGT	TCTAATTAGTGGGTTGGT	
GGATTCTCATTTGGCTAA	TTCAAATACACTATCTCGT	CTGACTAGCAACCTCCATGG	
TGATACTCTCAGGTCTTCA	ACTTCTTTCTATGGTAGT	AATTGTTCTCATCGCCG	
GATAGTTGCTCTTGGGAC	TTCCGTATTCTACCA	CACTGGAGCTAGGGTAGTT	
GCTTCTCAATTGAGAGTAC	TCCATCGGTCTTACTACTG	AGAAGATCATTTCA	
TGGTTCTTATAGCCCAATAT	TATTTAGTATGCCCTTC		
CCCTTCAAGGGAAGATT	TCAACAAGCATCCATCATA		
TGAAATGCCCATATGG	TATTTGAGACCATGAA		
CACTTCATCATCCTTATG	CCTGAGCACACATAACTAGA		
AGGACTTATGGGCCACTGAT	CCACTAATGACCCCTGAAAGT		
TCAGTAGCATTGGCGTC	GACGATACTATTGAGGTCC		
TTTCGACTTGTATGCCATC	GGAACATTCTATATGCT		
ATTTCAGCATTCCCAGGATT	ACGTCGGATATCGAGGATA		

279 **Supplementary Table 1: FISH probe sets.** DNA oligonucleotide sequences for  
280 detection of vRNA and mRNA of A/Panama and A/Mallard.

281

282 **Supplementary Table 2**283  
284 MSC Rank 2

Experiment		Predicted	
Segments	n	Segments	n
<b>23</b>	23	<b>27</b>	38
<b>35</b>	17	<b>37</b>	16
<b>37</b>	17	<b>23</b>	12
<b>27</b>	15	<b>35</b>	10

285  
286 MSC Rank 3

Experiment		Predicted	
Segments	n	Segments	n
<b>237</b>	14	<b>237</b>	31
<b>127</b>	7	<b>127</b>	12
<b>257</b>	5	267	7
234	5	<b>257</b>	4

287  
288 MSC Rank 4

Experiment		Predicted	
Segments	n	Segments	n
<b>1237</b>	10	2378	16
1257	5	<b>2367</b>	8
1267	5	<b>1237</b>	7
<b>2367</b>	5	2357	5

289  
290 MSC Rank 5

Experiment		Predicted	
Segments	n	Segments	n
<b>12367</b>	9	<b>12367</b>	10
23467	8	24567	7
23678	7	<b>12378</b>	5
<b>12378</b>	7	12468	5

291  
292 MSC Rank 6

Experiment		Predicted	
Segments	n	Segments	n
<b>123678</b>	19	<b>123467</b>	21
<b>123467</b>	13	<b>123678</b>	16
123457	10	123578	10
<b>123567</b>	10	<b>123567</b>	9

293  
294 MSC Rank 7

Experiment		Predicted	
Segments	n	Segments	n
<b>1234567</b>	41	<b>1234567</b>	57
<b>1235678</b>	41	<b>1235678</b>	31
<b>1245678</b>	26	<b>1245678</b>	25
<b>1234678</b>	17	<b>1234678</b>	19

295  
296 MSC Rank 8

Experiment		Predicted	
Segments	n	Segments	n
<b>12345678</b>	355	<b>12345678</b>	319

299 **Supplementary Table 2: Comparison between experimental and predicted**  
300 **abundances n of the four most abundant MSCs in each rank for Cell 18.** The four  
301 most abundant experimental and predicted MSCs in each rank are listed. MSCs that  
302 occur at a given rank in both the experimental and predicted MSCs are bold. Especially  
303 for the higher ranks 5 to 7 there is a good agreement between experiment and model.